

TGTGCTCATTAATTTTAATA TGTG ||| |||| |||| |||| ||| |||| ||
 TGGTATGCACTTGTTGTTTT TTCT TCAAT TTTAC TATTTTTTGT TCA GTATG GTA
 T
 TTATCATTTTTAACTTTTTC TTT T - TGT----- C - TAAT
 TT

GAM21 AATAACATTTGTTTTCATAT 7 TGAGAATTCT 2732 C TGTT TAT- - -- T TGGAT
 TTTTCATTTCTTCTTGATT TGAATAATGA AATAA ATT TTCA TTTTCATT TCT TCTTG ATTGA
 A
 GATGGATATAATTTCAATTC TATT |||| || ||| |||| || |||| ||||
 AGGATTAGATGATGAGAATT TTATT TAG AAGT AAGAGTAG AGA AGGAC TAACT /
 CTTGAATAATGATATTATT A TAAT TCTT T TT T TTAAT

GAM22 AATATGCTAGAGTTTCACTT 8 TTGGATGAAA 2733 GA TTCA C CT ---- AAATAAA
 AT- TG
 GCATTTACTTTAGCTTTTCA GAACAGCTAA GT CTTG ATTTA TTAGCT TTTTCATC
 TAACA AAGG A
 TCAAATAAATAACAATAAGG TTTA || |||| |||| |||| |||| |||| ||||
 TGACACCTTTAATGTTGGAT TA GAAC TAGAT AATCGA AAAGTAG GTTGT
 TTCC /
 GAAAGAACAGCTAATTTAGA TC ---- - TT CAAG ----- AAT AC
 TCAAGATCTTAGTACATT

GAM23 AATGGTAACAGTTGAAGGAC 9 TGAAGGACTA 2734 G C T- CTAA -- CG TT- CAAG
 TT
 TAAGAGTAGCTAAAGATGTA AGAGTAGCTA TTGAAGGA TAAGAG AG AGA TG TAG TA
 TATTTT TGATT A
 GCGTATTTATTTTCAAGTGA AAGA |||| |||| || || |||| || |||| ||||
 TTTTAAATAATCAAAGAGA AACTTTCT ATTTTT TC TCT ACGTC GT ATAGAG
 ACTAA A
 TATTTTGTCTGCAAATCTA - T TC CCTA AA TT TTT AAA- TA
 TCCCTCTTTTTTATTCTTTC
 AAATGCCATT

GAM24 ACAGTTTCCTAAATTTTAA 10 TTCTATGCTT 2735 TCCT--- TAA A- TCAA C
 ATTACTTAAAGTATTCAAAA GAAAGTAATA ACAGTT AAATTTT ATTACTT AAGTAT AATA
 G
 TACGATTATTCTATGCTTGA ATAG |||| |||| |||| |||| ||||
 AAGTAATAATAGAATTTTGT TGTCGA TTAAAGA TAATGAA TTCGTA TTAT A
 TTGTAGCTGT TGTTGT TAA AG TC-- T

GAM25 ACATTCGTTGTATAAAGAAT 11 TATAAAGAAT 2736 T GTA TCAATTGC AATTT T
 CAATTGCATTTGAAAAATTT CAATTGCATT ACAT CGTT TAAAGAA ATTTGAAA GC A
 GCTAACGTTGGTTTTAAATA TGAA ||| ||| |||| |||| ||
 ACTTTTTCTTTAGTAACGA TGTA GCAA ATTTCTT TAAATTTT TG A
 TGT - TG- TTTTCAA- GGT-- C

GAM26 ACCATCCATATGAACCTCTT 12 TATTGGAATA 2737 AT GAACC T GA G T

AGAGATGTTCCAAGTATATT GGTTTTGGAA ACC CCATAT TCT AGA TGTTCCAA TATA T
 ATATATTGGAATAGGTTTTG TTAA ||| ||||| ||| ||| ||||| |||||
 GAATTAAATATGGGGT TGG GGTATA AGG TTT ATAAGGTT ATAT /
 -- AATTA T GG - A

GAM27 ACCGATGAAATAATTA AAAAC 13 TGACACAAAA 2738 GAAA AAAAC GAACAA AC
 TTGTGGAACAAATGGACTTC CGAAATTAAA ACCGAT TAATT TTGTG ATGG T
 CTATGACACAAAACGAAATT GATT ||||| ||||| ||||| |||||
 AAAGATTGGT TGGTTA ATTAA AACAC TATC /
 GAA- AGCAA AG---- CT

GAM28 AGAAGAATTTTTTCTCTCC 14 TAACCAGATA 2739 T CTCCAA - CC
 AATGTAATCTCCAAAAGCAT AAAATTTTTC AGAAGAATTTTT TCT TGTAAT CT A
 TATAACCAGATAAAAAATTTT T ||||| ||||| ||||| |||||
 TCT TCTTTTTAAAAA AGA ATATTA GA /
 T CCA--- C AA

GAM29 AGATAACAATGGTTTGGGTG 15 TATTACCCAT 2740 AACAA T A-- AA
 AAATTTTTAACTACGAAAGT ACTAAAAGAT AGAT TGGT TGGGTGA ATTTTT C
 CTATTACCCATACTAAAAGA CT ||||| ||||| ||||| |||||
 TCT TCTA ATCA ACCCATT TGAAAG T
 GAAA- T ATC CA

GAM30 AGCTTACCAATATTAGTATT 16 TTGGTGCTGC 2741 TT- A TT GCA CC
 GTACCAACTGCAAGCCCTGC TGGTACTGGT AGC ACCA TATTAGTA GTACCAACT AGC T
 TGCTAAAGTTGGTGCTGCTG CCTG ||| ||||| ||||| ||||| |||||
 GTA CTGGTCCTGCT TCG TGGT ATGGTCGT CGTGGTTGA TCG G
 TCC C -- AA- TC

GAM31 ATAATATGAATTTGAATAAT 17 TCGGGTCTTG 2742 T TG AATA- ATTTACTTA G T A----
 C AATGT
 ATGAATTTACTTAAAGAAGT TTAAACATCA T AAT TGA AA AAG ATCCGA GAAAAT
 GTTT T
 ATCCGAAGAAAATCGTTTAA GTTA | ||| ||| || ||| ||||| ||||| |||||
 TGTTACTTAAAGACTATTTT A TTG ATT TT TTC TGGGCT CTTTTA CAGA A
 CAAACATCGGGTCTTGTTAA - GT CAAAG GACTACAAA G - ACAA T AATTC
 ACATCAGTTAGAAACGTTTG
 ATCATTTTAT

GAM32 ATAGCGGTGTTGTAATTTGT 18 TATTACAATC 2743 - TTGTAAT AGCGA
 AATGTAAGCGAAACACCTAT TTTACCGGTT ATAGC GGTG TTGTAATGTA A
 ATTACAATCTTTACCGGTTA AT ||||| ||||| ||||| |||||
 T TATTG CCAT AACATTATAT /
 G TTCT--- CCACA

GAM33 ATGAAGGAATGACAGGAAAA 19 TTGGATGGGA 2744 A AC AAAC AA A
 ACTTCTAAACAAAAATCTTT TATTCCTAAC ATG AGGAATG AGGAA TTCTA CAAAA T
 TGGATGGGATATTCCTAACA ATTT ||| ||||| |||| |||| ||||
 TTTCTACAT TAC TCTTTAC TCCTT AGGGT GTTTT /
 A AA AT-- AG C

GAM34 ATGATGTTGGCAATTTTAAA 20 TAGCATGGAT 2745 G GGCA TA A TAC CTA- T
 TG
 ACCATTACGGATAATCTAGA TCGAGATAAT ATATGTT ATTT AA CCAT GGATAAT GAAG
 AACAGA C
 AGTAACAGATGCCTTTTGTG AAC || ||||| |||| || ||||| ||||| ||||| |||||
 CCTTTAATTGTTGTCTAGCA TA TACAA TAGA TT GGTA TCTGTTG TTTC TTGTTT /
 TGGATTTCGAGATAATAAACA G ATAA GC A CGA TTAA C TC
 TGAT

GAM35 ATTCTTTCTCCAATAACTTC 21 TTGAATGTGT 2746 --- A TT CC C--- TCTTCT T-
 TCT
 GTCCTCAACCTCTTCATCTC TGATGGTATA TCT CCA TAAC CGT TCAA CTCTTCATC
 AATTCT CA C
 TTCTAATTTCTTCATCTCTT GAAA ||| || |||| || |||| ||||| ||||| ||
 CTGTTGGAAATTTCCGGTGG AGA GGT GTTG GTA AGTT GGGGGGTGG
 TTAAAGG GT /
 GGGGCATTTTGAATGTGTTG TAT A T- -- TTAC CCT--- TT CTT
 ATGGTATAGAAAGAAT

GAM36 ATTGCAAGAAACATGTGTTA 22 TGGAATGGGA 2747 A T C TGA ATGA CCTG
 TTCTACTTTTGTAGACAATG TGATCATGTT ATTGCAAG AACATG GTTATTCTA TTT T GACA
 TGATATA A
 ATGATATACCTGATGAAATG GCTT ||||| ||||| ||||| ||| | ||||| |||||
 TGTCATGTTATGGAATGGGA TGATGTTT TTGTAC TAGTAGGGT AAG A TTGT
 ACTGTGT T
 TGATCATGTTGCTTGTAGT G - - GT- ---- AAAG

GAM37 ATTTTGTATTACTTGTTCTGA 23 TAAGAGATTT 2748 C TCG-- --- ATATC - ---- A
 TT
 AAGTGTCTTTTATAATATCA AACTTTAATT TTGT AAAGT GTCTTTTATA AGTTT CT
 TCTTTA TTTG T
 GTTCTTCTTTAATTTGTT TGCA ||| |||| ||||| ||||| || ||||| |||||
 TGCAAGTGGAGATGTAGGTA AACG TTTCA TAGAGAATGT TCAAA GG AGAGGT
 GAAC /
 AACTTTCTGTAAGAGATTTA - TTAA ATT CTT-- T ATGT - GT
 ACTTTAATTTGCAAATTAGC
 AAGAT

GAM38 CAAATTCTACATTTGTATCA 24 TCAGTTATGG 2749 TC CATTT TT GGGA C-- C- GC
 A
 GTTATGGGAGATCCGTCAAT GAGATCCGTC T TA GTATCAG AT GATC GTCAATA
 AGGTTTC TTTTAAA C
 ACAGGTTTCGCTTTTAAAC AATA | || ||||| || ||||| ||||| |||||

ATTTTGAAATAGAAATTTCT
 AAAGTTT A
 TGTTGATTATGATCCAAAAT
 TTTTGATATTTTATATGGTT
 TG
 GAM39 CAATGTTGACAATTAAATTT 25 TCAAATGGGA 2750 ATG G AA A A AGA GGATT
 AATATTAACATAGATTTAGA TTGTGAAAGT CA TT ACAATT ATTTATATTA CAT TTTAGAAT
 A
 ATGGATTAGACATGGTTTTG G || |||||| ||| ||||| ||| ||||||
 AAAAAATGTAATATCAAATGG GT AA TGTTAG TAAA TATAAT GTA AAGTTTTG G
 GATTGTGAAAGTG GA- G GG C - AA- GTACA

 GAM40 CATGGCTTCCATTGGATTTG 26 TGAATGGCT 2751 G- T TTGG G -- AA--
 CTATTAAT
 GCACCGAAGTTTGACGTTCC TGCGGGATAT CAT GC TCCA ATTT GCA CCG
 GTTTGACGTTCC A
 TATTAATAGCTCCCTTGAAT TTGG ||| |||| ||||| ||| ||||||||
 GTCGAATGGAATGGCTTGCG GTA CG AGGT TAGG CGT GGT TAAGCTGTAAG /
 GGATATTTGGATGCAGATG GA T TTA- G TC AAGG TTCCCTCG

 GAM41 CGGTGATGGACTTCTTCTCG 27 TGATGGACTT 2752 T T C T - T T C T TC
 GTGATGGACTTCTTCTCGGT CTTCTCGGTG CGG GA GGA TTC TC TCGG GA GGA TTC TC G
 GATGGACTTCTTCTCGGTGA ATGG ||| |||| ||||| ||||| ||| ||| |||
 TGGACTTCTTCTCG GCT CT CTT AGG AG GGCT CT CTT AGG AG /
 - T C T T - T C T TG

 GAM42 CTTGGTTGATATTGTTTGTA 28 TATTGTTTGT 2753 G T- TG GTAAT TC A
 ATGGGGTTCTGAAAACAAGA AATGGGGTTC CTT GTTGA AT TTT GGGGT TG A
 TTCTGAATGGTTTTTAACGA TGAA ||| |||| || ||| ||||| ||
 AG GAA CAATT TG AAG TCTTA AC A
 G TT GT ----- GA A

 GAM43 GAAACTATGATGTGTGGATG 29 TATTACCACA 2754 A A G GGAA AAA ---- C A
 GAATGGTAAAAAAGTTAGAG GATTGACGCA GA ACTATG TGTGT GAT TGGTAA ACT
 TAGAG AG A
 CAGAAATCTTCTTTGGACCA CATG ||| |||| ||||| ||| ||||| ||| ||||| ||
 GTATATTACCACAGATTGAC CT TGGTAC ACGCA TTA ACCATT TGA GTTTC TC A
 GCACATGGTATC A - G GAC- ATA CCAG T T

 GAM44 GATGTTGAAATTTTAAATGT 30 TTAAATGTT 2755 T AAA- GTTATTAT AA GA
 TATTATTGGAAGGGGACAAT ATTATTGGAA GA GTTG TTTTAAAT TGG GGG C
 CTGACCACATCGCTAATTTA GGGG || |||| |||||| ||| |||
 AAAATAACAACCTC CT CAAC AAAATTTA ACC TCT /
 - AATA ATCGCTAC AG AA

GAM45 GCAAGCATT TTTGTACACATG 31 TGTACACATG 2756 C T TGATGA G A
 ATGAAGATTGTTTAGAAGGA ATGAAGATTG GCAAG AT TTGTACACA A ATTGTTT G
 CAGTGTTGTGTACAACGTAT TTTA ||||| || ||||| | |||||
 TTGT TGT TT TG AACATGTGT T TGACAGG A
 A C ----- G A

GAM46 GCTATCAATCTACAAGATCT 32 TACAAGATCT 2757 AT C C A GATA AC TGTA
 AAGTAGATATCCAACAGTGT AAGTAGATAT GCT CAAT TACAAGAT TA GTA TCCA AG T
 ATGATTCTATGGAAATACAT CCAA ||| ||| ||||| ||| ||| ||
 GCATCTTGTATGTTGGGAGT TGA GTTG ATGTTCTA GT CAT AGGT TC /
 GG T C A AA-- A- TTAG

GAM47 GCTATTTTTGTATTTAATTG 33 TAATACAAAA 2758 TTT- AAT - - GA
 ATTAAGTTGACTATGAGTAT TACCTCCAAT GCTATT GTATTT TG ATTA ACTT C
 AATACAAAATACCTCCAATA AGC ||||| ||||| || ||| |||||
 GC CGATAA CATAAA AC TAAT TGAG T
 CTC --- A A TA

GAM48 GGAGGAGATTTTGATTTAGG 34 TTAGGTATTT 2759 T--- GG TT ACA TC
 TATTTTAACATTAGGATGGT TAACATTAGG GGAGGAGAT TTGATTTA TA TTA
 TTAGGATGGTTA T
 TATCTTTTAACCATTTTAGA ATGG ||||| ||||| || ||| |||||
 CATAATTTGTTTAAATCAAC CCTCCTTTA AACTAAAT GT AAT GATTTTACCAAT /
 AACATTTCTCC CAAC TT TT ACA TT

GAM49 GGTTCAATTTGAATTGTTGT 35 TATCGCACCC 2760 TCATT A T- TA TTTT A TATC
 AATAATATTTTGAAGTTGAT AATATAATTT GGT TTG ATTG TG ATAATA TG GT G T
 CTATACCACCATATTTATTA TCAC ||| ||| ||| || ||||| || |||
 TCGCACCCAATATAATTTTC CCA AAT TAAC AC TATTAT AC C A C A
 ACC CTTTT A CC GC TTAT - - CAT

GAM50 GTATCAAAATGTACCATTCC 36 TAACGGAAAG 2761 C A -- A ----- TAATAA GA
 GTAATAAGATTTTATAATAA TGGATATTT GTAT AAAATGT CCAT TCCGT ATAAG ATTTCA
 ATA C
 ATAGACCATATACATATTGG TGTG ||| ||||| ||| ||||| ||||| ||||| |||
 AATAGTAGATTTATAACGGA CGTG TTTTATA GGTG AGGCA TATTT TAAGGT TAT /
 AAGTGGATATTTTGTGC T - AA A AGATGA TATACA AC

GAM51 GTATGAAATAAACAAGAAGG 37 TGCCTTCTAA 2762 A TAAACA-- CGTTT A
 TCGTTTTAAAGCATCGGCTT ATCTATTTTC GT TGAAA AGAAGGT TAAAGC T
 TATGCCTTCTAAATCTATTT AAGC || ||||| ||||| |||||
 TCAAGC CG ACTTT TCTTCCG ATTTCCG C
 A TATCTAAA T---- G

GAM52 GTTCTACGATGTTTCAGTAGA 38 TACGATGTTTC 2763 - -- GT- ATT GT
TATTTTTGGTGGTATAGATG AGTAGATATT GT TCTAC GATGTTCA AGAT TTTG G
GTCTCAATGAACGTTTAGTA TTTG || |||| |||| |||| ||||
GACAC CA AGATG TTGCAAGT TCTG AGAT G
C AT AAC GT- AT

GAM53 GTTGTTAGGTCATGTCAGAG 39 TCTGACACCA 2764 -- A-- ----- - AA
GCCCTGAAATTGATCAGGAG GACCTGAGAC GTTGTT AGGTC TGTCAGAG GC CCTGA
T
CGACCTGAAAACCTCTGACAC AGC |||| |||| |||| || ||||
CAGACCTGAGACAGC CGACAG TCCAG ACAGTCTC CG GGACT T
AG ACC AAAAGTCCAG A AG

GAM54 GTTTAGGAATTTGTTTATGT 40 TTAGGAATTT 2765 TGT TTA GG- T
TATGGGGATATGTGTGCATG GTTTATGTTA GTTTAGGAATT TTATG TGG ATATG G
TATACCAGTTCATGATTAAT TGGG |||| |||| |||| || ||||
TTTTAAAC CAAATTTTAA AGTAC ACC TGTAC T
TT- TTG ATA G

GAM55 GTTTGGAACGGAATGAGTT 41 AGGAACAGAA 2766 --- GGA- G C GA GT
TTCTTCTGTGACTGTTGTGA AAAGAATTAT GTTTGG AAC AATGA TTTT TTCTGT CTGTT G
AAACAGGAACAGAAAAAGAA TGGA |||| || |||| |||| ||||
TTATTGGAAGTTGAACTAAG CGAATC TTG TTATT AGAA AAGACA GACAA /
C AAG AAGG A A AG AA

GAM56 TAAACCAATATCAAATACCG 42 CGTAATGAAT 2767 AAT ATACCGC CA C ATATT
CTATACCATTATTACCTATT GTATACCTTG TAAACC ATCAA TATAC TTATTAC TATT T
ATATTTTTTCCAATACGTAA ATTA |||| |||| |||| |||| ||||
TGAATGTATACCTTGATTAG ATTTGG TAGTT ATATG AGTAATG ATAA /
GTTTA AT- CC----- TA C CCTTT

GAM57 TAAAGTAGATGAAAAAGAAA 43 TGAAAAAGAA 2768 A A GAAAGATA T AAG---
AGT
GATATAGAGGTGCAGAAGTT AGATATAGAG TAAAGT GATG AAAA TAGAGG GCAG
TTTTTGATCC G
TTTGATCCAGTGCCAGGATT GTGC |||| |||| |||| |||| ||||
AAAAAGAAATGTTGTTTCCTT ATTTCA CTAC TTTT ATTTCC TGTT AAAAATTAGG /
TAGATTTTGCATCACTTTA - G AG----- T GTAAAG ACC

GAM58 TATCAGGAACTTCTCGTGTT 44 TCAGGAACTT 2769 ACTT--- C C- - TT CAA
GCGCATAATTCATCAAACAT CTCGTGTTGC TATCAGGA CT GTGTTG GCAT AA CAT A
ATGTCTTAATGTTACAACAT GCAT |||| || |||| |||| ||||

TAGTATCCCCTTCTGATA

ATAGTCTT GA TACAAC TGTA TT GTA /
CCCCTAT T AT A CT TAC

GAM59 TCACCCGGATCTGTAACTGG 45 TACAGTTACG 2770 A- A--- GAGG G G A
AGGACCAGGTGGTAATATTG GGAGGATCGG TC CCCGG TCTGTAAC TG ACCAG T GTAT
CGGCTGGTACAGTTACGGGA GAGG || |||| |||||| ||||| |||
GGATCGGGAGGA AG GGGCT GGGCATTGAC TGGTC G CGT A
GA AGGA A--- -G T

GAM60 TCCATTTTATGTGAAGTTTC 46 TATGTGAAGT 2771 ---- - AGTT TTGTT T AAA
CCATTGTTCAATTGAAAAAG TTCCATTGT TCCA TTTTATG TGA TCCCA CAAT GAA G
AAATTCATTGTTTTTGGGAT TCAA ||| ||||| ||| |||||
CGTCATAAAATTACTGGG GGGT AAAATAC GCT AGGGT GTTA CTT /
CATT T ---- TTTT- - AAA

GAM61 TCGATTTTAGATTCTGAGAC 47 TTTGTTGAAA 2772 T A AAACGAG CAA AA-- A
GAACCA AACA
TAAACGAGCAATACAAGATG CAAAGTCCGA TTC G GACT CAATA GATGC TAGATTC TTT
TAC A
CAATAGATTCATTTGAACCA ATAT ||| |||| |||| ||||| |||
TACAACAATACAGTAAAAAG AAG C CTGA GTTGT TTACG GTTTAAG AGA ATG
/
AAGAGAATTTGAAGAGCATT -- AACAAA- --- AGAA - AGAAAA ACAT
TGTTGAAACAAAGTCCGAAT
ATAAAATTAG

GAM62 TGATGGAAGAGCCGTTTATA 48 TGGAAGAGCC 2773 - GCCGT TTCTGA G TTAC
ATTATGTC GC
TTTCTGAAGGTGGTCTTTAC GTTTATATTT AAGA TTATAT AGGT GTCT AGTCTT
TAGCGAA T
AGTCTTATTATGTCTAGCGA CTGA ||| |||| ||| |||| |||||
AGCTCCGTTTGCTAAGGACT TTTT AATGTA TTCA CAGA TCAGGA ATCGTTT
C
TTAGACGACTTGTATGTAAT A ATTGT TG---- G TT-- ----- GC
GTTATTTTACCGTCA

GAM63 TGGAGGTGCTATCGGTGGAG 49 TGAGGTCCTA 2774 ----- ATC A ATA T
GCATAAGAGTTTTTGGATTT CCAAAGCATT TGGAG GTGCT GGTGG GGC AGAGTT T
TGAGGTCCTACCAAAGCATT ATTT |||| |||| ||||| |||||
ATTTTTTCCA ACCTT TACGA CCATC CTG TTTTAG T
TTTTAT AA- - GAG G

GAM64 TGGTGTTGATGGATCATCTT 50 AGCCCATTTGT 2775 CAT ATG AC TT TATATA T- ----
T AT
ATGTCTGGAACGGTTCTGTA CAGTTCCTCC CTT TCTGGA GG CTG ATAATG TTTTGT
AAAA CTT T
TATAATAATGTTTTTGTAAG AGGA ||| ||||| ||| ||||| ||||| |||||

ATCTTATTCAAAGTTTTTCAT GAA GGACCT CC GAC TGTTAC GAAACA TTTT
 GAA /
 CACAAAGCCCATTTGTCAGTT AT- --- -- TT ----- CC CTAC - AC
 CCTCCAGGAAGTAACATTTT
 AATACCA
 GAM65 TGGTTTGAGGATGAGAAAGT 51 TTAACCACT 2776 TGA AGAAAGT CTTTT ----
 GGAC- TTC
 GTGGTTTCTTTTATAGCTTT ACGTCCGTGA TT GGATG GTGGTTT ATAGCT TTTTCT
 TTAT A
 TTCTGGACTTATTTTCATCCA CCA || ||||| ||||| ||||| ||||| ||||
 TAACACAAAGAAGAGTTGCA AG CCTGC CACCAAA TATCGA AGAAGA AATA
 /
 GCTATTAAACCACTACGTCC TG- AT----- T---- CGTTG AACAC CCT
 GTGACCA

 GAM66 TGTTGGATATAATTCAATTT 52 AGGAATTGAA 2777 TAT- CTTT--- T
 CTTCTTTACTTGTTAGTTCT TTTCGTTTTA TGTTGGA AATTCAATTTCTT ACT G
 TTATAAGGAATTGAATTTG ACA ||||| ||||| ||||| |||||
 TTTTAACA ACAATTT TTAAGTTAAGGAA TGA T
 TGCT TATTTCT T

 GAM67 TTGATTGTGAAATAACACCA 53 TGTGAAATAA 2778 T TA- A TTAC AT CC
 TTACTTAAATTTGCCATATC CACCATTACT TTGA TGTGAAA AC CCA TTAA TTG A
 AACCTTAATTTCTGGGTAAT TAAA ||||| ||||| ||||| |||||
 TTTCACATTCAA AACT ACACTTT TG GGT AATT AAC T
 T TAA - CTTT CC TA

 GAM68 TTGTGTTTTAGATAGTTGAT 54 TATTTTAATG 2779 ATA- T- T CTA CATA --
 TCA
 ATTTTAATGCATTTTCTAAA CATTTTCTAA TTAG GTTGATA TTAA GCATTTT AATTAAG
 TCAACT TTA A
 TTAAGCATATCAACTTTATC ATTA ||||| ||||| ||||| ||||| ||||| |||||
 AATATTTAATTGGTTGACTT GATC CAACTAT AAATT TGTAAAA TTAGTTC AGTTGG
 AAT T
 GATTCATAAAATGTTTAAAT ATTA TT - TAC ---- TT TTA
 TTATCAACATTACTAGAACCA
 AA
 GAM69 TTGTTGATCTTGAACCTTCTA 55 TAGGTTCAAC 2780 TT CTA A TT
 GAACTTGAACCTTGCGCGTAT AGGTTTTTGA TTGTTGATC GAACTT GAACTTG AC G
 AGGTTCAACAGGTTTTTTGAT TTAA ||||| ||||| ||||| |||||
 TAACAA AACAATTAG TTTGGA CTTGGAT TG C
 TT CAA A CG

 GAM70 TTTGTAAACGGTCTTTTTTAC 56 TGTAAACGGT 2781 --- C - AA--- GAG
 TAAACATGGAGGTCAACATG CTTTTTACTA TTTGTAA ACGGT TT TTTACT ACATG G
 TAGATGGGTGGACAAAACCG AACA ||||| ||||| ||||| |||||
 TTTTTTGCAAA AAACGTT TGCCA AA AGGTGG TGTAC T

TTT A C GTAGA AAC

GAM71 TTTTAATTTTAATTGTCCTG 57 GTGATGATGA 2782 A AATTG C TG AATTTAAT A TT
ATATT
TTTGTTATTAAATTTAATTC ACATGAAACA TA TTTT TC TGTT TTATTA TCTTC GAAGT
CTTCT A
TTCAGAAGTTTCTTCTATAT GAAA || ||| || ||| |||| |||| |||| ||||
TAACCTCAGAAGTTACTTCC AT AAAG AG ACAA AGTAGT GGAAG CTTCA GAAGA
/
GAAGGTGATGATGAACATGA C ACAA- T GT ----- C TT CTTCA
AACAGAACTAGAG

GAM72 TTTTCATGTAACATCCCCAT 58 TGGATTGAAA 2783 AAC CCATG T TGAA
GTTTAATCCTTCTGAAATAA CAATGGATTA TTTTCATGT ATCC TTTAATCC TC A
TTGATGGATTGAAACAATGG ATAT ||||| ||| ||||| ||
ATTAATATGAGAG GAGAGTATA TAGG AAGTTAGG AG T
AT- TAACA T TTAA

GAM73 TTTTCGATTCATACTTCTTT 59 TACAATAAAT 2784 ATAC----- T - TTACATC
AATAA
ATTTATTGTATTTTAATGTT AAGAATCTAA TCGATTC TTCTT ATTTATTGTATTT TAATG
AAGGT A
ACATCAAGGTAATAAAATTG AATG ||||| |||| ||||| |||| ||||
AACCTTATCTTCATTATAAA AGTTAAG AAGAA TAAATAACATAAA ATTAC TTCCA
/
TACAATAAATAAGAATCTAA GTAAAATCT - T TTCTA-- AGTTA
AATGGAATTGAAAA

GAM74 TTTGAGAATTTCCAGAAAGA 60 TGAAATGACA 2785 A TTCCAGA ATTA ATTTT ATG
C
TTAGCCATTTTTGTTAATGT GGTGAGCTTG TTTG GAAT AAG GCC TGTTA TTATTG A
TATTGCACCCGATGAAATGA CAGT ||||| ||| ||| |||| |||||
CAGGTGAGCTTGCAGTTGTT AGAC CTTG TTC TGG ACAGT AGTAGC C
CCAGA - TTGACG- GAG- ----- AA- C

GAM75 CTGACTTGCGACTCTGAATA 61 TATCAAAGAA 2786 -- CA C - TT TG
TTTGGGTGAAACCCATTTAT CCTTGAGTCA CTGACTT GG CT TGA ATA TGGG A
ATCAAAGAACCTTGAGTCAG G ||||| || ||||| ||||
GACTGAG CC GA ACT TAT ACCC /
TT AA A A TT AA

GAM76 CCTGCTGACGTATTGCGCAA 62 TGACGTATTG 2787 GA - C TG- C
CTGTGCAACTAATTGTGATT CGCAACTGTG CCTGCT CGT ATTGCG AAC TGCAA T
GTTTTGTAATAATGGAGCAG CAAC ||||| || ||||| ||| ||||
G GACGA GTA TAATGT TTG GTGTT A
G- A T TTA A

GAM77 GGGAAGTACTCTAACGACGG 63 TATTACTTAT 2788 C- A CG AG G AGAGA TC- CTTG
AA A A
AAGCGGAGCAAGAGAGCTCA GCGGAGGTGT TCT ACGA GA CG AGCA GC AG AGAGTT
TGAGGA GTT C
GCTTGAGAGTTAATGAGGAA TGCG ||| ||| || ||| || || ||| ||| |||
GTTACTGAACCTCCTTACAA AGA TGCT TT GC TTGT CG TC TCTTAA ATTCT
CAA T
TTCTATTACTTATGCGGAGG TA C AT CT G GGAGG TAT ATTA C- C G
TGTTGCGTCTTTATCGTCAG
AATGGGTTTTTC

GAM78 ACAATATCATAATCCATTGA 64 TATCATAATC 2789 A C TA- GA----- A
TAAAGTACCGATAATAGATA CATTGATAAA ACAATATC TAATC ATTGATAAAG CC
TAATAG T
ACTGTTAGCATAATGCGGAC GTAC ||||| ||| ||||| || |||
TTTTTATCGATTGATTAGAT TGTTATAG ATTAG TAGCTATTTT GG ATTGTC A
ATTGT - T TCA CGTAATACG A

GAM79 ACTATGAATTTAGACGATTT 65 TGAGTACAAT 2790 TTAGA TTC- T A CGTTG A---
AA-- TAA
CTTTGTAATTATACTCCGTT TCAGAACCTA CGAT TTTG AATT TACTC GAACGA TCTC
TAAA A
GGAACGAATCTCAATAAATA TCGA ||| ||| ||| ||| ||| ||| |||
AATTTTTTAATAAGAGAAAT GCTA AGAC TTAA ATGAG TTTGCT AGAG ATTT /
GTCGTTTGAGTACAATTCAG TGAA- TCCA - C ---- GTAA AATA TTT
AACCTATCGAAGTGTTTATA
GT

GAM80 AGATAGCAAGCTGTTGGCTA 66 TAGCAAGCTG 2791 CTG- AAAA- - T
AAAACGGTTTTTATCAGTGG TTGGCTAAAA AGATAGCAAG TTGGCT AC GGT T
TACGGCCAGATTATTTGCTA ACGG ||||| ||| |||
TTT TTTATCGTTT GACCGG TG CTAT
ATTA CATGG A T

GAM81 AGTAAGTTTTTTTTGTCTAG 67 TACTGTAAGT 2792 TTT- C- G TGTTT C-----
TCGCT T
TAGCGCTGATTGTTTTATTA ACTGGAAACT TTT GT TAGTA CGCTGAT TATTAA GTCG
AAG T
ACGTCGTCGCTAAGTTTTCT TGCT ||| || ||| ||||| |||| ||| |||
TTTTTCGGCCATCTTCATAT AGG CA GTCAT GCGGCTG ATAATT CGGC TTC
T
TAATATCTTCGTCGGCGGTA TCAT AT G CTCT ATACTTCTAC TTTT- T
CTGTAAGTACTGGAACTTG
CT

GAM82 ATCTCGTCTCCGACGTTTAA 68 TTCACGTCGA 2793 C --- TT T TTACC
CATCATTACCTGGCCGTTGC GCGACACGAG ATCTCGT TC CGACGT AACA CA T
TGTTACGTCGAGCGACACG AT ||||| || ||| ||| |||
AGAT TAGAGCA AG GCTGCA TTGT GT G

C CGA C- C TGCCG

GAM83 CAACTCTGGAATGGTTGAAT 69 TCGTTGGCTT 2794 TCTGG AATTTGT CGT -- C AA
TTGTGGCGTCGACCAGCGCG CGTACCTAAC CAAC AATGGTTG GG CGA CCAGCG GTA
C
TAAACCATATCGTTGGCTTC CATT ||| ||||| || ||| ||||| |||
GTACCTAACCATTATATTGT GTTG TTACCAAT CC GCT GGTTC TAT /
TG TTATA ----- AT- TC - AC

GAM84 CCTGAGCTATCAGTAAGTTG 70 TGAGCTATCA 2795 G ATCA--- A T TTCT
TAAATTCTATTAATTTTATT GTAAGTTGTA CCT AGCT GT AGT GTAAA A
ATTAACATCGTCGAGCTGGG AATT ||| ||| || ||| |||||
G GGG TCGA CA TTA TATTT T
G GCTGCTA A T TAAT

GAM85 CGGACTCATCACGCAACTGT 71 TACACAGACG 2796 T- CA CAA CG CAGA
GCGAAAGTCTCAGATCGCAA ACATGCTGTC CGGAC CAT CG CTGTG AAAGTCT T
GATTTTACACAGACGACAT CG |||| ||| || |||| |||||
GCTGTCCG GCCTG GTA GC GACAC TTTTAGA /
TC CA A-- AT ACGC

GAM86 CGTCGTACGTGGAAGTCGTC 72 CAGGAGCCGT 2797 A -TA G ---- C TTT ATAC
AA AC
TTACCGGCGTCCAGGAGCCG TTACGCTGAT GA GTCGTC T CCG CGTCCA GGAG CG
ACGCTG TTGTA AC G
TTTACGCTGATACTTGTAAC ACTT || ||||| | ||| ||||| |||| ||| ||||| ||
ACACGTTGTGTCGTGCAACAGC TT CGGCAG G GGC GCGGGT CCTT GT TGCGAC
AACGT TG /
AGCGTTTTGTTTCCCAATTG G TGC G TAAC T TT- GAC- GC TT
GGCGGCGGCGGTGACGGCGT
TGGTGTACGCG

GAM87 CGTGTCCGATAGATTGGTGT 73 TCACTCGTTT 2798 CCGATAGA G CT - C TCT T
CACCTCAGGCGGTCGTATCT GTGTGACATG CGTGT TT GTGTCAC CAGGCG GT GTA
ATA T
ATATTTATATTATTATCACT GAGC |||| || ||||| ||||| ||| |||
CGTTTGTGTGACATGGAGCA GCACG AG TACAGTG GTTTGC CA TAT TAT T
TGCACG TACG---- G T- T C TAT A

GAM88 CTCTTGATCCTGGCAATCTA 74 CCTGGCAATC 2799 TG C-- - ATCTAA T CATATTTT T
TTC
AACTAGCCATATTTTATAG TAAACTAGCC CTCT AT CTGG CA AC AGC TATAG TGA
C
TTGATTCCTATCTCGCCTAT ATAT |||| || ||||| ||||| ||||| |||
ATCTTTGCTGTACGTGACCA GAGA TA GACC GT TG TCG ATATC GCT T
GATTATTGAGAG GT TTA A GCA--- - TTTCT--- C CTA

GAM89 GAGAGGTTATCGCAGCTTAT 75 GAGGTTATCG 2800 G --- TA TG ACA
 CTTGAACACGATATTGGGAC CAGCTTATCT GAGA GTTAT CGCAGCT TCT A C
 AGTTGCGTTTGTAAATATTTT TGAA ||||| ||||| ||| |
 TTTT TAATG GCGTTGA AGG T G
 A TTT C- GT ATA

GAM90 GAGAGTCAAATTGATTTATA 76 TTAAAATTGA 2801 - TG ATA ACGAG TTA
 TAATAACGAGTTGCGATTTA TTCTGATTTT GAGAGTCA AAT ATTT TAATA TTGCGAT T
 TATTGTTGCAAGATATTTAA C ||||| ||| ||| ||||| |||||
 ATTGATTCTGATTTTC CTTT TAGT TTA TAAA ATTAT AACGTTG /
 C GT --- AG--- TTA

GAM91 GCGTCCAAATTTTACAGCGA 77 GAGCTTAAAC 2802 GT AA- A--- ATAT GA AACAA
 A C
 AATATTTCGAGAGCTTAAACA AACATGAACA GC CC ATTTTAC GCGAA TC GAGCTTA
 CATG ACAG T
 ACATGAACAGCTGGCTGTAC GCTG || || ||||| |||| || ||||| |||||
 ATGGTGAGCTCGGACACCTT CG GG TAGAATG TGCTT AG CTCGAGT GTAC
 TGTC G
 CGTCAACGTAAGATGCGGGG AG GCG CAAC CCAC G- G--- A G
 AGC

GAM92 GGAAAAAGCCAACAAGTGCC 78 TTAGCGCTGT 2803 AAAA ----- - CT G AC GT
 TTAGGATGGGACGTTACGTG GTTTCTCGGG GGA GCCA ACA AGTGC TAGGAT GG
 GTTAC G
 GTGTGGCCCAATCTTAGCGC TGGC ||| |||| ||||| ||||| || |||||
 TGTGTTTCTCGGGTGGCGCA TCT CGGT TGT TCGCG ATTCTA CC CGGTG /
 TCT ACG- GGGCTCTT G -- A -- TG

GAM93 GGATTCTAGTCTAGAACAAA 79 AGTCTAGAAC 2804 - TA- AGAACAAATTATA GG C
 TTATATCCGGGTTCAACAAC AAATTATATC GG ATTC GTCT TCC GTT A
 AGGAGCAGATACCGAATACC CGGG ||||| |||| ||| |||
 CC TAAG TAGA AGG CAA A
 A CCA CG----- A- C

GAM94 GGCTGCGATAACATCAATTT 80 TCACTCGTGG 2805 TG ATA ATTTTCT A ---- A AC
 TCTAGTAGATATTTTCGGAG TGTCACGTGG GGC CG ACATCA AGT GAT ATTTTCGG GA
 A
 AACACATCACCGAGAATGAC CC ||| || ||||| ||||| ||||| ||
 AATCACTCGTGGTGTACGT CCG GC TGTGGT TCA CTA TAAGAGCC CT /
 GGCC GT AC- GC----- - ACAG A AC

GAM95 GGGGTTGGTGGGGTTGGGGT 81 TTGCTGCAAC 2806 GG GGG G T ATGAT

TAGATATGATTGCTAAAATT AGAGCCAAAA GG TTGGT GTTG GGT AGAT T
 TGCTGCAACAGAGCCAAAAC CC || |||| ||| ||| |||
 C CC AACCG CAAC TCG TTTA G
 AA AGA G - AAATC

GAM96 GGTACTGCAGGGAATCGGGG 82 TACTGCAGGG 2807 - T AT TTCGC-- A C AA
 TTCGCTGTAGTGTCTGGAAGC AATCGGGGTT GGT AC GCAGGGA CGGGG TGT GTGT GG
 G
 TCTACACACACTCTTCTCCC CGCT ||| ||||| |||| ||| ||| ||
 TGTCTTGTGTGAACC CCA TG TGTTCT GTCCC ACA CACA TC /
 A T -- TCTTCTC - - TC

GAM97 GGTTGAGGAGATTATGATTG 83 TGAGGAGATT 2808 T AT- A A T CTTA CAA
 AGGTCGCGCTTATCTTCAA ATGATTGAGG GGT GAGGAG TATG TTG GG CGCG TCTT A
 ATCAAGGAATTCGCGCCCGA TCGC ||| ||||| ||| ||| ||| |||
 CGTACCCCTCTTCACC CCA CTTCTC ATGC AGC CC GCGC AGGA A
 - CCC - - - TTA- ACT

GAM98 GTAAAAATATCAAACATAGC 84 AAAAATATCA 2809 TC AGCA-- AT- TTT CG
 ATGAATTGGCTCGTTTTGCG AACATAGCAT GTAAAAATA AAACAT TGA TGGCTCG TG C
 CAACACTTGGGCCACCGTCA GAAT ||||| ||||| ||| ||||| ||
 AGGGACATGTTTTATTTTA TATTTTAT TTTGTA ACT ACCGGGT AC /
 T -- CAGGGA GCC TC- AA

GAM99 GTGACGTGGTGCGGCAAATC 85 TGCGGCAAAT 2810 A -- AAATCTT A A A
 TTGAGTAAAAGTGACGACGC CTTGAGTAAA GTG CGTGGT GCGGC G GTAAA GTG C
 CTTTACCGCCGCTCATCACG AGTG ||| ||||| |||| | ||||| |||
 CAC CAC GACTA CGCCG C CATTT CGC G
 - CT ----- C A

GAM100 GTTCATTCTAGTTCTGTAAC 86 TGTAACCGTT 2811 ATT TC- CC T TCTAT CT
 CGTTTTCGTCTATTATCTCA TTCGTCTATT GTTC CTAGT TGTA GTT TCG TAT C
 ACATACTCTTCGACAACTTG ATCT ||| ||||| |||| ||| ||| |||
 CAAACGCTGGTCAAC CAAG GGTCTG ACGTT CAA AGC ATA A
 CT- CAA -- C TTCTC CA

GAM101 TAACTCCAGGCCGTTGTTGC 87 GATAACAGTT 2812 C CCG - T- C AATA
 TATCACTGATAATAAACGA ATCTGGAATT TAA TCCAGG TTGTTG CTA CA TGAT A
 TCATTGTTTAGATAACAGTT A ||| ||||| |||| ||| ||| |||
 ATCTGGAATTA ATT AGGTCT GACAAT GAT GT ACTA /
 A ATT A TT T GCAA

GAM102 TCGTTTCAAATTTTCCGGC 88 AATCACGGGC 2813 TTCAAATTT C A G CC TG

AGCGCGTGACCCGATGACAT GCCTGATAAA TCGT TC GGC GC CGTGA CGA A
 TTGAATCACGGGCGCCTGAT AATG |||| ||||| ||||| ||||
 AAAAATGCGA AGCG AG CCG CG GCACT GTT C
 TAAAAAT--- T - G AA TA

GAM103 TCTAAAGGTATCTCTCTGAT 89 AAAGGTATCT 2814 --- - ATGGA TT
 GGACATTGAATTGCAGAACG CTCTGATGGA TCTAAAG GTATCTC TCTG CA G
 GATGGGATATATACTTTAGA CATT ||||| ||||| ||||| ||
 AGATTTT TATAGGG AGGC GT A
 ATA T AAGAC TA

GAM104 TGTCTTCGGTGAGGGGTAGC 90 TGAGGGGTAG 2815 CTT- A TGTT - G
 GTCGTGTTGGGTTCCGTGCA CGTCGTGTTG TGT CGGTGAGGGGT GCGTCG GGGT TCCGT
 C
 TACGGGTATCTCGACGCACT GGTT ||| ||||| ||||| ||||| |||||
 CCTCGCCGTCAAACA ACA GCCGCTCCTCA CGCAGC TCTA GGGCA A
 AACT - ---- T T

GAM105 TTGGCGGAGTGAACGTTGTG 91 TTACCGCCCA 2816 AGTGAA--- - TT TG
 GTGTTTGGTGATTTGTTTCA TCAGCAACGA TTGGCGG CGTTG TGGTG TGGTGATT T
 ATTACCGCCCATCAGCAACG TAAA ||||| ||||| ||||| |||||
 ATAAAGATGCTGCCAA AACCGTC GCAAC ACTAC GCCATTAA T
 GTAGAAATA G CC CT

GAM106 AAAATGTTTGTGGGAGCAGT 92 TGGGAGCAGT 2817 T T- GTAA A GACTT T ---
 G
 AAATGTACTATGACTTTATC AAATGTACTA AAAATGT TG GGGAGCA ATGT CTAT TA CTGG
 TCTT A
 TGGTCTTGACAAGAATCTCC TGAC ||||| || ||||| ||||| ||||| |||||
 AGTTATCAAAGTGGACATCC TTTTGCG AC TCTTTGT TACA GGTG AT GACC AGAA
 /
 ATGTTTCTCTCATGCGTTTT T TC ACC- - AAAC T TCTA C

GAM107 GAGAAGGCTGTTTCATATCCT 93 GGGGATGATT 2818 A TG TCA TACTTTT GG-- CTT
 CTTACTTTTCCAGGGTCTTC GTGGTCTACT GAG AGGC T TATCCTCT CCA GT C
 TAAAGCAAAATGGTGTCTAG C ||||| | ||||| ||| ||
 GGGATGATTGTGGTCTACTC CTC TCTG G GTAGGGGA GGT CG T
 A GT TTA TCTGT-- AAAA AAA

GAM108 TGCTCTAGTGTATTAACAAA 94 TAATACAGCA 2819 TA TTAA AT- - T AA
 TCTGTGTTGGTGTTTAAAGA GTTGGGCTTA TGCTC GTGTA CAA CTGTGTTGG TGTT
 AAAGAG A
 GAAAAGCTTTTTCAGCATCT CATG ||||| ||||| ||| ||||| ||||| |||||
 AATACAGCAGTTGGGCTTAC ACGAG TACAT GTT GACATAATC ACGA TTTTTC /

ATGAGCA

-- TCGG GAC T C GA

GAM109 TTCTATGTCCTGTAATAGGT 95 TGTGCAAGAA 2820 T --- AG--- AT TT
ACAATGTCTTTTTTTAAGGC GTTATACAAG TTC ATGTCCT GTAAT GTACA GTCTT T
TGTGCAAGAAGTTATACAAG GGCA ||| ||||| |||| ||||| ||||
GGCATGAA AAG TACGGGA TATTG CGTGT CGGAA /
- ACA AAGAA -- TT

GAM110 AAAGTTGCTGCCATTCTTGC 96 TTGCCAGATT 2821 CTGCCAT T C AC- AG
CAACAGAACAGAGTCCCTAT CTCCCAACTT AAAGTTG TCT GC AACAGA AG T
ATCTGTTGCCAGATTCTCCC T ||||| ||| ||||| ||
AACTTT TTTCAAC AGA CG TTGTCT TC /
CCTCTT- C - ATA CC

GAM111 AAGGAAGATTAGGTGCACAA 97 AAAAATGTCC 2822 TAG ACAATC C- TCCAGGT -
AACAC CC
TCTATTGTCATAAAAATGTC AGGTCAATTT GTGC TATTGT ATAAAAATG CAA TTTCTTC
CTT T
CAGGTCAATTTCTTCAACAC CTTC ||| ||||| ||||| ||| ||||| |||
CTCCTCAAAGTTATAGAAG CATG ATAACG TATTTTAC GTT AAAGAAG GAA
/
AAACTTGTTTCATCATTTTT TG- AACAA- AT TACTTT- C ATATT AC
ATTAGCAATAAACAAGTACG
TTTTTTCCTT

GAM112 AAGGGATTCAAAAAGAGTTA 98 TTTCAAAGGC 2823 T A A AAATA A T
AATATGAAAATGTGGTCATT TTATTGTGAT AAGGGA TCA AA GAGTT TGAAA TG G
TCAAAGGCTTATTGTGATTT TTCT ||||| ||| ||||| ||||| ||
CTTT TTTCTT AGT TT TTCGG ACTTT AC G
T G A AA--- - T

GAM113 AAGGGTCGGCTCCTTAACGC 99 AAGCAGCATT 2824 ----- TCC-- C CA- GAAAAAC
GTACTTTGA
TGTCAAGGAAAAACCTGCAG AAAAAGTCC GGT CGGC TTAA GCTGT AG
CTGCAGA G
AGTACTTTGAGTTGCTAATA GAAG ||| |||| ||||| || |||||
TCTGCAGACACTGAAGCAGC CCG GCCG AATT CGACG TC GACGTCT /
ATTA AAAAAGT GCCGAAGAAA ACAAAGAA TCAAA A AAG ACA---- ATAATCGTT
CAGCCCTT

GAM114 ACAACATGTAAGCGTTGGGT 100 TGGGTAAGAA 2825 CAT C T - CT ATC AT
AAGAAGATCTGGATCTGGAT GATCTGGATC ACAA GTAAG GT GGGTAAGAAG AT GG TGG
G
GACCCACCTTGTCTTCTTA TGGA |||| ||||| ||||| ||| |||
TCCTATCCTTATCCTTGT TGTT TATTC TA CCTATTCTTC TG CC ACC /
CC- C T C TT --- CA

GAM115 ACACGTCCGTGTTAGTGATG 101 TTA CTTGGAC 2826 GTTA----- GA T AGAT
 AGTATATGGACAGATTTGGT GAGAAAAGAA ACACGTCCGT GT TGAGTA ATGGAC T
 AGTCTATTACTTGGACGAGA ATGG ||||| || ||||| |||||
 AAAGAAATGGACGTGT TGTGCAGGTA CA GTTCAT TATCTG T
 AAGAAAAGAG G- - ATGG

GAM116 ACCTGATTCCCTTCTTCTGTT 102 TGCATAGCAA 2827 T- C - T AAAA C
 GCAGAATAAAAGGAACCAT GGAGAAATCT ACC GATT CTTCTT CTGT GCAGAAT GGAA C
 TCCGTTGGTTCTGCATAGCA CGGT || ||| ||||| ||| ||||| |||||
 AGGAGAAATCTCGGT TGG CTAA GAGGAA GATA CGTCTTG CCTT A
 CT A C - GTTG T

GAM117 ACCTGCACTCAAAATTACTT 103 AGCAGTAGTA 2828 ---- AACA A TA
 AACGAAGATGAT A A
 CTGGGGGTAACAATAGTAGC TCAATAACGA TTC TGGGGGT ATAGT GCAGTAG TCAAT
 GGTG TG T
 AGTAGTATCAATAACGAAGA AGAT ||| ||||| ||||| ||||| ||||| ||||| |||||
 TGATGGTGTATGATGACGATG AAG ACCCCCG TATTA CGTCATC AGTTG CCGT
 GC G
 CCGTTGACGCTACTGCATTA TCAA ---- - GC ----- A A
 TGCCCCCAAAGCTAC
 AGTGAAAAAT

GAM118 ACGATACGAGGATAGATTGT 104 TAGATTGTCT 2829 A A- T TCT T GTA AA C
 CTAGATGCAGTAGCAATCT AGATGCAGTA ACG TACGAGG TAGA TG AGA GCA GCA TCT
 A
 CACCGGACCTGTGTATGTTT GCAA ||| ||||| ||||| ||| ||| ||| |||
 TCATTTTAGATCTTGTACGT TGC ATGTTCT ATTT AC TCT TGT TGT AGG C
 - AG T --- - ATG CC C

GAM119 ACTTCTACTGTTTACACTTC 105 TCTACTGTTT 2830 A TC TAAA TTACC
 TGTAAGTGTTACCTTTCTT ACACTTCTGT ACTTCTACTGTTT CACT TG GTG T
 CCATAATCAAGAGTGAAAGT AAAG ||||| ||||| ||| |||
 AGTAGAAGT TGAAGATGATGAA GTGA AC TAC T
 A GA TAA- CTTCT

GAM120 AGAAAAAGCAATGGGTATCA 106 AAAAGCAATG 2831 ATGGGTA AAT AAT
 ATACAGATAATGGAGGATTT GGTATCAATA AGAAAAAGCA TC ACAGAT G
 GTTTGGAAGAATGGTGT TTT CAGA ||||| || |||||
 TTCT TCTTTTTTGT AG TGT TTA G
 GGTAAGA GTT GGA

GAM121 AGAAAGTACTACCATTTCT 107 TGTGGATAAA 2832 AAG A CC G A AT
 GTTGACAAGTATAGAGCTGT AAGGTGGTAA AGA TACTACC TTT TGTT ACA GT A
 GGATAAAAAGGTGGTAAATC ATCT ||| ||||| ||| ||| ||| |||

TCT ATGGTGG AAA ATAG TGT CG /
AA- - A- G - AG

GAM122 AGAACCGTATCTTGTTATCA 108 TTCAAAGCTG 2833 CC T TAT AA --- TCAGAAT
AATTTGAAAAGAACTCAGAA TACGCATGAT AGAA GTATC TGT CA TTTGAA AAGAAC C
TCATTACTTGTTTTTCCATT ACAT |||| ||||| || ||||| |||||
CAAAGCTGTACGCATGATAC TCTT CATAG ACG GT AAAC TT TTTTG /
ATTCT A- T CAT CG ACC TTCATTA

GAM123 AGAGGGCTAGTGTCTAAAAC 109 TCTAAAACGG 2834 CT- AACGGATA TT T AA CC
G A AAG
GGATAGGTTTTTACTACCAA ATAGGTTTTT GAGGG AGTGTCTAA GGTTT AC ACC AC
AACAG CC CC A
ACCCAACAGGCCACCAAGAT ACTA ||||| ||||| ||||| || ||||| |||||
GAAGGGGGTTGTTTAGTACG TTCCT TCGCAGGTT CCAGA TG TGG TG TTGTT
GG GG T
GTTGTTAGACCACAAAACT TTT CAAAAACA T- T CA AT G - AAG
TGGACGCTTTTTCTTTT

GAM124 AGCTCCTTTTACTGTAAGGT 110 TGTTATATGT 2835 --- G TG- A G
TTGGTAATGACAATGATAAT GTAGGAGGAG AGCTCCTTTTAC GTTAA GTT GT AT A
AATGTTATATGTGTAGGAGG CT ||||| ||||| |||||
AGCT TCGAGGAGGATG ATATT TAA TA TA C
TGT G TAA G A

GAM125 AGGTTTATGGAACCTCCTGGC 111 CAAGGTATTT 2836 A ACTC GC ATTT CC TCC
AAGGTATTTTGCCTCCCTG TGCCCTCCCT AGGTTT TGG A CTG AAGGT TGCCCT CTG T
TCCTCTTTTAGAGGGGCGGC GTCC ||||| ||| ||| ||||| |||
CTTACAGCCTCCAAAAACCT TCCAAA ACCT GAC TTCCG GCGGGG GAT C
A CC-- A- ---- A- TTT

GAM126 ATATAACAAGGGACAGACTT 112 CAGGAGTGGT 2837 C ACTTGT- TCCA GGTTCAA
CC T - A
GTAATGTTGTCCAGGAGTGG TCAAGGGATC AGGGA AG AATGTTG GGAGT GGGAT
TTC CTCT TGC A
TTCAAGGGATCCTTCTCTCT CTC
TGCAAAGCGTAGAGGAACAG TTTCT TC TTACAAT TCTTA CCCTG AAG GAGA
GCG /
TCCCCAAATTCTGTAGTAAC T GCACCCT GATG AAC---- AC - T A
ATTTCCACGCTTTCTTTTG
TAATAT

GAM127 ATCGTTCATTGTGTAAAAA 113 TATTACATTT 2838 ATT - AGT TG T TT T TG
AAAAA
GTATGGATGTGTTGAATTTG GTTTGTTTTG ATCGTTCA GTGT AAAA A GATGTG TGAA TGT
A ATGTT T
TTATGATGTTAAAAATAATA ACAC

AAAATATTGTACATTTTATT TGGCGAGT CACA TTTT T TTACAT ATTT ACA T TATAA
 A
 ACATTTGTTTGTGTTTGACAC C-- G GTTGT T T- -GT AAATA
 CTGAGCGGT

GAM128 ATGACGAAGAAGACGAAAAA 114 ACGAAGAAGA 2839 - ----- AAAA- G AA
 GATGTCAAGCAAGAAGTCTC CGAAAAAGAT ATG ACGAAGAA GACG AGAT TC G
 GAACCGTCCCCCATTTTTT GTCA ||| ||||| ||| ||| ||
 CGTACAT TAC TGCTTTTT CTGC TCTG AG C
 A TACCCCC CAAGC A AA

GAM129 ATTCACTTTTTTGTAACCCTA 115 TGTCAGGGTT 2840 -- T---- ATCA T G AT
 TCAACAGATTTGAATGATAA TTCACCAGAA ATTCACT TTTTG AACCT ACAGAT TGAAT
 ATA A
 TAGAATATGTTTCGTATTTGT ATAG ||||| |||| |||| |||| |||| ||
 CAGGGTTTTACACAGAAATA TAAGTGA AAGAC TTGGGA TGTTTA GCTTG TAT G
 GTGAAT TA CACTT C--- T - AA

GAM130 ATTTTCCTCCATGACGAAAC 116 TGATATGTCT 2841 T T C C T A- AGCTCT G
 ACTGGTGATATGTCTGGAGC GGAGCTCTGA ATTTTCC CCA GA GAAA ACTGG GAT TGTCTGG
 GAT A
 TCTGATGAATGTCTTGCCAG TGAA ||||| ||| ||| |||| ||| ||||| ||
 ATGCCATCCTAGTTTTTCTC TGGAAGG GGT CT CTTT TGATC CTA GTAGACC CTG A
 CTGGGGAAGGT - C - T - CC GTT--- T

GAM131 CAACAACAGTGCCAATGTAA 117 AACAGTGCCA 2842 A - AATG GA TGT - TT
 TGGAAGCTGTGGATAGTTTC ATGTAATGGA CAACA CA GTGCC TAATG AGC GGA TAGT C
 AATACTACTCCTTTGCTCGT AGCT ||||| |||| ||| |||||
 TAGGCACATGATGTTG GTTGT GT CACGG ATTGC TCG CCT ATCA A
 A A ---- -- TTT C TA

GAM132 CAAGTCCCACCGTGGTTCCT 118 TCAGAGGATG 2843 A ACCGTGGT GCT TT T T
 CTGGTTCTGCTTCTTCTTCT AAAGGGATAT CA GTCCC TCCTCTGGTTCT TC CT CTCAT G
 CATTGTATGAGTAGTGATGA G ||||| ||||| ||| |||||
 AGAATCAGAGGATGAAAGGG GT TAGGG AGGAGACTAAGA AG GA GAGTA /
 ATATG A AAAGT--- AGT T- T T

GAM133 CAATATGGATAGTTGTTGCC 119 TACCAGAAAA 2844 ATG T GC A C AACA AAC
 G
 TGATATCGAGGATAACACCA CAACTTCAAG CAAT GA AGTTGTT CTG TAT GAGGAT CCAG
 TGGCT G
 GAACTGGCTGGCAAGTTAAC ATTG ||| ||||| ||| ||||| ||| |||||
 CTGGATCTTCATACCAGAAA GTTA CT TCAACAA GAC ATA CTTCTA GGTC ATTGA C
 ACAACTTCAAGATTG GAA - AA C - ---- CA- A

GAM134 CAATTTGCTAAGGGTTTGT 120 CATCAGATGG 2845 - TAAGG --- TG AGGT TC
 GTTTGATGAGGTTGTCACAT CTCAAGATAT CA ATTTGC GTTT GT TTTGATG TGTCACA A
 CAATTGTGGCACATCAGATG TTGC || ||||| ||| || ||||| |||||
 GCTCAAGATATTTGCAAGTC GT TGAACG TAGA CG AGACTAC ACGGTGT /
 TG C TTTA- ACT GT ---- TA

GAM135 CAGACTTGTCGAAAGAGGAC 121 TAATAAGATT 2846 AAGA CAGAAAC C AA-- CC--
 -- - A
 CAGAAACTCTTATCATAATC GTCCACATCG TGTCGA GGAC TCTTATAT TCTA TCCAC
 CAT TGA G
 TACCTCCACCATTGAAGATT ACAA ||||| ||| ||||| || ||| ||||| |||||
 CGTATGTAGTGGAACCCATA ACAGCT CCGT AGAATA TA AGAT AGGTG GTA
 GCT A
 GAAAAGATAATAAGATTGTC ACA- TT----- A GAAA ACCCA AT T T
 CACATCGACAAGTACTG

GAM136 CAGATTGCACCAGAACCGAC 122 CTGGAACAGA 2847 AT- A C A TGC TG TTA
 TGTTGCTCCAGAAATGTGCA CGTTTCTGGG CAG TGC CCAGAA CG CTGT TCCAGAAATG
 CA A
 TTAACCTTTGTGTGTTTCTG CATA ||| ||| ||||| || ||||| ||||| ||
 GAACAGACGTTTCTGGGCAT GTC ACG GGTCTT GC GACA AGGTCTTTGT GT C
 AGCTG GAT - T A --- GT TTC

GAM137 CATATGATTTTTCAGTATTG 123 TTCAATGCAT 2848 TTT - TACA AA CAAAAAC
 AT
 TACAAGATTCTTCAACTACA GGGAATCGTG CATATGAT T CA GTATTG AGATTCTTC CTA
 AGA A
 AAAACAGAATATCTCTTTAC TG ||||| ||| ||||| ||||| ||| |||
 TTTTAGAGAAGGGTTTCAAT GTGTGCTA A GT CGTAAC TTTGGGAAG GAT TCT /
 GCATGGGAATCGTGTG - GG A ---- A- TTTCATT CT

GAM138 CATTTCTTCCCTGCAAACGT 124 TGCAAACGTA 2849 TT CT GTA - GA--- AG
 ATGGCGGTATAGAAGAGTTG TGGCGGTATA CA TCTTCC GCAAAC TGGC GGTATA AG T
 CCTGAAAATGTACTAGTCGG GAAG || ||||| ||||| ||| ||||| ||
 TTTGTCCGGAGGATTTG GT AGGAGG TGTTTG GCTG TCATGT TC T
 TT CC --- A AAAAG CG

GAM139 CCTTGCCAAGTGCGCATATC 125 TCACCAATTC 2850 AA G TATCAC TCAC-
 ACCTCCT
 ACGATCACTGATAAAACCTC CTTTGAGTAC CCTTGCC GTGC CA GA TGATAAA C
 CTCGTATATTATTTATCACC CGGG ||||| ||| || || |||||
 AATTCCTTTGAGTACCGGGC GGAACGG CATG GT CT ACTATTT G
 AAGG GC A TTC--- TAACC ATTATAT

GAM140 CGTCTGGGCGGAAGTGCAGT 126 ATCTCATAAA 2851 GG GAA-- C T CT G
 TTCCTCCCCGGGAGGGGCGA CACGACAGAT CGTCTG CG GTG AG TTC CCCC G
 ATCTCATAAACACGACAGAT G ||||| || ||||| |||||
 G GTAGAC GC TAC TC AAG GGGG G
 A- ACAA - T C- A

GAM141 CGTTACATTATTGCAGTTGG 127 AGTTGGTGTG 2852 A TT--- A TCCT CAA-- TCTTT
 TGTCTACATCAACGCTCTC CTACATCAAC CGTT CATT GC GTTGGTG ACAT CGCTC
 T
 TTTTCCCTCGAGCGCCGAAA GCTC ||||| ||||| ||||| |||||
 TGTTTTACCGACGGCTTTT GCGA GTAAT CG CAGCCAC TGTA GCGAG /
 TTAATGCAGCG C TTTTT G TTT- AAGCC CTCCC

GAM142 CTAAAATTGTCCAATACTTT 128 TTAAAGGCA 2853 -- CAATA-- GCAAAT AAAATC- G
 TTTT CT
 AAAGGCAAATTTTGAAAAAT AATTTTGGA TGTG CTTTAAAG TTTGG CATGTC
 GCTA TG C
 CCATGTCGGCTATTTTTGCT AATC ||||| ||||| ||||| ||||| ||||| |||||
 CAACATTTAGTGGACATGAC ACAG GGAATTTT AAATC GTACAG TGAT AC /
 AAACGCTAAACACTTTAAGG AA AAACCCA AC---- GCAAACA G TT-- AA
 ACCCAAAGACAAAGAAGATT
 TTAG

GAM143 CTAATACTGTTATCCTTCCT 129 TGTTATCCTT 2854 TAC CC CT A TTT
 ACTTCTGAGTTGTTAACTG CCTACTTCTG CTAA TGTTAT TTC ACTTCTG GT G T
 CCCAGGAGTTGAAAATGACA AGTT ||||| ||||| ||||| ||||| |||||
 AATTTAG GATT ACAGTA AAG TGAGGAC CG C /
 TAA A- T- C T AA

GAM144 CTCCACCTGAGGATGAAGAA 130 CACCTGAGGA 2855 C - G A AAGAA A ATTTCTAC AA
 GAGGATGATTTCTACCGCAA TGAAGAAGAG CT CA CCT AGG TG GAGG TG CGC A
 AAAGCGTGCCGCACCTCCAC GATG ||||| ||||| ||||| |||||
 CTGAGGATGAAG GA GT GGA TCC AC CTCC AC GCG /
 A A G - ---- - GCCGT--- AA

GAM145 CTCTTCATAGGAAACATTTA 131 ATAGGAAACA 2856 ----- ATG- T
 TGTGTTATTAGTGATAAGAA TTTATGTGTT CTCTTCA TAGGAAA CATTT TGTTA T
 GAATGGTACAATTTCTATT ATTA ||||| ||||| ||||| |||||
 CACCTGAAGAG GAGAAGT ATCCTTT GTAAG ATAGT A
 CCACTT AACATG AAGA G

GAM146 CTGGGTCGGTCTGATGTCAA 132 TGATGTCAAG 2857 - C AAGTTCGGA G T
 GTTCGGAGGGTGGACCTCTG TTCGGAGGGT CTGG GT GGTCTGATGTC GGGT GACC C
 GGTGACCCGATGTCAGATT GGAC ||||| ||||| ||||| |||||
 ACACCAG GACC CA TTAGACTGTAG CCCA CTGG T
 A - ----- G G

GAM147 CTGTTTTTGGAGTCAGTACG 133 GGA CTAGATA 2858 CAGTAC TG A CA T T CC-
ATA --- T
CGTGTGGATTCACATATTGT AGGCCTCATG GT GCGTG G TT CATAT G AGGCC TTTAGT
CCTGT TGA T
AGGCCCTTTTAGTATACCTG TGGC || ||||| | || ||||| ||||| ||||| |||
TTGATTTTTCAAGCGCAGGA CA TGCAT T AA GTGTA C TCCGG AGATCA GGACG
ACT T
CTAGATAAGGCCTCATGTGG AT---- GT A CG -- AAT --- CGA T
CAAATTGTACGTTAACACCA
TAGACGG

GAM148 CTTCAAATGAGATCCTTATA 134 TGGCATGGAT 2859 AATGAG C AAAA -- TGGA
AAAATGTTCCAAATGGATAG GATGATGATG CTTCA ATC TTAT ATGT TCCAAA T
GGTTTTGGATGGCATGGATG ATGA ||||| || ||||| ||||| |||||
ATGATGATGATGAAG GAAGT TAG AGTA TACG AGGTTT A
AGTAG- T GG-- GT TGGG

GAM149 CTTCTGGAGCTGCTTTAAA 135 TCGTGGAGCT 2860 TC -- TTAAAG TGCT
GGTTGTAGTGCTTGAATCT GCTTTAAAGG CT GT GGAGCTGC GTTGTAG T
GCAGCAAACGCAGCTCTCTA TTGT || || ||||| |||||
CAGAG GA CA TCTCGACG CGACGTC G
GA TC CAAA--- TAAG

GAM150 CTTGGACGTGAAAAGCGCGA 136 GTGCGCTTGG 2861 AAA- - GAA A CCCC TTAA
GGAC AAGA C GA
AGCAGCTCCCCCACTTAAAG ACGTGAAAAG G AGC GC GC GCT CAC AGGTGCACTT
GT GG GC A
GTGCACTTGGACGTAAGAGG CGCG | |||| ||||| || ||||| || |||||
CGCGAAGCAGCTCCCCCACT C TCG CG CG CGA GTG TTCGCGTGGA CA CC
CG G
TAAAGGTGCGCTTGGACGTG CCCC A AAG - AAA- CAGG AATT CCC- T AC
AAAAGCGCGAAGCAGCTCCC
CCACTTAAAGG

GAM151 CTTGGATAATGTTCTTGTGA 137 TCTTACAAAA 2862 AT- C AT AA ACA
ATATCAACAACAAGGATGAA CTCGTATCCG CTTGGATA GTT TTGTGA ATC CA A
GATCTTACAAAACCTCGTATC AG ||||| || ||||| || ||
CGAG GAGCCTAT CAA AACATT TAG GT /
GCT - C- AA AGG

GAM152 GAAGAGGTGAAGAATAAGGA 138 TGAAGAATAA 2863 A T GAAG ACA GC
GAAGGTACAGGACTAGCATC GGAGAAGGTA GAAG GG GAAGAATAAGGA GT GGACTA A
ATAGTCCCTCACAATCCTTG CAGG ||||| ||||| || |||||
TTCTTCCCCTTC CTTC CC CTTCTTGTTCTT CA CCTGAT T
- - AA-- CTC AC

GAM153 GAAGTGAGTGCAGCGCTATA 139 TGA CTGGATT 2864 - G C TAACTTC G G
 AACTTCTCCGGTGATTTGGC ACTTAGCCCT GAAGT GA TGCAG GCTA TCCGGT ATTT G
 GAGTGA CTGGATTACTTAGC GCGT ||||| || ||||| ||||| |||||
 CCTGCGTCAATTTC CTTTA CT GCGTC CGAT AGGTCA TGAG /
 A - C TCATT--- G C

GAM154 GAGGAGGAACAACAACGACA 140 GGAGGAACAA 2865 CAACA ACA A A T A
 CCAACTCAACCTTCACCTGA CAACGACACC GAGGAGGAA ACG CCA CTC ACC TC C
 CGGTGGAGATGGATACGTAG AACT ||||| ||| ||| ||| |||
 ATCTTTCTCCTC CTCCTCTTT TGC GGT GAG TGG AG C
 CTAGA ATA A G C T

GAM155 GAGGCTATCCAGATATCTAG 141 TGGAAAGGGT 2866 ATCTA -- GAAT--- A TC---- A
 TG CAA
 GTCGGAAGAATCCAGAAAC TACAATTTAT GGT CGGGAA CCAGA ACGAT TAGCC
 TTTC GAA T
 GATTCTAGCCATTTCTGGAA TGTA ||| ||||| ||||| ||||| ||||| |||||
 CAATCATTTCTGGAAAGGGT CCA GTCTTT GGTCT TGTTA ATTGG AAAG CTT
 /
 TACAATTTATTGTATCTGGT TA--- TG ATTACGT A TTTAAC G GT TAC
 GCATTATTTCTGGTACCATT
 TCTGGCACCTC

GAM156 GAGGTTGCAACAGCTGCAGC 142 CAACAGCTGC 2867 GC T- A AATACG A TT
 ATGGAATACGTTTTTCATTAT AGCATGGAAT GAGGTT AACAGC GCAGC TGG TTTC TTATT
 C
 TTTCATTAATAAAGGAAAAG ACGT ||||| ||||| ||||| ||||| ||||| |||||
 GCCAAGCTGTTTGTTGTTAG CTTTAA TTGTTG TGTCG ACC AAAGG AATAA A
 AATTC GA TT A GGA--- A TT

GAM157 GATAGTGATTACGGCATCTG 143 TACGGCATCT 2868 T TA GAAAAA - CGAAAAAC
 --- AAG
 TGAAAAATGTGCACGAAAAA GTGAAAAATG GATAG GAT CGGCATCTGT TGT GCA
 TCCC AAATAC C
 CTCCCAAATACAAGCTCCGT TGCA ||||| ||| ||||| ||||| ||||| ||||| |||||
 ATTTT TAGGGAACGAAAATG CTATT CTG GTTGTAGATA GCG CGT AGGG
 TTTATG /
 CTGCGATAGATGTTGCCGTC T CC ----- T AAAAGCA- ATT CCT
 TTTATC

GAM158 GATTAGTGATGATGAGGATG 144 TTAGTGATGA 2869 - GA GATATTGC A A
 ATATTGCCTTTATTGATTCC TGAGGATGAT GATTAGT GATGAT GGAT CTTT TTG T
 GAAGAAGAGTCTGAATCATC ATTG ||||| ||||| ||||| ||||| ||||| |||||
 TACTGATT TTAGTCA CTACTA TCTG GAAG AGC T
 T AG A----- A C

GAM159 GCACTACACTGCACTGGTGA 145 TCACTGCACT 2870 - - - AC A A AG TAA

CGTAGTAGTAGAAGTAGTAG	GCACTAGTAG	GC ACTAC ACTGC ACTGGTG	GT GTAGT GA
TAGTAGTGG T			
TGGTAATAGTCCACTATTGT	TAGT		
CACTGCACTGCACTAGTAGT		TG TGATG TGATG TGATCAC	CA CGTCA CT GTTATCACC
/			
AGTAGTAGTAGT	A A A	GT - - --	TGA

GAM160 GCATCATCTCCAACACATAC 146	TCCCCAGTGT 2871	T C- CAC-- TT	CGAGAAT
GTTC			
TTTGGATACGAGAATGTTGT	CGATTTTGAT	GCATCA CT CAA	ATACT GGATA GTTGTT
A			
TGTTTCATCCCAAACAACCTCA	AGCT		
AAATTATCCCCAGTGTGCGAT		CGTGGT GA GTT	TGTGA CCTAT CAACAA T
TTTGATAGCTGGTG		C TA TTAGC CC	TAAACT ACCC

GAM161 GCCTAGAGAAGTTATGCAAG 147	GAAGTTATGC 2872	-- G	AA-- - GG CTC G
TAATTGGTACTCTCTTGGAC	AAGTAATTGG	GCCT A AGAAGTTATGC	GT AATT TA TCTT G
AAGAACTAGAAATTGACGA	TACT		
CGGTATAGCTTCTGTAAAGG		CGGA T TCTTCGATATG	CA TTAA AT AGAA A
C	AA G	GCAG G	AG CAA C

GAM162 GCGATAGTAAGGATCCCAAT 148	TTTAAAGTTG 2873	G GGA	A CTGACT GAGG
TTTAAATGTCTGACTGGTT	GGAAAATTAC	GC ATAGTAA	TCCCAATTTTAAA TGT GGTT A
GAGGATAAAAACTGCATTAA	TGTG		
CATTTAAAGTTGGGAAAATT		CG TGTCATT	AGGGTTGAAATTT ACA TCAA /
ACTGTGC	- AAA	- ATTACG	AAAT

GAM163 GCGCCTTCATTTATTGTCGC 149	GCGAATCTAT 2874	CA TGT C A G A
AGAATCGGCCGATATTGTTG	GTCTGTAAAG	GCGCCTT TTTAT CG AGA TCG CCGAT T
GCGAATCTATGTCTGTAAAG	CAAG	
CAAGGCGT		TGCGGAA AAATG GT TCT AGC GGTG /
	CG TCT A A - T	

GAM164 GCTATAATGGGTTGTGGTAT 150	TAAGGTATAC 2875	TTGT A -- ATA A
ATAACCTTG AG AAC		
TATAAGGTATACTGTATTTG	TGTATTTGTC	ATGGG GGT TTATA AGGT CTGT TTTGTCA
CA ATC A		
TCAATAACCTTGCAAGATCA	AATA	
ACACTCGATAATGATGATGA		TATCC CCA AATAT TCCA GACG GAACAGT GT
TAG /		
CAAGGCAGCAACCTATTATA		---- C TA AC- - AGTA----- AA CTC
ACACCCCTATATATGGC		

GAM165 GCTCGTGTAATGAGGATCCT 151	GAAGGTGCTC 2876	GA TAAA- A A CT A- ----
AAA		

AAAGTCACGTGAAGGTGCTC GTGTATGGTT TCC GTC CGTG AGGTG CGTGT TGGTTGGC
CAAGGATGA T
GTGTATGGTTGGCCAAGGAT GGCC ||| ||| |||| |||| |||| ||||
GAAAATGCCATCATCTTTGA AGG CAG GCAT TCTAC GCATA ACCAATTG
GTTTCTACT G
AAACGTTAACCACGATACGG -- TATCG - C CG GC CAAAA ACC
CCATCTCTACGGACGCTATG
GAGCGAGC

GAM166 GCTTCTTCTAGGATCTGTAT 152 TAGGATCTGT 2877 --- A T CT CATCTC- AAATCT C
CACATTA
CTGCCATCTCTGCTCAAAAA ATCTGCCATC TTCTT CTAGG TCTG AT GC TGCTCAA GC
AGT A
TCTGCCAGTCACATTAAACGA TCTG |||| |||| |||| || || |||| || ||
TCCTACTGCTTTGTTGAGCA AAGGA GGTCT AGAC TA TG ACGAGTT CG TCA

/ CCAACACGTCTATCCAGAAT ACT A C TC CACAACC GTTT-- - TCCTAGC
CTGGTCAAGGAAGC

GAM167 GGAAGAAAGTCTTTCCATTT 153 TGGGATATAT 2878 A-- TTTCCATT CTTCT
CCCATTCTTCTTGATTGAGA TGACAAGTTC GGAAGAA GTC TCCCATT T
TGGGATATATTGACAAGTTC TTCC |||| | ||||
TTCC CCTTCTT CAG AGGGTAG G
GAA TTATAT-- ACTTA

GAM168 GGAAGATGGGTAAATAGTCC 154 TGGGTAAATA 2879 AT --- ATAA G G
CTATAATTGGTGATACGAA GTCCCTATAA GGAAG GGGTAAATAGTC CCT TT GT T
GTTGAGGAAAGACTGTTTGC TTGG |||| |||||| || ||
CCTTTCC CCTTT CCCGTTTGTGAG GGA AA TA A
-- AAA GTTG G C

GAM169 GGACATACTTGCTAGACTTA 155 TTGACAGGTA 2880 ----- CTAGAC A CCT GG
ACAATTGACCTATGGCCAAT TCATAATTGT GGACA TACTTG TTAACA TTGA AT C
TCTCAACTGTTGACAGGTAT CC |||| |||| |||| || ||
CATAATTGTCC CCTGT ATGGAC AGTTGT AACT TA /
TAATACT ----- C CT- AC

GAM170 GGATAATACTGTAGTTAATC 156 TCATTCTTTA 2881 TA- TCGCCA C TC A T AAAC
C-- GA G
GCCATGAAGCATTCACTTA AAAATTTAAC G GTTAA TGAAG AT ATTCTA CA CA TTTTA
CCTC AT A
ACATCAAAACTTTTACCCTC AATT | |||| |||| || |||| || || || ||
GAATGAAAATAGAGGACTTA T CAATT ATTTC TA TGAGAT GT GT AAAAT GGAG
TA A
AAACTGTTGTAGAGTCATTC TAA TAAAA- T C- - T C--- TCA A- A
TTTAAAAATTTAACAATTAG
TAACAAAGTCT

GAM171 GGATCGCCTGCTCTCATGTG 157 TGGGACGCTA 2882 CC CT--- TGAAC AAGA

AACCGTCTCGGGGAAGATTT TTATGCCAC GGATCG TGCT CATG CGTCTCGGGG T
TACCCTGGGACGCTATTATG AGCA ||||| ||| ||| |||||
CCCACAGCATGATCT TCTAGT ACGA GTAT GCAGGGTCCC /
-- CACCC TATC- ATTT

GAM172 GGCATAAGAAGCAGACACCT 158 AAGCAGACAC 2883 A AGAA ACCT G AA- T
TTCGTCCCAAAAGTTTAGAA CTTTCGTCCC GGC TA GCAGAC TTC TCCC AAGTT A
ATTTGAAGGGAGAGCCAGTC AAAA ||| || ||||| ||| ||| |||||
TGCCATGTAGCC CCG AT CGTCTG GAG AGGG TTAA G
- GTAC ACC- - AAG A

GAM173 GGCCCTGTTCCAGAAATGGC 159 CTGGAACAGT 2884 G - ----- TCGG
TGTCCAGAAATCTGGGTCCG CATTTCTGGA GGCCCT TTCCAGAAATGGCTGT CCAGAAA
TCTGGG A
ACAGATTCCAGAAACGTTTC AAGG ||||| ||||| ||||| ||||| |||||
TAACCATTCTGGAACAGTC TTGGGA AAGGTCTTTACTGACA GGTCTTT
AGACCT C
ATTTCTGGAAAGGGTT - A ACCAATCTTTGCAA TAGA

GAM174 GGCTAGCGCTAGAAGAACCT 160 TCGAATCTTC 2885 TA ----- - - CCCTCC C T
TT
TGCCCTCCGGAGACTCTGGG TTTTCGGGAG GGC GC GCTAGAA GAAC CTTG GGAGA
TC GGG C
TTCCATCCTCGAATCTTCTT TTCT ||| || ||||| ||| ||| ||||| |||
TTCGGGAGTTCTTTTTAGTA CCG CG TGATTTT CTTG GGGC CTTCT AG TCC C
TAGAAACAGCCTGCC TC ACAAAGATA T A TTTT-- A C TA

GAM175 GGGGAGGGATTTGTTTAGGG 161 GGAGGGATTT 2886 --- TTT --- A A C- TT TTG
GCTGGAGGAGGCTTGTTGAT GTTTAGGGGC GGGGA GGGATTG AGGGG CTGG GG GG
TTG GATG T
GTTGTTCTCGTCTCCAGAAC TGGA ||||| ||||| ||||| ||| ||| ||| |||||
CGCCGCCAGATTTCCCTCCA CTCCT TCCTAGAC TCCCT GACC CC CC GAC CTGC
/
GATCCTCCTTCCTC TCC C-- TTA G G AA CT TCT

GAM176 GGGTGGAGAAGAAGAGGAAC 162 AGAGGAACTT 2887 G AAGAA CTCCT AATATC
G
TTCCTTCAGCAATATCTGAA CCTTCAGCAA GGGTG AG GAGGAA TCAGC TGAAGT T
GTGTTTGCTTCATTACCAGC TATC ||||| || ||||| ||||| |||||
TGATAACGATTCCTCCTCAC CCCAC TC CTCCTT AGTCG ACTTCG T
CC - ----- AGCAAT ACCATT T

GAM177 GGTCCGAGCTGGGTTAGATG 163 TAGAATCTTG 2888 GCT GAT T - --- TT
GATTTCTAAGGTGGGTTATC TAACCCTCGG GGTCCGA GGGTTA GGATT CTAAG GT GGG
A

TCTGTGGCGTTTAGAATCTT ATT ||||| ||||| ||||| ||| |||
 GTAACCCTCGGATT TTAGGCT CCCAAT TCTAA GATTT CG TCT /
 --- GT- - G GTG CT

GAM178 GTAAAAAGAAGGAGAAAAAG 164 AAAAGAAGGG 2889 AAAA A - A C C--- T
 ATTC
 AAGGATAAAAAGAAGGGCGG CGGTGGTGGT GGAG AG AGGAT AA AAGAAGGG
 GGTGGTGGTGGTGA GA TCTG A
 TGGTGGTGGTGACGATTCTG GGTG ||| || ||||| || ||||| || |||||
 ATTCAGAAACAGATTCTTCC CCTC TC TCCTA TT TTCTTCTT CTACTACTACT CT
 AGAC /
 TCATCATCATCATCTTCTTC C--- C C C - CCTT T AAAG
 TTCTTCATCCTCCTCCTCCT
 CATCCGAAGAC

GAM179 GTACTCCATGTACACTGGAG 165 TGTACACTGG 2890 CA GGAGAAGGAAAA - AAATTT
 AAGGAAAAAGGGGTAAATTT AGAAGGAAAA GTACTC TGTACACT AGG GGT G
 GTATTAGAGCCACCTAAAGA AGGG ||||| ||||| ||| |||
 AAGAAGTGTACAAAGGGTGC CGTGGG ACATGTGA TCC CCG T
 AA AGAAAGAAA--- A AGATTA

GAM180 GTGCAGCATTATGTATAGTA 166 CAGCATTATG 2891 - A - ---- TAAAAA AAACC AT
 AAAAGCAAACCAGGATTTTC TATAGTAAAA GTG C GCA TTA TGTATAG GC AGG T
 TTTAGCCAAACTCTGTATAA AGCA ||| ||| ||||| || |||
 CATTAGTTGCCGTCAC CAC G CGT GAT ATATGTC CG TTC /
 T C T TACA TCAAAC AT--- TT

GAM181 GTTCTTCATTATACATGGAA 167 TGGAAATTGC 2892 C TTATACAT - TT- T T AATCA
 T T
 ATTGCCCTTGACGTATTGAA CCTTGACGTA GTT TTCA GGAAATT GCCC GACG AT GAA
 TGCG CG T
 AATCATGCGTCGTTCTCGCC TTGA ||| ||| ||||| ||| ||| ||| |||
 GCAAACGCTTCCGTTCTGTCT CAA GAGT CTTTGA CGGG CTGC TG CTT ACGC
 GC C
 TCGGGCAAGTTTTCTTCCCT T TTTCCCTT A CTT T C CGCAA C T
 TTTGAGTAAC

GAM182 GTTCTTCCGATTATACTGGA 168 TATACTGGAA 2893 CG A A----- ----- ATA
 AAGGGTATTGATCAATTGGC AGGGTATTGA GTTCTTC ATTAT CTGGA AGGGT ATTG
 C A
 CAATATACTAAAGACCCTGA TCAA ||||| ||||| ||||| ||||| ||| |||
 GAGAAAATCCAGATGATAGA TAGGAAG TAGTA GACCT TCCCA TAAC G T
 AGGAT A- - AAAAGAGAG GAAATCATA CG T

GAM183 GTTGTTTCGTCGTGGCTGTAG 169 TAGTAGCTTC 2894 TT-- T - --- TT- -- A AAG
 TAGCTTCCGTCGTTTTTACA CGTCGTTTT GTTG CGTCG GGC TG TAGTAGC CCG
 TCGTTTTTACA CTG G

ACTGAAGGAGCTAGTGTGAG	ACAA							
AGTGAAACGGTGTGCTGTTA		CAGT	GCAGC	CCG	GC	ATTGTCG	GGC	
AGTGAGAGTGT GAT /								
GCCCGTGCCCCGACGTTATT		TATT	C	T	CCG	TGT	AA	- CGA
GAC								

GAM184 GTTGTGTTGTTGAGTAGTA 170	TGAGTAGTAC 2895	TG	TT-	T	TA	A	CCAA-	TTTAATT
CAATATT CG								
CTTCCAATGGTATTTAATTT	TTCCAATGGT	GT	TTG	GT	GAG	GT	CTT	TGGTA TGTC
GAA T								
GTCCAATATTGAACGTAATT	ATTT							
CTACAGGCACCCTTCTACCA		CG	AGC	CA	CTC	CG	GAA	ACCAT ACGG CTT /
GTTCCAAGAGCACCTCCACC		GT	CGC	C	CA	A	CCTTG	CTTCCC- ACAT--- AA
GCCGATGGC								

GAM185 GTTTGCGAAATACGGGCAAT 171	TGTCACATAT 2896	AAATACGG	A--	TT	T
GTTTTATTATTTATAGATAA	GGCAACTACG	GTTTGCG	GC	ATGT	TATTATT A
TGTCACATATGGCAACTACG	CAGA				
CAGAT	TAGACGC	CG	TACA	GTAATAG	T
	ATCAA---	GTA	CT	A	

GAM186 TAATGTTGTTGTGTTGTATT 172	TTGTATTTTG 2897	-	-----	TT	ATA	A	GAA	TAA	G
A									
TTGTATATAGAGAAAAGAAT	TATATAGAGA	TT	GTTGTGT	TGTATT	GT	TAG	GAAAA		
TAAAA AA GTTA T									
AAAATAAAAGGTTAATATAA	AAAG								
TGTTGTCTTTTACATTTTCC		AA	CGATATA	ATATAG	CA	ATC	CTTTT	ATTTT	TT
TAAT /									
TAAACTTGATATAATAAACT		A	TCAAATA	TT	A--	-	AC-	CTG	G A
ATATAGCAAATATTA									

GAM187 TAATTTTTGATTACTCTTTT 173	TAGCGTGTAT 2898	T	C	C	T	A	-	ATTGA
GACATGT								
CTAGCGTGTATACAACCTGCA	ACAACCTGCAG	TT	GATTACT	TTTT	TAGCG	GTATACA	CTG	CAGC
AAAGGCAT A								
GCATTGAAAAGGCATGACAT	CATT							
GTAATTTCCAATGCTTTTAG		AA	CTAATGA	AAGA	GTTGT	CGTGTGT	GGC	GTCG
TTTTCGTA /								
CTGACGGGTGTGTGCTGTTG		C	A	T	-	G	A	A---
TAGAAAAGTAATCCAAGTTT								ACCTTTA
A								

GAM188 TAGCTAACCCAAAACCTTAC 174	TTGACAGATA 2899	TA	AAAACC	----	A	GA	TG	T A
AATTTAACTGGAAATACATG	ACCCTATTGT	TAGC	ACCC	TTACAAT	TTA	CTG	AATACA	G
CTG T								
GTCTGATGTAGTTTCTGTAT	AGAT							
TGACAGATAACCCTATTGTA		GTCG	TGGG	GATGTTA	AAT	GAC	TTATGT	T GAT /
GATGCGGGTGCTG		--	CGTA--	TCCC	A	AG	CT	T G

GAM189 TATCATGACTAATATATATA 175 TCAGAAGAAT 2900 TGA TATAT - CATTTC A CAC
GGATCATTTCTCTTTAGATA CACTATTTCT TATCA CTAA ATAG GAT TCTTT GATAAT C
ATCACCTATGTTATCAGAAG TAGA |||| ||| ||| ||| |||| |||||
AATCACTATTTCTTAGATTT ATAGT GATT TATC CTA AGAAG CTATTG /
GATA TTA CTT-- A ----- A TAT

GAM190 TATGGTCAAATGTCTGATTG 176 TCAAATGTCT 2901 A---- GAT A CAAT T C
TTAATAT TA
TAATGCAATTCCTCTATCTA GATTGTAATG TATGGTC AATGTCT TGTA TG TCCTC AT TA
TGGAG C
TTAATATTGGAGTACCTCTC CAAT ||||| ||||| |||| ||| |||| ||| ||||
CATAAATCGAGGATGAACAT ATACCAG TTACAGA ACGT AC AGGAG TA AT
ACCTC /
GCAAGACATTGAAAAGACCA AAAAG --- - AAGT C A ----- TC
TA

GAM191 TATGTTTTGTGGATGAAATT 177 AGAAATGTTT 2902 T TGAA TAA GAAGATG A
TCTTATAATGATGAAGATGT CTATTAGACA TATGTTT GTGGA ATTTCTTA TGAT
TAGACGA A
AGACGAAATTTTGTCTGAGA TA ||||| ||||| ||||| ||| |||||
ATAGATCACTAAGAAATGTT ATACAGA TATCT TAAAGAAT ACTA GTCTGTT T
TCTATTAGACATA T TTG- C-- GATAAGA T

GAM192 TCATGGAATAAATGTGCAGT 178 TTGGATGAAG 2903 T ATAAA -- -- C TAC- A- --
AC
CTTTCCCATATTACGTACTC ATACTGTACA TCA GGA TGTGCAG TCTT TCC ATAT GT
CTCC GC A
CGCACATGGCTAGGAGAAAC TCCT ||||| ||||| ||||| ||| ||||| || ||||| ||
AGATATATTGGATGAAGATA AGT CCT ACATGTC AGAA AGG TATA CA GAGG CG /
CTGTACATCCTGA - ----- AT GT T TAGA AA AT GT

GAM193 TCCAAGAAGCAGAGTCGTAT 179 AAGAAGCAGA 2904 CA AGA CG G GA AA G
GACCATTGACGTCAATGCGT GTCGTATGAC TC AGAAGC GT TAT ACCATT CGTC TGC T
GGGCAGAGGCGGAGGTGGTG CATT || ||||| || ||||| ||||| ||| |||
ATAAAGCGTTTCTGAGA AG TCTTTG CG ATA TGGTGG GCGG ACG G
AG --- AA G AG AG G

GAM194 TCCTCGACTACCAGACGAGA 180 TTCACAGTAT 2905 T CT CGA T CTG CC - CC
AT TC
TATGATGCTCTGGGGCCCTG TTGTCCCTTC CGA ACCAGA GATA GATGCT GGGC TGCT
TCGT TTTT ACCG A
CTTCGTCCTTTTATACCGTC TGGT || ||||| ||||| ||||| ||||| ||||| ||||| |||||
ACTTGGTTAGAAAAACGAT GTT TGGTCT CTGT TTATGA CTTG GTGA AGCA AAAG
TGGT /
AGTGTAGTTCACAGTATTTG - C- TCC - CA- AT T AA AT TC
TCCCTTCTGGTCTTGGA

GAM195 TCTATAGTGTACCAAGGGCA 181 TAGTGTACCA 2906 T CC C T ATTTA TTATC
 ATATCTTATTTACTGTTTTA AGGGCAATAT TCTATAG GTA AAGGG AA ATCTT CTGTT A
 TCATTTTTAGCAGAAGGTTT CTTA ||||| || |||| ||||
 TTCCTTTATTACTCTATGGA AGGTATC CAT TTTCC TT TGGAA GACGA /
 T TA T T ---- TTTT

GAM196 TCTGTTGACGTTTTTCTTTA 182 TTAGAGGATC 2907 AC T-- TTA CC--- A G TTAA
 AGTTCCTTCTCAGAAAGCGA AACAACTGTA TCTGTTG GTT TTCT AGTT TTCTC GAAA
 CGATTGA A
 TTGATTAAACACTTTAGTTG GAAC ||||| || |||| |||| |||| ||||
 GTTTTAGAGGATCAACAAC AGACAAC CGA AAGA TCAA AGGAG TTTT GTTGATT
 /
 GTAGAACCCAGCACACAACAGA A- CCC TG- CAACT A G TCAC

GAM197 TCTTGGTGACGCACACATTT 183 TGACGCACAC 2908 T T A- ----- A - AC
 ATAATACCCACATTGAGGTG ATTTATAATA TCT GG GACGC CACA TTT TAATACC C A
 TTAAAGAAGCAGTTGTGCCG CCCA ||| |||| |||| ||| ||||| |
 CGTCCCTAGA AGA CC CTGCG GTGT AGA ATTGTGG G /
 T - CC TGACGA A A TT

GAM198 TGAACGATAAACTTAAATCA 184 GATAAACTTA 2909 TTAA--- AA AGC
 ATTAATCCCCTTGAGCAGC AATCAATTAA TGAACGATAAAC ATCAATTA TCCCCTTG A
 TCCAGGGGGAGTGATTGATA ATCC ||||| |||| ||||
 ACATGTGTTTATCGTTTA ATTTGCTATTTG TAGTTAGT AGGGGGAC G
 TGTACAA G- CTC

GAM199 TGACCCGAGCCTTCCGCAAG 185 TTCACCGAGT 2910 C A TT AAGA AACCTA CGCA
 ATGAACAACCTAGTCAATCG GGTGGCCGAG TGAC CG GCC CCGC TGAAC GTCAAT G
 CAGCTTCATTGACGTTTACC TTA |||| |||| |||| ||||
 GAGTGGTGGCCGAGTTA ATTG GC CGG GGTG ACTTG CAGTTA /
 A - T- AGCC ----- CTC

GAM200 TGCACCAGAAACGACTGTTG 186 CTGGAACAGG 2911 A A TGC TA TTA
 CTCCAGAAACGTACATTAAC CGTTTCTGGG TGC CCAGAAACG CTGT TCCAGAAACG CA A
 CTTTGC GTGTTTCTGGAACA CA ||| ||||| |||| ||||| ||
 GGCGTTTCTGGGCA ACG GGTCTTTGC GACA AGGTCTTTGT GT C
 - G --- GC TTC

GAM201 TGCAGCAGAACGGTCTATAT 187 TCAGTGGAGA 2912 C G AT- G A- T
 TTTTACGTGGAGTTTTAACA TTACGGATGG TGCAG AGAAC GTCT ATTTTAC TGG GT T
 GTCAGTGGAGATTACGGATG TTTT |||| |||| |||| ||||| ||| ||
 GTTTTCTGTA ATGTC TTTTG TAGG TAGAGGTG ACT CA T
 - G CAT - GA A

GAM202 TGTATAGAAATTCCTCATTT 188 TGAGAGGCGT 2913 T--- TT- A T AA A TG- CCA
GG
GTGAATGATGTTGAAGAAAT ATTTTATTCA TCC CAT GTG ATGA GTTG GAA TAA
ACGTTTTTT AGCAGG T
AATGACGTTTTTTCCAAGCA CAAT ||| ||| ||||| ||| ||| ||||| |||||
GGGGTTGCCTGCTGAGAGGC AGG GTA CAC TACT TAAC CTT ATT TGCGGAGAG
TCGTCC /
GTATTTTATTCACAATTTCA TTTT CTC C T A- - TTA --- GT
TCCACCTCATGTTTTGGAGT
ATTTTATGCA

GAM203 TGTTCTCCTCCCATACTT 189 TGACCAGCTT 2914 C C A TTTCAA-- A CGA
TTGTTCTT A
TTCAATCAAAGCCGAGTCTT AGAATTTCTC TGTT TC TCCCAT TACT TC AAGC GTC
TGGATA T
GTTCTTGGATAATTTATCC CAGT |||| | ||||| ||| || ||||| |||||
ATGACCAGCTTAGAATTTCT ACAAGAGGGTA ATGA AG TTCG CAG ACCTAT /
CCAGTACATGGGACGAAACA - C C CCTCTTTA A AC- T----- T

GAM204 TGTTGTTGTCGTATCCAGAA 190 TGTCGTATCC 2915 T T C T AA- ATCA TC
AAATTGATCACATCTTCTTG AGAAAAATTG TGT GT GT GTA CCAGA AATTG CA T
GCACAATTCACCTCTGGTTAC ATCA ||| || ||||| ||||| ||
TGCCACTACA ACA CA CG CAT GGTCT TTAAC GT T
T C T T CAC ACG- TC

GAM205 TTATTGTTAAAAAATATGAT 191 TCAAATTAAT 2916 T AAATA-- AA T ACAACCCA T-
CA
TAAATGAGTAGAAACAACC TGGAGTAACT TTAT GTTAAA TGATTAA TGAG AGAA GAA
ATG A
CAGAATATGCAAGACATTTT TTGG |||| ||||| ||||| ||||| ||| |||
TCCAGTTCTCTCAAATTAAT AATA CGGTTT GTTAATT ACTC TCTT CTT TAC /
TGGAGTAACTTTGGCCATAA C CAATGAG AA - GAC----- TT AG

GAM206 TTCCAGAAATGGCTGTCCAG 192 CTGGAACAGT 2917 - CAGATTCC A
AAATCAGATTCCAGAACGT CATTTCTGGA TTCCAGAAATGGCTGT CCAGAAAT AGA A
CTATAACCATTCTGGAACA A ||||||||||| ||||| |||
GTCATTTCTGGAA AAGGTCTTTACTGACA GGTCTTTA TCT C
A CCAATA-- G

GAM207 TTCGGTTAAGTACATAGCCA 193 TTAAGTACAT 2918 AG ----- TCGT AAC C CTT
TCGTACGAAAACAAGCCACT AGCCATCGTA TTCGGTTA TACATA GCCA ACGAA AAG CA
T
TTCTCTGTCTTCTTCGTTTC CGAA ||||||| ||||| ||| ||||| ||| |||
TGGCGTCCATGTGTATCTGG AAGTCGGT ATGTGT CGGT TGCTT TTC GT /
CTGAA CT ACCTG CTT- C-- T CTC

GAM208 TTGACGCAATTTGGAGATGT 194 TGTAAGAAGA 2919 - GA-- ---- AGT---- CT
 AAGAAGAGTTGCGGAATTCT GTTGCGGAAT TTGACGC AATTTG GATGTA AGAAG
 TGC GGAATT G
 GTATGATTCCGTATTTGTTG TCTG ||||| ||||| ||||| ||||| |||||
 TTTCTTTAATACATCATAAT AGCTGTG TTAGAT CTACAT TCTTT ATGCCTTAG T
 AGATTGGTGTCTGA G AATA AATT GTTGTTT TA

GAM209 TTGTGTGCGTAAGGTTGCAG 195 TGACTTGACT 2920 GTGC TG- AA CGACA
 AATCAGTAGCGACAAAATAT ACCTTATTCC TTGT GTAAGGT CAG TCAGTAG A
 ACTGCTGACTTGACTACCTT AACG ||| ||||| ||| |||||
 ATTCCAACGA AGCA TATTCCA GTT AGTCGTC A
 ACCT TCA C- ATATA

GAM210 TTTGGCGAAATCGCAAATGG 196 TCTCTAACAC 2921 AA GCAA A-- C AGAG GT
 ACTGATTGGGCGTAAGAGGC CAGTCCATGA TTTGGCG ATC ATGGACTG TTGGG GTA GC
 G
 GTGAAGCAGTATCTCTAACA AGAT ||||| ||| ||||| ||||| ||| ||
 CCAGTCCATGAAGATATGCC AGACCGT TAG TACCTGAC AATCT TAT CG /
 AGA A- AAG- CAC C GA-- AA

GAM211 GCAGGCAGAAGTATGCAAAG 197 AGAAGTATGC 2922 ----- A AAA A CAATTA A
 AACCA G AAA
 CATGCATCTCAATTAGTCAG AAAGCATGCA GC AGA GTATGC GCATGC TCT GTC GC
 GGT TGG G
 CAACCAGGTGTGGAAAGTCC TCTC || ||| ||||| ||||| ||| ||| |||||
 CCAGGCTCCCCAGCAGGCAG TG TCT CGTACG CGTATG AGA CGG CG TCG
 ACC /
 AAGTATGCAAAGCATGCATC ATTAAC A AAA A ----- A ACCCC G CCT
 TCAATTAGTCAGC

GAM212 GTGTTGGTAAACAGCCCCACA 198 TGTCAGCTTT 2923 TAAACA A---- T CA AGAAA
 AATGTCAACAGCAGAAACAT GCACAAGGGC GTGTTGG GCCC CAAA GT ACAGC C
 ACAAGCTGTCAGCTTTGCAC CCAA ||||| ||||| ||||| |||||
 AAGGGCCCCAACAC CACAACC CGGG GTTT CG TGTCG A
 ----- AACAC - AC AACAT

GAM213 TCTAAGGTAAATATAAAATT 199 TAAGGTAAAT 2924 A TAA TTTA-- - A T
 TTAAAGTGTATAATGTGTTA ATAAAATTTT TCTAAGGTA ATA AATT AGT GT TAA G
 AACTACTGATTCTAATTGTT TAAG ||||| ||| ||||| |||||
 TGTGTATTTTAGA AGATTTTAT TGT TTAA TCA CA ATT T
 G TTG TCTTAG T A G

GAM214 AGTATTTTGGCGGTGAATCG 200 TTTGGCGGTG 2925 TT C -- T GGCG

GAM215 TGCCCGATGACGACGGCGCG 201 TTAAAGAGAT 2926 - G - G -- G CCATTTTA
CCAACGTA

GAM216 ACTGGGTCGGGTGGTCGTGC 202 TCCCCGGGAC 2927 G G C G A C TG TAC
CCGAGGGCTCTGCTACACTT ATTATCAGGC ACTG GTC GGTGGT GT CCCG GGG TC C A
GTGGATCCCCGGGACATTAT GCAG ||||| ||||| ||||| |||||
CAGGCGCAGT TGAC CGG CTATTA CA GGGC CCC AG G /
G A - - - T GT TTC

GAM217 TACAGCTTAGCACCCTGCT 203 CAGCTTAGCA 2928 G ACC G G CGAT AC
GCCTTGGAACGATGGGACCC CCACTGCTGC TACA CTTAGC ACTGCT CCTT GAA GGG C
TGCCCTGCCTTTGGAGGGAG CTTG ||||| ||||| ||||| ||||| |||||
CGGTCTGCTAGGTGTG GTGT GGATCG TGGCGA GGAG TTT CCC C
- C-- G G CCGT GT

GAM218 ACCCTGAGCCTCTCTGAGTA 204 TCAGTCATTT 2929 TG GCCT C TAC TA GA T
CATGACTGAGTGTAGCGCAG TTTATAGCCG ACCC A CT TGAG ATGACTGAGTG GCGCAGA
GGT G
AGAGGTTGTCGCTTCTGCGT ATTG |||| | ||||| ||||| ||||| ||
GTCACTCAGTCATTTTTTAT TGGG T GA ATTT TACTGACTCAC TCGCTCT TCG T
AGCCGATTGGGGT GTAGCC T TT- TG -- C

GAM219 CACTTCTGCTTCACCATCCC 205 AACGCTGACG 2930 TT TTCACC - C - AGT
CCTGCCAGCGTTGGTCTAGT GGGGCGATTT CAC CTGC ATC CCCCTG CAGCGTTGGT CT
G
GGAAAGAACTAACGCTGACG CTTG ||| |||| ||| ||||| ||||| ||||| ||
GGGGCGATTTCTTGACGCTG GTG GACG TAG GGGGGC GTCGCAATCA GA /
TG TC TTCTT- C A A AAG

GAM220 AAGCGTTTGC GTTTGCAAAC 206 TGCAAAC TCT 2931 TTTG- TT- AT TG TTT
TCTTCGCATGTTTCTTG TGT TCGCATGTTT AAGCG CGT GCAA C CTTCGCATGTTTCT TG
G
TTGTTTCAATAGAAACATGC CTTG ||||| ||| ||||| ||||||||| ||

GAGGGCTTGCTTTACGAATT
TCGCTT

TTCGC GCA CGTT G GGAGCGTACAAAGA AC /
TTTAA TTT C - TA TTT

GAM221 ACCTGTCATGGCACAGACTA 207 TCAGAGGAGC 2932 GCACA CTA A A T AT
CTCCATCATGGGTTTCAATA CATCACATAC ACCTGTCATG GA CTCC TC TGGGT TCA A
AGGTGACACTCAGAGGAGCC ATGA ||||| || ||||| |||||
ATCACATACATGATAGGT TGGATAGTAC CT GAGG AG ACTCA AGT A
ATACA ACC - - C GG

GAM222 ACGCGGGGAGGTGTATGATA 208 TACTATGATA 2933 CGG G G GCT T C A
GGCTATTAGGACGTGGATAC CATATCTAAA ACG GGA GTGTAT ATAG AT AGGA GTGGAT C
CTGTCCGCTCTTCGTTACTA TGT ||| ||||| ||||| ||||| |||||
TGATACATATCTAAATGT TGT TCT TACATA TATC TG TTCT CGCCTG C
AAA A G AT- C - T

GAM223 ACGTTGCCGAGAGGCGGCCA 209 GTTGGCACCA 2934 AG T A AAC CCCAAA
AATCACA
ACAAATGTTGGCACCAACAA ACAAACGTTG GCCG AGGCGGCCAACAAATGT GGCACCA CA
GTTG ACCC C
ACGTTGCCCAAAACCCAATC CCCA ||||| ||||| ||||| ||||| |||||
ACACAGTCTCAAGGGTCCTC CGGT TCCGCCGGTTGTTTACA CCGTGGT GT CAAC
TGGG A
GTCAACAAATGGTGGTGCCC CT C G AAA TGCTCC AACTCTG
ACATTTGTTGGCCGCCTTCT
GGCAACGT

GAM224 AGAGTTTCGGTCCTCTTATC 210 TAAAGTAATC 2935 - C TCC- TA T TAGATG TA
TATGTTTGTTACTTTTAGAT AATAACGGTA AGA GTTT GG TCTTATC TGTT GTTACTTT CC
T
GCCTATGCTGGAAGGTAAAG AGAT ||||| ||||| ||||| ||||| |||||
TAATCAATAACGGTAAGATT TCT CAAA CC AGAATGG ATAA TAATGAAA GG G
TTCCAAAACGTCT G A TTTT CA C TGGAA- TC

GAM225 AGGCCCTAACAAATGACAAG 211 TTAGTTAAAG 2936 AAAT AA TATA T AAGC -- T TG
TCT TGATA
ATATAGATTAGTTAAAGCAG CAGAACGATT GAC GA GAT AGTTA AGA ACGA TTAT ACT
CTC T
AACGATTTATTGACTTCTCT TATT ||| || ||||| ||||| ||||| |||||
CTGATATGAGCTGAGTGTAG CTG CT CTA TTAAT TCT TGTT AGTA TGA GAG
/
TTGATGATTTGTAATCTTAA ---- AC CG-- C ---- AA T GT TGT TCGAG
TTCATCGCTCCAGTCTAGGC
CCT

GAM226 AGGTGGCATATATTAGAGGG 212 TGGCATATAT 2937 GT TATTA G C--- ATAAA
CCAAG A
ACCCGGTCGCATAAATCTTA TAGAGGGACC AG GGCATA GAGG ACC GGTCGC TCTTA
CCTTG A

CCAAGCCTTGAAGTTAAGGA CGGT || ||||| ||||| ||||| ||||| |||||
 CTAAGAATGGCGACTCACTG TC CCGTGT CTCC TGG TCAGCG AGAAT GGAAT
 G
 GTGCCTCGCTTGTGCCGTCT TG TCG-- G TCAC GTA-- CA-- T

GAM227 AGTTTGACACGCTATTTGAA 213 TTTGACACGC 2938 -- - TA ----- TAAATC
 ATAATAAATCAAAAATATTT TATTTGAAAT AGTTTG ACA CGC TT TGAAATAA A
 ATTTTCATGATCCGACCGCGA AATA ||||| ||||| || |||||
 TGTTACAAGCT TCGAAC TGT GCG AG ACTTTATT A
 AT A CC CCTAGT TATAAA

GAM228 AGTTTGTTCACCTTCTGAGAA 214 TCTACTGTCT 2939 GTTCACTTCTG A ----- CA-- ---
 CAC
 TTCTACTGTCTACATACAGA ACATACAGAA TT AGA TTCT ACTGTCTA TACAGAAG
 GGTCA C
 AGGGTCACACCCATTGGCTA GGGT || ||||| ||||| ||||| |||||
 AACTTCTGTGCGACTAGACA GA TCT AAGG TGACAGAT GTGTCTTC TCGGT
 /
 GTCCCGGGGGAAGTCTAAAA AGCCATAAAAA G GGGCCC CAGC AAA
 TAC
 ATACCGAAGACT

GAM229 CATGGTATAAGCCAAAAATC 215 TAAGCCAAAA 2940 A-- AAAATCATTACT TC GT
 CCAAT-- GTCT
 ATACTTCCTCTTCCAGGGG ATCATTACTT AGCCA TCCTCT CAGGGGCTA CTG
 TAACT G
 CTAGTCTGCCAATTAAGTGT CCTC ||||| ||||| ||||| ||||| |||||
 CTGATCAAGTTACTAGAAAT TCGGT AGGGGG GTCTCCGAT GAT ATTGA /
 AGGATAGCCTCTGTGGGGGA AAC AAACACATTTC- T- AG AAAGATC ACTA
 CTTTACACAAATGGCTCAAA
 CACCATG

GAM230 CATGTTAATCACCTATAACT 216 TAGGACAGGA 2941 ATC-- ATAA TACA A
 GTACATCTTATAATCATATA GGTATCAATG CATGTTA ACCT CTG TCTTATA T
 GGACAGGAGGTATCAATGAC ACAT ||||| ||||| ||||| |||||
 ATG GTACAGT TGGG GAC AGGATAT C
 AACTA G--- ---- A

GAM231 CCAAGTTTGGATAGGTGAAC 217 TAGGTGAACA 2942 AA -- A AACACCCACTGA C A
 ACCCACTGACAGTAAGCTTT CCCACTGACA CC GTTT GGAT GGTG CAGTAAG TTTA A
 AAACCTTAGACTTTACTGCAC GTAA || ||||| ||||| ||||| |||||
 CATCCTTAAACAGGG GG CAAA CCTA CCAC GTCATTT AGAT C
 GA TT - ----- C T

GAM232 CCCGGCCACCCCTTGGGGGT 218 TCCCCGAAAC 2943 A C G CC TC T
 ACT
 TCTGGGGACACGGTGGCTGG CCCCAAGGGG CCCCTTGGGGGT TGGGGACACGGT
 GCTGGCTGCC GACA TAG TGGCC A

CTGCCCCGACATCTAGTTGG CGGC ||||| ||||| ||||| ||| ||| |||
 CCACTAGAGGGGCTGTCTAAG GGGGAACCCCCAA GCCCCTGTGCCA CGACCGACGG
 CTGT ATC GTCGG / C A A TT GA T GAG
 TGTCTTGGCAGCCAGCAACC
 GTGTCCCCGAAACCCCAAG
 GGGCGGCCGGG
 GAM233 CCGTAAATTCATCATCGTTG 219 TAAGACAAGG 2944 AAATTCAT G A GA GTTCATTT
 TTT
 TCATTATCGGAGAGTTCATT TGTTCACG CCGT CATC TTGTC TTATCG GA GTGA C
 TGTGATTCGATCTCATTTT G ||| ||| |||| |||| || |||
 CATCATCGGCGATAAGACAA GGCA GTGG AACAG AATAGC CT TACT G
 GGTGTTTCCACGG CCTTT--- - - GG ACTACTTT CTA

 GAM234 CGCCCATACAGCACACACCC 220 CAGCACACAC 2945 C- AACACAATTAC TG -
 CTCTATAACTC TG A
 AACACAATTACAACCTGCCCG CCAACACAAT ACAGCACA ACCC AAC CC CGCCC
 CACC GC C
 CCCCTCTATAACTCCACCTG TACA ||||| ||| ||| || |||| ||| ||
 GCACATGCGGTGTAGGGCGT TGTCGTGT TGGG TTG GG GCGGG GTGG
 CG A
 GGTGGTTTCGGCCTGGGGGT CA GGTCCGGCT-- GT T AT----- -- T
 ACTGTGCTGTGGCGGTG

 GAM235 CGGCCGTTGCGTCTTTTGTA 221 TGA CTGTTGT 2946 G - TTTT - T T T
 CAGGGTTTAGATGGTGTCT ACTCGCGATG CG CCGTTGC GTC GTACAG GGTT AGA GG G
 TCTGACTGTTGTACTCGCGA GCAA || ||||| ||| ||||| ||| ||| ||
 TGGCAATGGGCG GC GGTAACG TAG CATGTT TCAG TCT TC T
 G G CGCT G - - T

 GAM236 CTCGAATCACTAGGTGTGAA 222 TGACCAGCCG 2947 G----- G CCAT--- T CC TCATT
 T
 GCCCATCACATGACCTGTGT TATTCATGCA GT TGAAGC CACA GA TGTG
 CGGCTGGTCAAAACAC T
 CATTGCGCTGGTCAAAACAC TCTT || ||||| ||| ||| ||||| |||||
 TTGGTGTGTTTGACCAGCCGT CG ACTTTG GTGT CT GTAC
 GCCGACCAGTTTTGTG /
 ATTCATGCATCTTGTGTACA ATTTAAA G ATTACAT T AC TTAT- G
 TTAGTTTCAGGCAAATTTAC
 CACGATTAAG
 GAM237 CTTGCAGGCTGAGTAAATGT 223 TGGCGGATTC 2948 AA AAA TTCTCTG TG GA AG
 ---- TG
 AAAGGCTGGCGGATTCTCTG TCTGGCTGCG TGT GGCTGGCGGA GCTGCGGC G TAT
 G CTGCTGT A
 GCTGCGGCTGGGATATAGGC GCTG ||| ||||| ||||| | ||| |||||
 TGCTGTTGATTTACAGTAGG ACG TCGGCTGCCT TGACGTCG C ATG T
 GATGACA T
 CGCATTCGTAAACTGGCTGC -- GTG TG----- GT AA CT ACGCG TT
 AGTGTTCCGTCGGCTGTGGC

ACGGCTGAGG

GAM238 CTTTACTCGTCTCTTGTTC A 224 TTGACAGTTT 2949 - TC CAA T GAA----- --- C CA
C

TCATCAAGGTGAAGAATGTT TGTGAATTCT CTTGT ATCAT GG GAA TGTTAAGGA CA
TAC CTCAA T

AAGGACACTACCACTCAACT CCGC |||| |||| || ||| ||||| || ||| ||||
TTTTGAGCTGTGCTGCACTT GGATA TGGTG CC CTT ACAGTTCTT GT GTG
GAGTT T

CTTGACAGTTTTGTGAATTC C -- CG- T AAGTGTTTTG CAC C TC T

TCCGCGTGGTATAGGCAGAT

GAGTGAGAAAAG

GAM239 GACGGACGATACAGGCGCTT 225 TGGCTCAACC 2950 GACGAT CGC CA AT T CA

GGGCCCAAGAATTGTCCACA TGTCATACAC GACG ACAGG TTGGGCC AGA TG CCA T

TTTTTGGCATCTATGGCTCA GTT ||| |||| ||||| || |||

ACCTGTCATACACGTT TTGC TGTCC AACTCGG TCT AC GGT T

ACATAC --- TA -- - TT

GAM240 GATGCGTGATTTCTTGATG 226 TGCCTGATTT 2951 TTTCCTT TG AACTTTT---- ACA

TTGACAACCTTTTGTTC AAC CCTTGATGTT GATGCGTGA GATGT AC GTTCCA G

AGTATATGGAACCCTGTAAA GACA ||||| ||| || ||||

TTAGTTGATATCTTTTACGC TTACGCATT CTATA TG CAAGGT T

ATT TT----- GT ATTAAATGTCC ATA

GAM241 GCAGGTGAGTTGTGGCAGAG 227 TGTGGCAGAG 2952 GAGTT- GG ACTT TA

GGGACTTTAGTTTACATAAC GGGACTTTAG GCAGGT GT CAGAGGGG TAGTT C

TGCTCCTCTGAAGCTCCGGA TTTA |||| || ||||| ||||

GCCTGC CGTCCG CG GTCTCCTC GTCAA /

AGGCCT AA ---- TA

GAM242 GCTCTTTTTGTGCACTCGGT 228 TGAGGTTTGG 2953 TTTTGT A G A TT AA G CA
TGGAT

GAGGTTTGGTGAAGGTCTGG TGAAGGTCTG GCTCT GC CTC GTG GGT GGTG

GGTCTGGAGGG GC TGTT C

AGGGGGCCATGTTTGGATCT GAGG |||| || ||||| ||| ||||| || |||

TAATTAACGCTGTGCCTTCC CGAGG CG GAG TAC CCA CCGC CTAGACCTTCC TG

GCAA T

AGATCCGCCACCCATGGAGG CCT--- - G - - - G TC TTAAT

CTCCGGAGC

GAM243 GCTTTTAAGTTTCAGTGACT 229 AGAGGTGGCT 2954 -- TC -- ----- CTG TTTA AT
T

TTGGAGAGGTGGCTGATTTT GATTTTATTG GTT AGTG ACTTTGG AGAGGTGG AT

TTGGT TTG A

ATTGGTATTTGTAACCAACC GTAT ||| ||| ||||| ||||| || ||| |||

ACCAACATATACCACCTTTA CAG TCAC TGAAGCT TTTCCACC TA AACCA

AAC A

AGATATTTATCGAAGTAACA AG GT AA ATTTATAGAA ATA C--- CC C

CTTGGACGACGCAGAGC

GAM244 GGCACATTTCCATGGTATCC 230 GGGAAAGTAA 2955 C TATCCTTA-- GCTT A
TTATTGAGCTTTTTTCTTGT TCAAGATCCC GGCACATTTC ATGG TTGA TTTTCTTGT A
AAACGCGGGAAAGTAATCAA TAGT ||||| ||| |||||
GATCCCTAGTCCATTGAGAT CCGTGTAGAG TACC AACT GAAAGGGCG A
GTGCC T TGATCCCTAG AAT- C

GAM245 GGCGTCCGAGGTAGGAGATT 231 CGAGGTAGGA 2956 T G ----- GA GAT A CA
GATCCAAAGTGCAAATTCAC GATTGATCCA GGCG CC AGG TAG GATT CC AAGTG A
TTCGGTAAAGTCCACTGTGT AAGT |||| ||| ||| |||||
TTGGTTCCTGGGCGGCC CCGC GG TCC GTC CTGA GG TTCAC A
C G TTGGTTTGT AC AAT C TT

GAM246 GGCTTTGTGCCACGTAGAAA 232 TGGCGCGGTA 2957 -- ACGTA CAG --- TG CG
CTTAGT AG
GAGCAGGGCTTCTTGGCGCG GCCTTAGTGG TTTGT GCC GAAAGAG GGCT TCT GCG
GTAGC GGG A
GTAGCCTTAGTGGGAGAATC GAGA |||| ||| ||||| ||| ||| ||||| |||
TCGCTGCATCGCTGGGACTT AAACA CGG TTTTCTC CTGG AGG CGC CGTCG
CTC /
GGTCACTCTTTTGGTCGGCA GA CTGG- A-- TTC GT TA ----- TA
GACAAAGCC

GAM247 GGGCCTCAAACGGAAACCCT 233 TGGCAAAGTT 2958 CTCAAAC CC T T CC CA
TGTTCAAGGCTTCCGCCTGTT TTCACCCCGC GGGC GGAAAC TTGT CAGGCT CCG TGTT T
CATCTCAACAATTGGAGCCT CC |||| ||||| ||| ||||| ||| |||
GGCAAAGTTTTACCCCGCC CCGG CTTTGT AACG GTCCGA GGT ACAA C
C CCCCA-- A- - - TA CT

GAM248 GGGTCGAAGAATGGTTGTTT 234 TGGAATGGCT 2959 --- - G TTA- -- -
ATCTCCT
GGCAGCCTTATATTTGAGC GTAGAGCACA GGGTCGA AGAATGGT TGTTT GCAGCC TATT
TCGA GC T
ATCTCCTTTTTCTCGCGTT TCAT ||||| ||||| ||||| ||||| ||| |||||
GACCAATGGAATGGCTGTAG CCCAGTT TCTTACTA ACGAG TGTCGG GTAA AGTT
CG /
AGCACATCATTCTCCTTTGA TCC C A TAAG CC G CTCTTTT
CCC

GAM249 GGGTTCCTCATTTCTAGCTA 235 TAGACTATTA 2960 T T T- AG TTTG - AT- TG GCA
T
GTATTTTTTGATAGACTATT GGTGGGGCAT CC CAT TC AGCT TATTT ATAGA CT TAGG GG
TCTGCGTGC T
AGGTGGGGCATCTGCGTGCT CTGC ||||| ||| ||||| ||||| ||| ||| |||||
TTTGTATGCAGAAATTTGTC GG GTA AG TTGA GTAAG TGTCT GA GTCT TT
AGACGTATG T

TGCTGAGTTCTGTAGTGAAT - T TC CA TGA- T GTC GT AA- T
 GACAGTTCTGATATGGGAAC
 CC
 GAM250 GGTCCCACCCTACAGGTAA 236 CCTACAGGTT 2961 C C TAAT- TCCT-- AA
 TCCTCCTGGTTCAATCTGGG AATCCTCCTG GGTC CA CCTACAGGT CC GGTC T
 CTCCTATTGGTTAATACCTG GTTC ||||| ||||| || |||||
 TAGGTTGTGACC CCAG GT GGATGTCCA GG TCGGG /
 T T TAATT TTATCC TC

 GAM251 GGTGGCTGAACTTTAAAAGC 237 TGCCTTGGTG 2962 A- - - T- -
 ATGATCAGAACACAT GA
 GTATGGGGGTGGGGGCGATG GAGTTCAACT TTTA AAG CGTATGG GGG GGG GGCG
 AATCTACTCT T
 ATCAGAACACATAATCTACT ACT ||||| ||||| ||||| ||||| ||||| |||||
 CTGATTCTGGGGTGGATTCA AGGT TTC GTATATT CCT CCT CCGC
 TTAGGTGGGG T
 ACTAGCGCCATCCTTTCCAT GG C A TT A GATCAAC----- TC
 TATATGCCTTGGTGGAGTTC
 AACTACT
 GAM252 GGTTTGGGTAAGGTTTTGCG 238 TAAGGTTTTG 2963 - ----- T GA GAAC- GT AC
 T
 AGTTGAACTCTGTCGACGGA CGAGTTGAAC GGTTT GGGTA AGGTTT GC GTT TCT
 CG GGAT A
 TTATTATCCCGGTAGGACAA TCTG ||||| ||||| ||||| ||||| ||||| |||||
 AGACGGCCAAATCTCAATCA CCAA CCCGT TCTAAA CG CAG GGA GC CCTA
 T
 TATTTCTGCCCTAAACC T CTTTATACTAAC C G- AAACA TG -- T

 GAM253 GTGATGGTAGCCGATGTGGT 239 TAGCCGATGT 2964 - TG CTT C - TTAA
 GCTTGCCGCCATTAAC TTAT GGTGCTTGCC GTGATGGTA GCCGA TGGTG GC GC CA C
 TTGTGCTGCTTCCATTAATT GCCA ||||| ||||| ||||| ||||| |||||
 TGGTATATCATCAC CACTACTAT TGGTT ATTAC CG CG GT T
 A TA CTT T T TTAT

 GAM254 GTGGCTCCAATTATTCCGGT 240 TGTGATGTAG 2965 TC T- - A- T TTAT-
 GTG
 GAACATCACATTGCAGATTA CACGTGGCTA GTGGC CAATTAT CCG GTG ACATCACAT
 GCAGA GCGCATGCGC G
 TGCGCATGCGCGTGGAAGG TAAT ||||| ||||| ||||| ||||| ||||| |||||
 CGCGTGTGCCAAATTTTGTA CATCG GTTAATA GGT CAC TGTAGTGTA TGTTT
 CGTGTGCGCG A
 TGTGATGTAGCACGTGGCTA TT TC G GA - TAAAC GAA
 TAATTGTTGCTAC

 GAM255 TAATTGCATGTCTCATGGCT 241 TATTGCATAT 2966 T C GCT T C TTT TTA
 TGTCAATAAACACTTTAAGC AGATTGTAGT TAATTGCA GTCT ATG TG CAATAAA AC AAGCAT
 T

ATTTATGGTGTGTTTTCTGT TA ||||| ||| || || ||||| || |||||
 TTTATTGCATATAGATTGTA ATTGATGT TAGA TAT AC GTTATTT TG TTTGTG /
 GTTA - - --- - - TCT TGG

GAM256 TAGAGGATGTAGTAGAAGGT 242 TGTAGTAGAA 2967 T G GG GATA A- GACA
 GATACTACACAGACATAAAC GGTGATACTA TAGAGGA GTA TAGAA T CTAC CA T
 ATGGCGTAGAGGTTTTCTGG CACA ||||| ||| |||| | ||| ||
 TACTCCTTTA ATTCCT CAT GTCTT G GATG GT A
 - G TT GA-- CG ACAA

GAM257 TATTTCCCATTTGGTTGCCTC 243 ATTGGTTGCC 2968 - G CTCTAGTTCATA TC A
 ATCA
 TAGTTCATAGGAAATGTCTT TCTAGTTCAT TATTTCC CATT GTTGC GGAAATG
 TTCGAGAA CTTA C
 CGAGAAACTTAATCACTGCC AGGA ||||| ||| |||| ||||| ||||| |||||
 TGAGTTCTTGGAACCGTTTC ATAAGGG GTGA TAATG TCTTTGC AGGTTCTT
 GAGT /
 TGTAATGAGTGAGGGAATA A G ----- CA - CCGT

GAM258 TCATTCAGCCATGTGCTTAT 244 TGAAATGTTT 2969 T AT--- T TAT----- GC AAA
 CACTACAC
 CGGTTGGCTATTATTGCCAG GATCTGATGC G GCTT CGGT GGC TATT CAGAGAAC
 GTC C
 AGAACAAAGTCCACTACACC CTGC | ||| ||| ||| ||| ||||| |||
 TATACCCAAGACGTTCTCTG T TGAG GCCG CCG GTAA GTCTCTTG CAG T
 AAATGTTTGATCTGATGCCT T GTCCC T TAGTCTAGTTT A- --- AACCCATA
 GCCGCCCTGGAGTTTATAAT
 GAATGA

GAM259 TGCAGCTGAAATTGAGAATG 245 AAGCTCCGCC 2970 GAAATTGAGAAT AG AC
 GGCGGAGCTAGAGACCTGCT CTGTGGGTTG TGCAGCT GGGCGGAGCT AG C
 GAAGCTCCGCCCTGTGGGTT TA ||||| ||||| |||
 GTA ATGTTGG CCCGCCTCGA TC /
 GTGT----- AG GT

GAM260 TGCTGGAATTGATATCTTA 246 TATCTTATGA 2971 ----- A T CC AG C GG-- TT
 CATG
 TGATCTGACCAACAGAAGGA TCTGACCAAC ATCTTATG TC GA AACAGA GACA GG
 GGAG CTTGA T
 CACGGGGGGAGTTCTTGACA AGAA ||||| ||| |||| ||| ||| ||| |||||
 TGTAGCATCGAGTTCCAGAA TAGAGTAC AG TT TTGTTT TTGT TC CCTT GAGCT
 /
 CTTGTTTGTGTTGTTATTTTG GATATGTT - T TA GT - AAGA -- ACGA
 ACATGAGATTTGTATAGTTC
 ATATTTCCACA

GAM261 TGTAACATGTGCCAGAACCT 247 TGGGATGGGG 2972 A CAGAA G - TTTCA G - T
 AGCTCTATTTAGGGTGCCA CCTCTCTTAG TGTAAC TGTGC CCTA CT CTA GGGT CCA
 CCCATG G

CCCATGTGGCATGGGATGGG TAGG ||||| |||| |||| |||| ||||
 GCCTCTCTTAGTAGGTGGGA ACATTG ACGCG GGGT GA GAT TCCG GGT GGGTAC
 /
 TGCGCAGTTACA - TA--- G T TCTC- G A G

GAM262 TGTTCCCAAGATACGTTTGG 248 ACACCCGATA 2973 C TTGG ACC CTA G GTCT
 GGC-- TTC
 CGACCGTGTCTAATTTGTAG TCGGTATTTT CCAAGATACGT CG GTGT ATTT TA GACA
 TTAGTTT T
 TCTGACAGGCTTAGTTTTTC GGTG ||||| || |||| |||| ||||
 TTTACAAACTGAATACATGT GGTTTTATGCG GC CACA TAAG GT CTGT
 AGTCAAA T
 CTATGGGAATAACACCCGAT - TATA C-- A-- G AT-- ACATA CAT
 ATGCGTATTTTGGTGCA

GAM263 TGTTGTGTGGGATAAGCCCA 249 TTAAAGACAG 2974 G ATA C----- AT TC C CC
 AT- AA
 GGAATAGTTGTCTGGTTGCT CCATAACTTA TGTGGG AG CCAGGA AGTTG TGGTTG
 TCTT AGAG AC A
 CTTCCAGAGATACAAACACG TCCT ||||| || ||||| ||||| ||||| ||||| ||
 TCCACTTTTAAAGACAGCCA ACACCC TC GGTCCT TCAAT ACCGAC AGAA TTTC
 TG C
 TAACCTATCCTGGCCGATAT - GAA TATAGCC AT -- - AT ACC CA
 CTAAGCCCACAAACA

GAM264 TTATGTTTGTGATGATCACA 250 TTCCCTGCTA 2975 --- ATCA GAA---- CAT -
 TCTATG
 GGGAGGAATTTGACATGCAA CATCACCCCTG TTATGTTT GTGATG CAGGGAG TTTGA
 GCAAG AC G
 GACTCTATGGTGGCTTGTCC GACA ||||| ||||| ||||| ||||| ||||| ||
 TTGTTTCAGACTGCGTATTC AATACAGG CACTAC GTCCCTT AGACT TGTTTC TG
 /
 CCTGCTACATCACCCCTGGAC TCC ATC- ATGCGTC T-- C TTCGGT
 ATAA

GAM265 TTTTGCTACCATATCTATGT 251 TACCATATCT 2976 TA TAG TTAACCACTGTG TTTTCC -
 ----- - G
 AGAAGTTTTAACCACTGTGA ATGTAGAAGT TG AAGTT ATGCG GAAGGC AGGA
 TTG C
 TGCGTTTTCCGAAGGCAGGA TTTA || |||| |||| |||| ||||
 TTGGCGACAGCTCCTCCGTC AC TTCAA TACGC TTTCCG TCCT GAC G
 GCAGCCTTTCCACCGCATAA -- TTA ----- CACC-- ACGCTGCC C A
 CTTATTCATATGTGTGCCA
 AAA

GAM266 AAAGAACGTTTGGCAACGTG 252 TGCCATGAAG 2977 G TT AA AG---- CGG
 GTACAAGTGCGGCAATACAA TTTACGTTGT AAA AACGT GGC CGTGGTACA TG C
 AAGGAGTGTGCCATGAAGTT TT ||||| ||||| ||||| ||||| ||
 TACGTTGTTT TTT TTGCA TTG GTACCGTGT AC A
 G T- AA GAGGAAA ATA

GAM267 ACGTGCCAGTGGGTTGCGCG 253 TTCGTTGTGT 2978 A GG C - CGC ACAT
CCACACGGACGCGTCGCCGA GTGCGACGAC ACGTGCC GT GTTGCGCGC ACA CGGA
GTCGCCG T
CATTAACAGCGGCGACATTC GGGT ||||| || ||||| || |||| |||||
GTTGTGTGTGCGACGACGGG TGCATGG CA CAGCGTGTG TGT GCTT CAGCGGC A
TACGT G G- - T A-- GACA

GAM268 ATCGCCGTTGTACGACAATT 254 TTCATCAAAC 2979 - G - AA T TC GT CA ATC
TGATTGGGTCGTTGGTGGCA CGTTCGTGAA ATCGC CGTT TACGA C TTTGAT GGG GTTG GG
TGTA T
TGTAATCTAAAATACACACC ACGC |||| |||| |||| | |||| || |||| || ||||
GTCAACTTCATCAAACCGTT TAGCG GCAA GTGCT G AACTA CTT CAAC CC ACAT A
CGTGAACGCGCGAT C A T CC - -- TG AC AAA

GAM269 ATTTGATTCAAAAACGTGTT 255 TCAAATAAGC 2980 TTCAAAA T GG T T - ---
GTTTG ATC
GGTTGTCAAATAAGCGTAGA GTAGACTAGT TTTGA ACG GTT TTG CAAA AAGCGT AGA
CTA CGGC C
CTAGTTTGCGGCATCCCAA TTGC |||| |||| |||| |||| |||| |||| |||| ||||
GCCGGTCCATAGATATCTAG AACT TGT CAA AAC GTTT TTTGCG TCT GAT
GCCG C
CGTTTTTTTGCAAAAACCTTG TTTATAA T A- - T A ATA ACCTG AAA
TAATATTTTCAAAT

GAM270 CAACTCGTTTTGTCTCCGCT 256 TTGAATGGAC 2981 - CTCCGC- C TTCTA - T T
C-- CA
TCATTCGACAATTCTACGGC AATTTTGCTA T GT TTCATTCGA AA CGGCG GTG GCGTGT
ATATGC GT C
GGTGTGCGTGTTATATGCCG GAAC || ||||| || |||| ||||| |||| ||||
TCACTGTGCTAAGCGTGTTG A CG AGGTAAGTT TT GTTGC CAC TGCACG
TGTGCG CG T
CACGTCACGCGTTGGCTCTT T TTTTAAC T TCTCG G - T AAT TG
TTTTGAATGGACAATTTTGC
TAGAACGTTG

GAM271 CAGCTTGAAGATTTTGAATA 257 TGTCTCGACT 2982 ATT ATATTT TA- TC T TT--
AAC G
TTTATAGTGCTAGCATCCAT GCTTTAAGAT TTGAAG TTGA ATAGTGC GCA CA GTTATT
CGCGT TG T
GTTATTTTGCGTAACTGGT G |||| |||| |||| || |||| |||| |||| ||||
CCCAATGCGTTTTGATAGCT AATTTC AGCT TGTACAG TGT GT CGATAG GCGTA
AC C
TGAGTGTGCGCGCACTGTCTC GTC C---- CGC GA T TTTT --- C
GACTGCTTTAAGATG

GAM272 CGCAATTGCAGCGTGAATTT 258 AATTGCAGCG 2983 TG- AATT - TA
GCTCAGCTTTATTTACCGTG TGAATTTGCT CGCAAT CAGCGTG TGCTCAGCT TTATT C

GTGGCAGCTGGGCGTCGTGC CAGC ||||| ||||| ||||| |||||
 GTTGGATGTTGTG GTGTTG GTTGC GTGCGT GCGGGTCTGA GGTGG C
 TAG GCT- C TG

GAM273 CGCAATTCAGGCGGTAAAC 259 GGTAACGCT 2984 C----- ---- ----- AT C TG
 CAA A
 GCTTCATTGTGCTTTGCAAC TCATTGTGCT TT AGGCG GTAAACGCT TC TGTG TT
 CAA CTG C
 AACTGACATTAGCTTGTGAA TTGC || ||||| ||||| || ||||| || |||||
 CATACAGATTTATATAGCGT AG TCTGC CATTTGCGA AG ATAC AA GTT GAT
 A
 TTACAGTTCGTCTCTCATTT TTTTACTC TTGA TATATTT AC - GT C-- T
 TGAATTGCG

GAM274 CGCAGACTTTGATTTGAAAC 260 TGAAATTGGC 2985 --- A- GA TTCCA CCT
 GGACATTCCATCGTAAGCCT GTTGACAAAT CGCAGACTT TGATTTG AACG CA TCGTAAG
 T
 TATACTTATGAAATTGGCGT TATT ||||| ||||| ||||| || |||||
 TGACAAATTATTTAAGTTTG GTGTTTGAA ATTAAC TTGC GT AGTATTC /
 TG TTT AG G- TAA-- ATA

GAM275 CGGTGCCGTCGGGAATTGCT 261 AAGAATGTTT 2986 GAATT TAA ATTA T A
 GATGAACCAATT A AA
 TTAAGTATTAACGACGCTGA AGGCGACGCG G GCTT GT ACGACGC G CGCC ATAT
 CTTTGA A
 CGCCGATGAACCAATTATAT TCGT | |||| || ||||| ||||| ||||| |||||
 ACTTTGAAAATATTAAGAA C CGAA CA TGCTGCG C GCGG TGTA GAAATT /
 TGTTTAGGCGACGCGTCGTG ATT-- --- GTG- - A ATT----- A AT
 TGACAAGCTTACCTACTTTG
 CCG

GAM276 CGTCATGCCACATCGTGTTT 262 TAAACACGT 2987 G T T
 TACATTTTTTTGTTGAAAATG GTGGGATGAT CGTCAT CCACA CGTGTTTTACATTTTT G
 TAAACACGTGTGGGATGAT G ||||| ||||| ||||| ||||| ||||| |||||
 G GTAGTA GGTGT GCACAAAATGTAAAAG T
 G - T

GAM277 CGTGATTCATTAAACGGGCC 263 TGTTGTACAA 2988 T--- AAC -- C T AC
 ACTTTTTGCAATGGCACGCC ATTGCTGCTC CGTGAT CATTA GGGC CA TTT TGCAATGGC
 G
 GCTGTTGTACAAATTGCTGC AAAT ||||| ||||| ||||| ||||| ||||| |||||
 TCAAATAATGCCTTATCATG GTACTA GTAAT CTCG GT AAA ATGTTGTGCG /
 TTCC AAA TC T C CC

GAM278 CGTGCACGCACATATGCTTG 264 TCACTGGCAA 2989 --- - G GATT AATTAAAGA
 ATA AAATT
 AAGATGATTCCGGTGAAATT ATGTTGGAAG CACAT ATGCTT GAA AT CCGGTGA TTAT
 AGAGC T

AAAGATTATATAAGAGCAAA CGTA |||| ||||| ||| ||||| ||| |||||
TTTAAGCCGCTTTACAGTAA GTGTG TGC GAA CTT TA GTGCACT AATG TTTCG
/
TCACTGGCAAATGTTCTGAAG GAA G G AAC- ----- ACA CCGAA
CGTAAGGTGTGCCATCACG

GAM279 CGTGTGGGTAGATTTGAGGT 265 ACCAGCAGAT 2990 -- A- GAATATG
TGGAATATGACAAACAGCAA TAATGCCAAC CGTGTGGTA GATTG GTTG A
CCAGCAGATTAATGCCAACA ACG ||||| ||| |||||
CG GCACAACCGT TTAGAC CCAAC /
AA GA GACAAAC

GAM280 CGTTGTCGGAGCCGAGCACT 266 TGTCGGAGCC 2991 G GC A-- A A-- GGA
AGCGGGACAAAACGTAAAGG GAGCACTAGC CGTTGTC GA CG GC CT GCG C
CGCACCCGATTCCGACAATG GGGA ||||| || || || || ||
GTAACAG CT GC CG GG TGC A
G TA CCA C AAA AAA

GAM281 CTGCACAAACGTATACGGCG 267 TCAATGCTCT 2992 C T- GATTCCA TGCTCTC TT
CACA - G
TTGTGATTTCCATGTCAATG CTTAGTTTAA TA GGCG TGT TGTCAA TTAG TAA TAAT
ACAAAT G
CTCTCTTAGTTTAACACATA CACA || ||| || |||| ||| ||| |||||
ATACAAATGGCCATTTGTAA GT TCGC GCA ATAGTT AATC GTT ATTA TGTTTA
C
TTAGTTTTTGTCTAAATTT T TT ----- TTTA-- TT TTTG A C
TTTGATAACGTTGCTTTGT
AATAAATGCAG

GAM282 GAAGCATTCGAATTCAGTTA 268 TGGCAAAGTG 2993 - AA- G A CGCTAAC AA
TGCCGGCGCTAACGAAATTA AAACCCGACG GAAGCAT TCG TTCA TT TGCCGG GA T
ATCTAAACACTGGCAAAGTG TGTT ||||| || ||| ||||| ||
AAACCCGACGTGTTTC CTTTGTG AGC AAGT AA ACGGTC CT T
C CCA G - ACAAAT- AA

GAM283 GAAGCTATCCTCAACGAATC 269 TTCATCGTGT 2994 CT T AA AAGTTT CA T C
-T
GAGTCCAAGTTTCACGCAGA CGGGCTTGAC GAAG ATCC CAACG TCGAGTCC CACG
GAAACTC TTG CG C C
AACTCTTTGCCGCTCCAGTT GTTG ||| ||| |||| ||||| ||| ||||| ||| |||
GACAATGAGTTTCATCGTGT TTTC TAGG GTTGC AGTTCGGG GTGC CTTTGAG AAC
GT G C
CGGGCTTGACGTTGCGGATT TT C -- CT---- TA T A T A
TCTT

GAM284 GATAAACTTGTGCTGTTCA 270 TGTCACGCAC 2995 AAC T C TTCA- T- TT A- T
CGTTCAATGTTTTAATATGC ATCATCGCAG GATA TTG CG TG CGT CAATGTT AAT TGC T
TTAGCACAGTTTAAATGTT TCGT ||| ||| ||| ||| ||||| ||| |||

GTCACGCACATCATCGCAGT
CGTATC

CTAT GAC GC AC GCA GTTGTAA TTG ACG T
GCT - T TACAC CT TT AC A

GAM285 GATCCCAACGCGTTTGTATT 271 AACGCGTTTG 2996 CCA GTAT CG GACAAAAG
CA T
GACGGGTGACAAAAGCGAGG TATTGACGGG GATC ACGCGTTT TGA GGT
CGAGGTTAAAATG TTG C
TTAAAATGCATTGTCCGCAA TGAC |||| ||||| ||| ||| ||||| |||
CATTTTAACTTTGATTATAA CTAG TCGGTAAA ATT CCA GTTTC AATTTTAC AAC
C
CCAATTA AAAATGCGTGCCGA CCG ---- AA ATATTA-- -- G
TC

GAM286 GATGTCGACACATTTGATAC 272 TCGACACATT 2997 C A ATA T AAT
AATTTTGTG AATATCACTA TGATACAATT GATGT GACAC TTTG CAATTT GTTG A
ACAAGTTGCCAGAAGTGTTA TTGT |||| ||||| ||| ||||| |||
CATC CTACA TTGTG AGAC GTTGAA CAAT T
- A C-- - CAC

GAM287 GATTGTGAACGCGTAAAATC 273 TAAGCTAATC 2998 AAAATCAAC AGC TTTA C T
CATA T C T
AACTTTTAGTAAGCGTTTTA ATATAAATTA T TTTTAGTA GT ACA TAAGC AAT TAAA
TAAA CGG T
ACACTAAGCTAATCATATAA AACC | ||||| || ||| ||||| ||| ||||| |||
ATTAAACCGGTTTGCTGCTT G AAAATTAT CA TGT GTTCG TTG ATTT ATTT
GTC T
TATTTTACAGTTGCTTGTTG CATACA--- AA- ---- T - AC-- T C G
TACAATATTA AAAACATACG
CGCGTTGATC

GAM288 GCCAATTGTGTAAAGTTGTC 274 AAAGTTGTCC 2999 - G TC ACCA T C
CTGACCATGCTCACCTTGGT TGACCATGCT GCC AATT TGTAAGTTG CTG TGC CAC T
GGCAAACGTA GTTGACTTTA CACC ||| |||| ||||| ||| ||| |||
CAAGTTCGGC CGG TTGA ACATTT CAGT GAT ACG GTG T
C - T- GCAA - G

GAM289 GCGACACACAGGTGTTGTTC 275 GCTACATTTG 3000 - A - GTTCTATTAC TTGT
AC A
TATTACAAATGCTACATTTG TACATTGACT GCGA CAC CAG GTGTT AAATGCTACAT
ACATTG TT T
TACATTGACTTATCAAAAAT TATC |||| ||| ||||| ||||| ||| ||| |||
AATGTTTCGTGTAGCATTTAA CGTT GTG GTC CACAA TTTACGATGTG TGTAAT AA
C
AACACACTGCGTGATTGC A C A AA----- CT-- AA A

GAM290 GCTGTAGTAGTGATAGTAGC 276 TG TAGTAGTG 3001 AG- G ATA A TTACTAAT T
TTACTAATTATTTTATTC ATAGTAGCTT GCTGT TA TG GT GCT TA T

AATCTAGCAGCAACGGTAAC TACT |||| || || || ||
AACAGC CGACA AT GC CG CGA AT T
ACA G AA- A TCTAACTT T

GAM291 GGCAGTGGTAAGCTTGTAGT 277 TTACAGGCCT 3002 A TT-- GTTA----- G ACAG
AC
TACTGTAGCAGAGCACAGGT TTATATACCC GGC CTGGTAAGC GTA CTGTAGCAGA C
GTAAG T
AAGACTGATTTACAAGTTTG ATGT ||| ||||| ||| ||||| | ||||
TTACAGGCCTTTATATACCC TCG GACTATTTG CAT GACATTGTTT G CATT /
ATGTTTATCAGCGCT C TACC ATATTTCG - AA-- AG

GAM292 GTATTTATTAACGAGGCTTA 278 AAAAAGCTTT 3003 AT C-- ATTTAAAAG CGA
TTTAAAAGGAGCGCGAACA TATTTAGTGA GT TTATTA GAGGCTT GAGCG A
CGCTCAAAAAGCTTTTATTT TAAC || ||||| ||||| ||||
AGTGATAAC CA AGTGATT TTTCGAA CTCGC /
AT TAT AAA----- AAC

GAM293 GTGTGCTTCTCAACAAGAAC 279 CATGACAAAG 3004 CTTCT AA- TGA AG GTGA-
G AA GC
ATGACAAAGAGCGCGTTTGT AGCGCGTTTG GTGTG CAACAAG CA CAA AGCGCGTTT
AC CGT TG A
GAACGCGTAATGGCACACAA TGAA |||| ||||| || ||| ||||| || ||| ||
CGGTGGAGAGGATGCGCTAT CACAC GTTGTTT GT GTT TCGCGTAGG TG GCA
AC /
TGAATTGGAAGTTGTTGTCC CGCCT AAG TAA A- AGAGG - -- AC
GCCACAC

GAM294 GTTGACATGAATGTAACTT 280 TGTAACTTT 3005 AT - T--- AATT T C ACTCT
TTACGAATTGCTGTACCCGT TACGAATTGC GTTGAC GAATGT TAACTT TACG GCTG AC
CGTTG C
TGACTCTCTACAACGACGAG TGTA |||| ||||| |||| ||| ||||| ||||
TCTAGCCGTATCATAAGTTA CGGCTG TTTATA ATTGAA ATGC CGAT TG GCAGC /
CATATTTGCGTCGCGC CG C TACT --- C A AACAT

GAM295 GTTTTTAAAATTTCCAACAG 281 TCACCACTCT 3006 ATTC GTTT CT TT CCAT
TTT GT
GTTTTGTAAGTCATTAGCCA TGTTTACATT GTTTTTAAA CAACAG TGTA CA AG GTGAT
GAT A
TGTGATTTTGATGTATAAAT GTTG ||||| |||| |||| || || |||| ||
TTATCACCCTCTTGTTTAC CAAAAATTT GTTGTT ACATT GT TC CACTA TTA T
ATTGTTGTTTAAAAAC ---- ---- T- TC AC-- T-- AA

GAM296 TATCTCATCATGAGCAAACC 282 ATAACATTTA 3007 CT TCAT CT AACAA TTT
TTAAATAAAAAACAAATTTTT TTTGCGTTTG TAT CA GAGCAAAC TAAATAAA ATTT C

TCATATAAATAACATTTATT	TTTT	
TGCGTTTGTTCCTTTGTTG		ATG GT TTTGTTTG GTTTATTT TAAA A
TA	TT TTCT	C- ACAA- TAT

GAM297	TATTTGTAAAGCGAGTTCGC 283	TTCAGAGCAC 3008	TTC G - ACA- G CCGA A - C
T GC			
GAAGCACATGAGTCACCGAG	ATGAGTCACC	AGCGAG GC AA GC	TGA TCA GC TTGG CCT
GCTTT CAAGTA A			
CATTGGCCTCGCTTTTCAAG	GAGC		
TAGCATTATATTTGTAAAGC		TCGCTC CG TT CG	ACT AGT CG GACT GGA CGAAA
GTTTAT T			
AGGTTTCAGAGCACATGAGTC		--- G A AGCC G ACA- A T - T	AT
ACCGAGCATTGGCCTCGCTT			
TTCAAGTA			

GAM298	TGACATTTTAAAAAGCAAAT 284	AAAAGCAAAT 3009	TT -- A -- AAAA - CG-- GA
CGCAAAAAGCGTTTGACGTT	CGCAAAAAGC	TGACAT TAA AAAGCA ATC GCA	GC GTTTGA
TTGCTGTT A			
GCTGTTGAAACTGACGGCAA	GTTT		
AGATTTAAATAGCATGCAGG		GCTGTA ATT TTTCGT TAG CGT	CG TAAATT
AACGGCAG A			
ATGTGCTTTCGTTACTATGT		TC GC G GA A--- A	TAGA TC
CG			

GAM299	TGATCGCCAATTAATGACTT 285	CATCACAGCC 3010	A TAA A T - C CGCA T GTT
GTGTGCAAGCGCACCCATGC	GATATTGGCG	TG TCGCCAAT TG CT GTG TG AAG	CCCA
GCGC T			
GCGTTTAACGGCGCTGGGCA	ACA		
TACTTACATCACAGCCGATA		AC AGCGGTTA GC GA CAC AC TTC	GGGT CGCG A
TTGGCGACA	-	TA- C - T A ATAC -	GCA

GAM300	TGCGCGTTGAGGCGGCTACG 286	TGAGGCGGCT 3011	C T G CTAC - AAA-- AAT TT
CGCGGTCAAAGCAAAAATGA	ACGCGCGGTC	TG GCGT GA GCGG GC GCGGTC	GCAAA
GAC G			
CTTGTGGTTTTGTTTTCGTT	AAAG		
CCGATCGCAGCACCGCGTCA		AC TGCA CT CGCC CG CGCTAG	CGTTT TTG /
CGTTCA	T - G	A--- A CCTTG GTT GT	

GAM301	TGTCAATTGGCCAACAGCGC 287	TCAATTGGCC 3012	----- ---- AC AC TT
GACTTGTTAACCAACTGTGC	AACAGCGCGA	TGTC AATTGGC	CA AGCGCG TTG A
TTCTGAAATTGCCAATTTAA	CTTG		
AAAGACA	ACAG	TTAACCG GT TCGTGT AAC /	
	AAAAAT	TTAAA CT C- CA	

GAM302	TGTTGCCACGGTGATAATA 288	TGATATTGTT 3013	CACGG AAGTAA AAG TAT CG
AAGTAAGTCAAGTGTATGTG	AAACAAGGCA	TGTTGCC TGATAATA	GTC TG GTGGC A
GCCGACAAGCCACTGTCGAT	ACA		

ACAACGG ATTGTTAT TAG GC CACCG C
AACAA AG---- GTA TGT AA

GAM305 GGGTGAGGGGGGTTGAGTTT 291 TGAGGGGGGT 3016 GG GA TTT TG GCAATAAA
TCGGGGGTGAGCAATAAAAC TGAGTTTTCG GGGTGAGGG GTT G TCGGGGG A A
GTCGTCTATTGCCCCGACG GGGG ||||| ||| | ||||| |
AACAGTCTTTACCC CCCATTCT CAA C AGCCCC T C
GA G- --- GT ATCTGCTG

GAM307 AATTTTCATCGCATGAATACT 293 TTTACAGTAA 3018 C GAA G AAGC T T A TGC
GGAGATAAAGCTGTGTTGTG GTGTGATTAA AATTT ATCGCAT TACTG AGATA TG GTTGTG
GC CTT T
TGCAC TTTGCTATATGAGAG GTT ||||| ||||| || ||||| || |||
CTTACAACCATTGTGTTTAC TTGAA TAGTGTG ATGAC TTTGT AC CAACAT CG GAG
A
AGTAAGTGTGATTAAGTT T A-- A GTT- - T A TAT

GAM308 TATCAAGCGGGTTCTAATAT 294 TAATCGGAAC 3019 AG - TA A C A TA
ATCAAACGTGTATGACACGA GTCGAGTGGT TATCA CGG GTTC AT TAT AA CGTG T
TTATAATCGGAACGTCGAGT G |||| ||| |||| || |||| ||||
GGTG GTGGT GCT CAAG TA ATA TT GCAC /
GA G GC - - A AG

GAM309 CTTTGACTTTTCCTTTTGT 295 T GACTGGACC 3020 T C - TT-- ---- TT TT
 CCTTGTTCGATATTTATTAT TGGCATTCTA CT TGA TTTTC CT TGT TCC GTCGGATA T
 CTGACTGGACCTGGCATTCT GAGA || ||| ||||| || ||| |||||
 AGAGAAAATCACAG GA ACT AAAAG GA ACG AGG CAGTCTAT /
 C - A TCTT GTCC T- TA

GAM310 ACTTCTCTCGAGAGGGTGCC 296 TGTCAGGGCT 3021 CG AG G AA- CG A T
 TTGC
 CACTAAGCTGCGGCCTAGAC ATAGCCAAAG ACTTCTCT AG GGT CCCACT GCTG GCCT
 GAC AGC A
 TAGCTTGCAAGATTGCTGTC TGGG ||||| || ||| ||||| |||| |||| ||||
 AGGGCTATAGCCAAAGTGGG TGAGGAGA TC TTA GGGTGA CGAT CGGG CTG TCG
 A
 ATTACTTAAGAGGAGT AT A- - AAC AT A - TTAG

GAM311 GGAGAAATCAACAGTCTCGC 297 TTGAACGTGA 3022 --- A A - T C TT TTTT G-
 AT
 TCGTTATAGTTTTTGGTTGG CCTGATGAAT GGAG AA TCA CAG TC CG TCG ATAGT GGTG
 CATTCGGT T
 CATTCGGTATTACACCGGAT TGGG |||| ||||| ||||| ||||| ||||| ||||| |||||
 GAACAACCTCGCTATTGAACG CCTC TT AGT GTC AG GC AGT TATCG TCAAC
 GTAGGCCA /
 TGACCTGATGAATTGGA CTC AGG A A C T A -- C--- AA CA
 C

GAM312 TAGGGGTGCCTATTACAACA 298 TTGAATCACG 3023 A AA-- ----- -- T----- T
 CCGTGGTTATAA CACTGCTA AAGGGATGGT CT TTAC CACC GTGGTT ATAACAC
 GCTA C
 TCATTAGCGCCATACCAGAT GGTA ||||| |||| ||||| ||||| ||||| |||||
 GGAGTGTTATTGAATCACGA GA AATG GTGG CACTAA TATTGTG CGAT A
 AGGGATGGTGGTACGTAAAG - CATG TAGGGAAG GT AGGTAGACCATACCG
 T
 GAGCCCCTA

GAM313 GTCCTCTTTTACACCTCAGG 299 TGGCAAGGAG 3024 A TC- A--- T- G GG CAC - G
 AATAGT
 ACAGGCTGCCGTCTGGGCCA GTTTGTT CAG CACC AGGAC GGC GCC TCT GCCA CTG
 CGC CTTTCC T
 CACCTGCGCGCTTTCCAATA AGTC |||| ||||| ||| ||||| |||| ||||| |||||
 GTTACGCCAGGAGAGGCGTC GTGG TCCTG TTG TGG AGG CGGT GAC GCG
 GAGAGG /
 AGTTGGCAAGGAGGTTTGT - TCC AGAC TT - AA T-- T - ACCGCA
 CAGAGTCCTCCTGGTGGGAC

GAM314 GAGCTATTGCACAAGATGTG 300 TGGCAAGCAG 3025 T CA TG----- G A
 TTTGGTGTTAAAAGTTGATG TGTACCTTCT GAGC ATTG CAAGA TGTTTG TGTTAA A
 GCAAGCAGTGACCTTCTG TGCC ||||| |||| ||||| |||||

CCCAATGCTC

CTCG TAAC GTTCT ACGAAC GTAGTT /
- CC TCCATGTG G G

GAM315 CAGTGAGCTTCATCTAGATA 301 TGGCTTGCAC 3026 G ---- AGATA T
AAGCTAGCCTGAAGGCTGGC AGGATGATTG CAGT AGCT TCATCT AAGCTAGCC G
TTGCACAGGATGATTGAGGC AGGC |||| |||| |||||
TGA CTG GTCA TCGG AGTAGG TTCGGTCGG A
G AGTT ACACG A

GAM316 GGTAATCAAGAAGCTACGGA 302 AAGAAGCTAC 3027 - T - AAAA--- TC-- AAA
AACGTG
AAAAAGGTTTCCAAAAACAC GGAAAAAAGG GGTAATC AAGAAGC ACG GA AGGTT CAA
CACTCTC A
TCTCAACGTGATGCTATCGA TTTC ||||| ||||| ||| ||| |||||
GAGTGCTATTGATGCAACCT TTATTAG TTCTTCG TGC CT TCCAA GTT GTGAGAG
T
ATGACAATCTCGTTGCTTCT G T T AACAGTA CGTA ATC CTATCG
TGGATTATT

GAM317 GTACTCTGCACTGTTTGGTA 303 CTAGCAAATA 3028 - T A----- ACG T T T AGA
TGCACGTAGGTGACTTTGGT TAGATCTGAT GTACTC TGCACGTGTT GGT TGC TAGG
GACTT GG GACG T
GACGAGATGGACGTCTTCAA GGTG ||||| ||||| ||| ||| ||||| |||
GTTCTAGCAAATATAGATC CATGAG ATGTGGTAG CTA ACG ATCC TTGAA CT
CTGC /
TGATGGTGTATGAGTAC T T GATATAA --- - - T AGG

GAM318 TCTTACTGTCTAACGGATCT 304 TTTGT CATGC 3029 T AA TC-- A C A----- G
AACCAT
GAAAGGGTGTGCTCTGAAGC TTCTGAAGAT GTCT CGGA TGA AGGGTGTG TCTG
AGCAG TTGGG C
AGGTTGGGAACCATCCGATT GTTA ||| ||| ||| ||||| ||| ||||| |||||
ATCCAAGCTGCTGCAAAGAA TAGA GTCT ACT TTTTACAC AGAC TCGTC AACCT
/
ACAGAACACATTTTGT CATG G A- TCGT G A AAAGAAACG G ATTAGC
CTTCTGAAGATGTTAGGA

GAM319 ATACCATGTCTAACACGGCA 305 TGTGATCAAC 3030 C CTAACAC CA G TGCAT
GATCGACAGCTGCATAAGAC CCAAACATCG ATAC ATGT GG GATC ACAGC A
CGTTGTGATCAACCCAAACA TAT |||| ||| ||| |||||
TCGTAT TATG TACA CC CTAG TGTTG /
C AAC---- AA - CCAGA

GAM320 GTTTTCCGCGGACGATATAA 306 TGATTCTTTC 3031 G TATAAA CATCCT CACGTT
AA ACA A C
AAACCATCCTAGAATCGGAC GTTCTTCGTC CCGC GACGA AAC AGAATCGGA TATG
GT GCA GT T

ACGTTTATGAAGTACAGCAA AGCG ||||| ||| ||||| ||| ||| |||
 GTCTAAACCTGCCGCGATGT GGCG CTGCT TTG TCTTAGTCT ATGT CG CGT
 CA A
 ATCAATATCTGATTCTTTTCG A TC---- CTT--- ATA ACT AG C-- C A
 TTCTTCGTCAGCGGTAAC

GAM321 GGGGTTGTTTAAACGCGAGCA 307 ATAAAGCTAA 3032 T C- G- AACGTCG C
 ACGTCGATTATCTATATAAT GCAATTATAC GGGGTTGT TAA GC AGC ATTAT T
 AAAGCTAAGCAATTATACAG AGCT ||||| ||| ||| |||
 CTCC CCTCGACA ATT CG TCG TAATA A
 T AA AA AAA---- T

GAM322 AAATCCGTCATCAAACCCAC 308 TACCCGTCAA 3033 - C GG A C----- T TC----- - -
 CT
 GCGGGACGAGTCGTTGACGT TACAAACACC AA CC ACGCG ACG GT GTTGACG GTAT
 TTC CGAC GTA A
 GTATTCTTCCGACGTACTAC GTAA || ||||| ||| ||| ||||| ||| ||| ||| |||
 AATACAGTCGCGAATGTATC TT GG TGTGC TGC CA TAACTGC CATA AAG GCTG
 CAT C
 TATACCCGTCAATACAAACA T T AA - CAAACA C TCTATGT C A AA
 CCGTAACGTGTTGGTTTTGT
 AAACAGGATTT

GAM323 TATATACCCTGTTTCGATAAC 309 TGTTATCAAA 3034 ATA C AGC T - A- AT
 AGACGAGCCGTGTACAAGAA CGGGGCAGAT TAT CCCTGTT GATAACAGACG CG GT ACA
 GA A
 TATCGTCGATGTAGCCCGAT A ||| ||||| ||||| ||| ||| |||
 GTCTGTTATCAAACGGGGCA ATA GGGGCAA CTATTGTCTGT GC CG TGT CT T
 GATA GAC A A-- C A AG GC

GAM324 ACAACATTAACGGTCAACGG 310 TAATACTAGC 3035 C-- G A TATTAGAGAAA AG
 TC GGTG
 CGTAGAATTAGAATATATTA CGTTAGTGCC AACGGC TAG ATTAGAATA AAGAAACGGA
 GTA CGC C
 GAGAAAAAGAAACGGAAGGT TTGT ||||| ||| ||||| ||||| ||| |||
 ATCCGCGGTGCTAAAGCGTC TTGCCG ATC TAATTTTGT TTTTTTGTCT CAT
 GCG /
 TACGGTCTGTTTTTTTGT
 TAATACTAGCCGTTAGTGCC TGA - A ----- GG CT AAAT
 TTGTTGTTGT

GAM325 GATGAATGAACTGGGATACA 311 TCACTGGTGT 3036 GA AC-- - G A TA
 GTGGATACTTTATACGAGAT TCCAATATC GAT ATGA TGGGATAC AGTG AT CTT T
 CACTGGTGTTCCTCAACTATCA ATAA ||| ||| ||||| ||| |||
 TAATC CTA TACT ACCTTGTG TCAC TA GAG /
 A- ATCA G - - CA

GAM326 TGTGTTGATTTTGGATCGTA 312 AAAAAGGCAG 3037 G TC -- ATTAAG ATA-- G - TTA
 A TA

TCTTATCCCTATTAAGTTGG ATAAAGTGGG ATC TA TTATC CCT TTGG CG TTA CGTTC
 CCTC GGC T
 ATACGGTTACGTTCTTACCT TCCG ||| || |||| ||| ||| || |||| ||| |||
 CAGGCTATACGCCGAGGGAC TAG GT AATAG GGA AACT GT GGT GCGGG
 GGAG CCG /
 GGGCGATGGGTGGATGGTCA - GA AC AA---- GGTAG G A CAG - CA
 AAAAGGCAGATAAAGTGGAT
 CCGTCGGCTCA
 GAM327 CGGGTTAACGAGATGAAACA 313 TGGCAAGTTC 3038 TAA GAT AC GAC--- T AGA T
 AT
 CGGACTATGGAACAGAGCTA CCTAACATAA CGGGT CGA GAA ACG TA GGAAC GCTAG
 CA G
 GTCAATGGATGTCTGGCAAG CGTA ||||| ||| ||| ||| ||||| ||||| ||
 TTCCCTAACATAACGTACTT GCCTA GCT CTT TGC AT CCTTG CGGTC GT /
 CCTATCGCATCCG C-- ATC CA AATACA C AA- T AG

 GAM328 AGGTGCATTGGATATGATTA 314 GTGCATTGGA 3039 ----- A ATCC T G
 TCCTGTTTACGGAAGTGTAT TATGATTATC AGGTGCA TTGG TATGATT TGT TAC G
 ACGTCGATCATGCCGGAAGA CTGT ||||| ||| ||||| ||| |||
 ATTACAATTGCATCT TCTACGT GGCC GTACTAG ATA GTG A
 TAACATTAAGAA - CTGC T A

 GAM329 TTGGAAGTTACAAAATTTGT 315 AAAAGAGTGC 3040 A- TA T C --- GCA----- - --
 GAA
 ATCTATCTTTTCTGTAAAAG AATGCCCAGC ATTTGTATC TC TTT TGTA AAGAGT ATGC
 CC AGCA C
 AGTGCAATGCCCAGCAGAAC AGAA ||||| ||| ||||| ||||| ||| ||| |||
 AAAGTGCTCAGGTGTATGAG TAGGCATAG AG AAG ACATT TTTTCA TATG GG
 TCGT A
 ATCAAACTTTTCTATTACAC AA CC C C ATC AACTAGAG T AC GAA
 GAACGACCGATACGGATAAA
 ACTAGTTTTCA
 GAM330 GTGCTGCTGACGATGGTATG 316 CGTCACAGAA 3041 T A C A CG ATAA A - C
 CATTCTT
 GGGTGCCGCACCCGTGATAA ACAAAGGAGT GACGA GGT TGGGGTGC GC CC TG TG
 TGACGTG GTT TACG C
 TGATGACGTGGTTCTACGCA CGTA ||||| ||| ||||| ||| ||| ||| ||||| ||| |||
 TTCTTCTACTCAACCGTACA TTGTT CCA ATTCCATG TG GG AC AC ACTGCAC CGA
 ATGC T
 GCGCACGTACAGAAACAAA T - C A AA AAAG - G C CAACTCA
 GGAGTCGTACCTTAACCTTT
 GTTAGCGTGC
 GAM331 CGGCGTTGTTTTTCCTCTTT 317 TGGCATCATG 3042 GTTTTTCC TC A TG TC TGT
 ATAT
 CTGATACTGGATCGTCTGTC AGACGCGCGA CGGCGTT TCTT TGAT C GA GTC CGGCC
 C
 GGCCATATCTTACGGCCGTG AAAC ||||| ||| ||||| ||| ||| ||| |||
 ATCTCTGGCATCATGAGACG GCCGCA AGAG ACTA G CT TAG GCCGG /

CGCGAAAACGCCG

AAGCGCGC T- C GT C- T-- CATT

GAM332 TCGATACACAAGCGGCTGCC 318 TAGCCGTTCT 3043 CACAAGC TGCCATTT AA -- -
TATCCC

ATTTACGAATATAACTGGCC AACGCCTATC TCGATA GGC ACG TATAACTGG CCG AC
A
GACTATCCCACCCCACTGTG GA ||||| ||| ||| ||||| ||| ||
CGGTTCCGGTTATAGCCGTT AGCTAT CCG TGC ATATTGGCC GGC TG C
CTAACGCCTATCGA ----- CAATCT-- CG TT G TCACCC

GAM333 CGGTTAGCTGCCTTAACCCT 319 TAGCTGCCTT 3044 - CTTA CT-G TTG A AAACAAA
C CA AA

GGAGTTATTGTCTGGAACAA AACCTGGAG TAGCTGC ACC G AGTTA TCTGG AC
GCCCC TTA CG G
ACAAAGCCCCCTTACACGAA TTAT ||||| ||| | |||| ||||| || ||||| ||| ||
GCAGCGGTTAATGGGGCGGG ATCGACG TGG T TCAGT GGGCC TG CGGGG
AAT GC C
TGCCGGGATTGACTGTGATG C ---- TAG G TA- G GG----- T TG GA
GTGCAGCTACTTCTGCCG

GAM334 GGATGATGTAATTTTTACGG 320 TGATGTAATT 3045 GT----- T - CTTAACG G A
CACTTAACGACGAGGTTATT TTTACGGCAC GGATGAT AATTT TAC GGCA AC AGGTT
T

GACTTGGTATACTGCCAGTA TTAA ||||| ||||| ||||| || |||||
CGAATTTTCTATCCCAAAT CCTACTA TTAAG ATG CCGT TG TTCAG /
CATCC AACCTATCCTT C A CATA--- G T

GAM335 AAACCTCAGAACTGGGCAAG 321 AGAGGAATTA 3046 CTCA CT GC- ----- T
ACATTT AGA

TGCCGGTAGAGGAATTAACA ACATTTTCTA AAAC GAA GGGCAAGT CCGT AGAGGAA TA
TCTAC A
TTTTCTACAGAATTGAGTAG CAGA ||| ||| ||||| ||| ||||| || |||||
ACCTATTTCTTCTTACAAAA TTTG TTT TCCGTTCA GTCA TCTTCTT AT AGATG
T
CTGAAAACCTTGCCTCATTTA TCAA AC AAA AAACAT T CC---- AGT
ACTGTTT

GAM336 AAGACCCTGAGGTAAAAGCA 322 TGAGGTAAAA 3047 A GAGG GCTG CAG- T
GCTGCTCAGCTTTTGTCAAC GCAGCTGCTC AAG CCCT TAAAAGCA CT CTTTTC C
AAAAGATCCAGACTATGCTT AGCT ||| ||| ||||| || |||||
TTAGAGAAGGGCTT TTC GGGA ATTTTCGT GA GAAAAC A
- AGAG ATCA CCTA A

GAM337 AGTAACTTGTAATGCTGTGT 323 TGCCATGCAT 3048 ----- - GTTTA - GC
ATGGGTTTACAGGAGTTGCG AAGCATTGCA AGTAAC TTGTAATGCT GTGTATGG CAG
GAGTT G

GAM338 ATTCAGATTTTCATGTGTGTT 324 TCTTTAGGAA 3049 -- T G TG C G TTGATACAA
A TG
TTGGCACGCTGGGGCGCTTG CGTGCTCAGC TTCA GATTTCAGTGT TTT GCA GCTGGG CGC
CTAGA ATA C
ATACAACTAGAAATATGCTA TGTT |||| ||||| ||| || ||| ||||| || ||||| ||
TTATCTTTAGGAACGTGCTC GAGT TTGAAGT CATA AAA TGT CGACTC GTG
GATTT TAT T
AGCTGTTGAAAATACTGAAG AT - - GT - - CAAG----- C TA
TTTATGAGT

GAM340 ACCCTTGCATGGCAAGATCC 326 CATGGCAAGA 3051 GCAT- A TC GA TAC A
TGA CTTT TACCCAATCGGAT TCCTGACTTT ACCCTT GGCA GA CT CTTT CC A
AAAGAAGCTCTGCTTTCAAG TACC ||||| ||||| || ||||| ||
AGGGT TGGGAG TCGT CT GA GAAA GG T
AAGTT - C- A- TA- C

GAM342 CAAGTACTACACTGTTGTTA 328 AGAGATCTAG 3053 TACACT- GTTA C TAG
TGGATCCTTTAGTTAGTATC AGAAACTTAG CAAGTAC GTT TGGATC TTTAGT T
ATTAGAGATCTAGAGAACT CTCG ||||| ||| ||||| |||||
TAGCTCGTACTTG GTTCATG CAA ATCTAG AGATTA /
CTCGATT AGAG - CTA

GAAGGCTTCAGAAGGTGCTT CTTT |||| |||| ||| ||| ||||
 TGGTAG GATG TTCGT GAC CGG GAGA /
 GT GGAA TT AA ACTA

GAM344 GGCAGATTCGTTAATTCGTA 330 TAGCATCACT 3055 AAT A G CTC T G A C-- T --
 - GC

AGCAGATGAGCTCGATTGTG ATCTGCTGCG TCGTA GCAGAT AG GAT GT TAC CGGGT
 CGAT AAAGT TCA A
 TACACGGGTCCGATTAAAGT GTGT |||| |||| || ||| |||| |||| |||| ||||
 TCAGCAAATGAAAACTTTA GCGT CGTCTA TC CTA CG ATG GTCCG GCTA TTTCA
 AGT /
 TCGATAGCCTGGTAGCATCA T-- - - A-- - - - ATA - AAA AA
 CTATCTGCTGCGGTGTCTGAA
 TCTCGTC

GAM345 CAGAGCTGTCCTATCAACTC 331 TGGAAATCAGG 3056 G C T ACTCTT -----
 GA

TTGCTTGATTCCATAGGTGA CTGTAGACAG CA AGCTGTC TA CA GCTTGATTCCATA
 GGT T
 TAGAACCAGATATTTTTCTA CTAT || |||| || || |||| |||| ||||
 TGTGGAATCAGGCTGTAGAC GT TCGACAG AT GT CGGACTAAGGTGT CCA A
 AGCTATG A - - ----- ATCTTTTATAGA AG

GAM346 ACACAAGGACCCGCAATACA 332 TGGCAAGAAG 3057 A-- CCGCAAT-- AT ATGA T T
 CATCCATGATTGTCCAGTAT GTAGTGTAC ACACA GGAC ACAC CC TTG CCAGTA T
 TATACTGGCAAGAAGGTAGT CAAT |||| |||| |||| || |||| ||||
 GTCACCAATTAGTCCAACCTG TGTGT CCTG TGTG GG AAC GGTCAT /
 TGT CAA ATTAACCAC AT AAG- - A

GAM347 CCGACTGAGATCGCCGACGG 333 TGAGATCGCC 3058 A - -- A TGT T TTT GAA
 GC

TGTTTGTGAGTTTGTAGTG GACGGTGTTT CCG CTG AGATC GCCG CGG TTG GAG
 GTTAGT TGTGAC T
 AATGTGACGCTGAAGTCATA GTGA ||| || |||| |||| || |||| |||| ||||
 GAAACTGACTTCTCCAATCT GGT GAC TTTGG CGGT GTT AAC CTC CAGTCA
 ATACTG G
 TGATGGCAGGGTTTCCAGCT C C GA A CT- - TT- AAG AA
 GG

GAM348 CCACTGAGGTACAAAGATCT 334 TGAGGTACAA 3059 AG- CAA TGAAG AAGA
 TTCC

GAAGATTGATGTGAAGACAG AGATCTGAAG CCACTG GTA AGATC ATTGATGTG CAG
 C
 TTCCCCCCCCCTGAGTGCATC ATTG |||| || |||| |||| |||| ||||
 AGTGATTATTACAAGCAGT GGTGAC CAT TTTAG TGA CTACGT GTC /
 GG GAA TA- ---- GA-- CCCC

GAM349 TCCTGGTGCATCCAGTGATG 335 GTGCATCCAG 3060 - G CAG- GCCAA AG
 CCAATGAAAGAAATTCACGA TGATGCCAAT TCCT GGT CATC TGAT TGAA A
 ATCAATCAGATGGACCAAGG GAAA ||||| ||||| |||||
 A AGGA CCA GTAG ACTA ACTT /
 A G ACTA AGC-- AA

GAM350 AAACACTGGAAAGGTTTTTG 336 TCACCGAAAC 3061 T A T T TGAAAA T
 TGTACAGTTGAAAAGAGCTA CTTCTGTGTT AAACAC GGAA GGT TTT GTG ACAGT GAGC A
 AGCTCATTGTCACCGAAACC T ||||| ||||| ||||| ||||| |||||
 TTCTGTGTTT TTTGTG TCTT CCAAAG CAC TGTTA CTCG /
 - - C - ----- A

GAM351 ACTAGTTGTTGTTGTATTAA 337 TTAAAGCTTA 3062 GTT TT CT--- AT A TTTCA
 TCTTTGCAATGGTTATAAAG TGCAACCACT ACTA GTTGTGTGTA AAT TTGCA GGTT TAAAG
 A
 TTTCAAGGTGTTTTTAAAGC GTTT ||||| ||||| ||||| ||||| ||||| |||||
 TTATGCAACCACTGTTTTTA TGAT TAACAATAT TTG AACGT TCGA ATTTT /
 TAACAATGTTAGT TG- TT TCACC AT A TGTGG

GAM352 CAAGATAGTTTTTACAGCCG 338 TTTACAGCCG 3063 TA - C AT-- T CAA
 ATGATGTTGAGGACAAAGAA ATGATGTTGA CAAGA GTTTTTTA CAG CG GATGT GAGGA A
 ATTCTCTACGTCCCCACGAC GGAC ||||| ||||| ||||| ||||| |||||
 TGATAAAAGCATTCTTG GTTCT CGAAAAT GTC GC CTGCA CTCTT G
 TA A A ACCC T AAA

GAM353 CCTGTGTCTAAGAGTGTTAT 339 TGTCTAGTAT 3064 CT AGA --- TG
 AGATAAAGTGTGTAGCATTT AATATCTGTA C GTGTCTA GTGTTA TAGATAAAGTG T
 TGTCTAGTATAATATCTGTA GATA | ||||| ||||| ||||| |||||
 GATACTG G CATAGAT TATAAT ATCTGTTTTAC /
 T- GTC ATG GA

GAM354 CTTTTACATACTTTTTACAG 340 TTCACCCCAT 3065 ACAT TTA T TC- --- C A
 A
 CATGTTGTTCTGGGTTATTAC GTATGATGTA ACTTT CAGCATGT GT GGGT TATTA
 TATATGG GGTGAGTAAA G
 TATATGGAGGTGAGTAAAAG AACT ||||| ||||| ||||| ||||| ||||| ||||| |||||
 TTTTGTTCACCCCATGTATG TGGAA GTTGTACG CA CTCA GTAGT ATGTACC
 CCACTTGTTT /
 ATGTAAACTCCACACTGCAT TT-- --- T CAC AAT - - T
 GTTGAAGGTTTTTAAAG

GAM355 GATGAAATTTTTGACCCAC 341 TGAAATTTTT 3066 ----- ACC - ATAC
 TGAAATACTTTGGCTTCAGG GACCCCACTG GATGAAAT TTTTG CCAC TGAA T
 TGGCTGCAAAAATTCATGTT AAAT ||||| ||||| ||||| |||||
 TCATC CTACTTTG AAAAC GGTG ACTT T

TACTTA GTC G CGGT

GAM356 GCAAGAGGTTAGCGTGGTTG 342 AACTCTGGCT 3067 GT- G TT GAC A GA
TTGGTGGACGCAAGCAGATA ATAACCTTTT GCAAGAG TAGC TGG GTTGGTG GCA GCA T
GTGCATGTTTACACTAACTC T ||||| ||| || ||||| ||| |||
TGGCTATAACTTTTTGT TGTTTTC ATCG GTC CAATCAC TGT CGT /
AAT - T- ATT A GA

GAM357 GCAGAAGATGTTTGGTCTTC 343 TCTTCATTTA 3068 - C TT TGAAAA - GG C A
GG

ATTTACTGAAAAGTCTTTTG CTGAAAAGTC GATGTTTG GTCTT AT AC GTCTTT TGAATTCT
AAG TTGC TAT A
AATTCTGGAAGCTTGCATAT TTTT ||||| |||| || || ||||| ||| ||||| |||
GGAAAAGTGCGCAACCTTGA CTGTAAAC CGGAA TG TG CAGAAG GTTTAAGA TTC
AACG GTG A
AGAATTTGTGAAGACCTATG T - TT TATC-- T AG C C AA
TTTGTAAGGCTCAAATGTCG
ATTGT

GAM358 GCTATATGAATTCTTTCAAT 344 TTAATGCTGT 3069 T-TT A-- T TA T TC TTGT TT
TTT TA
ACTTCTTTGTTAATGCTGTA ATCAGTTTGT CT CAAT CTTCT TGT ATGC GTA AGT GAAG
AGGT GT T
TCAGTTTGTGAAGTTAGGTT GAAG || ||| ||||| ||| ||| ||| ||| ||| ||| ||| |||
TTGTTATTTACACCTCTTCT GA GTTA GAAGA ACA TACG CAT TCA CTTC TCCA
CA /
AATACTCTTACTGCATACAC TT GG ATG C -- T TC TAAT -- --- TT
AGAAGGTAATTGGGAGTTAT
TCTTCGAGT

GAM359 GGTGATAGTTTCACTATAGC 345 TACAGTTGTA 3070 TT----- A T TA
TTGTGCTTATGGTGGTACAG GGA CTCTACC GGTGATAG TC CTATAGCT GTGCT T
TTGTAGGACTCTACCCTGTT CTGT ||||| || ||||| |||||
ACT TCATTGTC AG GATGTTGA CATGG G
CCATCTC - - TG

GAM360 GGTGCTATATCTAATGTTGT 346 TGCTATATCT 3071 - T T TACA- AAGG -- A G - T
TG
TGTCTTACAGTCTAAAGGGC AATGTTGTTG TAATGT GT GTCT GTCTA GCA TGAA CA AG
GAAG GGATGC T
ATGAAACAGAGGAAGTGGAT TCTT ||||| || ||||| ||| ||| ||| ||| ||||| |||||
GCTGTTGGCATTCTTTCACT GTTATA CA CAGG TAGAT CGT ACTT GT TC CTTT
CTTACG /
ATGTTCAATTGTCAGTAGATC T - - CGCCC GA-- TT - A A - GT
CCGCGGACACATATTGTA
TATGTGGCAGC

GAM361 GGTTTTATAGTGTGTAATAC 347 TATTATGCGC 3072 TTTAT GTAA- G-- T CAT - AA
AA
ACAGAGTGCTCATGCATTAG AATATCTGTG GGT AGTGT TACACAGA TGC CATG TAGA
GG GCA G

AGGAAGCAAAGAATGCAGCC TAAG ||| |||| |||||| ||||| |||| |||
 ATCTATTATGCGCAATATCT TCA TCATA ATGTGTCT ACG GTAT ATCT CC CGT /
 GTGTAAGCCAATACTTATAC TAT-- ACCGA ATA C T-- A GA AA
 T

GAM362 GTGGCGCAAATAATACGGAT 348 GCGCAAATAA 3073 ----- A - -- AAT
 GAAGTAATAGAAGCTTCGTT TACGGATGAA GTGGC GCAA TAA TACGG ATGAAGT A
 ACCGTACTTATTGCTTTTTG GTAA |||| ||||| ||||| |||||
 CTAC CATCG CGTT ATT ATGCC TGCTTCG /
 TTTTT - C AT AAG

GAM363 TGGTTTGTCTACACAAGTAA 349 TCTACACAAG 3074 TTT - A AC A T
 CCCAGTAATGTTTACAGGAA TAACCCAGTA TGG GTCTA CACA GTA CC GTAA G
 TACGTGTGTTAGATTTTCTA ATGT ||| ||||| ||||| ||| |||||
 ATC TAGAT GTGT CAT GG CATT /
 TTT T G AA A T

GAM364 TTTGAGTGAGTATTGTGATG 350 TGAGTGAGTA 3075 GT- ACAT-- TA
 ACATACTTAAGAGGTCAACT TTGTGATGAC TTTGAGTGA ATTGTGATG ACT A
 GTATTACAATCGGTTACTCA ATAC ||||||| ||||||| |||
 AG GAACTCATT TAACATTAT TGG /
 GGC GTCAAC AG

GAM365 CTAATGTGACCGACTCAGCT 351 TGTGACCGAC 3076 T A - CAG-- T T
 GTTAGTTATAATTATCTAGC TCAGCTGTTA CTAA GTG CCGA CT CTGTTAG TA A
 AGACGCAGGTTTGGCTATTT GTTA ||||| ||||| || ||||| ||
 TAG GATT TAT GGTT GG GACGATC AT A
 T C T ACGCA T T

GAM366 CTATTAGGTACTCCTTTTGT 352 TACCGCAAAA 3077 ACTCC A AC- CA
 GGTAATGGACGACATGTTCT TGCACCTAAT CTATTAGGT TTTTGTGGTA TGG GA T
 AACCATACCGCAAAATGCAC GG ||||||| ||||||| ||| ||
 CTAATGG GGTAATCCA AAAACGCCAT ACC CT /
 CGT-- - AAT TG

GAM367 CTTTATTTAATGTTACTGAA 353 TGAGTACATA 3078 - TAC AAA ACC TCA
 AATGTGCTCATACCTAACAG CAAACGCGTA CTTTATTTA ATGT TG ATGTGCTCAT
 TAACAGTT A
 TTTCAACTTAACTGTTACAG TGGA ||||||| |||| || ||||||| |||||
 ATGAGTACATACAAACGCGT GGAATAGGT TGCG AC TACATGAGTA ATTGTCAA /
 ATGGATAAGG A CAA A-- GAC TTC

GAM368 GTGATTCAAGAAATCTACCA 354 TAACTGGTAG 3079 TCAAGA CA TT -- ACA A
 GCAATTTGACGCCATACAAG ATTGTCATCA GTGAT AATCTACCAG AT GACG CCAT AGC
 A

CAAATGCTCAAGTGGATCGT C ||||| ||||||| || |||| ||| |||
 CTTATAACTGGTAGATTGTC CACTA TTAGATGGTC TA CTGC GGTG TCG A
 ATCAC CTG--- AA TT TA AAC T

GAM369 ATGCTATGAACCAGAGAGCT 355 CAGAGAGCTT 3080 A A- CTTACCGTA C TT
 TACCGTATGCTTGGACTTAA ACCGTATGCT ATGCT TGAACC GAGAG TG TTGGAC A
 TGTTCAAACAGTAGATTCTT TGGA ||||| ||||| || |||||
 CTCAAGGTTTACAGAGTAT TATGA ACTTGG CTCTT AC AACTTG /
 G AA CTTAGATG- A TA

GAM370 CGCCTGAGGGACTTGTAGAT 356 TGAGGGACTT 3081 - GA G TAC A AATAA
 ACTTCAATAGGCAATAATTT GTAGATACTT CGCCTG AGG CTT TAGA TTCA TAGGC T
 TGAGCCTGTGAATTCTAAAG CAAT ||||| ||| ||| ||| |||||
 CACCTCCAGGTG GTGGAC TCC GAA ATCT AAGT GTCCG /
 C AC - T-- - AGTTT

GAM371 GCTTACAAGAGCTAAGCGTG 357 AGAGCTAAGC 3082 ACAA - CTG T TAG TG G
 GTATACTAGTTGTCATGCGC GTGGTATACT GCTT GAGCT AAG G G ATAC T TCATGC C
 CAGCGTGATGAATTGTATTC AGTT ||||| ||||| ||| |||||
 TGCTCTTAAGTTTACAGAGC CGAG TTTGA TTC C C TATG A AGTGCG C
 ACA- A TGT T TTA GT A

GAM372 GGCACAGAGTTACACCCAAC 358 TAAGTGGTGC 3083 A GA ----- CA C GTA GA
 TTCTACAGGTAGTGGATTGA TAATATAGCA GGC CA GTTA CACC ACTT TACAG GTG T
 CATACTGTATAAGTGGTGCT TGGC ||| ||| ||| ||||| ||||| |||
 AATATAGCATGGCC CCG GT CGAT GTGG TGAA ATGTC TAC T
 - A- ATAATC -- T A-- AG

GAM373 GTATTTATGTAAACCTGGT 359 TTAAACCTGG 3084 T -- - GTG CT A
 GGCCTAGCAGTGGTGATGC TGGCACTAGC GTATT ATGTAA AC CTG GCA AGCAGTGGTG
 T
 TACTACTGCTTATGCAAACA AGTG ||||| ||||| || ||| ||| |||||
 GTGTTTTTAAACATAATAC CATAA TACAATT TG GAC CGT TCGTCATCAT G
 - TT T AAA AT C

GAM374 TCAAACCTGGTAATGCTGCTA 360 TAACAGGCCT 3085 - ATG C A TATG
 TAAACGATTATGATTATTAT ACCATGTTTG TCAAAC TGGTA CTG TATAA CGAT A
 CGTTATAACAGGCCTACCAT A ||||| ||||| ||| ||||| |||||
 GTTTGA AGTTTG ACCAT GAC ATATT GCTA T
 T CCG A - TTAT

GAM375 TGATATTGTAGACTATGTGT 361 TATTGTAGAC 3086 A GACTA - T- TG
 CTGATGCACATGTTTCTGTG TATGTGTCTG TG TATTGTA TGTG TCTGA GCACA T

CTTTCAGATTGCAATAAATA ATGC || ||||| ||| ||||| |||||
 TAATACA AC ATAATAT ACGT AGACT CGTGT T
 - AAATA T TT CT

GAM376 AGCACGCTTGGGTCACTCCA 362 TGTCAATGCC 3087 CG TCACTCCAAAC - ACA- CT
 C
 AACGCGTGGGACAATCTGCA CCCACCGCC AGCA CTTGGG GCG TGGG AT
 GCAGAC T
 GACCTTGTCTGTCAATGCCC CCCA ||| ||||| ||| ||||| || |||||
 CCCACCGCCCCCAAGTATGC TCGT GAACCC CGC ACCC TA TGTCTG /
 T AT C----- C CCGG AC T

GAM377 CAGGCTTACGCGCATGAATC 363 TGAATCATG 3088 GCTTACGC- ATC CCCATGCCAA
 TCA C AA
 TTCCATCACCCATGCCAAAA TCTTCTCTCA CAG GCATGA TTCCATCA AAACC TCT
 C C
 ACCTCATCTCCAACATGAAG CTG ||| ||||| ||||| ||||| ||| |
 AATGGTTTTGATGGAATCAT GTC TGTACT AAGGTAGT TTTGG AGA G /
 GTCTTCTCTCACTG ACTCTCTC --- ----- TA- A TA

GAM378 GATGGTGAATCAAATGGCC 364 TGGTGAATC 3089 TG CAAATG--- ATTATAA GTT
 TATTATAACAGTTGTAAATG AAATGGCCTA GA GTGGAAT GCCT CA G
 GGAAGAGGCAAAAGTAAAGT TTAT || ||||| ||||| ||
 TTCATTGTC CT TACTTTG CGGA GT T
 GT AAATGAAAA GAAGG-- AAA

GAM379 GGAGGAAAAATGTTGTACAA 365 TATTGTACAG 3090 GGAAA --- AA ACAA
 TAAAGTTACAAAACAATTA ACCCATTACA GGA AATG TTGTACAAT AGTT A
 GCTATTGTACAGACCCATTA AATC ||| ||||| ||||| |||||
 CAAATCC CCT TTAC GACATGTTA TCGA C
 AAACA CCA -- ATTAA

GAM380 TCCCTCCTGAGTTGTGGACA 366 TGAATCATG 3091 T T GA-- A ATA GACTATA
 AGGTATAATATGACTATAAA GAAATATAAC TCCC CC GAGTTGTG CA GGT ATAT A
 TCAAACAATATGGAATCATG TTTG ||||| ||||| ||||| ||||| |||||
 GAAATATAACTTTGGGGGA AGGG GG TTCAATAT GT CTA TATA A
 - T AAAG A AGG ACAAACT

GAM381 TTACAAAAGTGGAAGATTG 367 AAAAGTGGA 3092 A TGG G GA ACAA-- A-
 GG ATT
 GGTAGGATGGATAGGAAATA AGATTGGGTA GGG AGAT GTAGGAT GATAG AATATTCC
 TATTT AAG ACT G
 TTCCACAATATTTAAAGGGA GGAT ||||| ||||| ||||| ||||| ||||| ||||| |||||
 CTATTGGGAGGTATCTTGGG TCC TTTG TATTTTA TTATT TTGTGAGG ATAAG TTC
 TGG /

AATAGGATTAGGAGTGTTAT A --- G A- ATTAGG GG TA AGG
 TATTGATTTTATGTTTACCT
 ACATTGGTTGA
 GAM382 AAATCCTCACAATGATATGT 368 TGATATGTTG 3093 CT T --- A TA- AGCT
 TGAATGTTAATTTAGCTAAA AATGTTAATT AAATC CACAA GATATGT TGA TGT ATTT A
 ACAAATGATGCAATCAAAGA TAGC |||| |||| |||| || |||| ||||
 TATGTCTTGTGTTGATTT TTTAG GTGTT CTGTATA ACT ACG TAAA /
 TT - GAA A TAG CAAA

 GAM383 GATTTCTCTGCTTTTGATGC 369 TGATTAGAGA 3094 C- GATG T TC
 TAGTCTTAGTCCATTTATGA AGCAGGTAGA GATTT TCTGCTTTT CTAGTC TAG C
 TTAGAGAAGCAGGTAGAATC ATC |||| |||| |||| |||| ||||
 CTAAG GGACGAAGA GATTAG ATT /
 AT ---- T TA

 GAM384 GCTGGTAATGTTGTTATTCA 370 GTAATGTTGT 3095 - G TTCAAT T -- --- -- G
 ATCTTTGGATGTGGGATTCC TATTCAATCT GCTG GTAATGTT TTA CTT GGA TGTGGGA
 TTC CAGGAT T
 AGGATGTTGTTCTGATGAAG TTGG |||| |||| |||| || |||| |||| || ||||
 GTTCCTACAATTCCTAAGTT CGAC CATTATAG GAT GAA CCT ACATCCT AAG
 GTCTTG /
 TAGAGATATTACTCAGC T A TT---- T TA TGG TA T

 GAM385 GGAATTTTGCTTTATGTAAT 371 TTGAGAGTCA 3096 T T C--- TG - AG--- GAAC- C
 TT
 ACAACAATTGAATCAGGATG TGAATTATGC TGCT TATG AATA AACAAT A ATC GAT
 ATTCTCA ATAA G
 AACATTCTCACATAATTGGT AGAT |||| |||| |||| |||| | ||| ||| |||| ||||
 TTGTTGAGAGTCATGAATTA ACGG GTAC TTAT TTGTTG T TAG TTA TGAGAGT
 TGTT /
 TGCAGATATTGGTTGTTTCAG T T TGAC GT A ACGTA AGTAC - TG
 TTATTTCATGTGGCAAAGTT
 TT
 GAM386 GGGGATTGATCTGTGCTATG 372 TAGCATCATT 3097 ----- - --- C T
 GTTCCTGGTGACCAGAGCTA GACTGTTTAT GGGGAT TGAT CTGT GCTATGGTTC TGG G
 TGGTTCTATAGCATCATTGA CCTC |||| |||| |||| |||| |||| ||||
 CTGTTTATCCTC CTCCTA ACTA GATA TGGTATCGAG ACC /
 TTTGTCAGTT C TCT - A

 GAM387 CTGGACTTTTAGTTACCCTC 373 TCCGCGGGCG 3098 T AC G ----- GT T A G
 C
 CGACCCGCCGCGTCTGCGGG GCGATCGTAA AGTT CCTCC ACC CGCCGC
 CTGCGGG GA GGCG TGG G
 TGAAGGCGGTGGCGACCACG ATGT |||| |||| |||| |||| |||| || |||| ||||
 TCTCTCCGCGGGCGGCGATC TCAG GGAGG TGG GCGGCG GGCGCCT CT
 CTGC ACC /

GTAAATGTGTCGGTGGAGGT
AGACTTGGACCCAG

T AT - CTGTGTAAATGCTA -- - - A

GAM388 CTGTGTCGGCGCGGTAGCGA 374 CGCGGTAGCG 3099 - ACTACA ----- TTT A -- -
C CG

CTACACCGCAGAGTTTTGTC ACTACACCGC C GGTAGCG CCG CAGAG TGTC C
GTTCC CGT TCGGG A
ACGTTCCCGTCTCGGGCGAA AGAG | ||||| || |||| |||| |||| ||||
CTCTTGAAACGCGGAGCTCG G CCGTTGC GGC GTCTC GCAG G CGAGG GCA
AGTTC A
CGACGCATCTCTGGTAACAC A GCGC-- CACAATG TAC C CT C A TC
CGGCGCGCGTTGCCAGCGCC
GCGCAG

GAM389 GACTGTATGGTCTATCTTAC 375 TGCCTCGTGC 3100 TATCTTAC---- T AAAC- AA---
TTAAA GC

GTCCATTTTCAAACTTATC GACGCGGATG GTC GTCCAT TTCA TTATCT GCATG
CAGA A
TAAGCATGTAAACAGAGCA AATC ||| ||||| ||||| ||||| ||||
ATATCTGCCTCGTGCGACGC TAG CAGGTG AAGT AGTAGG CGTGC GTCT
A
GGATGAATCTATGAATGTGG TCTCTAACCTTT T ATCTA CGCAG TCC-- AT
ACTTTCCAATCTCTGATTAT
GCATTT

GAM390 GCGCGATGCAATGGCCGCT 376 TGGCCGGCTC 3101 G- AAT- C A TC
ATAGACTGTCCGACGGGCTG TAGGTATGAG GCGC ATGC GGCCG CTATAG CTG C
TGGCCGGCTCTAGGTATGAG CGC |||| |||| ||||| ||||| ||||
CGC CGCG TATG TCGGC GGTGTC GGC /
AG GATC C G AG

GAM391 TGCTGTTTCCCGCCAATGAG 377 TGAGGTGGTT 3102 TT G T- CGCTTG TG TTAGA
CAC- GC

CGCTTGCGCTGAGGTGGTTAG AGATTGAGGG TGCTGT CCC CCAA GAG GC AGGTGG
TTGAGGG GTG C
ATTGAGGGCACGTGGCCAAC CACG ||||| ||||| ||| || ||||| ||||| ||||
ACCCACCCCTTAAGCTCGCC ACGACG GGG GGTT TTC TG TCCGCT AATTCCC
CAC /
TTGGTATCCTTTTTTGGGGG TC G TT CTA--- GT CG--- ACCC AA
GCTGCAGCA

GAM392 AGCGCCCCGGTCTACCCGTT 378 TACCCGTTTG 3103 TTGTGGAGGA - AA CA A
AA--- C AA C

TGTGGAGGAGCTGGCGCGCA TGGAGGAGCT CCGT GCTGG CGCGCAGA GCTA CGA
GG TCG GG CT T
GAAAGCTACACGAAGGAATC GGCG |||| ||||| ||||| ||||| ||||| ||||
GCGGAACTCTTTGGGGCCAT GGCA CGACC GCGCGTCT TGGT GCT CC AGT
CC GG T
GAACATGCCTCGCATGGTTC ----- A -- AC - GTACA A GG T
TGCGCGACCAGCACGGGTTC
ATGTCGGTGCT

GAM393 AAGCAAACTGGAGGACACC 379 CTTCACTC 3104 G ACAC C - - T - ATAT- AT--
T CG
GCGCGCAAGGTGTGTAGTGT TATGTGCCGT AGG CG GCGCA AG GTGTG AGTGTA TGGCA
AAC CA GAT C
ATGGCAATATAACATCATGA ACCT ||| || ||||| || ||||| ||||| ||||| ||| || |||
TCGCTTCATCTGTGCGGTTT TCC GC CGTGT TC CACAC TCATAT ACCGT TTG GT
CTA T
CTAGTGCCATTATACTTCAC G AT-- - A T T T GATCT CGCT - CT
ACTCTATGTGCCGTACCTGC
AATTCTACTT

GAM394 ACGTGACTGCTAATGCAGAC 380 TCTGACCAAC 3105 CTAAT AGA- C CG CGAT
TGGGTTCCGGTCAGAGACGAC CCGGCAAGGC ACGTGACTG GC CTGGGTT GGTCAGAGA A
A
GATAAATTTTATCTCTGACC TCAG ||||| || ||||| ||||| |
AACCCGGCAAGGCTCAGTCA TGCCTGAC CG GGCCAA CCAGTCTCT T /
CGT T---- GAAC - AT TTAA

GAM395 CATGATAGATAAGGTGCGCA 381 TAAGGTGCGC 3106 A--- C A C - - TCAT-- T --
T
TCTACCAAGGCATGACTGTC ATCTACCAAG GGTG GC TCTA CAAGG CA TGA CTG CA
CTCGGCC ATGTATT C
ATCATCTCGGCCATGTATTT GCAT ||| || |||| |||| || ||||| |||||
CGCAATGCATTGGGTCGAGC TTAC CG GGAT GTTCT GT ACTGAC GT GAGCTGG
TACGTAA G
TGTTTATTCAGTCACTGTTC TATA - - A T C TTATTT C GT C
TTGATAGGGCCATTATATAA
TCTATTCATG

GAM396 CCGAGGACAAGGAAATAGCG 382 TTGAAGCTTC 3107 AG - AA C-- TT A- A- A
CTTCAGGATTACAATCACAA CTGACTCCTA CCG GACA AGGA TAG GCTTCAGGA ACA
TCAC AGC G
GCAGTTGCTGGGTGAGATGT TGTT ||| |||| |||| ||||| ||| |||| |||
TCTTGAAGCTTCCTGACTCC GGC TTGT TCCT GTC CGAAGTTCT TGT AGTG TCG T
TATGTTGACGG AG A CA CTT -- AG GG T

GAM397 CCTTGACAGAGATTATCACA 383 TGTGGAGGCA 3108 TTATC AAT CTAC AAA - TC AAC-
CT ACT
CAATGCCTACGCAGAAAGAC AGGGTTTGAT ACAC GC GCAG GAC TT ACC
CCTCCATA GCCAT T
TTTACCAACCCTCCATACT GTTA |||| || |||| |||| ||||| |||||
GCCATACTTCGCATGGCTGT TGTG CG CGTC TTG AG TGG GGAGGTGT
CGGTA /
GGAGGCAAGGGTTTGATGTT T---- --- CAC- AAA T TT GAAC -- CGC
AAACTGCCACGCGTGTTGCT
CGTCATAGG

GAM398 CGGTGCTGAGGGGTTACAAA 384 TGAGGGGTTA 3109 GG T A CC ACTCC A
GCCGCGTTCACTCCGCATGT CAAAGCCGCG CGGTGCTGAG GT AC AAG GCGTTC
GCATGTCG G
CGAGCTTGACATGCCGAACG TTCA ||||| ||||| ||||| |||||

CAACTTCGTACAACCTTAGCA
CCG

GCCACGATTC CA TG TTC CGCAAG CGTACAGT C
AA - C AA C---- T

GAM399 GAGGTGTCGGTTGACGGAAA 385 TGA CTCTTTG 3110 GGTT - T C- CAACCG
GAGTTTTGGCCAGGGCGGCA CTGTCGACAC GAGGTGTC GACGG AAAGAGTT TGGC
AGGGCGG T
ACCGTTATAGATTCGTCTTT CTT ||||| |||| ||||| ||| |||||
CGCTATGACTCTTTGCTGTG TTCCACAG CTGTC TTTCTCAG ATCG TTCTGCT T
GACACCTT ---- G T CT TAGATA

GAM400 GCCTCTATTCATCAGACTGC 386 GCAGTCTGAT 3111 T- ---- --- AA -- C
CAAACCGTTTCAGGGCCGTG TATGACAATT GCC CTAT TCA TCAGACTGCC ACCGTTT
CAGGGC G
GCTTTGTAAACGGTAGGCA ATGG ||| ||| ||| ||||| ||||| |||||
GTCTGATTATGACAATTATG CGG GGTA AGT AGTCTGACGG TGGCAA GTTTCG T
GTTGGC TT TTAAC ATT A- TT G

GAM401 GTACTTCTACACCAGCGGGA 387 TGAGATCAGC 3112 ACACCAG AA A GA A -- C -
CAACGA TC
ACATGCAGAGATCGGCATGT ATGCACCCGA CGGG CATGC GA TCGGC TGTGGC AAG
GCA GGT GC A
GGCAAGCGCAGGTCAACGAG AGAA ||| |||| || ||||| ||||| ||| ||| ||| ||
CTCAGAGCCCAGAACCTTGC GCCC GTACG CT AGTCG AACTG TTC CGT CCA
CG /
CCTTCAGTCACAGCTGAGAT A----- AC A AG - AC C T AGACC- AG
CAGCATGCACCCGAAGAAGC
AC

GAM402 GTAGTCGAACTGGCTTACAC 388 TGGCAACTGG 3113 --- ACA C T ACGAA GGAAC A-
CCGA G
CCAGCTTGTCCAGGACGAAA GCCAAGTTAA TG GCTT CCCAG TTG CCAGG AA GCAT
CCAGAA AG G
AGGAACGCATACCAGAACCG TAGA || |||| ||||| ||||| || ||||| ||
AAGGGA ACTAAGATTCTGGA AT TGAA GGGTC AAC GTCC TT CGTA GGTCTT
TC A
CATGCCGAATTGGAAGCCTG AAT CC- - - GAAGG AAGC- CA AGAA A
GCAACTGGGCCAAGTTAATA
GACGAGACGC

GAM403 GTCAACAAGATAGGATGAAG 389 TAGGATGAAG 3114 A GCA ATAAACG A CGA AAC -
- AAG AC
ATGCAGGTTATAAACGTGAA ATGCAGGTTA G AGAT GGTT TGA CC ACTGGA GGAA
CTTC TTGTC C
CCCGAACTGGAAACGGA ACT TAAA | ||| ||| |||| ||||| ||||| ||||| |||||
TCAAGTTGTCACCAAGACAA C TTTG CCGG ACT GG TGGCTT CCTT GAAG
AACAG /
GAAGCATTCTTCGGTGGAT C AA- ACGG--- A --- --- AC --- AA
CAGGCAGGCCAAGTTTCCAT
CTTATCGAC

GAM404 GTCCGATTTCGATACAAGAAC 390 TTGAAGCCTG 3115 GA - AAGAAC- TG- T A
GCCGA T
CCTGTCATGTCTCACCAGGC GGGAGTATGA GTCC TTC GATAC CC TCATG CTC
CCAGGCT AATC G
TGCCGAAATCTGTGGATTGA AGTG |||| ||||| || ||||| ||||| ||||
AGCCTGGGGAGTATGAAGTG TAGG AGG CTATG GG AGTAT GAG GGTCCGA
TTAG T
GATGATAGGTATCAGGAAAG AA A GATAGTA TGA - G AG--- G
GAT

GAM405 TGAAACCTTCCGGAACACTACG 391 TGAGAACGAG 3116 A -- AA - T AA AA - T
ATGAAATCAAAGCCGTTCTC CCTGACATCC TGAA CCTTC CGG CTA CGA GA TCA GC
CGTTCTCGAGG C
GAGGTCATTCTTGAGAACGA TCGT ||||| ||| ||| ||| ||| ||| |||||
GCCTGACATCCTCGTTGGAG ACTT GGAAG GTC GGT GCT CT AGT CG
GCAAGAGTTCT A
CTGAAGAAGGTTCA - AA GA T C AC C- A T

GAM406 TGACGAAATGCCACACATTA 392 TGAGGAACAC 3117 C A- T - C ATCCA TAC
AT- TT
GGAGTGTGAGGAACACGGGC GGGCATCCAT CACA ATT GGAG GTGA GGAA ACGGGC
TGGGC CTGGGG TTC G
ATCCATGGGCTACCTGGGGA GGGC ||||| ||| ||||| ||||| ||||| ||||| ||||| |||||
TTTCTTGTGCAATTACCCTA GTGT TAG CCTC CGCT CTTT TGTCCG ATCCG
GATCCC AAG /
GACTGCCTACGCCTGTATTT T CG - A A C---- TCA ATT CT
CATCGCCTCCGCGATTTGTG
GGATGATGTCA

GAM407 ACTTGGTTTCGTCGGAAACT 393 TGGCAGGAGG 3118 T AAA C T G A ATT T--
TC
CCATAGTATTGTGGGTACTC CGCACGATTT GTTTCG CGG CT CATAG ATTGTG GT CTC
CCAGTAT AGTCCAGG A
ATTCCAGTATTAGTCCAGGT ATGA ||||| ||| ||||| ||||| ||||| ||||| ||||| |||||
CAGTTCTTGGACTTCTATAC TAAAGT GTC GA GTATT TAGCAC CG GAG GGTCATA
TCAGGTTT G
TGGCAGGAGGCGCACGATTT - GTG A - G - GAC TCT TT
ATGAAGGTGCTGTGAAATCG
TTGGAGGGGT

GAM408 CCGCCATAGTTGGGATTGGT 394 TTGGTTATCT 3119 G T----- G CT - TA AT TG G
TATCTTGGGGTTAGGATTGG TGGGGTTAGG CC CCATAG TGGGATT GTTAT TGGG GT GG
TGG CC C
TGCCGCTTGGTGCCGCCGTA ATTG ||||| ||||| ||||| ||||| ||||| ||||| |||||
CTCCCGGAATAACGAATTCC GG GGTATC ACCTTAA CAATA GCCC CA CC GCC
GG T
ATAATCACCTATGGGG - CACTAAT G AG T TG -- GT T

GAM409 GGGGTGCCTGGAGGAGCTCG 395 GAGGAGCTCG 3120 GT -- GA -----
CTGGGTTCTGTACTTCGGTA CTGGGTTCTG GGG G CCTG GGAGCTCG CTGGGT
TCTGTAC T

CGGAGAGGGACACACCCAGA	TACT				
CATGACCGAGTTTCCTCAGG		CCC C GGAC CTTTGAGC	GACCCA	AGGCATG C	
ATCGTCCC	TG TA TC	CAGTACA	CACAGGGAG	G	

GAM410	GAGGTCCACGAAGAGAAATG 396	TGAGATCAAA 3121	CACG - AAA- ---- - - TA
	CTATCCACCTAAATTGGATG	GAGCAACTAC	GAGGTC AAG AG TGCT ATC CA CC A
	AGATCAAAGAGCAACTACTA	TACT	
	CTTAAGAGACTTC	CTTCAG	TTC TC ACGA TAG GT GG A
	AGAA A ATCA	GAAAC A A TT	

GAM411	TCAGATAGTGCAAGCTTTTA 397	TAGTGCAAGC 3122	GA G AA A A G
	AAGAAGATAGGGCCTACTCT	TTTTAAAGAA	TCA TAGTGCAA CTTTT AGA G TAG G
	CCAGAAGTTGCACTGAATGA	GATA	
	AGT GTCACGTT GAAGA	TCT C ATC /	
	AA - CC -- C		

GAM412	TCTACTGCAGGGACAAGGAA 398	TATCACTAAG 3123	GCA CA-- - - GAGA AAG
	TGGGAGAAGAAGATCACTGA	ATCCCAGGTA	TCTACT GGGA AG GA ATGG AG A
	AGCCATATCACTAAGATCCC	GA	
	AGGTAGA	AGATGG CCCT TC CT TACC	TC /
	A-- AGAA A A	GAAG ACT	

GAM413	CCCAGGGCAAATGAATTTTT 399	TGGAAAGAGT 3124	CAGGG ATGAA --- AG
	CCAGCCTAAGATGTGGGCGT	ATGTTGAATA	CC CAA TTTTCCA GCCTA A
	ATGGAAAGAGTATGTTGAAT	AGG	
	AAGG	GG GTT AGAAAGGT CGGGT /	
	AATAA GTATG	ATG GT	

GAM414	GAAAGGGTGTTCTCAACTTG 400	AAGGGTGTTT 3125	A ----- CATTAC A
	GCTCATTTACTTGAATACAA	TCAACTTGGC	GAA GGGTGTTT TCAACTTGGCT TTG A
	ACCAAGCCAAGTTGACATAT	TCAT	
	CGAACACTCGTTC	CTT CTCACAAG	AGTTGAACCGA AAC T
	G CTATAC	ACCA--- A	

GAM415	GAATGGATGAACGATTATGT 401	TAGCACATGG 3126	A GA T AT AT
	TCTAAATCTATCAAAAGTTA	GGTTCATAT	GAATGG TGAAC TTATGT CTAA CT C
	GCACATGGGGTTCACTATTT	TT	
	TTTATC ACTTG	GGTACA GATT GA A	
	- G- C -- AA		

GAM416	GCATTTGAGGAAGCTATCGT 402	TCAGATCCAC 3127	A ATC- A TAT
	TAGAGTTATTGTATACTCAG	GGCTTTCGCA	GCATTTG GGAAGCT GTT GAGT T
	ATCCACGGCTTTCGCAAATG	AATG	

T TGTA AAC CTTTCGG TAG CTCA G
G CACC A TAT

GAM417 GCTGTATCTGAATCAAGATG 403 TGAGCTTCAG 3128 ATCAAGATGTACAAA GGTCT ----
TA - A
TACAAATGATGAGCTTCAGG GTCTTACCTC A TGATGAGCTTCA TACC TCAAG
TTTCG CTG T
TCTTACCTCAAGTATTTTCGC AAGT | ||||| ||| ||| ||| |||
TGATGCAGATGAAGAGTTTG T ACTGCTTGAAGT ATGG AGTTT GAAGT GAC
/
AATGCGGTACATATGAAGTT ----- ATAC- CGTA GA A G
CGTCATCAGAGCAGC

GAM418 TGAGAATGCGTGGTAATAGT 404 TGGGTTCGCT 3129 A- CG-- TAGT TT T TC TC
A
GTGTTTGGGTCGTCGCCTAT TTGCATTCT TGAG ATG TGGTAA GTGT GGG CG
GCCTATT TGT A
TTCTGTAATGACAAGTGGGT TTGC ||| || |||| ||| ||| ||||| |||
TCGCTTTGCATTTCTTTGCT ACTC TAC ATCGTT TACG TTC GC TGGGTGA ACA T
ATAACATCACTCA AC AATA TCTT T- - T- -- G

GAM419 TTGAAGATTTACTGGCATTTC 405 TTGGATGCTT 3130 G ACT G AA- AGGG
AAGAGTGAAAGTGTGAGGGA GAAGTCTTGA TT AAGATTT GGCATTCAAGA TGA GTGTG A
ACAAGCACACACATCATCTT A || |||| ||||| ||| |||
GGATGCTTGAAGTCTTGAA AA TTCTGAA TCGTAGGTTCT ACT CACAC A
G GT- - ACA GAAC

GAM420 AGATGCATTATTTGATATAT 406 AACACATATT 3131 T TAT C A GG
ATGCTGATGTGGACAATAAC TAGATACTGC AGATGCA TATTTGA ATATG TG TGT A
ACATATTTAGATACTGCATT ATTT ||||| ||||| ||| ||| |||
T TTTACGT ATAGATT TATAC AC ATA /
C --- - A AC

GAM421 GTACCTGTCCACCAGACGTT 407 TTGCTGACAA 3132 ----- C--- CG ATA TG G
GTTGATAAAGTTGAGGGTAC AATTTTACAG GTACCT GTCCAC AGA TTGTTG AAGT AG
G
TACACTTGCTGACAAAATTT TGGG |||| |||| ||| |||| ||| ||
TACAGTGGACTAGTTTAGGT TATGGA CAGGTG TTT AACAGT TTCA TC T
AT TTTGAT ACAT AA CG- CA A

GAM422 CTTTAATATGTGCATGGTTA 408 TGGCTAACTA 3133 - C TAAA ATG
GTTAAACATGGTTATGAATC TACACATCAT CTTTAAT ATGTG ATGGTTAGT CATGGTT A
AACCATGGCTAACTATACAC TGGG ||||| ||||| ||||| |||||
ATCATTGGGG GGGGTTA TACAC TATCAATCG GTACCAA /
C A ---- CTA

GAM423 GAATTAATACTTGAAAAAGC 409 TAGAATGCAC 3134 AAA A- T AAAC - C G - AA
C GT

AGATAATACTAAACTAACTA GGATGGAATT AGC GATAA ACT TAA CTAA TTT ATCT TGCA
TTCTAGAA AT C

ACTTTGATCTTGTCAAATTCT GGAT ||| |||| | ||| |||| |||| |||| ||||
AGAACATGTCAAATTTTTAG TCG CTGTT TGA ATT GGTT AAG TAGG ACGT

AAGATTTT TA /

AATGCACGGATGGAATTGGA ATA CA - A--- A - G C -- - AA
TTAAAGTTTGTCCACGCTATA
GCATGTGTTTT

GAM424 AGGGTTGATTATGATAATGC 410 ATAATGCATT 3135 T A - ----- TT TATCTTGCCA
C TTC

ATTTGGAAGGTATCTTGCCA TGGAAGGTAT AGGGT G TTATG ATAA TGCA TGGAAGG
ACA GTA C

ACACGTATTCCTCTTACTTG CTTG |||| | |||| | ||| |||||| ||| |||
TTCTTCCATGTAATCACCTT TCCCG C AGTAC TATT ATGT ACCTTCT TGT CAT

/

ATACATGAACGCCCT - A A CCAC TA -- ----- T TCT

GAM425 AGTCACTAATGTTTCATGTGG 411 TAATGTTTCAT 3136 T ATG-- TGAAGA CTATC AAAA
ATAAA TC

TGAAGAGAGCTCTATCGTTA GTGGTGAAGA C AATGTTC TGG GAGCT GTT GAATCT
CTGGT A

AAAGAATCTATAAACTGGTT GAGC | |||| | ||| ||| |||| ||||
CATTAGTAGAGATTCCAAT G TTACAAG ATC CTCGG CAA CTTAGA GATCA

/

TGGCTCAAACCTCTAATTAGG - GATTA TCAAA- TT--- C--- ---- TT
AACATTGTGTCT

GAM426 CTTGGCCCCATTTCTATTCCA 412 TCACGCTAGG 3137 TG ATT - A T CCCCATATA AGCT
AGTCGTCCCCCATAGAGAAG AAATAGAGGG CT GCCC TCTATT CC AG CGT GAGA G
CTGTAAATCTCACGCTAGG CTGA || |||| |||| || |||| ||||
AAATAGAGGGCTGAG GA CGGG AGATAA GG TC GCA CTCT T

GT --- A A - ----- AAAT

GAM427 CTTTGATAGAAGATCCTGCT 413 TAACAGACAA 3138 TAG T CT ACTAA--- ATG
AAAAC- AA

AGACTAATGTTAGAATGGTT TTGCTCCAGG CTTTGA AAGA CCTG AG TGTTAGA GTTA
AGGG T

AAAAACAGGGAATAGACCTT TCTT |||| | |||| | ||| |||| ||||
ATCGGATGACTCTAACAGAC GAGACT TTCT GGAC TC ACAATCT CAGT TTCC

A

AATTGCTCCAGGTCTTTCAG --- - C- GTTAACAG --- AGGCTA AG
AG

GAM428 GGAGTGCTTAGCAAGCGACC 414 GTGCTTAGCA 3139 G CGA GCC- AG

TAGCCAGGAGGATCCTTAGA	AGCGACCTAG	GGAGTGCTTA CAAG CCTA AGG G
TGGGGTTTTGATAAGTACTC	CCAG	
C	CCTCATGAAT GTTT GGGT TCC /	
	A TG- AGAT TA	

GAM429	AGGTGGATGAGTTTATTGAG 415	AAGCTGCGTT 3140	GGAT TTA GA GCC C T GCTA- T AAC
	CGAGCGGCTGCCGACGTTTT	CAACACTCTA	GAGT TTGAGC GCGGCT GA GTTT GG CT
	GCGCTTCCT C		
	GGGCTACTTGCGCTTCCTAA	GACC	
	CCAAGGGGGAGCGCCAGGCA		CTCA AACTTG CGTCGA TT CAAG CC GA
	GCGGAGGGG /		
	AACCTGAACTTTAAAGCTGC	GAT- C-- --	AA- T T AAACG C GAA
	GTTCAACACTCTAGACCT		

GAM430	CATTGGAACCTTGAATGGCAG 416	CAGTGCAAGT 3141	T GGC ATA C - CAA C TT GA- A ATC
	CACATATGGCTGGTCAAGCC	TACTCTGGGA	CT GAAT AGCAC TGG TG GT GC CTCGG
	TGGC CATTG CC G		
	CTCGGTTTGGCGACATTGAC	GCAA	
	CATCGAAGAGGCAGTGCAAG		GG TTTG TCGTG ACC AC CA CG GGGTC ATTG
	GTGAC GG A		
	TTACTCTGGGAGCAACGCAA	T ACT CA- A G A-- A	TC AAC - AGA
	CCAACGTGCTTCAGTTTTGG		
	TATGCCAATG		

GAM431	GCTCGTCGGTGCGGAACCCA 417	TGCGGAACCC 3142	T GA A- CC- TAG G
	GACCTCCCGTTAGTGGAACC	AGACCTCCCG	GCTCGTCGG GCG ACCC GACCT CGT TG A
	AGGTATGCTAAGGTCCCGGG	TTAG	
	TGTGCCTGATGAGT		TGAGTAGTC CGT TGGG CTGGA GTA AC A
		- G- CC ATC TGG C	

GAM432	GCTGGCGTATGACGGTTGCA 418	TGGCGTATGA 3143	--- TG T A A A C
	CACAGACCACCCACGGGGAC	CGGTTGCACA	GCTGG CGTA ACGGT GC CACAG CC CC A
	TGTGGGCTGCCGTTGTATGA	CAGA	
	CTCCAGC	CGACC GTAT TGCCG CG GTGTC GG GG /	
		TCA GT T G A - C	

GAM433	TTGAAGGTGTGAAGAGTTTC 419	TTGCTCAAGA 3144	TG G - G - A ----- TG
	TGGGACAAGGTGGTCTGTGC	GGCTGTTTGA	T AA GTGT GAA AGTTTCT GGG CAAG
	GTGGTCTG C		
	AACGGACCGCTGCTTTGACT	CACA	
	TGCTCAAGAGGCTGTTTGAC		A TT CACA TTT TCGGAGA CTC GTTC CGCCAGGC /
	ACATTTGA	GT A G G A -	AGTTTCGT AA

GAM434	CTCTTGCCCATGCATCAAC 420	TGGCCCATGC 3145	G -- ACTATTATAACT T
	TATTATAACTCGGGGGTATA	ATCAACTATT	CTCTT GCCCAT GCATCA CGGGGG A

CTCTTGTGATGTCAATGGGC	ATAA				
AGAGAG	GAGAG	CGGGTA	TGTAGT		GTTCTC T
	A	AC	-----	A	

GAM435	GGTGTGTTGTATAGGGTAATGA 421	TAGGGTAATG 3146	T--	A	T A AA	TG TGAT	T
	ATCAAGAGCCTGGTGATTCT	AATCAAGAGC	GG	GTTGTAT	GGGTAA	GA TC	GAGCC G
	TCTAG T						
	AGTTTTCTAGATTGGGCTTC	CTGG					
	AGATCCTTATTCATGCAACC			CC	CAACGTA	CTTATT CT AG	TTCGG T AGATC T
	TTCC	TTC	-	C	- AC	GT ----	T

GAM436	TACCAGTCTAGGTCAGAGGG 422	TGGAATGAAC 3147	AGA-	AG--	TT	ACGG	CT
	CG GG G						
	TTAAGGTATTGTTCAACGGG	TACAGAATAA	TAGGTC	GGGTTA	GTA GTTCA	GAATC	
	GGCT ACAT ATCG G						
	AATCCTGGCTCGACATGGAT	TTCG					
	CGGGAATGATGAATGTGAGG			ATCCGG	CTTAAT	CAT CAAGT	TTTAG TCGG TGTA
	TAGT A						
	CTTTGATTTGGAATGAACTA		ATAG	AAGA	--	AAGG	TT AG AG A
	CAGAATAATTCGATAGGCCT						
	AGTCCACTGTG						

GAM437	AGCTTAACCCGTTGAATGGT 423	GTACATTGTT 3148	T	CC-	-	AT T TC--	T CAG
	ACATTGTTCTCTTGTTGCC	CTCTTGTTG		AGC TAAC	GTTGAATG	GTAC TG TC	TTGG TGC
	C						
	AGCGATAGCATCCAATTTTG	CCAG					
	ATCAGTACACATTCAACAGC			TCG GTTG	CAACTTAC	CATG AC AG	AACC ACG G
	GTTGTGCT	T CGA		A	--	T TTTT	T ATA

GAM438	GAAGCGATGCTTAGGGTACC 424	GATCACAAAC 3149	A	GGT	C--	ATTAAGAGAT
	GA TTC					
	CACCGATAAGATTAAGAGAT	TTATCGACTT		G AGCGATGCTTAG	ACCCA	CGATAAG
	TTTGTGAT CAG C					
	TTTGTGATGACAGTTCCACA	GGGT				
	TCTGATCACAACTTATCGA			C TCGTTACGGGTT	TGGGT	GCTATTC
	GTC A					AAACACTA
	CTTGGGTCAATTGGGCATTG		A	AAC	TCA	-----
	CTAC					-- TAC

GAM439	GTAGCAGTGACTAGACAACT 425	TGGCAGGACG 3150	A	----	AA	TAAGC
	TGTCGGTAGTAAGCCTAAGT	TCTGGCTCTG		GTAGC	GTGAC	TAGAC CTTGTCTGGTAG C
	TTACTGGCAGGACGTCTGGC	TCAC				
	TCTGTCACAGTTAC			CATTG	CACTG	GTCTG GGACGGTCATT /
		A	TCTCG	CA	TGAAT	

GAM440	TAGCGGATATCATTTGATCG 426	TGGTATGGAA 3151	A	TT	C	AA TAAA--	TG - A
	GA						

GTGAATCTAAATCGTATTGT	TCCCGAGGCA	TAGCGGAT TCAT GAT GGTG TC	TCGTAT T
GA TTAG T			
GAATTAGGATCTACTGGATC	CCTA		
TATGGTATGGAATCCCGAGG		ATTGTCTA AGTG TTA CCAC AG	GGTATG A CT GGTC
C			
CACCTATTTGTGAATCTGTT		- T- T GG CCCTAA	GT T A AT
A			

GAM441 GCCTTGGGCGGATCTGTAAA 427	TGTAAACATT 3152	--- TCTG	----- G CATTATA
TC- T T			
CATTTGGGCCATTATACCTC	TGGGCCATTA	CCTTGGGC GGA	TAAACAT TT GGC
CCTC AG GCA C			
TCAGTGCATCAGTGTTCTAC	TACC		
CGAGGAGCCGAAAACATTGT		GGAACCTG CCT	ATTTGTG AA CCG GGAG TC
TGT A			
GTTTAATCTTCCTGTGTCCA		TGT TCTA TTACAA G A-----	CCA T G
AGGT			

GAM442 GTTGTGGTAGAACCGTCATT 428	GATGACAATA 3153	---- A TTAG G GG	TCA TG T
C C			
CATTTAGAATGGTTGTTGGG	TTATTATGAA	CC GTC TTCAT	AATG TTGTTG CTTTA AG TA
TAGTCAG AT A			
CTTTATCAAGTGTATTAGTC	GA CT		
AGCATCAGCATCTGGCTATT		GG CAG AAGTA	TTAT AACAGT GAAAT TT AT
ATCGGTC TA G			
ATGTTTAAAGATGACAATAT		TCCT - TTA- - A- --- GT T - C	
TATTATGAAGACTCCTGGTA			
ATACTGATGC			

GAM443 CCACCGAAACAAGATAATAA 429	TCTCCTGCCT 3154	AAT AGAA A GAT TA	
ATATTAGA TG--- AC			
ATGCAGAGAAGAGAATGGAG	ATTATATGTT	TAATA GCAG GAGA TGGA	TT TCA
TTGTG CCT G			
ATTTTATCAATATTAGATTG	AAAA		
TGTGCCTACGAAAAGGAATA		ATTAT CGTC CTCT ATCT	AG AGT AACGT GGA
A			
TTGCAATGACGGATATCTAT		C-- ---- - AT- GC -----	TATAA AA
CTCCTGCCTATTATATGTTA			
AAACAGGTGG			

GAM444 TAGTGTTAGAAATAGAAGAC 430	TGAGATGTTT 3155	AATAGAA AATAT - AT	
TTTAATATCAAGCATTTATT	GTTAGAAGTC	TAGTGTTAGA GACTTT	CAAGCATTT ATTT G
TATGGCAGGTGAGATGTTTG	AGTC		
TTAGAAGTCAGTCTAGTACT		ATCATGATCT CTGAAG	GTTTGTAGA TGGA /
A	GA-----	ATT-- G CG	

GAM445 AGAAGATTTTGTGTTTGCCT 431	TACAGCACAG 3156	TGTGTT C T GTA TT	
GTTGCAGTAGTTGTGCGTAT	TATGAATTTT	AGAAGATTT	TGC TGT GCA G G
GCTACAGCACAGTATGAATT	CT		
TTCT	TCTTTTAAG	ACG ACA CGT C /	
	TATGAC - T	ATG GT	

GAM446 TCAGTGAGTGGAAGGGAGTT 432 TTCGCTGCAA 3157 - GG GGGAG G AGA CAA C
GGA

AGAGGAAATAGAGCACAAGC GTTTTGTTTA TC AGTGAGT AA TTAGA GAAAT GCA GC
AATAGG A

CAATAGGGGAAATACCTATT AAGA || ||||| || |||| |||| || || |||||
CGCTGCAAGTTTTGTTTAAA AG TCATTTA TT AATTT TTTTG CGT CG TTATCC /
GAAATTGGATTTACTAGA A GG AAAGA G AA- --- C ATA

GAM447 GAGCTGTTTAAATGCAAGGA 433 TGGAGTGGGG 3158 AAA A AC- G AG T
AAGTT

CCTAAATGCTAAGCTGTATG TTTGGAGACC GAGCTGTTT TGC AGG CTAAAT CTA CTGTA
GGT T

GTAAGTTTAAAGAGCTTTAT TGGT ||||| ||||| ||||| ||||| ||||| |||||
GGAGTGGGGTTTGGAGACCT TTTGACAGA ATG TCC GGT TTG GGT GGTAT TCG /
GGTAAGACAGTTT --- G AGA G GA T AGAAA

GAM448 TACCTAAAAAAATTGCATT 434 TGAATGAGC 3159 AAAAAAAT T--- T G C- C G
AA

TGTATTGTGGGTCCTCCAGA CTGATGCACT TACCT TGCAT TGTATTG GG TC TCCAGA
ACA G A

CACAGGAAAGTCATGTTTTG TTAT |||| |||| ||||| ||||| ||||| |||||
GAATGAGCCTGATGCACTTT ATGGA ACGTA ACGTAGT CC AG AGGTTT TGT C /
ATGCAAGGTA ----- TTTC - G TA - A TG

GAM449 ACTGGTGCAGCTGAAGAAAT 435 TTCATAGTGA 3160 T C AA AATAC - A
ACCTATGGACACATTTGTTG TCCACTGTCC ACTGG GCAG TG GA CTATGGACA C T

TTCATAGTGATCCACTGTCC AGT |||| |||| ||||| ||||| |||||
AGT TGACC TGTC AC CT GATACTTGT G T
- - -- AGT-- T T

GAM450 CGCTCTTTTACCGGAGTTTC 436 TACCGGAGTT 3161 - T TTCTCGCC - TT

TCGCCACAAGCTTTTCGCGT TCTCGCCAC CGCT CTT TACCGGAGT CAC AAGC T
TTAGTGCTCAAATGCTTTGG AAGC |||| |||| ||||| ||||| |||||
TATAGGTAGTG GTGA GGA ATGGTTTCG GTG TTTG C
T T TAAACTC- A CG

GAM451 GCACCCCATGACTGGCAGAT 437 TGTGCAATTT 3162 ATGACT -- GG - A T
CATGGCTACGGGCGTGGAGG GTCCGCTAGG GCACCC GGCAGAT CATGGCTACG CGT

GG GGAGGCT A
AGGCTTACCGGCCTTCCCGA GGTG ||||| ||||| ||||| ||||| ||||| |||||
CGACGTGGCTGTGCAATTTG CGTGGGG CTGTTTA GTGTCGGTGC GCA CC
CTTCCGG C
TCCGCTAGGGGTGC ATCGC- AC A- G - C

GAM452 GGGGTCCAAAGAGGTTTCTG 438 TACTATGATA 3163 GAG AGCA C AC TTTAC
ACA GATG
AAGCAGCTCGGTACTCATTT ATCTGGCGTT GTTTCTGA GCT GGT TCAT
GTGGCTTTCGGGT CCCCT A
TACGTGGCTTTCGGGTACAC AGAA ||||| ||| ||| ||||| |||||
CCCTGATGAACAAAGGGGAC CGAAGATT CGG CTA AGTA CATCGGAAGCTCA
GGGGA /
TCGAAGGCTACTATGATAAT CGA G--- T AT T---- --- AACA
CTGGCGTTAGAAGCAGCATG
GGACCCC

GAM453 ACTGCCATGCTTTACCACGT 439 GTGAGCCCGT 3164 - CTTT CA TATTA AG A AC
CCTAT
TTATTATTCAAGACAGGTTT TGAAGACGGA ACTGC CATG AC CGTT TTCA AC GGTTC
CCGC T
AACCCGCCCTATTCCCTCAG GTTA ||||| ||| ||| ||| ||||| |||||
TGGTGAGCCCGTTGAAGACG TGGCG GTAC TG GCAG AAGT TG CCGAGT GGTG
C
GAGTTACATGCGCGGT C AT-- AG ---- -- C -- ACTCC

GAM454 ATTAGACTCGACAGGTTAGA 440 CAGGTTAGAG 3165 AC - G - TT- TAT-- ACC--
GT
GTCAGTTTGTATGCTCACC TCAGTTTGT ATTAG TCGAC AG TTAGAGTC AG TGT GCTC
CCT T
CCTGTTTAGAGGAACTAGAG ATGC ||||| ||||| ||||| ||| ||| |||
TTTAATGCATATCTAGACTC TGATT AGTTG TT AGTCTCAG TC ACG TGAG GGA T
TGAGTTGGTTGACATTAGT AC G G A TAT TAATT ATCAA GA

GAM455 TGAGTATGGAAAGAAGCTTT 441 TCACGGGTGA 3166 AAA--- -- T----- GGTG CCC
TT
TCTTCCGTGGTGTACCTGTC CGGATTCTAC TATGG GA AGCTTTTC TCCGT TACCTGT
GGGCTGT G
CCGGGCTGTTTGAAGCAGCT TGGA ||||| ||| ||||| ||||| ||||| |||||
CTCACGGGTGACGGATTCTA ATATC CT TCGAGAGG AGGCA GTGGGCA
CTCGACG /
CTGGAGAGCTATTCCCAAAC CAAACC TA TCATCTT ---- CT- AA
CTATACTCA

GAM456 ATGTATCGTAAGTTCTCTAA 442 TAAGTGTACT 3167 A G C---- CTATAGT A- ATAA
GTGTACTATAGTTGACAGTA ATAGTTGACA ATGT TC TAAGTT TCTAAGTGTA TGAC
GTATG T
TGATAATAGGGCATATAGGT GTAT ||||| ||||| ||||| ||| |||||
CATCATTATATTTGGATTAA TACA AG ATTTAA AGGTTTATAT ACTG TATAC /
AAATTTAGAAACAT A - AAATT TACT--- GA GGG

GAM457 CGATGATGAATATTACAAGA 443 TGATGAATAT 3168 GAATATTACAA-- T A TA

TTAGAAGTTATAGGATTAAC	TACAAGATTA	CGATGAT	GAT AG AGTTA G
TACTCATTGCACAAAATTAA	GAAG		
GATCATCG	GCTACTA	TTA TC TCAAT G	
	GAATTAAAACACG	C A TA	

GAM458 GTATTAATATGAATTATAGC 444	TCGCATGATT 3169	TTA	A	A	TAT TGAA- TC
GATGATTATATGATGAACAT	TATATGATTA	GTA	ATATGAATTAT	GCGATG	TTA GA CA T
CTATTTGAATTTTCCTTGGC	C				
TATCGCATGATTTATATGAT		CAT	TATATTTAGTA	CGCTAT	GGT CT GT A
TAC	TAG	-	C TC-	TTTAA	TT

GAM459 TACTAATATCCTTGACGAAT 445	CGAATGAAAT 3170	TATCC AC-	AATAT CA	AA
GAAATATATACATCTATAAT	ATATACATCT	TACTAA	TTG GAATGA	ATA TCTAT T
TAATAGAGATATCATAGTTA	ATAA			
TTTACCCAACTTTAGTA	ATGATT	AAC TTTATT	TAT AGATA /	
	TCA--	CCA	GATAC AG	AT

GAM460 CCACCAAGACAAGATAATAA 446	TCTCCTGCCT 3171	AG	AAT	AGAA	A G -- --	GA-
- T						
ATGCAGAGAAGAGAATGGAG	ATTATATGTT	ATAATA	GCAG	GAGA	TGGA ATT	TTAT
CAATATTC TTGTG G						
ATTTTATCAATATTCGATTG	AAAA					
TGTGCCTACGAGAAGGAATA		TATTAT	CGTC	CTCT	ATCT TAG	AGTA GTTATAAG
AGCAT C						
TTGCAATGACGGATATCTAT	A-	C--	----	-	A GC AC	GAAG C
CTCCTGCCTATTATATGTTA						
AAACAGGTGG						

GAM461 GGAAGACACATTATTTGACG 447	TAGAACGCTC 3172	CAC	T C -	AG	CT
ACGAGTTATACTCTATTATA	TTTCGATGAT	GGAAGA	ATTATT	GA GA CG	TTATA C
GAACGCTCTTTTCGATGATAA	AATT				
TTTTCC	CCTTTT	TAGTAG	TT CT GC	GATAT	T
	AA-	C T C	AA	TA	

GAM462 GATACAACGGTTACTATCAA 448	TGAATAGCGA 3173	CAACG	A ATA---	-	CG--	AA
A						
TATTATTCATTTAGCGATTA	GAGTGAGAGT	GTTACT	TCA	TTATTCAT	TTAG	ATTATGA
ATTATAATGA T						
TGAAAATTATAATGAATATT	GATA					
ATTATGATGATTATGATAGA		TAGTGA	AGT	GATAAGTA	GGTC	TAGTATT
TAGTATTATT /						
ACTGGTATGAATAGCGAGAG	ATAA-	G	GAGAGC	T	AAGA	AG A
TGAGAGTGATAATATATC						

GAM463 GCGTATCAAATGTAAATGAC 449	AATGACGCGG 3174	A	C AC	A	CAGATAACTAATG
CACA ATG AAA					
GCGGAACACATATCTCAGAT	AACACATATC	ATGACG	GGA	ACAT TCT	ATGTATCTA
AAC GG A					

AACTAATGATGTATCTACAC TCAG ||||| ||| ||| ||| ||||| ||| ||
 AAACATGGGAAAAGAAATCA TACTGC CCT TGTA AGG TACATAGAT TTG CT
 G
 GAGTTAGATAGATACATGGA A T A- A ----- AGA- AGA AAA
 AATGTATCCTCGTCATAGAT
 ATAGTAAGC
 GAM464 TCACTGACTAACCATATAAT 450 TTATTTGGCA 3175 C- AA- T GA- - CT
 AGATTATGTTCTTACAGACA AAGTCAAATG TCA TGA CT CCA ATAATA TTAT GTT T
 ATAAAAATATTATTTGGCAA A ||| ||||| ||| ||||| ||| |||
 AGTCAAATGA AGT ACTGA GGT TATTAT AATA CAG A
 AA AAC T AAA A AC

 GAM465 CACTTATTACTCCATTATTG 451 TCTCAGAATC 3176 TATTAC TAT GG ATGAACTT
 CACCAAA T
 GCGGAGGTCTGAGAATGAAC CGCTAATGGA CACT TCCAT TGGCGGA TCTGAGA
 TGGATT TG C
 TTTGGATTCACCAAATGTCC AACG ||| ||||| ||||| ||||| ||| ||
 TCAGATTAAATCCATCTCAG GTGA AGGTA ATCGCCT AGACTCT ACCTAA
 AC C
 AATCCGCTAATGGAAACGCA CGCAA- --- A- ----- ATTAG-- T
 GTG

 GAM466 ATATTACGTTCCCTGTCGGCG 452 TACAGTAGCT 3177 TT T C--- C CAAATTTCCCC -
 TA GAT
 ACAAATTTCCCCGCGCTGTA TTGCCACAA ATA ACG TC TGT GGCGA GC GCTGTAT
 TGT T
 TTATGTGATTTAGACGGTAC ATAG ||| ||| ||| ||||| ||| ||||| |||
 AGTAGCTTTGCCACAAATA TAT TGC AG ACA CCGTT CG TGACATG GCA /
 GATCGTTTTAT TT T ATAA C T----- A -- GAT

 GAM467 GCCAGCACCCGAGGAAGTGC 453 TTTGCAAGCT 3178 AGCACC -- T TT AAC TT
 GTC T
 TTTTGCAGAAAACCTTTGCG CTTCAACTTG GCC CGAG GAAG GCT TGCAGAA CT GCGT
 AGACG G
 TGTCAGACGTGACGTTTAAA ACGA ||| ||||| ||||| ||||| ||| ||||| |||
 CGTTTAGTTTTGCAAGCTCT CGG GTTC CTTC CGA ACGTTTT GA TGCA TTTGC /
 TCAACTTGACGAGGC AGCA-- AA T -- --- TT AA- A

 GAM468 CTCATGTGGTACGAGCTGAG 454 TGCCAAGTTG 3179 ACGA - GAT-- ACCC G
 ATGAGCGC T A C
 CAAGATCAACCCACACGCG ATAGGGGACG GCTGA GCAA CA CACCA CGTC CA
 CT TGGCAGGC A
 TCATGAGCGCCATCTATGGC TGGT ||||| ||||| ||| ||||| ||| ||||| |||
 AGGCCAGTGTCTGCCAAGTT TGA CT GT GTGGT GCAG GT GA
 ACCGTCTG G
 GATAGGGGACGTGGTGTGAG GTTG A AGACT GACT - GGGATA-- T - T
 TGTCAGATTGTATCAGTGT

GACCAAAAGAG

GAM469 CACCGAGGTGGTGAATA 455 TGGCCCAGCT 3180 A - AATATCAT A CT
TCATGCTGGGACCGGCCTTT CCAGATCACC CACCG GGTGGTGA CT GCTGGG CCGGC T
GAGCTGGCCCAGCTCCAGAT GCCG |||| ||||| || |||| ||||
CACCGCCGCGGTG GTGGC CCGCCACT GA CGACCC GGTCTG T
G A CCT----- - AG

GAM470 ATGTCTATGACATCCTTGAC 456 TATCATGGAT 3181 ATG----- TTGAC T
ATGATAATTAACGTTATCAT GTATTTTACG ATGTCT ACATCC ATGATAAT A
GGATGTATTTTACGAGACAT AGAC |||| |||| |||||
TACAGA TGTAGG TACTATTG A
GCATTTTA ----- C

GAM471 GATGGGTTAGTGAAAAAGGT 457 TGGGTTAGTG 3182 - G AAAAAGG A A- AAAC
GGCATCAGAATCCAGAACT AAAAAGGTGG GATGG GTTA TG TGGC TC GAATCCAG T
TGCTCCTGGATTGAGAGCT CATC |||| |||| |||| |||||
AATATGAACAATGACATTAT TTATT CAGT AC ATCG AG TTTAGGTC T
T A A AAGTATA - AG CTCG

GAM472 CGTTGCGGGAGCAATACAGC 458 TGCGGGAGCA 3183 T G AATA- CGAAAC G A- - A
A
GAAACCTGGCATATGGACGA ATACAGCGAA CGT GCGG AGC CAG CTG CAT TGG ACG
GG A
GGAACACCCGTACCGGACAT ACCT |||| |||| |||| |||||
GGCAGTACTGGGGCAGCTAC GCA CGCC TCG GTC GAC GTA GCC TGC CC C
CGCACG - A ACGGG AT---- G CAG A - A

GAM473 GGATGGACGCACCCTGGTGG 459 TCACCGGGGT 3184 ----- A -- C GAGA - TG
TGCCGTGCCGAGACCAAGAT GCGGCTGGAG GGAT GG CGCACCTGGTG GTGC GTGCC
CCAA GA A
GAACTCGTTGGGAGGGCGCG TGTC |||| ||||| ||||| |||||
CATCTCACCGGGGTGCGGCT CCTG TC GCGTGGGGCCAC TACG CGCGG GGTT CT
/
GGAGTGTCC TGAGG G TC - GAG- G CA

GAM474 GTCTGGTGTGGCCACAGTG 460 TAACAGAGGC 3185 T G TG- A G T- A C-- T
ATGA G
TTGTGCCTCATGTCGGTGGT TTCAGCAGTG G CTG TGT G CC CA TGTTG GCCTC TGT GG
GGTC ACC A
CATGAACCGAACGGTGGCCT GGAC | |||| | ||||| ||||| |||||
CCATAACAGAGGCTTCAGCA C GAC ACG C GG GT ACGAC CGGAG ACA CC CCGG
TGG A
GTGGGACTGGCAGCAGC - G GTA - G TT - ATA T --- C

GAM475 TGATGATTCACTGTCCTATG 461 TGTGGGAAAC 3186 -- G G - CA CAAGGAGA GC
TG GGATT T
AGTGTGTGACCATAGATCAA AGGAAGGCTC TCCTAT AGTGT TG AC TAGAT AGA CTGT
ACGT GT T
GGAGAAGAGCCTGTTGACGT A ||||| ||||| || ||||| ||| ||||| ||| ||
GGATTGTTTTTGCCGGAACG AGGGTG TCGCA GC TG GTCTA TCT GGTA TGCA
CG T
TTGATGGAGTCTATCTGGAG AA - G A AG ----- GA GT AGGC- T
TACGGACGCTGTGGGAAACA
GGAAGGCTCA
GAM476 TGCAGCCTTGGGAGCTTGGT 462 CAGCCTTGGG 3187 GGGA-- G GA AGC
CAGATGAGCAAAACAGATGG AGCTTGGTCA TGCAGCCTT GCTTG TCA TG A
GCAAGTGCAAGAGAGGCTGT GATG ||||| ||||| ||| ||
A ATGTCGGAG TGAAC GGT AC /
AGAACG G AG AAA
GAM477 AGGTCTCAGCCGTGCTCCGG 463 TGAGGTACAG 3188 C GGC A C ACAGT G
GT
CGCCTGAGCCTCACCCGCAC GTGGGGTATG AGGTCTCAG CGTGCTCC GCCTG GCCTCA
CCGC GGTT CCCTG C
AGTGGTTGCCCTGGTCAACA TCTG ||||| ||||| ||||| ||||| ||| ||||| ||||| |||||
GGGAGCCTAAGGTGGATGAG TCCAGGGTC GTATGGGG TGGAC TGGAGT GGTG
CCGA GGGAC /
GTACAGGTGGGGTATGTCTG T --- A A GAAT- - AA
GGACCT
GAM478 AGGTTCTGAGCGACCTCAAG 464 TGAGCGACCT 3189 G CT T TAG- - AAA AG C
T A
CTCCCTGGCTTAGCAGTCCA CAAGCTCCCT GC AC CAAGC CCCTGGCT CAGTCCA CCG
GA GC GGGGCGT GCG A
CCGAAAGAAGGCCGGGGCGT GGCT || || ||||| ||||| ||||| ||| || ||||| ||||| ||||| |||||
TGCGAACACGCATGCTCCGC CG TG GTTCG GGGATCGG GTCGGGT GGC CT CG
CCTCGTA CGC C
TCGCGCGGTTGGGCTGAGTT G TT - TTGA T GCG -- - - A
GGCTAGGGGCTTGTGTGGC
ATCCAGGCCT
GAM479 ATGATACAACCTGCTTTCACA 465 TCACTGACTC 3190 CT - - CTCCC AC CAA T
GA TT
AGGATCACTGACTCCCCCT CCCCTGACG GCTT TCACAAG GATCACTGA CCCTG GTATT
CCTA GG GGT T
GACGTATTCAACCTATGGGA TATT ||||| ||||| ||||| ||||| ||||| ||| ||| |||
GGTTTTTGCCAAACCCTAGG TGAG AGTGTTT CTGGTGGCT GGGGC CGTAG GGAT
CC CCG /
CAGATGCTACGGGGCGTTTC CG T A TTGC- AT AC- C AA GT
GGTGGTCATTTGTGATGAGT
GCCACAGTCAT
GAM480 ATGGGCATGGAATACCCCTC 466 TGGCCAGTTC 3191 - AAT-- G T- GAA - AC TG
T ATT
GAGCGGATGCGAACCGGAAG TCCGCTAGGG TGG ACCCCTC AGCGGA GC CCGG
AAGGC CTCG TTC GCC C

GCACCTCGTGTTCTGCCATT GGGT ||| ||||| ||||| || ||||| ||||| ||| |||
 CTAAGGCTGAGTGCGAGCGC ACC TGGGGGG TCGCCT TG GGTC TTCCG GAGC
 GAG CGG /
 CTTGCTGGCCAGTTCTCCGC T GTAAC A CT ACC G C- GT T AAT
 TAGGGGGGTCAATGCCATTG
 CCTAT
 GAM481 CATCTGGCCAGATGCTGTGA 467 GGAGATCTTG 3192 TG T GGT T TT C TT -
 C
 TGATGGTGGTGGTTGCCTTG GTGTCCCGGC CCAGATGCTG ATGA GGT GG TGCC GGTC
 TTCTCT GGCCTG TTCGA G
 GTCCTTCTCTTTGGCCTGTT CCTC ||||| ||||| ||| ||| ||| ||||| ||||| |||||
 CGACGCGTTGGATTGGGCCT GGTTCGCGC TGCT CCG CC GTGG CTAG AGGAGG
 CCGGGT AGGTT C
 TGGAGGAGATCTTGGTGTCC GT C GC- T TT - TT T G
 CGGCCCTCGTTGCGGCGTTT
 GGCTCGGGTG
 GAM482 CCGTCCGGCTGGTCTCCAAG 468 TGTCAAGGAG 3193 - T - AA -TG - T TT
 ATGTGTGCGAGAGGAGCTTA CGCCTGTTGG CCGT CCGGC GGT CTCC GAT G TGCGAGAG
 GAGCTTAT TG C
 TTTGTTGATCATATGGGCT AATG ||| ||||| ||| ||| ||| ||||| ||||| |||
 CTTTTTCGCGTGCTGTCAAG GGTA GGTTG CCG GAGG CTG C GCGCTTTT CTCGGGTA
 AC G
 GAGCGCCTGTTGGAATGG A T C AA TGT T T TA

 GAM483 CGGCTGATATCGGAGAAGCC 469 TGATATCGGA 3194 AGAAGCCGC - TC CT
 GCGGTGTTCTTCTCTGGGCT GAAGCCGCGG CGGCTGATATCGG GGTGT TCTTC TGGG
 C
 CGCCCCATTGAGGATGCACC TGTT ||||| ||||| ||||| ||||| |||||
 CTGATGTCAGCTG GTCGACTGTAGTC CCACG AGGAG ACCC /
 ----- T TT CG

 GAM484 CTCAGGGCCCTCTGCCCCGT 470 CATTGCGGGG 3195 A - G TG TAC
 GGTGTCACTACCCTTGTGGC AGGGGTGGTC CTC GGGCC CTCT CCCC GTGTAC C
 ATTGCGGGGAGGGGTGGTCC CGGG ||| ||||| ||||| ||||| |||||
 GGGG GGG CCTGG GGGG GGGG TACGGTG /
 G T A GT TTC

 GAM485 CTTGGTTTGCCTCCACCAGT 471 AGTGGTCGCG 3196 C-- A G CT A AGAT AGTTTA
 C T T
 GGTGCGGACTCGAAGATAGA ACTCGAAGAT CT CACC GTG TCGCGA CGA GAT GTGTGG
 GTGC AG TGGC C
 TGTGTGGAGTTTAGTGCCAG AGAT || ||||| ||||| ||| ||| ||||| ||||| |||||
 TTGGCTCTGCCACCTGCACC GG GTGG CAC AGCGCT GCT CTA CACGCC CACG
 TC ACCG /
 ATAGCCGCACTTGGATCATC TCC - - AG A GGTT GATAC- - C T
 GGATCGCGACACGGTGCCTG
 GGCTCTCCGAG

GAM486 GACTCGGTGTGGCGGAGGGT 472 AGGGTTACGT 3197 ---- GA CG G C- TT
TACGTCCGCTGCGACGCTGG CCGCTGCGAC GACTCGGTGTG GCG GGGTTA TCC CTGCGA
GCTGGGCCGATC G
GCCGATCTTGATGATCGGTC GCTG ||||| ||| ||||| ||| ||||| |||||
TAGCTATCGCGGGGGGAATG CTGGGCCACAT CGC TCTAGT GGG GGCGCT
CGATCTGGCTAG /
ATCTACGCGTCATACACCGG ACTG A- AA G AT TA
GTC

GAM487 GCCAGAGGAGTCGCTGGCGG 473 CTGCTCATCG 3198 A TC G TT TC
TGGTTGGGGTTCTTAGCCCT TAGCCCTCTT GCC GAGGAG GCTG CGGTGG GGGGT T
GCTCATCGTAGCCCTCTTCG CGGG ||| ||||| ||| ||||| |||||
GGT TGG CTTCTC CGAT GCTACT TCCCG /
G C- - CG AT

GAM488 GGCACGGTTGGTCCCGCTGA 474 TGCTATGGTG 3199 T T T-- TG TG GGGTGAAC
C
TCTTGCTGCTGCTATGGTGG GTGGGTGAAC GT GG CCCGC GATCT C CTGCTATGGTGGT
CAGCTGGCAGTC T
TGGGTGAACCAGCTGGCAGT CAGC ||| ||||| ||||| | ||||| |||||
CCTAGGGCTGCCGGCTGTGG CG CC GGGCG CTGGA G GACGGTGCCGCCG
GTCGGCCGTCGG A
AAGCCGCCGTGGCAGGTGAG T C CTT GT -- AAGGT--- G
GTCTTCGCGGGCCCTGCCCT
GTC

GAM489 GGGCACTTGGGAAATACTAT 475 TATTGCAGAT 3200 - AATACT AGG - T G
GCCTCAGGCACCATGGTCAC CCTCGGGTGT GGGCACTTG GGA ATGCCTC CACC ATGG
CACCCC G
CCCGGAAGGGGTGCCCGTCG CC ||||| ||| ||||| ||| ||| |||||
GTGAGAGGTATTGCAGATCC CCTGTGGGC CCT TATGGAG GTGG TGCC GTGGGG A
TCGGGTGTCC T AGACGT A-- C C A

GAM490 GTCCGCGGCCCAACTGGTGG 476 TGGGATCCTG 3201 - A GTG AG- - ATA- CTGTC
TA
GGGAGCTGGGTAGCCTATAC GGCCTGGGTG CC ACTG GGGG CTGGGTA GCCT
CGGGCCC GGTCTCGGCC T
GGGCCCTGTGGTCTCGGC AGGT || |||| ||| ||||| ||| ||||| |||||
CTATGTGGCTGGGATCCTGG GG TGGC TCCT GGCTCAT TGA GTCCGGG
CTAGGGTTCG /
GCCTGGGTGAGGTGTA CTG A G AA- GTG G GTGG TC--- TG
GGTGTCTAACGGTGGGAGT
CGCGTTGAC

GAM491 GTCGGCCTGCCTCCTGCGGC 477 TCGGTGCGGC 3202 T-- C G T TG - - -- A
ACCTGTGTGAGGGACTGCTG GTGGGGCCTC GTCGGCC GCCTC TGC GCACC GTG A GGGA
CT GCTGGCCCG G
GCCCAGACCGGGTCGGTTA GGCT ||||| ||||| ||| ||||| ||| ||| ||| |||||
GGTCCCATTCCATCGGTGC CAGTCGG CGGGG GCG CGTGG TAC T CCCT GG
TGGCTGGGC A

GGCGTGGGGCCTCGGCTGAC

CTC T G C C T A T A T C

GAM492 GTGCTGTTAGGCATTGGGAG 478 CCGGATCCCC 3203 TAGG T A G C GC TG CG
TG AA

AGTCCGGGAGCTGGCGCGTG TATGACGCAG GTGCTGT CAT GGG GA TCCGGGAG TG GCG
GGTG GGG C C

GGTGCGGGGTGCAACTAGTG CAC ||||| ||| ||| ||||| || ||| ||| ||
CTCTACGCCACCGCTACACC CACGACG GTA CCC CT AGGCCCTC AC CGC CCGC
CTC G /
TCCCGGATCCCCTATGACGC CA-- T - - C AT CA AT GT AT
AGCAC

GAM493 TATTTCCACAGAGCGACGCG 479 TCCACAGAGC 3204 A GAC CAGGA T AGATGTCGT
G T - TC

ACCAGGAAGCTTACCGTCAA GACGCGACCA GC GCGAC AGCT ACCGTCA GCT CG
TGA AAAGAGCG A

GATGTCGTGCTGCGTTGAAA GGAA || |||| ||| ||||| ||| ||| |||||
AGAGCGTCACGCGCTTTTTTC CG CGTTG TCGG TGGCAGT TGG GT ACT
TTTTTCGC /
TCATTGGGGTTGACGGTGGC - AT- TAG-- - ----- G T C GC
TGATGTTGCTAGCCTGTGTG
AGATG

GAM494 TCCCTGCGGACAGTGCCTGC 480 TGCAAAGACG 3205 - - GACA- GCC TG
GTCGGCTGAACTGTCGATGC AGGACGCACG T CCC TGCG GT TCGGTCGGC A
AAAGACGAGGACGCACGGGT GGTA | ||| ||| || |||||
A A GGG ACGC CA ACGTAGCTG A
T C AGGAG GAA TC

GAM495 TCGCATCATACGGGATGCCG 481 TCATCGGCGT 3206 ATAC C- TG -TG G A -
T

CGAGGACTTTGTCCTGCGGG CTTCCAGGAT TCGCATC GGGATGCCG GAGGACTT TC C
CGG C GTGCG TCATGGG T
CAGTGCATCATGGGTTTACC GTGA ||||| ||||| ||||| ||| ||| ||||| |||||
CGTGGTTGCGCGCCGTGGTG AGTGTAG TTCTGCGGC CTCTTGGA AG G GCC G
CGCGT GGTGCCC T
ATGAGGTTCTCATCGGCGTC GACC TA GT T GT - - T A
TTCCAGGATGTGA

GAM496 ATGACAAATTTTCAGGAAAAA 482 TCAGGAAAAA 3207 AAT G AAC GT- TT
CGGTGTTGTAATAATTCATT CGGTGTTGTA ATGACA TTCAG AAA GGTGTT AATAA C
TGTTTAAGACATTATTTGCT ATAA ||||| ||||| || ||||| |||||
GAACTCTGTCAT TACTGT AAGTC TTT TTACAG TTGTT /
CTC G A-- AAT TA

GAM497 GTTGACATCATTGAGAAAGA 483 ATCACAAATA 3208 ACATCA G - - CAAAACAA
G G

TTTGGATTTTTCCACAAAAC TTTTCAACA GTTG TTGAGAAA ATTTG GATTTTT CCA
TATG TCTT T

AATATGGTCTTGTAAGAG GCAA |||| ||||| ||||| ||| ||| |||
 TATATGGCGAAAATCACAAA CAAC AACTTTTT TAAAC CTAAAAG GGT ATAT
 AGAA A
 TATTTTTCAACAGCAAC GAC--- A A C ----- G A

GAM498 CTCACCTGACTGTCTCATGT 484 TGGAATGAGT 3209 --- GACT - GTA CT AA
 ATCCAGCTGAAACAAATCCT ACTGAAGAAA CTCAC CT GTCTCAT TCCAG GA C
 GGAATGAGTACTGAAGAAAG GTGA |||| || ||||| |||| ||
 TGAG GAGTG GA CA GAGTA AGGTC CT A
 AAA AGT- T --- -- AA

GAM499 GGACGAAAGTCTCAGCAACA 485 TATGTTGATG 3210 AA C G C- AG
 TGTATCCACAGTTTTGTGCT ACATCATCGT GGACGA GT TCA CAACATGTAT CAC T
 GTATATGTTGATGACATCAT CT ||||| || ||| ||||| |||
 CGTCT TCTGCT TA AGT GTTGTATATG GTG T
 AC C A TC TT

GAM500 GGATTTTGGCAGGTACGCCT 486 TTTGGCAGGT 3211 TAC C C----- ACA TCA C TC
 C C
 TGCTCCAGAAACAATTCAGC ACGCCTTGCT GGCAGG GC TTG TCCAGAA AT
 GCTAACCG TT AG TGTCC C
 TAACCGCTTTCAGCTGTCCC CCAG ||||| || ||| ||||| || ||||| || ||| |||||
 CAAGGACACTACGAATGGTT TCGTCC CG AAC AGGTTTT TA TGATTGGT AG TC
 ACAGG A
 AGTCATGCCTTTTGGATTAA C-- - AAAATT CCG C-- A CA - A
 AACAAGCCCCTGCTATTTTC
 C

GAM501 GCTTGGCGTTTGGATTGTCT 487 TATGACAATC 3212 CG -- TA----- AA
 ATTCCAATGCAAATAGCATT TTAAGAGACC GCTTGG TTT GGATTGTC TTCCAATGC A
 GGAGGGTATATATGACAATC AGGT ||||| ||| ||||| |||||
 TTAAGAGACCAGGT TGGACC AGA TCTAACAG GAGGTTACG /
 AG AT TATATATGG AT

GAM502 TGCCAGTGTTTGGCAGTTTT 488 AGTGTTTGGC 3213 A - TTTTACCG TG G- A GA
 TACCGTTGGTTGTGTAGAAT AGTTTTTACC TGCC GTGTTTG GCAGT TTGGT T TAG
 ATTGG A
 TGGGAAAGCTAATACTAAAG GTTG ||||| ||||| ||||| ||| ||| |||||
 TGACCGAGCATCCACTGTAC ACGG CGTAAAC TGTCA AGCCA G ATC TAATC /
 AAATGCGGCA - A CCTACG-- GT AA A GA

GAM503 TAGCTACGGGCAGAACTACC 489 TGACAAGCGA 3214 A A TAC- TG GA---- CTC
 AGTGCGAGTCAGTGCTCGTC GTGCTGCAAT TAGCT CGGGCAG AC CAG C GTCAGTG G
 CCGCTGACAAGCGAGTGCTG GTCC ||||| ||||| || ||| |||||
 CAATGTCCTGTCCGAGCTA ATCGA GCCTGTC TG GTC G CAGTCGC /
 - C TAAC GT AGCGAA CCT

GAM504 TTCTAGTACCGGTTCCCGTG 490 AGCGGGTGCT 3215 CC --- A--- CT- TCC C C-
CGCC
CGGCCTGCAGCGGGTGCTCT CTTGTCCCGC CGTG C GGCCTGC GCGGGTG CTTG CG
GGAGC GCGGCG G
TGTCCCGCGGAGCCGCGGCG GGAG ||||| ||||| ||||| ||| || ||||| |||||
CGCCGTATACGCCGTCTGCT GCAC G CCGGACG CGCCCGC GGAC GT TTTTCG
TGCCGC /
TTTGTTCAGGTCACGCCCGC -- T TC GGTG ACT TT- - TC ATAT
GTGGGCAGGCCCTGTCACGC
TGGACATCTA

GAM505 CGCAGCGCGACTTTCCCGAG 491 TACGTCTTCC 3216 C----- CTT C-- C C G GCA
GCGCACTGCCTGCTCCGGCA TGGACTTTTCG CGCAG GCGA TCC GAGGCG ACTGC T
CTCCG C
CTCCACGGAGGAGCAGTACG CAAC ||||| ||||| ||||| ||||| |||||
TCTTCCTGGACTTTTCGCAAC GCGTC CGCT AGG TTCTGC TGACG A GAGGC T
TTAACTCTGCG TCAATTTCAA TTC TCC A - G ACC

GAM506 AACAAATGGTGACGATTGTGT 492 TATCGCAGAG 3217 G GTTC T GA C----- G----
GTGC
TCTCATATGCGAAACTCGTG GAACCAGTCT GTGAC ATTGT TCATA GC AACT GTGACGT
GGGCGT T
ACGTGGGGCGTGTCGTGGAT ATG ||||| ||||| ||||| || ||||| |||||
AAGTTAACGACAGCGTGGCT CAAGG AGACG ATGTA AT TGGT CGGTGCG
AATTGA G
CCACTTTGGTTTTACATGTA - CT-- C TT TTCACCT ACAGC ATAG
TCGCAGAGGAACCAGTCTAT
G

GAM507 CAACCGGGCCTATTCTGAGA 493 TGAGATTTCC 3218 T -- T- G - G G TTT --
C
TTTCCGATGCTGCCAGATTT GATGCTGCCA C ATTCTG AGAT TCC AT GCT CCAGATTTA CT
GGAAAG CCTTCGA A
AGCTTTTGGAAAGCCTTCGA GATT | ||||| ||||| ||||| ||||| ||||| ||||| |||||
CATCTTACCAGATGTTTCAGG G ATTAGG CACG GCG CA GTC GAAGCCACC GG
GACTTG GACCATT T
AGGCCACCGAAGCTGAACTG - TC CT T A - - AG- TA C
CGTCGCACCTGGATTAGTCT
CGATTTT

GAM508 TGGCATATTTAAAGCGGCGG 494 TATCACAATG 3219 AAGC - - C - T G GCATA G C---
- TG G
CTTGTGCGTATCGTTGGGCT CTCGCTTATC GGCG GC TTGTG GTAT CG TG GCT CCC
GAT TCCGC C C
GCATACCCGGATCTCCGCTG TCTT ||||| ||||| ||||| ||||| ||||| |||||
CGCAAGTGGTGGATTGTTAT TCGC CG AACAC TATG GC AC CGA GGG CTA
AGGTG G A
CAGGGCAGGAAGCGCACCGT CTAT T T - T C G AGGAC A TTGTT GT A
GTATCACAATGCTCGCTTAT
CTCTTGATGAA

GAM509 GCAAAGTGGTGGTCGTTGGC 495 TGAAAGGAGT 3220 AA TG TC GA ACA
TCTTTGACAAATTACACGGC TAGCTCCGCT GC AG GTGG GTTGGCTCTTT CAAATT C
AATTTGAAAGGAGTTAGCTC CCTA || || ||| ||||| |||||
CGCTCCTAGC CG TC CGCC CGATTGAGGAA GTTTAA /
A- CT T- A- CGG

GAM510 TGATTGCGTTTATAGAATCT 496 TCACCAGTCT 3221 A CG - TA CAA- --
TCTAGCA
TAAACAAGTTTAAAGGCGTG TTAGATGACA TG TTG TTTATAGAA TCT AA GTTTAAAGGC
GTGATAAAT A
ATAAATTCTAGCAACACAAA TTCG || ||| ||||| ||| || ||||| |||||
TGTTTATCACCAGTCTTTAG AC AAC AAGTATCTT AGG TT TAGATTTCTG
CACTATTTG /
ATGACATTCCGGGATTTCTAT G AG T GC ACAG AC TAAACAC
GAAGACAAGCA

GAM511 GTCTTAAATCTGCCGTAGAA 497 TTAAATCTGC 3222 C T TAGAA TGATT T
GGACTAGGTGATTGCGTCTA CGTAGAAGGA GT TTAAATC GCCG GGACTAGG GCGTC A
TGATGCTCTAGTTCAAACCG CTAG || ||||| ||| ||||| |||
GCTGGTTTGACAC CA AGTTTG CGGC CTTGATCT CGTAG /
C T CAAA- ---- T

GAM512 GTTGTATGACTGCGAAAAGT 498 TGGCAAGTGA 3223 G CTGC AA-- A T TG CA
GAGA G - A
GCAAGTGGTTATTGTTGCCA CGATACCACT TATGA GAA GTGC AGTGGT ATTGT C GCC
AGAA CACG C T
GCCGAGAAGAAGCACGCATG CGCA |||| | ||| ||||| |||| | ||| ||||| |
GGCCGTGGTTCTGGCAAGTG ATACT CTT TACG TCACCA TAGCA G CGG TCTT
GTGC G G
ACGATACCACTCGCATAATC T TTC- CTAA C - GTAA ---- G C G
TTCCTTTTCATATGAC

GAM513 TCACTCCAGTCGTTTACACT 499 TTGGTTCCAC 3224 A -CG CAC TTCG AA AG
AT
GGGACCATTTCGAGAGAGGCA GCTGGGTAAT TC CTCCAG T TTTA TGGGACCA AGAGAGGC
ATGA AATT A
AATGAAGAATTATATTGATT CTGG || ||||| | ||| ||||| ||||| ||| |||
ACTTATCGGCCTCTCTTGGT AG GAGGTC A GGGT ACCTTGGT TCTCTCCG TATT
TTAG /
TCCACGCTGGGTAATCTGGA A T AT CGC ---- GC CA TT
GAGA

GAM514 TTCGCAGAAGGCTGGGGTAA 500 TGGGGTAACA 3225 CG AG- G A TCTG AC - C
CAGTAACGGGTCTGGGCACG GTAACGGGTC TT CAGA GCTGGG TAAC GTAACGGG GGC
GCTC TCT C
CTCTCTCCTGAGATGGGCGC TGGG || |||| ||||| ||||| ||||| ||| |||||
TTCTGTTGCGTTATCCAGTA AG GTCT TGACCT ATTG CGTTGTCT TCG CGGG AGA T
CCTCTGTAGA AT CCA - - ---- -- T G

GAM515 TTTTGGCTTGGATGTGGTCT 501 TACTGCAAGA 3226 ----- TG CT G AC
 ATGGGTCAAAAAGAACTAT TTTCCAAGCC TTTTGGCTTGGA TG GT ATGG TC A
 ACTGCAAGATTTCCAAGCCG GGA ||||| || || ||||
 GGA AGGGCCGAACCT AC CA TATC AG A
 TTAGA GT -- A AA

GAM516 CGACCAGTACAGATTCTTAA 502 TGGCAGGGTG 3227 ---- AT AAA GGC TAT-- T
 A AC
 AGGTCTGGCTTGAATATGCC GGGTTGTACT AGTA CAG TCTT GGTCT TTGAA
 GCCCATTTTGC CA CC T
 CCATTTTGTCTCAACCACTGA TCGA |||| || |||| |||| ||||| ||||
 GGCTGGCAGGGTGGGGTTGT TCAT GTC AGAA TCAGA AGCTT
 TGGGGTGGGACG GT GG /
 ACTTCGACAAAGACTCACAA CCGA CT CAC AAC CATGT - C AG
 GATCCTGAGCCTACTGATCG

GAM517 GGCTCTAGTAGTGCCGGCCC 503 GCACTGGCAC 3228 CTCT C CC C - CT
 CACTGTAGCCGCTGTAACGG CAGTACTACT GG AGTAGTGC GG CCA TGT AGCCG G
 CTAGCACTGGCACCAGTACT CTTA || ||||| || || ||||
 ACTCTTACC CC TCATCATG CC GGT ACG TCGGC T
 ATTC A AC C A AA

GAM518 GAAGTTTTTCTGAAGTAAAA 504 TGAAGTAAAA 3229 TTTC AAT CC ATAAG
 TGGTTGTTCTGAATAAGCA TGGTTGTTCC GAAGTT TGAAGTAA GGTTGTT TGA C
 AAAATCGTTAACGATCTATT TGAA |||| ||||| ||||| ||
 ATTTTAAATCAACTTC CTTCAA ATTTTATT CTAGCAA GCT /
 CTAA AT- TT AAAAA

GAM519 GTTGTACTTATTTTAAACCA 505 TTACAAGATG 3230 ----- AAACC - A T
 TGTAACAATGTCTTCAATG AGCAATTTCT GTTGTA CTTATTTT ATGTAA ACA TG C
 TCTTACATTACAAGATGAGC ACAG |||| ||||| ||||| ||||
 AATTTCTACAGC CGACAT GAGTAGAA TACATT TGT AC T
 CTTTAAC CAT-- C A T

GAM520 TGTTTAAACCAGCATTTAAA 506 TAGTACAACG 3231 T - T AT- - T GA A ATTACA
 TT
 CTTGTTATTATATATTACAT TTTAAGCTTA TTAAAC TTGT ATTATAT TA CATT GAAGA GTTT
 TAC TCTA G
 TTGAAGAGAGTTTATACATT AACA |||| ||||| ||||| ||||| ||||
 ACATCTATTGCACTAGAGTA AATTG AACA TGATATA AT GTAA TTTT CAAA ATG
 AGAT C
 CAAACCATTTTTTAATGATA - C - AGT A T AC C ----- CA
 TGAATATAGTACAACGTTTA
 AGCTTAAACA

GAM521 GTGTAAAAACAATTGCGCG 507 TTAAAAACAA 3232 AT- CG TAAC TT TAAAA-
AA GAT
ATTTAACGATTTTTTATTAA TTGCGCGATT GTGTAAAAACA TGCG ATT GATTTT AT TGG
ACAA G
AATGGAAACAAGATGTGATT TAAC ||||| ||| ||| ||| ||| ||| ||| |||
GTAACCAGCGACTATTTAAA CATAGTTTTTGT ATGC TAA TAAAA TA ACC TGTT
/
ATTAATTAATACGTATTGTG GTT A- TTAA TT TCAGCG AA AGT
TTTTTGATAC

GAM522 TACCGGTACATTAAACATTA 508 ATAACGTTTCG 3233 -- C ATA CA A
TAAACGCATGTTTATTAAAT ATGTTTAATC TACCG GTA ATTAAACATT AACG TGTTT T
AACGTTTCGATGTTTAATCTA TACA |||| ||| ||||| ||| ||||
CAACGGTA ATGGC CAT TAATTTGTAG TTGC ATAAA /
AA C C-- A- T

GAM523 AATTGGTCTGGGTCATATCA 509 TGAGATAAAT 3234 - CA A GAC GG T ACTGGAT
TG CT
TCAGACCAGAGGGGCCAGTT CCAGATTCAA G TCTGGGT TATC TCA CAGAG GCCAG TG
TGC CTTTTCA A
GACTGGATTGCTGCTTTTCA TT | ||||| |||| ||| |||| ||| ||| |||||
CTATCTGAGGAGGTGCACAT T AGACCTA ATAG AGT GTCTT CGGTT AC ACG
GAGGAGT /
TTGGCATTCTGCATGAGATA T A- - AC- A- T ----- TG CT
AATCCAGATTCAATT

GAM524 ACAGAGAGGGCAAGAATTGA 510 TGGCATATAC 3235 AGG--- A- A AG----- TAT T
G
ATGTTGAGCAGGATATTATG TCACAAGCTT AGAG GC AGA TTGAATGTTGAGC GA
TATGC CATGGG C
CTCATGGGGCTGTTTATGGC GGTT ||| || ||| ||||| ||| ||| |||||
ATATACTCACAAGCTTGGTT TCTC TG TCT AATTATAACTTG CT ATACG
GTATTT T
CAATATTTAATCTGAGTACG GGCGCA AG - GTTCGAACA CAT - G
CGGCTCTGT

GAM525 GAGGGTTAATTGATGGACTG 511 TAACACACTG 3236 TGAT- AC TAACT
TTGTATCTAACTTTACATG CGATGTTAGC GAGGGTTAAT GG TGTTGTATC T
TGGTATAACACACTGCGATG CCTT ||||| || |||||
TTAGCCCTT TTCCCGATTG TC ACAATATGG T
TAGCG AC TGTACA

GAM526 GTTCACTCCAGAGAAAAGGG 512 TTCGTTGTGC 3237 C CAG GTA TTTATCT GT
TAACAATTTTATCTGAAAGT CTTTTCTAAG GTTCA TC AGAAAAGG ACAAT GAAAGT T
GTTCAAGCTTTTCGTTGTGCC ATTG |||| || ||||| |||| |||||
TTTTCTAAGATTGGAC CAGGT AG TCTTTTCC TGTTG CTTTCG C
T AA- G-- ----- AA

GAM527 TCCCCAAGAGAGTGCTTCCA 513 TGGATAGATA 3238 - AG T GAG AA- TT T
TATTTGAGATCTGTGGCAAG TGGAGGTCTG TCC CCAAG AG GCTTCCATATTT ATCTGTGGC
GAC AC A
ACTTACTAGAGTTGTCATAG CTTG ||| |||| || |||| |||| |||| ||| ||
CTATGGATAGATATGGAGGT AGG GGTTC TC TGGAGGTATAGA TAGGTATCG CTG
TG G
CTGCTTGGAGGA A G- - --- ATA T- A

GAM528 TACACCCTGATGATGTACAC 514 TGATGTACAC 3239 ----- ---- TA-- - CC AAGC T
CACCTCTAAGCTCATAGATG CACCTCTAAG TACA CCCTGA TGATG CA CCA TCT TCA
A
ATCCAGACCTGGCTGAAATC CTCA |||| |||| |||| || ||| ||| |||
ATCACCAGTCGGGGACCCAA ATGT GGGGCT ACTAC GT GGT AGA AGT G
TGTA AACCCA GACC TAAA C CC CCT- A

GAM529 TCTCGTGGGTAGCTGACAGG 515 TAGCTGACAG 3240 T- - - CAG CT - - C
TGCCTGAGTACAGATCTCAT GTGCCTGAGT TCTCG GGGTA GC TGA GTGC GA GTA CAGAT
T
CTGTTACATCCTGCATATCA ACAG |||| |||| || ||| ||| || |||| ||||
TGCATGCCCCCGGGA AGGGC CCCGT CG ACT TACG CT CAT GTCTA /
CC A T A-- TC A T C

GAM530 GCCACATTGGACCACAGGTG 516 TATCACAGAC 3241 A T GA ACAG--- ACCA
GTGCCACCATTACAGGTATC TAAGGGACAT GCC CAT G CC GTGGTGCC T
ACAGACTAAGGGACATGAGG GAGG ||| ||| || |||||
C CGG GTA C GG CACTATGG /
A - AG AATCAGA ACAT

GAM531 CCATGATGTTGTTTATATGA 517 TGGAATGTGT 3242 ----- ATGAA A GTT
AATGCAATCCAAAGTTATTA GATGAGCGAT CCATGAT GTTGTTTAT ATGCA TCCAAA A
TTTGAATGTGTGATGAGCG CAAA ||||| ||||| |||| |||||
ATCAAATATATTATGG GGTATTA TAGCGAGTA TGTGT AGGTTT /
TATAAAC G---- A ATT

GAM532 TGGCCCCGTAAGAGGCAGTC 518 AGAGGCAGTC 3243 C C - - - --- AT- - GT
ATAGCTATGGCCGTGTTGGT ATAGCTATGG TGG CC GTAA GA GGCAGTCA TAGCT GG CC
G
CCTAAGGCTACATTGGCTGC CCGT ||| |||| || ||||| |||| |||
TGTCTTTATTGGTCCA ACC GG TATT CT TCGTCGGT ATCGG CC GG /
T T T G TAC AAT T TT

GAM533 TAGTCTCGTACGAACCTAAG 519 AGAGATCTTG 3244 GT AC A AA TG GT C AA T
GTGAGTGATTTCTCAATCT CCGAAGGCTC TA CTCGT GA CCT GG A GATTTC TC TCTT C

GAM539 ATTCCTTTTGCCACTGTTAT 525 TATCATATGG 3250 GT - - - A- --- C--- CA AA
ATA
ATGTACTTATAGACATGCTC GTGGTATAGA CT TATATG TA CT TATAG CA TGCTC ACCTTA
TAAGA TC T

CACCTTACATAAGAAATCAT AGGT II IIIII IIIII II IIII IIIII IIII II
ATAACAGATCTTAATAAGGT GG GTATAC AT GA ATGTC GT ACGAG TGGAAT ATTCT
AG A
TGATGAGCAAAGTGGACTGT -- T A T AG GAA TAGT A- -- ACA
ATAGATATCATATGGGTGGT
ATAGAAGGTT
GAM540 CATAAAATATATTTATAGAA 526 TACAATGGCC 3251 AA GAA TAAAAG A A TTT
CAA
GTCTAAAAGATTGTAATGAT ATATAAGTAT CATAA TATATTTATA GTC ATTGTA TGATC TAG
AC T
CATAGTTTACCAATTGAGTT AGAT IIII IIIIIII III IIII IIII III II
TCTAAGATTATACAATGGCC GTATT ATATGAATAT CGG TAACAT ATTAG ATC TG /
ATATAAGTATAGATTATG AG AC- ----- - A TT- AGT

GAM541 TGGTTAGATCATATATTTAA 527 TCATATATTA 3252 A TAAATTTTC CTC AGT
TTTTCGATCTCTAGAGTTCA AATTTTCGAT TGGTT GATCATATAT GAT TAG T
GCTATAATCACTTATATATG CTCT IIII IIIIIII III III
ATTGAATCA ACTAA TTAGTATATA CTA ATC /
G TTCA----- AT- GAC

GAM542 GATATATGTAATAAATGTAA 528 TGTAATGGTG 3253 -- AAATTA ---- G GGAG
GAA T
CAAAATTAATTTTGTTTCATG ATAATACAAA TAA ATGTAACA ATTTTGT TCAT AT
TATGCGGT TGTTA G
ATGGAGTATGCGGTGAATGT ATCT III IIIIIII IIIII IIII II IIIII IIII
TATGCTAACAAAATTGTATG ATT TATATTGT TAAACA AGTG TA GTATGTTA
ACAAT /
TAATGGTGATAATACAAAAT AA ACATC- TAAT G AT-- AA- C
CTACATGTTATATAATTATT
ATAAATGATC

GAM543 AGTATCATGATAAATTACAT 529 TATCACAATA 3254 TTACAT GGAA-- - A ATCAA A
GAA AATT
TGGAATATATATCACAATA TCAAGAATTA TAAA TG TATATAT C CAAT GA TTATCA
GATAT T
TCAAGAATTATCAGAAGATA TCAG IIII II IIIII I IIII II IIII IIII
TAATTTTACAATATCATGAT ATTT AC ATATATA G GTTA TT AATAGT CTATA /
AAATTACATTGGGAATATAT TAACT AAATCG A G CA--- A A-- ACAT
AGCTAAACATCAAATTTTAT
CAGAATACT

GAM544 ACCTGCCACTGTGTGTATGT 530 TATAACATGA 3255 T C---- - - A
GTTTAAATAAACATATAACA CATTTTTTGG ACC GCCA TGT GTGT ATGTGTTT A
TGACATTTTTTGGCTGGT CTGG III IIII III IIII IIIII
TGG CGGT ACA TACA TATACAAA A
T TTTT G A T

GAM545 ATATAAATTAGATGATTCAT 531 TAAATTAGAT 3256 - AT C T ACAA- C
TTCCATTATTTACAACAAAA GATTCATTC ATATAAATTA GATGATTC TTC AT ATTT CAAAAT
A

TCAATGTTTTGGAGAGGAAT	CATT		
TGTTGAAGAATTATTATGGT		TATATTTGGT TTATTAAG	AAG TG TAAG GTTTTG A
TTATAT	A	-- T T	GAGAG T

GAM546	CTGACACCCGGTTAGCTGAG 532	TACATCAGAA 3257	- CG A G GCTTCCGC-- G GA
T - A			
AGAGCTTCCGCCATGCTGGA	TGTTATTTTCG	CTGA CACC GTT GCTGA AGA	CAT CTG
GTA GTTG CGT T			
GTATGTTGCGTATGAACGTC	AATC		
AATTACATCAGAATGTTATT		GACT GTGG TAG CGACT TCT	GTA GAC CAT TAAC
GCA G			
TCGAATCTTCAGCGGATTTG		T TT G - AAGCTTTATT	A TA - T A
GTGTTCAG			

GAM547	GATAGCTATGAGGTGTTACA 533	TAGCTATGAG 3258	GA TTACAATGATAA C----
CA T			
ATGATAAGAAGACATGGCAA	GTGTTACAAT	GATAGCTAT GGTG	GAAGA
ATGGCAAGAC ATTTAAAA C			
GACCAATTTAAATCATTTT	GATA		
AGGTGTCTTGTGCATCAAAAT		CTATTGATA CCAC	CTTCT TACTGTTCTG
TGGATTTT /			
CTTCCACCATAGTTATC	--	----- AAAAC	-- A

GAM548	GTGTCGGTAAGCGGTTTTGT 534	TGGATGGACG 3259	C AAGC- T AA- TA AG
GTTAAGTCCGTTTACATATT	AGAACATCAA	GTGT GGT	GGTTT GTGTT GTCCGTT CATATT
G			
AGGGAAGATATGGATGGACG	GCTC		
AGAACATCAAGCTCAAGAAC		CACA CCA TCGAA TACAA	CAGGTAG GTATAG G
CACAC	- AGAAC C GAG	-- AA	

GAM549	ATCTTGGCAACTGCTGCATT 535	CTGCATTGGT 3260	--- GT---- TT TCC G GAC--- A
AC ACA			
GGTTCATCTTTCTGATCCTG	TCATCTTTCT	G CATTG	TCATCT CTGA TG AAT AGTGA
TG GTC T			
GAATGACAGTGAATGACGTC	GATC		
ACATATCCGACTACACTCAC		T GTGAC	GGTAGA GACT AC TTG TCACT AC CAG
A			
TACAAAAGTTGCATCAGTAG		ACA AATGCC T-	--- G AAAACA C AT CCT
ATGGCCGTAACAGTGACATA			
GCAGCACAGAT			

GAM550	ACGCTGAGAGTGTGATGCTG 536	TCAGTCCTTC 3261	T - AATAC T AT--- GATA- C---
--- TC			
CGACAATACGGTGCTGACAT	AAGTATGCGC	ATGC GCG AC	GG GCTGAC AGCT
TCATGG CCAG A			
AGCTGATATCATGGCCCAGT	GTCA		
CAAGCTGGATGAAATCCATG		TGCG CGT TG	CC TGACTG TCGA GGTACC
GGTC /			

GAGGCAAGCTCACGAGTCAG - A AACTT - AGCAC ACGGA TAAAGTA GA
 TCCTTCAAGTATGCGCGTCA
 CGTTGTCACGT
 GAM551 GGTCATTACGAGCACTAGA 537 TGTGTGCTCG 3262 C A AG AGAACAT CCAGA -
 A--- AAAA
 ACATGCACACCCAGAACTGC AGCAGTGGCG GGT ATT C G CACT GCACAC ACT GCGA
 CTCG G
 GAACTCGAAAAGAAGTCCGA GAAT ||| ||| ||| ||| ||| ||| |||
 GCGTATCGTAAGTGTGTGCT CCA TAAG GC GTGA CGTGTG TGA TGCT GAGC
 A
 CGAGCAGTGGCGGAATAACC A - G- CGAGCT- ---- A ATGC CTGA

 GAM552 TTTGTGTTGGACAATCCTGA 538 CCACCGGGAT 3263 --- ACA- A- CCG A CTG
 GGTGCCCCGGGCAAGGCTGTA AAGACCGGAG TTTGTGTT GG ATCCTG GGTGC GGCA GG
 T
 AATCCTGCCAGTACCACCGG ACAC ||||| || ||||| ||||| |||||
 GATAAGACCGGAGACACGAA AAGCACAG CC TAGGGC CCATG CCGT CC A
 AGG AGAA CA A-- - TAA

 GAM553 ATTCCATCGTTAGTAATCAA 539 TGTCAAGATA 3264 ATCGT- ATCAATCATCTAA- - - C
 AATCTT
 TCATCTAATCTATGCTTACA TAGGGAAATC ATTCC TAGTA TCTATG CTT ACA CTCT
 A
 CCTCTAATCTTATTACCCAG TTAC |||| |||| ||||| ||| |||||
 GGCTGTCAAGATATAGGGAA TAGGG ATCAT GGATAT GAA TGT GGGAA /
 ATCTTACCAAGTACTACAAA ATAAAC GAACCATTCTAAAG A C C CCCATT
 TAGGGAT

 GAM554 ATGAAAGCGATCTGTGTGTT 540 TCACCCGACC 3265 AA- TCT TTTA CG CA G TC
 ATCGGGTGACGTGCATGGTC ATTTGCTCCA ATG AGCGA GTG G TCGGGTGA TG TG
 TCGAG A
 GAGTCATTTTCGAACAACAA CAT ||| |||| ||| ||||| || |||||
 TCACCCGACCATTGCTCCA TAC TCGTT TAC C AGCCCACT AC AC AGCTT /
 CAT ACC --- ---- A- A- A TT

 GAM555 GAGCGTCACGTAGGCGATCT 541 TAAGATCGAC 3266 G- AGG GGGTAAC AG- AAA
 CA
 GGGTAACATTGAAGCGAAAA AACGTGATGA GA CGTCACGT CGATCT ATTGA CG AAAT
 A
 AATCAAACAGTTTGACCGAA GTC || ||||| |||| |||| || |||||
 ATCGATAAGATCGACAACGT CT GTAGTGCA GCTAGA TAGCT GC TTTG A
 GATGAGTC GA ACA A----- AAA CAG AC

 GAM556 GCGACGACTTGGGTCTCGGC 542 CCACCGGCAA 3267 GA C- C ATCCAT
 GGTCATCCATTGAGCAAGAC CTCGGGCGGT GCGAC CTTGGGT TCGG GGTC T
 CACCGGCAACTCGGGCGGTC CGC |||| ||||| ||| ||||

GC

CGCTG GGGCTCA GGCC CCAG /
GC AC A AACGAG

GAM557 GATCGCCGTCTGCTGATGTG 543 TGATGTGCGT 3268 C--- C ----- AAC- TG
CGTCGACGCCGAACCGTGTA CGACGCCGAA GATCG CGTCTG TGATGTGC
GTCGACGCCG CG T
GCGTCCACGGCGTCTGACTAT CCGT |||| |||| |||| |||| ||
ACGTACATTACGGACGACAT CTGGC GCAGGC ATTACATG CAGCTGCGGC GC /
CGGTC TACA - CATAT ACCT GA

GAM558 TCTTTTAATTCATTACGTCT 544 TGCAAAGTTC 3269 AAT A T- ACG ATC GCG A
TTGACGGCATCAGTTATAGC GAGTGAAAA TCTTTT TCATT CG CTTTG GC AGTTATA AG
A
GAGAACACTAATGTAATTAA GA |||| |||| || |||| || |||| ||
AGTATGCAAAGTTCGAGTGA AGAAAA AGTGA GC GAAAC TG TTAATGT TC C
AAAAGA --- - TT GTA AAA AA- A

GAM559 GGTGAAACTATTCCTTGATT 545 TATCATGCTG 3270 AACTATTC A -- T TAATTCTA A
A
CTGGTATTGATATTAATTCT TAGAACAAGA GGTGA CTTG TTCT GGTAT GATAT CA
TATGTGA A
ACAATATGTGAAAACTCGCA AAAC |||| |||| |||| |||| || ||||
TACTGCACTATATCATGCTG CCATT GAAC AAGA TCGTA CTATA GT ATACGCT
A
TAGAACAAGAAAACGTTACC GCAAAA-- - TG - TCAC---- C C

GAM560 ATTTACCAAACCTGATAACGT 546 TATTACACAC 3271 -- AA A C T T T ACAAAA -----
GAT
GTTTAATTTATTATTACAAA TTTAGCAGCG TTTAC CA CTG TAA GTGT TAAT TA TATT AGG
AGCG G
AAGGAGCGGATGTAAACGCT TGTT |||| || |||| |||| |||| || ||||
AAAACTCTGACGGGAATAC AAATG GT GAC ATT CACA ATTA AT ATAA TCT
TCGC T
TATATTACACACTTTAGCAG TT GC G T C T C GGGCAG CAAAAA AAA
CGTGTTGTAAAT

GAM561 ATAGTGATTGGTTAATATCT 547 TTGGTTAATA 3272 A- - ATCTAT AAGC - TAAC
ATGTCAAGCGGTTATAATAA TCTATGTCAA ATAGTG TTGGT TAAT GTC GGT TATAA A
CAAAGTTTATATACCTTCGG GCGG |||| |||| |||| || ||||
ATTATTTCTGTTATACTAACA TGTCAT AATCA ATTG TAG CCA ATATT /
TACTGT AC T CTTTAT GCTT T TGAA

GAM562 ATAATTTACTAGCTATTATC 548 TGAAACAATA 3273 CTA AT C A AAAA A
TGTTTAGTAGAAAACTATAA AGCGATAAAT ATAATTTA GCT TAT TGTTT GTAG CTATA C
CCTTATAGACTATGAAACAA TAT |||| || |||| |||| ||||

TAAGCGATAAATTAT

TATTAAAT CGA ATA ACAA TATC GATAT C
AG- -- - G A--- T

GAM563 GAAGCTATTATATAATATAA 549 TTAGTTGTAG 3274 T ATAA CG A AAAA
CCGATAAACAAAATCACGGT GAGATGTAG GAAGCTA TAT TATAAC ATA AC T
ATATTAGTTGTAGGAGATGT TTTT ||||| ||| ||||| ||| ||
TAGTTTT TTTTGAT GTA ATGTTG TAT TG /
T GAGG AT A GCAC

GAM564 GTATTTTCAGATTTTGGGTTC 550 AACACATATT 3275 TC - GGT AAA AAACG GAA
GG TAG
GAAAAAGATATAAACGATGG AATATCATTC GTATT AGAT TTTG TCGAA GATAT ATG
TTCTAG A C
AATTCTAGGGATAGCGCATT GATA ||||| ||||| ||||| ||||| ||| ||||| |
TACTAGAACACATATTAATA CGTAA TTTA GAAC AGCTT CTATA TAC AAGATC T
G
TCATTCGATAACAAGTATTT T- T AAT A-- ATTA- AC- ATTAC
TAATGC

GAM565 ACTACGTCTAAAGTAGATTA 551 TAAAGTAGAT 3276 A A A ---- -- A A--- AA
CAGACTACCTAAAGTAGAAC TACAGACTAC ACT CGTCTA AGT GAT TACAG ACT CCT
AAGTAG C
ATATTACTTACAAAGGAAGT CTAA ||| ||||| ||| ||||| ||| ||||| |||||
TCCTGTAATGATATCACTGT TGA GTAGAT TCA CTA ATGTC TGA GGA TTCATT A
AGATGAAGT A G - TAGTA CT A AACA AT

GAM566 GATGTTAGAGATCGCTGGGT 552 AACAGTAAAC 3277 - T A C - -- GAAAA T
ACTGGAAAATCCTTTTGAAA ACCGGCAGTT GA TGT AG GAT GCTGG GT ACTG TCCTT T
GGAACAGTAAACACCGGCAG ATTT || ||| ||| ||||| || ||||| |||||
TTATTTACGTTT CT GCA TT TTG CGGCC CA TGAC AGGAA G
T T A A A AA A---- A

GAM567 GACTTTAGGGACACAGGCGG 553 TGAAGTATTA 3278 - GACACAG AA- C--- TAAGT
A AA AG
TGAAGTATTACTTACTAAGT CTTACTAAGT AC TTTAGG GCGGTG GTATTA TTAC ACA
TCA GAC A
ACAATCAAAGACAGAGCAGT ACAA || ||||| ||||| ||||| ||| ||| ||| |||
TTGATGTTTAATGTAGACAC TG AGATCC TGCTAT CATGAT GATG TGT AGT
TTG G
TAGTACGAGTATCGTAAAC C AAAA--- GAG CACA TAATT - -- AC
CTAGACGTC

GAM568 GGTAAGTTACGCGGCTTATA 554 TAAGTTACGC 3279 - TA - CT ATCA-- AC
TCAAGCTTACAAAGAGTTGT GGCTTATATC GGTA AGT CG CGG TAT AGCTT A
ACGAATACACCGACGGGACT AAGC ||| ||| ||| ||| |||||
CTACC CCAT TCA GC GCC ATA TTGAG /

C GG A AC AGCATG AA

GAM569 GTCTTTGATGGCAGAAGTTG 555 TTATTGGAAA 3280 C GTAACCCC T TC C
TAACCCCTCCTAATTCATAT TTTCTCCATT GTCTTTGATGG AGAAGTT TCC AAT ATAT T
CTTAATATTATTGGAAATTT AAGG ||||| ||||| ||| ||| |||
CTCCATTAAGGAT TAGGAATTACC TCTTTAA AGG TTA TATA T
- ----- - T- A

GAM570 TGATACGGTCATAAAACCTA 556 TATTTTCATCC 3281 A CTAAC GG TGCGAAGTTTT
ATA A C TTG
ACGAAATATCAGGCCATGCG TGTGAAAATC AC GAAATATCA CCA GCGCCA GAC
GTC AACCA T
AAGTTTTGCGCCAATAGACA GTGT || ||||| ||| ||||| ||| ||| |||
GTCCAACCATTGTCACTGGT TG CTTTATAGT GGT CGTGGT CTG CAG TTGGT
/
TCGACGTCATGGTGCTGGAT - TCCTA A- ----- A-- - C CAC
GATATTTTCATCCTGTGAAAA
TCGTGTTA

GAM571 CAAAACCGTAATTTTCAGTGA 557 TTCAAGGACA 3282 CCGT- T AG T A AA
TATAGTAATAAAACCTAATA TTCTAAATTT CAAAA AAT TC TGA ATAGTA TA A
CTGTTCAAGGACATTCTAAA TG |||| ||| ||| ||||| ||
TTTTG GTTTT TTA AG ACT TGTCAT AT /
AAATC C GA - A CC

GAM572 CATATTAACTTTGTATCCCA 558 TGCCTTGGCG 3283 TTGT - - CAACG- C- A-- TAG
GA ACGG
AGCGTACAACGAGTCTGTTA GTCTAGGAAA T ATC CCAAG CGTA AGT TGTTAT TTCA
AC GTTC G
TATTCATAGACGAGTTCACG TGTG | ||| |||| ||| ||| ||| ||| |||
GGTAGAGAACGAGTATTTGA A TGG GGTTC GTAT TCA ACGGTA AAGT TG
CAAG /
AGACATGGCAAACTAGGGA TC-- C C CAGGGA AA CAG TTA AG AGAT
CTATGCCTTGGCGGTCTAGG
AAATGTG

GAM573 GAATTGATGTATGAATTCGA 559 TGATGTATGA 3284 - AAT GA G AG
CATGAATATAAGTACTATAT ATTCGACATG GAATTGATGT ATG TC CAT AATATA T
TAATGAGACATAACGTCAGT AATA ||||| ||| ||| ||||| ||
TC CTTGACTGCA TAC AG GTA TTATAT /
A --- A- A CA

GAM574 GCTAAAAATATGTATAGAAC 560 TGAGAGCTAA 3285 AAAA - AAC A - TTTAATTTT
GTATAGTTCTATCGTTTTAA CATGCTAATA GCTA TATGTAT AG GT TAGTTCT ATCGT A
TTTTAATACCGTGTACGATG TATA |||| ||||| || ||| ||||| |||||
AGAGCTAACATGCTAATATA CGAT ATATATA TC CA ATCGAGA TAGCA /
TAATACTAGC CATA A GTA - G TGTGCCATA

GAGGACAGAATGATGAACAA
 GAT
 GAM581 TTCTTACGTATATATGATTT 567 TATCATAACT 3292 TATA- T TT TTC CATAGA T
 ATGTTTCTATGATCATAGAG ACATATTTCC TTCTTACG TAGA TATGT TATGAT GTACT T
 TACTTTAAAGTATATCATAA TACA ||||| || ||||| ||||| |||||
 CTACATATTTCTACACTTT AAGAGTGT AT CT ATACA ATACTA TATGA A
 GTGAGAA TTCAC C TT TCA ----- A

 GAM582 CCTTCTAATGCAATACAAAG 568 TGTTATGCCA 3293 C- AATACAAAG -- CTCTATA T
 A AT
 CCGATGCCTCTATACGTGAC TGTATCTAGG CCTT TAATGC CC GATGC CGTGACAG
 AA GGA T
 AGTAAAGGAATTACTCCATT ATAT ||| ||||| || ||||| ||||| || |||
 CTGTTATGCCATGTATCTAG GGAA ATTGCG GG CTATG GTATTGTC TT CCT /
 GATATTACGGCGTTAATAAG TA GCATTATA- AT TACC--- - A CA
 G

 GAM583 TCCCTTGTTAACAGCTATCA 569 TGTTAACAGC 3294 CTT- TATCAAAA GG A
 AAATAGGATCACACGATATA TATCAAAATA TCC GTTAACAGC TA ATC C
 GTAAAACTGCTGTTGATTAA GGAT ||| ||||| || |||
 CGGA AGG TAGTTGTCG AT TAG A
 CAAT TCAAAATG A- C

 GAM584 ATATCCAAGAAGTTTTTCATC 570 ATAGGTATGT 3295 TTTCATCTA TATTC- - A A
 CA--- T
 TATAATAGGTATGTATTCTC ATTCTCCTAA GT TAATAGGTATG TCC TAATAC GAT GTAT
 ACTTT C
 CTAATACAGATAGTATCAAC TACA || ||||| || ||||| || ||||| |||||
 TTTTCTAAAGTAAACCATAC CG ATTGTCCATAT AGG ATTATG CTA CATA
 TGAAA /
 CATCAGTATTACGGATGCTT ----- CTTCGT C A C CAAA T
 CTATACCTGTTAGCTTCTGG
 GTAT
 GAM585 GGATGTTTAAGGAGATCCTC 571 TGGCCAGGGT 3296 G TAA ----- CGCA G GA
 GCAGGTCGATTAGGATATAC ATATATAACT GGAT TT GGAG ATCCT GGTC ATTAG T
 TGATGGCCAGGGTATATATA CCGT ||| || ||||| ||||| ||||| |||||
 ACTCCGTAAGATCT TCTA AA CTC TGGGA CCGG TAGTC A
 G TG- AATATATA ---- - AT

 GAM586 TCAGGGTCATGAGGTTTCAA 572 TGAGGTTTCA 3297 G GT TTCCTACTCGAAC- T-
 TAACT
 TTTCCTACTCGAACAGTGCG ATTCCTACT TCAG GTCATGAG TTCAAT AG GCGA T
 ATAACCTTTACTACTCGCTCC CGAA ||| ||||| ||||| || |||||
 TTACTTTTTTTCCGTATTGA GGTT TAGTATTT AAGTTA TC CGCT T
 ATATTTATGATATTGG A AT TGCCTTTTTTTCAT CT CATCA

GAM587 TGTTAAGGTAGCAGAAAATG 573 TAAGGTAGCA 3298 G ---- AAAT - AA
TTTTTGTAAACATGGCGCAAA GAAAATGTTT TGTTAA GTA GCAGA GTTTT TGT C
ACTCTGCAAACACTACATTGAT TTGT ||||| ||| ||||| |||||
A ATAGTT CAT CGTCT CAAAA GCG A
A CAAA ---- C GT

GAM588 GGTAAC TTATATATGTGACG 574 TATGTGACGA 3299 AACTTAT -- - AA -- ACA
AACATATGAAGCATGTAACA ACATATGAAG GGT ATATGTGAC GAACAT ATG GCA TGTA
G
GATTATACAAATGCGACATC CATG ||| ||||| ||||| ||| |||
ATGTTCTGTTATGTATTGA CCG TATGTATTG CTTGTA TAC CGT ACAT A
ACAAGCC AACAAAGT TC C AG AA ATT

GAM589 TGCGTGTGGCGAATTCCATA 575 TGGAAATGTGC 3300 - T GA--- AATATT AG
ATATTTCAAGAATATGACGA AGCCCATCGC TGCG TG GGC ATTCCAT TCA A
GATGGAATGTGCAGCCCATC A ||||| ||| ||||| |||
GCA ACGC AC CCG TAAGGTA AGT A
T - ACGTG GAGC-- AT

GAM590 TTGCAATTCCGGTGCCCAGA 576 TAACTGCTGC 3301 ATTCC GACAT A G CC--- A
CGACATCAGACAGTGATGCC GATAGTTTGG TTGCA GGTGCCCAGAC CAG CAGT ATG
TGCC T
TGCCATAGGCATATTACATA GTAT |||| ||||| ||||| ||| |||
ACTGCTGCGATAGTTTGGGT AGCGT TTATGGGTTTG GTC GTCA TAC ACGG /
ATTTATTCTGCGA CTTAT ATAGC - A ATTAT A

GAM591 GAAAGAGGTACGGTAGATCA 577 TACGGTAGAT 3302 A - TCAAAT T---- AA AC
AATGCTTAGAATTCTACTAG CAAATGCTTA GAAAG GGTA CGGTAGA GCT AG TTCT T
AGAAAGCTCCACCAGCTCCT GAAT ||||| ||||| ||| ||| |||
CTACTGATACCGCTTTC CTTTC CCAT GTCATCT CGA TC AAGA /
G A CCT--- CCACC GA GA

GAM592 GGGGTGCAGTTTTCTCTTAC 578 GTGCAGTTTT 3303 ---- TTC-- CAAC C A
ACAACCCCGGGCCAACGTTG CTCTTACACA GGGGTGCA GTT TCTTACA CCCGGG CA C
ACCTGGGTGTAGGATATACA ACCC ||||| ||| ||||| ||||| |||
GCCACGTGTA CTCC CCTCATGT CGA AGGATGT GGGTCC GT G
GCAC CATAT ---- A T

GAM593 TAGAGAGCGCATTCCCAGTG 579 TGGGCCAAAG 3304 A GC - AG AA T G G A
GAATATGTGATGCGTATGAT GCGAATGTAA TAG GA GCATTC CC TGG TA GT AT CGT T
GAATGACTGGGCCAAAGGCG TCCT ||| ||||| ||| ||| ||| |||
AATGTAATCCTTA ATT CT TGTAAG GG ACC GT CA TA GTA /
C AA C AA GG - G A G

GAM594 ACTTGGCAGACGGATCTTAC 580 TGGCAGACGG 3305 G CGG TTA CA--- T A
 AACCCCAAGTTCGACAGTGA ATCTTACAAC ACTTG CAGA ATC CAACCC AG TCG C
 CCTACAATGGGTTGATGATA CCCA ||||| ||| ||||| |||||
 AATCTGGTAAGT TGAAT GTCT TAG GTTGGG TC AGT A
 G AAA TA- TAACA C G

GAM595 TGAGGTGAATGTCAGACTGT 581 TACTCTGAAT 3306 T A -- CT ATGA TT G
 GTCATGACATACTTGGGGCG CAATCTCTTC TGAGG GA TG TCAGA GTGTC CATAC GGG C
 ACTCTGTATGGATACTCTGA A ||||| ||| ||||| ||||| |||||
 ATCAATCTCTTCA ACTTC CT AC AGTCT CATAG GTATG CTC G
 T A TA -- ---- T- A

GAM596 TGATGTATTACCAATCTGGA 582 TGAGATAGCT 3307 - - - - - C CACA GA - AA
 A

ACAACCCGTATCTTGCACAA GAATTGATTC TATTACC AATCTG GAA CAA CC CGTAT TTG
 AATTT CT TC GGA T
 ATTTGACTTCAAGGAATTT AATG ||||| ||||| ||| ||| ||||| ||| ||||| |||
 CTGAGATAGCTGAATTGATT ATAGTGG TTAGGC CTT GTT GG GTATG AAC TTAAG
 GA AG TCT T
 CAATGTATGAGGCATTGCTT G T C AC A T TTAG TC T AG T
 CTCGGATTGGGTGATATTT C
 A

GAM597 CTAACAACCTTTCTGCACCT 583 TTAGTGCTAA 3308 A TT T---- C CG TG
 AAGAACGCATATGACGCTAT ATTGATTGGT CTAACA CC TC GCAC TAAGAA CATA A
 GATTCTTAGTGCTAAATTGA GTTG ||||| ||| ||| ||||| |||||
 TTGGTGTTGG GGTGTTGT GG AG CGTG ATTCTT GTAT C
 - TT TTAAAT - A- CG

GAM598 GAATCTGCTGAAGGCTATGA 584 TTTCATGTGT 3309 GCTG- GC- C GTTATTAA A
 T C
 CTACATGGTTATTAAGAATG TCATAACACT GAATCT AAG TATGA TACATG GAATGG
 ATTGT CAA C
 GAATTGTTCAACCTTTTGAC TATA ||||| ||| ||||| ||||| ||||| ||||| |||||
 GATACCATTTCATGTGTTCA CTTAGG TTC ATACT GTGTAC TTTACC TAGCA GTT
 T
 TAACACTTATAAAGGATTC AAATA ACA T ----- A - T

GAM599 GCTTGAAGTCTTTAAATATT 585 TGCCTAAAGT 3310 TG TATT ----- TA----- T
 AA
 TGCTGGTTTTATTTATGTGT TAAAGTCAAA T AAGTCTTTAAA TGC TGGTTT TTTA
 GTGTCTTAG G
 CTTAGAAGTACTAAGATGCC CCAC | ||||| ||| ||||| ||||| ||||| |||||
 TAAAGTTAAAGTCAAACCAC G TTTAGAAATTT ACG ACCAAA AAAT
 CGTAGAATC /
 CTCTTGCATTTAAAGATTTT GT ---- TTCTCC CTGAAATTG C AT

GGTGC

GAM600 GTCATGATGCTTATAAATTT 586 TTTCATTGTG 3311 TGA AA T- C
GAAGTTGTTACACATAGCAA CATAAGCAGA GTCA TGCTTAT AT TGAAGTTGTTA A
TTTCATTGTGCATAAGCAGA CTGA ||| ||||| || |||||
CTGAC CAGT ACGAATA TG ACTTTAACGAT C
CAG CG TT A

GAM601 GTTGAGAATACTAACACTAT 587 TGAGAATACT 3312 T A TTTT CTGTT TGC TC
TC
GTTTTTGCCTGTTGACATGC AACACTATGT GT GAGAAT CTAACACTATGT GC GACA
AAGGTG ATGC A
AAGGTGTCATGCTCACAGTG TTTT || ||||| ||||| || ||| ||||| |||
TTTTGCTTTATTGTCTTTGT CA TTCTTA GATTGTGATATA TG CTGT TTTCGT TGTG
/
TACATATAGTGTTAGATTCT C - CAT- TTT-- TA- TT AC
TCAC

GAM602 TACAAAGGATTGGATGGTTG 588 TGTAATGCCA 3313 ATT TTGT T GAATT TAT
TCATTGCATCATACAGAATT TCTGCTTTTG TACAAAGG GGATGG CATTGCA CATACA GCA
T
GCATATTATATTGTTGTATG TA ||||| ||||| ||||| ||||| |||
TGTAATGCCATCTGCTTTTG ATGTTTTC TCTACC GTAATGT GTATGT TGT A
TA G-- ---- - ---- TAT

GAM603 TGATATTATACCTATTGAAC 589 TATTATACCT 3314 TT C-- GA GA CT - - TA
TTGAAGCTCCATTGCGTTTC ATTGAACTTG TGATA ATAC TATT ACTT AG CCATT GCGTT TC
T
TATGTTGACGGCGCTAATGG AAGC ||||| ||||| ||||| ||||| |||
TCCTGAAGTCAAGTATTTGT ACTGT TATG ATGA TGAA TC GGTAACGCGG AG G
ATTTTGTCA TT TTT AC G- CT T C TT

GAM604 TGGTTAGGAGATGAAGTCAT 590 TGAAATGTCT 3315 TT GAGA AT TG C G GC-- -
C C
TTGCCCTAGACATGTTATTG AGTGTGAGAC TGG AG TGAAGTC T C CTAGACAT TTATT
TAGT GATA CA A
CTAGTGATACCACACGTGTT TTCA ||| || ||||| | ||||| ||||| ||||| |||
ATCAACTATGAAAATGAAAT ACT TC ACTTCAG A G GATCTGTA AGTAA ATCA CTAT
GT C
GTCTAGTGTGAGACTTCACA TT AAC- --GT T A AAGT A T G
ACTTTTCA

GAM605 TTCTTGGAACCTGATGTTAT 591 TTAATGCTGC 3316 CTGAT A GC AT TCTTAAAC
G G G
TGTTAATGCTGCTAATGGTG TAATGGTGAT GAAC GTT TTGTTAAT TGCTA GGTGA
ACAT GGTGGT TC C
ATCTTAAACACATGGGTGGT CTTA ||| || ||||| ||||| ||||| ||| ||||| |||

GTCTGCAAGAGCCATCGATGT	CTTG	CAA GACAATTA ACGGT TCACT	TGTA
CTACCG AG A			
TTTCACTGGTGGCAAATTAA	-----	A- GG TT-----	G - A
CAGAACGTTCTAAGGA			

GAM606	TTTTATTTGTTTGTCTAGTAT 592	ACGGTGCTGT 3317	T - AT A AG AAA
	ACCACTAGTGCATAAATTAA	ACAGGCATAT	TTTTAT TGTGTTGT CAGT ACC GT TGCAT T
	CATGTAACGGTGCTGTACAG	AAAA	
	GCATATAAAA	AAAATA ACGGACA GTCG	TGG CA ATGTA T
	T T -- --	CAA	

GAM607	ACTTTGAGCTATCTTCAGTA 593	TGACATAGAT 3318	G ATCT GTA TA G A TA
	TTAGGTGGATATCTAGGTAG	CTACCTAGCA	ACTTT AGCT TCA TTAGGTGGA TCTA GT GTT
G			
	TTTAGATGATGACATAGATC	TGAT	
	TACCTAGCATGATTGAGCTG		TGGAA TCGA AGT GATCCATCT AGAT CA TAG /
	AAGGT	G GTT- AC- --	A G TA

GAM608	ATGAAACTGAGGGATGAAGC 594	AAGCTAAATA 3319	AA- GAG A AA CT AG- CA G
	GAAGA		
	TAAATACTGTAGGAGAGACA	CTGTAGGAGA	ATGA CT GGATG AGCTA TA GTAGG AGA
	TTAT GA T		
	TTATGGAGAAGATAAGAATT	GACA	
	GGTAATCTAGGTCTACTAGG		TACT GA CCTGC TCGGT AT CATCT TCT AATG TT /
	TGGCTACGTCCAAAAGCAAT		AAC AAA A GG -- GGA -- G AAGAA
	CAT		

GAM609	GGTCAGAATCCTGAACTTAC 595	TGTAAAAAGT 3320	GAA CT- -- AAGAA AA TGG
	A A		
	TAAGAAGCAGAAACATTTTT	GGTTTGCCAG	TCA TC GAACT TACT GCAGA CATTTTTTAT
	ACTCTG AGG A		
	TATTGGACTCTGAAGGAAAC	TGAC	
	CTATGGGGTGCTGTAAAAAG		AGT AG CTTGA GTGA CGTTT GTGAAAAATG
	TGGGGT TCC /		
	TGGTTTGCCAGTGACAGTTC		AG- ACT CA C---- G- TCG A A
	TCAGAGATGACC		

GAM610	TGTTATTATAGATTGCATGG 596	TGATATCATT 3321	- GC----- A GA T
	AGTCATCAGATGATAGCTCA	CTCAACTAAA	TGTTAT TATAGATT ATGG GTCATCA TGA A
	ATGATGATATCATTCTCAAC	TCTA	
	TAAATCTATGAATGACA	ACAGTA GTATCTAA	TACT TAGTAGT ACT G
	A	ATCAACTCT A A- C	

GAM611	CAGTATAGTGTGCACGTATA 597	TATAGTGTGC 3322	A---- A TATAACGTC AC
	ACGTCTGCAACGATATGCAA	ACGTATAACG	CAGT TAGTGTGC CG TGCA G
	AAAACAGTCGGCACGCTGCA	TCTG	
	AGAGCTG	GTCG	GTCGCACG GC ACGT A

AGAAC - TGACAAAAA AT

GAM612 CGCACGACGATTACGGTGAT 598 TGATATGGCG 3323 --- T - C-- GGTAC C GTT
ATGGCGCCTGGTACCACGCT CCTGGTACCA CGC ACGACGAT ACGGT GATATGG GCCT
CA GCTT T
TGTTTACGAAGCTGAAAAAG CGCT ||| ||||| ||||| ||||| ||| |||||
GTTACTCATATCGACCGTCG GTG TGCTGCTG TGCCA CTATACT TGGA GT CGAA /
TCGTCGTTCACTG ACT C G CAT AAAA- - GCA

GAM613 CCAAAATGCACGAGTGTGTA 599 TGTCACGTTC 3324 ---- - TAC AACG TT
CGCGTCAACGAAGGGTTTGT GTGCGATTCT CCAA AAT GCACGAGTGTG GCGTC AAGGG
T
GTCCTTGGATGTCACGTTCG ACTT |||| ||||| ||||| ||||| |||||
TGCGATTCTACTTGG GGTT TTA CGTGCTTGCAC TGTA G TTCCT G
CATC G --- G--- GT

GAM614 TCGGTAAATTTGTACAACG 600 TACGAAGATT 3325 ATT A C CC ACA AA CT G
AAAAC T A G
TCCGACTACACAAAAGTGCT TTTACACGTT TGT CAA TGT GACT CAA GTG AAAATTT TCG
GCCT TG G
AAAATTTGTGCAAAACTGCC GGGT ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
TATGGGAACGAGGTTACGAA ACG GTT ACA CTGG GTT CAC TTTTAGA AGC
TGGA GC A
GATTTTTACACGTTGGGTCA --- A A A- --- G- AT - AT---- - A
ACAATTGAGCATACGTA

GAM615 ATGTAATGGTGGCGGGTGTA 601 AATGGTGGCG 3326 A G GG TAAAA G CAAAGAAA
AAAGCGGGGTTGGCCAAAGA GGTGTAAAAG ATGTA TGGTG C GTG GCG GGTTGGC A
AAAAATGCGTAGTCGACTGT CGGG ||||| ||| ||| |||||
GTTACGAGTACCAGTGCAT TACGT ACCAT G CAT TGT TCAGCTG /
G - AG ---- G ATGCGTAA

GAM616 GGGTTAATAATAGTTTTTAC 602 TACACTGTAA 3327 -- G ACG- ATTAT T T GA AG
T AA
AGTGACGACAGATTATTGTA AACAAATGTGT GTTTT TACA TG ACAG TGTACAAA TG GC
GG TGTG GATA T
CAAATTGTGCGAGGAGTGTG CAAG |||| ||| ||| ||||| ||| ||| |||||
TGATAAATTTGTGTCTCACA CGGAA GTGT AC TGTC ACATGTTT AC TG CC ACAC
CTGT T
ACCAAGTTCAC TTTGTACAC CT A AAAA ---- C T AA A- T GT
TGTAACAATGTGTCAAGG
CTTGTGATCT

GAM617 GCCAGGAAGAGTTAATTTTT 603 AGAGTTAATT 3328 G--- A A AAATTAAAG- G
GT
AGAGATAAATTAAGTATTG TTTAGAGATA GCCA GAAGAGTTA TTTT GAGAT TATTGC
TTG A

CGTTGGTACTCGAGTAATGA	AATT					
TAACACACAATCTTAAAGGA		CGGT	TTTTTCGGT	AGGAA	TTCTA	GTAATG AGC /
CTGGCTTTTTTGCAATGGC		AACG	C	A	ACACACAATA	- TC

GAM618	AGGTTTTTAGAGGAGGTACC	604	GGAGGTACCG	3329	TTT	GTA	TACC	AT
	GATACCCAGACATATGCAAG		ATACCCAGAC		AGGT	TAGAGGAG	CCGA	CAGACAT G
	TGTTTGTTGGGAAC TTCTTT		ATAT					
	GGCTT		TTCG	GTTTCTTC	GGTT	GTTTGTG	C	
	---		AAG	----	AA			

GAM619	AAGGTTCTGAGCGACCTCAA	605	TAGCCGTCCA	3330	G	AC	C	G	TCT-	-	GCAAG
	A C										
	GCTCCCTGGTCTAGCCGTCC		CCGCAAGAAG		GA	CG	CT	AA	CTCCCTGG	AGCCGTC	CACC
	AAGGCCGGGGC TTG G										
	ACCGCAAGAAGGCCGGGGCA		GCCG								
	TTGCGAACACGCATGCTCCG				GT	TT	CC	GG	GATCGGTT	CGGGTTG	CGCG
	GGCCTCGTACG CAC A										
	GTCGCGCGGTTGGGCGGAGT				G	GT	G	-	GAGG	G	CT---
	TGGCTAGGGGCGCTGTTGTGG										- A
	CATCCAGGA										

GAM620	ACGTCATGGTTTTGGGGACG	606	TTGGGGACGG	3331	TG--	T	G	A	TCG-	A
	GCTACCTCGCGCAGCATGGG		CTACCTCGCG		ACGTCA	GTT	TGGGGAC	GCT	CC	CGCAGC T
	AACGTGCTTAAACGGGTTGC		CAGC							
	TGTTACGACATTCCA		ACCTTA		ACT	GTCGTTG	GCA	AA	TGCAAG	G
			CAGC	T	G	-	TTCG	G		

GAM621	AGTCCGCCGCCAGTTGGTG	607	TACGGGCCCT	3332	CAG	GA	-	-	CT	TTGT
	TT									
	GGGGAAC TCGGTAGTCTCTA		TGTCGGTCTC		CGCC	TTGGTGGGG	ACTC	GGTA	GTCT	
	ACGGGCCC CGGTCTCGGC A									
	CGGGCCCTTGTCGGTCTCGG		GGCT							
	CTTATGTGGCCGGGATCCTG				GGGG	CCACTCCTG	GGCT	ATCT	GAGG	TTCGGGGT
	TAGGGCCCGT /									
	GGGCTTGGGGAGGTCTACTC				CTG	GG	C	G	GG	CC--
	GGGGGTCTCACCGTCGGGG									GT
	TGGCGTTGA									

GAM622	CAAGGTCTCGGCAATCGTGC	608	TGAGGTCCAG	3333	GGCA	G	TG	T	T	CC-	GT
	TG										
	GCCGCCTGAGCCTTACTCGC		GTGGGGTACG		CAAGGTCTC	ATCGT	CGCCGCC	AGCCT	AC		
	CGCA GTG GGCCC G										
	ACCGTG GTGGCCCTGGTCAA		TCTG								
	CAGGGAGCCTAAGGTGGATG				TAGGGTCTG	ATGGG	TGGACCT	AGTAG	GT	GGAA	
	GAG GACAA /										
	AGGTCCAGGTGGGGTACGTC				C---	G	GG	-	-	TCC	
	TGGGAT									G-	
										CT	

GAM623	GCGGCCTGCCTCGTGTGGCA	609	TGGCACCTGT	3334	TG--	T	GT	-	A---	G
--------	----------------------	-----	------------	------	------	---	----	---	------	---

CCTGTGTGAGGGACTGCTGG	GTGAGGGACT	GCGGCC	CCTCGTG	GGCACCTGT	G	AGGG
CTGCTGGCCC A						
CCCGAGACCGGGTCGGTACG	GCTG					
TTTCCATTCCACAGGTGTG		TCGGAG	GGCGCGG	GTGGACACC	A	CCTT
TGGCTGGGCC G						
GCGCGGGACCGAGGCT		CCAG	T	TT C	TGCA	A

GAM624	GGCCCGAATCCTGTCCCACT 610	TGATTTGCCA 3335	-----	C-	ACT
	ACTGCTGAGGTGGGGCAATG	TCAAAAGTGG	GGCC	CGAATC	TGTCCCACT G
	ATTTGCCATCAAAAGTGGCC	CC			
		CCGG	GTTTAG	ACGGGGTGG	C
		TGAAACTACC	TA	AGT	

GAM625	GGTCTACGGTCCGGGCCAAA 611	CAAAGTGTTA 3336	A	CCG	AA - TT	ATTGAT	A
	CCC - AG						
	GTGTTACCATTGATGGGGAG	CCATTGATGG	CGGT	GGCC	AG TG	ACC	GGGG
	GCGCTACA TTCCGCA CC T						
	CGCTACACCCTTCCGCACCA	GGAG					
	GTTGCGGATGCGGAATGTGG		GCTA	CTGG	TC AC	TGG	CTCC CGCGGTGT
	AAGGCGT GG T						
	CGCCCTCTGAGGTTTCATCT		-	CGA	AG T TT	AGT---	- --- A CG
	GAGGTCAGCATCGAGATC						

GAM626	TCCCACCGGAACGTTTGGGT 612	TCAGAGGTAT 3337	GGGT-	- G - -	AACAACTG
	T C				
	TCTTCCCAGGAGTCCCCCCC	TGGGTGGGGC	GTTT	TCTTCCCA	GGA TCC CCCC CCTT
	CATGCTTC CGGCA T				
	CTTAACAACTGCATGCTTCT	GGGC			
	CGGCACTGAGGTGTCAGAGG		AGCA	GGGGGTCA	TCC GGC GGGT GGTT
	ATGGAGAC TGTGG G				
	TATTGGGTGGGGCGGGCCTC		TTTTG	C G G G	----- - A
	ACTGGGGGGTTTTACGAACC				
	TCTGGTGCG				

GAM627	TCTTGGTTTGCTTCCCACTGG 613	TCGGATCGCG 3338	--	GGG	A -	TGA	GAGT	TT
	C							
	GGGTCGCGACTCCAAGGTTG	ACACAGTGGT	T	TCCACT	GGTCGCG	CTC CAAGGT	TGTGTG	
	TTGG CCAGTTGG T							
	ATGTGTGGAGTTTGGTTCCA	TGAG						
	GTTGGCTCTGCCAGCTGCAC		T	GTGACA	AGCGCTA	GGC TCTAGG	ACGCCG	CCAC
	TCGACCGT /							
	CATAGCCGCACTGGGATCTT		TG	C--	- T	GTC	ATA-	G- C
	CGGATCGCGACACAGTGGTT							
	GAGCTCTCCGA							

GAM628	TGTCGCATCATACGAGACGC 614	TGAGGTCCTG 3339	TCAT	A C-	CCCT-	C CCA-
	GC G					
	CGCCAGGACCCTGAGCTGCG	ATTGGGGTCT	TGTCGCA	ACGAG	CGC	GCCAGGA
	GAGCTG GG A T GTCATG G					
	GCCAATGCGTCATGGGCTTG	TTCA				

CCCGTGGTGGCTAGGCGCGG	TGTAGGA CTGGG TTA CCTGGAG GCGCGG AT G
G GCCCGT C	
CGATGAGGTCCTGATTGGGG	CTTT G GT TAGCG - CG- T GT T
TCTTTCAGGATGT	

GAM629 TTATTTCCACAGAGCGATGC 615	GACCGTGGCT 3340	G CGA CACGA A AAGATGTCT
T GT - GT		
CACACGAAAGCTAACGGTTA	GACGTGGCTA AG TGCCA AAGCT ACGGTT TGC GT	
TGAGAAG AGC A		
AGATGTCTTGCTGTGTTGAG	GCCT	
AAGAGCGTAACACGCTTCTT	GA GGTGC CGGTG CCAGTT	GGG TT TTTTCTT
GCA /		
TTCTTTAGGGTTGACCGTGG	- TC- AGT-- -	----- A TC C CA
CTGACGTGGCTAGCCTGTGT		
GAGAT		

GAM630 TTTTATGGGCATGGTATCCC 616	TGAGGACTGG 3341	G-- C AGC - G---
TGC		
CCTCGAGCGTATGAGGACTG	TCGCCACCTT GCATG TATCCCC TCG GTATGAGGACTG GTC	
CCACCTTGTATT C		
GTCGCCACCTTGTATTCTGC	GTAT	
CATTCCAAGGCGGAGTGCGA	AATTG GCGCGC TCT TGACCGGCCGGT AGA	
GTGAGGCGGAACC /		
GAGATTGGCCGGCCAGTTCT	GGG C --- T GAGC TTA	
CCGCGCGGGGGGTTAATGCC		
ATCGC		

GAM631 ATCTTTTGTTAGTGGCCGTT 617	CATGACATAC 3342	- TT GTT GG C A
ACAGAGGGTGTCCGTGTGGA	TCTGTGGCCA ATCTT TTG AGTGGCC ACAGAG TGTC	
GTGTGG G		
GGACCACATGACATACTCTG	CTCG	
TGGCCACTCGTAACGGGAT	TAGGG AAT TCACCGG TGTCTC ACAG TACACC G	
	C GC --- AT - A	

GAM632 GTTGGTTCGGACGATGCAGT 618	TGGGGTGCCC 3343	TC A--- CAAGA A
CAAGAA- G		
CAAGATTAGGTGGGGTGCCC	AAGAAGACAT GTTGGT GG CGATGCAGT TT	
GGTGGGGTGCC GACATG C		
AAGAAGACATGGCACGTGTC	GGCA	
ACATATAGGCATCCCACTAA	CAACCG CC GTTACGTTA GA TCACCCTACGG	
CTGTGC /		
GGATATTGCATTGATGGCCT	TT GGTA TAG-- A ATATACA A	
TGCCAAC		

GAM633 ACTAAGGTATCACATGCAGC 619	TAAGGTATCA 3344	AA T- T A GA AA ATAGG
TATTTTGACAGAATTGGATA	CATGCAGCTA ACT GGTA CACA GC GCTATTTT CAG TTGG A	
GGATGAGAACTAAAGTTGAG	TTTT	
GAGGTGGCGCTTGTGTCTGC	TGA TCGT GTGT CG CGGTGGAG GTT AATC T	
TAGAGT	GA CT T - GA GA AAGAG	

GAM635 TATCCCTACATAGCCTGCTT 621 TTAAACAGGC 3346 ---- T C TAAAG ----- AA
AAAATGGA

A

TTATGATATATTTAACAGGC TCAA - - TA--- ATTAAGAA GA AGGGTAAG

TTGTAACCTCAAGGGATA

GAM637 CGCGGAAGCGTACGGCTTGA 623 TTAAAGCTGT 3348 GCG----- GAAGACAACC AA
AGACAACCAAAGGAAATTGT AACAGAATTT CGCGGAA TACGGCTT AAAGGA T
CCTTTTAAAGCTGTAACAGA TATT ||||| ||||| |||||
ATTTTATTCCGTG GTGCCTT ATGTCGAA TTTCCT /
ATTTTAAGACA AT----- GT

GAM639 CTTGGTAATGTAACGGTAAA 625 TAATGTAACG 3350 AA- -- ----- A CGA
GCAGGCACGAACAATGTCTG GTAAAGCAGG CTTGGT TGTA ACGGT AA GCAGGCA A
TATTTGAGATAACACCGTTC CACG ||||| ||| |||| || |||||
TACACAAGCCAAG GAACCG ACAT TGCCA TT TGTCTGT /
AAC GT CAATAGAGT A AAC

GTGTTGATCTCAGCGCTGCT CTGA ||||| ||| ||||| ||| |||||
 GGCTTGTTGCTGAGCGGTAC CTGAG CATG CGAG TCGTT GTT GGTCGTCGCGACTC
 A
 TGAGTC T G--- - - C- T

GAM647 AGACTTTTCTAAGCATGTAA 633 TTAGTGAATG 3358 C- CATGT - T GG ATGATAAT
 A
 GTATAGTTTCTTATGGAGAT GTTCAACATG CTTTT TAAG AAGT ATAGTTTC TAT AG
 GTTATTAACTTT G
 GATAATGTTATTAACTTTAG GAAA ||||| ||| ||||| ||| ||| |||||
 TGATGAAGTTAGTGAATGGT AGAGT TCGA CATT TCAAAGGT ACA TT
 GTGATTGAAGTA T
 TCAACATGGAACTATTACT TT AGT-- A - AC GGTA--- G
 GAAGCTTTTGAGAAGT

GAM648 AGCTATTTGTGGAAATGATT 634 CACCGGGTTT 3359 - TT GAAA CA TTA CAGCA
 CAAGTGAATTTATATCAGCA CCCATGGATA AG CTAT GTG TGATT AGTGAAT TAT A
 ATAAATAGATCTAGTTCACC CG ||||| ||| ||||| ||||| |||
 GGGTTTCCCATGGATACG GC TAGG CCC TGGGC ACTTGAT AGA /
 A TA TT-- C- CT- TAAAT

GAM649 GGTGGATACATTAAAGGATG 635 TGAGAGAAGA 3360 --- - T G AATTGAAAA GA
 CAAC- A
 AGAGAAGACCAATTGAAAA CCAATTGAAA ATACAT TAAA GGA GAGAGAA ACC GTA T
 TGAAAAC C
 GTAGATCAACTGAAAACACG AAGT ||||| ||||| ||||| ||| ||| |||||
 TGTGTTTTCTAATGGGCCTA TGTAAG TTCA TAT CTTTCA GTA TCC G
 TTTTGTG G
 TGGACTTTTCTATCACTTTT ATT C - G ----- GG TAATC T
 AGAATGTACTA

GAM650 ATAAAAGTTTAAGTAAGATA 636 AAAAGTTTAA 3361 A A TA- TATTTTCT - T AC
 CTTATTTTCTAGTAGCTAGT GTAAGATACT ATA AAGTTT AG AGATACT AGT AGC AGT G
 ACGTTGCTTGCTCATTTTTTC TATT ||||| ||| ||||| ||| ||| |||
 TAATAGTGTTTATTCTAAAA TAT TTCAAA TC TTTGTGA TTA TCG TCG /
 CTTATAT A A TTA TAATCTTT C T TT

GAM651 GCAACTTAATTACTGTCACC 637 TGGCAAGCAT 3362 CT A - CAC CA - T
 TCATTATAAATTCTCGATCG AGATAAGTAT GCAA TA TTA CTGT CT TTATAAATT CTCGA C
 GTCGGGCGGTTTATGGCAAG TTGC ||| ||||| ||| ||||| |||||
 CATAGATAAGTATTTGC CGTT AT AAT GATA GA GGTATTTGG GGGCT G
 T- G A C-- AC C G

GAM652 ACCGCGACAAGAATAGATTT 638 GATCACAGAA 3363 G AAGAA--- G TT GCCCC G
 A
 TGTGATCTTTTGCGCCCAT TGTGGTAAAC ACCGC AC TA ATTTTGTGATCTT GC ATGG
 CAC A

GAM653 TGAAATTGGATGGATATGGC 639 TGGGATGCAG 3364 A ATATG GTTAA AAG- A
ATCGTTAATCAAAAAGGGAT GTGCCAATCA TGAAATTGG TGG GCATC TCAAA GG T
GTTCAGGGTTTGGGATGCAG GTTT ||||| ||| |||| ||
GTGCCAATCAGTTTCA ACTTTGACT ACC CGTAG GGTTT CT G
A GTGGA ---- GGA T

ACTGAACGCGCGGATATGTT A C A ACTT- ATAGGCGCGCAA T A AC
TTCATTCTTACACGCATTAT
TGA CTG

GAM656 TAATGGATGTGTTTACCAAA 642 GAGAATGGTG 3367 A- TT AA G ATTA
TTGTTTAATTACATAATAGA CACAGACTGT TAATGG TGTGT ACCA TT TTTA C
GAATGGTGACAGACTGTTA TA ||||| |||| ||| || ||||
ATTGTC ACACG TGGT AA AGAT /
AG -- -- G AATA

GAM657 TTATGGACATCTTCCGTTAC 643 TGAAATAAAA 3368 A --- --- C G
TTCAGTGTTGGTCAATGCTG TCGGAATTTG TTATGG CATC TTCCG TTA TTCAGTGTT G
AAATAAAATCGGAATTTGAT ATGC ||||| ||| |||| || |||||
GCCGTAA AATGCC GTAG AAGGC AAT AAGTCGTAA T
- TTT TAA A C

GAM658 CCTGTGTGATAGTTTTGTTGG 644 TAGTTTGTTG 3369 - ---- TG CCAGT G - A
AGGAGGCCAGTATGTTTAGC GAGGAGGCCA CCTGTGTGAT AGTTT GT GAGGAGG AT TT
TAGCG T
GATGCCGCTGCAAGATTCTT GTAT ||||| || ||||| || |||||
CTCTGATCTGGGAGCTGATT GGGCGTATTA TCGAG TA CTCTTCT TA AA GTCGC G
ATGCGGG G GGTG GT ---- G C C

GAM659 GCGGATATAATGGCTGCTAT 645 TGATATGAGG 3370 ATAT- GC A- A AATTC
ACG
TAGGGACTCGTATAATTCGT CTCAAAGTGG GCGG AATG TGCTATT GGG CTCGTAT
GTCAA C
CAAACGCTATGTTGGCTGAT TAAC |||| ||| ||||| || ||||| ||||
ATGAGGCTCAAAGTGGTAAC TGCC TTGC ATGGTGA CTC GAGTATA CGGTT T
GTTTAGAACCGT AAGAT A- AA G GT--- GTA

GAM660 GTGGATGTCGATAATAGCGA 646 TCGATAATAG 3371 TA GCGAA A GT
AATGGATATGGTACACATAG CGAAATGGAT GTGGATGTCGA ATA ATGG TATG A
CTATAAATATTCGATATCCA ATGG ||||| ||| ||| |||
C CACCTATAGCT TAT TATC ATAC /
-- AAA-- G AC

GAM661 ACTCTTGACACCATTCCAT 647 TACCCGTTAT 3372 T C---- CATT C T
TTATACTAAATGTACCCGTT TTTACAAGTG AC CTTGTA AC CATTTA A
ATTTTACAAGTGT T || |||| || ||||
TG GAACAT TG GTAAAT /
T TTTAT CCCAT C

GAM662 GCTGAAGTAATTAATTTTTTC 648 TGAAGTAATT 3373 TG - TTTTTC C TTT ACTAGTT
TGCCCTCGTTTTTACTACAAC AATTTTTCTG GC A AGTAATTAA TGC TCGTT ACTACA T
TAGTTTTTCATCAATGTAGTG CCTC || ||||| || |||| ||||
ACGATGTATTGTTTAGTTAC TG T TCATTGATT ATG AGCAG TGATGT /
TCTTGGT GT C TGTT-- T --- AACTACT

GAM663 ACGAGTTAAAAAGGGTCATA 649 TGAGATAAGA 3374 A AAAAAG A --- A
TTTAAATTTAGTTGAGTTTA TTTAAAGCAC ACG GTT GGTC TATT TAAATTT G
TGAGATAAGATTAAAAGCAC GT |||| ||| ||| |||||
GT TGC CGA TTAG ATAG ATTTGAG T
A AAA--- A AGT T

GAM664 CGAGTTCGGTTTTGAAAAAC 650 ATGACATCAT 3375 AAAAC----- ----- TCA
AGC A
AAATGATGTCATTCTTGATC TTATATAATG A AAATGATGTCATT CTTGA
TGTTTTACG AG A
ATGTTTTACGAGCAGAATTC ACAT | ||||| |||| ||||| ||
TACCCGTAAAGCGAGTTCAG T TTTACTACAGTAA GGACT GCGAAATGC TC
T
GTTTAAAAACAAATGACATC ACAGTAATATA ACAAAAATTT TGA CCA T
ATTTATATAATGACATCATC
TCTGATCGCG

GAM665 TATGACTCAAGTTATGAGCC 651 ATGACATAGC 3376 A-- AGC GC
GTGTGCAAAACATGACATAG CTATGAGTCA TATGACTCA GTTATG CGTGT A

CCTATGAGTCATA TA ||||| |||| ||||
ATACTGAGT CGATAC GTACA /
ATC A-- AA

GAM666 TGGATAACGTAATAGAAATA 652 TAACGTAATA 3377 A A- TA C ATAA- G
CTATCTGTAATAAAGGATTC GAAATACTAT TGG TAACGTA TAGAAA CTAT TGTA AG A
TCAGAATACAATAGCTTTTT CTGT || ||||| |||| |||| || ||
TAGATATGTTACCA ACC ATTGTAT ATTTT GATA ACAT TC T
- AG TC - AAGAC T

GAM667 TTACAGCGTTAGGTGTTATA 653 TATGATATAT 3378 GGTG TCT A T CC C A
TTA AT
GTCTTAATATTTGTAGTACC CTACTATAAT TA TTATAG TA TA TTGTAGTA TATATTA TATA
TTGT AATAG T
TATATTACTATAATTGTTTA TAGT || |||| || ||||| ||||| |||| ||||
AATAGATTAAC TATTGTTAC AT AATATT AT AT AATATCAT ATATAGT ATAT GGCA
TTATC /
GGGTATATGATATATCTACT AAAA GT- G T CT - G TTG AA
ATAATTAGTATGTTATAAAA
AATAAAAACA

GAM668 GGTGATAAGTCTTATATAGC 654 TATTTTGCTA 3379 TCTT GCAA GAA A- ---
ACAA CT
AATATAGAAGTAAACATAGG ACTATGTAGT GTGATAAG ATATA TATA GTA ACATAG
GCAAA GTATT A
CAAAACAAGTATTCTAATAG ACAA ||||| |||| ||| || ||||| |||| ||||
ATATTTTGCTAACTATGTAG CATTGTTT TATAT ATAT CAT TGTATC CGTTT
TATAG A
TACAATATAAGTATATTAAT TAAT GA-- AA- GA AAT ---- AT
TTTGTTACC

GAM669 CGCAAAATATGCCTAGTGCT 655 TATAATGATA 3380 AAA TAGT---- T GGT CC A
CTGGTGTGCTTATATCCGTT GTGCTTTTTT CGCA TATGCC GC CT GTCGTTATAT
GTTCTG T
CGATACCGAATATATAATGA TTGG ||| |||| || ||||| ||||
TAGTGCTTTTTTTTGGTATA GTGT ATATGG CG GA TAGTAATATA TAAGC A
TGTG --- TTTTTTT T --- -- C

GAM670 CCGATAATGTAGAAAATATA 656 ATCAGATGTT 3381 AT AGA - A A - AG A TA
ACGTATGATTTACCTCAGGA GCTGTTTATG CCG AATGT AAATA TAACGT TGATTT CC TC
GAT GTA A
TAGTATAATTTACGATTTAG ATAT || |||| |||| ||||| |||| || ||||
ATGGAATCAGATGTTGCT GGC TTATA TTTGT GTTGTA ACTAAA GG AG TTA CAT /
GTTTATGATATTCCGG C- GTA C G A T AT G TT

GAM671 GAGTGTATAAAAGTAAAACA 657 TGGGATGTTT 3382 T AA - A GAACAAATA ATA
ACTGAACAAATACATGGAGT TAAC TTGGAT GAG GTAT AAGT AAAACA CT
CATGGAGTTTTT C

TTTTATACATCAAAAAATTT	ATCT			
TATGGGATGTTTTAACTTGG		CTC TATA TTCA TTTTGT GG		GTATTTTAAAAA A
ATATCTC	- GG A A -----	ACT		

GAM672	TATATGTCAAAATTACGACA 658	TATGTCAAAA 3383	A T AAATT	A TT- GG
	TTTACACGGAGAGTGT	TTACGACATT	TAT TG CA	ACGAC TT ACAC A
	AAAGTCGTTTTAATGTCAAA	TTAC		
	TA	ATA AC GT	TGCTG AA	TGTG /
		A T AATTT	A TTT	AG

GAM673	AAAAGCCAAACCACCGTTAA 659	GATTACGGTT 3384	TA---	CTGTTTTTACA -- T
	AGACT GTT			
	ACCGTAATTCTGTTTTTACA	CTGATACGGT	T AACCGTAATT	TGCTT C CAAAT ACAA
	CCAA T			
	TGCTTCCAAATTACAAAAGA	TACT		
	CTCCAAGTTTCAAGTTGGTG		A TTGGCATTAG	ATGAA G GTTTG TGTT GGT
	C			
	AGTTTGTGTTTGAGAAAGTA		TAGTC -----	A A - GAGT- GAA
	GATTACGGTTCTGATACGGT			
	TACTTACAAAT			

GAM674	AGTTATGACTACGTTAGTTT 660	TATGCTACTT 3385	TAG TG T---	-- TTGT-- T TG--
	A			
	GCTGGTTATGCTACTTTGTG	TGTGCAATTT	GT TT CTGGT	ATGC TACT GCAA TTCTAA
	AATGGTAT T			
	CAATTTCTAATGAATGGTAT	CTAA		
	ATTGGTGCTATTATTTT		CA AG GACCA	TACG GTGG TGTT AAGATT
	TTATCGTG T			
	AATTTGTCGTTTTGGTGTTG		TA- GT TTTT TT TTTTGC T	TTTA G
	CATTTTACCAGTGGAATAC			
	GTGTCTTACT			

GAM675	CAACCATGGACGGTTTTTGT 661	AAAGGCAAGT 3386	TG GGTTTTTGT	CA--- T-----
	ACAA- T			
	CAGTACAAAGGCAAGTGGGT	GGGTACAAGT	CCA GAC	CAGTA AAGGCAAG GGGT
	GTGCC A			
	ACAAGTGCCTATAGGTACAA	GCCT		
	ATGACCCTATAAGATTTTGT		GGT TTG	GTCAT TTCTGTTT CCCA CATGG T
	CTTGAAAATACTGTTTGTA		GT AAATGTTT-	AAAAG TAGAATAT GTAAA A
	AGTTTGTGGTTG			

GAM676	CAAGACTTCAAACTTTTGA 662	TTCACAGAAC 3387	AAAA T A T A
	TTTGTGAAATATGATTTCA	ATAAGGAGGT	CAAGACTTC CTT TG TTTGT GAAAT T
	CAGAACATAAGGAGGTTTTG	TTTG	
		GTTTTGGAG	GAA AC AGACA CTTTA /
		--- T A - G	

GAM677	CACCAATTAATAATACAGTT 663	TAAGGAAGAA 3388	TGAT A A--- AATT
	AAGAGAAGT CCT		

GATACAACACCTAAGGAAGA	TTTGTGTGTTA	ACAGT	ACA CACCT	AGGAAG	TGTTGTTA
TGAACG T					
ATTTGTTGTAAAGAGAAGT	AAGA				
TGAACGCCTTCCTCGTTCAT		TGTCA	TGT GTGGA	TCTTTC	GTAACAGT
ACTTGC /					
GACAATGTAGCTTTCTACCA		TAGT A	ACCA	GAT-	----- TCC
AGGTGATGTTGATACTGTTG					
TTAATGGTG					
GAM678 CAGACATCAGATACTGCTCA 664	TTACTAGAGC 3389	----	---	GC A-	- - C T T
TGCCTGTAATGCCAATCGTT	AAAGAAAGGT	CAGACAT	CAGA	TACT TC	TGC CT GTAATG
CAA CGT T					
TTAACGTTGCCATTACTAGA	ATTT				
GCAAAGAAAGGTATTTTCTG		GTCTGTA	GTCT	ATGG AG	ACG GA CATTAC GTT GCA
T					
TATTATGTCTG	TTAT	TTT	AA AA	A T	C - A
GAM679 CAGGTGAACTTGTGAGATTT 665	TAAGTCTATT 3390	A T	- TA -	TG AATT	T
GTAAAGTCTATTTGCAATTC	TGCAATTCAG	CAGGTG	ACT GTGAGA	TTTGT	AGT CTATT C
CAGC G					
AGCTGTTGCTGTCTGCGTGGGTG	CTGT				
GTACTATACAAATTCTCGCT		GTCCGT	TGA CGCTCT	AAACA	TCA GGTGG G
AGTGTGCCTG		G T	T TA T	GTCT--	T
GAM680 CCTGATGGCCGATGTTGATG 666	TGGCCGATGT 3391	----	TTG-	TCCTAA	T - GA
CTA					
ATCCTAAATTGATGGGATGG	TGATGATCCT	CCTGA	TGGCCGATG	ATGA	ATTGA GGG
ATGG CTATC A					
GACTATCCTAAGTGTGATAG	AAAT				
AGCTATGCCCTCAATGATTC		GGATT	ATCGGCTGT	TGCT	TAACT CCC TATC
GATAG G					
GTATGTTGTCTGGCTATGATC		CTAGT	TGTA	TAG---	- G GA TGT
TTAGG					
GAM681 GACATCTTGTACACACCTCC 667	TGTACACACC 3392	CTTGT	C--	ACT-	TT CTA-
ACAG TG					
GACTGTCAGTTATGGTTCTA	TCCGACTGTC	GACAT	ACACA	CTCCG	GTCAG ATGGTT
CATT GC G					
CATTACAGGCTGGTTTGCGC	AGTT				
AAAATGGCACAACCATCTGG		CTGTG	TGTGT	GAGGT	CGGTC TACCAA GTAA
CG T					
CTTTGTGGAGAAATGTGTTG		CCTGT	AAA	GTTT	-- CACG AACG TT
TCCGTGTC					
GAM682 GATGTACTACGTAATAGCTT 668	TTTGGTAAAG 3393	GT-	T	----	TTAAT TGTCTTTA
GAGT AA					
TGGTAAAGATCTTAATGCTA	ATCTTAATGC	AATAGC	TTGGTAAA	GATC	GCTAATA
GCC GC G					
ATATGTCTTTAGCCGAGTGC	TAAT				

AAGAGAGCTTTAGGCCTGTC
TTATCG GATCATTT CTAG TGATTAT CGG CG

A
TATTAGTGATCATGAATTTA TCT T AAGTA ----- CTGTC--- ATTT AG
CTAGTGCTATTTCTAATGCA
CATC

GAM683 GATGTTTCAAAAAC TACTCT 669 TACGTCTGAG 3394 T AAAAC T GTTTAC T A
AGGCGGTTTACACTTGTTGA TAAAATGGGC GATGTT CA TACTC AGGCG ACTTGT G T
TTTCACAAGTACGTCTGAGT ATC ||||| || ||||| ||||| |||||
AAAATGGGCATC CTACGG GT ATGAG TCTGC TGAACA C T
- AAA-- - A----- - T

GAM684 GCAGAGGATGTTTGTACTTG 670 AGAGGATGTT 3395 --- ----- - GAT
TTACGATAATAGTATACAAG TGTACTTGTT GCAGAG GATGTTTGTA CTTGT TAC A
GTTTCATACGAACGTTTTACT ACGA ||||| ||||| ||||| |||||
CTGT TGTCTC TTGCAAGCAT GAACA ATG /
ATT ACTTG T ATA

GAM685 GGAGTTTCTGAAATTGT TAA 671 TTAATACTGT 3396 T AT TGT TG - TCTAATGT T
TG- CTT
TACTGTCGCTGGCATTCCAT CGCTGGCATT AA TGTTA AC CGC GCATT CCA GTA
CTTGT GTAAAA T
CTAATGTGTATCTTGTTGGT CCAT ||||| || ||||| ||||| ||||| |||||
AAAACTTTAATTTTACACT TT ACAGT TG GTG CGTAA GGT CGT GAACA
CATTTT /
ACAAGCTGCTTTTGGTAATG T AT TTT GT T TTT----- C TCA TAA
CTGGTGTTTGTATGACATT
TTTGAGTCAC

GAM686 GGTGGCGTCTCTTTATTAGC 672 TACTATGACT 3397 C TTAT ACTACA G A
TACTATGACTACAAGACAGT ACAAGACAGT GGTGGCGT TCT TAGCTACTATG AGACA
TTTC T
TTCATCAGAAATGTCTGAAA TTCA ||||| || ||||| ||||| |||||
TCCATAGTAGCTACCAGAAA CCACCGTA AGA ATCGATGATAC TCTGT AAAG C
TGCCACC A CC-- CTAAAG - A

GAM687 GTCTTTAATATATTTTCAGGC 673 TAACATTAAT 3398 A TTTCAGG-- G - ----- T G
TT
TGTAAGTTCTAACATTAATT TGCGTTTTGA TTA TATA CTGTAA TTCT AACATTA ATTGCG
TTTGA CG A
GCGTTTTGAGCGTTAACTCG GCGT ||||| ||||| ||||| ||||| ||||| |||||
TCAAATTGCAATAATTTTAA AAT GTAT GACATT AAGA TTGTAAT TAACGT AAAC T
GC A
TGTTAAGAAGTTACAGAGAC A TTCAACAGA G A TTAA T - TC
AACTTTATGATAATTGC

GAM688 GTGAAACATTTTGGCGTTAC 674 TTTGGCGTTA 3399 - T- C GATAT GAAA- T
AACTTTGATATAACTGAAAG CAACTTTGAT GTGAAA CATTG GCGGTTACAA TTT AACT
GCAAG A

CAAGTATTCTTGCAAAGAGG	ATAA		
TTTTTAAAAATTGTAATGTT		TACTTT GTAGG TTGTAATGTT AAA	TTGG CGTTC T
TTGGATGATTTTCAT		A TT A ATTT- AGAAA T	

GAM689 GTGGTAAGAGTTTGCCGGCT 675	TGGAATGCTT 3400	GA - ---- TA- TT
ATTAAATTGAATTTTGGAAT	AATGGTAATG	GTGGTAA GT TTGCC GGC TTAAA G
GCTTAATGGTAATGCAATTG	CAAT	
CTAC	CATCGTT CG AATGG	TCG GGTTC A
	AA T TAAT TAA TA	

GAM690 GTGTGGAACAGCTTGAACCG 676	TCGAACAGCT 3401	-- CT -- G- GCT - CTTTT
TG TG		
TGTGCTCAGTCTAGACTTTT	TGAACCGTGT	GTGTC GAACAG TGA ACC TGT CAG TCTAGA
GAG GTGT C		
GAGTGGTGTGTGCTTATACTG	GCTC	
CTTTTTCTGGACCTGTTGAC		CATAG TTTGTC ATT TGG ACA GTC AGGTCT TTC
CATA /		
AAAGGTCATTATACTGTTTA		TA AT AC AA GTT C TT--- GT TT
TGATAC		

GAM691 GTTACAACAGACCTACTATG 677	TATTGGACAA 3402	A ACTATG ATTGG A-- G TA
- AG		
CTGGATATTGGACAAGCTCG	GCTCGCGTAG	AACAG CCT CTGGAT ACA GCTC
CGTAGCA TCAAG TGGC C		
CGTAGCATATCAAGTGGCAG	CATA	
CTCGCTATTTTGA CTGTTAC		TTGTT GGA GATCTA TGT TGGG GCATTGT AGTTT
ATCG /		
GAGGGTGGCTGTATTACATC		- GA---- CATTA CGG A C- T CT
TAGAGAGGTTGTTGTTAC		

GAM692 GTTACCAAGAGTTAAGTCAA 678	TAATATGCAA 3403	AGT CAATTT TTG GT TGT AA
A - CC		
TTTAGCCATTTGGATGTTGT	CCTTTCATTG	CCAAG TAAGT AGCCAT GAT TG GG
GCATAT AC AGAC T		
GTGGAAGCATATAACAGACC	TCAT	
CTTTGTTTAGTAATATGCAA		GGTTT ATTCG TTGGTA CTG AC CC CGTATA TG
TTTG /		
CCTTTCATTGTCATGGTTTT		AT- TCGTT- --- TT TTT AA A A TT
GCTGCTTATATTTGGTGAC		

GAM693 TATGCTTACTTTGGATGACC 679	TATTAAGGAT 3404	TT G T-- T C GA----- --- T
TT		
GTGGTTTAGCTCTAGACAAT	TGTGTTGACA	GGAT ACCG GGT TAGCT TA CAATGCA
CTTAGTGGTG GC A		
GCACTTAGTGGTGTGCTTAG	TAAA	
TGCTGCTATTAAGGATTGTG		TCTA TGGT CCA ATCGA AT GTTGTGT
GAATTATCGT CG /		
TTGACATAAATAAGCTATA		T- A CTT T A AAATACA TAG - TG

CCTTCTGGTAATCTTATTAA
 GTTTGATATA
 GAM694 TCCGTGGTTCATTTATTAAT 680 GTTCATTTAT 3405 T T ATTAA ----- G CAATC
 GGTGCGTGTGGTTCCCCTGG TAATGGTGCG TCCG GGTTCATT TGGTGCGTGTG GTTCC
 CCT GCTA T
 CTACAATCTTAAAAATGGCG TGTG |||| |||| || |||| |||| |||| |||| ||||
 AGGTGGAATTTGTTTATATG AGGC TCAAGT AA ACTACGTATAT TAAGG GGA CGGT
 T
 CATCAAATTGAACTCGGA - T ----- TTGTT T G AAAAA

GAM695 TGCTTACATGCCAATTGCAG 681 CATGCCAATT 3406 TAC ATG A ----- C A GA
 TT
 ACCCTACACATTTTGACATT GCAGACCCTA TGCT ATGCCA T CAG CC CTACA ATTTTG
 CATT AGAAG G
 GAAGAAGTTGAACTTTTAGA CACA |||| |||| | ||| |||| |||| |||| ||||
 TGCAGAGTTTGTAGAACCAG ACGG TATGGT G GTC GG GATGT TGAGAC GTAG
 TTTTC /
 GCTGTGGTGGTATTTTGGCA TTT -GT - ACCAA T - A- AA

GAM696 TGGGAATACCCTACTGCACG 682 TATGATGCCT 3407 GA TACT -- C T
 TCATACTATTCTTATATGAT GTTATGGGTA TGG ATACCC GCA CGTCATA TA T
 GCCTGTTATGGGTATGACTA TGAC ||| |||| || |||| ||||
 ATC TATGGG TGT GTAGTAT AT C
 AG TAT- CC - T

GAM697 TGTTTTGTTTGTTAATGACA 683 TTAATGACAA 3408 TG T AAAT AAT A
 AAATTACTGAATTCCAATTG AATTACTGAA TGTTT TT GTTAATGACA TACTG TCC A
 GATTACAGTATTGATGTCAT TTCC |||| || |||| |||| |||| ||||
 TGATAATGAAATA ATAAA AA TAGTTACTGT ATGAC AGG T
 GT - AGTT ATT T

GAM698 TTAATGCGTTACCTGAAGTT 684 TGACTTGTCT 3409 - CGT - AA - TTGTT ATGA
 CT
 AATGCAGACATTGTTGTCGT GTGATTAACC TTA ATG TAC CTG GTTAAT GCAGACA
 GTCGTGG GGTGT A
 GGATGAGGTGTCTATGTGCA AGCG ||| ||| |||| |||| |||| |||| ||||
 CTA ACTATGACTTGTCTGT AAT TAC ATG GAC CAATTA TGTCTGT CAGTATC
 TCACG T
 ATTAACCAGCGTATATCATA A TAT C -- G T---- AA-- TG
 TAA

GAM699 TTTCATTTTCTGATGACGTT 685 TGAAGTAAAA 3410 TGAT G TG AGACA AC T
 GAAGTAAAAGACATTGAACC GACATTGAAC TTTCATTTTC GAC T AAGTAAA TTGA CTG T
 TGTTTACAGAGTCAAGCTTT CTGT |||| |||| ||| |||| ||| |||
 GCTTTGAGTTTGAAGATGAA AAAGTAGAAG TTG A TTCGTTT AACT GAC T
 A T--- -GT CG--- GA A

GAM700 TTTTATGGCTTTAAAGATGC 686 TTAATGGTAT 3411 TG AAG CTTT TGA- T T
 TGTTACTTTTGCAACAGTTG TAGAGTGTTA TTTTA GCTTTA ATGCTGTTA GCAACAGT
 TCATAG GC T
 ATCATAGTGCTTTTGCCTAT AAA |||| |||| |||| |||| |||| ||
 GAAAGTGCTGTTGTTAATGG AAAAT TGAGAT TATGGTAAT TGTTGTCG AGTATC
 CG T
 TATTAGAGTGTTAAAA TG --- ---- TGAA - T

GAM701 ACAGTTCGTGAGTTTGTTAT 687 TTAATGGCTA 3412 T TA AC C- - TTTAT ATCG
 TTC TT
 TTCACGCACAGGACATTTTT TCGCTATTTT GTT GT TTTC GCA AG GACATT ATTAATGGCT
 CTAT AC T
 ATATTAATGGCTATCGCTAT ACTT ||| ||| ||| |||| |||| ||| ||
 TTCACTTTAGGTAATGTAGA TAG CA AAAG CGT TC CTGTAA TAATTGCCGA GATG
 TG /
 AGCCGTTAATTTCAATGTCA T CC A- CA A CTT-- A--- TAA GA
 CTA CTGCAGAAACCACTGAT
 TTTTGTACTGT

GAM702 ATTATGTTGCATTGCAGACT 688 TTGCATTGCA 3413 -- AGACT----- TTTA AATC
 GATGTTTTACAAGAAAATCA GACTGATGTT ATTATGTTG CATTGC GATGT CAAGAA A
 GAAATTCTTGCTGCATCTT TTAC |||| |||| |||| ||||
 TTAACAAAGCAATGACCAAC TGATACAAC GTAACG CTACG GTTCTT G
 ATAGT CA AAACAATTTT TC-- AAAA

GAM703 CTGCAGATGTTAGTGAGATG 689 AGATGTTAGT 3414 A TG ---- CA TT
 CTCACTTTGTACAAGAAAGC GAGATGCTCA CTGC GATGTTAG AG ATGCT CTT G
 GTTTACACTTGCTAATGTTA CTTT |||| |||| || |||| ||
 GTAG GATG TTGTAATC TC TGCGA GAA /
 A GT ACATT AA CA

GAM704 GAAACTAAAGGGCCTTTGTG 690 ACACGGGAAA 3415 TA C-- G C ATCA - AAT
 - TGT
 TGTTGACACATCACACTTCA TTGCCCTTTT AAGGGC TTT TGTGTTGA AC CACTTCAC
 TACCA ACGTTG C T
 CTACCAAATACGTTGCTGTT TC |||| || |||| || |||| |||| ||
 TATGCCAATGTTGGTAGGTG TTCCCG AAG GCACAATT TG GTGAGGTG ATGGT
 TGTAAC G /
 GAGTGCTAGTATTAACACGG -- TTA G A ATC- G --- C TAT
 GAAATTGCCCTTTTTC

GAM705 GTGCGTTGATGGTACAAACG 691 ATCACATCTC 3416 TGAT A G T-- C CAACC C-
 T AC
 GTTATGTGTTGCGACAACCT GCATAATGTT GTGCGT GGT CAAACG TTATGTG TG GA
 TAAT TTGC CTTT A
 AATCTTGCTCTTTACAAAGA TGAA |||| || |||| |||| || || |||| ||||

AGGCAATTATTATAGAATCA TATGCA CCA GTTTGT AATACGC AC CT ATTA AACG
 GAAG /
 CATCTCGCATAATGTTTGAA --- A - TCT A AAGAT TT - AA
 CCACGTAT

GAM706 TGGCAGATTTTGTTCAAATT 692 TAAGACGCTG 3417 TCAA AAA A ACAT TCTC-
 A T A
 GAAAATTGCAATGTCACATT CAAGAATTAA T TTGA TTGCA TGTC TTGTTAACATT
 GCTCTG GT GCAA C
 TGTTAACATTTCTCGCTCTG GTTA | |||| |||| |||| |||||||| ||||| || ||||
 AGTTGCAAACCATTGTGCCA A AATT AACGT GCAG AATAATTGTAG TGAGAC CG
 TGTT C
 GAGTATATTGATGTTAATAA TTG-- AAG C --- TTATA - - A
 GACGCTGCAAGAATTAAGTT
 ACAAATTGCCA

GAM707 GGCACCAAATTGATTTGTTG 693 TATAACAAAT 3418 ACCAAATTG - ACAA C - AA
 ATAACAAAGTTACAGATGGA AATCTCCGGC GGC ATTTGTTG ATA GTTA AGA TGG T
 ATTCTCACTCTTAGCCAAGT C ||| |||||| ||| ||| ||| |||
 ATATAACAAATAATCTCCGG CCG TAAACAAT TAT CGAT TCT ACT /
 CC GCCTCTAA- A GAAC- - C CT

GAM708 TTGGAATTAATGGGGTGGCT 694 TGAGGTAAAC 3419 G- G AA
 TAGCGAAACACTCGCTGAGG TCATTGATTT TTGGAATTAATGGG TG CTTAGCGA C
 TAAACTCATTGATTTCAA CAA |||||||||| || ||||||
 AACTTTAGTTACTC AT GAGTCGCT /
 AA G CA

GAM709 GTGTCTGAAGCGTATGCGAA 695 TCAGCGGCAA 3420 G- GC AAAT A CAAG CT -
 AT--- TCAATA
 AATCATTAATTGTCAAGTGC TACAGTGAAT CGTAT GA CATT ATTGT TGCC CTG TGCAG
 CGA T
 CCTCTGTGCAGATCGATCAA GTTG |||| | ||| |||| ||| ||| |||| |||
 TATTAAATATTCGTATTACT GCATG CT GTAA TGACA ACGG GAC ATGTC GCT
 T
 GTATCAGCGGCAATACAGTG TA A- GTT- G TA-- C- T ATTAT TATAAA
 AATGTTGTCTAGTACGATGTC
 GAGCAC

GAM710 ATCATAGATGAAATAGCAGG 696 GGAGGGACCA 3421 CAACTTCA CA G CG A--
 - AA
 AGGGACCAACTTCATCTCAA ACTTCATCTC TAGCAGGAGGGAC TCT AGACTT TAGC
 CTTTG TCGAAG CC T
 GACTTGTAGCCGCTTTGATC AAGA ||||||||| || ||||| |||| ||||| ||
 GAAGCCAATTGGGCCTTTGA GTTGTCTTCTTG AGA TTTGGG ATTG GAAGC
 AGTTTC GG /
 CAACGAAGAAGTTAGGGGTT A----- AA G AA AAC C GT
 TAAAGAAGTTCTTCCTGTTG
 TCTAGTAGGGT

GAM711 CGAGCGCTGAGGGATTTAAC 697 TGAGGGATTT 3422 C- TTAA AG C AATA

CAGGGTCTGGAATAGCGCAT	AACCAGGGTC	CGAGCG TGAGGGAT	CC GGT TGG G
CAACCACGGCATTCTCATC	TGGA		
TGCTTG	GTTCGT ACTCCTTA	GG CCA ACT	/
	CT C--- CA - ACGC		

GAM712 TTCCGTGACATTTGAGCTCC 698	TGCCCGTTTCG 3423	G TTTGA C C AC A ATCAA
AA GG		
TGTTGACGGGACCAACCCA	ATACGAGTCC	TTCC TGACA GCTC TGTT GACGGG CA CCC
CTGAGG AT G		
TCAACTGAGGAAATGGGAGA	TGTT	
TGACTTCGGGTTTCGGGCTGT		AGGG ACTGT TGAG ATAG TTGCCC GT GGG
GGCTTC TA /		
GCCCGTTTCGATACGAGTCCT	A TGTCC C C GT C CTTG-	AG GA
GTTGTCAAGGGA		

GAM713 GGCTTTGACTCCATCAAGAA 699	ACTCCATCAA 3424	TT--- -- CAA- AACATC - T
ACATCAGCAGATTTATCATG	GAAACATCAG	GGCT GAC TCCAT GA AGCA GA T
CTCTCAGATCAAAAATGGAA	CAGA	
TGTCTCAATGGCT	TCGG CTG AGGTA CT	TCGT CT T
	TAACT TA AAAA AGACTC A A	

GAM714 GTCTGATTATAGCATCATAT 700	TAGCATGAGA 3425	TA----- CA- A- CA
GTGAATCATCAATTTATAGC	ACTGAAAATA	GTCTGAT TAG TCAT TGTGAAT T
ATGAGAACTGAAAATAAATC	AATC	
ATCAGAC	CAGACTA GTC AGTA ATATTTA /	
	CTAAATAAAA AAG CG AC	

GAM715 AATTGAGGCATTAGAACATG 701	TTACCCGACT 3426	GCATTA --- T T TAATTC
CAAAC TA		
CTATAAGTTTAATTCGTAAC	TGTCGTCTGA	AATTGAG GAA CA GC ATAAGTT GTAA
TTGA C		
AAACTTGATACTATTCAATT	AATT	
ACCCGACTTGTCGTCTGAAA		TAACTC CTT GT TG TGTTCAG CATT AACT T
TTCAAAAACCTCAATT	AAAAA- AAA C C	CC---- ---- TA

GAM716 CAGGCATTGGAAGTTACAAC 702	TTGGTCCTGC 3427	--- A A TACA T AT
CAATTTGATGAGCAACTTGG	GTCCGGAGTT	CAGG C TTGGA GT ACCAA TTG G
TCCTGCGTCCGGAGTTTCCT	TCCT	
G	GTCC G GGCCT CG	TGGTT AAC /
	TTT A G TCC- C GA	

GAM717 GAAATATTTTAAGGCCCGTG 703	TGGCAGATTT 3428	TT GCC TG GT CT GA TC
GCAGATTTTGTCCGACTTAG	TGTCGGACTT	GAAATAT TAAG CG GCAGATTTT CGGA TA
TCT A		
ATCTTCAGTAGACATATTTT	AGAT	

CGGAGATTTGTGTTGAACTT
AATATTTTC

CTTTATA ATTC GT TGTTTAGAG GCCT AT AGA /
-- AA- TG -- TT AC TG

GAM718 GAATTGATGCATTGTATTTCG 704 ATGCATTGTA 3429 A C- A TTAA GA- - TG ----- -
AT

TTAAGAGTTAAGTTAGATGT TTCGTTAAGA TGC TTGTATT GTT AGAG GTTA TGTA CT AGA
AGCG C T
ACTTGAGAAGCGCATTGAAG GTTA ||| ||||| ||| ||| ||| ||| ||| |||
CCGCTGAAATATCTTGGGAT GTG GACATAA CAA TTTC CGGT GCAT GG TCT
TCGC G G
ACGGCATGGCAATCCTTTAA - AA A CTAA ACG A GT ATAAAG C AA
ACAAAATACAGGTGTTAATT
C

GAM719 GCGATGGCACGGGACCACTC 705 GTGCGCAACG 3430 ---- - GATA AT AG
TATTCCCTC

GATAGGTATTTTGTGTGTGA GAGCCGAGTG CACG GGAC CACTC GGT
TTTGTGTGTAC CG T
CAGCGTATTCCCTCTTCGCA TACG ||| ||| |||| ||| ||||| ||| |||
TATTCGAGGTGCGCAACGGA GTGC CCTG GTGAG CCG AGGCAACGCGTG GC
/
GCCGAGTGACGGAAGTCCA GAGA AAGGCAT ---- -- GA TTATACGCT
GAGCGTGCTGCGC

GAM720 GTTCTTGGAGTACATTCTCC 706 TGGAGTACAT 3431 TG CA TC -- GT G CG GGA
GTCCGGTGGAGTCGTGGGAC TCTCCGTCCG GTTCT GAGTA TTC CGTC CG G AGT TG C
AAGCATAACTACGTCTGTAGA GTGG |||| |||| ||| ||| ||| ||| ||| |||
CGTGAAC TACTTTGAGAAC CAAGA TTCAT AAG GCAG GC C TCA AC /
GT C- T- AT TG A AT GAA

GAM721 AAAGATGGAAGAACTGAGG 707 TGAGGAAATG 3432 - AAGAAA A TGT AT- CTGTC
- TACTT

AAATGTACAATGCACTGTCC TACAATGCAC AAAGAT GG CTG GGAAA ACA GCA
CGAACT GTCTG A
GAACTGTCTGTACTTAAAAA TGTC ||||| ||| ||||| ||| ||| ||||| |||||
TTCAGACAAGTTCGATGTTG TTTCTA CC GAC CCTTT TGT TGT GCTTGA CAGAC
A
ATGTTTTTTTCCCAGATGTGC A GTGTA- - TT- AGT A---- A TTAAA
CAATCTTT

GAM722 ACCGGAAACTGATCAAAATT 708 TGTCACCTTTC 3433 - AAA C A - T A G
ACGGAGAATGCGTTAGAGAT CATGATAGGT AC CGGAAACTGATC ATTA GGAGA TG CGT
AGAGATC GG T

CAGGGTGCCCGATCTTTATG TAGT || ||||| ||| ||||| ||| ||||| |||
TCACTTTCCATGATAGGTTA TG GTCTTTGATTGG TAGT CCTTT AC GTA TTTCTAG CC G
GTTTCTGAGT A A-- A C T - - C

GAM723 CAGCAAAGGTGGTTTTGGTG 709 TCGGGAAGA 3434 G TG A- TT T GACAAA AA
T GT

GATGGCGTTCCAGGGTGCGG CAAAGGAAAT GTTTTGG G TGGCG CCAGGG GCGGGAA
 GGA TTCTT CGAGA T
 GAAGACAAAGGAAATTCTTT TCTT ||||| | |||| ||||| |||| |||||
 CGAGAGTTAATTTCTGAAGAA TAGAGCC C ACTGC GGTCCC TGTTCTT TCT AAGAA
 GCTTT /
 GATCTAATTCTTGTCCTGG G GT GA T- - AA---- AG - AA
 TCGTCAAGCTGCCGAGATGA
 TCAGAAGAAG
 GAM724 CTAAAGTACTACACCGTTGT 710 TAGAACGGGT 3435 -- - -- GT GA C TAG
 GATGGATCCTTTAGTTAGTA TAGTAGTTAC CTAA AGTA CTAC ACC TGT TGGATC TTTAGT T
 TCATTAGAGATTTAGAACGG TTAT ||| ||| ||| ||| ||| ||| |||
 GTTAGTAGTTACTTATTAG GATT TCAT GATG TGG GCA ATTTAG AGATTA /
 AT T AT -- AG - CTA

GAM725 GTTACAACCTTTTATCGGTAA 711 TAAAAGGAGC 3436 TC-- AT---- C A TTC-- GT GC
 GC- C
 TACCGTCATCATTGCTTCGT CTTCTGCGGA TTA GGTA AC GTCATC TTGC GT CTT
 ATCAAT TCC G
 GTCTTGCATCAATGCTCCCG GATG ||| ||| || ||||| ||| || ||||| |||
 ATGGAAAAATTGATAAAAGG AAT TCAT TG CAGTAG GGCG CG GAA TAGTTA
 AGG A
 AGCCTTCTGCGGAGATGACA CCTT GTTGTT A A TCTTC AG AA AAA T
 GTTTGTTGTACTTTCTAAG
 GGTTGTGAGT

GAM726 AAGTACTACACCGTTGTGAT 712 TAGAACGGGT 3437 - -- GT GA C TAG
 GGATCCTTTAGTTAGTATCA TAGTAGTTAC AAGTA CTAC ACC TGT TGGATC TTTAGT T
 TTAGAGATTTAGAACGGGT TT |||| ||| ||| ||||| |||||
 AGTAGTTACTT TTCAT GATG TGG GCA ATTTAG AGATTA /
 T AT -- AG - CTA

GAM727 ATAGCGTTAGAGCTGGGATG 713 ATAAAGCTCA 3438 A TTAGA GAT-- GC TA
 CTTGCTGATACCTTTCTATAA AACCGGCGTA AT GCG GCTGG GCTT TGA C
 AGCTCAAACCGGCGTATTGC TTGC |||| |||| |||| |||
 AGT TG CGT CGGCC CGAA ACT C
 A TATG- AACT AT TT

GAM728 TGGAGTTGGTATTCAAAGCT 714 TACAATGCTT 3439 GGTA A TTTTG A A -
 GAAATGA
 TTTGACATTGAAGCATATGT CGGGTACGCT TGGAGTT TTC AAGC AC TTGAAGCAT TGT
 TACT T
 TACTGAAAATGATGATACCA TCGG ||||| ||| |||| || ||||| ||| |||||
 GAGTGTACAATGCTTCGGGT ACTTCAA AGG TTCG TG GGCTTCGTA ACA GTGA
 /
 ACGCTTCGGAAAACTTCA AA-- C CA--- - - T GACCATAG

GAM729 GCGAGCGATATTGTCATTAT 715 TATGATGATT 3440 AG - T A A - GA-- T

GATGATTAAGCGGAGCGGTC AAGCGGAGCG GCG CG ATA TGTCATTATG TG TTAA GCG
 GCGG C
 AACTGCAGAACGTGTAAAC GTCA ||| ||| ||||| || ||| ||| |||
 AATATAGTGGCGCTGTCCGA TGT GC TGT GCGGTGATAT AC AATT TGC CGTC A
 GTGT GA C C A A G AAGA A

GAM730 GTATAACAAGTTGAGGCAGC 716 TGAGGCAGCA 3441 C C T T TC TTT- -----
 AG
 AGTGTAATGTGTGGTCCGAT GTGTAATGTG GTTGAGG AG AGTG AATGTG GG CGA
 GCTAATTGTGCA CC C
 TTGCTAATTGTGCACCAGCC TGGT ||||| || ||| ||||| || ||| ||||| |||
 CGGCGAGAATATGTACGATT CAACTCC TC TCGC TTACAT CT GCT CGGTTAGCATGT
 GG /
 GGCTCACTCGCTTCTACATT T C - - TC CACT ATAAGAGC CC
 CGCTCCTTCTCAACGATTA
 C

GAM731 GTGTGTATTTCGCACGAGAAA 717 AAAAGTGGTT 3442 TAT AAA ---- TT- - -
 GAAGA G
 AAGTGGTTTGAGTACATGGT TGAGTACATG GTGTG TCGCACGAGAA GT GGT GAGT
 ACAT GGT CG A
 GAAGACGGAGACGATAAGCC GTGA |||| ||||| || ||| ||| ||| ||| |||
 GGTGTGACTTTTTGCCGAG TACAC AGCGTGTTTT CA CCG TTCA TGTG CCG
 GC G
 TACCAGTTTTTGTCGACCA C-- GAC TGAGC TTT G G AATA- A
 CAT

GAM732 TAAGATATTGGTTGACGGAT 718 TATTGGTTGA 3443 TGG ACGG CAGG GT
 ATGACAGGGCGTGCAGCAAT CGGATATGAC TAAGATAT TTG ATATGA GC G
 CGTATAGGACAAATGTATTT AGGG ||||| ||| ||||| ||
 TG GTTTTATG AAC TATGCT CG /
 TA- AGGA AA-- AC

GAM733 AGCTCAAAAGTGTAACCAAG 719 TAACAACTCA 3444 AA---- CCCA C G
 TCTGTTATGGAGCATAACAA GTTGCACCTCG AGCTCA AGTGTA AGT TGTTATG A
 CTCAGTTGCACTCGAATCTG AATC ||||| ||||| ||| |||||
 AGCT TCGAGT TCACGT TCA ACAATAC /
 CTAAGC TGAC - G

GAM734 AGTCGGGGTCGACGTCGCAA 720 TTCAACATGA 3445 GG C C C AC A A G
 CTCGAGTTGGAAGAATTAGC ACTGTTACTT AGTCG GT GA GT GCA TCG GTTGGAAG ATTA C
 ATTGGTACTTTCAACATGAA CTAC |||| ||| ||| ||| ||||| |||||
 CTGTTACTTCTACAACGACT TCAGC CA CT CA TGT AGT CAACTTTC TGGT A
 AA T T T CA A A T

GAM735 ATGGTACATACTTTGGCGAA 721 GTACATACTT 3446 - CTT- AACAT- TAT
 CATGTTGCTATGCTACGCGA TGGCGAACAT ATGGTAC ATA TGGCG GTTGC G

CTTAAAACGTTATATCTATG	GTTG		
GTACCGT	TGCCATG TAT ATTGC	CAGCG	C
	G CTAT AAAATT CAT		

GAM736 CATCAAGAGGGATATGGATG 722	AGAGGGATAT 3447	AA	T- A	TTG AG
AAGCCGTTGAGAGCAAACCTA	GGATGAAGCC	CATC	GAGGGATA	GG TGAAGCCG AG C
TGTGGTTTCACCTTTGTTTT	GTTG			
TCCAGATG	GTAG CTTTTTGT CC ACTTTGGT	TC A		
	AC TT -	GTA AA		

GAM737 GTCCTGAAGCAGCTAGGAAA 723	AAGCAGCTAG 3448	T GA A TAG	ATA TT AT - T
TATCCTTTACATGTTGAAAC	GAAATATCCT	G CCT AGC GC	GAA TCC TAC GTTG AAAC A
TAGCGTTTGCGATTTCGTATC	TTAC		
GGAAGTTCATTGCAGCTCAA		C GGA TCG CG CTT	AGG ATG TAGC TTTG G
GGC	- AC A TTA GA-	CT CT G C	

GAM738 TTGCTGACAAACTGCGCTCT 724	CTGACAAACT 3449	C	A C C TC	GACACAA G
AC				
TTTCTCGACACAAAGCTTGT	GCGCTCTTTT	TTG TGACAA	CTG GCT TTT TC	AGCTT
TTGTTGG A				
TGTTGGACACCACCAGCGGA	CTCG			
AGCTACTAGAAGAAACAGCT		AAC ATTGTT GAC CGA AAA AG	TCGAA GGCGACC C	
CAGGTTGTTATCAA	T	G T C GA ATCA---	- AC	

GAM739 GATATTGTAATATGTGAAAT 725	TATTGTAATA 3450	TG ATA	GAAA--	AA AT G A CAA
C AC				
GGGAAATTCTATTTTCAGCAC	TGTGAAATGG	GATAT TA TGT	TGGGA TTCT TTCA C CG	
GGA ATA T				
GCAAGGACATAACTTCATAT	GAAA			
TTCCCTACGGTGAAGGAACT		CTATA AT ACA	ACCCT AAGG AAGT G GC CCT TAT	
T				
CCCAGGATTAACAGGTATGA		GT GG- ATTAGG	C- -- -- ATC T AC	
TATC				

GAM740 GATGCCTGTGTTTCATGACGT 726	TGACGTAAAG 3451	- GTAAA	A G	CA--- GTG A
GA A				
AAAGCGAATTTTGAATGCTC	CGAATTTTGA	TTCATG AC	GCGA TTTT AATGCTC	GGA TCT
ATGCG GAAG G				
CAGGAGTGTCTAATGCGGAG	ATGC			
AAGAGAGTTTTGACGCATGA		AAGTAC TG	TGCT AAGA TTATGGG	CCT GGA
TACGC TTTT A				
GGAATCCATTACGGGTATTG		A AC---	- G	CATTA AA- G AG G
AGAATCGTCAGTACATGAAT				
GCATTGAATC				

GAM741 TGCAACCTCAAACGTAAATC 727	CAGGCGCGTA 3452	C	-----	AA CC
AT A				T CCCAA TAT

CAGGCGCGTATGTCCCAAG TGTCCCAAG CAA CTCA AACGT AT AGGCGCGTA GTC
 GTC TC AGTGC G
 TCTATTCATAGTGCAGATGC TCTA ||| ||| |||| | ||||| || || | ||||
 ATTCAGACGGCGTTTAGATC GTT GAGT TTGTA TG TTTGCGTAT TAG CGG AG
 TTACG A
 TATGCGTTTATGTAGATGTT T AGAAA GA TA C ATTTG C-- AC T
 AAAGATGAGTTTGCA

GAM742 TTGCTAATGATGAATACGTT 728 ATGTAGCCTA 3453 GA A CT- A- - A A- T T ACG
 CC
 ATTACTATTTTCATGTAGCCT TTAGTTGTTG AT ATACGTT TTA ATTC TGTAGC CT TT GT GT
 GCTG TTGG C
 ATTAGTTGTTGCTGACGTTG CTGA || ||||| || |||| |||| || || || || || ||
 GCCCCACCCAAGCAGTTGCA TA TATGTAG AGT TAGAG ACGTCG GA AG CA CG
 TGAC AACC C
 CGAGAAAGAGCTGCAAAGAG G- A TTT AA A A AG - T G-- CA
 ATTTTGAAGATGTATGATT
 ATTCTGCAA

GAM743 GTCAAAAGTTTTGTAAAAG 729 TATCAAAAGA 3454 AAA AAAAGAAA C GTAA
 AAATGATGTTCTTGTGGTA CGGAAGTAGA GTC AGTTTTGTT TGATGTT TTGTTG A
 AAGTTATAACAAAAATATCA C || ||||| ||||| ||||
 AAAGACGGAAGTAGAC CAG TCAAGGCAG ACTATAA AACAAT /
 A-- AAA----- A ATTG

GAM744 AAGATTGTGGTTTTGTTATG 730 TGCGAACAAG 3455 TG --- A TGGT
 CAGTTTGGTTATATTGACTG ACTTGTGTGA AAGAT T GGTTTTGTT TGCAGTT T
 CGAACAAGACTTGTGTGATT TTTT |||| | ||||| |||||
 TT TTTTA G TCAGAACAA GCGTCAG A
 GT TGT - TTAT

GAM745 AAGTATTAATACCTCTTGTA 731 TGCAATGCTC 3456 TAATAC C C GTGTTA
 GGGTCTTGACGCGTGTATG TGCAACAGAT AAGTAT CT TTGTAGGGT TTGCAGC T
 CTAAAGCTGCAATGCTCTG ATAC |||| | ||||| |||||
 CAACAGATATACTT TTCATA GA AACGTCTCG AACGTCTG G
 TA---- C T AAATTC

GAM746 AAGTTTGTGGATTTTGGCGG 732 TGACACTACT 3457 T GA G A T T T T
 GATGGAAGTTGTTTCATGTGT GTTCAGTCAA AAGTT GTG TTTTGGC GGATGG AGT GT CA GTG
 T
 TAGCACTGACACTACTGTTT AAGA |||| | ||||| |||| | || || ||
 AGTCAAAAGATACTAATTT TTTAA CAT AAACTG CTTGTC TCA CA GT CAC A
 T AG A A - - - G

GAM747 ACCCTGTATGGCCAAACTGT 733 TAGTTTATTT 3458 - ---- - TTTT GTGT T
 GCACG
 AGTTTATTTTGGAGGTTGTG TGGAGGTTGT ATGG CCAAAGTGT AG TTTA GGAGGTT
 GTAT GGAGTCCA T

TGTATTGGAGTCCAGCACGT GTGT ||||| || ||||| ||||| |||||
 AATATATGGATTCTATATT TATT GGTGGCA TC GAAT CTTCTAA TATA
 CCTTAGGT A
 AAAATCTTCTGTAAAGTCT T GTAT T TGT- AAT- T ATATA
 ATGACGGTTTGGTTTATACT
 GGAGT
 GAM748 AGATTTTCAGTTCATGCTTT 734 TTCATGCTTT 3459 AT C- TTTGG - TG-- T
 GGTGTAACGATGAGAAAGTT GGTGTAACGA AG TTTCAGTT ATGC TGTAACGA AGAAAGT
 A
 ATGACTTTCTATCCTCGTTT TGAG || ||||| ||||| ||||| |||||
 GCAAGCTGCATCTGACTGGA TC AAGGTCAG TACG ACGTT GCT TCTTTCA T
 AGCCT CG TC TCGA- T CCTA G

 GAM749 AGGGTCAGGATGTCATCTTC 735 AACCCGGTAA 3460 TCT-- -- AT GC- AGAG GCT AA
 -- CA
 AGCCAATTCGACAGCCTGAG TGTCGGTGGT GTCA TCA GCCA TCGACA CTG TCA CT
 CCAGA GCC C
 AGTCAGCTCTAACCAGAGCC AATG |||| || ||||| ||||| ||||| ||||| |||||
 CACAAGGTAATCTGGGGAGT CGGT AGT TGGT GGCTGT GGC AGT GA GGTCT
 TGG /
 AATGAACCCGGTAATGTCCG CTCGT AA -- AAT CCA- AAT GG AA AA
 TGGTAATGATGCTCTGGCAA
 CCTCCACTAT
 GAM750 CAGCTTTTAAAGGTTTAGC 736 TATTGCTGGT 3461 TT TAA-- T - CT TTTC TT
 ACAGCCTGTGGATTTCTTGG GCTATACTTG CAGC TT AGGT TAGCAC AGC GTGGA
 TTGGCA G
 CATTGACTGCTAGTTCTATT CTGT |||| || ||||| ||||| ||||| |||||
 GCTGGTGCTATACTTGCTGT GTTG AA TTCA ATCGTG TCG TATCT GATCGT /
 AATTGTTG TT TGTCG T G T- T--- CA

 GAM751 GCTTCAATGTTGCTATTACT 737 TGAGTAATAT 3462 TG-- - - - AG
 CGAGCCAAGAAAGGTATTCT GCAGTTGTTT GCTTCAA TTGC TATTACTCG AGC CAA GAA G
 TTGTGTTATGAGTAATATGC GAAG ||||| ||||| ||||| ||||| ||||| |||||
 AGTTGTTTGAAGC CGAAGTT GACG ATAATGAGT TTG GTT CTT /
 TGTT T A T T AT

 GAM752 GTTAAACGCGTGCGTGCTTG 738 AACGCGTGCG 3463 A- CGT T T G GA
 GGTGGCTTTGATGCTGAAG TGCTTGGGT GTTA ACGCGTG GC TGGGT G CTTT T
 GCGCTCATGCCACGCGTGAT GGCT ||||| ||||| ||||| ||||| ||||| |||||
 AGC CGAT TGCACAC CG ACTCG C GAAG G
 AG --- T - G TC

 GAM753 TAGTTGCTCCTTTGAGGATG 739 TGGTATCAAG 3464 T TC GGA A C T -- T
 AATTGACACCTAGCGATGTT TTACAATCAA TAGT GC CTTTGA TGA TTGA ACC AGCGA TGTT
 A
 TATCAACAACCTCGCTGGTAT AGCG ||||| ||||| ||||| ||||| ||||| |||||

CAAGTTACAATCAAAGCGTA
CTA

ATCA TG GAAACT ATT AACT TGG TCGCT ACAA T
- C- AAC G A - CA C

GAM754 TATAATAAGCAGATGGCTAA 740 TGGCTAATGT 3465 - - TGTCT TTAACT A G
TGTCTCTGTTTTAACTACAC CTCTGTTTTA TATA ATAAGCAGA TGGCTAA CTGT AC
CCCTTTA T
CCTTTAGTCTTAAAGGGGGT ACTA |||| ||||| ||||| ||| || |||||
GCAGTTTTTTAGTTATTTTGT GTAT TATTTGTTT ATTGATT GACG TG GGGAAAT C
TTATGTATG G T TTT-- ----- G T

GAM755 TATTAAGCCCAATTTAAAA 741 TTAAAGCCCA 3466 AAA T AG--- A- C T
CATTTGAGAAAGTAGATGGT ATTTAAAACA TATTAAGCCCAATTTA CATT GAGAA
TAGATGGTGTGT TA TAATT T
GTGTATACTAATTTTAAATT TTTG ||||| ||||| ||||| ||||| ||||| |||||
GATAGGACACACCATCTGTG ATAGTTTTGGGTTGAAT GTAA TTCTT
GTCTACCACACA AT GTTAA /
ATATTCTTAATGCTAAGTTG C-- - ATAGT GG A A
GGTTTTGATA

GAM756 TATTTGGAGTATATAAAGAA 742 TTGGATAGCT 3467 T AAGA A T C G
GTTGTACAATGACCTGGGTA ACAGTGTTAT TATTTGGAGTA ATA AGTTGT CAA GA CTGG T
ATCAGATCTTGGATAGCTAC TTTA ||||| ||||| ||||| ||||| |||||
AGTGTTATTTTAAGTA ATGAATTTTAT TGT TCGATA GTT CT GACT A
- GACA G - A A

GAM757 TCATGTGATGGTGGATTGTC 743 GTGGATTGTC 3468 AT- - T - - A
GCCGACTTCTTAAACAAGAA GCCGACTTCT TCATGTG GG TGGATTG CGC CGAC TTCTT A
TGTTGTGTGCAGTCTAGCCT TAAA ||||| ||||| ||||| ||||| |||||
AATACGTGA AGTGCAT CC ATCTGAC GTG GTTG AAGAA A
AAT G - T T C

GAM758 TCATTTGAGGAGCAGGATGA 744 TGTCTTGCCA 3469 GA----- AAAT A CTAT
AATTTACGCCTATACTAAGC ACACTTACTC TCATTTGAG GCAGGATG TT CGC A
GCAATGTCCTGCCAACACTT AAAT ||||| ||||| ||||| |||||
ACTCAAATGA AGTAAACTC CGTCCTGT AA GCG /
ATTCACAAC ---- C AATC

GAM759 TCTAAGGTTAAGGGTGTGCC 745 TTTTATGCAC 3470 GTT G C T TGTT TG GT-
GAT CGA
TAATATGCATGTTGTGGTAG AGTCTTTGTT TCTAAG AAGG TGTGC TAA ATGCA G GTA
GGAAAAT GC T
TGGAAAATGATGCCGATAAA TAGA ||||| ||||| ||||| ||||| ||||| |||||
GCTAATTTTCTTAATGCTGC AGATTT TTCT ACACG ATT TATGT C CGT TCTTTTA
CG /
TGTATTTTATGCACAGTCTT GT- G T T ---- GT AAT AT- AAA

TGTTTAGA

GAM760 TGCTATTAGTGCTAAGAATA 746 TTAGTGCTAA 3471 T--- A A- - - AC
GAGCCCGCACTGTCGCTGGT GAATAGAGCC TGCTA TAGTGCTAAG AT GAGC CC GC T
GTTTCCATACTTAGTACTAT CGCA |||| |||||||| || |||| ||
GACTGGCA ACGGT ATCATGATTC TA TTTG GG CG G
CAGT A CC T T CT

GAM761 TGGTACATTGAGTCGTGAAG 747 GTACATTGAG 3472 TG AAGATCT A AC-- TG
ATT
ATCTTGAGATTGGTTACACC TCGTGAAGAT TGGTACAT AGTCGTG TG GATTGGTT ACCG
G G
GTGGATTGTTCTTGCGGTAA CTTG |||||| |||||| || |||||| |||| |
AAAGCTAATCCATTGTGTAC ACCATGTA TTAGCAT AC CTAATCGA TGGC T /
GATTTGATGTACCA GT GTGTT-- - AAAA GT CTT

GAM762 TGTAGTTCCACAAGGTGGTT 748 TGTGATTGGC 3473 G CAAG GG T TG TT TT C
ATGTTGCCGATTTTGCATAT AGTGTGTTGC TGTA TTCCA GT T A TTGCCGATT GCATA
GGTT T
TGGTTCTTAACCTTATGTGA ATAC |||| |||| || || |||||| |||| ||||
TTGGCAGTGTGTTGCATACT ACGT AAGGT CG G T GACGGTTAG TGTAT CCAA /
GGAAATGCA A CATA TT - GT -- T- T

GAM763 TGTTGGCGCCATAGTGTTAC 749 CATAGTGTTA 3474 C TACAT T --- -----
AT
ATGTGATTACTTGTATAATC CATGTGATTA CGC ATAGTGT GTGATTACTTG ATA ATCCA
CTTATTGTTG A
CACTTATTGTTGATATTCAA CTTG || |||||| |||||||| || |||| ||||||||
CAGTGGGGATATATTGGATC GTG TGTTATA TACTAATGAAC TAT TAGGT
GGGTGACAAC /
TTTATCAAGTAATCATGATT A TTTAG - TTC TATATAG TT
TATATTGTAGTGCCACA

GAM764 TGTTGGTCGTGTGATTTCTG 750 TGTGGTACAT 3475 T TT-- CTT - AT---- TT- TT-
G
TTGTCTCTTTGTGGTACATG GGGTTCTAAC G GAT CTGTTGTCT TGTG GTAC GGG
CTAAC AGAGGAA A
GGTTCTAACTTAGAGGAAGA TTAG | || |||||| |||| |||| || |||| ||||||
AATTCTTCTTATGTTGGCTT T CTA GACAACAGG ACAT CATG CTC GGTTG
TCTTCTT A
CTCTTTTTGGTACTTACACA - TTTC TAC T GTTTTT TTC TAT A
TGGACAACAGCTTTATCTAT
GGCTGCAGCA

GAM765 TTCAGATGTTGATACTAAGT 751 TTGATACTAA 3476 -- A GTT-- GAT- T----- T
GTTTAGCTGATTCTGTCATG GTGTTTAGCT TCAGA TGTTG TACTAAGT TAGCT TCTGTCA
GTCTGCTG A
TCTGCTGTATCGGCAGGCCT GATT |||| |||| |||||| |||| |||||| ||||||

TGAATTGACGGATGAAAGTT AGTTT ACAAC GTGGTTCA GTTGA AGGCAGT
 CGGACGGC /
 GTAATAACTTGGTGCCAACA AT C ATAAT AAGT TAAGTTC T
 TATTTGAA

GAM766 TTGATCAATGGTATGAGTCT 752 TGTAGTAGAC 3477 TCA T TACA- AAGTT
 GT- CT
 ACATTTGGTCTAAGTTATTA CAGGATCTTG TTGA ATGGTA GAGTC TTTGGTCT
 ATTATAGTAACA ATGG T
 TAGTAACAGTATGGCTTGTC GCTC |||| |||| |||| |||| |||| |||| ||||
 CCATTGTTGTTGCTGTAGTA AATT TGTCAT CTCGG GGACCAGA TGATGTCGTTGT
 TACC G
 GACCAGGATCTTGGCTCTAC TG- - TTCTA ----- TGT CT
 TGTGTTTAA

GAM767 TTGATTTGTAAATTTAAGA 753 TTAAATGGCT 3478 T- G TT TGTT TG T -
 A
 GAGATTAAGCCTGTTTTTAA TTTTGTCTTA GTTAAAT TAAGA AGA AAGCC TTTAATG
 GTTAAAGC GTGC GAAAT A
 TGTGGTTAAAGCTGTGCGAA TTAT |||| |||| || |||| |||| |||| |||| ||||
 ATAAAATTTCTGCATGCTTT CGGTTTA ATTCT TTT TTCGG AAATTAT TAATTTCG
 TACG CTTTA /
 AATTTTATTAAATGGCTTTT TT G -- T--- TT - T A
 TGTCTTATTATTTGGCTGGA
 TTAA

GAM768 TTGTATATATTGCCGCGCAC 754 TGTGCAAATT 3479 TA- CACGAG A - GAT
 GAGTTGAACACCCAGATGTT ACGCGGCAAG TTGTATA TTGCCGCG TTG ACA CCCA G
 GATGGGTTGTGCAAATTACG TTTG |||| |||| || |||| ||||
 CGGCAAGTTTGTACAA AACATGT AACGGCGC AAC TGT GGGT T
 TTG ATTA-- G T AGT

GAM769 TTGTGAAGATCATAAGCCAC 755 TGAATGGTAT 3480 A T CAA TAAG
 AATATTCGTTTAAGTTGGTA GGTTTTTGGT TTGTG AGATCA AAGCCA TATTCGTT T
 ATGAATGGTATGGTTTTTGG CTAT |||| |||| |||| |||| ||||
 TCTATATAA AATAT TCTGGT TTTGGT GTAAGTAA /
 A T ATG TGGT

GAM770 GTTTGTCAAGTTTGTGGATT 756 TGACACTACT 3481 TC T GA G A T T T T
 TTGGCGGGATGGAAGTTGTT GTTCAGTCAA GTTTG AAGTT GTG TTTGGC GGATGG AGT GT
 CA GTG T
 CATGTGTTAGCACTGACACT AAGA |||| |||| || |||| |||| |||| |||| ||||
 ACTGTTTCAAGTCAAAAGATAC CAAAT TTAA CAT AAACTG CTTGTC TCA CA GT CAC A
 TAATTTTTTAAAC TT T AG A A - - - G

GAM771 CATGATGTTAATAGTGGTAC 757 TTAAGTGGCA 3482 TG TA TT C - C A -----
 AAT
 TACTTGTTCTACTGATTTAC AGGTATTTTT ATAG GTAC CTTG CTA TGAT TTA AAA ATCA
 AACACAGACAT T

AAAAATCAAACACAGACATA GTTG |||| |||| |||| |||| |||| |||| ||||
 ATTCTTGGTGTGTTTGTGTAA TGTT TATG GAAC GGT ATTA GGT TTT TAGT
 TTGTGTTTGTG C
 TTATGATCTTTATGGTATTA TT -- C- C T A C ATTAA GTT
 CTGGCCAAGGTATTTTTGT
 GAGGTTAATG
 GAM772 CTCACCTTCTAAACAATATCT 758 TTGATTGTAA 3483 C CAAT T AG T AG T
 ACTAGCTTTCAATCAAGATG GAGTGATTTT CTCACCT TAAA ATC ACT CTT CAATCA
 ATGGTGTTA T
 GTGTTATTTTTAATGCTGTT ATGA |||||| |||| |||| |||| |||| ||||
 GATTGTAAGAGTGATTTTAT GAGTGAG ATTT TAG TGA GAA GTTAGT TGTCGTAAT T
 GAGTGAG T ---- - - T -- T

GAM773 GTTATTAAAGATGGTGTAA 759 TTATAGTGTG 3484 TA TAAT A A TC- A TAG---
 - T
 GTATAGTGAGTTTCCTGCTA GTAGTACAAC T AAGATGGTG GTAT GTG GTT CTGCTATA
 CTATAGG TAC T
 TAACTATAGGTAGTACTTTT CACA | |||||| |||| |||| |||||| |||| ||||
 GTAAATACATCTTATAGTGT G TTTTACCAT CATA CAC CAA GATGGTGT GATATTC
 ATG T
 GGTAGTACAACCACATACTA GG ---- - - CAT - TACATAA T
 CCATTTTGGGTAAT

GAM774 TGTTTTTGATACTTTTAATT 760 TGTTATAGGA 3485 TTTTG T TACC T
 TCCTTACCAACGGCTTTTGC GATTTAAAGT TGT AACTTT AATTCCT AACGGC T
 TGTTATAGGAGATTTAAAGT GTAC || |||||| |||||| ||||
 GTACTACA ACA TGTGAAA TTAGAGGA TTGTCG T
 TCA-- T TA-- T

GAM775 TTCCCGATTGCAATATTGAG 761 TCGGTGCCCT 3486 GC ATT -- A
 GCTTGGCTTAATGATAAGTC CTCCATTAAA TTCCCGATT AAT GAGG C TTGGCTTA T
 GGTGCCCTCTCCATTAAATT TTGG |||||| || |||| ||||
 GGGAA AAGGGTTAA TTA CTCC G GGCTGAAT G
 A- CCT CT A

GAM776 GTCTTGGCGGTTTCAGTCGGC 762 TGGCGGTTCA 3487 TGG CA-- C AATAT TT
 AATATTCCACTTCGCGTGGA GTCGGCAATA GTCT CGGTT GT GGC TCCAC C
 TGGCTACAGTAAACCGGTGG TTCC |||| |||| |||| ||||
 AC CAGG GCCAA CAT CG AGGTG /
 TG- ATGA - GT--- CG

GAM777 CCGGTGCACAGCGAGCCCCA 763 TGTACACAAT 3488 CC TT ATATCT A GAA A
 TAAGTTTGT TG
 GTTGTCCGCATATCTGTACA ACGAATTGCA GC CAG GTCCGC GTAC CAATAC TTGC GG
 ACGTG A
 CAATACGAATTGCAGGTAAG GGTA || |||| |||| |||| |||| ||||

TTTGTACGTGTGACTCACGT CG GTC CAGGCG CATG GTTATG AACG CT
TGCAC /
TCGCAACGAGTATTGGTACT AA -- GTGCGT - AGC - ----- TC
GCGTGGCGGACCTGAAGCTG
GCGGTTCGACGG
GAM778 CGTGTATCCGCGACGCACGC 764 TGTGATGCCA 3489 A - GCA- AA AG AG
CAAGA
CAAGATGGAGTGGTATCGTA AACTGTCGGT CGTGT TCCGCG AC CGCC GATGG
TGGTATCGTAGTG TC G
GTGAGTCCAAGAGCGCCAAG GAAG |||| ||||| || |||| ||||| ||||| ||
AGCCGCTGTGATGCCAACT GCGCA GGGCGT TG GTGG CTGTC ACCGTAGTGTGCG
AG C
GTCGGTGAAGGGTATGCGGG - A GGAA -- AA CG AACCG
ACGCG
GAM779 TCGGTACCGTTTGAATTCGG 765 TATGACTATT 3490 ACCG ----- C G----- G
CCATAGTGCACGATCGTGAC TTGGATTAA TCGGT TTTGAATTC GG CATAGT CAC A
TTTAACTATGACTATTTTGG AACG |||| ||||| || ||||| ||
ATTTAAAACGATGCA ACGTA AAATTTAGG TC GTATCA GTG T
GCA- TTTA A ATTTCA C
GAM780 CGACGTGCGCGCCTACCAGA 766 TTCAACGTAA 3491 AGC TTCGTAC T
TTACAACCATC G CG
GCTTGATCGATTTCGTACTTT ACAATTCGAT CAG TTGATCGA TTTACGTT GAATA
TGTTTCG CGG G
ACGTTTGAATATTACAACCA CAAC ||| ||||| ||||| ||||| ||||| ||||| ||
TCTGTTCGGCGGCGGCACCG GTT AACTAGCT AAATGCAA CTTGT ACAAGT
GCC /
TGAACATGTTCAACGTAAAC AC- TAAC--- - ----- - AC
AATTCGATCAACATTGCGGG
TAGCAGACGCG
GAM781 AAGGGAAAATGCTTGAGGTG 767 TGAGGTGGCC 3492 AAA CT G-- GGACA- TT
GCCGGACACTTTTCGTTTGAC GGACACTTTC AAGGGA TG TGAGGTG CC CTTTCG T
GGAGGAGAAAAGGAAACATT GTTT ||||| || ||||| || ||||| ||
TCAGACATCTCTT TTCTCT AC ACTTTAC GG GGAGGC /
--- AG AAA AAAAGA AG
GAM782 GGGAAACTGAATCTTGAGGG 768 TGAGGGAGGG 3493 AAA AAT ----- GC A-- G
AGGGCGAGTCATGGGGGCCA CGAGTCATGG GGG CTG CTTGAGG GAGG GAGTC
TGGGG C
TCCCAATAGACTTACCTCGT GGGC ||| ||| ||||| ||||| ||||| ||||| ||||| ||
GGAACCTCAGGCAGCCC CCC GAC GGACTCC CTCC TTCAG ACCCT C
--- --- AAGGTG A- ATA A
GAM783 TGCGGATTTTTTTGGGAAAGG 769 GGTCATGTTT 3494 - -- AAAGG TAG - AAG
GAA GA
AAGCATAGTGGCCTGTGCCA ATGACTCAAC TGCG GATTTTTT TGGG AAGCA TGGCCTG
TGCC TTT TGC G

AGTTTGAATGCGAGGAAGCA	AAAA	
AAAAAGGCAGTAGGTCATGT		ATGC CTAAAAA ACTC TTTGT ACTGGAT ACGG AAA
ACG G		
TTATGACTCAACAAAAATCA		A CA AGTA- --- G AA- --- AA
CGTA		

GAM784 TGCTGTCGTGGCTTTGGCTT 770	TTTGGCTTGG 3495	TG- TTT---- -- - TG TAGTT G
TA G		
GGCTCATGCTGGATAGTTGG	CTCATGCTGG	TGC TCGTGGC GGCTT GGCTCA TGC GA
GGAT GC GG T		
ATGGCTAGGGTGAAGTGTGAT	ATAG	
CCTTCTGGCGCTGAGCCTTG		ACG AGCACCG CCGGG CCGAGT GCG CT CCTA
TG TC G		
GGCCTGTATACGCCACGAGA		TAG CATATGT TT C GT T---- G -- A
TGCA		

GAM785 ATAAACCCGTCACCTGTTAAT 771	AACCCGTCAC 3496	A - AA AATT CAC
CAATTGGATCACGATAAATT	TGTTAATCAA	ATAA CCCGTCA CTGTT TC GGAT G
CTTGGAAGCAGTTGATGGGG	TTGG	
TTAT	TATT GGGTAGT GACGA AG	CTTA A
	G T -- GTT- AAT	

GAM786 CGGCTCAGGTGAGAAGACAG 772	TCAGGTGAGA 3497	T ----- GA A--- G- - AC
TAGCAGCTGTCACGAAGGAC	AGACAGTAGC	CGGC CAG GTGAGAA CAGT GCA CT GTC
G		
AAGGATGTGAACGCTGGTTC	AGCT	
TCATGGGAAAATTGTGCCG		GCCG GTT TACTCTT GTCG TGT GA CAG A
	T AAAAGGG G- CAAG AG A GA	

GAM787 TCTCTTGTGGTTTCAAGATT 773	TAATACTGTA 3498	GATTT CGATGC C--- AT-- TTGT-
----- G		
TTTGCGCGATGCTACAGCGA	CGCAACATGA	TTGCG TACAG GACATT ATACC
GAAC T		
CATTATATACCTTGTGAACG	TAGC	
TGTGTTTGGTATTCTCCTTG		AACGC ATGTC CTGTAA TATGG TTTG G
GTATTACAAATGTCTAATAC		AGTAC ----- ATAAT ACAT TTCCTCTTATGG T
TGTACGCAACATGATAGCGG		
CGACAAGGGA		

GAM788 TGATCCATACATATTATTGC 774	TAGGATGCGT 3499	--- TATTA TG C CT CCTACCAT
A		
TTGGCATGATCTCACCTACC	CATTTTGAGC	TGATCCATA CA TTGCT G ATGAT CA
TCTTGTA C		
ATTCTTGTACACATGTATAG	GAGG	
GATGCGTCATTTTGAGCGAG		ATTAGGTAT GT AGCGA T TACTG GT AGGATATG
A		
GTATTGAAATATGGATTA		AAA TATGG GT T C- ----- T

GAM789 AGAAGAAGAGGAAGAAGAAG 775 TCAGTGCCTC 3500 A AG- A GAA- AA- - A A CC
 - C A
 CGGAAGAAGAAGCGATGGAC ATTTACGCCG AGAAG AG GA GAA GCGG GAA GA GCG
 TGGA AGGA G CTGC G
 CAGGAGCCTGCAGAAGTAGA TAAA ||||| || ||| ||| ||||| ||||| ||||| |||||
 CTTCTTTTCAGTGCCTCATT TCTTT TC CT CTT TGCC TTT CT CGT ACTT TCCT C
 GATG A
 TACGCCGTAAAATTCGTCAA G GAA G AAAA GCA A C G -- T A A
 GCTGTTTCT

GAM790 TCCCCCTGCAAGAAGTGCCA 776 TCAGCGGTTT 3501 CCCTGCAA C A T G G A
 AGATAACGGTTGAAGGAGTC TCGTGACATT TCC GAAGTG CA GA AAC GTTGAAG AGTC A
 AAGGGATTTTTTCAGCGGTTT TTGG ||| ||||| || || ||||| |||||
 TCGTGACATTTTGGA AGG TTTTAC GT CT TTG CGACTTT TTAG G
 ----- A G T G - G

GAM791 TGCTGCTCAAGGAGAATGTG 777 AAGGAGAATG 3502 TG ----- A - CA
 GATCTTGGGCAACATTCGAC TGGATCTTGG TGC CTCAAGG AGAATGTGG TC TTGGG A
 GACCCGCATTCTGTATTGCC GCAA ||| ||||| ||||| || |||||
 TTGGGTGGCA ACG GGGTTCC TCTTACGCC AG AGCTT /
 GT GTTATG C C AC

GAM792 CCATGACAGTAGATGTGGAA 778 TGTGGAAAAT 3503 A CAGTA T CT ----- GC
 AATTCTGTATCGTCTGCTAA TCTGTATCGT CC TGA GA GTGGAAAATT GTATC GTCT T
 AGACTCGGTGGATATTAGAT CTGC || ||| || ||||| ||||| |||||
 TTTTCACTCTCAGGG GG ACT CT CACTTTT TAG TATAG CAGA /
 G ----- AT GTGGCT AA

GAM793 GAGGAGGGGTTGCATTCGTA 779 TGGTATCTTC 3504 G G A TA TTGA A
 GAAGGTTTGACGTTAGAAAA ACTGAAGTAA GAGGA GG TTGC TTCG GAAGGT CGTT G
 TGGTATCTTCACTGAAGTAA TTGT ||||| || ||||| ||||| |||||
 TTGTCCT CTCCT TT AATG AAGT CTTCTA GTAA A
 G - - CA TG-- A

GAM794 TGGGGGTAACAATAGTAGCA 780 AGCAGTAGTA 3505 AACA A TA AACGAAGATGAT
 A A
 GTAGTATCAATAACGAAGAT TCAATAACGA TGGGGGT ATAGT GCAGTAG TCAAT
 GGTG TG T
 GATGGTGATGATGACGATGC AGAT ||||| ||||| ||||| ||||| ||||| |||||
 CGTTGACGCTACTGCATTAT ACCCCCG TATTA CGTCATC AGTTG CCGT GC G
 GCCCCCA --- - GC ----- A A

GAM795 GGTACATGTGGCCCTTCTCT 781 TGATATGCAT 3506 ----- - GCTT A G AA GA
 A
 GCTTTGCAAGTGGGGACAAA GAAGGAAGAA TTCT CT TGCA GT GGGAC AAATAA
 GACGCTAGA C

AATAAGAGACGCTAGAACGT ACAA |||| || |||| || |||| || |||| ||
TTAGTGTTTTATTTGGTTCT AAGA GG ACGT TA TCTTG TTTATT TTGTGATTT /
GATATGCATGAAGGAAGAAA TTAGGACAGTAACA A AAGT A G G- -- G
CAATGACAGGATTTGGGAAA
ATATGGCC
GAM796 GGTGTATAATTGTACTCTAT 782 TATAATTGTA 3507 TGT- ACT G AGC
GTTGTCTAGCTTTAAGAAAA CTCTATGTTG GG ATAATTGT CTATGTT TCT T
TGTAGTGATAGTTATTTGTC TCTA || |||| || |||| ||
C CC TATTGATA GATGTAA AGA /
 TGTT GT- A ATT

GAM797 GGATGAGGCAAAGTTTGTGC 783 TGAGGCAAAG 3508 - GC TT C----- TA TTT
CTATACCTTTATTTGGCGTG TTTGTGCCTA GGAT GAG AAAG TGTG CTA CC A
GAACCTTTACACCCTTTACT TACC |||| || |||| || |||| ||
CAATTC CTTA CTC TTTC ACAT GGT GG /
 A A- CC TTCCAA GC TTT

GAM798 TCTTAAAAATGCAAAAAAGC 784 TATTGTATTG 3509 AAAAA C- ---- AA- A AT T
AAA
 CCCCAACTGATTTAACGATG GGAAAATCAA CA GCCC CAACT GATTT CGATG CGG
TTTGACTTT ATG A
 ACGGATTTTGACTTTTATGA ACAA || |||| || |||| || |||| || |||| ||
 AAAATACATAAGGTCAGATA GT TGGG GTTGA CTAAA GTTAT GTT AGACTGGAA
TAC /
 TTGTATTGGGAAAATCAAAC A---- CT ACAA AGG - AT - ATA
 AAGTTGTCGGGTATGTTTAG
 TGAGA
GAM799 AAGGTTAACAATTTTCTTGA 785 TGGATAGTAT 3510 TCTT T CAATT TAAATTGG
TTC CAAA
 ACATACCAATTGTACTATTA TTCTAGTTGT TTT GAACA AC GTACTAT CCAAAGAG
ACTTTGT A
 AATTGGCCAAAAGAGTTCAC TCTT || |||| || |||| || |||| || |||| ||
 TTTGTCAAAAGATTATAAAG AAA CTTGT TG TATGATA GGTTTTCTT TGAAATA
/
 TTCTTCTTTTGGATAGTATT TCTT - ATCTT ----- CT- TTAG
 TCTAGTTGTTCTTCTAAAAT
 GGCTGTCCCT
GAM800 TAGTAATCAAACCTCAAGCAA 786 TGTCAAACGT 3511 AATCAA T AAA---- C AAC
AAATATA-- GA
 ATTTGCACATGGAACCTGATA ATAAGCTTGG TAGT AC CAAGC TTTG ACATGG TGAT
CT A
 AATATACTGAAAGAAGACGA TCAA |||| || |||| |||| |||| |||| ||
 CGATAATCAACCATGTCAAA GTCA TG GTTCG AAAC TGTACC ACTA GA A
 CGTATAAGCTTGGTCAAAGA GAAAC- - AATATGC - A-- ATAGCAGCA AG
 CTG

GAM801 CTGACCATCGAGGAGCACGT 787 TAGCATGTGC 3512 ----- TC -- TC ACCTCT
GTTATTCTAGACCTCTCTTC CGTCCTCTTT CTGAC CA GAGGA GCACGTGTTAT TAG C

CAGCTAAGATAGCATGTGCC GTTT |||| || |||| |||| |||| ||||
 GTCCTCTTTGTTTCCCAAGT GACTG GT CTCCT CGGTACGATA ATC /
 CAG AACCTTT TT GC GA GACCTT

GAM802 GAAGTAGCGAACCTCTGCTC 788 GTGAGCAGGA 3513 T - CT G C
 ACTGCCCGGGCCCTCCGGA GTTGCGCTTT GAAG AGCG AAC CTGCTCACT CCCGGG C
 GGTGAGCAGGAGTTGCGCTT TC |||| |||| |||| |||| ||||
 TTC CTTT TCGC TTG GACGAGTGG GGGCCT /
 - G AG A C

GAM803 GAGGAAGTGGGTCCAACCTTT 789 GGAAGTGGGT 3514 - T AC CCTA
 ATCCCTATAGTGATAGAA CCAACTTTAT GAGGAAGTG GG CCA TTTATC T
 ATGGCCGTACTTCCTT CCCT |||| |||| |||| |||| ||||
 TTCCTTCAT CC GGT AGATAG A
 G - AA TGTG

GAM804 AATTTACTCCCTATTTTCGG 790 TCCCTGGTTA 3515 A TTTCGG GT ATAC GTAAATG
 G
 AGTCAATACGGGATAGTAAA CATATGGGGA AATTT CTCCTAT A CA GGGATA TT A
 TGTTGAAAAAATATCCCTG GAAA |||| |||| |||| |||| ||||
 GTTACATATGGGGAGAAATT TTAAAGAGGGGTA T GT CCCTAT AA A
 - TACA-- TG ---- AA----- A

GAM805 GAAATGGTAGGCAATGTGGC 791 GGAGGAATGA 3516 GCA GT GAA-- A GATGA--
 AGA T
 ATGTCTGAAAAAGAGGAGGA TGAAGTATCT ATGTGGCAT CT AAAG GGAGGAAT
 AGTATCTC CTTAT T
 ATGATGAAGTATCTCAGACT CAGA |||| |||| |||| |||| ||||
 TATTTATAAGGGAGATACT TATACTGTA GA TTTC CCTTCTTG TCATAGAG
 GAATA /
 GTGCTGAGTTCTTCCCTTTG G-- TG AGGAG - AGTCGTG G-- T
 AGGAAGGTATGTCATATGAA
 TCCATTTT

GAM806 TGTTGAAATTATTCTCCAGT 792 TCTCCAGTAA 3517 T TT AAATTTCTGGTA - A- C
 A
 AAATTTCTGGTAGCGCCTCT ATTTCTGGTA TG TGAAA ATTCTCCAGT GCGCC TCT
 ATTT TAGC C
 AATTTCTAGCACAGTTGAAG GCGC |||| |||| |||| |||| ||||
 ATGAGGATGGTGCATTGGGG AC ATTTT TGAGGGGTTA CGTGG AGG TAGA
 GTTG /
 AGTTTTTTTACCA C TT ----- T AG A A

GAM807 CGCCTTGACCCTGGCCACCC 793 TAGCGGCGAG 3518 TG CCA CT -- A TTCTCCT ---
 --- C
 TAGCGGCGAGCGCGTTTCTC CGCGTTTCTC CC G CC AGCG GCG GCGCGT GAGACTT
 GAAGCAAG C

CTGAGACTTGAAGCAAGCCT CTGA || | ||| ||| ||||| ||||| |||||
TCTTGTTTCTCTCAATGAGT GG T GG TCGT TGC CGCGCA CTCTGAG
CTTTGTTC T
CTCTGTCTACGCGCACGTAG GT CA- TT GA A TCTGT-- TAACTCT T
TGCTTTGGACTTGGGGACCA
GAAGGCG

GAM808 CGCGTTGGTGTATGAGGTAGA 794 TGAGGTAGAC 3519 GTT G GTA ---- - TG --- GT
- GGC
CGATGTCCCTGGCGCCGGGG GATGTCCCTG CGC GGT ATGAG GACG ATGT CCC
GCGCCG GG C CTG A
TCCTGGGCAGAGGCGGCGGT GCGC ||| ||| |||| ||| ||| ||||| || | |||
CTGTTTGGTGTGTTGGGGAACA GCG CCA TACTC CTGC TACA GGG TGTGGT TC G
GGC G
TGCCCGCGTCGCTCATGACC --- G G-- GCCCG A GT TTG TG C GGA
GCG

GAM809 GCGGTCTGGGCCCGATCAG 795 TGAGGTGCC 3520 ----- G CCTGAAG -- T- -
- AA
GCCCTGCACGTCCCTGAAGG GCCGAGGGTC AGGCCCT GCAC TC GTCAGCT TCTGGT
GAGG ACG TCA G
TCAGCTTCTGGTTGAGGACG TGGC ||||| ||| || ||||| ||||| ||| ||| |||
TCAAAGAGCTGGTCGTAATT TCTGGGA CGTG AG TAGTTGG AGACCG TTTC
TGC GGT A
TTTGCCAGACAGGTTGATGA GCCGCC G ----- AC TT A T CG
GGTGCCCGCCGAGGGTCTGG
CCCGACCCGC

GAM810 ACAGATGTAGATATTACACA 796 TCAATAGTAA 3521 G T CA AATC A GTTT-- G
TTT
AGGTAATCTTAGATAGTT CATCTGTTGT ACAGATGTA ATA TACA AGGT TTAT GATA
ATC TGTT T
TATCGTGTTTTTTATTTAAC ATTA ||||||| ||| ||| ||| ||| ||| ||| |||
GGATTTAATATATCAATAGT TGTTTATAT TAT ATGT TCTA GATA CTAT TAG GCAA
A
AACATCTGTTGTATTATATA A T TG CAAT A ATAATT - TTT
TATTTGT

GAM811 TATATTGATGTATATAATGC 797 TGATGTATAT 3522 T TA- C T TC C TCT
ATGTGTTCTAATTCTATCTT AATGCATGTG TATATTGA GTA TAATG ATG GT TAATT TA T
CATTAAAATTATTGCCATCT TTCT ||||||| ||| ||||| ||| ||| ||| |||
GTAAATTTACTTAATATA ATATAATT CAT ATTGT TAC CG ATTAA AT /
- TTA C - TT A TAC

GAM812 ACGTGGTTTCATTGCTGTTG 798 TCACTGATAA 3523 ----- T C T C A TTCCT
CCAAAAAGTTTATTCCTATC AATCTTCAAC ACGTGGTT TCA TG TGT G CAAA AGTTTA A
AATTAAATTGTTTGACACAT CACG ||||||| ||| ||| | ||| |||||
CACTGATAAAATCTTCAACC TGCACCAA AGT AC ACA C GTTT TTAAAT /
ACGT CTTCTAAAAT C T - A G TAACT

GAM813 TCCTCTGATGTAGTTCCCTT 799 TGATGTAGTT 3524 - CC TTCCATTTTTTT GTA
AAGTT AGC GT
TTTCCATTTTTTTCTCATGG CCCTTTTTCC TG TAG TT CTTT CTCATG TTGTGA
GGCCC TG A
TATTGTGAAAGTTGGCCCAG ATTT ||||| || ||||| ||||| ||
CTGGTAAACAGGGTCTCATA ATATC AA GAGA GAGTAC AATACT CTGGG AC
/
AGTGCATGAGTTTAGAGCAA T AC TTT----- GTG ---- -- AA
ATCTATACAGATGA

GAM814 TTATCAGGATTAGAACATTT 800 TGAGGTGTTT 3525 AGA TTTG ---- TTTAG A- --
AG G
GGGACAGTGAGGTGTTTAGT AGTAAAAATG T ACA GGACAGTG AGGTG TAAAA
TGGTGGG CA CACA A
AAAAATGGTGGGCAAGCACA GTGG | ||| ||||| ||||| ||||| || |||||
GAAGTGTGAATGTCCCCGCT A TGT CCTGTTAT TCTAC GTTTT GTCGCCC GT
GTGT A
GGGTTTTGAAAATCATCTAT GAA CTTA TGTA TAAAA GG CT AA G
GTTATTGTCCATTCTGTAAG
AGTCCAGGTAA

GAM815 GATGTGACATTCGGATAGGT 801 TGTGACATTC 3526 A- ----- AATG G GC
TAATGGTTGGGTCGCGCAGA GGATAGGTTA GATGTG CATTCGGA TAGGTT GTT GGTC
G
CCGATAAAGCCTGCAACGT ATGG ||||| ||||| ||||| ||| |||||
ATTCTGAGTGAGTATATT TTATAT GTGAGTCT GTCCGA TAG CCAG /
GA TATGCAAC AA-- G AC

GAM816 TGTCTGTAGGTGCCGAGATA 802 TCTCCGTTAA 3527 A- --- C C
AGCAGCCTTATCTCCGTTAA ACTCCACAGA TGTCTGT GGT GC GAGATAAG A
ACTCCACAGACA CA ||||| ||| || |||||
ACAGACA TCA TG CTCTATTC G
CC AAT C C

GAM817 TAGCGGATATCATTTGATCG 803 TGGTATGGAA 3528 A ATTT C AA TAAA-- TG - A
GA
GTGAATCTAAATCGTATTGT TCCTGAGGCA TAGCGGAT TC GAT GGTG TC TCGTAT T GA
TTAG T
GAATTAGGATCTACTGGATC CCTA ||||| || ||| ||||| ||||| ||| |||||
TATGGTATGGAATCCTGAGG ATTGTCTA AG TTA CCAC AG GGTATG A CT GGTC
C
CACCTATTTGCGAATCTGTT - CGT- T GG TCCTAA GT T A AT
A

GAM818 TAGCGTATAAAAATATTCAA 804 TCACCGTTTG 3529 - ----- A G T TG ATG
AATGGGGATGAGGATGATAA GGTATTCGTT TAGCG TATAAA AATATTCAAA TGG GA
GAGGA ATA A
TGATAATATTGTCTTCTCAC TTCT ||||| ||||| ||||| ||||| ||||| ||||| |||||
CGTTTGGGTATTCGTTTTCT ATCGC GTATTT TTATGGGTTT GCC CT CTCT TAT
/

ATGTTTATGTCGCTA

T GTATCTTTTGC

- A - GT AAT

GAM819 TGTTTTTTTCTTTTAATGCC 805 TTAATGCCAT 3530 TTTC - - T T --- AAA
ATGCGTAGTCTCCAAAAAAA GCGTAGTCTC TGTTTT TTTTAAT GC CA GCGTAG CT CC A
GGTCAAAGTTATGCTGTGCA CAAA ||||| ||||| || ||||| || ||
ATTA AAAACACAAGATA ATAGAA AAAATTA CG GT CGTATT GA GG /
CAC A T - - AACT AAA

GAM820 ACCATAGCCCCTTGCTGCTT 806 TTAAAGCAAA 3531 T CCTTGC- C
TAATGCTGCCATTAAAGCAA TTCATGGCTT ACCA AGCC TGCTTTAATG T
ATTCATGGCTTTGGT TGGT ||||| ||||| |||||
TGGT TCGG ACGAAATTAC G
T TACTTAA C

GAM821 TATGGGAATATTCTGGTAAA 807 AAAAGTGCAT 3532 GG TC- A- - GTATCAAT TC
AGTGCATGTATCAATTTTAG GTATCAATTT TATG AATAT TGGTAAA GTG CAT TTTAG G
TCGTTTTTGGATTTCTGTAA TAGT ||||| ||||| ||||| |||||
TGTTACGATTTGCTATGTGT GTAC TTATG ATCGTTT CAT GTA AGGTT T
ATTTTCATG TT TGT AG T ATGTCTTT TT

GAM822 TTAAGCAGCCGCGAACTCGT 808 AAGCAGCCGC 3533 A GAACTC GTTA
TAATAGTTACTTTGATGTTA GAACTCGTTA TTAAGC GCCGC GTTAATA C
ACTCAGGTGGTGGCTTGG ATAG ||||| ||||| |||||
GGTTCG TGGTG CAATTGT T
G GACT-- AGTT

GAM823 GAGAAGAGTCTGGACTGTAA 809 TTCGTTTGAC 3534 GA C CT ATTT- - --- T
TTTTTAAATAATAAGATATT TCGCTATTTT GA AGAGT TGGA GTA TTAAAT AATAA GATATT
A
TATTAATATCCAATTATTCG CATG || ||||| ||||| ||||| ||||| |||||
TTTGA CTCTCG ACCT TAT AGTTTG TTATT CTATAA T
CTCTCTTC TC T T- CGCTC C AAC T

GAM824 GGATCTGTCGTTTTTAAAGA 810 TATCATGATT 3535 AAAGATAAAA C - - ATCTTTAA--
A TC
TAAAAGAGAGACGTTTGAAT CTTTTGTTTT T GAGAGA GTTT GAATTA TAAAA
ATGATA TATT T
TATAAAAATCTTTAAATGAT GCTA | ||||| ||||| ||||| ||||| |||||
AATATTTCTACTAATATATC G TTCTCT CGAA CTTAAT GTTTT TACTAT ATAA A
ATGATTCTTTTGTTTGCTA C----- - T C GTTTTCTTAG - TC
ATTCTAAGCTCTCTTCGAAA
GCATTAGCTCC

GAM825 CCACCGCAATAGATCCTGTT 811 TATCGCATTT 3536 C AA TCC TA - A C
AGATACATAGATCCTCGTCG TCTAACGTGA CCA CGC TAGA TGT GATA CAT GAT C

TGATATCGCATTTTCTAACG TGG ||||| |||| | ||||| |||||
 TGATGG GGT GTG ATCT ACG CTAT GTG CTG T
 A CA TTT -- A - C

GAM826 AGATCAGAGGCCATAACCTC 812 TGGGTTCTTG 3537 - CC ACCTC AAAAAAAG CT
 T A T
 ACAGTGGCAAAAAAAGCAGC TATTCTGAGA AGATCA GAGG ATA ACAGTGGC CAG
 GTATAAG GCC ATG A
 TGTATAAGTGCCAATGTATC CTGA ||||| |||| | ||||| || ||||| |||||
 TATGGGTTCTTGTATTCTGA TCTAGT CTCT TAT TGTCAGT GTC TATGTTT TGG
 TAT T
 GACTGAGTCACTGTATCAAT A -- AACTA AGTCAGA- T- T G C
 ATTCTCATGATCT

GAM827 TAGAACTATTTGGGGGTTGA 813 AACACTGTTG 3538 - GGGG- GT GAG C AAAT
 C CTAATGCC
 GTGTGAGACAACAGCTGTTG TGCTATCAGA T TTG TTGA GT ACAACAG TGTTGT
 GGTGTTTG GC A
 TAAATGGTGTGTTGCGCCTAA AAAA | ||| ||| || ||||| ||||| ||||| ||
 TGCCAGTTTTTGATGCCAAA G AAC GACT CG TGTTGTC ACAATA CCATAAAC CG
 G
 TACCTATCATAAACTGTTG G AAAAA AT --- - CTAT - TAGTTTTT
 TGCTATCAGAAAAACAAGGT
 AGTTCCTCTG

GAM828 ATGTAAGTTATAAATTGGTT 814 TAAGTTATAA 3539 ----- TT AA
 CCAAAACATATTGGCCAATA ATTGGTTCCA ATGTAAGTTATAAAT TGG CCAA C
 CTCATGTTTATGGCTTACAT AAAC ||||| ||||| || |||||
 TACATTCGGTATTTG ACC GGTT A
 TACTCATA -- AT

GAM829 GAAGCAATAGATGATTTCTA 815 TAGATGATTT 3540 - T TCTA ACTGAAATAT-- GT--
 TTCTATT
 CGACTGAAATATAGAATAGT CTACGACTGA GAAGCA ATAGA GATT CG AGAATA
 TCATT T
 TCATTTTCTATTTGTAAAAT AATA ||||| ||||| || || ||||| |||||
 AATGATTTATATTCTCTCCT TTTCGT TATTT CTAG GC TCTTAT AGTAA /
 AAAAATACGATCGATCCTTT A C CTA- ATAAAAATCCTC ATTT TAAAATG
 ATATGCTTT

GAM830 TTGCGAAAAGGCATACATAT 816 AAAGGCATAC 3541 - C CA ATC - GACC
 GATCAATATCAGACCTACAA ATATGATCAA TTGCGA AAAGG ATA TATG AATAT CA T
 TGAATGTTTCCATAATATCC TATC ||||| ||||| || || ||||| ||
 CTTTATCGCAA AACGCT TTTCC TAT ATAC TTGTA GT /
 A C A- CT- A AACA

GAM831 CGGTAAGTTGACGTGCGTCG 817 TGACGTGCGT 3542 A - CG GGAA GA A
 GAATCGGAAGCAACAACGTG CGGAATCGGA CGGT AGTTG ACGTG TC TCG AGCAAC A

TGCTCGAACAGAAACATGTG AGCA |||| |||| |||| || |||| ||||
 CAACTCATTG GTTA TCAAC TGTAC AG AGC TCGTTG C
 C G AA ACA- -- T

GAM832 TCCTGAAATCTGAGTGATCT 818 TGAGTGATCT 3543 TG C - - C TTC AA CAC
 GATTTCGACAAATCATCACCA GATTTCGACAA TCC AAAT TGAG TG AT TGA GAC ATCAT C
 CGTATGGTCGTCATTTCAAA ATCA |||| |||| |||| |||| |||| ||||
 TACACCTCACGTTTTGGGA AGG TTTG ACTC AC TA ACT CTG TGGTA A
 GT C C A A TTA C- TGC

GAM833 AGTATTGACCCACGAGTTAT 819 GGAAATGGAT 3544 C--- TAACAAA AAGAC T CT-----
 - T GT
 AACAAAGTCAAAGACCCATT ATGACAACCC A GAGTTA GTCA CCATTT CCTA CCAT
 GAGT A
 TTCCTACTCCATTGAGTGTA TAAT | |||| |||| |||| |||| ||||
 AAATTCATGGTTGACAATTT T CTTAAT CAGT GGTAAA GGAT GGTA CTTA /
 AGGAAATGGATATGACAACC TTTA CCCAA-- ATA-- - TTAACAGTT - AA
 CTAATTCATTTTGGGAAGAT
 GCT

GAM834 GAAACGATACCAGTTTTTAAA 820 TTTCTTAGAT 3545 AA C GT ACA T G
 CAGAATACGGATGCGATGGC GTTATCGACT GA CGATA CA TTAA GAATACGGA GC A
 TTTGTATTTCTTAGATGTTA C || |||| || |||| |||| ||||
 TCGACTC CT GCTAT GT AGATT TTTATGTTT CG T
 CA T -- C-- - G

GAM835 GTGGTTTAGCAGCAACATTG 821 TACCCATCAG 3546 TA GCAA ATTAA GT
 GTGATTAAACCGTACGAGGT TGATATGCAA GTGGTT GCA CATTGGTG ACC A
 ACCCATCAGTGATATGCAAC CTAC |||| || |||| |||| ||||
 TAC CATCAA CGT GTGACTAC TGG C
 -- ATA- CCA-- AG

GAM836 TACATTTAAATCCGTA ACTA 822 TTAGATCTGA 3547 T AA GTAAC -- A GTGA
 GATCAGATCATGAGTGTGAA CGTCTAAGGA TACA TTA TCC TAGA TCAGATC TGAGT A
 TCTAGCTTAGATCTGACGTC AGTA |||| || |||| |||| |||| ||||
 TAAGGAAGTAACTGTG GTGT AAT AGG ATCT AGTCTAG ATTCG /
 C GA A---- GC - ATCT

GAM837 TGTTTTCAGGACAGGAGAGG 823 TAATAAGTAC 3548 T A GGAG AG CCTG T
 CCAGTAGATCCTGTTATTAA GCTGGCTTAA TGTT TC GGACA AGGCCAGT AT TTATTAA T
 ATTATTTAATAAGTACGCTG TGTC |||| || |||| |||| |||| ||||
 GCTTAATGTCCGATAATA ATAA AG CCTGT TTCGGTCG TG AATAATTT /
 T - AA-- CA ---- A

GAM838 TTTGTATCACCTAGACGGTG 824 AGAAGAGCAA 3549 TA CCTAGAC - A CAAGCTCT A
 ATG- A- A

AGTTACGGATCCTAATGAGT ATCCTAATGA CATCT TGTTTAG TTACGGA TGA TTAAGA
 CATC A
 TATTAAGAAATACATCGAAC GTTA |||| |||| |||| ||| |||| ||||
 GGATGAACGAAGGTTGTTTT GTAGA ACAGATC AATGTTT ACT AATTTT GTAG
 /
 AAGTTGATCACATACTTTGT T T CATAC- AGTTG GTTGAAGCAA GC
 AATCTAGACATAGATGTGGA
 AGAACGGT
 GAM845 GATCAAGGCCCTCCGTATAA 831 TTGCATAATA 3556 AG A G C
 TGTAATGTTCCAAAGGTTT CGGAGGGTTC GATCA GCCCTCCGTAT ATGTAAAT TT C
 GCATAATACGGAGGGTTCTG TGAT |||| |||| |||| |||| ||
 ATC CTAGT TGGGAGGCATA TACGTTTG AA /
 CT A G A

GAM846 GATTCACACTACAGGCGGCATG 832 TTCACATTTT 3557 T G A AA T C T AAT
 AAAATGTGAAAACCTCTCCC TAAGTTGTAT GAT CACTACA GCGGC TGAAATGTGA ACCTC
 CC GC AGA A
 GCTAGAAATAGAATCTGCTG GTAG || |||| |||| |||| |||| || || || ||
 GGGGGTTTACATTTTTAAGT CTA GTGATGT TGTG ATTTTACACT TGGGG GG CG TCT
 /
 TGTATGTAGTGTATC T A A -- - T - AAG

GAM847 TCCCCTGTGAAGTTTAATGC 833 TGACAGCATG 3558 GT TTTA TA C TC T
 TGTATCGGAACCCTTCGTTT ACCTTTCTGG TCCCCT GAAG ATGCTG TCGGAACC TTCGT
 GG G
 GGTGACCACGAATGGTTCTG GGGA |||| || |||| |||| |||| || ||
 ACAGCATGACCTTTCTGGGG AGGGGG TTTC TACGAC AGTCTTGG AAGCA CC /
 GA TC CAG- -- T -- A

GAM848 TCTCCTAAAAGAAAGTTGTA 834 AAAGAAAGTT 3559 AA TG CC TAA
 TTCTGCCCGGTAGTCCGTTT GTATTCTGCC TCTCCT AAGAAAGT TATTCTGC
 GGTAGTCCGTTTG G
 GTAAGGTCTTGAACGGACTG CGGT |||| |||| |||| |||| |||| || ||
 CCGCAGAATAGCTTTCTTGA AGGGGA TTCTTTTCG ATAAGACG CCGTCAGGCAAGT G
 GGGGA G- -- -- TCT

GAM849 GAAAGGCATGTGGGTTAATG 835 ATCATACCAC 3560 C G - TA AAA-- TAC- A- TT
 ATTAAATCAGGTACTATGCC AGGTACCTTT GAAAGG AT TG GGT ATGATT TCAGG
 TATGCC TC T
 ATCTTTAGTGAAAGGCATGT T |||| || || || || || || || || || || ||
 TTTCTTGGGCATAAATCATA TTTTCC TG AC CCA TACTAA GGTTT GTACGG AG A
 CCACAGGTACCTTTT A G A -- ATACG TTTT AA TG

GAM850 GGCTTGTTTTCCCATATTAG 836 TAAAATGGGA 3561 -- TT A GAT ATGC GG
 ATTGATATGCTATACGAGGA TCACAGAAGC GGCT TGT TCCCAT TTA TGAT TATACGA A

GATTGTGTATGATTATAAAA C |||| ||| ||||| ||| |||||
 TGGGATCACAGAAGCC CCGA ACA AGGGTA AAT ATTA ATGTGTT /
 AG CT A --- GT-- AG

GAM851 GGTTGTATTAAAGGCTTAAT 837 TAATGCTGTA 3562 GGCTTAATTT T AATACC TGT
 TTCAGCTTTATCAATACCTA TTTAATACAA GGTTGTATTAAA CAGC TTATC TAG A
 GTGTAAATCTAACAGATAAT CT ||||| ||| |||
 GCTGTATTTAATACAAC TCAACATAATTT GTCG AATAG ATC /
 AT----- T ACA--- TAA

GAM852 GGAAGTTCGCGAGATCCTCGG 838 TGAGGTCCGC 3563 A - GGGTCC GTC T AGA C-----
 - G TGAC
 GTCCGATCTCAGTCTCGTCG GTAGAGCGAC TC CTC GATCTCA TCG CG GAGCGC
 CGCTGC CT A
 AGAGAGCGCCCGCTGCGCTT TTGG || ||| ||||| ||| ||| ||||| ||
 GACAATGTAGAGCAGCGCCT AG GAG CTGGAGT AGC GC CTTGTG GCGACG
 GA /
 TGATGTGTTCCAGCGCGATG C C ATGCGC --- - GAC TAGTTCC A TGTA
 AGGTCCGCGTAGAGCGACTT
 GGACAGGTCC

GAM853 CGATGAATACTTTAATGACG 839 TATAATGTCT 3564 A TT-- T CC T ATA-- TT
 TTATACCTCTACATAATGCT TATCTCGTAT CGATG ATAC TAA GACGTTATA TC AC ATGC A
 TATAGCGTGCAACGTTGATA ATAT |||| ||| ||||| ||| |||
 TAATGTCTTATCTCGTATAT GTTAT TATG ATT CTGTAATAT AG TG TGCG /
 ATTG A CTCT - -- T CAACG AT

GAM854 CAGTATCTCGTGATAATTTT 840 CAATACGTTT 3565 TC G ATAATTTT TT A
 TCTCATTTA
 TCATTGACGAATTGCGTCTC GACCAAAGCA CAGTA TC TG TCA GACG ATTGCG T
 ATTTATTTCTATAACTGCAA GGAT |||| ||| ||| ||| |||||
 TACGTTTGACCAAAGCAGGA GTCAT AG AC AGT TTGC TAACGT /
 TCTACTG CT G GAAACC-- -- A CAATATCTT

GAM855 GGAAGCAATGATTTTTTACAT 841 TCGCAGGAAC 3566 ATGATTTTT AGT AAATTTTA
 C- T- TT
 AGTGTTCTGCAAATTTTAA TCGGTGTTGT GGAAGCA ACAT GTTCCTGC ATAC TCT
 CAAG C
 TACCTCTTCAAGTTCACTTT TTCT ||||| ||| ||||| ||| ||| |||
 GTTGGATAGTATCGCAGGAA TCTTTGT TGTG CAAGGACG TATG AGG GTTT
 /
 CTCGGTGTTGTTTCT ----- GCT C----- AT TT CA

GAM856 GGTTTCAGCCGAGGCAATGT 842 CGAGGCAATG 3567 TTC- C- AT TAC CCTGGT -
 TTT
 TTACATAGTCCTGGTGCTTA TTTACATAGT GGT AGC GAGGCA GTT ATAGT GC TTAA C

ATTTCCATTTTAATGCTTGT CCTG ||| ||| ||||| ||| ||||| || |||||
 AACTGTTTGAAGTGTCTCCA CCA TCG CTCTGT CAG TGTCA CG AATT C
 GCTTTTCACC CTTT AC -- TT- TATGTT T TTA

GAM857 CCATTCTTAATAATCGTCAG 843 TTAAACTGT 3568 AATA - - TT GTTAAA T T-
 TCAACA
 TATTTAAACTGTAAATGTT TAAATGTTGG CCATTCTT ATCGT CA GTA TAAACT TGT GG
 ATA T
 GGTATATCAACATCTATCTT TATA ||||| ||||| ||| ||||| ||| || |||
 ATTTCCCGCAGTATAAGGTT GGTAAGGA TAGTA GT CAT GTTTGG ACG CC TAT
 /
 TGTTACATGTATGATGTTCA CTTG T A T- AATATG C TT TCTATC
 GGAATGG

GAM858 GTTTGTACTGCAAAAATAAT 844 TATGGTAAAA 3569 - AAA-- AA - T
 ATCTATTTTGTTCGAAG TTAAATAGTA GTT TGTACTGC AAT TATC TATTTTGT
 ATATGGTAAAATTAATAGT GTAC ||| ||||| ||| ||||| |||||
 AGTACACAAC CAA ACATGATG TTA ATGG ATAGAAGC T
 C ATAAA AA T T

GAM859 TGATTTTGGTTTACATGTAA 845 TATCACATGC 3570 - TTA A TT-TG C
 TACATTTTGAAGTCTTTGAT GCCGGCAGTC TGATT TTGGT CATGT ATACA T AA T
 TTTGTATCACATGCGCCGGC A ||||| ||||| ||||| ||||| | ||
 AGTCA ACTGA GGCCG GTACA TATGT A TT /
 C C-- C TTT GT C

GAM860 TGTACTGCAAAAATAATATC 846 TATGGTAAAA 3571 AAA-- AA - T
 TATTTTGTTCGAAGATA TTAAATAGTA TGTACTGC AAT TATC TATTTTGT
 TGGTAAAATTAATAGTAGT GTAC ||||| ||| ||||| |||||
 ACA ACATGATG TTA ATGG ATAGAAGC T
 ATAAA AA T T

GAM861 CCCC GCGATGATTTTCCGG 847 TGCCCGGCCG 3572 GA-- C CC A AC
 TGATGCCCCGGACAGGCTCC TTATCGAAAA CCCC GCGAT TTTT CGGTGTATG CCGG
 CAGGCTCC C
 ACCTCGGGGTCTGCCCGGCC AACA ||||| ||||| ||||| ||||| |||||
 GTTATCGAAAAACAGAATT GGGGCGTTA AAAAA GCTATTGC GGCC GTCTGGGG /
 GCGGGG AGAC A C- C CT

GAM862 CGCTTCAGTTGTTACATGT 848 TGGCACACGT 3573 G A A TTT A
 ACCATTTTCGACCGCGTGGC GAACGGTGAA CGCTTCA TTGTTTAC TGT CCA CGC C
 ACACGTGAACGGTGAAGTG GTG ||||| ||||| ||| ||| |||
 GTGAAGT GGCAAGTG ACA GGT GCG /
 - C C --- C

TTCACTTTTATTATT

TTAT TATTT TATGAAAG GTCTA TCTT C
- TCACTT T ATT C

GAM869 ACGATAATAACTCCTTCATG 855 AAAGGGATTT 3580 TC C- AA-- TTTCG CT ---
TTATC

TTAAAAGGGATTTCGTTTAC CGTTTACTAC ATAAC CTT ATGTTAA GGGA TTTACTAC GT
TCATAT T
TACCTGTTTCATATTTATCTT CTGT ||||| ||| ||||| || ||||| || |||||
CTTTGTATGATAAACTCGTA TATTG GAA TATAGTT TCTT AAATGATG CA AGTATG
/
GTAAAACTTCTGTAATTGAT CT AT AATG CA--- CT AAT TTTCT
ATTAAAGTCGTTATTACCTT
CGT

GAM870 CTATATAAGAAAATATAGCT 856 TAAGAAAATA 3581 T G C CCAA TT
ACCAAAGATTTATCATCTAT TAGCTACCAA CTATA AA AAAATATAG TA AGAT A
ATCTATGTTTTGTTCTATAG AGAT ||||| ||| ||||| || |||||
GATAT TT TTTTGTATC AT TCTA /
C G T A--- CT

GAM871 GCTAGTTTATAGTCGTGATA 857 TAGTTTATAG 3582 TT A ATA TAT
AACGTATCTATCGTTATCCA TCGTGATAAA GCTAG TATGTCGTG AACG C
CGACGTATCTAGT CGTA ||||| ||| ||||| |||||
TGATC ATG CAGCAC TTGC /
T- - CTA TAT

GAM872 TAGACTTATGTGGTCCGCGA 858 TTATGTGGTC 3583 T GTCC AT TT
TGAAGATTTTATGATCTTCC CGCGATGAAG TAGACTATGTG GCG GAAGAT T
GTACATGTTAGTCTA ATTT ||||| ||||| ||| |||||
ATCTGA TGTAC TGC CTTCTA A
T A--- -- TG

GAM873 TCTTCCTAGGTTCTGAAGGTG 859 AATCACACAA 3584 TC - CGAAG C TATATTAA
ACTTGTTTTATATTAATTAA ACCATAGTTA TCT CTA GGTT GTGA TTGTTT T
CTCCATAAACAATCACACA GA ||| ||| ||||| ||||| |||||
AACCATAGTTAGA AGA GAT CCAA CACT AACAAA T
TT A ACA-- A TACCTCAA

GAM874 AGTATTATATGTTGGTAAAG 860 TATCTGACAC 3585 GTT AAAG A CAAC
GTCAAGATATACAACGTGCA CGTATGGTAC AGTATTATAT GGT GTCA GATATA G
TTATATCTGACACCGTATGG T ||||| ||||| ||| ||||| |||||
TACT TCATGGTATG CCA CAGT CTATAT T
--- ---- - TACG

GAM875 GTTGTAGGTGCAGATGCTGC 861 TGGCCAGACG 3586 A AGA C - -- CA---- - G G
AGA

CGACGAAACGCAGCGGCTCG	CTGTGCATCC	GTTGT GGTGC TG TGC CGACGAA ACG
GCGGC TC GG CAGC G		
GGGCAGCAGAGGTAGCTGGC	CGTC	
CAGACGCTGTGCATCCCGTC		CAGCG CCGCG AC ACG GCTGCTT TGC TGTCG AG
CC GTCG /		
CTTCGTGCGCACCAAGCGC		A A- C C CC CCTACG C A G ATG
CAGCGAC		

GAM876 GTTTGAAGTCCTCGTCCGTC 862	TGGCCTGCGT 3587	- CCT C C CTCCT CA
TCCA GC CC		
TCGATCTCCTGCAGCACTAG	TGATGCGCAC	GTTTG AAGT CGT CGT TCGAT GCAG
CTAGGT GCCCG GG A		
GTTCCAGCCCCGGCGGCCAGA	GTAA	
CCACGGGCAACACCTGGCCT		CAGAC TTCG GCA GCG AGTTG CGTC GGTCCA
CGGGC CC /		
GCGTTGATGCGCACGTAAGC		C AAT C T ----- C- CAA- A- AG
TTCCAGAC		

GAM877 TTCCCATAGCCTGTCTAACT 863	TCACCAGAAT 3588	- GTCT- C CC GTT G
AGCCTTCCCGTGAGAGTTTA	GCTAGTTTGT	TTCC CATAGCCT AACTAGC TTC GTGAGA
TAT A		
TGAACATGTATCTCACCAGA	AGAG	
ATGCTAGTTTGTAGAGGCTA		AGGG GTATCGGA TTGATCG AAG CACTCT GTA A
TGCGGGA	C GATGT T AC AT- C	

GAM878 TATCCGTGTTAACGTCGATC 864	TGAGATCGTA 3589	C T A - ACTA TTG TA-- AATA
T		
ACTAACATTTGTACTAACGA	TGATGCTACA	TATC GTG TA CGT CGATC ACAT TAC ACG
TCTA A		
ATATCTATATCTAGAGAAAC	GATA	
GTATATGTGAATATGTGAGA		ATAG CAT GT GTA GCTAG TGTA GTG TGC AGAT T
TCGTATGATGCTACAGATA		A C A T AG-- TAA TATA AAAG C

GAM879 TAGGAGCATTTTCCAAAGAA 865	GAGCATTTTC 3590	TTCCA AT TA
TTTATATATATTATAATCTT	CAAAGAATTT	TAGGAGCATT AAGA TTATA T
ATTTAATGTTTCTG	ATAT	
	GTCTTTGTAA	TTCT AATAT /
	TTTA- -- TA	

GAM880 GTTGCCTCTGCGTATCGCTA 866	TACAATGTTT 3591	-- A- -- A- -- GTTTC- AC A
ACATA		
GTTTCGAGCTCGGGTTTCCGA	CGATGCAACT	GCGT TCGCT AGTTTCG GC TCGG
CGAAGCA GTA CAC T		
AGCAACGTAACACACATATC	GAAA	
CTATAGTGTACAATGTTTCG		TGTA AGCGA TCGAGC CG AGTC GCTTTGT CAT
GTG C		
ATGCAACTGAAAGCAACGAG		TT GA AA AA AA AACGTA AA - ATATC

CTAAAGCGAAGATGTTTTGC
AGGCGAC

GAM881 TCGAAACCATATCTGCGTGG 867 TGATATGTTC 3592 AAC G CCTTTAATTC C G
GCCTTTAATTCCATATCCGA CCAGTAGGTA TCGA CATATCTGC TGGG CATATC GAG C
GGCGTTCTGATATGTTCCCA TGTC |||| |||||| ||| ||||| |||
GTAGGTATGTCGA AGCT GTATGGATG ACCC GTATAG CTT /
--- - TT----- T G

GAM882 GTTAGTGATCCGTCATGCAT 868 TGAAATGCAT 3593 T T T
TTCATATTCTGTTCCGGCAT GACGGATCAC GTTAGTGATCCGTCATGCATTTCAT CTG T
CTGAAATGCATGACGGATCA TAAT |||||||||||||||| || |||
CTAAT TAATCACTAGGCAGTACGTAAAGT TA GGC /
C C C

GAM883 CTCGCTTCGACATTCCGGGT 869 TGGAGTGGTC 3594 TT A TC TAAAC ATTTG ACA
-- CG
AAAACGCGTATTTGGCCCTA GGGGAGGGCA CTCGC CG CAT CGGG GCGT GCCCT CT
TTATTTCTGA T
CACTTTATTTCTGACGTTTC GGCG |||| |||| ||| |||| || ||||||||
TATGGAGTGGTCGGGGAGGG GAGCG GC GTG GCCT TGCG CGGA GG
GGTGAGGTAT T
CAGGCGTAAGGATTCCGCGT TC - C- TAGGAA GA--- GG- CT CT
GCGCTGCGAG

GAM884 GTTGAAGTAGTTCTTGAC 870 TGAAGTAGTT 3595 G G TC A CGT GGG
GGGCGTACACCGGGATCAGG CTTGTACAGG GTTGAA TA T TTGTAC GGG ACACC A
TGTCTCGTGCAATTGTGGTT GCGT |||| || |||| ||| ||||
CGAC CAGCTT GT G AACGTG CTC TGTGG /
G - TT - --- ACT

GAM885 TTGAAGTCGATATTGTCGCA 871 TCGCAGCCCC 3596 AAG A - CCCT T - A
GCCCCCTGCTCCAGAGCT CCTGCTCCCA TTG TCGAT TTGTCGC AGCC GC CC CAG G
GGAAGTCCGTGCGCTTCTTG GAGC || |||| |||||| |||| || ||||
TAGGCGGGGTTGGGCA ACG TTGGG GCGGATG TCTTC GC TG AGG C
GG- - T GCGT C A T

GAM886 GAGACTTGATAGATATTAGT 872 TCACCACGTG 3597 - - TAG TA- TTGAA
GATGAATTGAAAATTATTT TGTTCAGGA GA GA CTTGA ATAT GTGATGAA A
TATCACCACGTGTGTTTCAG TCAT || |||| ||| |||||
GATCATC CT CT GGA CT TGTG CACTATTT A
A A TTG CAC TTATT

GAM887 GGCTATTCTGGCGGCTAGAA 873 TCTGGCGGCT 3598 C TA TAAT GA TGT
TGGCATAATCCGATGTTGT AGAATGGCAT GG TATTCTGGCGGC GAATGGCA CCG TGT G
GTAGTACAAGTGGCTGCTAT AATC || |||||| ||||| ||| |||

GAM893 TGGCCATAGCTTCGCTATAC 879 TAGCTTCGCT 3604 G -- AT T
CCCACCACAACCACCAC ATACCCACC
CATAGCTTCGCTATACCCACCACAACCACCACCAC ACC GGACAC GGCC T

GATAGGTCTTTGGGATGTAA CGGG ||||| ||||| ||||| ||||| ||
 AGCAGCTGCCCCGGGGTCCC CCCT GGGCCCGTC CGA TGTAGGGTTTC GG /
 G GA AA T ATAGAC

GAM900 GCTGAGGGAGCTCACCCAAC 886 TGAGGGAGCT 3611 ---- A- -- AC A- A C
 ACCGTCGCCACGGAGTCCGG CACCCAACAC GCT GAGGG GC TC CC AC CCGT G
 CGGATCGCGGCCCTCCCAA CGTC ||| |||| || || || ||||
 GC CGA CTCCC CG AG GG TG GGCA C
 AACC GG CT GC CC A C

GAM901 CTTTCAAATTCAATATTTCT 887 TCTGCAGGAT 3612 C A C T A A AC- AACAAATA
 AGCAAGATAACTTTTTCTAT ATTAACTTT CTTT AA TT AATATT CT GCA GATA TTTTCTAT
 C AACAAATACCAACTTCAGAT AAAG |||| || |||| || |||| ||||
 GGAAAAATCGTATCTGCAGG GAAA TT AA TTATAG GA CGT CTAT AAAAAGGTA C
 ATATTAACTTTAAAG T C T - - - GCT GACTTCAA

GAM902 TAAAAAGTGATATAATGCA 888 AAAAGTGATA 3613 GA TAAT--- T T - T G
 TTTTGTGTTGAATTCGCAAG TAATGCATTT TAAAAAGT TA GCA TT TGTTTG AA TC C
 ATTTACAAATATAATTGTTA TTGT ||||| || ||||| ||||| |||||
 ACTCCTGGAAC TTTTCA GT TGT AA ATAAAC TT AG A
 AG CCTCAAT T T A T A

GAM903 ATTAAATCATTAATTTCTTT 889 TATCAAATAA 3614 TC TTTC ATC TG
 ATTTGATAATCGTTTGACTG ATTTTAAAT ATTAAA ATTAA TTTATTTGATA GTT A
 GCATATCAAATAAATTTTTT CCTT ||||| ||||| ||||| ||||| |||||
 AATCCTTTAGT TGATTT TAATT AAATAAACTAT CGG /
 CC TTTT A-- TC

GAM904 TATATTCCCAATGTAATTTA 890 TATTGTGATA 3615 CCC ATT TG TAA ATC
 TCATGATATTGTAAAATTAT TATATTCCCA TATATT AATGTA TATCA ATATTG AATTAT T
 ATCTTCTGATAATTCTTGAT ATGT ||||| ||||| ||||| ||||| |||||
 ATGTGATATATATTCCCAA ATGTAA TTATAT ATAGT TATAGT TTAATA T
 TGTA CCC --- GT TC- GTC

GAM905 ATGTGATCTTGTGGAGTTGT 891 GGCAATGACA 3616 G G- GA C
 TTGCATTAGGCAATGACAGA GAAAGGTAAC ATGT ATCTT TG GTTGTGTTG A
 AAGGTAACAT AT ||||| ||||| ||||| ||||| |||||
 TACA TGGAA AC TAACGGAT /
 A AG AG T

GAM906 CTTTTTGCAATATGAAATTT 892 TATGAAATTT 3617 TT-- T----- A -- TTAA
 TTTGA

TCATTTGTGTCTGCTATGTC	TCATTTGTGT	TTCATTTG	GTCTGCT TGTCAT ATACAGCT
CTG C			
ATATACAGCTTTTAACTGTT	CTGC		
TGACCTTTTCAGGGTTGTGT		AAGTAAAC	TAGATGA ATAGTA TGTGTTGG GAC
/			
GAATGATAAAGTAGATTGTT	ACCT	TATAGTTGT	A AG ---- TTTTC
GATATCAAATGAATCCATGA			
CATATTGTAG			
GAM907 GACGTCTCCAGGCCTGTACT 893	TGGTAAGCAT 3618	C CT-	AATT C AGAATA- ----
- TT			
CTTTTAGAATTCTCATGCAG	ACTGCATAAG	TGTA CTTTTAG	CT ATGCAGTG CAGCTGT
GTTT CAT T			
TGAGAATACAGCTGTGTTTC	CTAA		
ATTTTGGTGCAAATTATGG		ACAT GAAAATC	GA TACGTCAT GTCGACG TAAA
GTG /			
CAGCTGGTAAGCATACTGCA	- AAC	---- A	ACGAATG GTAT C GT
TAAGCTAAAAGCAATACAAT			
AGGAGATTTT			
GAM908 TGATGGGCGTCTCTGTGCAG 894	CAGCAGCTTC 3619	A T -	TT GC TCT CCCAG
TT			
CAGCTTCTCGCACTCTGTCT	TCGCACTCTG	TG TGGGCG CTCTGTG	CAGCAGC CTC AC
GTCTG CTTG T			
GCCCAGCTTGTTTTGCAAGA	TCTG		
TCTAGATGTAGAGTTGCTGC		AC ATTCGC GGGGCAT	GTCGTCG GAG TG TAGAT
GAAC /			
TGATACGGGGTCGCTTACCA	C T A	TT A- ---	CTA-- GT
GAM909 GAATTCCACGGTGTTGTGGT 895	TCCAGAGAAA 3620	CCAC	GTGG - AGA T
CTGACATAGATGCATTAGTG	CACCAAAAAT	GAATT	GGTGTT TCTG ACAT TGCA T
CACATGTCCAGAGAAACACC	TC		
AAAAATTC	CTTAA	CCACAA	AGAC TGTA ACGT A
	AAA-	AG--	C C-- G
GAM910 TATAGACTGGTAGCGGTGGG 896	TGAAAAGGCT 3621	TGGTA T G- T	TCAGA T
GTTGGTGTCTTTTCAGTCAG	TCAAAGTCCT	TATAGAC	GCGG GGG TTGG GTCTTTTCAG
AGGGC T			
AAGGGCTTCGCCCTCTGAAA	CTGC		
AGGCTTCAAAGTCCTCTGCA		ATATTTG	CGTC CCT AACT CGGAAAAGTC TCCCG /
ATGTTTATA	TAA--	T GA T	---- C
GAM911 CTGGATAGGTAACACTGGAA 897	TAGGTAACAC 3622	A---	GAAGAGGACGCAAG A
AGA TA- T			
GAGGACGCAAGACGGCTTAT	TGGAAGAGGA	GG	TAGGTAACACTG ACGGCTT TAG
TGCT CAAA G			
AGAGATGCTTACAAATGAGT	CGCA		
TTGGGTGGCACCTGAAGTC		CC	ATTCGTTGTGAC TGCTGAA GTC ACGG
GTTT A			

GA----- - CC- TGG G

AATCCCATTTGATATATGGA ATAG ||| ||| ||||| ||| || |||| |||
AAGGTGTCCTTCGCACTTCT CAG TTC ACGCTTCCTGT AAA GT GTTTA CCT A
TGAC TTC - GG G ATATA C A

GCCAT /
AGCGAGACTGTTGATTCTC
C

ATCCTTATCGAAGTAGATGG CATC ||||| |||| | | |||||
CTA ATCGGT AGATG GCTA TCC AGTTG /
-- AA T--- T TT

TGCTGAGTTTGTTGTTTCC ATGA ||| ||||| ||||| |||
TAA AAT TTTTGTTGTTT AGTCG TAG T
CC G ---- ATA

TTTGAA G
TAATGGATTATTGATGACTC G TA-- T A TT C GAA
AA

CAATTGTGATATATCCAGAG TGG ||||| ||||| ||||| ||
ATATCTTGTAATGG GGTAATGTT TATAGAGAC CTATATA GTG A
C ---- -- TTA

GAM918 AGAGATAAAACTTTTTTACG 904 TGAGACCATC 3629 -- AC ----- A A AAGA A T
 ACTCCATCAGAAAGAGGTTT GAAGGAGACT AGAGATA AACTTTTTT GA CTCC TC GA
 GTTTT ATA T
 AATATTTTTGTGAGACCATC CCAT ||||| ||||| || ||| || |||||
 GAAGGAGACTCCATCAGAAA TTTTAT TTTGGAGAAA CT GAGG AG CT CCAGA
 TGT T
 GAGGTTTAATATTTTT AA GA ACCTCA A - A--- G T

GAM919 CTTTTTTACGACTCCATCAG 905 TAATATTTTT 3630 A CTCCA G G T A G GACCA -
 AAAGA
 AAAGAGGTTTAATATTTTTG GTGAGACCAT T CGA TCA AAAGA GTT AAT TTTTT TGA TCG
 AAGAGAG G
 TGAGACCATCGAAGAGAGAA CGAA | ||| ||| ||||| ||| ||||| ||| |||||
 AGAGATAAAACTTTTTTACG A GCT AGT TTTTT TAA TTG AGAAA ACT AGC TTTTTTC
 A
 ACTCCATCAGAAAGAGGTTT - ACCAG G A T G G ACCTC A AAAAT
 AATATTTTTGTGAGACCATC
 GAAGAGAG

GAM920 CTTTTTTACGACTACTCCAT 906 TAATATTTTT 3631 CTACTCCA G G T A G GACCA -
 AAAGA
 CAGAAAGAGGTTTAATATTT GTGAGACCAT GA TCA AAAGA GTT AAT TTTTT TGA TCG
 AAGAGAG G
 TTGTGAGACCATCGAAGAGA CGAA || ||| ||||| ||| ||||| ||| |||||
 GAAAGAGATAAAACTTTTT CT AGT TTTTT TAA TTG AGAAA ACT AGC TTTTTTC
 A
 ACGACTCCATCAGAAAGAGG ACCAG--- G A T G G ACCTC A AAAAT
 TTTAATATTTTTGTGAGACC
 ATCGAAGAGAG

GAM921 ACACTCAAAAAGGAAGTTTC 907 TCCACAGTAG 3632 A AA T - TTT TGT CA AG- -
 CCCA AAC
 TCTCGTTTTGTGCGTGTGG GCGATCCAGA GG GT TCT CTCG TTGTCG TGG TG TGCC
 ACTG GATA T
 CATGAGTGCCACTGCCCAGA CCAT || ||||| ||||| ||| || ||||| |||||
 TAACTTTTTGTATCCACAGT CC CA AGA GAGC GACAGT ACC AC GCGG TGAC
 CTAT T
 AGGCGATCCAGACCATTGAC - AA C C CT- T-- AG CTA A AC-- GTT
 AGTCCGAGCAGACACAACCA
 GAAGAGTGT

GAM922 GCTCCCTGAACAAAAACCAT 908 TCCCTGAACA 3633 TCC ACAA T AA
 ACCAAAAGGGTTTGTTCAA AAAACCATAC GC CTGA AACCA ACC A
 AATCAGCACGC CAAA || |||| ||||| |||
 CG GACT TTGGTTGG /
 CAC AAAAC T GA

GAM923 GTGGAATTGCAGACTATTCC 909 TGAAGTAAGA 3634 ----- T CT A-- TT--- TCGT C C
 TTC
 TGGCTGAAGTAAGAGAATTG GAATTGACTT AT CCTGG GAAGT AGAGAA GACT ACT
 AG GCGG T

ACTTCGTA CT CAGCGCGGTT CGTA || |||| |||| |||| |||| |||| ||||
 CTTTTCTG CACTAAGTTTCA TA GGACC CTTTA TCTCTT CTGA TGA TC CGTC
 /
 GTCTCTCTTTCTCTATCATT AAATTCT C -- CTA TCTCT CTT- A A TTT
 TCCCAGGCATTCTTAAACTT
 TTGAGTTTCTC
 GAM924 ATGTGGCACTATCGATGCTG 910 TCATATCGAA 3635 CA--- - CT TT C AC AT TCA
 TCTTCACGCACGCATGTGTC TAGATCCACC ATGTGG CTAT CGATG GTC CA GC GC GTG
 A
 AAACGCCGCCGCCGCCCTGT ACAT ||||| |||| |||| |||| |||| ||||
 CGATCATATCGAATAGATCC TACACC GATA GCTAT TAG GT CG CG CGC A
 ACCACAT ACCTA A AC CT C C- GC CGC

 GAM925 CTGGAGCTGCGTGGGGCCAT 911 GAGCTGCGTG 3636 GT G AG- TG
 AGGGTGAGACCACGATGGCA GGGCCATAGG CTGGAGCTGC GG GCCAT GG A
 CTGAGTAGCTCCAG GTGA ||||| || |||| ||
 GACCTCGATG TC CGGTA CC /
 AG A GCA AG

 GAM926 GACTGTACACCGGCTGCCAG 912 TGTACACCGG 3637 - ----- CG CA G TG A
 TGGATTGCAATGTGATGCAT CTGCCAGTGG GAC TGT ACAC GCTGC GTG AT C A
 CAGCAGCGTGTCTTATACA ATTG |||| |||| |||| |||| ||||
 TGTC CTG ACA TGTG CGACG TAC TA G /
 T TATTCC -- AC G GT T

 GAM927 GGGCACCCGGCGATGATGTG 913 TGTAATGCCA 3638 ACCC ATGAT AGGC C
 TTGCACCAGGCGTCCCCAGA AATGCCAAGT GGGC GGCG GTGTTGCACC GTC C
 CGGTGTAATGCCAAATGCCA CC |||| |||| ||||| ||||
 AGTCC CCTG CCGT CGTAATGTGG CAG C
 AA-- AAAC- ---- A

 GAM928 GTCGGTCAGCGGTAAGTTCA 914 TTGAATGCCG 3639 C A- AGCAG CAC C TCC --
 CC GT
 GCAGGGTGGCCACCGCAGTG CCACCGGGAC AG GGTA GTTC GGTGGC CG AGTGTT
 ATGTGC GTCCA AT T
 TTTCCATGTGCGTCCACCAT CATG || |||| |||| |||| |||| |||| |||| ||||
 GTTCCAATACTGGATAGGCA TC CCGT CAGG CCGCCG GT TCGCGA TACACG
 TAGGT TA C
 CATAGCGCTTGAATGCCGCC - AC GCCA- TAA - --- GA CA AC
 ACCGGGACCATGCCCTGGCC
 GAC
 GAM929 TCCAATCCATCATATGACAC 915 TATGACACGG 3640 A - A ACG AAA TGC
 GGCCGCAAAATGAGCTGCGA CCGCAAAATG TCC AT CCATCAT TGAC GCCGCA TGAGC G
 GCTGCTCGGCTGTGGCGTTG AGCT |||| ||||| |||| |||| ||||
 AGTGGTGGCATGGGA AGG TA GGTGGTG GTTG CGGTGT GCTCG A
 G C A --- CG- TCG

GAM930 GTAAAAGGATTATTGCATTT 916 AAAGGATTAT 3641 A T-- CATT TA-- TC T TTT
 ATTAAGTATTAACATTAT TGCATTTATT GTA AAGGAT ATTG TATTAAGTAT AAACATTA
 TA ATA T
 CTATATATTTTGAATTATTT AAGT ||| ||||| ||| ||||| ||||| |||||
 ACTAATGTTTGAATATATTT CAT TTCCTG TAAC ATAATTTATA TTTGTAAT AT TAT
 G
 AATACAATTTTGTCTTGTA G TTT ---- TAAG C- T TAA
 C

GAM931 TTCAGTCTCCTTAAATTCTT 917 TCACCAGAAT 3642 TCT TT-- TCCACGATAC T TTT
 CCACGATACGGTTGAGACTA TTCAATGGTT TTCAG CC AAATTCT GGT GAGACTA G
 TTTGGCTTTAGTTTCACCAG TCTG |||| | ||||| ||| |||||
 AATTTCAATGGTTTCTGAA AAGTC GG TTAAAGA CCA CTTTGAT G
 TTT TAAC ----- - TTC

GAM932 CTCCTGTAGCCCCCAGTAAA 918 TGTCATTCTC 3643 - - CC C TA ATTT G A
 TGGATTTCAAGGAGGGACCG TTGGACTAAC CTCCT GT AG CC AG AATGG CAG GAGGG C
 TCCTTGCTGTCAATTCTCTTG GAGG |||| | ||| |||| ||| |||||
 GACTAACGAGGAG GAGGA CA TC GG TC TTACT GTC TTCCT C
 G A A- T TC ---- G G

GAM933 GCTGGAGGAGTTCGTCGGGC 919 TGGCTCGAGG 3644 TG -- - T AACTC C ATTC---
 T
 TCAACTCCGCAGCCATATTC GCCTGTCGCA GC GAG GAGTT CG CGGGCTC CG AGCCAT
 ACA C
 ACATCCATGTTTCTCAAATG GCTC || ||| |||| | ||||| || ||||| |||
 GCTCGAGGGCCTGTCGCAGC CG CTC CTCGA GC GTCCGGG GC TCGGTA TGT
 C
 TCGTCTCTGGC GT TG C T A---- - AACTCCT A

GAM934 GGGGAGGTGATCACAGCGCG 920 GGAGGTGATC 3645 AGCGC - - - - - T GG- TTT- A-
 CT T GTC
 TCATGTTCTCCGGCAGCTTT ACAGCGCGTC GTCAT G TTC CC CAGC ACAT GAGGGT
 CCG CAT A
 ACATAGAGGGTCTCCGTCAT ATGT |||| | ||| ||| ||| ||||| ||| |||
 GTCATCAATGTTGGTCACCT CAGTA C AAG GG GTCG TGTG CTTCCA GGT
 GTA /
 TCAGGTGTTTGTGCTGAAAG ---- A TAATG T AAA TGTT GA CT T ACT
 GTGAAGTAATCAATGACAGT
 CACCTTCCCC

GAM935 GATAACATTCCATTTTCAAC 921 TTATAACTAA 3646 TCC CAACT C T C
 CACCATCT
 TGATCTTTTATTTACAATAA AAAATCCTAC GATAACAT ATTTT GAT TTTTA TTA AATAA T
 CACCATCTTCAATATTTTAA TAAA ||||| |||| | |||| | |||||
 TTATAACTAAAAATCCTAC CTGTTGTA TAAAA CTA AAAAT AAT TTATT /

TAAAATATGTTGTC

--- TCATC A C A TTTATAAC

GAM936 TAATAAATCTGACTTAGTTA 922 TTCATATAAT 3647 A CTTA -- AG
AATATGTGGATTTAGTTAAA TTTAATATTT TAATAA TCTGA GTTAAA TATGTGGATTT T
AATTCATATAATTTTAATAT CAGA ||||| ||||| ||||| |||||
TTCAGATTGTTA ATTGTT AGACT TAATTT ATATACTTAAA T
- TTA- TA AA

GAM937 TTCATTTTTTTTAATTTTGG 923 TAACAAATTT 3648 T A TT TA- TAC C TC
GTATACGTACATTTGTTCTA TGTAATTCCT TTCATTT TTTTA TT GGG TACG ATTTGTT TAT T
TTCTACATGTAACAAATTTT TTAG ||||| ||||| || ||| ||||| |||||
GTAATTCCTTTAGATAAAAT AAGTAAA AAAAT GA TCC ATGT TAAACAA GTA /
AAATGAA T A TT TTA TT- T CA

GAM938 ACGCGCCTTTAATGCTGCTC 924 AGCAGCATTT 3649 TTT----- - T
GAATATGTGCCATAGTTCTGA AATTGCTAAT ACGCGCC AATGCTGCTCGAAT ATG G
GCAGCATTTAATTGCTAATT TGGT ||||| ||||| ||||| |||||
GGTGCGT TGC GTGG TTACGACGAGCTTG TAC /
TTAATCGTTAAT A C

GAM939 GAGTTGAGCACCCACCTTGTA 925 TTCCCGGGCA 3650 - ACCACCTT A TGT T ATC
TACCTGTGTGAATATATCTT TACGCTCAAC GAG TTGAGC GTAT CCTG GAA AT T
TCAGTCTTCCCGGGCATAACG CTC ||| ||||| ||||| |||||
CTCAACCTC CTC AACTCG CATA GGGC CTT TG T
C ----- C C-- C ACT

GAM940 TTTGTACCCATCCTCCACCA 926 TACCCATCCT 3651 - TCCACCA AAT
ATGTTTTCTCAATAATAGAG CCACCAATGT TTTGT ACCCATCC ATGTTTTCTC A
AAAACATCATCTGGGTGGGT TTTT ||||| ||||| ||||| |||||
GACAGA AGACA TGGGTGGG TACAAAAGAG /
G TCTAC-- ATA

GAM941 CAGACATGATGACGGTGATA 927 TGACCGGGCT 3652 CAT-- --- G CTTT
CTTTTTATATATGACCGGG CATTTTCTT CAGA GATGA CGGTATA T
CTCATTTTTCTTCTG CTG ||||| ||||| ||||| |||||
GTCT TTA CT GCCA TAT T
TCTTT CGG G ATAT

GAM942 CCATAGCTTACAGGATAGGG 928 TAGCTTACAG 3653 TTA G T GAA CT G
AAGCCTGCGGCGCCGTCAGC GATAGGGAAG CCATAGC CA GA AGG GC GCG C
AATCTTCATGATGTTGTGG CCTG ||||| ||||| ||||| |||||
GGTGTTG GT CT TCT CG TGC G
TA- A - AA- AC C

GAM943 CGGTGGCCAGGGGCGATGCCG 929 TGGCCAGCTG 3654 C- ---- CCGC CG - G C
CG
ATGAGCAGGCCCGCCAGCAC CTGAAGCTTG ATGC GA TGAGCAGGC CAGCA GC GGCCA
CTGCCA AGGTCCA C
GGCGGCCAGCTGCCACAGGT TTCA ||| || ||||| |||| || |||| |||||
CCACGCCCTGGGCCTTGCG TACG CT ACTTGTTCTG GTCGT CG CCGGT GGCGGT
TCCGGGT /
GTGGCCAGCTGCTGAAGCTT TC ACACC AA-- -- A - - CC
GTTCAACACATCCTGCATGC
TGCTGCTGCTG

GAM944 GCCAGAGGTATTTTTTTGTT 930 AGAGGTATTT 3655 A--- TTTT---- A - TG
AGGTCTGATGTTTTCGGAAC TTTTGTTAGG GCC GAGGTA TTGTT GGT CTGA T
CAAATAATTACGTTTTACT TCTG ||| |||| |||| ||||
TTACAAGGC CGG TTTCAT AATAA CCA GGCT /
AACA TTTGCATTT A A TT

GAM945 GTGCTCAGCTAAACTTTGC 931 TCAGCTAAAA 3656 ----- AAA ---- - C ATA
AACAAGCATCTTTATATTCT CTTTGCAACA GTGCTCA GCT ACTTTG CAA CAAG ATCTTT
T
AAAGGGTATTTGATTGGATT AGCA ||||| ||| |||| ||| |||||
CAAAGTACAAGCTTCATTTG CATGAGT CGA TGAAAC GTT GTTT TGGGAA T
AGTAC TTA CTT ACA TTAG A A ATC

GAM946 GAACGATTGGATTTTCAAAG 932 TGGCTCGAGT 3657 - TCAA TTT TC
TTTCCATTTCTACAATGGCT TCGATATGTT GAACG ATTGGATTT AG CCATT T
CGAGTTCGATATGTT C |||| ||||| || ||||
CTTGT TAGCTTGAG TC GGTA /
A C--- --- CA

GAM947 GAGTGGACGCTGACATTCTA 933 TTAGTAGATG 3658 G --- TTCTAGT TC C
GTGATT
GTATGCTTTACCTCTTTAGT GTAAAGCGTT GAGTG AC GCTGACA ATGCTTTACC
TTTAGTGA TTCA G
GACTTCAGTGATTGAGTATG GTTA |||| || ||||| ||||| ||||| ||||
ATGAATTACTAGATGGTAAA TTCAT TG TGATTGT TGCGAAATGG AGATCATT AAGT
A
GCGTTGTTAGTTATGTGTAC G TAT ----- T- - AGTATG
TT

GAM948 GCATCGAGACCAATGGCGAC 934 TATCCCACTT 3659 ----- A CCAA C C CTTA
AGGCTTATGAAACCTATCCC CTCCCGAAAA GCA TCG GA TGG GA AGG T
ACTTCTCCCGAAAAATTGC ATTG ||| ||| ||| ||||
CGT AGC CT ACC CT TCC /
TAAAA C CTTC - A AAAG

GAM949 TCTGCACCTGCTTAAGATTT 935 AACACAGTCA 3660 - C- CTTAA TT C AG
 CTGCGTTCTAGTATAAGAAC TCCCCACAGT TCTG CA CTG GAT CTG GTTCT T
 ACAGTCATCCCCACAGTTTG TTGC |||| || ||| ||| |||||
 CCAGA AGAC GT GAC CTA GAC CAAGA A
 C TT ACCC- CT A AT

GAM950 AGCAATGCCCAATTGACCCA 936 TCACAAAATC 3661 A CCAATTG AG ----- --
 ATG
 AGTCGATAAGTTTGTGATCA TCTTAATCTT AGC ATGC ACCCA TCGATAAG
 TTTGTGAT CAG T
 GATGTGGAAGTGTGATCACA ATCG ||| ||| |||| ||||| ||||| |||
 AAATCTCTTAATCTTATCGG TCG TACG TGGGT GGCTATTC AAACACTA GTC
 G
 TGGGTACCCTAAGCATCGCT C AATCCCA -- TAATTCTCTA CT AAG

GAM951 GGAACAGTGTGATCAAACC 937 TGTCCCATT 3662 - GT CAAACC A ----- A CCT C
 CTTA
 TAGATGCATCGAGCCCTATG AGCCCGGAAA GGA ACA GTTGAT TAG TGCA TCG GC
 ATGG GACAGG T
 GCGACAGGCTTATCAAACCT ATTG ||| ||| |||| ||| ||| ||| |||||
 GTCCCATTTAGCCCGGAAAA CCT TGT CGACTA ATC ACGT GGC CG TACC
 CTGTCC /
 TTGCACCTACCTCATCAGCT A GT CTCC-- C TAAAA C ATT - AAAC
 GTGTATCC

GAM952 GGCACATAATGTAGCACAAAC 938 TTCAACGGGT 3663 CATAA- AC G T
 TGATCAAAA A T
 GCTGTTGAATGTGTACTGAT TAAGCTGTAA GGCA TGTAGC AAC CTGTTGAATG GTAC
 TTGG TGCTA C
 CAAAATTGGATGCTATCGCT CAAA |||| ||||| ||| ||||| ||||| ||||| |||||
 GGCAACCAAGAGAACAATGT CCGT ATGTCG TTG GGCAACTTAC CATG AACC
 ACGGT G
 ACCATTCAACGGGTAAAGCT TAAACA AA - - TAACAAGAG A C
 GTAACAAATTGCC

GAM953 GATAGCTTTGTTGATCTATT 939 TAGCTTTGTT 3664 T C - A AT C T G
 TCCCTATCCGATGGTTAGTG GATCTATTTT GA AG TTT GTTG TCT TTC CTA CC A
 AACAAGACGACTAAACCTCT CCTA || || || |||| ||| ||| ||| ||
 C CT TC AAA CAGC AGA AAG GAT GG /
 C C T - AC T T T

GAM954 GTAATCTGGGTAGACATCTA 940 TAAGATGAGA 3665 AGACA - - T AACT T - T
 AA T
 AGATGAGAATTCTAAACTA ATTCTAAAC GT TCT AAGAT GAGAAT CTAA AC AGAACT AG
 GGTAA GTGAG C
 CTAGAACTAGTGGTAAAAGT TACT || ||| ||||| ||||| ||| ||||| || ||||| |||||

GAGTCTTTTCACAATTGCCCG
CACTT T
TGAGTTCTGTTTTGTTGGCA
TTCTTGATCTTCAGAGCCAC
AGATGC
GAM955 GTAGGAGGAAAATTCTTCAT 941 GGAGGAAAAT 3666 ---- A -- CATT AA
TTCAGAAAGCCTGACACAAG TCTTCATTTG GTAGG AGGA AAT TCTT TCAG A
ATAATTATCCTATAACTTAC AGAA |||| |||| |||| ||||
CATTG TCCT TTA AGAA AGTC /
AATA A AT CAC- CG
GAM956 TCAGAGTGTCCCATACTATC 942 TGGAATGGTT 3667 --- CCCA CCAA- G GA A
CAA AAC
CAAAGAAGCAGATCATGACT CCATCTAATA TCAG AGTGT TACTAT GAA CA TCATG CTA
CA A
ACAACAAACATAAGTGGAAGT GTGA |||| |||| |||| |||| |||| ||||
AGCATGGAATGGTTCCATCT AGTC TCACA GTGATA CTT GT GGTAC GAT GT T
AATAGTGAACACTAAGCTGA GAA A--- ATCTAC G AA - CAG GAA
GAM957 TGTCCAAGAATACATGACAC 943 TCCAAGAATA 3668 -- T CACTACCAA AA
TACCAAAGAAACCCCTTTT CATGACACTA TGT CCAAGAATACA GA AAG A
TTGTATTCTTGGCTACA CCAA ||| |||| |||| ||| |||
ACA GGTTCTTATGT CT TTC C
TC T ----- CC
GAM958 TTGCAGGAAAAATCAAGCTT 944 AAGAAGCTTG 3669 AAA AA G TT --- TT T T
TAACAGGTTTCCAAGATTTT GTGTTTGGCA TTGCAGGA ATCAAGCTTT CA GT CCA AGA TT
GTG A
TGTGTAACACCAACTTCTTA A ||||| ||||| ||| ||| ||| |||
TTGGGGATGTGAAGAAGCTT AACGTTTT TGGTTCGAAG GT TA GGT TCT AA CAC /
GGTGTTTTGCAA G-- AA G GG TAT TC C A
GAM959 ATCAGGCCCTTTAGTTGTCA 945 TATGTTGTAA 3670 C CCCT T CCCTA A
ATATCCCTAATACATCAGTA CTAATATACT AT AGG TTAGTTG CAATAT ATAC T
TATGTTGTAACATACTAATACT TTGT |||| |||| |||| |||
TTGT TG TTC AATCAAT GTTGTA TATG C
T ATAT - ---- A
GAM960 ATCTTAAAATTTCTTTCTCT 946 TTAAAGGCTT 3671 TTTCT TCTGTTCCAT CGT-- A
ACATAT CA TCT
GTTCCATTTGTCGTACGTAT GTTTCATAC TTC TTGTCGTA ATAAG TC GT
GGATAA T
AAGATCACATATGTCAGGAT GATA ||| ||||| |||| || |||||
AATCTTTATTTGTCTCTATT AAG AATAGCAT TGTC GG TA TCTGTT /
AAAGGCTTGTTTCTATACGA CT--- TTTTGTGTT ATCTT - AAAT-- TC TAT

TAATTTGTTTTTGAATCTT
TTGAGTAT

GAM961 TTTGATAAATTAATATATGT 947 TAAATTAATA 3672 -- A- CG ATCC TG A TTAT C T GT
GCGCTTAATCCTCTGGAAC TATGTGCGCT GATAAAT TAATAT TGTG CTTA TC G AC CT
ATGAA ATCG T
TATCTCATGAATATCGGTTT TAAT ||||| ||||| ||| ||| || | || || ||||| ||||
TTGATTTCATTAGTATTGTA CTATTTA ATTATA ATAT GAAT AG T TG GA TACTT
TAGT /
TTTGAAAAATAAGTATATAA TT AA AT AAAA TT A TTAT T - TT
AATATTATTATTTATCAAA

GAM962 CCCATGTGGCTTTGAGCAAA 948 TCACGGGTCG 3673 T - AAA AA CATGTT GTT
AGCTG C - TT
GAAACCGCATGTTTCGATGTT CTCGCTAGCC GCT TGA GC GA CCG CGAT AGAT ATTG
AGTG CTTG G
AGATAGCTGATTGCAGTGCT GTCT || ||| || || ||| ||| ||| ||||| ||||
TGTTGTTCAAGCCGCTCAAT CGA GCT CG CT GGC GCTG TTTA TAAC TCGC
GAAC /
ACATTTTtagtCGTTATCAC T T --- G- ACTATT ATT CA--- - C TT
GGGTCGCTTCGTAGCCGTCT
GGG

GAM963 GCGTGTGTGTAAACACCTTC 949 TCAGTCTATT 3674 --- ACACCTTC ATCTGG T C
--- AAA
AAGGCGCATCTGGAGATTTA AGCGCTTTCA GTGT GTGTAA AAGGCGC AGATT ATC
CATC TGGG C
TCCCATCTGGGAAACGCAGC TTAC ||| |||| ||||| ||||| ||| ||| |||
CCAATTGATGTGGTCAGTCT CACA CACATT TTTCGCG TCTGA TGG GTAG
ACCC G
ATTAGCGCTTTCATTACACA AGA AC----- ATTA-- C T TTA GAC
GAACACGC

GAM964 TACAAGCTGTAGCAATAGTG 950 AAGGATCTAT 3675 A -- A TA AA- - ATA AT TT
CTC
AAGGATCTATACTGCAATTA ACTGCAATTA TACA GCT GT GCAA GTG GGAT CT CTGCA TA
CCC C
TTCCCCTCCAGTGGGTTTAT TTCC ||| ||| || ||| ||| ||| ||| ||| ||| |||
ATGTAGAGAATCTGCCCAT T ATGT CGA CA CGTT TAC TCTA GA GATGT AT GGG /
TGCAACAAAGCCTGTA C AA A -- CCG A --- AT TT TGA

GAM965 TCGTTAGAAACGTTGATAAA 951 AAGGATATTG 3676 AAC AAC A - A--- TG- AA
AT
CTTTGAAAGGATATTGTGGG TGGGTTTAAT TCGTTAGA GTTGATA TTTGA AG GAT TTG G
GTTT TGT T
TTTAATGTATTTGCGCACGA GTAT ||||| ||||| ||||| ||| ||| ||| ||| ||| |||
ACACTGCAACAACATCACTG GGTAATCT CAACTGT GAGCT TC CTA AAC C CAAG
ACG T
TCGAGAATGTCAACCTCTAA C-- AA- G A CAAC GT A C- CG
TGG

AGTGTTCATTATATAAACA AGTTTAAAGT TTGTGG AAAACA TAAGTGTTT T
 CTTGTTAATGTTTTACCATA GTTT ||||| ||||| |||||
 A AATACC TTTTGT GTTCACAAA A
 A AATT- TAT

GAM973 GCTCTCGAACGATGGGACTG 959 TATCTCATCG 3684 ----- A C TA T C
 TTTAGCTCTACCAGTAGTGC TGC GCAACAC GCTCT CG ACGATGGGA TGTT GC CTA C
 CAATATCTCATCGTGCGCAA CGGG |||| || ||||| |||| ||||
 CACCGGGGC CGGG GC TGCTACTCT ATAA CG GAT A
 CCACAAC G - C- T G

GAM974 ACCACGTCTAGTCGTATCAG 960 TGGCTTGTA 3685 C-- GTCG C ATT GATTAA T
 CATTTAT
 CCATAATTTTAAGATTTAAT TAGATCCTTG GTCTA TAT AGCCATA TTAA TTTATT
 AATACAT T
 TTATTTAATACATCATTTAT GT |||| || ||||| |||| ||||| |||||
 TCCTGCTAATGTATTTAATA TAGAT ATG TCGGTAT AATT AAATAA TTATGTA /
 AAAAATTAATATGGCTTGTA TCC A--- T --- AAA--- T ATCGTCC
 ATAGATCCTTGGT

GAM975 ATGTTTTTTATCTCTTTCAG 961 TTCATCATCG 3686 T -- TCAGT-- - TA T
 TATGTGAATAGATAGGTATT AATTTAAGAG ATGTTT TT ATCTCTT ATG TGAATAGA GGTA T
 TTATCTCTATTCATCATCGA ATCC ||||| || ||||| || ||||| |||||
 ATTTAAGAGATCCGATAAAC TACAAA AG TAGAGAA TAC ACTTATCT CTAT /
 AT T CC TTTAAGC T -- T

GAM976 CTTCAATTATGAATTGATTCT 962 TGTAATGTCT 3687 T T --- G TAT-- C-- CA TT
 TAG TT
 TGAGGTATAAACCTAACACA TTCATGTTAT A GAAT GATTCT T AGG AAAC TAACA AA
 ATATTAT AC T
 AATTATATTATTAGACTTTT AAGT | |||| ||||| | |||| |||| || ||||| ||
 CGTATGTAATGTCTTTCATG T TTTA CTAAGA G TCC TTTG ATTGT TT TGTAATG
 TG /
 TTATAAGTTTTTAATCCTGG - T TAA G TAATT AAT AC TC TA- CT
 AATAGAATCTATTTTAATGA
 GG

GAM977 GCCATAGTCATAGCATCCGG 963 TCGTCGGAGC 3688 C A C- A T- - G A TCA
 CTTATCCGCCTCAGTTGTCA TGTACACCAT GC AT GT ATAGC TCCGGC TAT CC CCTC GTTG
 T
 TAAACCAACGAGGAGGAATA AGC || || || |||| ||||| || || ||||| |||||
 TCGTCGGAGCTGTACACCAT CG TA CA TGTCG AGGCTG ATA GG GGAG CAAC A
 AGC A C CA - CT A A - CAA

GAM978 GTTAATACGTCTTGCACGTA 964 TATAATTATT 3689 - C- CTAT CC
 ATCTATTATAGATGCCAAGA TTGTAAGATG GTTAATA CGTCTTGCA GTAAT TATAGATG A
 TATCTATATAATTATTTTGT ATGT ||||| ||||| ||||| |||||

AAGATGATGTTAAC

CAATTGT GTAGAATGT TATTA ATATCTAT A
A TT AT-- AG

GAM979 TTGGTAACTCATTCTATATA 965 TAGGATATAC 3690 A TC ----- G T GTT
TGCTTTTCCTTGTTGATGAAG TCAATAGAAT TTGGTA C ATTCTA TATAT CT TCCTT G
GATAGGATATACTCAATAGA TTGT ||||| I ||||| ||||| II |||||
ATTTGTACCAA AACCAT G TAAGAT ATATA GA AGGAA /
- TT AACTC G T GTA

GAM980 CTTCAATTATGAATTAATTCT 966 TGTAATGTCT 3691 T ATTA --- G TAT-- C-- CA TTT
TAG TT
TGAGGTATAAACCTAACACA TTCATGTTAT A GA ATTCT T AGG AAAC TAACA AA
TATTAT AC T
AATTTTATTATTAGACTTTT AAGT | || ||||| I ||| ||||| || ||||| ||
CGTATGTAATGTCTTTTCATG T CT TAAGA GTCC TTTG ATTGT TT GTAATG TG /
TTATAAGTTTTCATCCTGG T ATC- TAAG TAATT AAT AC TCT TA- CT
AATAGAATCTATCTTAATGA
GG

GAM981 GAACTAGATATATTAATAAA 967 TATATTAATA 3692 A- ATAAAGTACTC A TT
GTACTCATTAGGCAGTTTAT AAGTACTCAT GAACT GATATATTA ATTAGGC GT A
GGCAGCTTGATAATTAGATA TAGG ||||| ||||| ||||| ||
TAGTATATTCCAGTTC CTTGA TTATATGAT TAGTTCG CG /
CC ATAGATTAA-- A GT

GAM982 GACATTCTATTTTTTGTGGA 968 GTGGATTAGT 3693 ---- GTATACTCTC ----- A
TT TA
TTAGTATACTCTCTTCCCTC ATACTCTCTT TTTTGTGGATTA TTCCCTCTA TC TG
CAC C
TATCATGTTCCTACTACTGGTG CCCT ||||| ||||| || ||| ||
TCCACGATGACAAATATCTA AGGATACCTGAT AAGGGAGAT AG AC GTG /
GAGGGAATATAATATAGTCC CCGT ATAATAT--- CTATAAACAGT C CT GT
ATAGGATGCCAATCTAGCAA
TGTC

GAM983 GATACGAATATGTCTTTGTT 969 TTAAACATAT 3694 T GTCTT AACA TTT AAT
AAAAACAGTTATTTTCTGAA GATATTCGTT GA ACGAATAT TGTTAAA GTTAT CTG A
TATTTCTAGTTTGTAATTT C || ||||| ||||| ||||| ||
AACATATGATATTCGTT CT TGCTTATA ACAATTT TAATG GAT T
- GTAT- ---- TTT CTT

GAM984 TGTGATAATTTATGTGTGAG 970 TCCACGTTTT 3695 T- TG--- A A
GCAAAATTTGTCCACGTTTT TTAATTTTGT TGTGATAA TTA TGTG GGCA A
TAATTTTGTGTTATA TATA ||||| || ||||| ||
ATATTGTT AAT GCAC CTGT T
TT TTTT - T

GAM985 TTGTACTTTTTGTTGGATCG 971 TACCCGCAAC 3696 ACTTTTTGT- A-- ATTAT - C
 ACGGATTATTAATAGTGACA GATTCATCCC TTGT TGGATCG CGG TAATA GTGA A
 TTTACGTATTGTACCCGCAA CTCT ||| ||||| || ||||| ||||
 CGATTCATCCCCTCTGAACA AACA ACTTAGC GCC GTTAT CATT /
 A AGTCTCCCCT AAC CAT-- G T

GAM986 AGTTTGGTATATCAGCCATT 972 TATCAGCCAT 3697 TGG -- G ACT-- AG
 TTGCTCAAGAATTGTATACT TTTGCTCAAG AGTT TATATCAGCCATTTT GCTCAAGAATT TAT
 CA G
 CAAGGTATGTTACGTGGAA AATT ||| ||||| ||||| ||||| ||| ||
 TTCTTGGGTTAAAGATGGCT TCGA GTATGGTCGGTAGAA TGGGTTCTTAA GTG GT /
 GGTATGATAGCT TA- AT G CACTT AT

GAM987 CAGCTGAGTTACAACCTCCGA 973 TGAGTTACAA 3698 CTGA AA GA CT-- ACCC
 CGACTTGGTTGACCCTCCAA CTCCGACGAC CAG GTTAC CTCC CGA TGGTTG T
 CAACCATTCAATTGAAGGGGC TTGG ||| ||||| ||||| ||||| |||||
 GTAACCTG GTC CAATG GGGG GTT ACCAAC /
 --- C- AA ACTT AACC

GAM988 CTCAACCCGGGCCGTAGCAG 974 AACCCGGGCC 3699 - G - GCAG- -- A
 CCGCAAGTTTGTAGGATCA GTAGCAGCCG CTCAAC CCGG C CGTA CC GCA G
 ATACGCGTCGGTGTTGAG CAAG ||||| ||||| ||||| ||||| |||||
 GAGTTG GGCT G GCAT GG TGT T
 T - C AACTA AT T

GAM989 GCAACAACGCCCCAGAATGT 975 TGTCACAGAA 3700 A A -- AGAA- CT A TC
 GCTTAAATTCTCCACGAATA TCGGGTTGCG GCA CA CGC CCC TGTG TA ATTC C
 TGTCACAGAATCGGGTTGCG CTGT ||| ||||| ||||| ||||| |||||
 CTGTGC CGT GT GCG GGG ACAC GT TAAG /
 - C TT CTAAG T- A CA

GAM990 TCCGAATGGTGCGTCCTTAT 976 TATAACAAC 3701 GAA C- CC T--- AT
 ACATATACATTATGTATTAC CCACCACAAG TCC TGGTG GT TTATACA ATAC T
 TTGTATAACAACCTCCACCAC GA ||| ||||| ||||| ||||| |||||
 AAGGA AGG ACCAC CA AATATGT TATG /
 AAC CT AC TCAT TA

GAM991 CATCCTGTCCAAGAATTGTA 977 TCCAAGAATT 3702 G-- G ACTCAG TA
 TACTCAGGGTATGTTACGT GTATACTCAG CATCCT TCCAAGAATT TAT GG T
 GGAATTCTTGGGTTGAGGAT GGTA ||||| ||||| ||||| ||||| |||||
 G GTAGGA GGGTTCTTAA GTG CT /
 GTT G CA--- TG

GAM997 ACATTTTCCATTTATAACAC 983 TATGTTAATA 3708 TT- -- - CT A GATCATTT
TTTT T
TTATGTATTAACTTTGATCA ATTATGGTGT ATT CCAT TTAT AACA TATGTATT ACTTT
ATATT CAT A
TTTATATTTTTTCATTATTA GGTG III IIII IIII IIII IIII IIII IIII IIII
TGTTGATATTAACAAAAGTG TGG GGTA AATA TTGT ATATATAA TGAAA TATAG
GTA T
AATATATATGTTAATAATTA TGT TT A -- G ACAAT--- TT-- T
TGGTGTGGTGT

GAM998 ATCTAATGATGACGTAACCA 984 TGACGTAACC 3709 - T C AACC A T CAGC
AGAAGTGTATCTACAGCCAA AAGAAGTGTA ATCTAA TGA GA GT AAG AGTGTA CTA C
TTTAGCTGCATTATTTTAG TCTA ||||| ||| || ||| ||||| |||
CATCTCGTTTAGAT TAGATT GCT CT CG TTT TTACGT GAT /
T - A ATT- A C TTAA

GAM999 CTTCAATTATGAATTAATTCT 985 TGTAATGTCT 3710 T ATTA --- G TAT-- C-- CA TT
TAG TT
TGAGGTATAAACCTAACACA TTCATGTTAT A GA ATTCT T AGG AAAC TAACA AA
ATATTAT AC T
AATTATATTATTAGACTTTT AAGT || ||||| ||| ||| ||||| || ||||| ||
CGTATGTAATGTCTTTTCATG T CT TAAGA G TCC TTTG ATTGT TT TGTAATG TG
/
TTATAAGTTTTTAATCCTGG T ATC- TAA G TAATT AAT AC TC TA- CT
AATAGAATCTATCTTAATGA
GG

GAM1000 GGAAGAGATGTAACGGGAAC 986 AGAGATGTAA 3711 -- ACG CTG TG
TGGGTTTGTGATTACACAAA CGGGAAGTGG GGAAGAG ATGTA GGAA GGTTTGT A
CTATTCTAATACATAGTTCT GTTT ||||| |||| ||| |||||
TCT TCTTCTT TACAT TCTT TCAAACA T
GA AA- A-- CT

GAM1001 TTTTGTGGATTAGTGTACTC 987 GTGGATTAGT 3712 GTGTACTCTC ----- A TT
TA
TCTTCCCTCTATCATGTTCA GTACTCTCTT TTTTGTGGATTA TTCCCTCTA TC TG
CAC C
CTACTGGTGTCCACGATGAC CCCT ||||| ||||| || |||
AAATATCTAGAGGGAATATA AGGATACCTGAT AAGGGAGAT AG AC GTG /
ATATAGTCCATAGGA ATAATAT--- CTATAAACAGT C CT GT

GAM1002 ACCTCAGTCGGTGTCCGACG 988 TGCCGAGCGT 3713 CA-- - ---- - TC G AGCAT-
CAC
CCGGCAGTTCCCGGGGTAGC GAGTACGAGA CCT GTCGGTGTC CG ACGC CGGCAGT
CCG GGT ACGC A
ATACGCCACAGTTGCGTTTCG TACC || ||||| || ||| ||||| ||| |||
GGGACCGTGCGCGCTGCCGA GGA CAGCCATAG GC TGCG GCCGTCTG GGT CCA
TGCG /
GCGTGAGTACGAGATACCGA ACCG A ATGAG A CC G GGGGCT TTG
CGCCAAGGT

GAM1003 CGAGTATAGTTCGTTGAATC 989 TTTGGGATGA 3714 G TG CA T G AAT-- GG- G- TT
GTA AG A
AAGGCTTTGGGATGAAATCT AATCTAGGTC T AAT AGGC TTG GATGA CTA TCC GG
GCCA GT GGG T
AGGTCCGGGTTGCCAGTAGT CGGG | ||| ||||| |||| ||| ||| ||| |||
AGGGGATGTCTTCGCGTGGT A TTG TTTG AGC TTGCT GAT AGG CC TGGT CG
TCT /

CCGAGGAGTATAGTGTTC
 GTTGCGATGTTTGAGTTGA
 AGCATGCTCG
 GAM1004 GAAGATTATGGCCAACCCAA 990 TATGGCCAAC 3715 T C ACC A C -- C
 TTCCATACTCCGTCGAGTC CCAATTCCCA GAAGA TATGG CA CA TT CCAT ACTC G
 CGTGGTAGATGTAATGTCCG TACT |||| |||| || || |||| ||||
 TATTCTTC CTTCT ATGCC GT GT GA GGTG TGAG T
 T T AAT A T CC C
 GAM1005 GCGTCCAGCAGCACGAAAT 991 CAGCAGCACG 3716 T -- C GC TAT
 GCGGCGCGCGGTATAGATCC AAATGCGGCG GGCG CCAGCAGC ACGAAATG GGC GCGG A
 GCCGGCCCGTTTCGTCCGCT CGCG |||| |||| |||| |||| ||||
 GCTGGCGCT TCGC GGTCGTG TGCTTTGC CCG CGCC /
 - CC - GC TAG
 GAM1006 GGGTGAGGCCGGGGCGGAAG 992 TGAGGCCGGG 3717 T C ---- C - T T CG
 GCGGGTCGTCTCGTTCTAAGC GCGGAAGGCG GGG GAGGC GGGGCGG AAGG G GG CG
 CGTT T
 ACGTCGTCTCCCTTCTTC GGTC |||| |||| |||| |||| ||||
 ACCGCCTCGTCTCCCC CCC CTCTG CTCCGCC TTCC C CC GC GCAG A
 - - ACTTC C T T T CA
 GAM1007 TGTGGAGGTGTGTTGTAATG 993 GAAAGTATAG 3718 TTGTA TG T- A T A A
 CCCCCTCCTCC--- T- C
 GTGTTGAGATTGTGAAAGTA CCCCCTCCT TG A GTG TG GAT GTGAA GTAT GC
 GCG CCC C
 TAGCCCCCTCCTCCGCGTC CCGC || | || |||| |||| |||| ||||
 CCCCCGGGGCCCGTCCTTTC AC T TAC GC CTG TACTT CGTG CG TGC GGG
 C
 TCCTCCTTGCAAGTGCGTTCA TTGCC GT TT - T G A TTCCTCCTCTTTCC CC G
 TTGTCCGTTTATTGTCCGTT
 CATTCTCCGCA
 GAM1008 TGTTGACGAGCATACCGTAT 994 TGACGTAGAC 3719 ACG A TC - GA TGTA T
 AGT TAAAC
 CTCCCTGACGTAGACGGTGT GGTGTATGTT G AGCATACCGT TC CC TGACGTA CGG TGT
 GCAACG CC A
 ATGTTGCAACGAGTCCTAAA GCAA | |||| || || |||| || || |||| ||
 CAGTAATGGTGTGTTGTACG C TTGTGTGGTA AG GG GTTGTAT GTT GCA TGTTGT
 GG /
 GTTTTGGTATGTTGCGGCTG AAG - TC C G- TTG- - GT- TAATG
 AATGGTGTGTTGAACGGCG
 GAM1009 CACGAGGTTTTGTTTGGCCT 995 TCAGGTGCCC 3720 T TG TA CC AG - GATATAA
 GG TCT
 ACCCCGCAGGTCAGGTGCCC ACTGATATAA TTG T GCC CC GC GTC AGGTGCCCCACT
 CGCGTT TAAAT C
 ACTGATATAACGCGTTGGTA CGCG ||| | || || || |||| |||| |||| ||||

AATTCTCTGTTATTTAGACG AAC G TGG GG CG CGG TCTACGGGTGG GTGCAG
ATTTA T
TGAGGGTGGGCATCTAGGCT -GT CC CA CT A GA----- -- TTG
CGCACGGCCGGTTGGCAAGT
TCCTGAAGCGG
GAM1010 GTTTCGTCTCTGGCCAGCAT 996 TGGCGCGGAT 3721 T- --- - T A T
TCCGCGCATATTTAAATGG GTCTGCGTGC GTTTCG CTCTGGC CAG CAT CCGCGC TATT A
CGCGGATGTCTGCGTGCCAG CAGG ||||| ||||| ||| ||||| ||||
GGTTCGAAAT TAAAGC GGGACCG GTC GTA GGC GCG GTAA /
TT TGC T - - A

GAM1011 TGTCAAAGTGGTAGTGCCCTG 997 CAAAGTGGTA 3722 A - T C -- - CGC- TTAAACA
TTGCACGCGTCTTTAAACAT GTGCCCTGTTG TGTCA AGT GG AGTGC TGT TG CA GTCT T
CAAAAATGGGCTTCCTGTCA CACG ||||| ||| ||||| ||| ||| ||||
TTACAGCACTTCTAACTATG ATAGT TCA TC TCACG ACA AC GT CGGG /
ATA A A T - TT T CCTT TAAAAAC

GAM1012 GTAAATAAGCACGCTTTAAA 998 TGTAAGGGT 3723 -- -- G AA- A AA
TCAAACAACAACAGGTTGTA ATGTTTTTAT GTAAATAA GC AC CTTTA TCA ACAAC C
TGGCTGTAAAGGGTATGTTT TTAC ||||| || ||||| ||| |||||
TTATTTAC CATTTATT TG TG GAAAT GGT TGTTG /
TT TA G GTC A GA

GAM1013 GTGTAAGCTTCAGCGATGGG 999 TGAAATCTGG 3724 -- TAAAGCTTGAAA C G C
A-- - C
TTAAAGCTTGAAAGCATCCA ATGCCGCCCA GCGA TGGGT GCATCCA GA TTTTG TCTG
GT TGATGGC G
CGAGTTTTGCTCTGAGTTGA TGTT ||||| ||||| ||||| ||| ||||| ||| |||||
TGGCCGCCGTTATCACACCC CGTT ACCCG CGTAGGT CT AAAGT AGAC CA
ACTATTG C
GCAGATGAAATCTGGATGCC GT C----- - - - GCC C C
GCCCATGTTGCTGATCGTTA
TAC
GAM1014 GAGATTATATCTTACACCTC 1000 TGAGAGAGAT 3725 T---- CACCTC G A
AGTCTCGTCTTAGAAAGTTT TACATCTTAA GAGAT ATATCTTA AGTCTC TCTTAGAA G
CTGAGAGAGATTACATCTTA GATG ||||| ||||| ||||| |||||
AGATGTCTTACATCTC CTCTA TGTAAGT TTAGAG AGAGTCTT /
CATTC TCTACA - T

GAM1015 TGA CTCCTGAATTACCATT 1001 TTCGTAGAGG 3726 C- AATTA A C- A
TATCACAATAGCATTGTTG CCAAGTAAGT TGACT CTTG CC TTTAT ACAAT G
TAGAGGCCAAGTAAGTCA CA ||||| ||||| ||| ||||| |||||
ACTGA GAAC GG AGATG TGTTA /
AT C---- - CT C

- A AGC A G

GAM1023 GAGGCCTCGCTGACGAAGT 1009 TCTTATACTC 3734 C GAC AC - AA
TAAGATACAACCTGTGATCT ATGGTAGGCC GAGGCCT GCT GA TGTAAGAT AC C
TATACTCATGGTAGGCCTT TT ||||| || ||||| ||
TTCCGGA TGG CT ATATTCTA TG /
- TA- C- G TC

GAM1024 TGCCGGCAGAGTACCAAAAG 1010 TGAGAGAGGC 3735 AGAG CAAAA- CA AATA TG
AATCCA TTGT
TCCACCTCAATATCTTGTAAG GACCTGTAAG TGCCGGC TAC GTC CCTC TCT TA
GCTCG A
ATCCAGCTCGTTGTAATACC TAGT ||||| ||| ||| ||| ||| || |||
GAGCGATATGAGAGAGGCGA ACGGTCG ATG CAG GGAG AGA AT CGAGC /
CCTGTAAGTAGTAGCTGGCA ATG- AATGTC C- ---- GT AG---- CATA

GAM1025 TGCTCAGTTATCTTTTGTGG 1011 ACCACATATG 3736 TCA CTTT-- TGCC
TTATGCCAGATACTAACCAC CAATAACGCG TGC GTTAT TGTGGTTA A
ATATGCAATAACGCGCA CA ||| |||| |||||
ACG CAATA ACACCAAT G
CG- ACGTAT CATA

GAM1026 TTGCTGAGACATCCCAGAAG 1012 TGAGACATCC 3737 A--- AGAAG C
GGACACTTGTGTCCGGGGAT CAGAAGGGAC TTGCTG GACATCCC GGACA T
GTTGCAATAGCAA ACTT ||||| ||||| ||||
AACGAT TTGTAGGG CCTGT T
AACG G---- G

GAM1027 CGCGCGAGAACTGTGTTTCG 1013 GCACGGGTAC 3738 AGAAA TT - T
TGCAGCGTATTCGTTAGCAC GGACGCCGCG CGCGCG CTGTG CGTGC AGCG A
GGGTACGGACGCCGCGCG CG ||||| |||| |||| ||||
GCGCGC GGCAT GCACG TTGC T
CGCA- GG A T

GAM1028 GGATGATGTA CTCTCGGGGGGGG 1014 TGATGTACTC 3739 T CTC - GCCTTC-- T T
ATGCCCTTCCTGGTTGGTCGC GGGGGGGGATG GGATGA GTA GGGGGG GAT CTGGT GG C
CACTAGTTTCACCAATCGCC CCTT ||||| ||| ||||| ||| ||||| ||
CCCCTATTTTATCC CCTATT TAT CCCCC CTA GATCA CC /
T --- G ACCACTTT - G

GAM1029 TATTGTGACCGCTTCCCTGC 1015 TGTGCAGGGT 3740 CC TT- TATAACTAAG TA
ACTATAACTAAGAGCTAATT ATGTTTTACA TATTGTGA GC CCCTGCAC AGC A
GCTGTGCAGGGTATGTTTTA GTA ||||| || ||||| |||

CAGTA

ATGACATT TG GGGACGTG TCG /

T- TAT ----- TT

GAM1030 GAACGTGATTGCTCCGCTGG 1016 TGTCTCGCTC 3741 G A G - CT --- CC TG T G
AACTTCCCGCGAGATTGTCT GAACCTGTTC GAAC TG TT CT CCG GGAAC TTC GCGAGAT
TC TTT A
TTTGAGAAAACGAATGTCTC CTCT |||| |||| |||| |||| |||| ||||
GCTCGAACCTGTTCTCTCTGG CTTG AC AA GA GGT CTTG AAG CGCTCTG AG AAA G
TAGAAACAGTTC - A - T CT TCC CT TA C A

GAM1031 GGAGTGGTAAGCGGCCATCA 1017 AGTGGTAAGC 3742 A G -- A- AAT G
CTCGAATTCTAGAGTTAGAC GGCCATCACT GGAGTGGTA GC GC CATC CTCG TCTA A
GAGGAGGTGTTGTAGCTGCC CGAA |||| |||| |||| |||| ||||
ACTCT TCTCACCGT CG TG GTGG GAGC AGAT G
- A TT AG --- T

GAM1032 CCTGCTTGTCCCGTGTGTCC 1018 TGAGGACGAC 3743 G C- G T
TCATCTTCTGACGAGGATGA GATGACGAGG CCT CTTGTC CGT TGTCCTCATCTTC G
GGACGACGATGACGAGGAGG AGG |||| |||| |||| |||| ||||
GGA GAGCAG GCA GCAGGAGTAGGAG A
G TA - C

GAM1033 GCGCTGCCGGGCGCTGCGGCC 1019 GGAGGTAGAC 3744 C CG C CT A A CGCA
GCG
CTCGGGGAGGTAGACGGGTC GGGTCGCAGG GCG TGC GGC TGC GGCC CGGGG GGT
GACGGGT GGGGC C
GCAGGGGCGCGCCAGTCCC GGCG |||| |||| |||| |||| ||||
CATCTGTTAGCCGCCCTGTG TGC ACG CCG ATGTCGG GTCCC CCG TTGTCTA
CCCTG /
GCTGTATGCCGCATCGT T -- T T- G A C--- ACC

GAM1034 GGAGGCCGATTGTGGCGAAA 1020 GCGAAAGATG 3745 CC - - A T C G-- TT CT
GATGTGGCGGGCGGGTTTTT TGGCGGGCGG GGAGG GAT TGTG GCGAAAG TG GG GGGC
GGTT TA T
ACTTATTGTTGACCGCAGTC GTTT |||| |||| |||| |||| ||||
CCCCCGCTTTTGCATACGT CCTCC CTA GCAT CGTTTTTC GC CC CCTG CCAG GT /
ATCTCCTCC T- T A - C C ACG TT TA

GAM1035 TGCACATCGCGTGAAGCGCC 1021 TCACCCGGTA 3746 ACA C- A-- - T ATACA TA
CA
CCCTTCCATACATGTAGGTC GGGGGTCGTA TGC TCG GTGA GCG CCCCT CC TG
GGTC C
CACAAAGGCTCTCACCCGGT TATT |||| |||| |||| |||| ||||
AGGGGGTCGTATATTATAAC ACG AGC TATT TGC GGGGGA GG AC TCGG A

GAGCCGCA

CCG AA ATA T T CCC-- TC AA

GAM1036 TGCATGTCACAGAACTGTTT 1022 TGTCACAGAA 3747 G --- AAC TCCAAT A
ATCCAATAACGCACTGTGTT CTGTTTATCC TGCAT TCA CAG TGTTTA AACGC C
TCATTTTGAACACTGATATG AATA ||||| ||| ||||| |||||
AGATGCA ACGTA AGT GTC ACAAGT TTGTG /
G ATA --- TTTACT T

GAM1037 CAGCAGGTTGAAGATGCCCA 1023 TGTGGAAGTC 3748 TG G GC TTG---- TC -- - T
AAC
GCTCCTTGAGGCTCATGAGC GTCATAGGCC T AAGAT CCA TCC AGGC ATGA GCT
CCACGG CATGCGG A
TCCACGGTCATGCGGAACAT TGGT | ||||| ||| ||| ||| ||| ||||| |||||
GCGCCGCGTGCTGTGGAAGT A TTCTA GGGT AGG TCCG TACT TGA GGTGTC
GTGCGCC T
CGTCATAGGCCTGGTACTCG TG G AA CTCATGG GA GC A - GCG
GAAATGGGGATCTTGTACTT
GCTG

GAM1038 GCAGGTCGCACGGCTGGTAG 1024 AGAGGTAGTC 3749 - GCA TGGTA TA C - -- CGC
T CC
AGGTAGTCCAGGCCCTCGCC CAGGCCCTCG GC AGGTC CGGC GAGG GTC AG GC CCT
CG AGGTGC A
GTAGGTGCCCAGCAGCGCCT CCGT || ||||| ||| ||| ||| ||| ||| |||||
CGCACAGGAAGCTCTTGGCC TG TCTAG GCCG CTCC CGG TC CG GGA GC
TCCGCG G
GCCTCGATGCCGAAGATCTC C AA- TAG-- GC T T AA CAC - AC
GT

GAM1039 GCGGGGTTTCAGGTGCGTGAG 1025 CTCGCGCACG 3750 - TC --- AG GTAC A AAG
AT
GAAGACGTACTCGATGAAGT TCCTCTACCA GCGG GGT AGG TCGTGAGGA AC TCG TG
TCG G
CGATGTCCGAGACGCCGAAG CCGC ||||| ||| ||||| ||| ||| ||| |||
AAGTAGTTCTCGCGCACGTC CGCC CCA TCC ACGCGCTCTT TG AGC GC AGC /
CTCTACCACCGC A TC TGC GA AAGA C AG- CT

GAM1040 TCGCGACGAAAGCGCGAGTG 1026 TGTCTGGCG 3751 ACGA-- AGTG C CC AGA
TCC G C
CGCCACGGGGCCCGGCAAGAG AGAGCGCGCT CGCG AAGCGCG CGCCA GGGC GGCA
GCGCGCG CT TTGT C
CGCGCGTCCCTGTTGTCTG TCTT ||| ||||| ||||| ||| ||||| |||||
GCAAGAGCGCGCGTCCCTGT GCGC TTCGCGC GCGGT CCTG TTGT TCGCGC
GA AACG T
TGTCTGGCGAGAGCGCGCT CTTTTC GAGA - -- CCC --- G G
TCTTTTCCGCGG

GAM1041 AGCGAAGCTAGCCAACCAGT 1027 TGTCAAGTGG 3752 -- T T T- TT- AAG
TCGTA TTT

CTTTACTTTGCTTCTTGAGA GACAGTGGTT GCCAACCA GTCTT ACTT GC TC GAG
 TGCGCCTAT GATTT A
 AGTGCGCCTATTCGTAGATT GGCT ||||| |||| ||| || ||| ||||| ||||
 TTTTACATCAGATCCATAGG CGGTTGGT CAGGG TGAA TG GG CTC GCGCGGATA
 CTAGA C
 CGCGAGCTCTGTGGTTGTCA GA - C TT TGT GA- C---- CTA
 AGTGGGACAGTGGTTGGCTC
 TCTGTGTAGTT
 GAM1042 GCTTGACTGAGGCAACGTAA 1028 TGA CTGAGGC 3753 TG- - AA G G TCGC
 ACT G
 TCGATGGACATATCATCGCC AACGTAATCG CT ACTGAGGCAA CGT TC ATG ACATATCA
 CAGCATAC TGTGCG C
 AGCATACACTTGTGCGGCAT ATGG || ||||| ||| ||| ||||| ||||| |||||
 CGCATGGTATGTTGAATTTG GG TGA CTTCGTT GTA GG TAT TGTGTGGT GTTGTATG
 GTACGC A
 GTGTGTGTATAGGCAATGTT TTG T AC A G TTAA --- T
 TGCTTCAGTGTGGC
 GAM1043 GGAGGATTTCTGAAGAGTGTT 1029 TGAGATTTCA 3754 GA AA- G TG T
 GGGTTGTGCAACCTGAGAT ATGGAAGCTC GGAG TTTCG GAGT T GGTTG C
 TTCAATGGAAGCTCC C |||| |||| ||| ||||
 CCTC AAGGT TTAA A CCAAC /
 G- AAC G GT G
 GAM1044 CCTGGGCAGCCTAAGGGCCA 1030 CAGCCTAAGG 3755 TG - G-- --- CTT TCAGCT
 CTG
 TGTGCCTTGGGAGTCAGCTG GCCATGTGCC CC GGCAGC CTAA GGCCAT GTGC GGGAG
 GCGC T
 CGCCTGTTTTCGTGCCCCAC TTGG || ||||| ||| |||| ||| |||| ||||
 CTCCCCGCGCCGTGTGGCCG GG CCGTCG GGTT CCGGTG CGCG CCCTC CGTG
 T
 CGTTGGTGCTGCCTGGG GT T GCG TGC C-- CACCC- CTT
 GAM1045 TCGTTTAACTTTTTTCAAAT 1031 TCTAAAAATC 3756 ATTTCC TCA C--- TC
 AATTC CA
 TCATTTCTGTTTCACCTAT AAAAATTCTA TTTTCAAATTC TGTT CCTAT TCTAAAA AAA
 TATGA T
 CTCTAAAAATCAAAAATTCT TGAC ||||| ||| |||| ||||| ||| ||||
 ATGACATTTTATATCTTTA AAGAGTTTAAG ATAA GGATG AGGTTTTT TTT
 ATATT /
 TTTTTTGAATAAGTAGGAT GTTT-- TTA AATA TA CT--- TT
 TAATATTTGGAATTTGAGAA
 AAATTATCGA
 GAM1046 TCTGGTCTGATTACATGTCT 1032 TGTGTAACGA 3757 CATGT AGAA C CC - C----- C
 GA
 CAGAACAGGCTGCCAGGCCA CCCTACCTGT A CTC CAGG TG AGGC CAG TACGC
 AGCGCCAGGG T
 GCTACGCCAGCGCCAGGGGA GCCT | ||| ||| ||| ||| ||||| |||||

TGGGTCCTGGCGCTGTGTAA T GAG GTCC AC TCCG GTC ATGTG
 TCGCGGTCCT G
 CGACCCTACCTGTGCCTCCA CTTT- ACA- C C- T CATCCCAGCA - GG
 CCCTGACAGAGTTTCTAAAC
 AGACCCGA
 GAM1047 CATGAGACTTTCCACGGCGG 1033 TAGCTAATTG 3758 - ----- - C T --- GCGTA
 TT A
 ATAGCTAATTGCAGGGAGGC CAGGGAGGCG GACTTT CCAC GGC GGATAG TAAT GC
 AGGGAG GAG TC G
 GTAGAGTTTCAGAGGATCCT TAGA ||||| ||| || ||||| |||| || ||||| ||| ||
 TGATCACTCCCTTCGGCGTT CTGAAA GGTG CCG CCTATT ATTG CG TCCCTC
 TTC AG A
 ATTATCCAGCCGCAAAACGT C CAAAACG A - - GCT ACTAG CT G
 GGCAAAGTCTCCTG

GAM1048 CATTGCAACTGTCCAGGTGG 1034 TTGACCATGT 3759 T TC- G G CA
 GCGACTACCATGAAGTAGTT GTGTCAGTTG CA TGCAACTG CA GTGG CGACTAC T
 GACCATGTGTGTCAGTTGCA CATT || ||||| || ||||| |||||
 TTG GT ACGTTGAC GT TACC GTTGATG G
 T TGT G A AA

GAM1049 GCAGGCAGATGTGTAGGTAT 1035 TTGGTTCCGT 3760 GG GA GTAG TC TAGG- ---
 GT A
 GTCAGGGGTAGGTCCGGGAC CGGAATACTT GCA CA TGT GTATG AGGGG TCC
 GGGACCAGA AGC A
 CAGAGTAGCAAATGCTTTTG CCCT ||| || ||| ||||| ||||| ||| ||||| ||||| |||
 GTTCCGTCGGAATACTTCCC CGT GT ACG TATGC TCCCT AGG CCTTGGTTT
 TCG A
 TCCGTATGGCAGTGAATGC AA G- G--- C- TCATA CTG -- T

GAM1050 GGTTGGAAATTACACGACTG 1036 TGAAATGCTA 3761 T A C- AATT TG ATAC
 GCGTAATTTTTGGTATACAT TCTCGGTCAT GGTTGGAAAT AC CGA TGGCGT TT GT A
 TATGGCTGAAATGCTATCTC TTCT ||||| ||||| ||||| || ||
 GGTCATTTCTAACC CCAATCTTTA TG GCT ATCGTA AA CG T
 C - CT ---- GT GTAT

GAM1051 GTAGTCCAATTCTAAGCAAT 1037 TTCATTA ACT 3762 A AAT-- C- TTAACC
 GAGTATTAACCATCTACTTT TAGATTTCCG GT GTCC TCTAAG AATGAGTA A
 ATTCATTA ACTTAGATTTC GACA || |||| ||||| |||||
 GGACAGC CG CAGG AGATTCTTACTTAT T
 A CCTTT AA TTCATC

GAM1052 TCCCGCTCCATTAGCACAGC 1038 TCAGCAGGTA 3763 CT G ACA ATAATTC AAA-
 CCCCC
 TTGTTGAATAATTCTAGAAA AGGTGGTGGG TCCCG CCATTAC GCTTGTTGA TAG TGC
 A

TGCCCCCAATGTAGCACTC	ACGG			
CCTATCAGCAGGTAAGGTGG		AGGGC GGTGGT G	TGGACGACT	ATC ACG /
TGGGACGGGA	AG	- GAA	----- CCTC	ATGTA

GAM1053	TTTTATTGGCGTGTTTATGA	1039	TGGAGTGC	3764	TG-	TTT	----	C	-----	- AA
	TTCCTCCCGCTTCGCGCCAA		GGTTGAAATC		TTTTAT	GCGTG	ATGATT	CCTC	CGCTTCGC	
GC CA T										
	ATTACTGAGCGAAATGTGGA		GTCA							
	GTGCGAGGTTGAAATCGTCA				AAAATA	CGTAC	TGCTAA	GGAG	GTGAGGTG	CG GT
T										
	TGCAACATAAAA		CAA		---	AGTT	C	TAAAG	A CA	

GAM1054	TGATATATTACACGTTTTTG	1040	TATATTACAC	3765	CGT	CAAC	CT
	AGCAACTTTAACTATATTA		GTTTTTGAGC		TGATATATTACA	TTTTGAG	TTTAA A
	ATTCAGGATGTGATGTGTTA		AACT				
			ATTGTGTAGTGT		AGGACTT	AAATT /	
			---		----	AT	

GAM1055	CGGTCCGAGCCATGAACTGC	1041	TCGCCGACAG	3766	CGAGCCA	CT C	AAC C T
	GCCGTGCGCAACATACCCGT		CGCCTTCACA		CGGTC	TGAA GCGC	GTCGGC ATA CCGT T
	TTCGATGGATATCGCCGACA		AGAT				
	GCGCCTTCACAAGATTGACC				GCCAG	ACTT CGCG	CAGCCG TAT GGTA C
G			TTAGAAC		C- A	C-- A	G

GAM1056	TGTGAACCAGACAGTTGAGG	1042	TCAACGCCTT	3767	CA	GAGGC	G	A	TGC	AAC	T
C AA TT											
	CGTATGTGAACGGTGACCAT		GGACACCGTT		AGA GTT	GTAT TGAACGGTG	CCA	CGT	GAT		
GC GG CAAAA T											
	GCCGTAACGATTGCCGGAAC		CGAT								
	AAAATTTATTTTGGGCCAG				TCT TAA	CATA GCTTGCCAC	GGT	GCA	CTG TG CC		
GTTTT /											
	TGTCAACGCCTTGGACACCG				-- AAA--	-	A	TCC	A--	- A GG	TA
	TTCGATACAAAAATTCTGGT										
	TTACA										

GAM1057	CTACTGATTGGTTACGCCCA	1043	TTGGTTACGC	3768	-	-	CCAAAA	CCC
	AAAATCCGACCCAGCCATTG		CCAAAAATCC		CTAC	TGATTGGTTA	CGC	ATCCGA A
	GATAAAACGTGCTAGCCAAT		GACC					
	CAGGTGG				GGTG ACTAACCGAT	GTG	TAGGTT	G
			G		C CAAAA-	ACC		

GAM1058	CTGGGCACAGTTTGATAATG	1044	TCCACTGAAA	3769	-----	TT	A	AAGAT
	TAAGATCTCCCCACACTGTC		TGTCATAATT		CTGGGCA	CAGT	GATA	TGT C
	CACTGAAATGTCATAATTGC		GCCC					
	CCAG		GACCCGT		GTCA	CTGT ACA	/	
			TAATACTGTAAA		C-	C	CCCCT	

GAM1059 TTTGAAATTTGGGTCCGCTG 1045 GCACCAGAGG 3770 TTTG GT G GA- T
 GGATATTTAAATAGCACCAG GTCAGTTTTC TTTGAAA G CC CTGG TAT T
 AGGGTCAGTTTTCAGA AGA ||||| | ||||| ||
 AGACTTT C GG GACC ATA A
 TGA- TG A ACG A

GAM1060 CGCATTCTTAGGAGTCTCAC 1046 TGTGAAACTG 3771 - C--- - -- C A A
 AAGCACCGCTGTGAAACTGA ACCATAAATA CGC ATT TTA GG AGT TCACA GC C
 CCATAAATAAAATCGCG AAAT ||| ||| ||| ||| ||| ||
 GCG TAA AAT CC TCA AGTGT CG /
 C AATA A AG A - C

GAM1061 AGTAAAAGTCCCGTCTTCTA 1047 TCACACTTTT 3772 TCCCG TA C AA----- G
 AGTGTGCAGGTGTGAGTAAC GCATTGGGGA AGTAAAAG TCTTC AGTGTG AGGTGTGAGT
 CTTT A
 TTTGAAAAAAGACCCGCAAA AATG ||||| |||| |||| ||||| ||||
 ACTCACACTTTTGCATTGGG TTATTTTC AGGGG TTACGT TTCACACTCA GAAA A
 GAAATGTCTTTTATT TGTAA -- T AAACGCCCA A

GAM1062 GGTAAGTTAACAGAGTTTTT 1048 TAAGTTAACA 3773 A G TTT AA TG
 TATAAAAATCTGGTATGATT GAGTTTTTTA GGT AGTTAACA AGT TTATA AATC G
 CTATAAGCTTGTTAACTAGC TAAA ||| ||||| ||| ||||| ||||
 T TCG TCAATTGT TCG AATAT TTAG T
 A - --- C- TA

GAM1063 AACCCATAGGATACGTGGAG 1049 TAGGATACGT 3774 A ---- GGGA- G GA
 TGGGGAAGGGTTTGAGGAAT GGAGTGGGGA AACCCATAGG TACGTGGA GTG AGGGTTT
 AG A
 ACACCCCAAGCTTGTTGGCC AGGG ||||| ||||| ||| ||||| ||
 AGTTCTTTCACGTCCTATG GGGTATCCTT GCACTTTC CCG TCGAACC CA T
 GG - TTGA GTTGT C CA

GAM1064 ACCCAGCGACTCAGGTCCGC 1050 TCACAGTTAA 3775 - - TC CG- G
 GGGAGTCCTCTCACAGTTAA TCATGATGTT ACCCAGCGA CTC AGG CG GGA T
 TCATGATGTTGTTGG GTTG ||||| ||| ||| ||| |||
 GGTTGTTGT GTA TAA GA TCT C
 A C TT CAC C

GAM1065 ACGGGTTGCCACTGAAGAGC 1051 TGAAGAGCCT 3776 TG TG T A TC----- TG G
 CTTGATCAGTTTCGTGTGGT TGATCAGTTT ACGGGT CCAC AAGAGCCT GATC GTT G TG
 T
 CTGGGCTGCCCTTGAAGAAC CGTG ||||| ||| ||||| ||||| ||| ||

CTGACTAAGGCTTGCCAGTT
AAC

CAATTG ACCG CGGAATCA TCCA GAA T GG C
-- TT G A GTTCCCG CG T

GAM1066 GCTTCGTCTTTGGCTTGCTG 1052 TGAGATCCTC 3777 T T T GAGA TT G GG-TT
G C TG

GTGGGAGAAGAGTTGGACGG GGT TTGGACG TGGCT GCTGG GG AGAG GGACG
TGAGATCCTC T G ACG AGT G
TGAGATCCTCGGTTTGGACG CAGT ||||| ||| ||||| ||||| | |||||
CAGTTGGTGAAGCCGTGGTT TGAGG ACCGG TG TCAT TGTCT TTTAGGAGTT G G
TGC GAA /
GGTGTGAGGATTTCTCTGT C G C T--- GC C GTG TT G C GT
CGTACTTGTGCGGCCAGGGAG
TCCTGGATGAG

GAM1067 AAAATTACAACACTCCTTAT 1053 TACAACACTC 3778 - A C - A ACA GCGTAG A A
TT

AAAACTTACAGCTGCGTAGT CTTATAAAAC AAATTA CA CA TCCTT ATA AACTT GCT TG
GAGGTG TAAGTG G
GAGAGGTGATAAGTGTTGCA TTAC ||||| ||| ||||| ||| || ||||| |||||
TCACTTGACCTTACAGTTC TTTAAT GT GT AGGAG TGT TTGAA CGA AC TTCCAC
GTTTAC C
AAAGCACCAAGTTATGTGGA T C - G A CCA AACTTG A - TA
GGATGCTGTTAATTTT

GAM1068 AACCAGGATTCATATGGTGG 1054 GAGCACATGT 3779 GGA T - C- - A
TGCTTCCGTGTGTCTATATT TGAGCATCCA AACCA TTCATA GGTGG TGCTT CGTGTG TCTAT
T

GTAGAGCACATGTTGAGCAT TCTA ||||| ||||| ||||| ||||| ||||| |||||
CCATCTATGGATGGTT TTGGT AGGTAT CTACC ACGAG GTACAC AGATG /
--- - T TT G T

GAM1069 ACCAGTTTTGCCTAATTTTG 1055 TGAGTGCAAC 3780 ----- TT--- TG T ATTGAAG TG
CT

AACCTTTCAGGATTGAAGGT CCTGAAGGTT ACCAGTTT TGCCTAA T AACCTT CAGG G
CTCATG T
GCTCATGCTTTCTATGAGTG TGAT ||||| ||||| | ||||| ||| | |||||
CAACCCTGAAGGTTTGTATGT TGGTCGAA GTGGATT A TTGGAA GTCC C
GAGTAT /
CCTTAGGTGCTGACAAGCTG CAGTC CCTGT GT - CAA---- GT CT
GT

GAM1070 ACCTATAGGTAGCCCCGTCT 1056 TGAGTACTGC 3781 -- C CGTCTGT TG T TAT
A A T

GTGATGATGTTGTTGCTGGT AACAGTGTTA ACCTATAG G TAG CC GATGA TTGTTGC GGT
GCT ATTCT GT T
TATGCTAATTCTAGTTTTGA TTTG ||||| | ||| ||||| ||||| ||| ||||| ||
CAAGAATGAGTACTGCAACA TGGGTATC C GTC GG TTATT GACAACG TCA TGA
TAAGA CA T
GTGTTATTTGTAAGGTCTGT T T T AATGT-- GT - --- G A G

CTCTATGGGT

GAM1071 CATACTGGGTTTACCTTTCC 1057 TTTACAATTA 3782 T- TTC- G TAACG TAA
ACA- A
TAGCGAAGTTGTAAACGGTA CAGTTTGCTA TT ACCT CTAGCGAA TTGT
GTAGGCGTGTGAT AACC GAT A
GGCGTGTGATTAAACACACA GATT || ||| ||||| ||| ||||| ||| |||
GATAATAATTGTTGGGTAA AA TGGA GATCGTTT GACA CATTTGTACACTG TTGG
TTA T
TGTCACATGTTTACAATTAC CT TTTA - TTAA- TAA GTTG A
AGTTTGCTAGATTTAGGTTC
AAGTCAGCAG

GAM1072 CCTGGTTATGTTACACCTAT 1058 TTCACACTCA 3783 TTATGTT CCT GC TCAT C-
CTCA
GTTTGCGTGCTTGTCAATTGC AGCATAAGAC CCTGG ACA ATGTTT GTGCTTG TG TATC
C
TATCCTCACTTTTGATGTTT ATTG |||| ||| ||||| ||||| || ||||
ACACTCAAGCATAAGACATT GGACC TGT TACAGA TACGAAC AC GTAG /
GTTTTTCCAGG TTTT--- --- A- TCAC TT TTTT

GAM1073 CTGCTTTTTGGTATGTTGAG 1059 TTTGGTATGT 3784 GC G T CGTT ATA TC
ACGTTTGGATATGTCTTCTG TGAGACGTTT CT TTTTGTAGTTGAGA TGG TGTCT T
TAGACACCATTCTCAACTTG GGAT || ||||| || ||||| ||| |||||
GCAAAGGATGG GG GGAAAC GT CAACTCT ACC ACAGA /
TA G T T--- --- TG

GAM1074 CTTTCTATTATGATGGAACA 1060 TATGATGGAA 3785 TC TT - ---- - CC
CTATACTATCCCACCGATGG CACTATACTA CTT TA AT GATGG AACACTAT ACTATC A
TAATAGTGTGTGCCTATCT TCCC ||| || || ||||| ||||| |||||
GTTTAAAGAAG GAA AT TG CTATC TTGTGATA TGGTAG /
GA TT T CGTG A CC

GAM1075 GAGCATTGTAATGTACATAG 1061 TGA CTGCTG 3786 TTGTA CA-- AA- - - T T
AAACGAGCATGTGGCTTCTG TCTGGCCATA GAGCA ATGTA TAGA CGAG CAT GTGGC TC
G
GTGATGCCATAATGACTCGC CATG |||| |||| ||| ||||| ||||| ||
TGTCTGGCCATACATGATTG TTCGT TACAT GTCT GCTC GTA TACCG AG G
CTT TAG-- ACCG GTC A A T T

GAM1076 GCAATTAGGGTTTTCTAACG 1062 TGAGTCTGGT 3787 ATTA TT A TG TTT TG
CTGAA G
GTGTTGATTTTGTGTCAGA GACTACATTA GCA GGGT TCT ACGG TTGAT GT TCAGAC
GGTTGC T
CCTGAAGGTTGCGTTGTAAC AACC ||| ||| || ||||| ||||| || ||||| |||||
TGAGTCTGGTGACTACATTA CGT CTCG AGA TGCC AATTA CA GGTCTG TCAATG

/

G--- -- C CA CAT GT AG--- T

GAM1081 TCCCTGTCATGGCCCCTGGT 1067 AAGCAGCGCT 3792 GG C- GT G T AT A- -- -
G
CCTTGGGTGTGAGCGTATTG CCATTAAGGC GTCAT CC CTG CCTTGG TG GAGCGT TGTT
AGCT CCAG AATAAT A
TTAAGCTCCAGAATAATGAG AGAA ||||| || ||| ||||| || ||||| ||||| ||||| ||||| |||||
ATTATTCCTGGTAAGCTGAA CGGTA GG GAC GGAATT AC CTCGCG ACGA TCGA
GGTC TTATTA /
GCAGCGCTCCATTAAGGCAG GA AA -- - - -- AG AT C G
AAGGAGATGGCATAGTTGGA

GAM1082 TCCGATTGGACTGATGTTTC 1068 TCATTGCGTC 3793 GA- AC- - A A T A- T A
 T GACTACAGGTTGGCAAATG TATTTGCAGC TCC TTGG TGAT GTTCTG CT CAGGT GGC
 AATGA GTC A
 ATGTCAAGGACTCATTGCGT GGAA ||| ||| ||| ||||| || ||||| ||| ||||| |||
 CTATTTGCAGCGGAAACTAT AGG AACC ACTA CAAAGGC GA GTTTA CTG T TACT
 CAG /
 CAAGGCCAAGGAGGA AGG GGA T - C T CG - G

GAM1083 TGATATATTTGGTGAGGATT 1069 TAAGACAGCA 3794 T G TTTTAA A AC C A
 TTAAGTCATATGACCTGCTG CTCTTCAACA TGA ATATTTG TGAGGA GTC TATG CTG
 TGGAAT T
 GAATATGATTTTACGGAGCA AGTA ||| ||||| ||||| ||| ||||| ||| ||||| |||
 TAAGACAGCACTCTTCAACA ACT TATGAAC ACTTCT CAG ATAC GGC ACTTTA /
 AGTATTTCA T A CACGA- A GA - G

GAM1084 TGCTACTAAGCTTAACATTG 1070 TATCAAGGAC 3795 TAA TA C CT ---- C T
 AG T
 TTACCTCTGATATCGATTCT AATGATGGCA T CATTGT CCT TGATATCGATT TAT AAT GTA
 CCAGCGTG GGA G
 TATAATCGTATCCAGCGTGA AGGT | ||||| ||| ||||| ||| ||| ||| ||||| |||
 GGGATGTGTCCACTACGCTG G GTAACA GGA ACTATAGTTAA ATA TTA CAT
 GGTCGCAT CCT T
 GTACCATTTGGAATATAATT TA- -- - T- AGGT C - CA G
 GATATCAAGGACAATGATGG
 CAAGGTGGTA

GAM1085 TGCTTAAGAACCTTATTGAT 1071 TGATACGCAT 3796 T G - A --- T - ----- A
 GGTGTTGAAAATCCGTGTCT GATTTCAGCC GAT GTG TTGAAA TC CGTGTC TAT GGGT
 TGGG T
 TATGGGTTGGGATTACCCAA ATGA ||| ||| ||||| || ||||| ||| ||||| |||
 AGTGCGATAGAGCACTGCCC CTA TAC GACTTT AG GCATAG ATA CCCG
 ACCC T
 AATATGATACGCATGATTTT - G C - TAC T A TCACGAGATAGCGTGAA A
 AGCCATGATCTTAGGCTCTA
 AGCA

GAM1086 TGTACTGGTGATGTTGCTAT 1072 GTGCATTGGT 3797 - TGATGTT T T- GGTTGTA GC
 T A
 GTTTGTGCATTGGTTGTACT TGTACTGGCT TACT GG GC ATGTT GTGCATT CTG
 T TACTGG GTTGAC A
 GGCTTACTGGTGTTGACAAA TACT ||||| || ||||| ||||| ||| ||||| |||||
 GGTCAGCCTAGTGATTGAGA ATGA CC TG TACAA CACGTAA GAC AGTGATC
 CGACTG A
 AAATGCACTTAACATGTTGT A TGT---- - TT AA----- TT - G
 CCAAGTACA

GAM1087 TGTCCACATGGTCTTAACATA 1073 TCAATGTAGG 3798 T - TC AA AGTT TAA
 CATTGGCAAAGTTGTTGTAG AAAACCTGTA TG CCAC ATGG TT CTACATTGGCAA
 GTTGTAGT A
 TTAAAGGTACTACAATTGTT GTGG || ||||| ||| || ||||| |||||

GTCAATGTAGGAAAACCTGT
AGTGGCA

AC GGTG TGTC AA GATGTAAGTGT TAACATCA /
- A CA AG GT-- TGG

GAM1088 TGTGAATCTCGTCGTCGTTG 1074 GGATGTAACC 3799 T - G CG -- C - C GT
ACGAGGATGTAACCCCTCAAC CTCAACACCA TGTGAA CTCGTCG TC TTGA AGGATGTAA CC
TCAAC AC ACTG C
ACCACTGGTCGTACAGTTGT CTGG ||||| ||||| || ||||| || ||||| || |||||
CGTTGATGGACTTGCAATTCT ACATTT GGGCAGT AG AGCT TCTTACGTT GG AGTTG TG
TGAC G
TCGAGAGTGACGGGTTTTAC T G - -- CA T C T AT
A

GAM1089 TGTTACGGATGCACCAATTG 1075 TGAAGTAGAC 3800 - TGC A G G GTGAT AG A
CC- - G
ATTCCGAGGGTGATGAAGTA TCCTCTGCAC GTTAC GGA ACCA TT ATTCC AGG GA TAG
CT TCTGC ACCT A
GACTCCTCTGCACCTGAGAA CTGA ||||| ||||| ||||| ||||| ||||| ||||| |||||
GGTGGCAGATGTGGCTAACT CGGTG CCT TGGT AG TAGGG TCC CT ATC GG
AGACG TGGA G
CTGAACCTGGGGATGATGGT T TC- - - G AAGT- CA - TGT G A
CTTCCTGTGGCA

GAM1090 TTTTGAGTGTTTTATGCCTA 1076 TCACTGGTCT 3801 TTA CTAC -- CC -- CTTG
ATG- G
CAATCCCACAGTGTCCAGCA TAATACAATG T TGC AATCCCACA GTGT AG CAGTG
AAGAGATTG GTG T
GTGCTTGAAGAGATTGATGG TGGG | ||| ||||| ||||| ||||| ||||| ||||| |||||
TGGTAGCATATGGCGGTCTT A ACG TTAGGGTGT CATA TC GTCAC TTTTCTGGC
TAC A
TTATCACTGGTCTTAATACA --- TTT- AA AT TG TA-- GGTA G
ATGTGGGATTTTTGCAAGCG
TCTTAAAG

GAM1091 CGATGACGGGTGGGTTGACG 1077 TGGCACGTCG 3802 GG- G -- AA TG G -- GGG
AATGCTGGTGGCCTCGGGGA AAGCTGACGA CGATGAC GT GGT TGACG TGC GT GCC TC
G
GAAGAACGGCGGCTGGCACG AGTC ||||| ||||| ||||| ||||| ||||| |||||
TCGAAGCTGACGAAGTCATT GTTACTG CA TCG GCTGC ACG CG CGG AG A
G AAG G AA -- GT G CA AAG

GAM1092 CTAAGAGAGGTGCGGCAACC 1078 TGGATAGGTT 3803 GAGGTG G G GGA
GTGTCGCGGTGGACGGTGCT GTTGAAAGCG CTAAGA CGGCAACC TGTC CGGT C
GGATAGGTTGTTGAAAGCGT TCTT ||||| ||||| ||||| ||||| |||||
CTTGG GGTCT GTTGTGG ATAG GTCG /
GCGAAA - - TGG

GAM1093 GAGCTCTGCGAGCAAGCGAG 1079 TGCGAGCAAG 3804 T- AA G CCTG ---- GATA
GGTGATGTCCTGGGGTGCGA CGAGGGTGAT GAGCTC GCGAGC GCGAGGGT ATGT GGGT
GC A

GGAATTTTCAGAACTTGATT	ATTCCGGACA	GGAAATCTTGTT	TGGAAT	AGAACTT
ATTCCT A				
TCCTCAAGAGGAGATGGGTT	AGGT			
CTTTATTCCGGACAAGGTTT		CTTTTGGAAACAG	GCCTTA	TCTTGGG TAGAGGA A
TC	-----	TT--	-	G

GAM1101 GGATGAGGCCGTTTGTCTCG 1087	TGAGGCCGTT 3812	GC TT-	CC C ATT
GCCTCGCTGATTTTTTGCAC	TGTCTCGGCC	GGATGAG CG	TGTCTCGG TCG TG T
GAACTGAGATATATCGTTCT	TCGC		
CATTC	CTTACTC GC	ATAGAGTC	AGC AC T
	TT TAT	A-	- GTT

GAM1102 GTGTATACACTTTGTATTTA 1088	TATCACAACG 3813	- TGTATT T A T
CTTTGAGATATACTTTGTGT	TGCCCTAAGA	GTGTATACA CTT TAC TTG GATATAC T
ATCACAACGTGCCCTAAGAT	TGTG	
GTGTGCAC	CACGTGTGT GAA	GTG AAC CTATGTG /
	A TCCC--	C A T

GAM1103 TCATGGACTCAAGGGTCTCG 1089	TCACTGAGAA 3814	----- GG C AC- G
CTGATGGGTACGAGAAATTC	ACTAGCTTTC	TCATGGACTCA AG TCTCG TGATGGGT GA A
AAATCTATCACTGAGAAACT	TGGG	
AGCTTTCTGGGTTTATGA	AGTATTGGGT	TC AGAGT ACTATCTA TT A
	CTTTCGA AA C	AAC A

GAM1104 AACGTGGTGGGTTTGGCGGT 1090	TGGCGGTCTC 3815	G - CG GAC TTC A TT G- GG C
CTCGTCCCCGACGGCGTTCA	GTCCCCGACG	TGGGTTT GCGGT CT TCCCC GGCG ACC CC
CGT AGCTG GCTT G		
CCACCTTCGTGAGCTGGGGC	GCGT	
TTCGTGAGGCGCAGCTGGAC		GCTCGAA CGCCA GA AGGGG CCGC TGG GG GCA
TCGAC CGGA T		
GTCGGGGTCGCCCTGGGGGA		G T TG GTC --- - CT GG G- G
GTAGTACCGCGAAGCTCGTC		
AACTCGCGTT		

GAM1105 GCACCGATGCCGTGCCGCTG 1091	TGCCACGTCA 3816	GA G - T AGAGAA AC
GCGTTGCGCCGAGAGAACGA	GCTGGCAGGT	GCACC TGCC TGCC GCTGGCGT GCGCCG
CGAC G		
CACGGAGTCGCGGTGCCACG	GAAG	
TCAGCTGGCAGGTGAAGGTG		CGTGG GTGG ACGG CGACTGCA CGTGGC GCTG /
C	AA - T C	----- AG

GAM1106 GTGGGTGTGGTTCGGGGGGC 1092	TGTGGTTCGG 3817	C- GG-- G G G GA AG G C
CATT TT		
GGATGCGTTCCGCGGGGACG	GGGGCGGATG	TT GG GGC GATGC TTCC CGGG CGCGG G
GG GG GCTCGCG C		

CGGAGGGGGCGGCATTGCTC CGTT || || ||| |||| |||| |||| | || ||| |||||
 GCGTTCCCCCGCGGGCCAC AG CC CCG TTACG AGGG GCCT GTGCT T CC CC
 CGGGCGC C CA ACGA G G G GC AT G A ---- CC
 CGTTATCGTTCGTCCGGGGG
 AGGCATTGGCCAGCACCACG
 ACCACACCCAC

GAM1107 TCAGATTGGAGATGTTGCCG 1093 TGTGCAACAC 3818 A- - A - GT TC
 GCGTGGTCCTTCCTGGGGTT TACCAGGACT TCAG TTGG AG TGTTGC CGGCGTG CCT C
 CATGTTGTGCAACACTACCA GA |||| ||| ||||| ||||| |||
 GGACTGA AGTC GACC TC ACAACG GTTGTAC GGG /
 AG A - T TT GT

GAM1108 GTCTGGGCGTCACGCGTTGT 1094 TGACGTAGAA 3819 TGG- C TG A AG GC -
 AGAA ACT A
 CGCATGAGCGCGCGGTTGAC GGCCGACTCC C GCGTCACG GT TCGC TG C GCGGT
 TGACGT GGCCG CCG G
 GTAGAAGGCCGACTCCGAGA GAGA | ||||| || ||| ||| ||||| |||| |||
 TCGGCCGGCCGTTGGCGTCG G CGCGGTGC CG GGCG GC G CGTCG GCTGCG
 CCGGC GGC A
 CGCTGCAGGTCCGCGCGGTT TCGA - TT C CT GA C GTTG C-- T
 GCCGTGGCGCAGCTGAC

GAM1109 TGACGAAGCCGTTGGCCTCG 1095 CGGCGAGCCG 3820 A AG- -- -- CG --- G CAC
 TCGGCCTCGGCCACGTTCCA CCCAGACGGA TG CGA CCGTT GGC CTCGTCCGCCT GCC
 AC TTC G
 CGAACCGAAGGTGAAGGTGC TCTT || ||| |||| ||| ||||| ||| ||| |||
 AGGCCGGCGAGCCGCCCAGA AC GTT GGCAG CCG GAGCGGCCGGA TGG TG AAG
 A
 CGGATCTTGCA - CTA AC CC CG AAG G CCA

GAM1110 GCGTACGTGCAGGTAATGTA 1096 TACTTTGCCC 3821 CGT A--- T - AA
 TCAATAAACGTTGTATACT CCGGTTTCTA GCGTA GC GGTAAGTAT CAAT A
 TTGCCCCCGGTTTCTACGC CGC |||| || ||||| |||||
 CGCAT TG CCGTT CATA GTTG /
 CTT GCCC T T CA

GAM1111 ATAATAGGAACATGATATTT 1097 ATAGGAACAT 3822 A T AT--- CATTTC
 TCTGTACCATTTACCAACA GATATTTCT ATAATAGG ACA GAT TTTCTGTAC A
 AGTATAGAAATGCGAATCTG GTAC ||||| ||| ||| |||||
 TATCTATTAT TATTATCT TGT CTA AAAGATATG C
 A - AGCGT AACAAC

GAM1112 ATCTATGATTCCGGTATTCA 1098 TTTACGGAGA 3823 AT TCCG TTA- GTGA TA
 G
 TTTAGATATGTGATATCTTC TGAAATATCC ATCT GAT GTATTCAT GATAT TATCTTC
 TAAATATAT A

TATAAATATATGAGCATATA TCTA |||| ||| |||||| |||| ||||| |||||||
 TTTACGGAGATGAAATATCC TAGA TTA TATAAGTA CTATA GTAGAGG ATTTATATA
 G
 TCTATGAATATATATTGCAG CG TA-- TCTC AA-- C- C
 AT

GAM1113 GAACAACAAAGCGATTATTG 1099 AACAATAACA 3824 ACA A- CCTGATC
 TTTTACCTGATCCCATAATA CGCTTCTGTT GAACA AAGCG TTATTGTTTTA C
 TGGAACAATAACACGCTTCT C |||| |||| |||||||
 GTTC CTTGT TTCGC AATAACAAGGT /
 C-- AC ATAATAC

GAM1114 TATGAAAACCTGTTTTATCT 1100 GATCTCATGG 3825 CT TT TC- TT T C AAT
 CTATTTGTAGACTTAGTTAA ATTTTATTAC TATGAAAA TGT TA TCTA TG AGA TTAGTT G
 TGAAAAATTAGATCTCATGG ATTT |||||| ||| || ||| |||||||
 ATTTTATTACATTTTCATG GTACTTTT ACA AT AGGT AC TCT GATTAA /
 -- TT TTT -- - A AAA

GAM1115 TTTCTCGAATTGGCGGTCTC 1101 TGGCGGTCTC 3826 TG ----- --- ----- G
 TAGCTGCTGGATGATATCCC TAGCTGCTGG TTTCTCGAAT GCGG TCTCTAG CTGCT
 GGAT A
 ACTATGGTAGTTACTGGAGA ATGA ||||||| ||| |||||| |||| |||
 TTCTAACTTGGCCCGTATAT AAAGAGCTTA TGCC AGAGGTC GATGG CCTA /
 TCGAGAAA TA CGGTTCAATCTT ATT TATCAC T

GAM1116 ATCGTATTGTGGTTATATGG 1102 TCAGTGTCTC 3827 ATTG T C A- TAA
 CTACAATTTTATAATGAGTT ATGATCAATG ATCGT TGGTTATA GG TAC ATTTCA T
 GAAGTCAGTGTCTATGATC ACGA |||| |||||| || ||| |||||
 AATGACGAT TAGCA ACTAGTAT CC GTG TGAAGT G
 GTA- - T AC TGA

GAM1117 ATTTGGAGCTTTAATAGTAA 1103 TATTATATGT 3828 AA TAA CT CC T TCACTAA
 A G
 GAACCTCCTAATATATCCGTG TTGAGTTTGT CTTT TAG GAACTC AATATAT GTGTA GTGG
 TAC GATTGTA T
 TATGTGGTCACTAATACAGA TTAG |||| ||| |||||| |||||| |||| ||| || |||||||
 TTGTAGTTCTATAATCGTAA GAAA ATT TTTGAG TTGTATA TATAT CATT ATG
 CTAATAT T
 ATAATTTACCTATATTATAT AG TG- T- T- C TAATAA- - C
 GTTTGAGTTTGTTTAGAAAA
 GTAGCTAAGT

GAM1118 GATACGAATATGTCTTTGTT 1104 TTAAACATAT 3829 T GTCTT -- - TTTTCTG
 AAAACAGTTATTTTCTGAA GATATTCGTT GA ACGAATAT TGTTAAAA ACA GTTA A
 TATTTCTAGCTTGTAATTTT C || ||||||| |||||| || |||||
 AACATATGATATTCGTTCTC CT TGCTTATA ACAATTTT TGT CGAT /
 - GTAT- AA T CTTTATA

GAM1119 GGAAGAGATGTAACGGGAAC 1105 AGAGATGTAA 3830 -- ACG CAG TG
 AGGGTTTGTGATTTCGCAA CGGGAACAGG GGAAGAG ATGTA GGAA GGTTTGT A
 CTATTCTAATACATAATTCT GTTT ||||| |||| ||| |||||
 TCT TCTTCTT TACAT TCTT TCAAACG T
 AA AA- A-- CT

GAM1120 TTTTAGGAACTATGTTTCATG 1106 TTAGGAACTA 3831 TCA TCCT GC
 TATTAAACTATC T
 GTATCCTGGCGAATATTAA TGTTCATGGT TTTTAGGAACTATGT TGGTA G GAA
 AATGATA G
 ACTATCAATGATATGATTAT ATCC ||||| |||| | ||| |||||
 CGTTTTTCATCTTTTATCACC AGAATCTTTGATATA ACTAT C CTT TTGCTAT A
 ATATAGTTTCTAAGA CC- TTT- TA ----- T

GAM1121 AAAATGCTACAAATAATAAT 1107 TTACATGGTC 3832 TATAATTT C T TG ATG----
 CG T
 TTAAATATAATTTATTTTA GATCTGAAGT TAATTTTAAA ATTTTA ATT ATTATGTA GTAC
 TTG GG A
 CATTTATTATGTATGGTACA TTTA ||||| |||| || ||||| ||| ||| ||
 TGTTGCGGGTATCTCAACAA GTTAAAATTT TGAAGT TAG TGGTACAT TATG AAC
 CT T
 ATAATTAGTATTACATGGTC ----- C C -- ATTAATA AA C
 GATCTGAAGTTTTAAAATTG
 TAGTTTGTGTT

GAM1122 AAGCAGTTTCTTGGATAATT 1108 TGACATGATT 3833 C T -- TC-- TTGT
 TCCATAGTTGTTGAATCTAT GAGTCCAGAA AAG AGTTTCT GGAT AATT CATAG T
 GACATGATTGAGTCCAGAAG GCTA ||| ||||| ||| ||| |||||
 CTACTT TTC TCGAAGA CCTG TTAG GTATC /
 A - AG TACA TAAG

GAM1123 ATGAACAGTTGGCTGTCCAA 1109 TGTGTTTCAGC 3834 AC GC CCAA - GA T
 TGAACACAGATGTGGAAGCT AACAACTTCA ATGA AGTTG TGT TGAACACA GATGTG AGCT
 T
 TTAGAGCTATACATTATGTG T ||| |||| ||| ||||| ||||| |||||
 TTCAGCAACAACTTCAT TACT TCAAC ACG ACTTGTGT TTACAT TCGA A
 -- A- ---- A A- G

GAM1124 CGTAGACAATTTGATATAAA 1110 TCTGATGCCG 3835 AG TATAA C G C T
 TTCATGGTGTGAGCATCTTC TAAATGTTTA CGT ACAATTTGA ATT ATGGTGT AG ATC T
 TGATCTGATGCCGTAAATGT AGTT ||| ||||| ||| ||||| ||| |||
 TTAAGTTGTGCACG GCA TGTGTAATT TAA TGCCGTA TC TAG C
 CG TG--- A G - T

GAM1125 TTATAATAAATTGTTTTTGC 1111 TAAATTGTTT 3836 T - ---- T TG C
 TTTTGTGGGCGGCGCCCGTC TTGCTTTTGT TTA AATAAAT TGTTT TTGCTT TG GGCGG G
 TCCATGAGCAATTGTAGGCA GGGC ||| ||||| |||| ||||| || |||||
 CATTTATTTTAA AAT TTATTTA ACGGA AACGAG AC CTGCC /
 T C TGTT T CT C

GAM1126 CGACCATGCTAGGGGATTGT 1112 AGGAGCAGAG 3837 ATG GGGGA TG ---- G
 TGTCTGGGTTTGGAGACAG ATGGAGGGTT CGACC CTA TTGT TCCTGGG TTTG A
 ATGAGTCCCAGGAGCAGAGA G ||||| ||| ||| ||||| |||||
 TGGAGGGTTG GTTGG GGT GACG AGGACCC AGAC G
 GA- AGA-- -- TGAGT A

GAM1127 AAGCCATGTTTGGAGACTTT 1113 TGTGGTTTGT 3838 GT--TG A C T - G A T
 CTGTGGTTTGTTCCTCAATAC TCCAAATACT AAGCCAT T G GA TTTC GTG GTTT TTCCA
 ATACTC C
 TCTCTCGAGTGTCTGGAAGA CTCT ||||| | || ||||| ||| ||||| |||||
 ACATGCGAAAATCACTGATG TTTGGTA A C CT AAAG CGT CAAG AAGGT TGTGAG T
 GAATGGTTT AGGT GT A A - A - C C

GAM1128 ACTATCAACTGTGTAGCGTG 1114 TTCTCAGATA 3839 ---- GATT T AG CAGAT- T C
 ---- T
 ATTTGTGAAAGGGCTCAGAT AAGTGGCCGT G TAGCGT TG GAA GGCT TTTGAG GT
 ATCGAA GAC T
 TTTGAGTGTATCGAAGACT TCCA | ||||| ||||| ||||| ||||| ||||| |||||
 TTCGTCAGAATTTGATATTC T ATCGCA AC CTT CCGG AGACTC TA TAGTTT
 CTG T
 TCAGATAAAGTGGCCGTTCC CTTAG AGTT - G- TGAAAT T - AAGA C
 ATTGAACGCTAGATTCTACA
 GTTTTCAGT

GAM1129 AGCTTATTACTTGCTGAAGG 1115 TGAAGGACCT 3840 CTT TGA C -TA CA--- GA -
 T
 ACCTTGTGTACCGCAAGCTG TGTGTACCGC AGCTTATTA GC AGGAC TTGT G CCG AGCT
 TAG GTTTCAT T
 ATAGGTTTCATTTTGATGAA AAGC ||||| || ||||| ||| ||| ||||| |||||
 GCTCTAAAAGTTCATTACGG TCGAATAGT CG TCTTG AATA C GGC TTGA ATC
 CGAAGTA T
 CGCCATAATGTTCTGTGCTG --- TG- T C GC ATTAC AA T G
 ATAAGCT

GAM1130 CTGGAGATGTTGCCTTCTAT 1116 TAAGGAATTT 3841 -- T TTTGA T -- AA - GA -
 C
 TTGAGTGCTAAGGAATTTTA TACAAAGTTA GTT GCCT CTA GTGC AAGGAAT TTTACA
 GTTA AAG ATA CCT A
 CAAAGTTAAAGGAATACCTC AAGG ||| ||||| ||||| ||||| ||||| ||||| |||||
 AAAAGGTTATAACTTCTAAC CAA CGGA GAT CATG TTCCTTG AAGTGT CAAT TTC
 TAT GGA A
 AGTGTGAAACGTTCTTGTA AG - CG--- - CA GA C AA T A

CGCTAGAGGCGAAACGACTC
CGG

GAM1131 GGCCCAGAAGGTAACAGGGA 1117 TTGGTCAGAG 3842 G A G-- ----- AA TGGGAC
GT- A
CGGTGACCGAATGCGAGAAG CGCTGTGTAG ACA GG CG TGACCGAAT GCGAG GGACC
CTCTT TC A
GACCTGGGACCTCTTGTTCA ACCT ||| ||| ||||| |||| |||| |||| ||
ACCGATAAAAGAGATATTGG TGT TC GC ACTGGTTTA TGTTC CTTGG GAGAA
AG C
TTCAACTTGTGATGCCCAAT G - GAG ACCCGTAG AA TTATA- AAT C
TTGGTCAGAGCGCTGTGTAG
ACCTCGTAGCC

GAM1132 TCCTGTTTCCTCCTGCTGTA 1118 TGCTGTATTG 3843 TC- T -- T AG AGAA CAT
TTGATAGGTCAGAAGGAAGG ATAGGTCAGA TCCTGTT CTCC GCT GTA TGAT GTC
GGAAGG T
CATTTTACCTTCCGTGGACG AGGA ||||| ||| ||| ||| ||| ||| |||||
GTCATTACTTGGTGGAGAAT AGGACGG GAGG TGG CAT ACTG CAG CCTTCC /
GGCAGGA TAA - TT T G- GTG- ATT

GAM1133 ATGCGGGCCAGGTCAGCGGG 1119 TAACAGGCCC 3844 C --- G-- AC G- G G
TACGGCGGTGGTGCTGGACA GCCCACGGTG ATG GGGCC AGGTCA C GGGT GGC GT
GTGCT G
GCATAACAGGCCCGCCACG ATCT ||| |||| ||||| ||| ||| ||| ||| |||||
GTGATCTGACGGCCCCCAT TAC CCCG TCTAGT G CCCG CCG CA TACGA A
C CAG G CA C- GA A C

GAM1134 GCGTTAGCCATGATGGTTGC 1120 TCGCAAAC 3845 A - - C G G
CTGGGTCTTGGAAGAGAGCT CGTTGAGGT GCGTTAGCC TGATG GTT GC TGG TCTT G
GCGCAAAC 3845 GATG ||||| |||| ||| ||| ||| |||
ATGC CGTAGTTGG GTTGC CAA CG GTC AGAG A
A T A C G A

GAM1135 GCGGAGTCGGCAAAGAGCA 1121 TGAATGGGA 3846 AAA G CTGG G C -- ATGG
AAGAAA T TC
CTGGCGGGCGGCAGGCTGGA GACGAGGCCA GC GA CA CGG CGG AGG CTGG
GTCTCCCA CC TGGC G
TGGGTCTCCCAAAGAAACCT GAAC || ||| ||| ||| ||| ||||| |||||
TGGCTCGGGGCCATGGAATG CG CT GT GCC GCC TCC GACC CAGAGGGT GG
ACCG /
GGAGACGAGGCCAGAACCTC AAG - AGTA G - AA GGAG AA---- T GG
CGGCCGATGATGTGAAGCC
GAACAGCC

GAM1136 GCACCGCAAGCCACGTACAT 1122 TATGACGAAT 3847 - A---- -- A T A A
TGTAACCTCAAAAGAGGAATA GGCCGAGATG GCACC GCA GCCA CGT CAT GT CCTC A
TGACGAATGGCCGAGATGCT CTGG ||||| ||| ||| ||| ||| |||
GGTGC CGTGG CGT CCGT GCA GTA TA GGAG A
T AGAGC AA - - A A

GAM1137 GGCAACCTTGAAGTTCTGAC 1123 TGAGATCCGA 3848 CTT A - - AACT TG CTCAGACTATCTTGCAGCTTGTT TCAAGAACTC GGCAAC GA GTTCT GA CG ATCT CAGCTTGTTT A
TCTCAATTTTAAACGAGCTG GTTG ||||| || ||||| || ||| |||||
AGATCCGATCAAGAACTCGT CCGTTG CT CAAGA CT GC TAGA GTCGAGCAAA /
TGCC --- - A A C--- -- TTTT

GAM1138 GGTGAGCTCCCCAAGTTTTA 1124 TGAGCTCCCC 3849 ----- GTTTTACT T AAA
CTTCTCTAAACAAAAAGGAT AAGTTTTACT GGTGAGCT CCCCAA TC CT C
GCTCGGATTGGGGCACGAAG TCTC ||||| ||||| |||||
CTCACC CCACTCGA GGGGTT AG GA A
AGCAC AGGCTCGT - AAA

GAM1139 GAATCATCACCTGAGACGAA 1125 TCAGTGTTGT 3850 AGA- AA- ----- T G ----
AAAA- T
GACTGGTTGGTCGGTTATGG CGTCATAGGT CG GACTGGT TGG CG TTATGGCG
TACTGACTA TGG G
CGTACTGACTAAAAATGGTG GCCG || ||||| ||| ||||| ||||| |||
GCCAGATTGTAGTCAGTGTT GC CTGGCCG GCC GT GATACTGC GTGACTGAT
ACC /
GTCGTCATAGGTGCCGGGTT GTAC AGA CTTGG - G TGTT GTTAG G
CGCCGGTCAGACGCATGCAG
GTGAGTGGGC

GAM1140 GCTGGTTGTAGCTGCCGGCG 1126 TAGCTGCCGG 3851 TG G C - GTGATGG GGGGG
TGATGGCTTTTCGGGGGTGTA CGTGATGGCT GC GTT TAG TG CCGGC CTTTC T
ATGGAGAGACGAGCCGGTCA TTCG || ||| ||| ||||| |||||
CTTGGAATTGGT TG TAA GTT AC GGCCG GAGAG G
GT G C T AGCA--- GTAAT

GAM1141 GCTTGGGACGTTACCCAAGA 1127 CGGGATCCGA 3852 A --- AAGA - GTTGCTG
T GAA
GTGCTCGGGTTTGTGCTGT GACGCGAAGG GCTTGGG CGTT ACCC GTG CTCGGGTTT
TGCA GC C
GCATGCGAACGAAGCCTGCG GTTC ||||| |||| ||| ||||| ||||| |||||
GGATCCGAGACGCGAAGGGT TGAGCCC GCAG TGGG CGC GAGCCTAGG GCGT
CG /
TCGGACGGCCCGAGT G GCT AAG- A ----- C AAG

GAM1142 GAGGTTTTTCGATTGTCTAA 1128 TGGCTAGGTA 3853 TT G GT ATGG G
TGGCGAACGTCGGTTTGGCT GTAGGTGACC GAGGTT TC ATT CTA CGAAC T
AGGTAGTAGGTGACCTT TT ||||| ||||| ||| |||||
TTCCAG GG TGA GAT GTTTG C
T- A TG CG-- G

GAM1143 GCTTCGGTAGTTGCTGCGTC 1129 TTCGGTAGTT 3854 T G- G T AA
 TGTGTAATTGATGCCGATGA GCTGCGTCTG GCT CG TAGTTGCT CGTC GTGT T
 GCGACTGGACGAGC TGTA ||| || ||||| ||| |||
 CGA GC GTCAGCGA GTAG CGTA /
 - AG - C GT

GAM1144 GGACGATCGTGGCGAGCAGG 1130 TGGCGAGCAG 3855 TG CAG T CTA T -
 GAAAATG - ACC
 GTCTCTAGTTGTGGGGAGCT GGTCTCTAGT TCG GCGAG GG CT GTTG GGGG AGCTTGT
 TGCT CCAGC T
 TGTGAAAATGTGCTCCAGCA TGTG ||| |||| ||| ||| ||||| ||| |||||
 CCTCAGGCTGGAAGTAATGC AGT TGTTT CC GA TAAC CCCT TCGGACG ATGA
 GGTCG /
 AGGCTGTCCCCAATAAAAGC GT CTA - AAA - G TA----- A GAC
 CATCTTTGTTGTGATTTC

GAM1145 TGGTAGCAGTTGCCCCTAAT 1131 TTTCACATGG 3856 GG G -- - T TGCCC
 GGATATAGTGTGCCCGTTTA TGGGGGCAGA T TAGCA TTGCCCTA ATG GA ATAGTG G
 TTATTATTTACATGGTGGG TGCT | |||| ||||| ||| || |||||
 GGCAGATGCTGTTG G GTCGT GACGGGGGT TAC CT TATTAT /
 TT A GG A T TATTT

GAM1146 GTTAAATATTGTCCTTATAT 1132 AGGTATGAAA 3857 TAAAT CC A CTTC
 ATTCATCTTCTATTTTCGTGA ACAATTCATA GT ATTGT TTATAT TTCAT T
 AGGTATGAAAACAATTCATA C || |||| ||||| |||||
 C CA TAACA AGTATG AAGTG A
 TACT- AA G CTTT

GAM1147 TAGAAAATTTTAAAATATCG 1133 TACTATATCT 3858 AATTTT --- - CT-- T T
 TATAGCTTGTAGTTATCTTT TCTATAGCGA TAGAA AAAATA TCGT ATAG TGTAGT ATC T
 TGATACTATATCTTCTATAG ATGT |||| ||||| ||| ||| ||||| |||
 CGAATGTATTTTATATTCT ATCTT TTTTAT AGCG TATC ATATCA TAG T
 A ATAT-- GTA A TTCT - T

GAM1148 GACGTTGTTTCCAGGAGCC 1134 TTAAATGTGA 3859 TTTCCA CATAAACTGCTG A
 GT-- AA
 ATAAACTGCTGTGTGGTTAA TTCCAATGTC GTTCG GGAGC TGTGGTTA
 ATGTGATTCCAAT CC G
 ATGTGATTCCAATGTCCAAG CAAG |||| |||| ||||| ||||| ||||| |||
 CTGGTGTAGTTGGGGTCATA TAAGT CCTTG ATACCGGT TATACTGGGGTTG
 GG /
 TCTGGCCATAGTTCCATAAA TTA--- CTAAATACCTTG C ATGT TC
 TCGTTCCATTTGAATGTC

GAM1149 GGTCGTTTAAATTGATACTC 1135 TCGTTTAAAT 3860 ATT-- TA T T C- GA TT

TGTGTCGGCTGGACTTTGAG	TGATACTCTG	GGTCGTTTAA	GA CTC GTG CGG TG C T
AACAAACCGCACGAGATTCT	TGTC		
AAAATTAACGATC	CTAGCAAATT	CT GAG CAC GCC AC G /	
	AAAAT TA - - AA AA AG		

GAM1150 TCGTTCAATAGATCTGGCAA 1136	GTTGTTGTGG 3861	C A G TTTTC AT
CAATTTTTCCTATTAAATCT	AATTGTTAAC	TCGTT AATAG TCTG CAACAA CTATTAA C
CTTGATAGTTGTTGTGGAAT	GG	
TGTTAACGG	GGCAA TTGTT AGGT GTTGTT	GATAGTT /
	- A - ----- CT	

GAM1151 ATAAAAATATTTTTACGACT 1137	TGAGACCATT 3862	CGA CA-- AGAAA - A T
CCATCAGAAAGAGGTTTAAT	GAAGAGAGAA	ATAAAAAATATTTTTC CTC TC GAGGTTT ATA
T		
ATTTTTGTGAGACCATTGAA	AGAG	
GAGAGAAAGAGAATAAAAAAT		TGTTTTTATAAAAAAT GAG AG TT CCAGA TGT T
ATTTTTGT		AA- AAAG AGAAG A G T

GAM1152 ATGGTTCATGCGGTGTTATA 1138	AGCAGCAATA 3863	T- CG A- C A AT
TCGCTGTTTATTATGATTAT	GCAATATATA	ATGG TCATG GTGTT TAT GCTGTTT TTATG T
ACATGAAAGCAGCAATAGCA	TGAC	
ATATATATGACTTCAT		TACT AGTAT TATAA ATA CGACGAA AGTAC A
	TC A- CG A - AT	

GAM1153 TTTGTGGTGTGCCTGAATCG 1139	TGAATAGGGT 3864	C-- CTCGAT C CAA
CTCGATTAACCCTACTCATC	TATCGATTCA	TTTGTGGTGTG CTGAATCG TAACCCTA
TCATC T		
CAATTTTCAGATGAATAGGGT	GACA	
TATCGATTTCAGACACACGCT		GAATATCGCAC GACTTAGC ATTGGGAT AGTAG T
ATAAG	ACA T----- A ACT	

GAM1154 TTTTCTTAGTACAAAAGTC 1140	TAAAACTTG 3865	A- G- AT--- AAAA G
AATGTTTTAAAATATATGGA	TGTGAAATTT	TTTTTCTT GTACAAA TCA GTTTT
TATATGGACAA A		
CAAGAATTTGTCTGTATAAA	TGTA	
AACTTGTGTGAAATTTTGTA		AAAAAGAA CATGTTTT AGT CAAAA ATATGTCTGTT A
CCAAAGAAAAA	AC AA GTGTT ---- T	

GAM1155 GAGATGGTTTTGATCCAAGG 1141	TTGGATCTAA 3866	---- TT G G
TTGATTAATGTTGGATCTAA	CTGTAGTACT	GAG ATGGTT GATCCA GTT A
CTGTAGTACTC	C	
	CTC TGTCAA CTAGGTT TAA T	
	ATGA T- G T	

GAM1156 GCAAAACAATATTGACCGTT 1142 TATCCAGAGA 3867 AACA A - TCGAT
TCGA TTC
ATAAATGTCTTTGTGCGATGA TATCTTGTA GCAA ATATTG CCGTTATAA ATGTCTTTG
GATATAT CGC C
TATATTCGACGCTTCCAATT TGGC ||| |||| |||| |||| |||| ||||
GTGATATATCCAGAGATATC TGTT TATAGC GGTAAATGTT TATAGAGAC CTATATA
GTG A
TTGTAATGGCGATATCTTGT C--- - C ---- - TTA

GAM1157 TTGGAAATCCTGTTTCAAAG 1143 TGATATACTC 3868 TCCT- CAA AC T CTTT
TAAC TTATATCATCTTTATA ACAAATTTTC TTGGAAA GTTT AGTA TTA ATCAT A
ATATGATCTGATATACTCAC TTTT ||||| ||| ||| ||| ||||
AAATTTTCTTTTCCAA AACCTTT TAAA TCAT AGT TAGTA /
TCTTT CAC AT C TAAT

GAM1158 TATTATCATTACATGTATTA 1144 TATGATACAC 3869 - ATTACA A AAAACT
CACTTACA
ATATCAAAAACTGAGAACA CAAAGGATTA TATTA TC TGTATTA TATCAA GAGAA A
CTTACAATTACTTTTATTCT ATA ||||| ||||| ||||| ||||
TTTCATTGATATGATACACC ATAAT AG ACATAGT ATAGTT TTCTT T
AAAGGATTAATA T GAAACC - ACTT-- ATTTTCAT

GAM1159 GATATCCTAGCATTGTGAAG 1145 TATCCTAGCA 3870 T- - GTGAAGTAGAA TAT
ATC
TAGAACATTAAATGTATTGG TTGTGAAGTA GA ATCCTAG CATT CATTAAATG TGGGG
A
GGATCAGATTCCTACCATTT GAAC || ||||| ||||| ||||| ||||
AGTGGATGCCTGGGATCTTC CT TAGGGTC GTAG GTGATTTAC ATCCT /
TC C ----- C-- TAG

GAM1160 GCTTCGTATGCATTGAATTA 1146 TGCCATGAAT 3871 CG - TTA AATCG- A CCAAAG
CCAATCGCATGAGCAGCCCA TACGGCTTCG GCTT TATG CATTGAA CC CATG GCAGC
T
AAGTTACGTTGCTGCCATG ATGA ||| ||| ||||| || ||| |||||
AATTACGGCTTCGATGATAT CGAA ATAT GTAGCTT GG GTAC CGTCG T
AGAAAGC AG A C-- CATTAA - CTTGCA

GAM1161 GGCCATGGTGCAATGCACCA 1147 GTGCAATGCA 3872 CAT A- - A TC
TCGAACGTTCTCATGCGTCT CCATCGAACG GGC GGTGCA TGCA CCATCG ACGT T
GGTGGATGCAGATGCGCCGC TTCT ||| ||||| ||| ||||| ||||
C CCG CCGCGT ACGT GGTGGT TGCG C
--- AG A C TA

GAM1162 AACTGTAGTGCTCAAATACT 1148 TGTAGTGCTC 3873 - CTCAAA C - - AC
 CATCAGATTTTTTACCGGAA AAATACTCAT AACTGTA GTG TACT AT CAGATT TTTT C
 AAGTAATTTGCATTAGTGCC CAGA ||||| || ||| ||||| ||||
 TCCATGTACAGTT TTGACAT TAC GTGA TA GTTTAA GAAA G
 G CTCC-- T C T AG

GAM1163 CCGTTATAAATGTCTTTGTA 1149 TATCCAGAGA 3874 - TAGAT - GCT
 GATGATATATTCGATGCTTC TATCTTGTA CCGTTATAA ATGTCTTTG GATATATT CGAT T
 CAATTGTGATATATCCAGAG TGG ||||| ||||| ||||| ||||
 ATATCTTGTAATGG GGTAAATGTT TATAGAGAC CTATATAG GTTA /
 C ---- T ACC

GAM1164 GGAAATCCTGTTTCAAAGTA 1150 TGATATACTC 3875 TCCT- CAA AC T CTTT
 ACTTATATCATCTTTATAAT ACAAATTTTC GGAAA GTTT AGTA TTA ATCAT A
 ATGATCTGATATACTCACAA TTTT |||| ||| ||| |||||
 ATTTTCTTTTCC CCTTT TAAA TCAT AGT TAGTA /
 TCTTT CAC AT C TAAT

GAM1165 GGAACGTCTGATGAACAAAA 1151 TGAAATCTTT 3876 ACG--- G ACAA A TG CTT
 GTA TG
 GTAAAGATATTGACTTGGAT ACTTGATCAG GGA TCTGAT A AGTAAAGAT T A GGATG
 TTTTC A
 GGTATTTTCTGACAGAAAAAC GATA ||| ||||| ||||| ||| ||||| ||||
 ATCTTTGAAATCTTTACTTG CCT GGA CTA T TCATTTCTA A T TCTAC AAAAG /
 ATCAGGATAAAATCC AAAATA G ---- A GT --- --- AC

GAM1166 ACGGGATTGCTTAGCATCA 1152 TGAGATCTTT 3877 T CATCACC-- CGA- CTTTT
 CCAAAGACGAAGGCTTTTTT AACGCAAAAT ACGGGATT GCTTAG AAAGA AGG T
 ACAACCTGAGATCTTTAACG TAAG ||||| ||||| ||||| |||
 CAAATTAAGTAATCCCGT TGCCCTAA TGAATT TTTCT TCC /
 - AAAACGCAA AGAG AACAT

GAM1167 GTCATATGAAAGGAAGATTA 1153 TGGCAACAAT 3878 A AAG- TTA - C CA T ---- C
 GCC
 TGCGAGTGGTATCGTCACTT AACCACTTGC TATGA GAAGA TGCGAGTGGT AT GT CT GCC
 AGAA CACG C
 GCCAGAACCACGGCCCATGC ACTT |||| |||| ||||| ||| ||||| |||||
 GTGCTTCTTCTCGGCTGGCA ATACT CTTTT ACGTTCACCA TA CA GG CGG TCTT
 GTGC /
 ACAATAACCACTTGCACTTT C GACG C-- A A AC T CTCT C GTA
 TCGCAGTCATACAAC

GAM1168 GAGGTGTAACTTTTGCAGAA 1154 TACAATCTTA 3879 --- A C A ----- C A T
 TATCTTACGATAGTAACATT AGTTTCTTTA GAGG TGTA CTTTTG AGA TAT CTTA GAT
 GTAACAT A

AAGATGTTACAATCTTAAGT	TACT						
TTCTTTATACTTTTCAGAAAGA		CTCC	ATAT	GAAGAC	TTT	ATA	GAAT CTA CATTGTA A
TATATTCCCTC		CTT	A	-	C	TTTCTTT	T A G

GAM1169 GTGATCAGGACAGACAGGAG 1155	TGGCAATCAC 3880	G	-	AC-----	CA CAG CG
GT C					
GTCAGTCAGGACGGCCGGGG	CAGCCTCCTC	GT	ATCAGGAC	AG	AGGAGGT GT GA
GCCGGGGC CC T					
CGTCCCTGCGGGCCCTGGCA	CCCC				
ATCACCAGCCTCCTCCCCCT		CA	TAGTCCTG	TC	TCCTCCG CA CT CGGTCCCG
GG G					
GCTGGTCCTGATGAC	G	G	GTCCCCC	AC ---	AA -- C

GAM1170 GATGAGTAACCAGTAATAAC 1156	TGAGTAACCA 3881	-	ACCA	C CA-	TTAA
TTCATGAATTAAATCAGTTT	GTAATAACTT	GATG	AGTA	GTAATAA	TT TGAA A
CAAATAATTTATTACACAAT	CATG				
ACTGTATC	CTAT	TCAT	CATTATT	AA	ACTT T
	G	AACA	T	TAA	TGAC

GAM1171 AAATCCTAGCAAGAATATCA 1157	TGGAAACATC 3882	A A	CA---	C AAC	C
AGCATCTC CC G					
TCTAGACCTAAACGTTCCCA	TAGCTCTAGA	CA	GA	TAT	TCTAGA CTA GTT CCAAATA
CACAG TGAT A					
AATAAGCATCTCCACAGCCT	ATCT				
GATGAAAATCATTCTGTGAT		GT	CT	ATA	AGATCT GAT CAA GGTTTAT GTGTC
ACTA A					
TTATCATATTTGGAAACATC		C C	CTCTA	C	CTA A ACTATTTA TT A
TAGCTCTAGAAATCTCATACT					
CCTGCTTATT					

GAM1172 AGAAGTAGAGTAAGACATCT 1158	TAAGACATCT 3883	-	A A ---	GATTAT	ACT TCA
TGATTATGAACTTAGTGGCT	TGATTATGAA	AGAAGTA	GAGT	AG CA	TCTT GA TAGTGGC
G					
CAGAAGCGCCGCTATCCGAA	CTTA				
AAAGATTCTGCCTCACTCTT		TTTTCAT	CTCA	TC GT	AGAA CT ATCGCCG A
ACTTTT	T	C C	CTT	AAAGC-	--- CGA

GAM1173 CTCTTAGACCCTTCTTTAAA 1159	ACACCAGAAA 3884	--	AAAA--	AA---	G CCAC -
CAA- AGAG					
ATAGAATTGGTGGTAGCCAC	TCCTAACAAA	T	TCTTT	TAG	TTGGTG TAG CAAAGA GG
TCTCC T					
CAAAGAGGCAATCTCCAGAG	CAAA				
TTAACGGAGAAAAACCATCT		A	AGAAA	ATC	GACCAC ATC GTTTCT CC AGAGG
/					
TTGATCCTAACACCAGAAAT	CC	CAAACA	CTAAA	A	CTA- A AAAA CAAT
CCTAACAAACAAAGACCAGG					
GTTTGGAG					

GAM1174 ACTCTGTAGATTAGCTGTAG 1160 TAGCTTATAG 3885 T A--- TAG-- TA- C A--- G-
C

CTTATAGCTCTCACTGTATG CTCTCACTGT ACTC GTAG TTAGCTG CTTA GCT TC
CTGTATG AC T
GACCTTGTAGTATACAGAAT ATGG ||||| ||||| ||| ||| ||||| ||
AGAAAGTGCTTGAGAATTTCTGAG CATC AGTCGAC GAGT TGA AG GACATAT
TG /
AGCTGACACACTACGAGT - ACAC TTAA TCG A ATAA GA T

GAM1175 ATAGAATGTGTAGGTCCTGA 1161 TCGTAAGGGC 3886 ----- GTA- G A TG- ----- G
AAG

TGAGAATGGTGCTTGGTGTA CACTAACATC AGA ATGT GGTCTATGAGA TGG CTT
GGT TAC T
CAAGTTAGAGTAGACCTACC CAAC ||| ||| ||||| ||||| ||| ||| ||| |||
ATGAAAAGACTCCATCTCGT TCT TACA CCGGGA TGCTCT ACC GAA CCA ATG
T
AAGGGCCACTAACATCCAAC CAACC ATCA A - TCA AAGTACCAT G AGA
TCTAT

GAM1176 TCTCTGGATAGTTCTGCATA 1162 AACTTGCAGC 3887 T A TT TAAGC AT
AGCAGTTTAATAAGTAAACT TCTGACCTGA TCTC GG TAG CTGCA AGTTTA A
TGCAGCTCTGACCTGAGA GA ||||| ||| ||||| |||||
AGAG CC GTC GACGT TCAAAT /
T A TC ----- GA

GAM1177 AGTTTCTCCCAAATGAAGTA 1163 GAGCTTCCAT 3888 C A GAAGT A A-- A TTC -----
TTG TA

CTCAACAGCACAAATGGAATT TGGCACCGTC CA AT ACTC AC GC CAATGGAA GTTCTGG
GAT TCA C
CGTTCTGGGATTTGTCATAC GAGT ||| ||||| || ||||| ||||| ||| |||
TTTGAAATGTCTAACACTAG GT TA TGAG TG CG GTTACCTT CGAGATC CTG
AGT /
AGCTTCCATTGGCACCGTCG A C AACC- C CCA - --- ACAAT TAA TT
AGTCCAAATCTGAGAGAAAC
T

GAM1178 GGATAATTTTAAAGGTGAAT 1164 AGATGTATGA 3889 T A----- CT CAA T CA
TT

CTCTTCTTGCAAGCAGATGT TAAGAGCCAA TAAAGGTG ATCT TCTTG GCAGATGTATGA
AAGAGC AGTG G
ATGATAAGAGCCAAGTGTTG GTGT ||||| ||| ||||| ||||| ||||| ||||| |||||
CTTCATTAGCTCTTTTCATG GTTCCAC TAGA AGAAC TGTTTGCCTACT TTCTCG
TTAC C
CGTTTGTCTACAAGACAGAT C CACACTCA C- ATC T A- TT
ACTCACACCACCTTTGCAAT
TGTCC

GAM1179 GGTCTGTAATAGTGTAAGAC 1165 AATAGTGTA 3890 CT A A AC AATAC TCA C
A

ATATTCAATACGATTCAGAT GACATATTCA GGT GTAAT GTGT AG ATATTC GAT GATTGTG
GTC A

TGTGCGTCAAATGACTCACA	ATAC		
ATCATCATCAATACGAATAT		CCA CATTACACA TC TATAAG	CTA CTAACAC CAG A
CACTAACACCATTACCAACC		AC C A AC	CATAA CTA T T

GAM1180 GTGATAACCTCCTAACCTCC 1166	TAAAGGGAAT 3891	ACCTCC CC ACGA	A T CA
G TT GG			
CTACGATGTAAACAAGTGTG	TTGTTTCAGTA	GTGATA	TAA TCCCT TGTAACA G GTGGC
AAAT T C A			
GCCAAAATGTTTCGGATAAG	TCAC		
GGAAATTTGCCACTCTGTTT		CACTAT	GTT AGGGA ATATTTGT C CACCG TTTA A G
T			
ATAAAGGGAATTTGTTTCAGT		GACTT- TA A---	- T -- A GG AA
ATCAC			

GAM1181 TTATAATTTTATCAACCTTT 1167	TTCAAAGGCT 3892	AAT A --- G	ACTTGA CGT
GGAATACGTACCGACTTGAC	GATAAATTAA	TTAT TTTATCA CCTTTGGAA	TAC TACCG
CAGC T			
AGCCGTAAAGCTGACGGTA	TAA		
GTAGTTTTTCAAAGGCTGAT		AATA AAATAGT GGAACTTT	ATG ATGGC GTCG /
AAATTAATAA	ATT C	TTG - A----	AAA

GAM1182 AAGAAGGAGACCACGTTGAG 1168	TGACCAGCTG 3893	-- -- C A C T GC
TCCGTTTGCGCAGCGGCTGA	GTTGCTCCCA	AAGAA GGAG ACCA GTTG GTC GTT GC A
TGACCAGCTGGTTGCTCCCA	TTCT	
TTCTT	TTCTT CCTC	TGGT CGAC CAG TAG CG G
	AC GT - - - T GC	

GAM1183 CGTTGTCAAAGCAGTAATTA 1169	TCAAAGCAGT 3894	- A- AG ATTA TC
ACTATTTCTAGTGATAGTGG	AATTAECTAT	CGT TGTCAGC TA ACTATT T
AGTGAGGTTGGTGGCAGACG	TTCT	
	GCA ACGGT TTG GT	TGATAG A
	G GG GA GAGG	TG

GAM1184 GAGGCCAATGGTTGCTTTGG 1170	TCGCGAGTTG 3895	ATGGTT- TG A- TTT
GGCAGAGCGGTTTGAGTCCG	GAAGATGGCT	GAGGCCA GCTT GGGCAG GCGG G
TGCCTGCTCGCGAGTTGGAA	TC	
GATGGCTTC	CTTCGGT	TGAG CTCGTC TGCC /
	AGAAGGT CG CG	TGA

GAM1185 TCTCCATCAGTCAAAAGTTG 1171	TGAGAAAACA 3896	- AAA-- TT - AA C - C----- C
TGA		
AGAAAACACGGCCTCCACCT	CGGCCTCCAC	TCCA TCAGTC AG GAG AA CA GGCCT CCA
CTG TTTGA T		
GCTTTGATGATCTTTCGAAC	CTGC	
GGTTAATTTGGTGGGCCATG		AGGT AGTTAG TC TTC TT GT CCGGG GGT GGC
AAGCT /		

GATTGCTTTCTGAGAAGATT
GAGTGGAGA

G AAGAG T- G AG A T TTAATT - TTC

GAM1186 CGGTGATAGGTTTTTCTCCC 1172 TAGGTTTTTC 3897 G TTTCT ATA A T
ACCATAAGCACCAGTTTTTG TCCCACCATA CGGT ATAGGTT CCCACC AGC CCAG T
GCGCTGGGTGGGTAGCTTGT AGCA ||||| ||||| ||||| |||||
AGCTG GTCG TGTTCTGA GGGTGG TCG GGTT /
A T---- G-- C T

GAM1187 GCTCTTGGGCTAACGGCGGC 1173 GCAGTGCCGG 3898 - TAA G G AGAC TA
TGGTT A TGT
GGCTGCTTAGACTTACCGGC CGGCGCCTGA GCTCTT GGGC CG CGGCG CTGCTT T
CCGGCCC CC GTGG C
CCTGGTTCCAGTGGTGTCCC GGAG ||||| ||||| ||||| ||||| ||||| |||||
ATCTACGGTTGGGTCTGGCGA CGAGGA TCCG GC GCCGT GACGGA A GGCTGGG
GG CATC C
ACAGGCAGTGCCGGCGGCGC G CG- G - CA-- GC TT--- - TAC
CTGAGGAGC

GAM1188 GGATCGCCTGACGGGGCGTA 1174 TGAAATGTCC 3899 A-- - T AAAT AGA C
AATGAAGAGCGGCCAGCGCC CGTCCGGACG GG TCG CC GACGGGGCGT GA GCGGC A
GCCGATCTGAAATGTCCCGT GAGA || ||||| ||||| ||||| |||||
CCGGACGGAGACC CC GGC GG CTGCCCTGTA CT CGCCG G
AGA A C AAGT AGC C

GAM1189 AATTCACCGTTGCTGTTAGC 1175 AAGCTGCAGG 3900 A G - AATG- - T AA G
TTCA
CAATGGTATTTCTTCAAGCG GGGGTTGGGC AATTC CCGTT CTGTT AGCC GTA TTTC TC GC
GCTCATC A
GCTCATCTTCAACAGTTGGT GGGG ||||| ||||| ||||| ||||| ||||| ||||| |||||
GAGTGGTACGGTGAAGCTGC TTGGG GGCGG GGCGG TTGG CGT GAAG GG TG
TGAGTGG C
AGGGGGGTTGGGCGGGGGCG - G G GGGGA C T CA G TTGA
GGGGTT

GAM1190 ATGCTACTAATAGGCAGTCA 1176 AGGCAGTCAT 3901 AAT A- T- - AT- G
ATCCTTCT A
TTGCGGGTGGGATATGGTGG TGCGGGTGGG ACT AGGCAGTC TTGCGGG GG GAT G
TGGGGGAGT TTGC A
GGGAGTATCCTTCTTTGCAA ATAT ||||| ||||| ||||| ||||| ||||| |||||
GTGCGGCCGCGTAGACTTCT TGG TCTGTTAG GACGTCC CC CTA T ACTTCTTCA
GGCG G
TCAGTGAGATCGCCTTCCTG CCT GG TT G GAG G GATGCGCC T
CAGGGGATTGTCTTCCGGTA
CAGTGT

GAM1191 CATGAGGAGGGTTTCAAAGT 1177 TGTGATCCCA 3902 CAA TTGACAAA A - C AGCG
AGTGT - A
TGACAAAAGTTGCATCCTGC GTGGGCAGCT TTT AG AGTTGC TC CTG GA TCATACGC
AGTCG CC T

GAAGCGTCATACGCAGTGTA ACGA ||| || ||||| ||||| ||||| ||||| |||||
 GTCGCCATCGGTTCGATTCCC AAA TC TCGACG GG GAC CT AGTGTGTG
 TTAGC GG /
 GTGTGTGATCCCAGTGGGCA AC- TTAAAGCA - T C --- CCC-- T C
 GCTACGAATTTCTCAAAATC
 TTCATTGGTG

GAM1192 GTGATAGTTTATACCATTCA 1178 TAGTTTATAC 3903 AG- T - ATATA TT CT
 ATATAATCGCTTCATCCTTT CATTCAATAT GTGAT TTTA AC CATTCA ATCGC CATC T
 AGATGGTGTATCCTGAATGCG AATC |||| |||| ||||| ||||| |||||
 TTTAAAAAATTAT TATTA AAAT TG GTAAGT TAGTG GTAG /
 AAA T C CC--- -- AT

GAM1193 TAGCTTTCATAGTTAGATAC 1179 TTAGATACAT 3904 ----- GTCTCA- --- T A CT
 AT
 ATGGTCTCAGAAGTAGGATT GGTCTCAGAA AGTTAG ATACATG GAA GTAGGATTA
 GTAAC TCAG TCG A
 ATGTAACATCAGCTTCGATA GTAG ||||| ||||| ||| ||||| ||||| ||||| |||||
 AAATGACTGGGTTATTTAGT TCAATT TATGTAC CTT CATTCTGAT TATTG GGTC
 AGT A
 CTTACACATTCGCTCATACA GCCAG ATACTCG ACA T - -- AA
 TGTATGACCGTAACTACAG
 AGTCTA

GAM1194 TCGTAAGATACTCCTTCATG 1180 TATGAAGTAA 3905 A C-- GAAC TCA A
 AACATAATCAGTTACAAAAC AGTATCTACG TCGTA GATACT CTTCAT ATAA GTT C
 GTTTATATGAAGTAAAGTAT A ||||| ||||| ||||| ||||| |||||
 CTACGA AGCAT CTATGA GAAGTA TATT CAA A
 - AAT ---- TG- A

GAM1195 GCCGCCTGAGAGCCTGGACG 1181 TGGCAGCTCG 3906 - A CC A T - A- - AG
 TGCTCCAGAAGGTCGCGGTA CCGTTTCCTA GCC GCCTG GAG TGG CG GCT CCAGA GGT
 CGCGGT A
 GATAGCCGTGCACTCCTCTG GGTA ||| ||||| ||| ||| ||||| ||| |||||
 GCAGCTCGCCGTTTCCTAGG CGG TGGAT CTT GCC GC CGA GGTCT TCA GTGCCG /
 TAGGC A C T- - T C CC C AT

GAM1196 TGAGCAGGTTTGGTATCAGC 1182 TTTGGTATCA 3907 GG--- G C AGCA- A
 GAGAGCAGCACAAGCGATCC GCGAGAGCAG TGAGCA TTTG TAT AGCGAG GC C
 CTCGTTTCATGGCAAAAATCA CACA ||||| ||||| ||||| |||||
 TGTTTA ATTTGT AAAC GTA TTGCTC CG A
 ACTAA G C CCTAG A

GAM1197 TGGTGAGGTACAATCGGGTT 1183 TGAGGTACAA 3908 GAG T TTTCT TG TCT
 TCTCTTGTCTCTCCTCGAA TCGGGTTTCT TGGT GTACAA CGGG CT TTC C
 TGGGCCTGTTGTGCACCA CTTG ||||| ||||| ||||| |||||
 ACCA CGTGTT GTCC GG AAG /
 --- - ----- GT CTC

GAM1198 TGTCTGAACGAGCGGGTATA 1184 TACAGCAGTT 3909 AACGA-- - TAC G C AC
 CGCGGTCGTACCGTACTCCC ACCGCGCGAG TGTCTG GCG GGTA GC GT GTACCGT T
 ATGGTACAGCAGTTACCGCG AATG ||||| ||| ||| ||| |||||
 CGAGAATGCAGGCA ACGGAC CGC CCAT TG CG CATGGTA C
 GTAAGAG G --- A A CC

GAM1199 GGAAGTAGTCACCCTGACCT 1185 TACCACGTAG 3910 A- T CC TG C ---- AAA C CA
 GTTTGTGGAAAGCCTGCCCA TGCCAGATTG GG AGTAG CA C A CTGGT TGTGG GC TGCC
 A
 AGAAGGCATGTACCACGTAG GTTT || ||||| || | ||||| ||||| || |||||
 TGCCAGATTGGTTTGCTGCT CC TCGTC GT G T GACCG GCACC TG ACGG G
 AGCC GA - TT GT A TGAT A-- T AA

GAM1200 TATTGGTAGTCATAATAAGT 1186 GTCACAGTTT 3911 A TAATAA CA T G
 GACCCATCATCCGGAGACGG GACCACCAGT TATTGGT GTCA GTGACC TCA CCG A
 TTGAATGGTCACAGTTTGAC A ||||| ||||| ||||| |||||
 CACCAGTA ATGACCA CAGT CACTGG AGT GGC G
 C TTGA-- TA T A

GAM1201 TCTCAAGTGCAGTAGCTGCA 1187 TCAAGTGCAG 3912 T C A C- C - C ATT
 ACTTTGGACATTTGGAGATT TAGCTGCAAC TC CAAGTG AGT GCTG AA TTTG GA ATTTGGAG
 G
 GGTAAGTCCAAATTTTGCGA TTTG || ||||| ||| ||||| || ||||| ||||| |||||
 GATTTCCAGTAACTCGCTTG AG GTTCGC TCA TGAC TT GAGC TT TAAACCTC G
 TGA T - A CT A G T AAT

GAM1202 TTCTCCAAGTGTTGGTAACC 1188 TGGGTTGCCT 3913 TT-- - AAC A C T ACT AACAA
 T G T
 AAAGTCAAAAGCAGTCAACC TTCTTGACAT GGTAAC CA TCAA AG AG CAACC CATT
 GGT GTT TCAAC G
 ACTCATTAACAAGGTTGTTG GAGT ||||| || ||||| || ||||| ||||| ||||| |||||
 TCAACTGTTGTTGAAAATTG CCATTG GT AGTT TT TC GTTGG GTAG CCG TAA
 AGTTG T
 CCCAGATGGGTTGCCTTTCT CTCT A AC- C - C --- AC--- T A T
 TGACATGAGTTACCTCTCCA
 GTTGGAAGAA

GAM1203 CGGCGGGGTCGTGCTGGAGT 1189 TGGCACACGT 3914 G - AGT-- CGAA C
 TGG GA G
 TGTGTGCCATCGAAACCGTG GGAATTAGCA CGGCG GGTCG TGCTGG TGTGTGCCAT
 ACCGTGG TC AG GGG C
 GCTCTGGAGGAGGGGACCCC GTGG ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 AACTGACCCATGGTATGGCA GCTGC CCGGT ACGATT GCACACGGTA TGGTACC AG
 TC CCC /
 CACGTGGAATTAGCAGTGGC A G AAGGT ---- C --- AA A

CACGTCG

GAM1204 GCAGAGGCGTCCTGGAGGCC 1190 TGAGGTGGTG 3915 G T A--- T- G T ----- -
AAATT--- TT
TTGAGGTGGTGGGAGGCGAA GGAGGCGAAA GCGTCC GG GGCC TGAG TGG GGG AG
GCG GAC T
ATTGACTTTAAGTCTACCTT TTGA ||||| || ||||| ||||| ||||| |||||
GGCGCTCTGAATAAACCCCC TGCAGG TC CCGG GTTC ACC CCC TC CGC
CTG /
AGCTTGTTGGCCAAAGCTTG - T GAAA TT G - AAATAAG T GGTTCAT AA
GACGTTGC

GAM1205 TGGGTAAGCAACTTGCCAGT 1191 TGAGCTGGCT 3916 G AG TT - AA A
TCTACAATTTTTGATGTCGG CGTTGGTGGT TGG TA CAAC GCCAGTTC TAC TTTTGT
AGGCGTATGAGCTGGCTCGT CA ||| || ||||| ||||| |||||
TGGTGGTCA ACT GT GTTG CGGTCGAG ATG GGAGGC G
G G- CT T C- T

GAM1206 ACGGTCTTGACGTACATGAA 1192 TGACGTACAT 3917 C G T ATA T A C T
TAGTTGCATGACCAGGGTTT GAATAGTTGC ACGGT TTGAC TACA GA GT GC TGA CAGGG T
TCTTGATCGGCACTCTGTGG ATGA ||||| ||||| ||||| ||||| |||||
TTAAACTGT TGTCA AATTG GTGT CT CA CG GCT GTTCT /
- - - --- - - A T

GAM1207 GAACCACTGGGTCATCGGTT 1193 TGAGCTGTAT 3918 C T--- TCAT--- TG A ATTAGA
TGGACACAATTAGAGTATCC AACTCCCTTT GAA CAC GGG CGGTT GAC CA G
ATGGTCTGAGCTGTATAACT CGTG ||||| ||||| ||||| |||||
CCCTTTCGTGTTTC CTT GTG CCC GTCGA CTG GT /
T CTTT TCAATAT GT - ACCTAT

GAM1208 TGGTCGATTCTGTATGGACA 1194 TACCTGCTGG 3919 AT- G TA- ----- TT TG
T A
GGGGTACCTGCTGGCCTCTT CCTCTTTGAG CTGT GGACAG GG CCTGCTG GCCTCT
GAGT T CT G
TGAGTTGTTCTAGCAAGTGT TTGT ||||| ||||| ||||| ||||| |||||
GGCTCCGGGAGGCGTCCTTC GGTA CCTGTT TT GGACGGT CGGAGG CTCG
G GA C
ATACTTTGGCAGGGATTGT GTT G TAG TTCATACTTCCTG GC GT T A
TGTCTTGATGGGAAAGATT
A

GAM1209 TTAAAGTCTCCCTAATCAGT 1195 TGGCTGGTGG 3920 - A- T- G G C
TTAGCAGTTGATGGGCAAG TTTTGATGAA TTAAAGTCTCC CT ATCAG TTA CAGTT ATGGGC
A
CCTATGGCTGGTGGTTTTGA GTGG ||||| ||||| ||||| ||||| |||||
TGAAGTGGGGGCTTTGA AGTTTCGGGGG GA TAGTT GGT GTCGG TATCCG /
T AG TT G - A

GAM1210 ATATTGACCGTTATAAATGT 1196 TATCCAGAGA 3921 A - TCGAT TCGA TTC
 CTTTGTGCGATGATATATTCG TATCTTGTA AATTG CCGTTATAA ATGTCTTTG GATATAT
 CGC C
 ACGCTTCCAATTGTGATATA TGGC ||||| ||||| ||||| ||||| |||
 TCCAGAGATATCTTGTAATG TATAGC GGTAATGTT TATAGAGAC CTATATA GTG A
 GCGATAT - C ---- - TTA

GAM1211 GAAGAGGTTGGAATATCAAC 1197 AGAGGTTGGA 3922 T A A T---- GAAAGAAAA
 AGT AC
 TAGTTGCTGAGAAAGAAAA ATATCAACTA GAAGAGGT GGA TATC ACTAG TGCTGA
 AGTTA TCT A
 GTTAAGTTCTACAAAAGATA GTTG ||||| || ||| ||||| ||||| ||||| |||
 ACTAGAACGTGATCGGTATC CTTCTCCA TCT ATAG TGATC ATGGCT TCAAT
 AGA /
 TTTCTAGTAGATATCTTACC T - A TTTCT AGTGCAAGA --- AA
 TCTTC

GAM1212 TAATTTCTATAGTTTGTAAT 1198 TCTATAGTTT 3923 -- T- AATA C
 ATGGAGCTTTTTCCACGCGT GTAATATGGA TAATT TCTATAGT TGT TGGAG T
 TACTATAGAGTGATTA GCTT |||| ||||| || ||||
 ATTAG AGATATCA GCG ACCTT T
 TG TT C--- T

GAM1213 TCTCCGTTAAAGTGATAAGC 1199 TAAAGTGATA 3924 -- AA- TAAGCAAACC TCA
 AAACCTATTGTGCTCAGCAT AGCAAACCTA TCTC CGTT AGTGA TATTGTGC G
 GCATAGTATCCCAACTCTTA TTGT ||| ||| |||| |||||
 CTGTAAACGTTGAGG GGAG GCAA TCATT ATGATACG /
 TT ATG CTCAACCCT- TAC

GAM1214 GGAAAACGTAAAGGTGGGCC 1200 AAAGGTGGGC 3925 AA AA GC --- CT-- A C AG
 CGGTCAGCTGGACGTCCGAG CCGGTCAGCT GGA ACGT AGGTGG CCGG TCAG GG
 CGTC G T
 TCTCCGATGCCTAACCTGAT GGAC || ||| ||||| ||| ||| |||||
 ACCTGGATCTACCTATGTT CCT TGTA TCCATC GGTC AGTC CC GTAG C /
 C -- -- TA CAT CAAT - CTC

GAM1215 GGTCCAAGTCCCGGGTCTTG 1201 TGGAGTGGTG 3926 ----- GGT G GTAT GT
 GGAGGGATGTATTTGGGTGG ACTTTCTGTG GGTCCA AGTC CCG CTT GGAGGGAT TTGG
 G
 AGCCAAGAGTCTCTCTGGAG GACT |||| ||| ||| ||||| ||||
 TGGTGACTTTCTGTGGACT TCAGGT TCAG GGT GAG TCTCTCTG AACC G
 GTCTT T --- G AG-- GA

GAM1216 GTCCATGTTGATCAGGTCAT 1202 TCTGATCAAA 3927 G----- --- GG T TT AA

CGGCCGTGGGTTCAAAGTCA ACTCAGTGGA GTCCAT TTGATCAGGT CATC CCG GGG CA
 G
 TGGTTCCCGGGGATGCTCAT C ||||| ||||| ||| ||| ||
 CTGATCAAACTCAGTGGAC CAGGTG AACTAGTCTA GTAG GGC CCT GT T
 ACTCAA CTC G- - TG AC

GAM1217 TCCGTCGACCTGACTTAGAG 1203 TCCAGGGGCT 3928 G A--- TG TTA TC AACT
 TCTCTGTCTACACACTTCAC CCTGTTGGGA TCC TCG CC AC GAGTCTCTG TAC T
 AGGTATCCAGGGGCTCCTGT TACC ||||| || ||||| ||
 TGGGATACCGAGGGA AGG AGC GG TG CTCGGGGAC ATG /
 G CATA GT TC- CT GACAC

GAM1218 CCGAGCATTATCCACTTCT 1204 TTCAAAGTCT 3929 ACTT ACTCT T ATATTA- T -----
 - TCCGAAT
 AAACCTCTGTACGTTAATGAT TCGGTTATCG CTAA GTACG TAATG TTGA AAC AGCA
 T
 ATTATTGATAACAGCATCCG TACT ||||| ||||| ||||| ||||| |||||
 AATTACATTTTTGCTTTATA GATT CATGC ATTGC AACT TTG TCGT /
 TAGGTTTCAAAGTCTTGCCT ---- GCACT T GTTCTGA - GATATATT TTTTACA
 TATCGTACTCACGTTAGTTT
 GAATGTAAAG

GAM1219 TTTTAATGCGTTCTTGATCT 1205 TTAATGCGTT 3930 TCTT A CTT- --- C
 AACAGTCTTTCCTTTAACCG CTTGATCTAA TTTTAATGCGT GATCTAAC GT TCCT TTAA C
 ATTAACAGGATACTGCGT CAGT ||||| ||||| || |||||
 TAGGTTTCGTATGCATTAATA AAAATTACGTA TTGGATTG CG AGGA AATT G
 TGC- - TCAT CAA A

GAM1220 CGCCGTCGGAAGGAGCGCT 1206 TGGAAGGGAG 3931 CTC -- GTG GC CC
 TCCCGTGCCGCGTACAGCCC CGTCGGTCTC CGCCGTCGGA GATCG C TTCCC CC GTACAG
 C
 GTCTGTATGGAAGGGAGCGT TTCC ||||| ||||| ||||| ||||| |||||
 CGGTCTCTTCCGACGGCG GCGGCAGCCT CTGGC G GAGGG GG TATGTC /
 TCT T C AA- -- TG

GAM1221 GCGTTCCATGAGTTCCAGAA 1207 TGCCATGGTA 3932 TT GA - GAAGC AAA
 GCGCGGTAAAACGAACTGCC ACAATGGTTC GCG CCAT GTT CCA GCGGT A
 ATGGTAACAATGGTTCGT GT ||||| ||||| ||||| |||||
 TGC GGTA CAA GGT CGTCA /
 TT A- T AC--- AGC

GAM1222 GGCCACGTACCGTTGGATCG 1208 TGACGAGATT 3933 TACCG- G CA AGC CAACC
 TT
 CGTCCACGAAGCGCTGCCAA CAGAATGACC GGCCACG TTGGATC CGTC CGA GCTGC
 GA T
 CCGATTTTTTCCTTCGCGGT GTGG ||||| ||||| ||||| ||||| ||||| ||

ATTGATGACGAGATTCAGAA
TGACCGTGGCC

CCGGTGC GACTTAG GCAG GTT TGGCG CT /
CAGTAA A TA A-- CTTC- TT

GAM1223 AGCACGCAGATGGAGGCGGT 1209 AGATGGAGGC 3934 A - ---- C C - TT TG
CCTGTTGCTCTTTTTTAGCT GGTCTGTTG AGC CGCAGAT GG AGG GGTC TGT TGCTCTTTT
AGC C
GCAGCGCTTGAGAGAGCATG CTCT ||| ||||| || ||| ||| ||||| |||
CATGGCCCCTGGCACCGGTC TTG GCGTCTG CC TCC CCGG ACG ACGAGAGAG TCG
A
TGCGGTT - G ACGG - T T T- CG

GAM1224 GCGAGGGGCGAGGTATTAAG 1210 CGAGGTATTA 3935 - A---- GA ACCGCG
GGGAAAAAAGGACCGCGGGC AGGGGAAAAA GCGAG GGGCG GGTATTAAGGG AAAAAGG
G
TAATCCCTTTTTGATCTTTA AGGA ||||| ||||| ||||| |||||
ATACCCCGCGCGCCCGCTCG CGCTC CCCGC CCATAATTTCT TTTTCC G
C G GCGCC AG CTAATC

GAM1225 TGTGACGTTCTTCTCGCCGT 1211 TGGCATCCAG 3936 T-- T- G CA GCGAA G TGA
CCAGGTGGCGAATCAGGCGC AGGGCGCTGA TGTGACG TCTTC CGCC TC GGTG
TCAGGC CT A
TTGAAAAACAGGTCTGGCAT AGAT ||||| ||||| ||||| |||||
CCAGAGGGCGCTGAAGATAT ACGCTGT AGAAG GCGG AG CTAC GGTCTG GA A
TGTCGCA TAT TC G AC ---- - CAA

GAM1226 ACATTAATACTATTGGAAAC 1212 TGAGGTCAGG 3937 A TT GG A- - AA A-- AAA A
AG- AC
ATTTGTGAGGGTCAATCCAG CATCACACTT AA CA TGTGA GTC ATC CAGAAG TTTG GAGA
TGG AG TG A
AAGAATTTGAGAGAAAATGG GTTC ||| ||||| ||| ||||| ||||| ||||| |||
AAGAGTGACATGACAAAAC TTT GT AACT CGG TGG GTCTTC GAAC CTCT ATC TC
AC T
ACTAAATCTCAAACAAGACC - TC A- AC A CA AAA AA- A AAA AG
TTCTGAGGTCAGGCATCACA
CTTGTTCTGT

GAM1227 GCTGAAGTTCTTAGATGTTT 1213 TGAAGTTCTT 3938 A- GTTTG AG GG
GCATAGCATTGGATTTGATG AGATGTTTGC GCTGA GTTCTTAGAT CAT CATT A
AATGAGAATCTAGGAATCGT ATAG ||||| ||||| ||| |||||
CAGC CGACT TAAGGATCTA GTA GTAG T
GC AGA-- A- TT

GAM1228 TCAATATTTTCTGATGATGA 1214 TGAGATGACA 3939 AT - - C- A G AAAAGGG
AT
GATGACAGGCTTCATTAGAA GGCTTCATTA TTCTG GATGAGA TGA CAGG TTC TTAGAAGCT
TGCT TTTTGA G

GCTGTGCTAAAAGGGTTTTT GAAG ||||| ||||| || ||||| ||||| ||||| |||||
AATGATATAAAAAGAGGCAA GAGAT TTATTCT ACT GTCC AAG AGTTTTTGA ACGG
AAAAAT A GG G A AA G A AG----- AT
AGTTTTTGAGGAAAACCTGA
TCAGTCTTATTGGTAGAGAT
GGTGA
GAM1229 TTAGGCTTTAGATGGGTGAA 1215 AACACTGATT 3940 GGTGAA T A T G AAGA AGTA
TG AA--- AAT
TTTGTCAAGTTTTGGTGACC AAGACATTGC G TT GTCA GT TTGGT ACCT CT T AGGACC
GTT G
TAAGACTAGTATTGAGGACC AGTC | ||||| ||||| ||||| || ||||| |||||
AAGTTAATGACGAGCAGAAG C AA TAGT CA AACCG TGGA GA A TCTTGG CGA
/
GGTTCTTGAGAGAGAAGAGG AG---- T - C - GAA- GAG- GT GAAGA GCA
TGCCAACACTGATTAAGACA
TTGCAGTCCA
GAM1230 AAGGAGTAAAGCCAGCTGGT 1216 TTAAACACTA 3941 TG - CTGA ACAC
TATGCTGATAAGAACACAGG ACTGGCTGGT AAGGAGTAAAGCCAGC GTTA TG TAAGA A
CATCTTAAACACTAACTGGC TTTA ||||| ||||| ||||| ||||| |||||
TGGTTTTACTCCTT TTCCTCATTGTCG CAAT AC ATTCT /
GT C AA-- ACGG

GAM1231 AGTTTATCAACAGCATTAAC 1217 AAGCACCAGC 3942 TTA- C C CCTA A- C AC AC
CTATGGACTCTTATTACTAA ATTAATCTTT AGT TCAA AG ATTA TGG CT TTATT TA A
CACTATACCAATAAAGCACC TGAC ||||| ||||| ||||| ||||| |||||
AGCATTAATCTTTTGACACT TCA AGTT TC TAATT ACC GA AATAA AT C
ACT TCAC T - ACG- AC - CC AT

GAM1232 CCAGGTAAGGGAGCGAGCTG 1218 TAAGGGAGCG 3943 AG C C T TT C - TC
TTGGATTATTGTTTCTGACA AGCTGTTGGA CC GTAAGGGAG GAG TG TGGATTA GTTT TGA
CA A
TCAATCTGCTCAAAGCTTAA TTAT ||||| ||||| ||||| ||||| |||||
TCTACCAACTCCCTCCCTTA GG CATTCCCTC CTC AC ATCTAAT CGAA ACT GT A
CAGG A- C A C T- - C CT

GAM1233 GTAAGAGGGGTGCGATCCGG 1219 CCAGAACCTG 3944 C C ATGCTA C CC-- AT
TTATGCTACTCGGACCAGCA ATCACACCTC GTAAGAGGGGTG GATC GGTT CT GGA AGC
C
TCATGCTTTAATCCCAGAAC TCTT ||||| ||||| ||||| ||||| |||||
CTGATCACACCTCTCTTAC CATTCTCTCCAC CTAG CCAA GA CCT TCG /
A T ----- C AATT TA

GAM1234 GTAAGGAGTGGTGAGGTCGG 1220 TGAGGTCGGG 3945 G A ATG AATG C CA AT
GTATGCTAATGGGACCACAG TATGCTAATG GTAAGGAGTG TG GGTCGGGT CT GGA CA
GC C
CATCTAGCCTGATCCAGAGA GGAC ||||| ||||| ||||| ||||| |||||

CCTGACCCCAGCGCTCTTTA
C

CATTTCTCGC AC CCAGTCCA GA CCT GT CG /
G C GA- ---- A C- AT

GAM1235 ACATCTGGGAGTGCTTCAAT 1221 TCAAATGTGG 3946 AT- TTC GATAT -- G-----
T G

CTGTTCAAGTGAAGATATGTT ATCCTGCCAG TTCA CTG AGTGAA GTTCA AATGTG
ATCC GCCAGG T

CAAATGTGGATCCTGCCAGG GGTC ||| ||| ||||| ||||| ||||| ||||| |||||
GTCACCTGGTTGGATATGGA AGGT GAC TTACTT CAAGT TTATAC TAGG
TGGTTC C

TAGGCATATTAATGAACTAC CTT TT- ACCAT AA GGATAGGTA T A
CATTCAATTTTCAGTTCTGGA
GTCACCTCTGT

GAM1236 ACATGGTTTGACAAGTTTTA 1222 TAAAATGTTT 3947 - TT GTTTT T -- A TG TGT
GTAAAATGTTTTTTTCAAAG TTTTCAAAGT AC ATGG TGACAA AG AAAAT GTTTTTTTCA AG
TAG T

TGTAGTGTTCTTCTAGTTTC GTAG || |||| ||||| || ||||| ||||| || |||||
TGAAGAAAACCTGTTTTCTT TG TACC ACTGTT TC TTTTG CAAAAGAAGT TT ATC /
TAATTGTCATCCATAGT A T- AAT-- C TC C TG TTC

GAM1237 CACTATGGTGGCAAGATGTC 1223 TATGGTGGCA 3948 TA- - AG T A
TCCCATCTGGGGATGTGATG AGATGTCTCC CAC TGGTGG CA ATGTC CCC T
CCCGCCACGTGTG CATC ||| ||||| || ||||| |||
GTG ACCGCC GT TGTAG GGG C
TGC C AG - T

GAM1238 GACAGGACTCTCCTGGCATT 1224 TAGCCAGGCT 3949 CT ---- ATT G
TGATGCTGTTATAGCCAGGC CAGGCTTCCT GACAGGA CT CCTGGC TGAT C
TCAGGCTTCCTGTT GTT ||||| || ||||| |||
TTGTCCT GG GGACCG ATTG /
TC ACTC AT- T

GAM1239 GGTCTCATTGTGGCCATCTC 1225 TTTATTGTTT 3950 TCA-- G CATCT-- A TATAAAT
AAAAAATATATAAATTTAAA ACCTGCTAGA GGTC TT TGGC CAA AAATA T
AATTATTTATTGTTTACCTG AGAT ||| || |||| ||| |||||
CTAGAAGATATGACC CCAG AA ATCG GTT TTTAT /
TATAG G TCCATTT A TAAAAAT

GAM1240 TGTCTCGCACACAACCTTAC 1226 ACCACATCTT 3951 ACAACTTACTACT AC C C-- -
CA CTG TT
TACTGAATGAACCACGGATG TGTGTCATTT C GAATGA CA GGATG TTTC CTTCT GAT
TGGAT A
CTTTCCTTCTCAGATCTGTG TTAA | ||||| || ||||| ||| ||||| ||| |||||
GATTTATCTGTCCAATCGGA G TTTACT GT TCTAC AAAG GAAGG CTA ACCTG
T

AGTGAAACACATCTTTGTG
TCATTTTAAATCAGCCCCGT
TAAAGGTACA

GAM1241 GATATATGGGCACTATTATC 1227 TGACGTGCGC 3952 - CACTATTA C - CGCAT -
A

CGGTGACGTGCGCATAGTTG ATAGTTGAGC GATATA TGGG TC GGT GACGTG
AGTTGAG CG C

AGCGACGTGCGACTCGACTTA GACG ||||| ||| || ||||| ||||| ||
CGTCTATCCGAATCTCCCAT CTATGT ACCC AG CTA CTGCAT TCAGCTC GC G
TGTATC T TCTA---- C T ---- A T

GAM1242 GGCGGGGAGTCTTGAGTGAA 1228 TGAAGTGCAT 3953 C - T TG ATAGTGAA AC
GTGCATAGTGAAGATGGACT AGTGAAGATG GG GGG GAG CT AGTGAAGTGC GATGG T
GTCCATTAGAGGCAGGCGCT GACT || || || || ||||| |||||
TCACTGGTCTCGCCCCC CC CCC CTC GG TCACTTCGCG TTACC /
- G T -- GACGGAGA TG

GAM1243 CAAGGCTGGATAAGCAAATT 1229 TAAGCAAATT 3954 C A --- A GTT CTTCAAGTTT
TT

GAGTTACATGCTTCAGTTTT GAGTTACATG CAAGG TGG TAA GCAA TTGA ACATG TTC
T

TCTTTCATGGACATTAATCT CTC ||||| ||| ||| ||||| ||| |||
TATGTTATCAGATTGTAAAT GTTCC ACC ATT TGTT GACT TGTAT AGG C
TAACCAACCTTG A A AAA A AT- TCTAATTAC TA

GAM1244 GAGGCATGATTGTAAGTGTG 1230 TACTACACGC 3955 G T- GTA A TC
TAAGTGTGAGTCCTTTTTAT TCAGATTCTT GAG CA GATT AGTGTGTA GTGTGAG C
ACTACACGCTCAGATTCTTG GGCT ||| || ||||| |||||
GCTC CTC GT TTAG TCGCACAT CATATTT /
G TC AC- - TT

GAM1245 TACAGCTCACTATATTACTT 1231 CAGCTCACTA 3956 - CTATATT- CTC- TAAA
CTCGCTAAAATAAATGTTCT TATTACTTCT TACAG CTCA ACTT GC A
AAAGTTATTCAATTGAGTCT CGCT ||||| ||| ||| ||
GTG GTGTC GAGT TGAA TG T
T TAACTTAT ATCT TAAA

GAM1246 TGTGTTTCGCGCCACAGCAT 1232 GTAAAGGAGT 3957 C ---- A ACTA
GAAAATTCACACT TTA

TACTAATGAGAAAATTCACA TGTGGTTAAA TGTGTTT GC GCCACAGC TT ATGA
TGTC A

CTTGTCTTAACTTGACATTT GCCA ||||| || ||||| || ||| |||
TAATAGCCAATCGTAAAGGA ATACAGA CG TGGTGTG AG TGCT ACAG /
GTTGTGGTTAAAGCCAGACA C AAAT - GAAA AACCGATAATTTT TTC
TA

GAM1247 AAGTTATGCAGCATTTCATA 1233 TGAGATTTTT 3958 AT G TC TTT A - T
 TTAAACTCGTTAATCGTTA GTTTAATGTG AAGTT GCA CATT ATA AA CTC GTTAA C
 ACTGAGATTTTTGTTTAATG TTCA ||||| ||| ||| || ||| |||||
 TGTT CAGCTT TTCGA TGT GTAA TGT TT GAG CAATT /
 CT - TT TT- A T G

GAM1248 ATATTGACCGTTATAAATGT 1234 TATCCAGAGA 3959 A - TCGAT TAGA TTC
 CTTTGTGCGATGATATATTAG TATCTTGTA A ATATTG CCGTTATAA ATGTCTTTG GATATAT
 CGC C
 ACGCTTCCAATTGTGATATA TGGC ||||| ||||| ||||| ||||| |||
 TCCAGAGATATCTTGTAATG TATAGC GGTAATGTT TATAGAGAC CTATATA GTG A
 GCGATAT - C ---- - - TTA

GAM1249 GACTGTAGTGCTCAGATACT 1235 TGTAGTGCTC 3960 - CTC A C - --- A
 CATCAGACTTTTTACCGGAA AGATACTCAT GACTGTA GTG AG TACT AT CAG ACTTTTT C
 AAGTAATTTGCATTAGTGCC CAGA ||||| ||| || ||| ||| |||||
 TCCATGTACAGTT TTGACAT TAC TC GTGA TA GTT TGAAAAG C
 G C-- C T C TAA G

GAM1250 TGATACCTTTGTACGACATT 1236 TACCTTTGTA 3961 AC T TAA T
 AATGCTATAGTAACATGTTG CGACATTAAT TGAT CTTTG ACGACAT TGC A
 TCCGAAGCAATTA GCTA ||||| ||||| ||||| |||
 ATTA GAAGC TGTTGTA ATG T
 AC C CA- A

GAM1251 TTGTGATTGTTTCATGATATC 1237 TTCATCATGT 3962 T T--- T ATC TC T C
 GTTTCGGATGTTACCTATGT GCCAACGTCT TTG GAT GT CATGAT GTT GGA GTTAC T
 AATTCTCTAATTCATCATGT CAA ||||| || ||||| ||| ||| |||||
 GCCAACGTCTCAA AAC CTG CG GTACTA TAA TCT TAATG A
 T CAAC T CT- TC - T

GAM1252 CAATGCTTTTTAGGAGACTT 1238 TGGCAAAGGA 3963 - AGA CAT T ---- - C
 TCATCCATCTGGTCAGAAAA GCCATAGAGG CAATGCTTTTTTA GG CTTT CCATC GGT CAG
 AAAAGA T
 GACTATTTTTTTTATTGTCAA GCGT ||||| ||||| ||| ||||| ||| |||||
 GCTTGGTGGCAAAGGAGCCA GTTGCGGGAGAT CC GAAA GGTGG TCG GTT
 TTTTTT A
 TAGAGGGCGTTG A GAG C-- T AACT A T

GAM1253 CCTCGTAGAGGCGGGTGAGG 1239 CATTGCATGA 3964 T AG GAGG - T A AGAT
 AC TG -- T
 GCGTGCTTGAGATGCAGATG GCCCGTAGCT CC CGTAG GCGGGT GCG TGC TG GATGC
 GGT T ATTT C A

AATGGGCCACCTTCCTAAAG	GAGGACGGAA	CC TC CACCGG AAGGTTCTGTTG A
GCAGGAG	AT----- T -- GT	AC

GAM1260 GATTTTCGTCCACCCGTGGT 1246	CACCCGTGGT 3971	TCCA- CG TG --- GA G
GAGAGGCTGCGACTACGAAA	GAGAGGCTGC	GATTTTCG CC TGG AGAGGCT GC CTAC A
GTAGAGTTAAAGCTTCTATC	GACT	
CAAAGGAAAATCGAGAATC	CTAAGAGC	GG ACC TCTTCGA TG GATG A
	TAAAA AA TA AAT A- A	

GAM1261 GCCTACTGTTGCGTTTGTTA 1247	TTAATGTTAT 3972	A-- G G TTT TAT A T
TCCT		
ATGTTATGGACACACGTATT	GGACACACGT	GCCT CT TT CG GTTAATGT GGAC CACGTA
TGAGGA T		
GAGGATCCTTTGTATTCTTC	ATTG	
ATTATGTGGGTCCTACATTG		CGGG GG AA GT TAGTTACA CCTG GTGTAT ACTTCT
T		
ATCTTGGAAGGGATCGGGC	CTA G G TC-	T-- G T TATG

GAM1262 GCGAGTGACACGTGGATGTG 1248	TGACGAGACT 3973	GAC T----- A T
TCTCGTCGAGTTGCATATGA	CGAATCATCT	GCGAGT ACGTGGATG GTCTCGTCG GT G
CGAGACTCGAATCATCTACG	ACGT	
TTAGCTTGC	CGTTTCG TGCATCTAC	CAGAGCAGT TA /
	AT- TAAGCT A C	

GAM1263 AGCTAAGGCTAAGAGAGCTT 1249	TAAGAGAGCT 3974	TA- A C GTTGA --- -----
-- GA		
GAGGTTGAGCGTATGCCCGG	TGAGGTTGAG	AGGC AG GAG TTGAG GC GTATGCC
CGG A		
GAAGACTGAAAGATATATTC	CGTA	
ACACAGGTATACAAGGTGGT		TTCG TC CTC AACTC TG CATATGG GTC /
GCTCAACTCGCTGGTGCTTT		TGG G - GTGG- GAA ACACACTTATATAGAAA
AG		
AGCT		

GAM1264 GAGGATGATGGTGTTTATAC 1250	TGACCACGAT 3975	G TATACTGATGC GA CT
TG--- C		
TGATGCTGAGAGTGCTGTCA	CAATTTGATC	GAGGAT ATGGTGTT TGA GTG GTCATTG
GGTA T		
TTGTGGGTACTAGTGCTATT	TCAA	
GTTAATGACCACGATCAATT		TTCTTA TGTCATAA ACT CAC CAGTAAT TCGT A
TGATCTCAATACTGTGATTC		G CTCTAGTTTA- AG -- TGTTA G
TT		

GAM1265 GCCGCAAGCTTACCTGTTAT 1251	AAGCTTACCT 3976	--- T ATTA TT GTC
TAAGGCCAATTTTAGTAGTC	GTTATTAAGG	GCCGCAAGC TTACC GTT AGGCCAAT TAGTA
T		

TCGGTGCTAATTGGTCTGAA	CCAA		
GATGGTGATGTGTTTGTGGC		CGGTGTTTG AGTGG TAG	TCTGGTTA ATCGT /
	TGT - AAG- -- GGC		

GAM1266	GTAGTAGGTTAGTTGAACTA 1252	TAAAGAGTCT 3977	T G	A- TA TT	GGGTTC	--
A	AAGAGTCTATGGTTTTCTAG	ATGGTTTTCT	GGT A TTGAACTAAAG	GTC TGGT	TCTAG	
TGGTGGC	GGCGGTG T					
	GGGTTCTGGTGGCGGCGGTG	AGGG				
	ATTTCACTGTTGAGTTACCA		CCA T GATTTGATTC	TAG ATCA AGATC	ACCATTG	
TTGTCAC T						
	ACTAGAACTACTGATGCCTT	- G	CG TC	-- A-----	AG	T
	TAGTTTAGGTACCACTAT					

GAM1267	TGAGGCCCTTCCTTTTGAAA 1253	CGACTAGAGA 3978	- TTG	GTTTATT	C C G	TTT
T- T	CATGGGTTTATTTAAATCTC	ATTTGTTACT	TCCTT AAACATGG	TAAAT TCTCT GT	TGTAT	
AG ATCGGG G	TCTCGTGTGTATTTTAGTAT	GTGT				
	CGGGTGTTCGTATCTCTTTT		AGGGG TTTGTGTC	GTTTA AGAGA CA GCGTA	TC	
TAGTCT /						
	ATGCGACTAGAGAATTTGTT	G	TAA	ATT----	- T -	TTT TC T
	ACTGTGTTTAATGGGGAGTT					
	TGAGGGTCTTA					

GAM1268	ACGCTTAGCAAACGTGGACC 1254	TATCTCAACA 3979	- AACG-	ACCTACCCG---	A -
T	TACCCGTGAGAAATGATGGG	GCCTGCTCGC	ACGCTTAG CA	TGG	TGAGA AT
GATGGG C					
	TCATCCATCTATATCTCAAC	CGAT			
	AGCCTGCTCGCCGATTGATG		TGCGAGTC GT	GCC	ACTCT TA CTACCT /
	ACTGAGCGT		A AGTTA GCTCGTCCGACA	A T	A

GAM1269	CCTGGTAGGTAGCATGGTTC 1255	TAGCATGGTT 3980	TA	- T CA	CGTGGA	----- T
CC	ATCATCTGCGTGGAATCCTA	CATCATCTGC	CCTGG GGTAGC	ATGGT CAT	TCTG	ATCC
TATAC GC C						
	TACTGCCCCCTGCCGTGTAT	GTGG				
	CTTTGGATCAGACAATGATC		GGATC CTATCG TGCTA	GTA AGAC	TAGG	ATGTG
CG /						
	GTAGCTATCATCTAGG	TA	A - AC	-----	TTTCT	C TC

GAM1270	CCTTGGAAGAGTGGACACT 1256	TGGAATGTAG 3981	TT AA G	AC-- --	C A TA-	G
AT						
	GAACTCCATACCATAGCCTG	TAATCAAATA	CC GG AGA	TGGAC	TGA ACT CAT CCA	GCCT
TAAGA T						
	TAAGAATTTCTCTTAAGGTA	GTCC				
	TCTGGAATGTAGTAATCAAA		GG CC TCT ACCTG	ACT TGA GTA GGT	TGGA ATTCT /	

T- GA - ATAA AA T A CTA - CT

GAM1271 CTCTTTGCTAGCTTTAGGAC 1257 TACCCGAAGA 3982 G TACT C CCCATAAT T -
CT-- - GA
CTACTATATCTACCTCCCCA GAGTGTTCAG TA GACC ATAT TACCT GAA CGC CTTTTTG
TGTC CC C
TAATGAATCGCCTTTTTGCT GTAC || ||| ||| |||| ||| ||| |||| ||| ||
TGTCCCGACCAAGGCGATGT AT CTGG TATA ATGGA CTT GTG GAGAAGC
GTAG GG C
ACCCGAAGAGAGTGTTCAGG G CTT- C ----- - A CCAT C AA
TACATATTTTCGGTCGTAGCC
GCTCTCAGAAG
GAM1272 TGCTACCCAATCATCTCTGA 1258 AACAGTGTTC 3983 CCC - C - T CTAATCAC
GCACTTTCCTTGGGCTAATC AAGTATGGTT TGCTA AATCAT CT TGAGCACT TTCC TGGG
A
ACAAGCACTTTCTCCACGGA TGGC |||| ||||| || ||||| ||| ||||
ACAGTGTTTAAGTATGGTTT ACGGT TTGGTA GA ATTTGTGA AAGG ACCT A
GGCA --- T - C C CTTTCAG

GAM1273 ATCATACCACTCCCGCTCAA 1259 CAAGCACTTG 3984 - C CCGCT C AGCT
GTGCCTTGAAAGCTGGCAAA CCGACTGGTA ATCA TACCA TC CAAGTGC TTGAA G
TTCAAGCACTTGCCGACTGG CTGA |||| ||||| || ||||| ||||
TACTGAT TAGT ATGGT AG GTTCACG AACTT G
C C CC--- - AAAC

GAM1274 CCAGTGTCAATACGGTAATT 1260 TACGGTAATT 3985 - A TTTCAAGA T T
TCAAGATTGACTCCTTCTGG TCAAGATTGA CCAGT GTCAAT CGGTAA TTGAC CC T
GTCAACCAAGTTTACTGCAT CTCC |||| ||||| |||| ||||| ||||
TGACTACTGG GGTCA CAGTTA GTCATT AACTG GG C
T C TGAACC-- - T

GAM1275 GGAAGTATCCAGCCCCCTTCG 1261 AGAGATTGCA 3986 C T TTC ATA G C CCC -
C
TCTGCAATAATCTCGGACCT GATGGGGCTG GGAA TA CCAGCCCC GTCTGCA ATCTC GA CT
CTG AGT A
CCCCTGAGTCAACGCTACAG GTGT |||| ||||| ||||| ||||| ||| ||||
AGAAGATCAGAGATTGCAGA CCTT GT GGTCGGGG TAGACGT TAGAG CT GA GAC
TCG A
TGGGGCTGGTGTTC

GAM1276 TATGCTATCATCCTCAAATC 1262 TTGAATATAC 3987 --- C AATCA AAAGAG TTTAT CT
CT GTCCGA
AGACAAAGAGATTCGTTTAT TGGTCCCTGA C AT CTCA GAC ATTCG ACAC TGA
ATAAT A
ACACCTTGACTAATAATGTC GCAT | |||| ||| |||| ||||| |||||

CGAATTATAAGATTATTTAT G TA GAGT CTG TAAGT TGTG ACT TTATTA T
CATTGTGTTGAATATACTGG CCC C CC--- GTCATA ----- TT AT GAATAT
TCCCTGAGCATCCCGATGGC
ATA

GAM1277 ACGGATCAATCACTTTTGAC 1263 TCACCGGGGA 3988 T T A-- G GTAC TA
CGTGGGTACAGTCTATATGA AACAGAAAGTG ACGGA CAA CACTTTTG CC TGG AGTC T
TTTCACCGGGGAAACAGAAG CTTG ||||| ||||| || ||| |||
TGCTTGTTTCGT TGCTT GTT GTGAAGAC GG GCC TTAG /
- C AAA G ACT- TA

GAM1278 CCAATGAGTGTAATAATTTA 1264 TAATTTAGAA 3989 A TA - AATTT CAACATG- G A
CA TT CA
GAATTTACCCCAACATGGTG TTTACCCCAA A TGAGTG ATAATTT AG CACC GT TG CT
GTCG TGT G
TGACTCAGTCGTTTGTGAGA CATG | |||| ||||| || ||| || ||| |||
AGCAGGTGATAAAGATAGAC T ACTTAC TGTTAAA TC GTGG CA AT GA TAGT
ACG /
AGAATATAGGTGCCTTGCTC A -- C GTTCC ATATAAGA G A AA GG AA
AAATTGTCATTCAATGG

GAM1279 CCCATATCTTTTAGACAATC 1265 TAGCTTCCAC 3990 ATCTT AATC TT ACCACC TC
T GTG-- T
TGGTAGCTTCCACCACCATC CACCATCCCC CCCAT TTAGAC TGGTAGC CC A CCCT
GAA GTCT C
CCCTTGAAGTGGTCTTCCAA TTGA ||||| ||||| ||||| || | ||||| |||
GACACCGATTCCAGGGTGTA GGGTG GGTCTG ATCATCG GG T GGGG CTT
CAGA C
AAAACGGTTGCTACTAACGT ACTT- CA-- TT CAAAAA GT C AGCCA A
CTGGTTCAGTGGG

GAM1280 GTGTTTCATTGTTGGCAACCC 1266 TACACATGGG 3991 TT TGGCA T A ----- A
TAAT
TTGATGTACTGGGATGGTAA TGCGATGGTC GTG CATTGT ACCC TG TGTAC TGGG
TGG A
TATTTCTCAACCCATTAAAT AC ||| ||||| ||||| ||||| ||||| |||
TCTGTACACATGGGTGCGAT CAC GTAGCG TGGG AC ACATG ACCC ACT /
GGTCAC TG ----- T - TCTTAAATT A CTTT

GAM1281 ACTAATGGTGACGTAAAAGA 1267 TGACGTAAAA 3992 GG- AAAGA AAG TC
CAAAGTTCCTCAATGGAGTA GACAAAGTTC ACTAAT TGACGTA CA TTCC A
TGAAGTACGTCGAAAGTTGG CTCA ||||| ||||| || |||
T TGGTTG GCTGCAT GT GAGG /
AAA GAA-- AT- TA

GAM1282 ACTTATAGGTCACCATTTGGA 1268 TAGGTCACCA 3993 G ATTG T CATTTT G
TGTTGCCGCATTTTAACTC TTGGATGTTG ACTTATAG TCACC GA GTTGCCG TAACTC A
GAAAGGGTTATTACGGTAAC CCGC ||||| ||||| || ||||| |||||

TCGGTGATTATGAGT

TGAGTATT AGTGG CT CAATGGC ATTGGG A

- ---- - ATT--- A

GAM1283 CTATCGGTCCCAGGACAGGT 1269 AGAGATGGAG 3994 CAGGA- GAC A ATTCCAAA
- C- TT T

ATGACTTCCATCTATTCTAT AAATACTTGG CC CAGGTAT TTCCATCT TTCT AGTT GC
AA GTCAA A

TCCAAAAGTTGCCAATTGTC GCAA || ||||| ||||| ||| || |||||
AATATTTGACCTTTACGCAA GG GTTCATA GAGGTAGA AAGA TCGA CG TT
CAGTT /

GCTGAAAAAGAAGAGATGGA AAACGG AA- G AAAAG--- A CA TC T
GAAATACTTGGGCAAAGGAA
AATGG

GAM1284 CTGGCGGCCCGTCCTGCATC 1270 TGGCATCAGA 3995 C-- TC- C - A - AATCTG T
AGT C CT

CAATCTGCCCAAATCTGTCT GTCGGACACC GG CCG CTG AT CCA TCTGCC CA TCT
GTATG CTGT AC C

TGTATGAGTCTGTACCTCA GTTG || ||| ||| ||| ||||| || ||| ||||| |||||
ATGTCACAGTCCATATAGAA CC GGC GAC TA GGT AGGCGG GT AGA TATAC
GACA TG A

TCTGCGGCGGATGGCATCAG ACA TGA - C - C CTA--- - CT- C TA
AGTCGGACACCGTTGG

GAM1285 GGAGGTAATTGGGCAACACA 1271 TTGGGCAACA 3996 ---- - CGC A GA
CGCTATGAGAAAGTGATAAGC CACGCTATGA GGAGGT AATTGGGCAACA CA TATGAGA GT
T

GTTTCGTACATTGCTGTTGT GAAG ||||| ||||| ||||| ||||| ||||| |||||
CCGATTTTAGACTTCC CCTTCA TTAGCCTGTTGT GT ATGCTTT CG /
GATT C TAC G AA

GAM1286 TCTGTAGATTGTTACCTCC 1272 TACCCTGCAA 3997 C AATA----- TC AAATC A-
GAT CT A

AATATGGTCTCTACCCTGCA ATCTCCAACA CA CTCC TGG TCTACCCTGC TCCA CA
TGCGCA TC C

AATCTCCAACAGATTGCGCA GATT || |||| ||| ||||| ||||| ||||| ||||| |||||
CTTACCAGGTATGTGTATG GT GAGG GCC AGGTGGGATG AGGT GT ATGTGT
GG C

GCTGGAGTAGGGTGGAATCC C GTAAAACGG TA ---- CG --- AT A
GGGCAAAATGGGAGCTGAGA
CACCATCATCA

GAM1287 TGTTGGTAGGATGAAAGAGA 1273 TGAAAGAGAA 3998 A A G TT G G
ATCAATTAAATGTGGAACG TCAATTAAAT TGTTGGT GGATG AAGA AATCAA AAAT TG A
ATTTTTGGTTATCTTGCATC GTGG ||||| ||||| ||||| ||||| ||||| |||||

CACTAATA ATAATCA CCTAC TTCT TTGGTT TTTA GC A
- G A -- - A

GAM1288 AATAAACGTTTTTTTCTAAGA 1274 TGAGCTACTG 3999 AC CTAAGA G TCCA CT

TTTGTGAGCTACTGATCCA ATCCAAAAAG AATAA GTTTTTT TTTGTGACTACTGA
AAAAGG A
AAAAGGCTATAATCTTTTTC GCTA |||| ||||| ||||| ||||| |||||
AGTAGTTAACAGAAATAAGA TTATT CAAAGAA AGACAATT GATGACT TTTTCT T
AACTATTATT AT TAA--- - ---- AA

GAM1289 CCATGAGGTACACTGTTATT 1275 TGAGGTACAC 4000 - AC--- T AG AC
AGGTAACAAGTACACAATTA TGTTATTAGG CCATG AGGT ACTGT ATT GTA A
CAGTATGAAACCTGCATGG TAAC |||| ||| |||| ||| |||
GGTAC TCCA TGACA TAA CAT /
G AAGTA T CA GA

GAM1290 GTGCGGTGGAGGAGGTACTG 1276 GGAGGTACTG 4001 ----- GG GGGTGTA G TG
CA- TT
GGTGTAGAGGATGGCCAGGT GGTGTAGAGG GTGC GGTGGA AGGTACT GA GA GC
GG G
TG TAGTCGGTGTGTCGTCG ATGG ||| ||||| ||||| || || || ||
TAGGTGCCTGGTTCACCGGT CGCG CCACTT TCCGTGG CT CT TG CT T
GATGCGC TAGTGG GG ATG---- G GT TGG GA

GAM1291 CAACGATAACTGATGATGAT 1277 CATCACATAA 4002 AC-- - GTT C- TTAC
GTTTGTGATGTTTCTTCTTA TCTATTATCA CAACGATA TGATGAT GAT TGTGATGTTT TTC
A
CATAACGAACAAGGCATCAC ATGG ||||| ||||| ||| ||||| |||
ATAATCTATTATCAATGGTA GTTGCTAT ACTATTA CTA ACACTACGGA AAG /
TCGTTG GGTA T AT- AC CAAT

GAM1292 TCCATACTATGTGATCACCT 1278 TATGTGATCA 4003 - T A CACC TCC AG
CTATCCGTTAAGTGAATAAC CCTCTATCCG TC CA ACT TGTGAT TCTA GTTA T
ATTAGAATCCATTATAAGTT TTAA || || || ||||| ||| |||||
GAGA AG GT TGA ATATTA AGAT CAAT G
A - - CCTA TA- AA

GAM1293 TTCTATAAATATATATTCTA 1279 TATTAAAATG 4004 ATATATT CGTCG TT A TT---
TC T TAA
GATATTCGTCGTTAATATTT TTTAGCTAGT CTAGATATT TTAATAT GC AACTT TATG
TAT GA A
GCAAACTTTTTATGTCTATT TTTT ||||| ||||| || ||||| ||| |||||
GATAAACTTTTCTATATCAT GATTTGTAA AATTATA TG TTGAG GTAC ATA CT
A
GTCCGTGAGTTCGTATATTA TGATC-- ---- -- C TGCCT T- T TTC
AAATGTTTAGCTAGTTTTTG
TTGAA

GAM1294 GATGTGCGATTCTTTGCGTA 1280 TATCAAACAT 4005 TC T T TCA- G GC CTTC
TA

TAAATATTTTAAATATATTT ACTT ||| || ||||| || ||||| ||| |||| |||||
 ATGTTAGGAACCAAAATGTA AGA CT AATTT TT AAATGT AGG ATTG ATTTATA /
 AACTTTTTTAAATCTAGA T A T C AAAACCA ----- T TAA

GAM1301 TTTTAATTACAGTCATTAGT 1287 TATAACATTG 4012 TTAGTTCTC TCCCA A T T CTC
 ---- ATA
 TCTCAGTGTTGTTCCCAAA TCGTTGTAAT CAGTGTTGT AAA TAT ATG GC ATCTA
 TAATAA T
 AATATTATGTGCCTCATCTA TAAG ||||| ||| ||| ||| || ||||| |||||
 TAATAAATATTGCATTATTA GTTACAATA TTT ATG TAC CG TAGAT ATTATT T
 TATCTAGATAGCCCATTTGTA ----- ---- A T C A-- CTAT ACG
 ATTTATAACATTGTCGTTGT
 AATTAAGAGA

GAM1302 CCAGGCGCAATGGAGTGAGA 1288 TTAAATCCGA 4013 A C ----- G- G A
 GGCCGGACCACTGGCGTTTT GATAATTGCC CC GG GCAAT GGA TGAGA GCCGG C
 AAATCCGAGATAATTGCCCG CGG || || ||||| ||| ||||| |||||
 G GG CC CGTTA CCT ATTTT CGGTC C
 - - ATAGAG AA G A

GAM1303 CTGGTGCTAGTAGGGACGTT 1289 AGCAGCAACC 4014 G AGTA GA- --- GG TG---
 G
 TGTGCTGCTGGTCATATTTG CGAACGCGAC CTGGT CT GG CGTTTG TGCTGCT TCATATT
 TAGC T
 TAGCGTCGCTGAAGTCGATG CAGG ||||| || || ||||| ||||| ||||| |||||
 TGAAGCAGCAACCCGAACGC GACCA GA CC GCAAGC ACGACGA AGTGTAG
 GTCG /
 GACCAGGACCAG G ---- AGC CCA -- CTGAA C

GAM1304 GTTTCATCTGACGTGATAGT 1290 TGACGTGATA 4015 CAT-TG T- G - TG GTGT
 TACGGTGATTGTTGTGTTAT GTTACGGTGA GTTT C ACGTGATAGT ACG TG AT TT T
 AAGATGATGTAGCGTTTGCT TTGT |||| | ||||| ||| ||| ||
 GTTACGTTGGTAAAAGAT TAGA G TGCATTGTCG TGC AT TA AG /
 AAAT GT TT G G GT AATA

GAM1305 CCAGAAACCAAGTACCAGTC 1291 TTCAGAGAAC 4016 A - A ACCAG AG TT AAA
 TTC GA T
 TCAGTGTTACCTTAAAGTGT GTGGCTTTTCG CC GAAA CCA GT TCTC TG ACCTT GTGTGT
 AT CAGTAT A
 GTTTCATGACAGTATTACCG G || ||||| ||| ||| ||||| || |||||
 TGCTGGGGTTGCACACACGC GG CTTT GGT CA AGAG AC TGGAA CACACA TG
 GTCGTG C
 AAGGTTTCAGAGAACGTGGCT - C G ----- -- T- CG- CGT GG C
 TTCGG

GAM1306 CGTCGATGTCAAAGTGAAAC 1292 TGCAATGATG 4017 T- A ---- TT TG GG A A GT G
 ----- T

CTACGGTTTAGTGCATCAGG ACCTTGCTGT GAA CCT ACGGT AG CATCA GCAA CC TC
 AC TG GGG G
 GCAAACCATCGTACGTGGGG TGAA ||| ||| |||| | |||| ||| ||| ||| |||
 TGAACCCAGAATACAGGTTA CTT GGA TGTCTG TC GTAGT CGTT GG AG TG AC
 CCC A
 GAGGTTGCAATGATGACCTT CC C AAGT T- CA AA - - AT G ATAAGA A
 GCTGTTGAAAGGCTTCCCCT
 TGTCCCTCG
 GAM1307 GGTCTGTCATGGCCCTGCCG 1293 TGACGAGGCA 4018 TC CA CC GTCAA A A A C
 A
 TCAATCATGATCTTGTGATA CGAGATAGGC GG TGT TGG CTGCC TC TG TCTTGTGTCAT CTT
 TC G
 CTTCTCAGCGAAAAGATGAC AGTA || ||| ||| |||| || |||||||| ||| ||
 GAGGCACGAGATAGGCAGTA CC ACA ACC GACGG AG AC GGAGCAGTA GAA AG /
 CCAAACACTCC TC A- AT ATAG- C - - A C

GAM1308 GTTGCAAGTCTCTTCATTTCA 1294 TGAGAAGGGC 4019 G ----- ATT A C
 ACAGCCATGCCGTTGAGAAG ACAATCATAC GTT CAGT CTCTTC TCAAC GC A
 GGCACAATCATACTGGAAC TGGA ||| ||| |||| |||| ||| ||
 CAA GTCA GGGAAG AGTTG CG /
 G TACTAACAC --- C T

GAM1309 GTCTGTTTTTGTCTGTTTC 1295 TCTGACACTA 4020 C TTT TC TCTTTACT C CCT
 TCT
 TTTACTATGGTCTTCTACCT CAACCTCATA GT TG TTGT TGTT ATGGT TTCTA TCA C
 TCATCTCTTCTGATTTTGGA C ||| ||| ||| |||| |||| |||
 AAACCATCTGACACTACAAC CA AC AACA ACAG TACCA AAGGT AGT /
 CTCATAC T TCC TC TC----- A TTT CTT

GAM1310 TTTGCGCAGGTACGCGGAAG 1296 GCAGGTACGC 4021 G T G CAAC ---- C
 TCCACAACCCCGGCGTGAGT GGAAGTCCAC TTTGC CAGG ACGCG AAGTCCA CCC GG G
 TTCAGCGGAGCGGTGGACTC AACC |||| ||| |||| |||| ||| ||
 CTGCGGACCTTGCA ACGTT CCAG CGTCC CAGGTGG GCG GA T
 - G T CGAG ACTTT G

GAM1311 CCTGTACACTTGTTGTTTCA 1297 TGTACACTTG 4022 - TTGTTTCA - TGGG GT
 GCCTTGTTGGGACGCGGTGTA TTGTTTCAGC CCTGTACA CTTG GCC TTG ACGCG G
 CGCGTAGTCAGCGGCCGAGA CTTG |||||| ||| || ||| ||||
 TGTACGGG GGGCATGT GAGC CGG GAC TGCGC /
 A ----- C TGA- AT

GAM1312 CGCCGTCGTGTAGCGTGAAT 1298 GGAAAAGTGC 4023 TGT C ATTC - GT
 TCCATTTTTCCTGCAGTCCG TATTACCTCT CGCCGTCG AG GTGA CATTTTTCCTG CA C
 TGATAGGAAAAGTGCTATTA TTGA |||||| || ||| |||||||| ||
 CCTCTTTGATGGCG GCGGTAGT TC CATT GTGAAAAGGAT GT /

TTC - ATC- A GC

GAM1313 CGTCGATGTCAAAGTGAAAC 1299 AAAGTGAAAC 4024 TG C- TC-- AG G--- A TG--
C GT
CTCCGGTTCAGAGCATCAGG CTCCGGTTCA AAG AAACCT CGGT AG CATCA GAC CACCA
GT TTCGGG G
ACACACCATGGTCTTCGGGG GAGC ||| ||||| ||| || ||||| || |||||
TGAAGCCCGAGTACAGGTTG TTC TTTGGG GTCG TC GTAGT TTG GTGGT CA
GAGCCC A
GTGGTTGCAATGATGACCTT CG AA TCAT CA AACG - TGGA T GA
ACTGCTGAAGGGTTTGCCTT
TGTCCTCAAG

GAM1314 CTGAGGCGATCCATGCCTTA 1300 TGGCAAGGAT 4025 --- - A TTA AG
ATCCAGTCGCGGATGGCAAG CAGCTTGACC CTG AGGC GATCC TGCC ATCC T
GATCAGCTTGACCAG AG ||| ||||| ||||| |||||
GAC TTCG CTAGG ACGG TAGG C
CAG A A --- CG

GAM1315 GACAATGCGAGTCTTGCCGG 1301 TGGCAAGCAA 4026 C --- CACGT CCATC AA
CACGTACTTTCTCCATCGGG ACTTGATTG GA AATGCGAGT CTTGCCGG ACTTTCT
GGGCG T
CGAATTTCTCCTTCAGGAA TC || ||||| ||||| ||||| |||||
GGTCTGGCAAGCAAACCTTGT CT TTATGTTCA GAACGGTC TGGAAGG CCTGC /
ATTCTC C AAC ---- ACTT- TT

GAM1316 GCCAACACACGGTGTGGCGC 1302 TCACCGGGCC 4027 A A TGT G TA----- GA
GGTGTATGGGAGAGCCAGTC CTTGTGGTAG GCC AC CACGG GGC CGGTG TGG G
GAGTCACCGGGCCCTTGTGG GC ||| ||||| ||||| |||||
TAGGC CGG TG GTGTT CCG GCCAC ACC /
A - C-- G TGAGCTG GA

GAM1317 GAACAGTTGGAGGATGGCGT 1303 TCACCGTTGT 4028 GTT- C - CA- TTGTC
TTGTT GGA
TCAGCCAACAGTTGTCGTGG AAAGTGTGAA GAACA GGAGGATGG GTTCA GC ACAG
GTGG GGGTCT G
TTGTTGGGTCTGGAGTAGAA TTCC |||| ||||| ||||| || ||||| |||||
GACCTTCTTTTCACCGTTGT CTTGT CCTTCTACC TAAGT TG TGTT CACT
TCCAGA T
AAAGTGTGAATTCCATCTTC GTTC T G AAA GC--- TTTCT AGA
CCTTGTGTTT

GAM1318 GTGTTCACTAGAGTCTTCAG 1304 TGGAATCCGA 4029 ACTA-- CT A A GC
AATCCACTCGGCGTTTCGGGT ACTCCGTGCG GTGTTC GAGT TC GA TCCA CTG G
GGAATCCGA ACTCCGTGCGG GAAC ||||| ||||| ||||| |||||
AACAC CACAAG CTCA AG CT AGGTGGGC /
GCGTGC -- C A TT

GAM1319 TGTCAAGGCTCTGCCGTCCA 1305 TGACGAGGCA 4030 CAA T GT AACA A A C
ACATGATCTTGTCTGTA CTTT CGAGGTAGGC TGT GGC CTGCC CC TG TCTTGTCTG CTTTTC
G

TCCGCGAAGAGATGACGAGG AGTG ||| ||| ||| || || ||||| |||||
CACGAGGTAGGCAGTGCCGA ACA CCG GACGG GG AC GGAGCAGTA GAGAAG /
ACA AG- T AT AGC- - - C

GAM1320 GAATTTGGAATCCAACATTG 1306 TATAATTAAT 4031 TCCA A GG-- T
ATATATATTGGAATTAGTAT GTTCCAAAT GAATTTGGAA ACATTGAT TATATT AAT A
TATAAGATATAATTAATGTT TT ||||| ||||| ||||| |||
TCCAAATTT TTAAACCTT TGTAATTA ATATAG TTA G
---- - AATA T

GAM1321 TTAGCATCAATAAATTTATT 1307 TCAATGTATT 4032 T TT ---- CTA TTAAAT TTC --
CA

ACATGTAATACATCTAACTT TTTTACATGT AAAT TA ACATGTA ATACAT ACT ATCT TAT
ACATT A
TAAATATCTTTCTATACAT TTTA ||||| ||||| ||||| ||| ||| ||| |||||
TCAACACAATGTCTATATCC TTTA AT TGTACAT TATGTA TGA TAGA ATA TGTA
C

AGATTGACAGTCAATGTATT C TT TTTT AC- CAGT--- CCT TC CA
TTTTACATGTTTTACATTTA
AATGTTAAAA

GAM1322 ATCTTACAGCCCAGATGCGT 1308 AGAGATCTGG 4033 ACA-- GCG TATT T
TTTAATATATTTGTAATCAT GTAGACCAAG ATCTT GCCCAGAT TTTTAATA TG A
TTATTAGAGATCTGGGTAGA AT ||||| ||||| ||||| ||
CCAAGAT TAGAA TGGGTCTA GAGATTAT AC A
CCAGA --- TT-- T

GAM1323 GTGCGATTTCTGAAGGCCATG 1309 TCAGTGCAGA 4034 TTCG G- A---- - --- G
ATC

ATGTATTGATCTTGGGAGGC TCCCATGGAA GTGCGAT AAG CCATG TGTATTGA TCT TG
GAGGC A
ATCAAAAGCTTCACAGTCAG CTTA ||||| ||| ||||| ||||| ||| ||| |||||
ACTCAGTGCAGATCCCATGG CACGCTG TTC GGTAC ACGTGACT AGA AC CTTG
/
AACTTATTGTCTGCAC TTA- AA CCTAG C CTG A AAA

GAM1324 TGGCTTTTGGAGAACACCAG 1310 TTGCTCACTT 4035 GC T- CACCA- C C AA G
GAAC ATT

ACCAACGTCAGCCAACCAGT TTTTTTCCTC TG TTT GGAGAA GA CAA GTCAGCC CCA
TCG AGGATCG A
CGGAACAGGATCGATTAGCG AAAA || ||| ||||| || ||| ||||| ||||| |||||
TGATTCTCAATGATGGCGGC AC AAA CCTTTT CT GTT TAGTCGG GGT AGT
TCTTAGT /

TGATTTGCTCACTTTTTTTTT
CCTCAAAATCA

TA CT TTTTCA C - C- - AAC- GCG

GAM1325 TTGTACTTGTATTCTCTCCC 1311 TCACTGTGGA 4036 T-- T CTTT A --- A- TC
TCATAACCG AAG

TTTTAGTAGATTACAAATGT GTGGATCCCC G ATTCTCTC TAGTGATT ACA ATG CGAT
AGG A
CCGATTCATAACCGAGGAAG GAGT I ||||| ||||| ||| ||| ||| |||
ACGTGCCTATCGTTCATACT C TAGG GAGG GTCA CTAA TGT TAC GCTA TCC
C
GTCATAATCACTGTGGAGTG CCC T T--- - TAC CA TT ----- GTG
GATCCCCGAGTATGA

GAM1326 GAGTCGGTTCACCTAACAGCA 1312 TAACTGCTGC 4037 TC - AACAA- T A C AACC
TGTAATTGTCCGGTTTAACC AACAAAGTGA GAG GGTT CACT GCA GTA TTGT CGGTTT T
TTTTTGAAATCGTATAACTG AACT ||| ||||| ||| ||| ||| |||||
CTGCAACAAAGTGAAACTAT CTC TCAA GTGA CGT CGT AATA GCTAAA T
CTC TA A AACAA - C T GTTT

GAM1327 GGAAAAGTTTAGAAACTTGT 1313 TCGATAAACT 4038 AACT ----- C GTC C - T -
GAAA

CGATAAACTCCTTGTCCGCG CCTTGTCCGC GA TGTCG ATAAA TCCTT CG GGA GG
CTTTAATA TG A
GAGGTCTTTAATATGGAAAA GGAG || ||||| ||||| ||| ||| ||||| |||
CTGAACATTGTTGGAGTCCT CT ATAGT TGTTT AGGGG GC CCT CC GAGGTTGT
AC C
TCCACGTAGGGGACTTTGTA GTAT CTGTGCAA C AT- A T T T AAGT
ACGTGTCTGATATATGTCAT
AAACTCGTCC

GAM1328 TAGATAGTCGAGCGACGATA 1314 TAAAGTGTAC 4039 A---- GA-- AA--- G TT A G
AT

AAGTGTACGTTTACATACCG GTTTACATAC TAGAT GTCGAGC CGAT AGT TACGT AC
TACC CCG G
CCGATGTTCCGGGGTAAGTA CGCC ||||| ||||| ||| ||| ||||| ||| ||||| |||
CGTGACTGTTTAATCGAATG GTCTA CGGCTCG GCTA TCA GTGCA TG ATGG
GGC T
GCTCGGCCTATAATCTG ATATC GTAA ATTTG - -- A - CT

GAM1329 TCTGGGATTCTTGCTAGGCG 1315 TCCCTGGGCA 4040 T CTT --- TGAA TG TCC A
TCC

TTTGTGAACCTGGTCCGGAT GACGTGGCCT TC GGGATT GCTAGGC GTTTG CC G GGAT
CAAG C
ACAAGTCCCGGTCTTGATCC GGTT || ||||| ||||| ||||| ||| ||| ||||| |||
CTGGGCAGACGTGGCCTGGT AG CCCTAA TGGTCCG CAGAC GG C CCTA GTTC

/ TCAATCCCTGA T CT- GTG --- GT --- - TGG

GAM1330 AGGTGGAAAAATTTGTACTA 1316 TGGAAAAATT 4041 A ----- T TC TC- A A- GT
 CTCTTAAATCATAGTAAATA TGTACTACTC AGGTGGAAAA TTTG TAC AC TTAAA ATAGT
 AAT TTT T
 TTTGTTTCAGAAGCATTGAC TTAA ||||||| ||| || |||| |||| ||| |||
 TGTATTTTAAACGTTGTAAA TCCACCTTTT AAGC ATG TG AATTT TGTCA TTA AAG
 T
 TAGCCGAATTTTCCACCT - CGATAA T C- TTA G CG AC

GAM1331 GCGGTGAGAGCGGCTTGTTT 1317 TAGCAGTATT 4042 ----- TAT--- -- G CCCA-
 AC
 TAGCAGTATTTGGTTACGCC TGGTTACGCC CTT GTTCTAGCAG TTGGTTA
 CGCCGGGCTC TAC TTC C
 GGGCTCGTACCCCATTCACC GGGC ||| ||||||| ||||| ||||||| ||| |||
 CTGGAAATCATGTGGGGTCC GAG TAAGATCGTT AACCAAT GCGGCCTGGG GTG
 AAG C
 GGCGCTTAACCAATTCATTT TTCTGA TTA CTT TC - TACTA GT
 TGCTAGAATAGTCTTGAGCC
 GCGCCGGCCGC

GAM1332 GGAACAGGACAAATGCAATA 1318 TAGTATTTCC 4043 C - ---- A AAA
 TAAAGTTAATATAGTATTTT TTGATCTTTT GGAA AGGA CAA ATGC ATAT G
 CTTGATCTTTTTCC TCC |||| |||| ||| ||||
 CCTT TTCT GTT TATG TATA /
 T A CCTT A ATT

GAM1333 GTGAAATTGCTGTCAGACTG 1319 TATTGCAAAC 4044 -- A -- G TG AT GAA AC- A T
 TTCA
 CGGTCCCTGCATTTTGAAGG CAAAGAACGG TGCTGT CAG CT GCG TCCC C TTC GGT
 CAATG CT GACT C
 TACCAATGACTTGACTTTCA TGGG ||||| ||| || ||||| | ||| ||| ||||| |||||
 CTTAATAGTTTCAGTATTGCA ACGGCG GTT GA CGT GGGG G AAG CCA GTTAT GA
 TTGA T
 AACCAAAGAACGGTGGGGGG AC A AA G GT GC AAA AAC - C TAAT
 TGCAAAGATTGCAGCGGCAG
 TGACAC

GAM1334 TAATTCCATAAACCCAGCCT 1320 CATAAACCCA 4045 C CAGCCTATG-- T TCTT
 ATGTAGTTTGTTCCTTTAGT GCCTATGTAG TAATT CATAAACC TAG TTGTT T
 ATAACAATCTAAAAAATTCC TTTG |||| |||||| ||| |||||
 ATGGTTTATGTAGTTG GTTGA GTATTTGG ATC AACAA A
 T TACCTTAAAAA T TATG

GAM1335 TTAAGCTTTT 4046 T GTAT AAAC T GAG T GGGA
 GA- ATT
 GTTAAACTGTGTTGAGATTG TAGTAATACC ACT GTGTT GTGTT ATTGGGA GT
 TAATCACA GCTC A
 GGATGTGGGATAATCACAGA TGAA ||| |||| |||| ||||| || ||||| |||||
 GCTCATTAAAGGGTAAGTG TGA TACAA CATAA TGATTTT CG ATTAGTGT
 TGGG /

TGATTAAAGCTTTTAGTAAT T AAT- AGTC- --- - AA-- GAA AAA
 ACCTGAAACATTAAAGTTAG
 TTATAAAGTAG
 GAM1336 TAAAGTTAAGTTTAAATCTG 1322 TAAGTTTAAA 4047 TTA- AA- GCAAA CG
 GCAAATGTTTCGTAAAACGGC TCTGGCAAAT TAAAG AGTTTA TCTG TGTT T
 AACAGAATGTAAATTCCTTC GTTC |||| |||| ||| |||
 TTTA ATTTC TTAAAT AGAC GCAA /
 TTCC GTA AACG- AA

 GAM1337 TACGATTCTTTTGTCTGAAT 1323 TTACGTAAAT 4048 T C T TAACC CCCGATAAA
 A
 ATTTTAAACCATGTACCCGA AAAATCTTTA TACGA TCTTTTGT TGAA ATTTT ATGTA
 GCTG G
 TAAAGCTGAGTTCAGTTACG ACAA |||| |||| ||| ||| ||| |||
 TAAATAAAATCTTTAACAAA ATGCT AGAAAACA ATTT TAAAA TGCAT TGAC T
 AGATTCGTA T - C TAAA- ----- T

 GAM1338 GCGGATATCATTAGACAATT 1324 TTAAGTTT 4049 C--- TT ATT
 GTAGTATATTCTCACGTATT AATATCTATA GCGGATAT ATTAGACAA GTAGTAT C
 ACTTGTTTAATATCTATATC TCCG |||| |||| |||| ||||
 CGC CGCCTATA TAATTTGTT CATTATG T
 TCTA -- CAC

 GAM1339 TAGTATCTTAGCTGTTAATG 1325 TTAATGTTGT 4050 CTTA -- TGTTTTCTTAC - T
 G- GA
 TTGTTTTCTTACTAACGGCA TTTCTTACTA TAGTAT GC TGTTAATGT TAACG GCA GAT
 TAAAGGG T
 TGATGTAAAGGGGATAATCC ACGG |||| || |||| || |||| |||| ||||
 TTTAGAATCTTGACGTTAA ATTATA TG ACGATTACA ATTGC TGT CTA
 ATTCCT /
 CATTAGCACCGTGTAATATT ATG- CC ----- A T AG AA
 A

 GAM1340 ATCGTCGAAGATCTTGTAAC 1326 TCACTGGGTG 4051 G- AA T G ACT GT
 TAACAGTGGTAGATTGATCA TGACGCGAAG ATC TCG GA CTT TA AACAGTG A
 CTGGGTGTGACGCGAAGTTC TTCA ||| || |||| || ||||
 AAG GAA TGA CG AGT TG CACTAGT G
 CT AG C G GGT TA

 GAM1341 CTAGTCGATTGTGAGTTTGA 1327 TGACGGGGAG 4052 TT AATATAG AA C ---
 ATATG-- CCG
 ATATAGACTGTCAACTGTCC TTGATTGGAT GTGAGTTTG ACTGTC CTGT CTGG TCAA
 TTAGAG C
 TGGTCAAATATGTTAGAGCC TTAA |||| || |||| || |||| ||||
 GCATGGATTTGGCTTAAGGA AATTTAGGT TTGAGG GGCA TGTT TTGA
 GGTTTA A

GTTGT TTTGTGACGGGGAGT TA TAG---- -- G TTG GGAATTC GGT
 TGATTGGATTTAAATTTGTT
 AAAATGGAGTC
 GAM1342 TCCAATCAGTCTCTCAGCAT 1328 TCAGTGTATG 4053 CA- ---- G TTAATGG T AA
 TGG TG CT
 GCACTTTAATGGGATTTGCT GTGAGAAATG AT GTC TCTCA CATGCACT GATT GCT
 ACGTT GC T G
 AAACGTTTGGGCTGTCTGTG GGCC || ||| |||| ||||| ||| ||| ||| || |
 AGTGGCGTTGATGTAGTAGT TG CGG AGAGT GTATGTGA CTGA TGA TG TAG
 CG G T
 CAGTGTATGGTGAGAAATGG CAC GTAA G ----- - -- TTG GT AG
 GCCACGTTGGA

 GAM1343 TGAGGGCTAGGGGTTTCTGA 1329 TGAAGTCGAA 4054 G TT GAAGTTT G G AGT
 AGTCGAAGTTTCGGAGGTTT GTTTCGGAGG TGAGGGCTAG GG TCTGAAGTC C GAG TTTG
 C
 GAGTCGTAGCAAGGCTTGGG TTTG ||||| || ||||| | ||| |||
 GCTTCAGATTGTTGGTTTTT GCTTTTGGTT TT AGACTTCGG G TTC GAAC G
 G G -- ----- G G GAT

 GAM1344 CACCGTATAGCTGTTGCCGT 1330 TCACCGCGGC 4055 -- - - TT ----- ACG A AAT
 - T
 TGGAGGCCTGCACGGCCAGC GCATATTGGG AG CTGTTGCC G GGAGGCCT GC GCC
 GCGGT ATGTTCC GT G
 GGTAATATGTTCCGTTGTAA TCTC || ||||| | ||||| || ||| ||| ||||| ||
 CGGGAGCATCACCGCGGCGC TC GGCAACGG C TCTCTGGG CG CGG CGCCA
 TACGAGG CA T
 ATATTGGGTCTCTCTCGGGC CC T G TC TTATA --- - C-- G A
 AACGGTCTCCAGGCGGTG

 GAM1345 GCGTCCTCGATGGTGAGCTC 1331 TGAGCTCGAG 4056 C T -- A GG ACA G -
 GG G
 GAGGATGGGGATGGACACGA GATGGGGATG CGTC TCGATGG GAGC TCGAGG TG GATGG
 CGATG AGC CTTCC CG C
 TGGAGCCTTCCGGCGGCGGT GACA ||| ||||| ||| ||||| || |||| ||| ||||| ||
 GAAGGGGGCGCTGCATCGGC GCAG AGTTGCT TTTG AGCTCC GC CTACT GCTAC
 TCG GGGGG GT G
 CTCATCAGCGCCTCGATAGT C - AT - GA CCG G C AA G
 TTTCGTTGACGACGC

 GAM1346 AGTCTTTCTTCTCTAATTTA 1332 TTAGATAAGA 4057 CT- TTC-- A T
 ATAGTATTCTATTAGATAAG TTCCTGAACT AGT TTC TCT ATTTAATAG A
 ATTCCTGAACTCACT CACT ||| ||| ||| |||||
 TCA AAG AGA TAGATTATC T
 CTC TCCTT A T

 GAM1347 GCCGTAATATCCTAGATACA 1333 TGTCACGTAT 4058 TAATAT AG A - CA GG
 TGGCATAACAGAATGGAGTA AGAGGCATCG GCCG CCT ATAC TGGCA TAA GAAT A

ATTCCTTTACTGTCACGTAT GC |||| ||| |||| |||| ||| ||||
AGAGGCATCGGC CGGC GGA TATG ACTGT ATT CTTA G
TAC--- GA C C TC AT

GAM1348 GGCAGCCAAATGCAAGGGTG 1334 CAGCCAAATG 4059 - C- AAGG T- T
TTTGATTTAGATTATTACAC CAAGGGTGTT GGC AGC AAATGC GTGT TGAT T
GCATTTATGTTAGCT TGAT |||| |||| ||| ||||
TCG TTG TTTACG CACA ATTA A
A TA ---- TT G

GAM1349 GTAGTTTTTCCATAACGCTA 1335 TACCATGGTA 4060 TTTTT --- TT TTT TATA TTA
TTCTATTTTTATCATATATG GTGTTATTTA GTAG CC ATAACGCTA CTAT TATCA TGTTG
T
TTGTTATAAACTAATACTTC GGCT |||| || |||| |||| |||| ||||
TGATACCATGGTAGTGTTAT CATC GG TATTGTGAT GGTA ATAGT ATAAT A
TTAGGCTCTCTAC TCTC- ATT -- CC- CTTC CAA

GAM1350 TCGACATTATAGGATAGTAA 1336 CATTATAGGA 4061 GA A- A TAAT TTT A
TAGTTTTATAGATTCTATGT TAGTAATAGT TC CATTAT GG TAG AG TATAG T
TCCTTCCTCTAACC GCATAG TTTA || |||| |||| || ||||
TGCAGA AG GTGATA CC ATC TC GTATC /
AC CG A TCCT CTT T

GAM1351 TGTGCCAGTTCTTAGATTCT 1337 TACTATACCA 4062 AGTTCT CTT- --- GCTTTC
TTGTAGTATTTTACATGCTT TAATCTATTA TGTGCC TAGATT TG TAGTATTTTA CAT C
TCCATTAACAATGAAATAGG GGTA |||| |||| |||| |||| |||
ATACTATACCATAATCTATT GCATGG ATCTAA ATATCATAGGAT GTA A
AGGTACG ATT--- TACC AAA ACAATT

GAM1352 TGTTATATTTTATTTATGTT 1338 TGAAAATAAT 4063 TT- - TTCT AAT- AAG
CTAA
CTGAAAATAATTTATAAGCT TTATAAGCTA TGTTATA TTATT TATG GAAAAT TTAT
CTATTAA T
ATTA ACTAATTGCCTTAATA TTAA |||| |||| |||| |||| |||| ||||
GATCATAATCAGGTTTTTCT ACAATGT GATAG ATGC TTTTGT AATA GATAATT /
TCGTACGATAGTTTTGTAAC TTT C TTC- GACT CTA CCGT
A

GAM1353 TTCTTTTTTATTATTTAGTAG 1339 TACCGTGTTA 4064 TT ATTTA TACA - ATCT TA
TATGGTATATACATCGTTAA TAATATTAAG TTCTT TATT GTAGTATGGTATA TC GTTAAT
C G
TATCTCTAGTAGTTCCGTTA AA |||| |||| |||| |||| |||| ||||
ATAGAATTATACCGTGTTAT AAGAA ATAA TATTGTGCCATAT AG TAATTG G /
AATATTAAGAA TT ---- TA-- A CCTT AT

GAM1354 ACACGATAGACGTATTCATC 1340 TGAAATGTAA 4065 CGTAT TCT TTACCATCC A TA--
CA A AA
TCTAACTATCTTACCATCCG TTTGGACTCT GA TCA CTAACATC GA TCCA ACAT
TCAT CCC C
AATCCATAACATCATCATAC TCCA || ||| ||||| || ||| ||| ||| |||
CCAACAAAGGGATGAAATGT CT AGT GATTGATAG CTAGGT TGTA AGTA
GGG A
AATTTGGACTCTTCCAGAAT AAAC- TTT TAAGACCTT C TTAA A- - AA
GATAGTTAGTTTTGACAAAT
CTAAACGTAT

GAM1355 CAACGTA CTGTGGGTCTTTG 1341 TTCACATTTT 4066 TA GTCTT T CTTT
TGTATCCTTTT CACAAGATT ACCACAGGTC CAACG CTGTGG TGTG ATC T
CACATTTTACCACAGGTCGT GTTG |||| |||| ||| |||
TG GTTGC GACACC ACAC TAG C
TG ATTTT T AACA

GAM1356 CATAAGCTGGATAAATCAAA 1342 TAAGATTCTT 4067 A T AAC TC AC CGCC-- C-
AA AA
CTCTTCTCGTCAGAAACGTA TCACCAATAC GAT AA CA TCTTCTCG AGAA GTAT
AAGAATTT TCTT TC T
TCGCCAAGAATTTCTCTTAA ATTC ||| ||| ||||| ||| ||| ||||| ||| ||
TCAATTCAGAAAAAGATAAG CTA TT GT GGAAGAGT TCTT CATA TTCTTAGA AGAA
AG T
ATTCTTTTACCAATACATTC C - C-- -- A- ACCACT AT AA AC
TTGAGAAGGCTGTTTCATCAA
GTTTCATG

GAM1357 CTCGAGTATTTAAATCTAGA 1343 AGAAAAGTAA 4068 CTA AGTAATT - T
ACTCCAGC ACCT A
AAAGTAATTAGGTATTTTTA TTAGGTATTT TTAAAT GAAA AGGT ATTTT AAAACAT GCC
CATC G
AAACATACTCCAGCGCCACC TTAA |||| ||| ||| ||||| |||| ||| |||
TCATCAGAAGATGTTCCGGC AATTTA CTTT TCCA TAAAA TTTTGTG CGG
GTAG A
AAAAGGTGTTTTCAAATAA TAC AC----- A C GAAAA--- CCTT A
CCTCATTTCCATATTTAAGA
CTCAAAG

GAM1358 CTGTAGCAGAGGATCCCGTA 1344 TAGCAGAGGA 4069 A A G C- AAAGTTA- AA- CG--
- A
AAGTTATCTCTAAGAGCCGT TCCCGTAAAG CTGT GC GA GAT CCGT TCTCT GAGC
TAGCTG A
AGCTGAAATAGCTAATGGAG TTAT ||| ||| ||| ||| |||| ||| ||||
CTCCCAAGAGAAATCCAAAA GACG CG CT CTA GGCA AGAGA CTCG ATCGAT /
CGGAAATCATCAGCAGCAG A A A AA AAACCTAA ACC AGGTA A

GAM1359 GGATAAGATAGTGTACTTTT 1345 TAAGATAGTG 4070 --- - TGTAC- CCCAC --- --
AAATATA
GCCACACCCGTATCTCCAG TACTTTTGCC GGA TAAGA TAG TTTTG ACC CGTA
TCTCCAG A

```

AAATATAAATAGTAACTGGA      CACA      ||| ||||| ||| ||| |||||
GGATTACGAATGGTAGACTC      CCT ATTCT ATC  AAGAC  TGG GCAT GGAGGTC

/

AGAAAACCCTCTATTCTTAA      TAA  T TCCCAA  TCAGA TAA TA  AATGATA
ATTCC

GAM1360 GGTGACATAAGTGCATCAGG 1346 TGACATAAGT 4071  T  CATCA T TTC  A
TAATTTCAAGGAAAAGATTT      GCATCAGGTA  GG GACATAAGTG  GG AAT  AAGGAAA G
CTTTATTTTCAATATCACTT      ATTT      || ||||| ||| |||||
GTGTTCC      CC TTGTGTTTAC  CT TTA TTTCTTT /
-      TATAA T ---  A

GAM1361 GTAGGATTCCATATCTCATC 1347 TCATCTGGAG 4072      CC- C C-- AGA  CAT  TACA
TGGAGACAGATCATCTAGTA      ACAGATCATC  GTAGGATT ATAT TCAT TGG CAGAT CTAG
A
CAAAGCCCTAGTATCTGCC      TAGT      ||||| ||||| ||| ||||| |||
CAATCATGAAATATAGTAGT      CATCCTGA TATA AGTA ACC GTCTA GATC  A
CCTAC      TGA  A CTA C-- T-- CCGA

GAM1362 GAACAGGTAATACCTCTGCC 1348 ACAGGTAATA 4073      -  -- T--- CC  TT
GGATATTTGTTGTATCTAA      CCTCTGCCGG  GAACA GGTAATA CC  CTG GGATAT C
CAGTGCTGGAATATTGCCTT      ATAT      ||||| ||||| ||| |||||
GTTG      CTTGT CCGTTAT GG  GAC TCTATG G
T  AA TCGT AA  TT

GAM1363 GAATGGGTGTATGCCATGTT 1349 TGGTTTGAAA 4074  C GTTA  T  A ----- CCAA  TG -----
C
AGGCATTCCAGAGGTGGGCG      GATGGTCCTC      AT  GGCAT CCAG GGT  GGGCG  AGGAT T
AAGCTGTGC G
CCAAAGGATTGTAAGCTGTG      TGTC      || ||||| ||||| ||||| ||| |||||
CCGCGGTATGGTTTGAAAGA      TG  CTGTA GGTC CCG  CCTGT  TCCTG A
TTTGGTATG C
TGGTCCTCTGTCCAAGATGC      A AAG- - - TAGAA  C---  GT GAAAG  G
CCTGGATGTGCAAGTAGCTG
CTACCCATATC

GAM1364 GATGAAGTTTTTGTGACCGG 1350 TGAAGTTTTT 4075  G  T - GTCA  AACA GTT
TCAGTGGTAACACCGTTTGT      GTGACCGGTC  GAT AAGTTTT GTGA CCG  GTGGT  CC T
AGGAGCCACATATGGATCAC      AGTG      || ||||| ||||| ||||| |||
GAAACTTGTC      CTG TTCAAAG CACT GGT  CACCG  GG /
-  -  A ATA-  A--- ATG

GAM1365 TGTATCCTGAGTAAAAGTGT 1351 AAAAGTGTTA 4076  A  - - TTAGAA  ---
CCAGAAAC
TAGAATTTGTAAATGGAGCC      GAATTTGTAA  TGT TCCTGA GTAA AAGTG  TTTGTAAAT
GGAG  A
AGAAACAGAATTAGAACTCT      ATGG      || ||||| ||||| ||||| |||

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TGTATTTGCAGAAAGTTTGC
TTGTTACATTAGGAGGCA

ACG AGGATT CATT TTCGT AGACGTTTA TCTC G
G A G TTGAA- TGT AAGATTAA

GAM1366 CTGAGGCAGCCGTAGAGGTA 1352 TGTGAAACA 4077 A GTA TATT GA- GAG
ATCAAAA G TG
TTCAGGATGTGAGCATAGTA GTACTGTCTT GGCAGCC GAGG CAG TGT CATAGT GT
TGAATTGCT A
TCAAAAGTGTGAATTGCTTG CAGA ||||| ||| ||| ||||| |||||
ATGGGTAATTCGAACGCTGT CTGTCCG CTTC GTC ACA GTGTGC CA
GCTTAATGG /
GGAAACAGTACTGTCTTCAG - AGA T--- ATG AAG ----- A GT
AGGCTGTCCAG

GAM1367 GGATCAGAAATAAAGTCTTG 1353 TCGAATGAAA 4078 ----- T GCA GTTA CTG
GTAG GGAATC
CAGTTTGATGTTAATGAAGT GTTTTGTTAT ATAAAG CTT GTTTGAT ATGAAGT GGAT
AGCCT T
CTGGGATGTAGAGCCTGGAA ATGG ||||| ||| ||||| ||||| ||| |||||
TCTGAAACGAAGGCTGTCCA TGTTTT GAA TAAGCTA TGCTTTA CCTG TCGGA
G
TTTCGTATCGAATGAAAGTT TATAT - AG- ---- --- ---- AGCAAA
TTGTTATATGTTCTGATCC

GAM1368 GGTTTACGTATTTTTGGAGG 1354 GGAGGTAGTT 4079 GTA GT ----- G TAC A
TAGTTGGTATACGCGTTTAG GGTATACGCG GGTTTAC TTTTGGAG AG TT GTA GCGTTT
G
TAGAATGCTTACGAGAAGGT TTTA ||||| ||||| || ||||| |||||
TTGTCTCCGGGAGTAGATC CTAGATG AGGGGCCTC TT GA CAT CGTAAG T
--- TG TGGAA G T-- A

GAM1369 GTAGTCGATGTGCAATGTGC 1355 TCGAATGTGC 4080 ----- G C A--- GA --- -
AT
GTGCTCTGAGGACAGATTGG GTGCTCTGAG GATGTC GAATGTGC TGCT TG GGACA
TTGGAA GT CTTT C
AAGTCTTTATCGTGGAGTAC GACA ||||| ||||| ||||| ||||| ||||| |||||
GTTTCCAGGTGTCTCATGC CTATAG TTTGTATG ACGA AC TCTGT GACCTT CA
GAGG /
AAAGCAGGTATGTTTTTTCG TAGCTTT G A GTAC G- TTG T TG
ATGATATCGATGTAC

GAM1370 GTTTGTTGGAAGGTATCTTT 1356 GAAGGTATCT 4081 T - ----- TTT A- - GG
CATAAGTTTGGCGGGTTGCC TTCATAAGTT GTTTG TG GAAG GTATC CAT AGTT TGGC G
ATAGCTGGGTGTGCATACAT TGGC ||||| ||||| ||||| ||||| |||||
ATATTTCTCATTAAT TAAAT AC CTTT CATAG GTG TCGA ACCG /
T T ATATA CT- GG T TT

GAM1371 TATGGTCCAGTTGAAATTAG 1357 GTCCAGTTGA 4082 - GA AG- T AG- A

ATTTCATTATAGGAAAAGAT	AATTAGATTT	TATGGTC CAGTT AATT	ATTTCAT AT	GAA A
TTGAGATCGTGAAATAAAGA	CATT			
TTGAAATTGTGATCGTA		ATGCTAG GTTAA TTAG	TAAAGTG TA	TTT G
	T AG AAA	C GAG A		

GAM1372	GAGTATGTGAGTTTTGTGTT 1358	TGAGGCAGGC 4083	TA AGTTT	CA- TG
GCC				
	GAGGCAGGCCACTTGCACTT	CACTTGCACT	GAG TGTG	TGTGTTGAGGCAGGC CT
	CACTTGCACT T			
	GCATTGCCTTCCAAATGCAG	TGCA		
	GTGAGAGATAGCCTGCTTTA		TTT ACAC	ACACAATTTTCGTCCG GA GTGGACGTAA T
	ACACATATCCCACAGGTTT		GG CCTAT	ATA GA ACC

GAM1373	GCAAGTCTCTTGCGGAAAAG 1359	CGGAAAAGCT 4084	A CT C-	-	ATTATTTA
	CTATTTTCAAATACATTATT	ATTTTCAAAT	GC AGT CTTG	GGAAAAGCTAT	TTTCAAATAC A
	TAATTACAAACGTATTTGAA	ACAT			
	ACATAGCTTTTCCAACAAGC		CG TCA GAAC	CCTTTTCGATA AAAGTTTATG	/
	AACTAGC	A AC AA	C	CAAACATT	

GAM1374	GCAGATCTTATGCTTGTGTCAG 1360	TCAGTTAAAG 4085	CTTATGCT	A CC -	TTTTT
	TAAAGCCCCGGAATGTTTTT	CCCGGAATGT	GCAGAT	TGTCAGTTA AGC	GGAAT GTT T
	TTTAAATTAACAATTCCTGC	TTTT			
	TGTAAGTACACAACAAAAT		CGTCTA	ACAGTCAAT TCG	CCTTA CAA /
	CTGC	AAACAAC-	G T-	A TTAAT	

GAM1375	GTAGCTAGGGTGGTGAGTGG 1361	TGAGCAACAC 4086	A TG T	GC GC	A
	CGCTCGCAGCAGCTAGTGAG	TCCCTGCCCC	GTAGCT GGG	G GAGTG	GCTC AGCAGCT G
	CTGCTGAGCAACACTCCCTG	AGCT			
	CCCCAGCTAC		CATCGA CCC	C CTCAC	CGAG TCGTCGA T
		C GTC	AA --	G	

GAM1376	TACCCGCTCCGTGGAGTAGT 1362	AGACTCGCCT 4087	C--	T --	A A C G C ATT
	CAGACGCGTCGTATCTTTAA	GACCACTAGC	TACC	GCTCCG GG	AGT GTCAG CG GTC TAT
	TTTA T				
	TTTTACTGAAAATAAGACTC	CCGG			
	GCCTGACCACTAGCCCGGAG		ATGG	TGAGGC CC	TCA CAGTC GC CAG ATA AAGT /
	TACAGGTA	ACA	-	GA C	C T A A CAT

GAM1377	TGCATGTCTCTTGCTAGGTA 1363	TTTGTCCAGA 4088	A TC T C	- C T	GTC T A
	GCCTGTACAAAACAGTCCTT	CTAGCCTAAC	TGC TG	TC TG TAGGT	AG CTG ACAAAACA CT
	TTTTA T				
	TTTTAATGTAAAACAGTGTT	ACGA			
	TTGTCCAGACTAGCCTAACA		ACG AC	AG AC ATCCG	TC GAC TGTTTTGT GA AAAAT /
	CGAACCAAGCA	A CA C A	A A C	---	C G

GAM1378 CGTCTCCCCGGGGGAAAACA 1364 TCCCCGGGGG 4089 GAAAA--- GATA - AC
AC TC
GGATAGCTTCCGGAGTCTCC AAAACAGGAT CGTCTCCCCGGGG CAG
GCTTCCGGAGTCTC CAT GC GG A
ATACGCACGGTCACCCACG AGCT ||||| ||| ||||| ||| || ||
CACATGTGAGACTTCGGGGG GCGGGGGGGCTCC GTC CGGGGGCTTCAGAG GTA
CG CC /
CGCTGGGCCAAGACCTCGGG AGAACCGG G--- T CA CA CC
GGGGCG

GAM1379 GGATCCAAAGGTTGTGAGCT 1365 TGGCGGCGAG 4090 AAA G ----- TG GAGA- -
A C
GGCGGCGAGATTGATGCCCA ATTGATGCCC GGATCC GGTT TGAG C GCGGC TTG
ATGCC TCG T
TCGCTACGGGGGTATACAGA ATCG |||| ||| ||| | ||| ||| ||||| |||
CGGAGCCGTTGGTGATAAGA CCTAGG CCGA ACTC G TGCCG GAC TATGGG
GGC /
TCTCAAAGCCGGATCC --- A TAGAATAGT GT AGGCA A - A

GAM1380 CTGGATGACTATCGGCAGAC 1366 TAACACATAG 4091 GACT AGAC - ACCC CA
A
ACTTGTACCCCAGGGTCCAC TATAAGTCGA CTGGAT ATCGGC ACT TGT CAGGGTC
CTCCAAGT C
TCCAAGTACATACTTGGAGA TTTA |||| |||| ||| ||||| |||||
AGATCCTGTAACACATAGTA GACCTA TAGCTG TGA ACA GTCCTAG GAGGTTCA A
TAAGTCGATTTAATCCAG ATT- AATA T CAAT AA T

GAM1381 GGATTTTTCAGTATTTAGGG 1367 TTAGGGATAT 4092 TTCAG ATATATTC TCC TA
ATATATTCGATGAGATTCCA ATTCGATGAG GGATTT TATTTAGGG GATGAGAT AGTTA
T
GTTATATCTTTAATTTCTAT ATTC |||| ||||| ||||| ||||
CTTATCTTCTAAATAATCAG TCTAGA ATAAATCTT CTATTCTA TTAAT C
ATCT CTA-- ----- TCT TT

GAM1382 GGTGCGAAAATAGACCACA 1368 AGCAGCAAGA 4093 A AGA A C CC A CC T
CCACCCTCATGCTGTTCTT AAGTGATGAG GGTTGCGA AAT CC CA CAC TC TGCTGTT
TTGAA T
GAATTTCTTCAAAGCAGCAA GCAT ||||| ||| || ||| ||||| ||||
GAAAGTGATGAGGCATTATC TTAACGCT TTA GG GT GTG AG ACGACGA AACTT T
GCAATT A C-- A A AA A -- C

GAM1383 TACACGGCAACAACCACACG 1369 CAGAGTAGGG 4094 G AACA CAC - A A T T T
TCCCCACCTATATCTTCCTT GGAGATATAT TACAC GC ACCA GTC CCC CCTAT TCT CCT
CAAT A

CAATTAAATTGTAGGCAGAG	GGTA	
TAGGGGGAGATATATGGTAC		ATGTG CG TGGT TAG GGG GGATG AGA GGA GTTA /
TCGCAGTGTA		A CTCA ATA A - - C T A

GAM1384 TGAGATTACACAAGGATATCC 1370	AACACCATTA 4095	T C	C- G CTACC	CCAAGC-
C TAC				

GATGCTGCTACCTCCAGGCC	CCTATCCTGG	GAT CA AAGGATAT	CGAT CTG	TCCAGG
ATGGTGT TGTA A				

AAGCATGGTGTCTGTATACA	AAAC	
AGCTACAAACACCATTACCT		CTA GT TTCCTATG GCTA GAC AGGTCC TACCACA

ACAT /				
ATCCTGGAAACAACAGAATC		T T	TA A AACAA	TATCCAT A CGA

GATGTATCCTTTTGTATCAT				
CA				

GAM1385 TGGAGAAGGTTGCTGAGTCG 1371	TTATACGGCT 4096	A G C	A ACG- CA
TAAGAGAACGTTCCATTTGA	CACCAAGCTC	TGGAG AG TTG TGAGTCGTA GAGA	TTC T

AAAACCTCTTATACGGCTCAC	CTCC	
CAAGCTCCTCCA		ACCTC TC AAC ACTCGGCAT TTCT AAG /

	C G C	A CAAA TT	
--	-------	-----------	--

GAM1386 TTCCAAGATAATGGAGCCCC 1372	TGTGATGCGT 4097	A G C - AAACC	A A C-
CA- C A			

CAAGTAAAACCCGCAATCAA	GCATACGTTG	TA TGGA CCC CAA GTA	CGCA TCA
AATCATCAG AG GC ATAGC T			

AATCATCAGCAGCAGCCATA	TGGG	
GCATAAGCTGTAGCGTACTC		AT ACTT GGG GTT CAT GCGT AGT TTGGTAGTC TC

CG TGTCG A			
ACTGATGGTTGTGATGCGTG		C A T G ACGT- - G	AC ATG A A

CATACGTTGTGGGATTCAT			
AGATCGGAA			

GAM1387 TTGAATTCTGAATAGGAAAAT 1373	ATGACATTTT 4098	A AA----- AA- TCA A - CGT
GAATCAATGTAATTTGGTAT	ATCCATCTTA	TTGA TTCG TAGGA ATGAA ATGT ATTTGGT

ATG T			
GCGTTTAACATAATCAAATG	CTAC		

ACATTTTCATCCATCTTACTA		GACT AAGC ATTCT TACTT TACA TAACTA TAC /
CCAGCGAAATCAG		A GACCATC ACC --- G A AAT

GAM1388 AATACAATAACAAAACCCCC 1374	TTACATGCGA 4099	TA- AACCCC	TATGT T
GCGTGTAAGATATGTTTGGA	AGAGTTGTAT	AATACAA ACAA	CGCGTGTAAGA TTGGA A

TATCTCCAGTTCTTACATGC	TTTG	
GAAGAGTTGTATTTTGTATT		TTATGTT TGTT GCGTACATTCT GACCT T

	TTA GAGAA-	T---- C	
--	------------	---------	--

GAM1389 AATGCTATCTATTGCATTTA 1375	TTGCATTTAA 4100	TAT	AA-- TCCAAG T
AAGATCCAAGTTCTGTTGAA	AGATCCAAGT	AATGC CTATTGCATTT	AGA TTC G

AACGCTCTATTAATAATGCAA	TCTG	
-----------------------	------	--

TGGTGTATT

TTATG GGTAACGTAAA TCT AAG T
T-- ATTA CGCAA- T

GAM1390 TTCATATGTAATATATATGC 1376 TGTAATATAT 4101 TA-- TA- CGT CT
CGTCTAAACTTCCTTTTGGT ATGCCGTCTA TTCA TGTAATATA TGC CTAAA T
TTGCAAGTTATATTATAATT AACT |||| |||||| || ||||
TTGAA AAGT ATATTATAT ACG GGTTC C
TTTA TGA TTT TC

GAM1391 AGCGGTGTCACAGACTTTTC 1377 TGGAATCCCA 4102 TCA TTCAGCTAAGAAA-
CAAT TTATC T A
AGCTAAGAAATCCATGACCT CAACTTTTAG GGTG CAGACTT TCCATGACCT AG
GGTG GAA T
CAATAGTTATCGGTGTGAAA GTCT |||| |||||| |||||| || |||| ||
TAATTCTCACCTTTCCCTCC TCAT GTCTGGA AGGTATTGGA TC CCAC CTT
A
AAGGTTATGGAATCCCACAA C-- TTTTCAACACCCTA ACC- CCTTT T A
CTTTTAGGTCTGCTACTGCT

GAM1392 CGCACTCAGTCGTGCCTGTG 1378 TGCAAACAGC 4103 C C-- CT - - TCT TTCC-
G
CAAACAGCTTGTTCTGTATT TTGTTCTGTA CGCACT AGT GTGC GTGCA AACAGC TTGT GTA
GC T
CCGCGTAGCCTGTTTACTGC TTCC |||| || |||| |||||| |||| || ||
AACGCTGTTCTGCACTTGCA GTGTGG TTA CACG CACGT TTGTGCG AACG CAT CG /
CAAAATTTGGTGTG T AAA TT C C T-- TTGTC A

GAM1393 GAGGGCTTGCTGTGTTTGCA 1379 TGTTAACTTG 4104 TT GT---- T TGTC T TG
TGTCGCCATTAACGTGTGTTG ATGAGCTTGC GAGGGC GCT GTT GCA GCCAT AAC T
TTCGTGGCTGTAACTTGAT CCTC |||| || |||| |||| ||||
GAGCTTGCCCTC CTCCCG CGA CAA TGT CGGTG TTG G
TT GTAGTT T ---- C TT

GAM1394 GCACTGTGTTGACTCTGATG 1380 TACCATATGG 4105 T TG T - --- TTC
GTATGCATTCCTGATTGCTT TGTTGGCAGC GCAC GTGT AC CTG ATGGTAT GCA C
TATACCATATGGTGTGGCA TGC |||| || |||| |||| ||
CGTGC CGTG CACG TG GGT TACCATA CGT T
- GT T A TTT TAG

GAM1395 ACATGAGAGAGAAATTGCC 1381 TGAGAGAGAA 4106 T TT--- --- --- ACTTG - G
CC
AGCACTTGGTAGATCTTTTG ATTGCCCAGC ACA GAGAGAGAAA GC CCA GC GTA
GATCTTTT AT T
ATCCTTTAATGAAAAGATCA ACTT |||| |||||| || || || |||| ||
TACATCCGGCAAATGGTTTG TGT TTCTCTCTTT CG GGT CG CAT CTAGAAAA TA
T

CTCATCTTTCTCTCTTTTGT

T CTACT TTT AAA GCCTA A G AT

GAM1396 ATGGTTGTGGAGGTTGGTTC 1382 TGAGATCATC 4107 T -- TA T- CAC
AATCAACTGT TTC

ATAGCTTGTTGACACTTCAA CAGGCCCTGA GGTTG GGAGGTT G GTTCA GCTTG TGA
TTCAA GAGT T

AATCAACTGTGAGTTTCTTG ACGC ||||| ||||| | ||||| ||| ||||| |||||
CACTCTTCAATATCATTGAG CCGAC CCTTCAA C CAAGT CGGAC ACT GAGTT
CTCA /

ATCATCCAGGCCCTGAACGC T G G CC CT A-- ACTATAACTT CGT
GAACTTCCTCAGCCAT

GAM1397 GTATTAGGACAGTTCAACAG 1383 TAGGACAGTT 4108 GA C TAATG-- ---- TG ---
CT AAAT

TAATGAGTGGAGTGGTTCTG CAACAGTAAT TAG CAGTT AACAG AGTGG AG GTTCTGCT
GC CTG T

CTGCCTCTGAAATTAATCCC GAGT ||| ||||| ||||| ||||| || ||||| || |||||
AGTTGCTCAAGCAGAACGTC ATC GTCAA TTGTT TCACC TC CAAGACGA CG
GAC A

TGTTACCACTAACTTCTTTG TC - TCTTCAA ATTG TG ACT TT CCTA
TTAACTGCTCTAATAT

GAM1398 ACCCCGTTGCTTAAATACTT 1384 TCAAAAGTAG 4109 TT AAA T AA
TTGTTGAAACAAATCATCAA GAAGCTCGGG ACCCCG GCTT TACTTTTG TGA C
AAGTAGGAAGCTCGGGGT GT ||||| ||| ||||| |||
TGGGGC CGAA ATGAAAAC ACT A
T- GG- T AA

GAM1399 ATCGTTGGTGCTGCAGTCTG 1385 CTGCAGTCTG 4110 GC- C AA CG A AT CA
CATAACTCGTAGTTGATTCT CATAACTCGT ATCGTTGGT TGCAGT TGCAT CT T GTTG
TCTCTA A

CTACAAAAATAGAGACATAA AGTT ||||| ||||| ||||| || | ||||| |||||
CCGTAAGCCATGCAAAGTGC TGGTAGCTA ACGTCA ACGTA GA G CAAT AGAGAT A
ATTAATCGATGGT ATT A CC AT C AC AA

GAM1400 GAACGAAAGACTTTAATGGT 1386 TTTAATGGTG 4111 A AAG - T--- AT AAA- A AA
GTGACATCAAACGAGTACAA TGACATCAAA GA CGA ACTT TAATGG GTGAC C CG GTAC
T

TAAAGTACCCGAAGCGGCGT CGAG ||||| ||||| ||||| ||| | |||||
CACTAGTCCATTGAAAGTAA CT GCT TGAA GTTACC CACTG G GC CATG A
TCGCTC C AA- A TGAT CG CGAA C AA

GAM1401 GACTGTGCAGCTGGGATCCT 1387 TTACAGGTTC 4112 C G AAA CTC CAACTOC A TA
TTTCT T
AAAAGGCTCAGCCAACTCCC AATAGCTTTA GCAG TG GATCCTA GG AGC CC TGTA
ATACTCT AGA T

CATGTATAATACTCTTTTCT CCCA ||||| ||||| || || || |||| ||||| |||
 AGATTGCTCTTTCCAGAGTA CGTC AC CTAGGGT CC TCG GG ACAT TATGAGA
 TCT G
 TCTTACAGGTTCAATAGCTT A A AAC ATT ATA ACTT - TC CCTT- C
 TACCCAATGGGATCACAAC
 GCTGTC

GAM1402 GCTCTTGTGGTAAAGTAATT 1388 TGTGGTAAAG 4113 G TAA C T- T ----- GG
 GACCATGTTTCTTCCAGCTG TAATTGACCA GCTCTTGTG TAAAG TTGAC ATGT TCT CCA
 GCT T
 GTAAAGTTATGAATTGGTAG TGTT ||||| ||||| ||||| ||||| ||||| |||
 ACCGCATAGTCAAACCCCTT TGAGGACAC ATTTC AACTG TACG AGA GGT TGA /
 AACACAGGAGT A CCA A CC T TAAGTAT AA

GAM1403 GGACCAAGCGCCATTACTGT 1389 TGAGGTGCCA 4114 C - CATTACT AG AA- - C-
 CCA- CA AA
 GTAGCGAAATGCCAAACTCG GAACGAAATT CAA GCGC GTGT CGA TGC CAAA TCG
 GGCACC AGC G
 CCAGGCACCCAAGCAAGATG TGAG ||||| ||||| ||||| ||||| ||||| |||
 CTGAGGTGCCAGAACGAAAT GTT CGCG CATA GCT ACG GTTT AGC CCGTGG
 TCG /
 TTGAGCAAAGTCGAATACCC A A AACAACC A- GAA A AA AAGA AG TA
 AACAAGCGCATTGATCC

GAM1404 GTCAATAGGAATAAATTGGC 1390 TAACACCAGA 4115 A - C T A
 GTTTTAAGAACTTGTAACA TTTATCCCTA GTCAATAGG ATAAAT TGG GTT TAAG A
 CCAGATTTATCCCTATTGAC TTGA ||||| ||||| ||||| ||||| ||||| |||
 CAGTTATCC TATTTA ACC CAA GTTC /
 C G A T A

GAM1405 TTCTCAATTGATATATCTGT 1391 CGGCACATGA 4116 TGATATATC - ACTCTT---- A
 - C
 AAATTGAACTCTTTGTATTG AAAACGGTCA TTCTCAAT TGTAAT TGA TGT TTGGTAC
 TGCAT A
 GTACTGCATCAAATGCAGGT CATT ||||| ||||| ||||| ||||| ||||| |||
 ACCGGCACATGAAAAACGGT AAGGGTTA ACATTTA ACT ACA GGCCATG
 ACGTA /
 CACATTTACATAAATATTGG TAAAT---- C GGCAAAAAGT C G A
 GAA

GAM1406 TTGGTGTATTTGGTGCTTCC 1392 GTGTATTTGG 4117 G TT CT C T TC - C T TT-
 CT
 GTCTTCTGATCGTAATCTCT TGCTTCCGTC TTGGT TAT GGTG TC G CT TGAT CGTAAT TC
 AGC GTGC C
 AGCTTGTGCCTCCACGCATT TTCT ||||| ||||| ||||| ||||| ||||| ||||| |||
 CTGCTGAATTACGAATCAAG AACCG ATA TCAT AG C GA ACTA GCATTA AG TCG
 TACG C
 CGATATACTTTATAGGCCAA G TT AT - - - A - - TCT CA

GAM1407 CTAATTGTTTCACTGTCTCG 1393 TGTCTGAACA 4118 T TTC- C-- TG - TA
 TG TAGTCATATTTTGTACTG ACAGTCCCCA CTAA TGT ACTGT TCG TAGT CA T
 TCTGAACAACAGTCCCCACA CATT ||||| ||||| ||| ||||| ||
 TTTGG GGTT ACA TGACA AGT GTCA GT /
 T CCCC ACA CT T TT

GAM1408 CTGAGCATAACCATTATATG 1394 TGATATCCAA 4119 A AACCATT C- ----
 CAATCTCCAGT TC
 TACTGATATCCAAACAATCT ACAATCTCCA CTG GCAT ATATGTA TGATA TCCAAA
 GGCCT T
 CCAGTGGCCTTCTGATAGGC GTGG ||||| ||||| ||||| ||||| |||||
 CTTAGAAATCACTTTGGACC GAT CGTA TATACAT ACTAT AGGTTT CCGGA
 G
 ACTTATCAAATACATATTCC A CTCCT-- AA TCACC CACTAAAGATT TA
 TCATGCATAG

GAM1409 TCGAAATTTTGACGCAATGG 1395 AAGAAGCTTA 4120 C TT - -- A CTTATA - C--
 CAT
 TTAGATTATGTCAAGAAGCT TAATTATAAG TTGA GCAATGG AG ATTATG TC AGAAG
 ATTATAAG C CTC C
 TATAATTATAAGCCCTCCAT CCCT ||||| ||||| ||||| ||||| ||||| ||||| |||||
 CTAGTGAGTTTGTCTTATAA GGCT CGTTATC TC TGATAC AG TCTTC TAATATTC G
 GAG T
 TGTCTTCTCGAACCATAGTG - C- G CA C TG---- T TTT TGA
 CTCCTATTGCTCGGTTTTTC
 GG

GAM1410 TCTCCGTATCATTAGTTAGA 1396 TAACTGAGTC 4121 T CA--- CC----- A A- TAAT
 TCCAAGATGTATTTGTAATT AAGTCCGGGG TCTCCG AT TTAGTTAGAT AAG TGT TTTG
 T
 GTTATCAGAAGGCGCTTTAA A ||||| ||||| ||||| ||||| ||||| ||||| |||||
 TTCCATCTAACTGAGTCAAG AGGGGC TG AGTCAATCTA TTC GCG AGAC G
 TCCGGGGA C AACTG CCTTAAT - GA TATT

GAM1411 TTCACACCTGAACTCACTTT 1397 TGGCTAGTTT 4122 CTCA--- - C TCATTTCC T TT -
 TT T
 AACATAATATTTCAATTCCT AAATGCTAAT TGAA CT TTAA ATAATATT TTAA CTG CC
 CATTG CT C
 TAATCTGTTCCCATTTGTTCT GATG ||||| ||||| ||||| ||||| ||||| ||||| |||||
 TCGTAGTTTAGTGTGGCTAG ACTT GA AATT TATTGTAG AATT GAT GG GTGAT
 GA G
 TTAAATGCTAATGATGTTA CCTTATC C T TAATCGTA T C- T TT T
 TTTAACAGCTATTCCTTCA
 TACGTGTATA

GAM1412 AACCTCTAGAACCATATCCC 1398 TGAGAAGTTC 4123 ATCCCT- TT- AT TG TT--- TC---
 - ATG
 TCTTCTTTACAATGCTGAGA CTTGCCACA CCAT CTTC TACA GC AGAAG CCT
 GCCA CATA A

AGTTCCTTCGCCACATAATG TAAT ||| ||| ||| || ||| || ||| |||
 AATTGTATGTTGGCCTTTCA GGTA GGAG ATGT CG TTTTC GGA CGGT GTAT
 A
 GGTCTCTCTTTTTGGCCTGT ATCTTTT CGT C- GT TCTCT CTTTC T GTT
 ATGCGAGGTTTTCTAATGGT
 TCTTTTGTAAT
 GAM1413 CTATTATGACAAACTTATAC 1399 TATGACAAAC 4124 A TTATAC TT T
 TCTTTCATCATTGCTGGATT TTATACTCTT CTATTATG CAAAC TCT CA C
 GTTTCGATAATAG TCAT |||||| ||| ||
 GATAATAC GTTTG AGG GT A
 - TT--- TC T

 GAM1414 GACCCACACAAAATTGGCA 1400 TTAAATCCAA 4125 C ACAAAA C T- CCA TG
 TTTTGTCCAGCTGGTTGTC ATTAACGTGG GACCC AC TTGG ATTT TGT GC G
 ACACATTAAATCCAAATTAA GTC |||| || ||| ||| ||| ||
 CGTGGGTC CTGGG TG AACC TAAA ACA TG /
 - CAATTA - TT CAC TT

 GAM1415 TGGTGATTAGGTCTGTTGG 1401 TGATTAGGT 4126 GG TT- TC T TGA
 TCTATTGTCAATGAATGTTT CTGTTGGTCT TGGTGATTTA TCTG GG TAT GTCAA A
 GATTATATCCCTTCCAGAAT ATTG |||||| ||| || ||| |||
 AAGTCACCA ACCACTGAAT AGAC CC ATA TAGTT /
 A- CTT CT T TGT

 GAM1416 AGCTTGCGACGTACACTAGA 1402 TGATATCGTA 4127 TTG- ACTA A T CA
 ATGTTATTGCCATACTGTAT CGTCGACTTG AGC CGACGTAC GA TGTTAT GC T
 GATATCGTACGTGCGACTTGC CT || |||||| || ||||||
 T TCG GCTGCATG CT ATAGTA TG A
 TTCA ---- - - TC

 GAM1417 GGTCTACTCGGACGGCTCTG 1403 TGCGATGTTG 4128 T CGA TC -- A ATCG
 TCGCAGTTCACCATCGTGCG TTGCTAAGTC GGTC ACT G CGGC TGTCGCAG TTC CC T
 TCGGGAATCCTGCGATGTTG GACC |||| || | ||| |||||| ||| ||
 TTGCTAAGTCGACC CCAG TGA C GTTG GTAGCGTC AAG GG G
 C AT- TT CT - CTGC

 GAM1418 GTCATACTTAGGTATATACA 1404 TGTCGTACAT 4129 TA -T GT--- A--- TTCCT--
 TTCT TGT
 ATGCTACCTTGTCGTACATC CAATTCCTCA TACAATG C ACCTT CGTAC TCAA CAAAT
 CGT G C
 AATTCCTCAAATTTCTCGTT AATT |||||| ||| ||| ||| |||
 GGTCTTCTGCGCTGTTTGTG GTGTTAC G TGGA GTATG AGTT GTTTG GCG
 C /
 TATTCTTGACTAGGTATGTG -- TT AGTGT GATC CTTATTT TC-- TTT
 TGAAGGGTTGTCATTGTGCT

GAM1419 GTCCTGGCGACTATGAAAT 1405 TTTCATAGTT 4130 C - - AT TTGA TTCCG TA
GCTTAAC TTGAGCGGTTCCG CGTCCATCAA GTT GTGG CGA CTATGAA GCTTAAC GCGG
TG G
TG TAGCTCAATTCCGTGTGT C ||| ||| ||| ||||| ||||| ||| ||
GT TAAGTTT CATAGTTTCGTC CAA TACC GCT GATACTT TGAATTG TGCC AC /
CATCAAC C T T -- TGTG TTA-- TC

GAM1420 ACCATCAAGCCACAATCAGT 1406 TCACCGGCTG 4131 C AAGC AAT T - T GTTGC
TCCGG A CG
AACTGAGTCAAAGTTGCCAG GAATTTCTGT C ATC CAC CAG AA CTGAG CAAA CAGAGTA
TGGA AG C
AGTATCCGGTGGAAGCGCG TTCC | ||| ||| ||| ||||| ||| ||||| ||| ||
TCTGTGGCACAAACGCACAC C TCC TGT TTA GG CGGCC ACTA CACACGC
CGGT TC /
ATCACCGGCTGGAATTTCTG G CTT- CT- A T - ---- AAACA G TG
TTTCCCTGCC

GAM1421 CAGGCGAACCTTTTTGGTAGA 1407 TGCGATACCA 4132 G A T-- AGAAC C
ACACGCACCAGGTGCGATAC CCTAAGCTTC CAG CGA CCT TTGGT ACGCA C
CACCTAAGCTTCACC ACC ||| ||| ||| ||||| |||||
CCA TTC AAT CCATA CGTGG /
C G CCA G---- A

GAM1422 CAGTTGTCGAAGATGCCACC 1408 GATGCCACCC 4133 TG G- C CC T CT C A AC
CTGTGCCTCGCCCACCACTA TGTGCCTCGC CAGT TC AAGATG CA CTG GC CG CC CC T
AAAGTAGTAGGAAAGCCATT CCAC |||| || ||||| || ||| || |||||
AGGAGGCGTTGCTCCA ACCT CG GCGGAG AT CCG AA AT AT AA /
-- TT G TA A GG G G AA

GAM1423 CGTCACTAGCGGCCGCGAAG 1409 AATCAAAGCA 4134 A C CGAAGA A TCCACCT
A
ATTGCAGCTTCCACCTGCAT AGTGGCATCC CGTC CTAG GGCCG TTGC GCT GCATGTC
T
GTCATGTTCTGTCGATTGACG ACAG |||| ||| |||| ||||| |||||
AATCAAAGCAAGTGGCATCC ATTG CACC ACGGT AACT AGC AGCTGCT G
ACAGTTA A T GAACGA A AGTT--- T

GAM1424 CATCATTTGTCAGGCTACCA 1410 TTAAATGGAG 4135 TC- A ATC AAAGC T TTATC
TATCTTAAAAGCACCTCATT TCTCTGTAAG CATCATTTG AGGCT CCAT TTA ACC CAT T
TATCTTCCTTATGTGGTTAA TGAT |||||| |||| ||| ||| |||||
ATGGAGTCTCTGTAAGTGAT GTAGTGAAT TCTGA GGTA AAT TGG GTA /
G GTC - --- ---- T TTCCT

GAM1425 GCGTCTCTTTTCGAACCATAT 1411 TTGAGCCATA 4136 T C CC AA A CA

GGTTAACAATTATGTGCATG TTTTGAGAAA GCG CT TTTCGAA ATATGGTT CAATT TGTG T
 CCATAAGTTGAGCCATATTT GTTG ||| || ||||| ||||| |||| ||||
 TGAGAAAGTTGC CGT GA AGAGTTT TATACCGA GTTGA ATAC /
 T A -- -- - CG

GAM1426 TATGGTGCTTGGTCAAGAAC 1412 GTGCTTGGTC 4137 - G GAACC AA AA
 CCATAAATAAACCTGCGTA AAGAACCCAT TATGGTG CTTG TCAA CATA TA A
 TGTGATTGAGCAAGTCATCA AAAT ||||| |||| |||| |||| ||
 TA ATACTAC GAAC AGTT GTAT GT /
 T G AGT-- GC CC

GAM1427 TCATAGTTCAAGCCCAACTC 1413 TTGGTCTAGA 4138 - ---- A C C AAA
 TTTGAAAAGTGTAGAAAGTT TACCACTCAT TCAT AGT TC AG CCAACT TTTG A
 GGTCTAGATACCACTCATGA GA |||| ||| || || ||||| ||||
 AGTA TCA AG TC GGTGA AGAT /
 C CCAT A T A GTG

GAM1428 TGAACCTACTTAGGTCATTTC 1414 TCGAATGTAC 4139 C T - CTTT T
 CTTTGGATGGAATCAGTTCT CTAGTAATTT TGAA TTA CT AGGT CATT C GGATGGAA C
 GTTTCGAATGTACCTAGTAA CA |||| |||| |||| |||| |||||
 TTTCA ACTT AATGA TCCA GTAAG TTTGTCTT A
 T - T C--- G

GAM1429 TGTTATGTCATCATTATTAA 1415 TAAAGTGGCA 4140 T T T TTAA T GTT AC T AGT
 AGTGGCAGTTTGGAAGTGT GTTTGGAAGT TGTTA G CA CATT A AG GGCA TGGA TGT TT
 T TTAGTTTGCAACACAAGTCC GTTT ||||| || ||||| || |||| |||| ||||
 ACTGTGCCCCCTCTCTTAATG ACAAT C GT GTAAT TC CCGT ACCT ACA AA /
 TGCTAACA -- - TCTC C GTC GA C CGT

GAM1430 TTGGTCTCTTGAGGTATAAG 1416 TGAGGTATAA 4141 CTCT ATAA C T T TA
 TGCTGTTTGTCAAGTAACTC GTGCTGTTTG TTGGT TGAGGT GTG TG TTG CAAG A
 CTTGTCAACCATATCAAGCC TCAA |||| ||||| || || |||||
 TTATGTCGCCAA AACCG ATTCCG TAT AC AAC GTTC C
 CTGT AAC- - C T CT

GAM1431 AGTCGAGATTTCGATCCATTTC 1417 TTGGTCCTCA 4142 C TCCATTCCC CTTT G CCT
 A CCTTGAGCTTTGACGAAGTC ACTCGAATCT AGT GAGATTTCGA TTGAG GAC AAGT GA A
 CTGAAAACCTCACTTGGTCCT CTAC ||| ||||| |||| || |||| ||
 CAACTCGAATCTCTACT TCA CTCTAAGCT AACTC CTG TTCA CT A
 T C----- --- G --- C

GAM1432 CAATGGTTTCAGTTTCCATC 1418 TATGATGGAT 4143 A- TT GTT C G TGT
 ATGCTTGGTGGTGTAGTTCC GTTACCAGCT CA TGGT CA TCCATCATG TTG TGG A
 AGCAAATATGATGGATGTTA G || ||| || ||||| ||| |||
 CCAGCTG GT ACCA GT AGGTAGTAT AAC ACC /
 CG TT --- A G TTG

GAM1433 GTCCAGATCGAAGTCGATGG 1419 TGTCATCTAG 4144 C A- -- T -- TT CT
 TCATGTTCTTCTCCTCGAGA ACTTTGAAAC GT CAG TCGAAGTC GATGG CAT GTTC CTC C
 GTTGGACCTATGTCATCTAG TGAA || ||| ||||| ||||| ||| |||
 ACTTTGAAACTGAAC CA GTC AGTTTCAG CTA CTACT GTA CAGG GAG /
 A AA AT - TC TT AG

GAM1434 GTTGGTTCAAGCAGTAGAAC 1420 TAGGGTAGCC 4145 AA TAG TTC T GA
 GGTTCCCTTTCTTACTGAGAT CTGTTGATTT GTTGGTTC GCAG AACGG CT TCTTACT G
 GGTAGGGTAGCCCTGTTGAT GCCA ||||| ||| |||| |||||
 TTGCCAGAACCAAC CAACCAAG CGTT TTGTC GA GGGATGG /
 AC TAG CC- T TA

GAM1435 GTTTC AATTGGTGCAGCTGT 1421 CAGCTGTGAA 4146 AATT C ATGTTT TCTT CA
 GAATGTTTCGAGTCTTGTTCA TGTTTCGAGTC GTTTC GGTG AGCTGTGA GAG GTT G
 GATCAACTTTTTCTTTGGT TTGT |||| ||| ||||| ||| |||
 CGCAGCTCTGCTTTGAGAGA CAGAG TCGT TCGACGCT CTT CAA A
 C AGTT C GGTTTC TTT- CT

GAM1436 TTCCAAAAGTATGTGTTTTT 1422 TGGGATGTTT 4147 AA - T----- T GT
 CTTTGGTATTATATGGGATG CTGACACCAT TTCC AAGTATG TGTT TCCT TG A
 TTTCTGACACCATACTTGAG ACTT ||| ||||| ||| ||| ||
 GAA AAGG TTCATAC ACAG AGGG AT T
 AG C TCTTTGT T AT

GAM1437 TTGAGTATTTAACTGAATT 1423 TTAAACTGA 4148 AT T T GT TG GAA TG--- T- G
 T TG T
 TGGGTGTTTGATTGAACTTG ATTTGGGTGT TTAAAC GAATT GGGT T ATT CT TTCAAGT
 TT AT G TT A
 TTCAAGTTTTGATTGTGTTT TTGA ||||| ||||| ||| ||| || ||||| ||||| ||
 AAAATGTTGTGAACTGCTTG AGTTTG CTAA CTCG A TAG GA AAGTTCG AA TG T
 AA /
 AAGATTTAGAAGATTGATTG TT - T TTGT AA- TTTAG TC G T GT A
 CTCTAATTCGTTTGATTCT
 TGA

GAM1438 ACCTTTCCTTGTC AATGAGTCAT ACCTT TGTC ATGA TC TG TGGAAGTAGT
 CTTCCC
 TCCATGTCCTGGAAGTAGTC AATGAGTCAT ACCTT TGTC ATGA TC TG TGGAAGTAGT
 TGCTT T
 CTGCTTCTTCCCTTTATACT AGAT |||| ||| ||||| || ||||| |||||

GAGCACCAACCGCTGCTTTC TGGGA ATAG TACT AG AC ACTTTCGTCG ACGAG
 T
 ATGTTCAATGAGTCATAGAT CTGCT A- G TA TTGT CCAACC TCATAT
 ATCGTCAGGGT

GAM1439 GAATCTATTGAGTCCTCTCA 1425 TAACATTTTC 4150 TGA CATTCTC AC TGAA AA
 TC
 TTCTCAGTGTTACGGCATGA AGCAAGAGGA GAATCTAT GTCCTCT AGTGTT GGCA AG
 TGGG C
 AAGAATGGGTCCCTTCCAAG CGTG ||||| ||||| ||||| ||| || ||||
 CTGCTTGCTAACATTTTCAG CTTGGGTG CAGGAGA TTACAA TCGT TC ACCT /
 CAAGAGGACGTGTGGGTTC TG- ACGACTT -- TCG- GA TC

GAM1440 GCCCTGTGAGTGAGGAGCTA 1426 TGAGTGAGGA 4151 - -- GCT TG TC- T
 ATTGTGTCAAATGATTTTT GCTAATTGTG GCC CT GTGAGTGAGGA AAT TG AAAA G
 CTTCATGATTTCTCACTTA TCAA ||| ||||| ||| || ||||
 TTAAGTGGT TGG GA TATTCATCCT TTA AC TTTT A
 T AT --- GT TTC T

GAM1441 GCTTTGCCTTGTAGACGAAC 1427 TTACTATTAA 4152 ACGA- - TCAAC AA TCCTC
 TT ATTA A
 AGTGTTCAACACTCCAAGAT ATTCAAGGAG TTGTAG AC AGTGT ACTCC GA ATAGT
 TGCAG TTG G
 CCTCATAGTTTTGCAGATTA TTGC ||||| ||||| ||||| || ||||| ||||| ||||| |||||
 TTGAGATCGACTGTATTACT AACGTT TG TCGCG TGAGG CT TATCA ATGTC
 AGC A
 ATTAAATTCAAGGAGTTGCG GTCCG C T---- AA TAAAT TT ---- T
 CTCGTGCCTGTTGCAAGATT
 GCAATGT

GAM1442 GTTTAGCATAACTGGTTTGT 1428 TTAAAAGCCT 4153 TAACT GTTATACTTG A
 TATACTTGAAGAAATCTTTC CTTTGTTGAG GTTTAGCA GGTTT AAGAA T
 TTAAAAGCCTCTTTGTTGAG C ||||| ||||| |||||
 C CGAGTTGT CCGAA TTCTT C
 TTCT- AA----- T

GAM1443 AAGATAGGCTATCTTCAACC 1429 TAGGCTATCT 4154 T CTATC AC- T A
 ACTAATTTCACTGGGAATTG TCAACCACTA AAGA AGG TTCA CAC AATTTC C
 TGTTGTGAACCTCTACCTCTC ATTT ||||| ||||| ||||| |||||
 TT TTCT TCC AAGT GTG TTAAGG T
 C ATCTC GTT - G

GAM1444 CTCAAATGTATGCATTGTGC 1430 TGA CTGGTAA 4155 GC T- GAAC GTAT---- - A -
 T AG
 GAACTTGTGGTATTGTACAA ATTGTACGCA T ATTG GC TTGTG TGTACAATTT TTA
 TCATG CT GTGG A
 TTTTAAATCATGCTTGTGGA AAGC | |||| || ||||| ||||| ||||| |||||

GACGCCACTAGACATGACTG A TGAC CG GACAT GCATGTTAAA GGT AGTAC GA
 CACC /
 GTAAATTGTACGCAAAGCAA GT TT ACGA AACGAAAC T C A T GC
 TACAGAGCAGCTTCAGTTGA
 TATCATTTGAG
 GAM1445 GATGACTCACTTCAGACATT 1431 CATCGCGAAC 4156 C TCAGA - AACCA
 TATACAATA A---- CCA
 TTCGCGGTGAACCACGTATA AATGAGTGAT GA TCACT CATT TTCGCGGTG CG GCC
 TGCA C
 CAATAGCCATGCACCACCAC TTAT || |||| ||| ||||| || ||| |||
 ATGCAACACCGGCCGCAATG TT AGTGA GTAA AAGCGCTAC GC CGG ACGT
 C
 ATCGCATCGCGAACAATGAG T ---- C ---- TAGTAACGC CCACA ACA
 TGATTTATT

 GAM1446 TACTAAGCAATACTTTTCGCA 1432 TGAAATGCCC 4157 T-- TT----- CT AAA C GAG
 T CA
 CTAGGAAATTTGCGCATGAG AAACACCTTG GCAA ACT CGCA AGG TTTG GCAT
 TGA CCTA A
 TGATCCTACAAAATAGGTTG CGTC ||| || ||| ||| ||| ||| ||| |||
 AAATGCCCAAACACCTTGCG CGTT TGA GCGT TCC AAAC CGTA GTT GGAT
 /
 TCAATAAAATTCTTAGTTCC CCT TTCTTAAATAACT -- AC- C AA- - AA
 TTGCTTGGTG

 GAM1447 TCCGATCTTCATATGCCAAA 1433 TTTGTTGGAA 4158 - T ATA GC - TT
 TAACCTTTTGTATGGGTCTAT GAAGTTCAGG TCC GA CTTC T CAAATA ACCT T
 TTGTTGGAAGAAGTTCAGGA A ||| ||| | |||| |||
 AGG CT GAAG G GTTTAT TGGG G
 A T AAG TT C TA

 GAM1448 TTCTGATTTATTCCTCGTCC 1434 TGATTTATTC 4159 TTC TCCGAG G
 GAGATGAGAAATCATAATTG CTCGTCCGAG TTCTGATTGA CTCG ATGA A
 AGCCCTAAATCAGAA ATGA ||||| ||| |||
 AAGACTAAAT GAGT TACT A
 CCC TAA--- A

 GAM1449 ATGGAGACTGATAGTTTAGG 1435 TAGTTTAGGC 4160 AC GAATTCT C
 CACTTGAATTCTGCCTAGGT ACTTGAATTC ATGGAG TGATAGTTTAGGCACTT GC T
 CATGAAAAGGTGCTTAAACT TGCC |||| ||||| ||||| ||
 ATCGCTTCCGT TGCCTT GCTATCAAATTCGTGGA TG A
 C- AAAGTAC G

 GAM1450 CAGGACTTCAAGTGCTGTGT 1436 TGTGTTAGTA 4161 T A - T A AG -- CT
 TAGTAGCCTAGAGGCGTTTC GCCTAGAGGC CAGGAC TCA GT GCTGTGT AGT GCCTAG GC
 GTTT G
 TGTTAAACCAGCTCCTAGGC GTTT |||| ||| || ||||| || ||||| || |||

GTTCTG GGT CG CGACACA TCA CGGATC CG CAAA /
T A T - A CT AC TT

TAGTGAAATTATGCTGGTTA TTAT ||| ||| || ||||| ||||| ||||| ||||| |||
 TGTAATGCAAAATTTCACTA TAG AGG GT TTCCGCGGC CGCGAC
 GACATCACTTTAA ACG T
 CAGCAGCGCATCGGCGCCTT A TTCACAA A TA -- A TAATG
 ATGAACACTTGGAAGATGGG
 GG

GAM1453 CCTAGGCCCCGAGTGGGGTG 1439 TGGCTTCCCA 4164 T C TG G G GTATCT
GTTGGGAAGGCAGTTTTGTA AACACTCTGT CC AGGC CCGAG GGGTG TTGGGAAG CAGTTTT
C

TCTCTGGCAAAAAAGCTGGC TTGG || |||| |||| |||| |||||| ||||||

TTCCCAAACACTCTGTTTGG GG TCTG GGTTT CTCAC AACCCCTTC GTCGAAA T

TGTCTTGG T T GT A G AAACGG

GGAGTGAATGAGAAGGCAGT TGGA ||| || |||| ||| ||||| ||||| ||||| ||||| |||||
TTTGTGTATCAGAAAAGAAA CAC AC CAGGT TCG GGCTCGCCTCA
ACTCTTCCGTCGAAA A
GCTGCCTTCTCAGACTCCGC C - C----- T G-- GAAAAG
TCGGTGCTCTGGACCACCAC
ACCCACCAGAG

TGTAATTGATTCCTAATACT GACG ||||| ||| ||||||||| ||| ||||| |||
TCAGAAGTCTCCGGACGGTG CTTTGTGGCAGGCCTCTGAAGA TCAT AATCC AGT A
TTTTC T - CT - TT TA

ATACTGTGTAGAAGAGATTG GGGAACTTCT GAGAGCT CGT CAGATA
GTGTAGAAGAGATTGG AACTTC GT GTT C

GGA	ACTTCTGTCGTTAACCC	GT	CG						
TAAG	CACCGAAGTTTCGGTC			TTCTCGG	GCG	GTCTAT	TACGTCTTCTCTGGCT		
TTGAAG	CA CGA /								
TCTTCTGCATGCTATCTGGC				-	-----	CG	-	C -	ATC
GGGCTCTT									

GAM1457	GAGGTCTAGGGTCTGCAGAA 1443	TAAGGTTTAC 4168	A----	A--	A C	AG T	ACGT
T GTT							

TGCCAGAGCCCCGAGTGTA	AAGGTTTACGAGGA	GGT TT T	GAGGAACGTG	TGC	GA	TGCCAG GC CCG TG	
GGTTTACGAGGAACGTGGTT	TTGTTTCTAAAACACCTAGC	CCAA C	GTTT				
TCCTCGTGGATCTTTAAACG	GCGCCTGGCAAATCCACGA	GCAGACTCTC		ACG	CT	ACGGTC CG GGC	AT TTCTAGGTGCTCCT
				AGCAC	AAA	- C	AA - CGAT C AAT

GAM1458	GCGAAACACTGAATCAAGAT 1444	TGAGATCTTG 4169	AAT	CT	TA	GCC	
CTCACCTCACTGTAGTTGTG	TGCAGTGTTT	GCGAAACACTG	CAAGATCTCAC	CACTG	GTTGT		
T							

CCTGTGACAATCCAGTGCTG	TGAGATCTTGTGCAGTGTTT	TGT					
TGT		GT-	TC	C-	GTG		

GAM1459	GCGGGATACCGCGTAAGATA 1445	TAAGATAGAA 4170	T	A	GT	GTCTC	
GAAAGGGTTGGCTATGTGTC	AGGGTTGGCT	GCGGGATACCGCG	AAGATAG	AAGG			
TGGCTATGT T							
TCTGGTAAACATAGTTACAC	TTTCTATCTTCGCGGTGTT	TTGT	ATGT				
				TGTTTTGTGGCGC	TTCTATC	TTTC	ATTGATACA /
				-	C	AC	AATGG

GAM1460	GCGTGAGATATTAGGGAACC 1446	TGAGATATTA 4171	T	A	ACC	T AAG	
TGGACCGCTGTGTAAGAAAA	GACCAGTTCAGGTACTCTAG	TGTCTCCCGC	GGGAACCTGG	GCG	GAGATATTAGGG	ACCTGG	GCTG GT A
			ACCG				
				CGC	CTCTGTGATCTC	TGACT	TGAC CA A
			C	A	---	-	GAA

GAM1461	GGTATCGGGTTTCACTATCC 1447	TTAACGCTTT 4172	G	CTATCC	CC	-	TCCTTGT T
CGTCCACAGTTTCTTGTAGA	TACATCTTCTCCTGCTTGTT	AACGCTTTTGAAGCCGAT	ACC	TTGAAAGCCG	GGTATCGG	TTTCA	CGT ACA GT AGA A
			ATAC				
				CCATAGCC	AAAGT	GCA	TGT CG TCT C
			G	TTTTC-	AT T	TCCTCT-	A

GAM1462	GGTGGGGGGTTTCAAGAGTGAA 1448	TATTTCAACA 4173	---	GG	A G	AGA	A C A TC
CGAGGAGAGGTATTGCAGTG	ATTCTCTGTGAGATATTTCA	TTCA					
AGTG TTC T							

ACACCACCCCTCGTTCAGTC
CGAGTTCCCAAACACC

CCAC CCC GAG CT ACTTGCTCC CCA AAC TTAT GAG /
AAA TT C G CCA C T A TG

GAM1463 GTATATACCACACACCCGTA 1449 TCAGTACGGA 4174 T C A -- TTAT
TAGATTGTGTTTATTTTGCT TGTGTGGTGT GTA ATACCACACA CCGTAT GATT GTGT T
ACACCTAATCAGTACGGATG CTAT ||| ||||| ||||| ||| |||
TGTGGTGTCTAT TAT TGTGGTGTGT GGCATG CTAA CACA T
C A A TC TCGT

GAM1464 GTCACACCCGAGGTAGTGAT 1450 CGAGGTAGTG 4175 A C -- A - G G G C
CTGCTGAAGGCTGGGGTGCT ATCTGCTGAA GTC CAC CGAG GTAGTG TCTG CT
AAGGCTGGG T CT T
CTTGAGGACCTAGCTTTGGT GGCT ||| ||| ||||| ||||| || ||||| |||
CAGACCATTACTGCTCGTGT CAG GTG GCTC CATTAC AGAC GG TTTCGATCC A GA T
GGAC - T GT C T - - G G

GAM1465 TCAAAATCCTGTGAATCGTC 1451 TGGATCAACC 4176 TC A CGA G GT T T AA
CGAGTGAGTCAAGTGTGTG CTGACGATGC TCAAAA CTGTG ATCGTC GT GA CAG TG
GTGT G
TAAGCCATACTCACCTGGAT ACAG ||||| ||||| ||||| || || ||| |||
CAACCCTGACGATGCACAGT AGTTTT GACAC TAGCAG CA CT GTC AC CATA /
GTTTTGA GT G TCC A AG C T CC

GAM1466 TGGCTTAAGCAGTCTGTGAC 1452 GTTCACAGAC 4177 - C C TTGTAT
ACTTAAGTTTTGTATAAAAA TCTTAGGACC TGG CTTAAG AGTCTGTGA ACTTAAGTT A
ATAATTTAAGTTCACAGACT A ||| ||||| ||||| |||||
CTTAGGACCA ACC GGATTC TCAGACACT TGAATTTAA /
A - - TAAAAA

GAM1467 TGGGCGTCTGTGTAGAGGAG 1453 AGAGGAGAGG 4178 CG T A A AC- G A
AGGAGGACTTGCGATTAGTC AGGACTTGCG TGGG TC GTGT GAGGAGAGG GG TTGCGATTA
TC T
ATGGAGTAATCGTAACTACC ATTA |||| || ||||| ||||| || ||||| |||
CCTCTCCTCCACACCGAGTC ACCC AG CACA CTCCTCTCC CC AATGCTAAT AG /
CCA TG C C - ATC G G

GAM1468 ATGTCAATTCATTAGCTTTC 1454 TTCAAAGCG 4179 C ATTA CT TA CAT
TTGATAATATCATTAACCGT TAGGATTACG ATGT AATTC GCTTT TGA ATAT T
ATTCAAAGCGTAGGATTAC T |||| ||||| ||||| ||| |||
GT TGCA TTAGG CGAAA ACT TATG A
- ATG- -- -- CCA

GAM1469 CGACCAGCCTGCGCTTGATT 1455 TCAGTTTTCA 4180 AGCC ATTT A TA G

TGAATTAATTTTAAGAGTAA	TAAGTGTA	CGACC	TGCGCTTG	GAATT	ATTT	AGA	T
TTTCCAAGTCAGTTTTTCATA	CGGT						
AGTGTAACGGTCG		GCTGG	ATGTGAAT	TTTGA	TGAA	TTT	A
	CAA-	ACT-	C	CC	A		

GAM1470	AGATGTCTGTTATCAACCAT	1456	TGTTATCAAC	4181	TCT	TA	C	TT	TC	A	-	C	G
	TTGTTGCGCAATGTCTGCGA		CATTTGTTG		AGATG	GT	TCAA	CA	TGT	GCGA	TGTC	TG	GAA
T													
	AGTGTTCCATGACAATCGTT		CGAA										
	ATATCTGTTTGAATGCTCTC				TCTAC	CG	AGTT	GT	ATA	TGCT	ACAG	AC	CTT /
	ATCT		TCT	TA	T	CT	T-	A	T	-	G		

GAM1471	CAACTGAAGCGTTCTGAGTG	1457	TGAAGCGTTC	4182	---	GA-	GA	ACA--	G
	ACGACAGGGAGACCAAAGGC		TGAGTGACGA		CAACTGAAGCG	TTCT	GT	CG	GG A
	GAAACAAAGGAAAGCCGCTT		CAGG						
	CAGTTG		GTTGACTTCGC		AAGG	CA	GC	CC	G
			CGA		AAA	AA	GGAAA	A	

GAM1472	CGACCATCGATTTTGCTGAC	1458	TATCAGCAGT	4183	A	A	ATT--	C----	T
	TGTGTAACCGCGTTCTATCA		TTACCGAGGG		CG	CC	TCG	TTGCTGA	TGTG A
	GCAGTTTACCGAGGGCG		CG						
			GC	GG	AGC	GAC	GA	CT	GCGC A
			-	G	CATT	ATCT	T	C	

GAM1473	GGCTATGTATGGGGCTTTTC	1459	TTGAAAGGCT	4184	GT---	CAATGG	CA
	CAATGGAGGCCAAATGCTTG		CCATTCCTAA		GGCTAT	ATGGGGCTTTTC	AGGC A
	AAAGGCTCCATTCCTAATAG		TAGC				
	CC		CCGATA		TACCTCGGAAAG	TTCG /	
			ATCCT		-----	TA	

GAM1474	GTCGATTAAGGATGTGATTT	1460	TGACGTGTTT	4185	--	GA	A	----	AC	T	---	TC
CC												
	TGAAACGCACTCGTTGGAGG		CAACCTTAAA		GTCGATT	AAG	TGTG	TT	TTGAAACGC	TCGT		
GGA	GGG	TAAA	A									
	GTCTAAACCAACTTTGAGCC		CACG									
	CAGTTTCATGACGTGTTTCA				CAGTTGA	TTC	GCAC	AA	AACTTTGTG	AGTA	CTT	CCC
GTTT /												
	ACCTTAAACACGGA		CTTCCA		CC	AG	A	TTCC	C-	-	TGA	GA
	GTTGAC											

GAM1475	GTGTTTTAGCTTGATGCTTG	1461	CATCGCAGTT	4186	----	-	C	CCAT	G
	ACCATCGGATACGTCATTAA		GATTTAAGCG		GTGTT	TTAGCT	TGATG	TTGA	CG A
	CATCGCAGTTGATTTAAGCG		C						
C			CGCGA		AGTTGA	GCTAC	AATT	GC	T
			ATTT		C	-	ACT-	A	

GAM1481 GACGTAGTGGGACTCTTGGT 1467 TCAGATCGTA 4192 C - C TTTTCTTC
TCAACAAACACTA TGG
CTGATGCGCTTTTTCTTCTC GATTTCCTACT GGA TCT TGGTCTGATG GCT TCGTAG
GCGGAA C
GTAGTCAACAAACACTAGCG GTGT ||| ||| ||||| ||| ||||| |||||

GAATGGCTTTTTCTGCGCAT CTT AGA GCTAGACTAC TGG AGCGTC CGTCTT
/
ATCTGCGACGTTTCGGTCAT T T - CTTTGC-- TATACG----- TTT
CAGATCGTAGATTTCCACTG
TGTT
GAM1482 GTTCCACGAGCGTCGTGAAG 1468 TAGAAGGCTT 4193 C GT- TG G G TG
GCTTTGAAAGTTGATTACT TGTGTGAGTT GTTC ACGAGC CG AAG CTTTC AAAGT A
TTAGAAGGCTTTGTGTGAGT TGTG |||| |||| || |||| ||||
TTGTGAGC CGAG TGTTTG GT TTC GGAAG TTTCA /
- AGT GT - A TT

GAM1483 TCCGAATAAGATGTGATGG 1469 TGATGTGAAT 4194 - C T - AAT -- G TT CA--
C TC
GCGCTGATGTGAATGTTCTC GTTCTCGTCT TGT GATGGGCGC GA TGTG GTT CTC TCTTG
GGCTG AC TTC A
GTCTTGTTGGCTGCAACCTT TGTG ||| ||||| || ||| |||| |||| || |||
CTCAGCTGGACGTAACCTCAG ACG TTACCCGTG CT ACAC CAG GAG AGGAC CCGAC
TG AGG G
CCTTCAGGAGAGCTGACCAC C T C C --- TC - TT TCAA C TC
ACTCCGTGCCCATTTGCACA
AATTTTCCCA
GAM1484 CATATTGATCGATTAGATCG 1470 TCGATTAGAT 4195 TA A A G T- A A A G
CCTA
AGCTTTGAAAAGGTTAACAT CGAGCTTTGA CA TTG TCGATT GATC AGCT TG AA GGTTA CAT
TGTGGC T
GTGTGGCCCTATATTTGCCA AAAG || ||||| |||| |||| |||| |||| ||||
TAATGGTGACCATTACATCG GT AAC AGCTAA CTAG TCGG AC TT CCAGT GTA
ATACCG /
GCTGGATCCAATCGAACAAC CC A C G CT A A G - TTTA
CTG

GAM1485 CATTCAACAGTTTGCGAGTC 1471 TCAACAGTTT 4196 - - GAGTCC CTTT TC
CAACTCTTTAGTTTCTTCGA GCGAGTCCAA CATTCAA CAGT TTGC AACT AGTT T
CTTTAGTTAAAAGCAGTGCT CTCT ||||| |||| |||| ||||
GCTTGAGTG GTGAGTT GTCG GACG TTGA TCAG /
C T AAAA-- TT-- CT

GAM1486 GCTCTTCTACGTGATCTTTT 1472 TTTACAGATG 4197 TCTAC A-- TTTC- - CTA T
TTCAATTCTTCTGCTATGGA GAATTATAAT GCTCT GTG TCTTT AATTCT TCTG
TGGACAT A
CATTATAGTGTTTACAGATG AGAG |||| || |||| ||||| |||| |||||
GAATTATAATAGAGACCCCA CGAGA TAC AGAGA TTAAGG AGAC ATTTGTG T
TATTCTAGAGC TCTTA CCC TAATA T --- A

GAM1487 TGGAATATTATCTTTGGATA 1473 TGTCATAACT 4198 AT-- CTT AT - T AAGCA AAC
GTTGTA CTGATAAGCAATTC TCATAAATAG TGGA ATTAT TGG AGTTGT AC GAT
ATTCACA G

ACAAACGCTACTGTGGATAT	TCTT							
CGAGTCTGTCATAACTTCAT		ACCT	TGATA	ACT	TCAATA	TG	CTG	TAGGTGT C
AAATAGTCTTGTCCA		GTTC	AAT	--	C T	AGCTA	CAT	

GAM1488	AGGCTGTAAAACTGATTATT 1474	AAAACTGATT 4199	-	-	TGAAG	CAAC	
ACTTTTCCC	A						
GAAGTCATCAACGCACACTT	ATTGAAGTCA	AGGCTG	TAAAACT	GATTAT	TCAT	GCAC	
CCC G							
TTCCCCCAGAAGGGTATCA	TCAA						
ATCGGTGCTGCTGTGAATGA		TCCGAT	ATTTTGA	CTAGTA	AGTG	CGTG	GGG A
TCGAGTTTTATTAGCCT		T	G	----	TCGT	GCTAACTAT	A

GAM1489	GCCTTTCCCTTCACCTTTGG 1475	AGAGATAGTT 4200	CCCTT	CTTT	TTTC	A	AT	CT--
AG	C	GT						
CAGAGATAGTTTCGAAGTCA	TCGAAGTCAT	CAC	GGCAGAGATAG	GA	GTC	TGC	TCAA	
C TGG ACT A								
TTGCCTTCAAACGTGGCACT	TGCC							
GTAAAAGTTCCAGTTGATCC		GTG	TTGTCTCTGTC	CT	CAG	ACG	AGTT	G ACC
TGA /								
TGCATCGACATCCCTGTCTC		AGTT-	T---	C---	A	CT	TCCT	-- T AA
TGTTTGTGTTGACTAGCGC								

GAM1490	GGATCAACAAAGCGAACAAA 1476	TTCACAAATT 4201	C--	-	AA	G	-	TC	-	ATC
GTTGTAGTCTGTAGGATCGT	TGCGTGTTTT	GGAT	AAC	AAAGCG	CAAA	TTGT	AG	TGTA	GG	
G										
ACCCGTACATGTTACAAAT	CGTT									
TTGCGTGTTTTCGTTCCCAT		CCTA	TTG	TTTTGT	GTTT	AACA	TT	ACAT	CC	/
CC	CCC C	GC	A	C	GT	G	CAT			

GAM1491	GGCGCCAAAGTTGCGGATAA 1477	TTGAATTCTA 4202	CCAA---	-	TAA	TA	C
GTTCAGGATAACTTGATCA	GCAACTGAGA	GGCG	AGTTGC	GGA	GTTCAGGA		
ACTTGAT A							
ATGTTCAAGTTCTTGAATTC	CTTC						
TAGCAACTGAGACTTCGCC		CCGC	TCAACG	TCT	TAAGTTCT	TGGACTTG	A
	TTCAGAG	A	---	--	T		

GAM1492	AATGTGATATCCAGTTGTAA 1478	TAAGTGAGCC 4203	GA	----	A----	GTCAACTA--
- AGT						
GTGAGCCAAAAGTGTCAACT	AAAAGTGTCA	TATCCAG	TTGTAAGTG	GCCAAAAGT		
CGTG CAT T						
ACGTGCATAGTTTTCGTGTC	ACTA					
ATGATCCACTAAAATTTTGG		ATAGGTC	AATGTTTCGC	TGGTTTTTA	GTAC	GTG
/						
GTATTTCCGCTTGTAATGTT		AG	TTTGT	CTTTA	AAATCACCTA	T CTT
TCTGGATAGAATATT						

GAM1493 CAGTTCTCCGGTAATCTCCT 1479 TGAGATGATT 4204 - T TC TT AT AACCTT -
T
CATTAAGGAATCCCAACCCT CTGGTAGAAC CAGTTCT CCGG AATC CTCA AAGGA CCC
GTAG AATT T
TGTAGAATTTTGAGATTCCT TG ||||| ||| ||| ||| ||| ||| ||| ||| |||
ACTGTCCAGGGTCCTTTGAG GTCAAGA GGTC TTAG GAGT TTCCT GGG CATC
TTAG G
ATGATTCTGGTAGAACTG T - TA -- -- ACCTGT- C A

GAM1494 CCTTTGAGAATGTTTCTAGG 1480 TATCTTGAGG 4205 TT- T TCTA TC T TCTT T
TCCTCGTCAGTTGGTTCTTC ACCAGCTTCT CCT GAGAA GTT GGTCTCG AG TGGT CG A
GTA CTTGTCTGCTATCTTGA TTAC ||| ||||| ||| ||||| || ||||| ||
GGACCAGCTTCTTTACAGG GGA TTCTT CGA CCAGGAGT TC ATCG GT C
CAT - ---- -- T TCT- T

GAM1495 GCTGATATGCTTTGGAAATG 1481 TGATATGCTT 4206 TGCTTT AT C T
ACTATGCTTAATCTGTTCCCT TGGAAATGAC GCTGATA GGAA GA TA G
CTTTTATCAGC TATG ||||| ||| |||
CGACTAT CCTT CT AT C
TTTCT- GT A T

GAM1496 GTACAAGTGCATGTTAATTA 1482 ACAAGTGCAT 4207 - ---- - - T TA
GTTTGTA AATTCAATCTGCA GTTAATTAGT GTACAA GTGCA TG TTAAT TAG TTG A
TTAGTCGT CAGCTGTACATT TTGT ||||| ||||| || ||||| ||| |||
GTAC CATGTT CATGT GC GATTA GTC AAC A
A CGACT T C T TT

GAM1497 GTCTAGCTGAGCCACGAGGT 1483 TAGCTGAGCC 4208 GC A G AC--- - TAG-- C
CACAGATCTTAGTGACGCAT ACGAGGTCAC GTCTA TGAGCC C AGGTC AGA TCT TGACG
A
ACGTTGAGGTTAGATTCTTC AGAT ||||| ||||| ||||| ||| ||| |||
CAGGGCCTGAGGTTCAATAG CAGAT ACTTGG G TCCGG TCT AGA GTTGC T
AC A- A- GACCT T TTGGA A

GAM1498 GTGTGCAGCGGCCCACTCCT 1484 TGAGTAGGAG 4209 TG C A- C TG T ATG
CATGTCTGTA ACTGATGCCT GGCTCCTGTG GTG CAG GGCCC CT CTCA TCTG AACTG C
CCTAGTTTCAGATGAGTAGG TAC ||| ||| ||||| || ||||| ||| |||||
AGGGCTCCTGTGTAC CAT GTC TCGGG GA GAGT AGAC TTGAT C
GT C AG T -- T CCT

GAM1499 TGAAAATGCAACCTACACAT 1485 TGTTATTGTT 4210 ATG TAC T A TC
GTAAAGTCTCTAGGATGTTA TTGGTTGGAG TGAAA CAACC ACA GTAA GTC T
TTGTTTTGTTGGAGTTTCA TTTC ||||| ||||| ||| ||||| |||
ACTTT GTTGG TGT TATT TAG /

GAG TTT - G GA

GAM1500 CGTGTGAGTCGATTAGTCGT 1486 ATAAAGATCG 4211 G A C ----- G - --
GTAT
TTCAGTTCGGGATTCTTGAT GCTGTTTTAA TCGTTTC GTT GGGAT TCTT ATGATA GA
AGGCAAA T
GATAGAAGGCAAAGTATTAC ATCC ||||| ||| ||||| ||| ||||| || |||||
TAATTTGCTTAGTCATATCA AGCAAAG TAG TCCTA AGAA TACTAT CT TTCGTTT
A
TAAAGATCGGCTGTTTTAAA - A T AATTTGTCGGCT A A GA AATC
TCCTTGATAGAAACGAGTCA
ACAGACACACG
GAM1501 GATAATTTATTAATATAAAG 1487 TAATTTATTA 4212 A AAAG-- AGA-- AT-- C T- -
CTCA
CGTATTTAGATATTGCAATG ATATAAAGCG T ATAT CGTATTT TATTGCA GT TCACTAC
GC CTGA G
TCTCACTACTGCCTGACTCA TATT | ||| ||||| ||||| || ||||| || |||
GTTATATCGGCGTCTGTAGT A TATA GCGTAAA ATGACGT TA AGTGATG TG
GGCT T
GAAATTGAATGCAGTAACAT C CTAAAA ATACA AAGT A TC C ATAT
AAAATGCGAAAATCATATCA
ATAAATGCGTT
GAM1502 GTAATTTGTCCGAGATAGCA 1488 TAGCATTAGT 4213 TCC A - T GCA A
TTAGTCAAATCTGCAAACAT CAAATCTGCA GTAATTTG GAG TAGC ATTAG CAAATCT AAC T
AGTTAAAGATTTGTTAATAG AACA ||||| ||| ||||| ||||| |||
CTAGTTCTAAGTTAT TATTGAAT CTT ATCG TAATT GTTTAGA TTG /
--- G A - AA- A

GAM1503 TACAACGCGTAACAAAGGGT 1489 TGAAATCATC 4214 AA GG- ACC GCCC- AA
CGCCCACA AT
GGACCTAATAGCCACAGAA GCCCACAGCT AAC AG TGG TAATA ACAGA CTGAAATCAT
GCTCT A
ACTGAAATCATCGCCACAG CTAT ||| || ||| ||||| ||||| ||||| |||||
CTCTATAAAAGAGTGCTTTA TTG TC GCC GTTAT TGTCT GACTTTGGTG
TGAGA /
GTGGTTTCAGCCTCTGTCAA AA ATA A-- ATAAC CC ATTTG-- AA
TATATTGACCGATACTAAGT
TACGTTGTA
GAM1504 TGAGATAGTATCAGACACTG 1490 TGAGTACGTA 4215 ATAG A G GAA C---- A A
TGGAAGTGGCACGTAATTCA CAACCTACCA TGAG TATCAG CACT TG GTGG ACGTA
TTCATT A
TTAAGAATGAGTACGTACAA ACAG |||| ||||| ||||| ||| ||||| |||||
CCTACCAACAGAGTGCTGAT ACTT ATAGTC GTGA AC CATC TGCAT GAGTAA /
AATCCTTCA CCTA - G AAC CAACA - G

GAM1505 TTAGGATCTGCATTGTCTGG 1491 TCACCAGGAA 4216 CTGCA -- A TA TC
TAATTTATCATCATTTGAAT CAAATAAAAT TTAGGAT TTGT CTGGT ATT TCA A

AGTCACCAGGAACAAATAAA CCTA ||||| ||| ||||| ||| |||
 ATCCTAA AATCCTA AACA GACCA TGA AGT /
 AAATA AG C TA TT

GAM1506 TTCGAAAGTTCCTTCAAGAT 1492 AGCTGTTCTA 4217 TCA TTTC ATATA TC A--- T C
 TC T AG

TTCGTGGCATATATACATCA GTCTCATCGA AGA GTGGC TACA AGC GCTG TCTAGT
 TCA GA GAC T
 GCAGCTGTTCTAGTCTCATC TGAC ||| |||| ||| ||| ||| ||||| ||| |||
 GATGACAGTATTGTCTTCTT TCT TACCG ATGT TCG CGAC AGGTCA AGT CT
 CTG A

GAACTGGACCAGCATTAGCT TC- ---- CG--- CT ATTA C - T- T TT
 TCTGTAGCGCCATTCTCTGG
 GATCAATCGAA

GAM1507 TTTGTGGGTAAATTGTACAAT 1493 TGAGATAGCA 4218 -- T- CAATG AA TA AG
 TAACA - G

GGCAATGTCTCTACGAGGAT TTACTIONAAT G GG AATTGTA GC TGTCTC CG GATCCT
 TGTT TTCTT T
 CCTTAACATGGTTTTCTTGT TCTC | || ||||| || ||||| || ||||| ||||| |||||
 TCAAGAATAACCGAGCATGG C CC TTAACAT CG ATAGAG GC CTAGGG GCCAA
 AAGAA T
 GATCAACGGTGAGATAGCAT AA TC CATTA -- TG AA TACGA T C
 TACTACAATTCTCCAACACA
 AA

GAM1508 ACGATCTCAGTGTACAAGTT 1494 AAAGAGCTGT 4219 CA TGTAACA AA AA CC
 CCTCCATA TACC ACA

TTGTAACATTTGAAAACCAA CGAACTGAGA AGTTT TTTGA ACC TATC ATT AATGCA
 TC G
 TATCCCATTCCTCCATAAAT TCCG ||||| ||||| ||| ||| ||| ||||| ||
 GCATACCTCACAGCTAGAAC TCGAG AACT TGG ATAG TAG TTACGT AG /
 TGCATTGATCAGATAAGGTG TG ----- G- A- AC ----- CA-- ATC
 TCAAAGAGCTGTGCGAACTGA
 GATCCGT

GAM1509 AGGCATCAAACCTCCTCTGAA 1495 TTAAGTGCAA 4220 A TCCT A AATC A T TAG
 CTTGAATCCACATTTAGATA GCTCAGTAAT AGGCATCA AC CTGA CTTG CAC TT AGA A
 GAGTTTCTTAAGTGCAAGCT GTAT ||||| || ||| ||| ||| |||
 CAGTAATGTATGGTGCCT TCCGTGGT TG GACT GAAC GTG AA TCT /
 A TAAT C ---- - T TTG

GAM1510 TAGTGGTTGCACTTGCAATT 1496 TGAGATCGCA 4221 TT ---- A TTTGA TTT
 TCATCATGTTTGAGACTTTA CTATGAGTGT TAGTGG GCACT TGC ATTTTCATCATG GAC A
 AATGTTCCATGGTGAGATCG TCCA ||||| ||||| ||| ||||| ||| |||
 CACTATGAGTGTTCATTA ATTACC TGTGA ACG TAGAGTGGTAC TTG /
 T- GTATC C C---- TAA

GAM1511 TTTGTGTGGTATGCATGTAT 1497 TGTGGTATGC 4222 ---- -- - ATCA TTCTAAAA ATT
 CAGACTTCTAAAAGCCATTG ATGTATCAGA TTTGTG TGGT ATG CATGT GAC GCC G

AAGAGGCGTCCATGACATGA CTTC ||||| ||| ||| ||||| ||| |||
 CATTTCATCAATTATCACAAA AAACAC ACTA TAC GTACA CTG CGG A
 TATTA CT A GTAC ----- AGA

GAM1512 GAAGAATTGAAAAGAGTCTT 1498 TTTGTCCAAG 4223 ATT A TTTT TT
 GTTTTGGGTTTTTCATAAAT GCTCTTCTCT GAAGA GA AAGAGTCTTG GGGTTT C
 TTTGTCCAAGGCTCTTCTCT CATC ||||| || ||||| |||||
 CATCTTT TTTCT CT TTCTCGGAAC TTAA /
 ACT C CTGT TA

GAM1513 GAGAGCTTTGAAGAGAAAGA 1499 TGTAATCGAT 4224 T- AAGAGAAA TGA T
 TTTGAAGAATGAATTCTGTA GCAATTGCTT GAGAGC TTG GATT AGAA G
 ATCGATGCAATTGCTTTT TT ||||| ||| ||| ||||
 TTTTCG AAC CTAA TCTT A
 TT GTAG---- TG- A

GAM1514 GTCCTTCACTTTAATTAAAA 1500 TCAGTTTAAA 4225 --- TTAAAA C C TACT
 AGCTCAGTTCGTATACTAAC GCCATGAAGG GTCCTTCA CTTTAA GCT AGTT GTA A
 CCTATTAAGTCAAGTTAAAG GC ||||| ||||| ||| |||||
 CCATGAAGGGC CGGGAAGT GAAATT TGA TCAA TAT /
 ACC ----- C T CCCA

GAM1515 GTTGAGTATTAGGATTGTGC 1501 TGAGTATTAG 4226 T A CCAAAC TT-- -- CAT
 CAAACTGAAATTGGGCTCTG GATTGTGCCA GTTGAGTAT AGG TTGTG TGAAA GGGCTCT
 GC C
 CCATCCATCGCCAAGAGCCT AACT ||||| ||| ||||| ||||| ||||| ||
 CCTCTTTCACCACAAACCTG TAAC TTATG TCC AACAC ACTTT TCCGAGA CG C
 TATTCAAT - A C----- CTCC AC CTA

GAM1516 TTGTGTGAGTTACTATCATG 1502 TGAGTTACTA 4227 TG T ACTA - AA
 CGCAGAAACCGCTTTGTGTA TCATGCGCAG T TG GAGTT TC ATGCGCAGA C
 TCGACATGAACTCTATGG AAAC | ||||| || |||||
 G AT CTCAA AG TATGTGTTT C
 GT - GTAC C CG

GAM1517 GATGGATTGGTAAGCTATGT 1503 TAAGCTATGT 4228 TT T TA---- TTCTCA TAA
 GTCTTCTCAATGGTAAACTG GTCTTCTCAA GATGGA GG AAGC TGTGTC ATGG A
 CCCATGCCTTGACACAATTC TGGT ||||| || ||||| ||||| |||||
 TTGTTTCCCCTTCATT TTA CTT CC TTTG ACACAG TACC C
 CC - TTCTTA TTCCG- CGT

GAM1518 GTCACTGAAATGCGCCATTA 1504 TGAAATGCGC 4229 C ----- CATTATCT TG A
 TCTGTCTGAAAGTTGGACGC CATTATCTGT GTCA TGA AATGCGC GTC A A

GCATTATCCATCACTGGC CTGA ||||| ||||| ||| |
CGGT ACT TTACGCG CAG T/
C ACCTA ----- GT G

GAM1519 TTGCGCCATTGTTGTAAAAA 1505 TATCAGAGCC 4230 C----- TA AAT CTAAC -----
AA
TTGTTCTAACTTTTGATAAT AAACATCATT TTGCG CATTGTTG AA TGTT TTTTGATA
ATGTTG A
GTTGAAAATACAGCATCACT GCCA ||||| ||||| || ||||| |||||
CCTATCAGAGCCAAACATCA AACGT GTAACAAC TT ACAA GAGACTAT
TACGAC A
TTGCCAACAATGCCATCAAT AACTACC CG ACT ACC-- CCTCAC AT
GCAA

GAM1520 AACATCAATGTCGCAATTTG 1506 CAGAATGTCG 4231 C - GT - A G
TATTGTCCAATACAGAATGT GTGATTCGTG AACAT AA T CG CA TTTGTATT T
CGGTGATTCGTGTT TT ||||| || || |||||
TTGTG TT G GC GT AGACATAA C
C A TG T A C

GAM1521 ACCATTCCAAGTCACTGTGT 1507 TATCATAAGC 4232 TTCCA CTG- TA GAT
GTAAGAAGATTATATTCTAT TTGACTACAT ACCA AGTCA TGTG AGAA T
CATAAGCTTGACTACATTTG TTGG ||||| ||||| ||||| |||||
GT TGGT TCAGT ATAC TCTT /
TTACA TCGA TA ATA

GAM1522 CTCCCTGATCTATGTATCTA 1508 TAATACCATT 4233 CT TA--- C A ACTC
GCGGTGTTATTATAAACTCT GGATGCACCA CTCC GATC TGTATCTAG GGTGTTATT TAA T
CAACATTGGAATAATACCAT TTGG ||||| ||||| ||||| ||||| |||||
TGGATGCACCATTTGGTCCCG GAGG CTGG ACGTAGGTT CCATAATAA GTT C
GAG CC TTACC A G ACAA

GAM1523 CTCGTTTCATAAAGAGATCA 1509 TCAGGAATCC 4234 TT A T-- TCCAAA TATAA
TCT
GGAATCCAAAGAGCTATAAA AAAGAGCTAT CTCG TC TAAAGAGA CAGGAA GAGC
ATAGA C
TAGATCTCTGGTTCTATGCT AAAT ||||| ||||| ||||| ||||| |||||
CCTCGTTTCCTGTATTCTTT GAGC AG ATTTTCT GTCCTT CTCG TATCT T
TTAAGATCGAG T- A TAT TGCTC- ---- TGG

GAM1524 GACATACATACTATCTTTAA 1510 TGAGATCTTC 4235 C TT----- CTCT C--- AAT-
- T
TAGAACTCTTTTCATCCAGT TATTTTATCA CATA TATCT AATAGAA TTTCAT CAGTTG
GGA T
TGAATGGATTCGTCCTTAAC TTTT ||||| ||||| ||||| ||||| |||||

C CAACTGATTAATGAGATCTT GTAT GTAGA TTATCTT AGAGTA GTCAAC CCT
 CTATTTTATCATTTTCCAGA A CCTTTTACTATT CT-- ATTA CAATT G
 TGATATGTATGTC

GAM1525 GCGCAATTCATTTTCGGGTT 1511 TAATATCGAC 4236 CAATTC T GT T
 TAAATTCTTTAATATCGACA AATTCATAC GCG ATT TCGG TTAAA T
 ATTCATACGC GC ||| ||||| |||||
 CGC TAA AGCT AATTT /
 ATACTT C AT C

GAM1526 GCTTTCCAGACGACTCGAGC 1512 TAATCGTTTCG 4237 TCC- C- CT T TCTT
 CTCTTT
 CTTTATTATATTCTTGTATC AACTCGTCTC GCTT AGACGA TCGAGC TTAT ATAT GTAT T
 TCTTTTCTCTTTCGTATTGT CCCA |||| ||||| ||||| ||||| |||||
 GTATATAATCGTTTCGAACTC CGAA TCTGCT AGCTTG AATA TATG TATG C
 GTCTCCCCAAGC CCCC CA CT - TGT- CTTTCT

GAM1527 GTGGTAAGAACCGATAGGTT 1513 TAGGTTATTG 4238 C----- AG C GTAT-
 ATATT
 ATTGACATTGTATGGTTTTA ACATTGTATG GTGGTAAGAA CGAT GTTATTGA ATT
 GGTTTTAA C
 AATATTCTATAACTTGAGAC GTTT ||||| ||||| ||||| ||||| |||||
 TTGATAGATATTAATGACGA CACTATTTT GTTA CAGTAATT TAG TCAGAGTT T
 ATTGAAAATTATTTTATCA ATTAATA AG A ATAGT CAATA
 C

GAM1528 GTGTAGATTTGATACGGCTA 1514 TCTGGCGGCT 4239 T T ATAC T TA TAAT
 GA TGT
 TTCTGGCGGCTAGAATGGCA AGAATGGCAT G GTAGA TTG GGC ATTCTGGCGGC
 GAATGGCA CTG TGT G
 TAATCTGGATGTTGTGTAGT AATC | ||||| ||||| ||||| ||||| |||||
 ACAAGTGGCTGCTATTTCTG C CATCT AAC CTG TGAGACCGTCG TTTATCGT GGT
 ACA T
 CTGCCAGAGTGTCCAATTCT - T ---- - TC C--- GA TGA
 ACC

GAM1529 TACAAAGGAGATGATTTATC 1515 TGATTTATCG 4240 ----- TTATCGAT TT - C
 TC A
 GATGGTATTAAGAATTCGTT ATGGTATTAA ACAAAGGA GATGAT GGTA AAG AATT
 GTTTT GAC T
 TTTCGACATCCGTCAAAACC GAAT ||||| ||||| ||||| ||||| |||||
 AATTCCTTTTGCCTGTATC TGTTTCCT CTACTA CCGT TTC TTAA CAAAA
 CTG C
 ATCCAGTTTTCCATCCTTTG ACCTTTTGAC TGT----- TT C C -- C
 TA

GAM1530 TCATTAATAGGGACTTGACG 1516 TGACGTACGT 4241 T GGAC- C A
 TACAAAATGATCG CT ATAA

TACGTAGCGTACAAAATGAT AGCGTACAAA TTAA AG TTGA GT CGTAGCG TTC
 GGTATATAG A
 CGTTCCTGGTATATAGATAA ATGA |||| | |||| | ||||| || |||||
 AGAGTCCTATATATTTGAAA AATT TC AGCT CG GCATTGC AAG TTATATATC
 G
 ATCGTTACGGCTCGATTAAA - AAATT - - TAA----- T- CTGA
 CTTTAATGA

GAM1531 TGATGGCTGATAGTGCTACT 1517 TGGCTGATAG 4242 -- TAG- CTGCAC T
 GCACAAGATTTCCAATCTTT TGTCAGTCA TGATG GCTGA TGTCA AAGATT C
 GACAATTTTCAGCACCATTA CAAG |||| | |||| | |||| | |||| |
 ATTAC CGACT ACAGT TTCTAA /
 CA TTTA ----- C

GAM1532 AATGGTAGCGCATCTTTAAC 1518 TAGCGCATCT 4243 C CTTT - TT CT
 TCGTCAGTTAGCTCTTTCTT TTAAGTCGTC AATGGTAGCG AT AACTCG TCAG AG C
 TTGATCGAGTTCGTCGCTAC AGTT ||||| || |||| | |||| |
 TATT TTATCATCGC TG TTGAGC AGTT TC T
 - C--- T T- TT

GAM1533 GACTTGATAGATATTAGTGA 1519 TCACCACGTG 4244 - TAG TA- TTGAA
 TGAATTGAAAATTATTTTAA TGTTCAGGA GA CTTGA ATAT GTGATGAA A
 TCACCACGTGTGTTTCAGGA TC || |||| | |||| | |||| |
 TC CTGGACT TGTG CACTATT A
 A TTG CAC TTATT

GAM1534 GGCTATTCTGGCGGCTAAAA 1520 TAAAATGGCA 4245 C TA TAAT GA TGT
 TGGCATAATCTGGATGTTGT TAATCTGGAT GG TATTCTGGCGGC AAATGGCA CTG TGT G
 GTAGTACAAGTGGCTGCTAT GTTG || ||||| |||| | |||| |
 TTCGGCTGCCAGAGTGTCC CC GTGAGACCGTCG TTTATCGT GGT ACA T
 T GC C--- GA TGA

GAM1535 GTGCTGAGGTCTTTCAACGA 1521 TTTCAACGAT 4246 - GATC TTTCAACA TA ---
 A- AA
 TCTTGTTATTTATTTTCAAC CTTGTTATTT TTCAAC TTGTTATTTAT AG AGATTTTTC CAA
 GTTTT A
 AAGTAAGATTTTCCAAAGT ATTT |||| | ||||| || ||||| || |||| |
 TTTAAAACCAAATAGTTGT GAGTTG AATAATAAATG TT TCTGAAAAG GTT
 TAAAA A
 ATGAAAAGTCTCGTTCGTAA T AGCC C----- GC TAT GA CC
 ATAATAACCGAGTTGAGTTT
 ATCCTTATAT

GAM1536 TACAAAGGAGATGATTTATC 1522 TGATTTATCG 4247 ----- TTATCGAT TT - C
 TC A
 GATGGTATTAAGAATTCGTT ATGGTATTAA ACAAAGGA GATGAT GGTA AAG AATT
 GTTTT GAC T

TTCGACATCCGTCAAAACC	GAAT								
AATTCCTTTTTGCCTGTATC		TGTTTCCT		CTACTA		CCGT	TTC	TTAA	CAAAA
CTG C									
ATCCAGTTTGCCATCCTTTG		ACCGTTTGAC		TGT-----		TT	C	C	-- C
TA									
GAM1537 TCGCTTCTATCTTGTTTAGA 1523	TGACTAGATA 4248	CT	GTTT	TT	TAAA	TCTC--			
ACATA									
TTTATTTTTATAAAGTTTAG	AACTATCAGT	CG	TCTATCTT	AGATTTATT	TA	GTTTAGTC			
CTTCCA A									
TCTCTCCTTCCAACATAATA	AAGT								
AACGTGGAAGTCATCTGACT		GC	AGATAGAG	TTTGAATGA	AT	TAGATCAG			
GAAGGT T									
AGATAAACTATCAGTAAGTT	--	ATAT	CT	CAAA	TCTACT	GCAAA			
TTATAGAGATAGACGA									
GAM1538 GGCCATTTTTAATATTTAAG 1524	TAAGTGATAC 4249	CC	TT-	-	AA	ATA	AAAC		
TATTTA									
TGATACAAACTATCTCGAC	AAAACATCT	GG	ATT	TAAT	ATTT	GTG	CA	TATCTCGACT	
A									
TTATTTAACTCTTTAGTCGA	CGAC								
GATATATGGACACAGATAGT		CC	TAG	ATTG	TAGA	CAC	GT	ATAGAGCTGA	/
TATATGATAACC	AA	TAT	A	--	AG-	AT--	TTTCTC		
GAM1539 TACAAAGGAGATGATTTATC 1525	TGATTTATCG 4250	-----	TTATCGAT	TT	-	C			
TC A									
GATGGTATTAAGAATTCGTT	ATGGTATTAA	ACAAAGGA	GATGAT	GGTA	AAG	AATT			
GTTTT GAC T									
TTTCGACATCCGTCAAAACC	GAAT								
AATTCCTTTTTGCCTGTATC		TGTTTCTT		CTACTA		CCGT	TTC	TTAA	CAAAA CTG
C									
ATCCAGTTTGCCATTCTTTG		ACCGTTTGAC		TGT-----		TT	C	C	-- C
TA									
GAM1540 TATCTTGTTTAGATTTATTT 1526	TGACTAGATA 4251	GTTT	TT	TAAA	TCTC--				
ACATA									
TTATAAAGTTTAGTCTCTCC	AACTATCAGT	TATCTT	AGATTTATT	TA	GTTTAGTC				
CTTCCA A									
TTCCAACATAATAAAAGTG	AAGT								
AAGTCATCTGACTAGATAAA		ATAGAG	TTTGAATGA	AT	TAGATCAG	GAAGGT	T		
CTATCAGTAAGTTTATAGA		ATAT	CT	CAAA	TCTACT	GAAAA			
GATA									
GAM1541 TTCACTCGTTTCATAAAGAG 1527	TCAGGAATCC 4252	A	TT	A	T--	TCCAAA	CTATAA		
TCT									
ATCAGGAATCCAAAGAGCTA	AAAGAGCTAT	TTC	CTCG	TC	TAAAGAGA	CAGGAA	GAG		
ATAGA C									
TAAATAGATCTCTTGTTCTA	AAAT								
TGTTTCCTCGTTTCCTGTATT		AAG	GAGC	AG	ATTTTCT	GTCCTT	CTC	TATCT	T

CTTTTAAAGATCGAGGAA

- T- A TAT TG---- CTTG-- TGT

GAM1542 CAAACGGAGTAAAATAAATA 1528 TTAGTATTTT 4253 C GTAA T C ATGC
TCATTAATATATGCTCTAGA TATTAATCCT CAAA GGA AATAAA AT ATTAATAT T
TATTAGTATTTTTATTAATC TTG ||||| ||||| ||||| |||||
CTTTG GTTT CCT TTATTT TA TGATTATA /
- AA-- T - GATC

GAM1543 CTCGTTTCATAAAGAGATCA 1529 TCAGGAATCC 4254 TT A T-- TCCAAA CTATAA
TCT
GGAATCCAAAGAGCTATAAA AAAGAGCTAT CTCG TC TAAAGAGA CAGGAA GAG
ATAGA C
TAGATCTCTGGTTCTATGTT AAAT ||||| ||||| ||||| |||||
CCTCGTTTCCTGTATTCTTT GAGC AG ATTTTCT GTCCTT CTC TATCT T
TTAAGATCGAG T- A TAT TG---- CTTG-- TGG

GAM1544 GGACATGTAACTTGACAAA 1530 TGTAAACTTG 4255 CA- AACT AATTG TTG
AATTGTGACTTTGTTATTGG ACAAAAATTG GGA TGTA TGACAAA TGACT T
TCAACCTTTGTTGTACAAAT TGAC ||||| ||||| ||||| |||||
TCC CCT ACAT GTTGTT ACTGG T
TAA ---- CCA-- TTA

GAM1545 GGTCTATGTCTCTTATTAGA 1531 TTAGAGATTT 4256 TAT CTC A CTTC A-- ATA
GATTCAGCTTCTGGAATAG CAGCTTCTGG GGTG GT TT TTAGAGATTTTCTAG TGGAAT
GGATA A
GATAATAATTAATATCTATA AATA ||||| ||||| ||||| |||||
ATTTTATTGAGGTTTCTGAC CCAG CA AA AGTCTTTGGAGTT ATTTTA TCTAT T
AATTACTTTGACC TTT TT- C ---- ATA AAT

GAM1546 TACAAAGGAGATGATTTATC 1532 AACCAATTCC 4257 ----- TTATCG - TT - C
TCA A
GACGGTATTAAGAATTCGTT TTTTGCCTG CAAAGGA GATGAT AC GGTA AAG AATT
GTTTT AC T
TTTCAACATCCGTCAAACC TATC ||||| ||||| ||||| ||||| ||||| |||||
AATTCCTTTTGCCTGTATC GTTTCTT CTACTA TG CCGT TTC TTAA CAAAA TG
C
ATCCAGTTTGCCATTCTTTG ACCGTTTGAC ----- T TT C C C-- C
TA

GAM1547 TCTATCTTGTTTAGATTTAT 1533 TGA CTAGATA 4258 GTTT TT TAAA TCTC--
ACATA
TTTTATAAAGTTTAGTCTCT AACTATCAGT TCTATCTT AGATTTATT TA GTTTAGTC
CTTCCA A
CCTTCCAACATAATAAAAGT AAGT ||||| ||||| ||||| |||||
GGAAGTCATTTGACTAGATA AGATAGAG TTTGAATGA AT TAGATCAG GAAGGT
T

AACTATCAGTAAGTTTTATA
GAGATAGA

ATAT CT CAAA TTTACT GAAAA

GAM1548 ATCGTAACGAGACGGAATCC 1534 TGGGTTCCGG 4259 AGA- A -- A-- T
AAAGAACACGCCCGATCTTA GGGCGTTACG ATCGTAACG CGGAATCCAAAGA CAC GCCCG
TC T
AGACCACGGGCACGTGTCTT AT ||||||| ||||||||| || ||||| ||
TGGGTTCCGGGGGCGTTACG TAGCATTGC GCCTTGGGTTTCT GTG CGGGC AG A
AT GGGG - CA ACC A

GAM1549 ATGGGATTAAATACCAGGGA 1535 TTAAATACCA 4260 A - AG GA G GG TC ATG A
- CTG T
TACAGGCTGTAGGTTCCGTA GGGATACAGG GG TTAAAT ACC G TACAG CTGTA T GGTA
GGT CCA GG GAG G
ATGGGTACCAGGCTGGAGTG CTGT || ||||||| || | ||||| |||| | ||||| || |||||
ACTCATACCATGGGATTAAA CC AATTTA TGG T ATGTC GACAT G CCAT TTA GGT CC
CTC /
TACCAGGGATACAGGCTGTA A A CT GG G AG GA AAA G A ATA A
GGTTCGGTAATTTAAACCTA
T

GAM1550 CCGTTTATCAAAATGGAAAA 1536 TGGAAAAATT 4261 TTTA A - -- AAA
ATTAAGGCTTTGCGTTAAAA AAGGCTTTGC CCG TCAAA TGGAAAAATTAAG GCT TTGCGTTA
T
TCTGCTAACGCAAAGGGCAC GTTA || ||||| ||||||||| || |||||||
TTAATTTTCCAGTTTGGAC GGC GGTTT ACCTTTTAAATTC CGG AACGCAAT C
TCGG TCA- G A GA CGT

GAM1551 GAAGTTACATTCCGACATAC 1537 TGGGTCCCTT 4262 A C ATAC C AAA C----
ACGCA
AAGCGGACCCAAAAAACAC CCACGTCGCA GAAGTT CATT CGAC AAG GGACCCAAA ACAC
CCA A
CCCAACGCAAAACAACCTGGA ATGA ||||| ||||| ||||| ||||| ||||| ||||| |||||
GACTGTGTCTTTGGGTCCCT CTTTAG GTAA GCTG TTC CCTGGGTTT TGTG GGT
A
TCCACGTCGCAATGAGATTT A C CACC - C-- TCAGA CAACA
C

GAM1552 GAATACGGCCAACGCGCCAG 1538 CGGCCAACGC 4263 CGC G AAC CCTCCA A
GTA AAT CT
CGTCCAACCGCCCTCCAACC GCCAGCGTCC CAA GCCAGC TCC CGC ACCGTGC GCGCC
TATTG TGC T
GTGCAGCGCCGTATATTCGA AACC || ||||||| ||||| ||||||| ||||| ||||| |||||
ATTGCCTTCCGCACGAATAC GTT CGGTGCG AGG GCG TGGTACG CGCGG
ATAAGC ACG /
GGGGCGCAGCATGGTCGCGG A-- G --- C----- A GGC --- CC
GAGGCTGGCATTGCGCAATA
TTC

GAM1553 GACGCCGTTAATAATTGGCA 1539 TAAACTGCGA 4264 G AATAA-- A A - GC- C
TAG

GTAAACTGCGAAAGGGCGTA AAGGGCGTAC GAC CCGTT TTGGC GT AACTGCG AAAGG
 GTACATCG AG T
 CATCGCAGTAGTGATTTTAC ATCG ||| |||| |||| || ||||| |||| ||||| ||
 GATGTGCACACCTTTCCGCG CTG GGCGA AACCG CA TTGGCGC TTTC
 CGTGTAGC TT G
 GTTACCGCCAACAACAAAA - AAACAAC C C C ACA A TTA
 GCGGGTC

GAM1554 GGCGGGTTCGACCCATTGAC 1540 TGCGATCGCG 4265 C C AT C CTC - GCA
 CGCATCCTCGGTGGCCGGGC GGGTCTGACC GG GGGTT GACCC TGA CGCATC GGT
 GGCCGG G
 AGAGGCCGGCCGGCCAAAGG CACC || |||| |||| || ||||| || |||||
 TGCGATCGCGGGGTCTGACC CC CCCAG CTGGG GCT GCGTGG CCG CCGGCC /
 CACC A T GC A AAA G GGA

GAM1555 GGGCGCTGGGGGTGATATGT 1541 TGATATGTTC 4266 C GT A C CTTAC
 TCTGATGACCGCCGCCTTAC TGATGACCGC GGG GCTGGGG GATATGTTCTG TGAC GCCGC
 G
 GTTTGCAGCGGTGTCAGCGG CGCC ||| ||||| ||||| ||||| ||||| |||||
 AACATATTCTCCCGGCTCC CCC CGGCCCC TTATACAAGGC ACTG TGGCG T
 C T TC G - ACGTT

GAM1556 TAACGGCGACTTTGGGCAGC 1542 TTGGGCAGCG 4267 CGA T- CGAA A CT- AAA
 AAATT
 GAATCAGTGTCTGTGCGAAA AATCAGTGTC TAACGG CT TGGGCAG TC GTGT GTCGC
 CCCTGTT T
 CCCTGTAAATTTAAACACA TGTC ||||| || ||||| || ||||| ||||| |||||
 ACAGGGAGCGCGACTAAACA GTTGTC GG ACTCGTC AG CACA CAGCG
 GGGACAA A
 CGGACTAACTGCTCATCGGG CCG CT AATC G AAT CGA CACAA
 CCCTGTTG

GAM1557 TGGTGTTGCAATGCATTAGG 1543 TTAGGGAATC 4268 ----- CA AT T A AA -
 CTC
 GAATCTAAAAACGAAATCCT TAAAAACGAA TGGT GTTG ATGC TAGGGAA CTAAA ACGA
 TCC TG G
 GCTCGGTAACACGGAAATTG ATCC |||| |||| |||| ||||| ||||| ||||| |||||
 TCTTTAGTTCCCTACAGCAT ACCA CAAC TACG ATCCCTT GATTT TGTT AGG AC
 G
 CACAACAATTGTAAACCA AATGTAA AC AC - C AA C AAT

GAM1558 AGCCGTGGGACAACCTTCCC 1544 TTGAATCTCC 4269 GA ACCTTCCCTTT CCTGC -
 TCCTTG
 TTTGGAGCCTGCGTTCACAT TGCACCACGG AGCCGTGG CA GGAG GTTCA CA T
 CTTGTCTCTCATTGTTGAA CT ||||| || |||| ||||| ||||| |||||
 TCTCCTGCACCACGGCT TCGGCACC GT CCTC TAAGT GT C
 AC ----- ---- T TACTCT

GAM1559 CAAATGCTTTGTTTTGTTGT 1545 TGTGCATTGT 4270 CTT TTGTT - GA
 GCTGACAGAATCATGTTGTG TGACATCATT CAAATG TGTT GTGC TGACA A
 CATTGTTGACATCATTTG TG ||||| ||| ||| |||||
 GTTTAC ACAG TACG GTTGT T
 T-- TTGT- T AC

GAM1560 CGATGAAATAAGCTTGAATT 1546 TGAAATAAGC 4271 A- TA ATTC CTC
 CCAGGTTTGCTCCTGATTAG TTGAATTCCA CGATGA A AGCTTGA CAGGTTTG C
 ATTTGCGTCAAGTTCGTCCT GGTT ||||| | ||||| |||||
 CATCG GCTACT T TTGAACT GTTTAGAT T
 CC GC GC-- TAG

GAM1561 GTGCCACCAAAAAGATCTGA 1547 TGAGATTTTG 4272 - - ----- G TG
 AATGAGCTTTGAGATTTTGA AATTCTTCTT GTG CCA CCAAAA AGATCT AAA A
 ATTCTTCTTTTGGTTGGTCA TTGG ||| ||| ||||| ||||| |||
 C CAC GGT GGTTTT TTTAGA TTT /
 T T CTTCTTAAGT G CG

GAM1562 GTGGAAGATCAATGTATTTA 1548 TTCAGAATAC 4273 G A T C T A CAC G
 GGATCTCCAGATGTACCAAC ATTGGTGTTT GTGGAA ATCAATGTATTT GGA CTC AGA GT
 CCAAC GAG T
 CACGAGGTGTCTCTTAGTTG CAT ||||| ||||| ||||| ||| ||| ||| ||| ||| |||
 GACTCTTGAGTTCAGAATAC TACCTT TGGTTACATAAG CTT GAG TCT CA GGTTG CTC
 G
 ATTGGTGTTCCAT G A - T - - ATT T

GAM1563 TCTGGCTCGATCCGATGTTT 1549 ATCAAAAGCG 4274 ATCCG G G ACC
 TGGATGTCACCTCATAGAAA TAGCGAGCTA TCTGGCTCG ATGTTTT GAT TC T
 TCAAAAGCGTAGCGAGCTAG GA ||||| ||||| ||| |||
 A AGATCGAGC TGCGAAA CTA AG C
 GA--- A A ATA

GAM1564 CGTTGAGGTAGAAGACAAAC 1550 TGAGGTAGAA 4275 T G GAA-- AACTC T
 TCGCGTAACCGTTGTCCGTT GACAAACTCG CGT GA GTA GACA GCG A
 ATACGTCACG CGTA ||| ||| ||| |||
 GCA CT CAT CTGT TGC A
 - G ATTGC ----- C

GAM1565 GGATTACAGAGTATAACATA 1551 TACAATAGTG 4276 TA GA ATAACA GA ATA
 GAGTATAATATAGAGTATAC ACGTGGGATC GGAT CA GT TA GTATA T
 AATAGTGACGTGGGATCC C |||| ||| ||| |||
 CCTA GT CA AT CATAT A

GG G- GTG--- AA GAG

GAM1566 TCTGGTATACACCCGTCTCG 1552 CACCCGTCTC 4277 TATA C C A- AA TA
TGGTACGAAGTAGAGCGCGG GTGGTACGAA TCTGG CA CCGTCT GTGGT CG G G
CACCACCGGACGGATGCAGT GTAG ||||| || ||||| ||||| || |
CCAGA AGACC GT GGCAGG CACCA GC C /
TGAC A C CG G- GA

GAM1567 CAGTGCTCCAGCGGCGTTTC 1553 TGAGATTGAG 4278 AG C - CGT -- G
GGTCCACGTGTCCTGGAGCA ATCCCGGGAG CAGTGCTCC CGG GTTTCGGTC CA GTC CTG
A GTTGA CTGAGATTGAGATCC CGTT ||||| || ||||| || || |||||
CGGGAGCGTTG GTTGCGAGG GCC TAGAGTTAG GT CAG GAC /
-- C A --- TT G

GAM1568 GCCGTCGATATCGGAACTGA 1554 TATCGGAACT 4279 C TA- A A- TCA C
CGAAAGAGCTCATGTGCCGC GACGAAAGAG GCCGT GA TCGGAACTG CG AAGAGC TGTG
C ACGCTGTTCTTGACGTAGTT CTCA ||||| || ||||| || ||||| |||||
TTGAAACTCCACGGC CGGCA CT AGTTTGTGAT GC TTCTTG GCAC /
C CAA - AG TC- G

GAM1569 GCCTGCTGCGTCTCATGGAT 1555 TTGGTCCAAG 4280 - CG TCA AG CG
CAGAAGTTGCGGACCCAAAA TGGTTTAGCG GCCT GCTG TC TGGATCAGA TTG G
TTTGGTCCAAGTGTTTAGC AGGC ||||| || ||||| ||||| |||||
GAGGC CGGA CGAT GG ACCTGGTTT AAC A
G TT TGA AA CC

GAM1570 TGTAGGCGCTGCTGCACTTC 1556 TAGCTGCAGG 4281 C --- T A - CCTA TC G A
AGC- T GGGTAGCTGCAGGCCGCCTA CCGCCTAGCG TGC ACT CGGGTAGCTGC GGC CG GCGCT
CA CTG GCT TGC C GCGCTTCCAGCTGAGCTAGC CTTC ||||| ||||| ||||| ||||| ||||| |||||
TGCTCCTGTACCAAGGCCAG ACG TGG GCCCGTCGGCG CCG GC CGCGA GT GAC
CGG ATG C TGTCAGCGCCGAGCCGCGGC C CGC - - A ---- CT - - AACC T
TGCCCGGGTCGCGCACCAGC
GTCTCG

GAM1571 AAAGGAGCCGTAATTCCTAA 1557 AGCCGTAATT 4282 - AATGAGCA AG GT
TGAGCAGCATATAGCGCGGT CCTAATGAGC AAAGGAGCC GTAATTCCT GCATAT CGCG
G GTGACGCGGTGTGCGAAGGG AGCA ||||| ||||| ||||| |||||
ATTATAGGTTCTTTT TTTTCTTG TATTAGGA CGTGTG GCGC T
A AG----- -- AG

GAM1572 ATATTTGAGATTAAGTTGTG 1558 TGTAAGCGT 4283 TAACT- CTTTTTCCAT--- A C
GCAT ATACCA
CTTTTTCCATATGTAAAGCG AACAATGGCA AT TGTG ATGTAA GCGTAA AATG
TTTGT T
TAACAATGGCATTTTGTATA TTTT || ||| |||| |||| ||||
CCATTTTCACGCACAAATCAA TA ACAT TACGTT CGTATT TTAC AAACA T
CATTCTTATGCTTGCATTTT TTACTC CTTTAACATTTTT - C AACT CGCACT
TTACAATTTCTACACTCATT
ATCTAAACAT

GAM1573 CAAAATTGGTGTGGCTCCA 1559 GCGAGCACAA 4284 TT CTCCAATT- ACA AATCAA-
AATAACTCAA A AAT
ATTTGCCACAGTGTTTAATC ACACAAACAC GG TGCC GTGTTT TGCT CC
TATCA C
AATGCTAATAACTCAACCAT ACGG || ||| |||| ||| || ||||
ATCAAATCCTTGTGATAGGC CC ACGG CACAAA ACGA GG ATAGT C
GAGCACAAACACAAACACAC TT ATATGCTAT CA- CACAAAC GC----- - GTT
GGCATATCGTATACCTTCAT
CACATTTTCG

GAM1574 CAACAGCATGGAGCGCGTCA 1560 TAGAATAAGC 4285 AGCG A- ATTT- A C ATT---
A- GT
ACGCCAGATTTAGCATATCC TTCAGACTGG G CGTCA CGCCAG AGC TAT CTATTA
GACCA CACCAG A
TATTAATTGACCAACACCAG CGAG | |||| |||| |||| |||| |||| ||||
GTATTTTGGTGAGTGGTTCC C GCAGT GCGGTC TCG ATA GATGAT TTGGT
GTGGTT /
ATGATAGTAGAATAAGCTTC CAA- GA AGACT A A AGTACC GA TT
AGACTGGCGAGTGACGAACC
CTTGTTTTTG

GAM1575 CCTGATACTATTTAACGTAT 1561 TTCAAAGGTA 4286 T TAAC A A GA
CTTTAAATAAGGGATAAACC CAATAGTTCC CCTGA ACTATT GTATCTTT AATA GG T
ATATTCAAAGGTACAATAGT GG |||| |||| |||| |||| ||||
TCGGG GGGCT TGATAA CATGGAAA TTAT CC A
- ---- C A AA

GAM1576 GCTGTCGTTGGTGTGTTTT 1562 TAACGAAAAA 4287 C TGTTT A G
TTTTCGTAATATGAAATATA GCACCAATTG GCTGT GTTGGTGT TTTTTCGT ATAT A
ACGAAAAAGCACCAATTGCA CAGC |||| |||| |||| ||||
GC CGACG TAACCACG AAAAAGCA TATA /
T ---- A A

GAM1577 GCTTCCGGACAATTCAATGA 1563 TGTAACGTT 4288 ---- TTC TG TCA C - GTTG
AA- TC
TTCAATCTGTAAACGTTGTA GTAAATTAGA GCTTCC GGACAA AA AT AT TGTA AAC
TAAATTAG G A
AATTAGAAAGTCAAACAAATT AGTC |||| |||| || || || |||| || ||||
AATTTAGGTTCTGCAAATGT CGAAGG CCTGTT TT TG TA ACGT TTG ATTTAATT
C /

GTTGTTTTTGTCCAACAAGG
AAGC

AACAA T-- GT TG- A C G--- AAA AA

GAM1578 GGCAATATTTTCCGCAATCT 1564 TGAGATTGGT 4289 A TTTCCG ATTA T
CATATTAGTGTTCATCATCAT ATCGTATAGC GGC ATAT CAATCTCAT GTG C
GAGATTGGTATCGTATAGCC C ||| ||| ||||| |||
CCG TATG GTTAGAGTA TAC A
A CTATG- C--- T

GAM1579 GTACCTATTTTGAGTAGGCG 1565 CGGGGTTATG 4290 C T GTA- C ----- G CTAAA -
A
GGGTTATGGCACTAAAACGC GCACTAAAAC GTA CTAT TTGA GG GGG GTTATG CA AC
GCTT A
TTAATAAGCTGTCTAAATGA GCTT ||| ||| ||| ||| ||| ||| ||| |||
CGTAACTTTTTCCCCCATCA CGT GATA AACT CC CCC CAATGC GT TG CGAA /
TCAACATAGATGC A C ACTA - TTTT A AAATC T T

GAM1580 TAGACATTTTCATCAGAATCA 1566 TATCCGAACC 4291 - - CGAA-- GAGA G TT
TCAT C G
GTGCGAAAGAGAGATTGGAG ATCTGAATTA CATCAGAAT CA GTG AGA TTGGA ATG
CAATT TTTGG TT T
ATGTTCAATTTTCATTTTGGC CACA ||||| ||| ||| ||| ||| ||| ||| |||
TTGTTAAACCCAAATTAGTT GTAGTTTTA GT CAC TCT AGCCT TAC GTTGA
AAACC AA T
GCCATATCCGAACCATCTGA A A ATTAAG ACCA A C- TT-- C A
ATTACACATGAATTTTGATG
GGGCTTGTTTA

GAM1581 AAATTCTGTTGCTACTAAGT 1567 TTGAATCAGA 4292 TGC TAAG AAGAG
GATTCAACAGAAGAGAGTAG TGTGTTTGCA AAATTCTGT TAC TGATTCAACAG A
CTTGTTGAATCAGATGTGTT GGAT ||||| ||| ||||| |||
TGCAGGATTT TTAGGACG GTG ACTAAGTTGTT /
TTT TAG- CGATG

GAM1582 AAGAGAGTCAGTGCCTGGAG 1568 TCAGTGCCTG 4293 G T CCT GT- TT - AG
TTGTTCTTTCAACAGGATGG GAGTTGTTCT AA AGAG CAGTG GGA TG CTTT CAAC G
TTGAAAAGGGTGTTGTCCTC TTCA || ||| ||| ||| ||| ||| ||| ||| |||
TACTGTCTCTGTT TT TCTC GTCAT CCT GT GAAA GTTG A
G T CT- GTT GG A GT

GAM1583 GATTGCAAGTATATATGCAG 1569 TGACATATTT 4294 TT A- --- - ----- G
GAGCTAGCGGAAGCAGACTG GATATGATGT GA GCA GTAT ATATG CAGGAGCTA GC G
TTTATAGCTTCTGACATATT CTC || ||| ||| ||| ||||| ||| |||
TGATATGATGTCTTC CT TGT TATA TATAC GTCTTCGAT CG A
TC AG GTT A ATTTGTCAGA A

GAM1584 GCTGGTGATATGTCTGTTTT 1570 TGATATGTCT 4295 A CTGTTTTAT T A
 ATCTTGTTTCATAGTATGTA GTTTTATCTT GCTGGTGAT TGT CTTGTT CAT G
 ACAAGTCTGTTAATACATTA GTTT ||||| || ||||| ||
 TTAGC CGATTATTA ATA GAACAA GTA /
 C ATTGTCT-- T T

GAM1585 GCTTTAGGTATGAAAAATGA 1571 TGA CTCAATG 4296 T TA- AA- AAG TT CC
 AAGCATGTTTGCAAGTTTCC TTTCACCTTC GCT TAGG TGAAA TGA CATGT GCAAGTTT A
 AAGAAAATTTGTTTG CATGA TATA ||||| ||||| || ||||| |||||
 CTCAATGTTTCACCTTCTAT CGA ATCT ACTTT ACT GTACG TGTTTAAA A
 AGC T TTC GTA CA- TT AG

GAM1586 GGCTAGATGTCTGTTTGAGA 1572 TATTTTGAGC 4297 T T G TAAAA
 ATATTTAAAAAGTCAGTGAT TGA CTCTAGT GGCTAGA GTC GTTT AGAATATT A
 ATTTTGAGCTGACTCTAGTT T ||||| ||||| ||||| |||||
 TTGATCT CAG CGAG TTTTATAG G
 - T - TGA CT

GAM1587 TCAAGAGTAGATATAGCATT 1573 TAGCATTTTG 4298 G AGA A TTGT A- G T
 TTGTAAAACTGAAAGATCAT TAAAACTGAA TCAA AGT TATAGC TT AAAACTG AA ATCA C
 CAGTGGTGTTAGCGGTTTTT AGAT ||||| ||||| || ||||| |||||
 TCTAAGTTGTAAAACTGTTG GGT TCA ATGTTG AA TTTTGGC TT TG GT A
 G G AA- - TCTT GA G G

GAM1588 TCTAGTTGTATGAAGCTTAT 1574 TGTGTAGTTT 4299 T C CGT T---- CATCATCTGA
 CCA C T
 ATCTAGCGTATCATCAATGT CAGTATCTAG GCT ATAT TAG ATCA CAATGT ATATGA
 GT GTGAA G
 CATCATCTGAATATGACCAG G ||||| ||||| ||||| ||||| ||||| |||||
 TCGTGAATGTTTTCATCACC TGA TGTG ATC TAGT GTTATA TGTACT CA
 TACTT T
 TATCATGTATATTGTTTCTT - T AC- TCTTT ----- ATC C T
 GATCACTATGTGTAGTTTCA
 GTATCTAGG

GAM1589 AGTAGAGATGGTTGTTAGTG 1575 TGATATGTTA 4300 TT T -- - - TAT AG--- CCA
 T A
 TGGTTCCACAGAGAATATCC TCTAGCAAGG GGTTG AG GT GGTTCCA CAGA GAA CC
 AGATG ATATT GAG A
 AGAGATGCCAATATTTGAGA CTTT ||||| ||||| ||||| ||||| ||||| |||||
 AGATTCTGATATGTTATCTA TCAAC TC CA TCGAGGT GTTT CTT GG TCTAT TATAG
 CTT G
 GCAAGGCTTTTCA TTTGTTGG CT - GT T A TC- AACGA TG- T A
 AGCTTGACCTTCCA ACTATC
 CTTAGTAGCCT

GAM1590 ATGTTCTGAAACAATAATAC 1576 TATAACAGTG 4301 T CT - T TGTT -- TG A AA
 TCT

TTTTAGGGTCATTTGTTTTG	GTGTTTCTGC	ACAA AATA TT TAGGG CATT TTGTTATGC AC
GGG CA AAAG T		
TTATGCACTGGGGACAAAAA	AATA	
AGTCTTGGTTTTTGGTGGCT		TGTT TTGT AA GTCTT GTGG GACAATATG TG TTC GT
TTTT /		
TTGGTGGGTATAACAGTGGT		- AT C T T--- GG GT G GG TGG
GTTTCTGCAATATGTTTTGT		
TTCACTTATGT		
GAM1591 GTGTTGTTTTTTGTTGTATG 1577	TACACAGGGT 4302	TG TTT GTA T TTAGTT
TAATATT TT CA		
TAGCTATTAGTTCCCATAAT	TTGGGTTCCC	TGT TT TGTT TG AGCTA CCCA TCCTGT
GTATGC T		
ATTCCTGTTTGTATGCCAT	TGGC	
ATGCGTACACAGGGTTTGGG		ACG AG GTAA AC TCGGT GGGT GGGACA
CATGCG /		
TTCCCTGGCTCCAAGAATGT		GT TT- GA- C CCCTT- TT----- -- TA
TGATGGCAC		
GAM1592 TTATGAGTTTAGGCCACATC 1578	TCATTCATAA 4303	C T T - GTTTTGTGTGG A
TG C C		
GTAAGTATTATTTGAATGAG	TTATCTTTAT	CAT GTAAG AT ATT TGAATGA TTTACAT TAT
GCA TGTGT G		
TTTTGTGTGGTTTACATATA	TATG	
TTGGCACTGTGTCTGGGATGC		GTA TATTT TA TAA ACTTACT GAATGTG GTG TGT
ACGTA G		
ATTGTTTGTGGGTGTAAGTC		T C T T ----- G TT T G
ATTCATAATTATCTTTATTA		
TGTGGCAGTA		
GAM1593 TTTTCAAGTAATTATGAGGTTG 1579	TAAGATCTTT 4304	A TG TT A
GTTTTAAGAAGAGTTTTAAG	TGTAGGTATT	TTTCAGTA TTA AGG GGTTTTAAGA G
ATCTTTTGTAGGTATTGAAA	GAAA	
	AAAGTTAT GAT TTT CTAGAATTTT A	
	G GT -- G	
GAM1594 CCTAATATTCAAAGTGTTTA 1580	CAAAGTGTTT 4305	CA --- AA GTT AC
TAAGGTGGTTGTACCACGCT	ATAAGGTGGT	CCTAATATT AAGT GTTTAT GGTG GT C
ACACCAGTAAATAAACTTA	TGTA	
CGATATTAGG		GGATTATAG TTCA TAAATG CCAC CG /
	CA AAA A- AT- CA	
GAM1595 GATTATATGATACTGCAACT 1581	TACTGCAACT 4306	A A--- G CC TT TCTA ---
CCTTTC AA		
GGTGCGCCTGTTTGTCTAAG	GGTGCGCCTG	GAT CTGCA CTG TGCG TG TG AGATC
TAGCGT TGG A		
ATCTAGCGTCCTTTCTGGAA	TTTG	
AGCCCATCACGTTATTTGAT		TTG GGCGT GGT ACGC AC AC TCTAG ATTGCA
ACC /		
CTCCCACTCACCCGCAGTGG		A GTTA G CC TC CC-- TTT CT---- CG

ATTGTGCGGAGTTAAGTCAA
 TC
 GAM1596 GTTACGTTCAATCTGATTTT 1582 TGGGATCCGC 4307 - G TC TT----- CTG-- A G G
 TCCACCACTGCGAAAATGTG ATCTGTAAAG GTT AC TTCAA TGAT TTCCACCA CGAA AT
 TG C
 GCACCAGGTATTTCGATTAAT TTGA ||| ||||| ||| ||||| ||| |||
 GGTGGGATCCGCATCTGTTA CAA TG AAGTT ATTG AGGGTGGT GCTT TG AC A
 AGTTGAAGTCAAC C - GA TCTACGCCT AATTA A G C

GAM1597 TAGTGAGAGCGTAGTTAAAA 1583 GAGCGTAGTT 4308 T- GTTAAAA A- GGAA
 GATGAACAGGAACTAGATGT AAAAGATGAA TAG GAGAGCGTA GATG ACA C
 CACATTAGCGAAATATGCTT CAGG ||| ||||| ||| |||
 TCTTCTG GTC CTTTCGTAT TTAC TGT /
 TT AAAGCGA AC AGAT

GAM1598 AGACTGACACAGTGGCCAGT 1584 TTTGACAGTT 4309 A C - C ATTTAGTCAAG G
 T-- TCA
 ATTTGACTACCACATTTAGT TGGTGATGGA GTGG CAGTATTTGA CTA CAC CAAA
 TGTTAG TTTGCA T
 CAAGCAAAGTGTTAGTTTTG TCAG ||| ||||| ||| ||| ||| ||| |||
 CATCATTTTCTGCGAGTATT CACC GTTGTGGACT GGT GTG GTTT ACAGTT
 GAGCGT T
 TGACAGTTTGGTGATGGATC A T A A ----- G TAT CTT
 AGGTGTTGTCCACAAAGTGA
 GTTT

GAM1599 AGCCTGAGGCGCTCGGGGAA 1585 TCCACAGACC 4310 CC G GAAA G GTC C T --
 GG
 AATGAGGTCGGCCAGGTCCG CTTGAGTTCT AG TGAG CGCTCGGG AT AG GGC AGG CCG
 AGGC T
 AGGCGGTGGTGCGCTCGTCG TCTG || ||||| ||| ||| ||| ||| |||
 AACCCGGTCCACAGACCCTT GT TTCT GAGTTCCC CA CT GGC CAA CTG CGCG G
 GAGTTCTTCTG C- T AGA- C --- C G CT TG

GAM1600 AGCTCCTCCTCGTGCTCCGC 1586 TGGGACGGCC 4311 CC T-- --- G TCACATA G
 AATCT-- A
 GGGCGTCACATAGCCCAGGT GCGTCGGAGG CT TCCTCG GCTC CGCG GCG GCCCAG
 TC CGATGG T
 CAATCTCGATGGATTCTCTCC TGGC || ||||| ||| ||| ||| ||| |||
 ATCTCTTGCATGTCTGGGAC GT GGGCGG AGGC GCCG CAG GGTCTG TA
 TACCTC T
 GGCCGCGTCCGAGGTGGCGG CG TGG TGC G ----- - CGTTCTC C
 GGCTGGG

GAM1601 TCTAAGGTAAGCTTTATGTT 1587 TAAGGTAAGC 4312 -- T CC- TATCAAATGTAA GG A
 AACT- A C
 TCCATCAGTATCAAATGTAA TTTATGTTTC AGCTTTA GTTT ATCAG GT AG GACT
 GT CTGC A

GTGGAGAGACTAACTGTACT	CATC				
GCCAAGGCAGAGCCACGGAG		TCGAAAT CAAA	TAGTC	CA TC CTGA	CG
GACG A					
TCCTAAACCTGATCCAAAAC		GA C ACC	-----	AA -	GGCAC A G
CTAAAGCTAGTGTGTTTAGA					

GAM1602 TGGAACAGCCAGGTGAGGTA 1588	TGAGGTACTT 4313	GCCAG G - T	GGGG C G
CTTCTTGTGGGGCTTACACT	CTTGTGGGGC	TGGAACA	GT AGGT ACT CTTGT CTTA ACT G
GGAGCTGGAGCTCGGTCTCG	TTAC		
TTCCCGGTGAAGAACAAAGA		TCAGAAA	AG GGCC TTG CTCTG CGAG GTC A
CT	CAAGA T C -	GCT- - G	

GAM1603 AAAGTCCTGATGGGATTCCA 1589	TGGGATTCAA 4314	C ATG--	C CA ----	C
CCACAGCAGTCTTAGCTCTA	CTACAGCACT	AAAGT CTG	GGATTCCA CA GC	AGT T
TAGTCCTGATGGGATTCAAC	TT			
TACAGCACTTT		TTTCA GAC	CTTAGGGT GT TG	TCG T
	C ATCAA	A CC	ATATC A	

GAM1604 GACCTGAGCTTTTGCAATTA 1590	TGAATTGCGT 4315	CT CTTT--	A CC
AGTCCTTAAGTGAATTGCGT	GCCTCCTTGA	GAC GAG	TGCAATT AGT T
GCCTCCTTGAGTC	GTC		
	CTG TTC	GCGTTAA TCA /	
	AG CTCCGT	G AT	

GAM1605 GATAAGTGGATTGAGAACGG 1591	TAAGTGGATT 4316	- AACGGAAA -	C-----	-
AAT				
AAATGACGATTCGGCCTGGG	GAGAACGGAA	GATAAGTGGAT TGAG	TG ACGATTCCGGC	
TGGG GCAC C				
GCACAATCTGCCGTGTACCC	ATGA			
AACTTTGCTGGATCGTACA		TTATTCACCTA GCTC	AC TGCTAGGTCTG	ACCC
TGTG T				
CTCGCATCCACTTATT		C -----	A CTTTCA A CCG	

GAM1606 GCCCGACACCCAGGAAACAG 1592	TACTACATTT 4317	CC CA- AAACA CT	T A ATA
C			
GCTTGGCAATTGTGGATAGA	GCCACCGCAC	GC GACACC GG	GG TGGCAA TGTGG TAGA
GGTA T			
ATAGGTACTCCTACCCCATC	CAAC		
TACTACATTTGCCACCGCAC		CG CTGTGG CC	CC ACCGTT ACATC ATCT CCAT C
CAACGGTGTCTGC	T-	CAA ACG-- --	T - ACC C

GAM1607 TCATGAAACTGGTTGCACAA 1593	TGGAATGTGT 4318	AA --- TG A - A G
TTCTGCAAACGTGGCTTCAC	GATTTGTAGC	TCATGA CTG GT CACA TTC TGCA ACGTG C
GTCTGTATGGAATGTGTGAT	GTCG	
TTGTAGCGTCTGTA		AGTGCT GAT TA GTGT AGG ATGT TGCAC T

GC GTT GT A T C T

GAM1608 TTGCTGCGTCTTTCTGGAT 1594 TTAGATCCAG 4319 - TTTC T T AGC ATCTTCT
AC

TCTGATGGAGCCATATCTTC	CTACGATGCG	TTGC TCGTC	CTGGAT CTGA GG	CAT
GTTC A				
TGTTACAAGGGACCTTACG	TGCA			
ATGACCCTTAGATCCAGCTA		AACG GCGTAG	GACCTA GATT CC	GTA CAGG /
CGATGCGTGCAA	T	CATC	- C A--	GCATTC- GA

GAM1609 AACAAAGTGCGTACTAATGGG 1595 TAATGGGTCT 4320 T --- GTCT G A TG CTTTAT
- AAA

TCTGGTGGTAACTGTATCTT	GGTGGTAACT	ACAAG GC	GTACTAATGG	GGTG TA C TAT
CCGGTTG AC C				
TATCCGGTTGACAACTCTA	GTAT			
GTGTAATTGGTTATGTGGGT		TGTTC CG	TATGATTGCC	TTAC GT G GTA GGTTAAT
TG T				
GGCATTACCGTTAGTATAA	- AAA	AT--	G G GT	TT---- G ATC
AGCCTTGTT				

GAM1610 CCACCCTCCGCCGCCATGTG 1596 CGGGATCCTC 4321 TCC C T - CC
GGTCCGTTCCCGCGACGGGA ATGTGGCTCT CCACCC GCCGC ATG GGGTCC GTT C
TCCTCATGTGGCTCTGGGT GGGT ||||| ||||| ||||| |||||
G GGTGGG CGGTG TAC CCTAGG CAG /
TCT - T G CG

GAM1611 CCCCTCCCCGTGTCATTAAA 1597 TACATAGACA 4322 ----- TTAAAACG TAC
CAATAAAATCACA AGA

ACGGTGTATGTACAGGACAA	CTGACGCGCG	CCC	CGTGTC	GTGTATG	AGGA
TCGGG C					
TAAATCACATCGGGAGACT	CTAG				
TTTTCTGGGACAAAATATAT		GGG	GCGCAGT	TACATAT TTCT	GGTCT T
CTTTATTATACATAGACACT		ATCGC	CACAGA--	TAT ATATAAAACAG--	TTT
GACGCGCGCTAGGGAGAGG					

GAM1612 CCGATATACGCTTTCTCTTT 1598 TCATTGAACT 4323 - TTTCTCT- TTTA A G TA
TAAAA

CTTTATTAGTAGGTAGCTGT	GAATAATACC	CCG ATATACGC	TTC	TTAGT GGTA	CTGT
GCAA T					
TAGCAATAAAATAGAAGTTT	TGCG				
GCATGCAGTATCATTGAACT		GGT TGTGTGCG	AAG	AGTTA CTAT GACG	CGTT A
GAATAATACCTGCGTGTGTG		G	TCCATAAT TCA-	- - TA	TGAAG
TGG					

GAM1613 CGAGCGGGACGCGGGCCGCG 1599 TGAGCGAACC 4324 - GC AC CG GT CC T-
- AG

ATGAGCGAACCGCCGGCGGC	GCCGGCGGCG	CGG GCC	GATGAGCGA	CGCCGG	GCG
GGCG AGGCA	GGACGGT	CG C			

GGTGGCGCCAGGCATGGACG GTGG ||| ||| ||||| ||||| ||| ||| ||||| |||||
GTCGAGCCCCCGCCGTCCC GCC CGG CTGCTCGCT GCGGCT TGC CTGT TCCGT
CCTGCCGGC C
TCTGCCTTGTCTGTCGTTCCG T -- -- -- TG -- CTC CC
CGTCGCTCGTCGGCTCCGCC
GTCCTTCTCG
GAM1614 CGCCATGCCCTGGTCGTGCC 1600 CGTCATGACC 4325 - GCCC C GTT
GGTGTCTTCTCGGCCGTCATG GTCAATGAGC CGC CAT TGGTCGTG CCGT T
ACCGTCAATGAGCG G ||| ||| ||||| |||||
GCG GTA GCCAGTAC GCCG C
A ACT- T GCT

GAM1615 CGCCACCGCCATCCCCTGA 1601 TCTCATGGCG 4326 ---- TCCCC TT TG C
GGCGTTCGTGGTCGTTGCTG GTGTAGCGGC CGCC CACCGCCA TGAGGCG CG GT G
TGTGTCTCATGGCGGTGTAG G ||| ||||| ||||| || ||
CGGCG GCGG GTGGCGGT ACTCTGT GT CG T
CGAT ---- -- GT T

GAM1616 TCTTGTTCAATTATCATTCT 1602 TAGTATGTGT 4327 A G C CT --- CC - GCAACGT
CT A
TTTTGCTCATCTCCGTGGCA ATATATGGTT TC TTCTTTTT CT AT CCGTG GCAC ATTA CA
TGGA GCCG C
CCCATTACAGCAACGTTGGA ATAG || ||||| || ||||| ||| ||||| ||||| |||||
CTGCCGACCCCGGCTTTTCA GG AAGAAAA GA TA GGTAT TGTG TGAT GT ACTT
CGGC C
TGATAGTATGTGTATATATG - A - TT ATA TA A ----- TT C
GTTATAGAAAAAAGAAGGTA
AAATACAGA

GAM1617 CGACGTCGGGATCGCCCGTG 1603 TCGAAGACGG 4328 T C--- GAGCA CACAAC
TGCA
AGCATGAAACACAACATAAA TATACGTCTC CGACGTCGGGA CG CCGT TGAAA
ATAAAGGGG T
GGGGTGCATACGTTTTCTT GATG ||||| || ||||| ||||| |||||
TATTTTCGAAGACGGTATAC GCTGTAGCTCT GC GGCA GCTTT TATTTCTT A
GTCTCGATGTCG - ATAT GAA-- ----- TTGC

GAM1618 CGTCTCGGAAAAGCCGTTCTG 1604 TCGGAAAAGC 4329 AG GATGAGC GT - C----- G
GA G C
ATGAGCGCGTCCATCTGCGA CGTTCGATGA AAA CCGTTC GC CC ATCTG GAC CC
CCTGTTG TCT C
CGCCGACCTGTTGGTCTCCT GCGC ||| ||||| || ||||| ||||| ||||| |||||
GAGAGTAGCGGGAAGGAGTC TTT GGCGGG TG GG TAGGC CTG GG
GGGCGAT AGA T
TTTTTGTTGCGATCGGGTGT GA ----- TG C TTGTTTTT A AA G G
GGGCGGAGTTTCTGGGACG

GAM1619 CTCTTTTTCGAGCAGCTGAT 1605 TGAGGGACTC 4330 TT AG AT----- AGT- T GA
AG

GGAACCAGTTCTCTTCGGGA	GGGTTCTCG	CTCTTT CG CAGCTG	GGAACC TC
CTTCGG TTGT A			
TTGTAGAAAGCGAGTCTGAG	TAGG		
GGACTCGGGTTCTCTCGTAGG		GAGAGA GC GTTGAC	CCTTGG AG GGAGTC
AGCG /			
GCAGTTGGGCGTAGAGAG	T- GG	GGGATGCT	GCTC - TG AA

GAM1620 GTACGCGGTGAAGGTAAGTT 1606	CGTGCATGCC 4331	A GT T CA TG---	T TGGGA
GTC-- GG			
GCTTCCAAAAGGCGTG	GAGTTCGTCT	G AAGT GCTTC AAAGGCG	GGTGT GC
ATGGTGG GCA A			
TTGCTGGAATGGTGGGTCG	TTGA		
CAGGAAAATGTAAAGTCGC		C TTCA TGAAG TTTCTGC	CCGTA CG TGCCGCT
TGT A			
CGTGCATGCCGAGTTCGTCT	G TG - --	TTGAG - -----	GAAAT AA
TTGAAGTACTTGTCGTA			
CTACT			

GAM1621 TGTTGGGCGACGTTGGCTAT 1607	TGAGATGGCC 4332	GG G-- A - - AT---	G- C
CCGCTCTATGTCGTTGAGAT	ATTGGGAAGC	TGTTG CGACGTT	GCT TCC GCT CT GTCGTT
AGAT G			
CGCTATCTGAGATGGCCATT	AGGA		
GGGAAGCAGGAGGCGAGGAC		ACGAC GTTGACG	CGG AGG CGA GG CGGTAG
TCTA C			
GTTGTACAGCA	AT	GAG - A A GTTAC	AG T

GAM1622 AAAGTGATATATAGGATGAG 1608	TAGGATGAGT 4333	T TTCTTTA- CA
TTCTTTAATTTTCAAATAAA	TCTTTAATTT	AAAGTGA ATATAGGATGAG ATTTT A
ATGATCTGTCTTTATCTTGT	TCAA	
ATTTTACTTT	TTTCATT TATGTTCTATTT	TAAAA /
	T CTGTCTAG TA	

GAM1623 CTGGCACGTGATTGAAGCTA 1609	TAATGTATCT 4334	G GATTGAAG - AA- AG A A
TCTAATGTATCTATTAGTTC	ATTAGTTCAT	CTG CACGT CTAT CT TGTATCTATT TTC TCT
T		
ATCTATTTGGAGAAAGATGG	CTAT	
ATGCAGAGGGTATAGATGTG		GAC GTGTA GATA GG ACGTAGGTAG AAG AGG T
GCAG	G -----	T GAG A- - T

GAM1624 GAACATCATTTTTTAAGGAGT 1610	TGAGGTGCTT 4335	AC T T AG T C - GT
GTGAACCATTTCTCTTGAT	CTCATTTTCT	GA ATCA TT TA GAGTG GAA CATTTC TCTT A
AGAGATGAGGTGCTTCTCAT	ATGA	
TTTCTATGATTGATAATC		CT TAGT AG AT TTTAC CTT GTGGAG AGAG /
	AA T T CT T C T AT	

GAM1625 GAGTGTGTTGAATGTCTGGT 1611	TTCTCAGTTT 4336	G -- -GG G
-----------------------------------	-----------------	------------

TGGGGTAAGGGGGTGTCTTT	TAGGGATTCA	GAGTGTGTTGAAT TCTGG TTG G TAAGGGG T
TGTTCTCAGTTTTAGGGATT	ATAT	
CAATATATTC	CTTATATACTTA GGATT GAC C GTTTTCT /	
	G TT TTT G	

GAM1626 GAGTTTGGATGCCAGTTTAT 1612	TCATTGGGTG 4337	G - GTTTA TT T
CAATGTTTGCTAATGTATCA	GTGGTATGCC	GA TTTGG ATGCCA TCAATG TGC A
TTGGGTGGTGGTATGCCAAG	AAGG	
GTT	TT GAACC TATGGT	GGTTAC ATG A
	G G GGTG- T- T	

GAM1627 GCTGTGAATGCTAGCATGGG 1613	TAGCATGGGT 4338	TG C- GGTG - AGT
TGTCATATCAGCAGTGGGGG	GTCATATCAG	GCTG AATG TAGCATG TCATATCAG C G
TTTGGTGTGAGAATATGCTA	CAGT	
TATATTTCCAGT	TGAC TTAT ATCGTAT	AGTGTGGTT G /
	CT AT AAG- T GGG	

GAM1628 GGGCGAGGTCAATATTGGCC 1614	TGGGAACTAT 4339	CCCC-- AGG-- ATA -- ---
TAG GT		
CCCCTAAGGGGTTTCATAGGA	ATATAGGAAT	TATTGG CCTA GGTTC GGAGAAT GCT
CCATATC AT T		
GAATGCTCCATATCTAGATG	GTAC	
TTATGTAGTGATGTGGGTTA	GTGACC	GGAT TCAAG TCTCTTA TGA GGTGTAG
TG /		
GTAAATTCTCTGGGAACTAT	ATGTAA	ATATA GG- AA TTG TGA TA
ATATAGGAATGTACCAGTGT		
ATTCTGCACC		

GAM1629 GGTGGTATATATATTGACTT 1615	TCACAACTAT 4340	T TTGT A G G TG GA AG A
-- GT AT		
GTGAATCCATCCTGGGGTGG	AGGTGTTGTT	ATAT GAC GA TCCATCCT G G GCA TA
AGTTG TGACG TG T T		
CAGATAAGAGTTGATGACGT	GGGG	
GGTTATTGAGGTCAAGTGTC	TGTG TTG	CT AGGTAGGG T T TGT AT TCAAC ACTGT
AC G /		
ACAACTATAGGTGTTGTTGG	T TGT- C	G - GT GG A- - GA TG AG
GGATGGACTCTGTGTTTGTG		
TAAATGCTGTT		

GAM1630 GTATCTGCAGGTCAGAATTC 1616	TTACATTGAG 4341	A GTAGAA GT AA T T ---- -
G C		
AGTAGAAGGGTTAAATCATG	ATATTCCATG	GAATTCA GG TA TCA GTGT GGGAT
CTCTAGT CTTTGT CC A		
TGTTGGGATCTCTAGTCTTT	AATG	
GTGCCCAAAGGATAAAGAAT	TTTAGGT	CC AT AGT TACA TTCTG GAGGTTA
GAAATA GG A		
TGGAGGAGGGTCTTACATTG	A	AAGTA- TT AG - - GGAG A - A
AGATATTCCATGAATGGATT		
TAGAAGATAT		

GAM1631 TCTGTTGTTACAATTATTGT 1617 TATCAATAAA 4342 GTT A - TT
 ATGTTTGATCATATCAATAA TGTAATTAAG TCT GTTACA TTATTG TATG T
 ATGTAATTAAGG G ||| ||||| ||||| |||||
 GGA TAATGT AATAAC ATAC G
 AT- A T TA

GAM1632 TTCCAGTTGTTGAAGGCTGT 1618 TTGGGCATCT 4343 TTGTT- A C T TTTCAT - TT
 CTTGATTTTCATCCATGCAT ATTTGTTTTT TTCCAG GA GG TGTCT GAT CCA TGCA G
 TGTTTGCAATTGGCAGTTATT TGGA ||||| || ||||| ||| |||||
 TGGGCATCTATTTGTTTTTT GAGGTT TT TC ACGGG TTA GGT ACGT /
 GGAG TTTTGT A T T TTGAC- T TT

GAM1633 TTGATGAGGTCTAGGATGAG 1619 TGAGGTCTAG 4344 G TC - G ATT TTTG
 ATTTTCAGAATTTGTGAGTT GATGAGATTT TTGAT AGG TAG GAT AG TTCAGAA T
 TCTGGATACTGTCTCTGAGC TCAG ||||| ||| ||| || |||||
 CTATTAA AATTA TCC GTC CTG TC AGGTCTT /
 - GA T - AT- TGAG

GAM1634 TTGGTTATGGTATCCTCTGG 1620 TATGGTATCC 4345 T- --- AAAAAAAGAAAG G -----
 A G
 AGTTGGGGGGGATAAAAAAAG TCTGGAGTTG TGGAGT GG GGGGAT CACAT A
 ATCAG TTCCAT A
 AAAGCACATGAATCAGATTC GGGG ||||| || ||||| ||||| ||||| |||||
 CATGAAAATGGAAATTGATA ACCTCG TC TCTCTA GTGTA T TAGTT AAGGTA
 A
 ATAGTTTGTATGTGATGATCT TT GAG GTA----- G TTGATAA A A
 CTGAGCTTTGCTCCATCATG
 GCCATATCCAG

GAM1635 CAAATTTCTATAATTGGTGT 1621 TCAGATCGAC 4346 ---- T T - CG GC C C T AA GA
 TGCT
 CACCGCGGCAGCTCTAGCCC CCGGACTACA TATAAT GG GTC AC CG AGCT TAG CC GG
 GATCTG AGCT T
 TGGAAGATCTGGAAGCTTGC GTTA ||||| || ||||| || ||||| ||||| |||||
 TTCAATGGCTCAGATCGACC ATATTA CC CAG TG GC TTGA ATC GG CC CTAGAC
 TCGG /
 CGGACTACAGTTAGCGAAGT TCTA - - A AA GA C A C AG -- TAAC
 AGACCCATTATAATCTTAAT
 CTAAATCTG

GAM1636 GAAGGAGGGTTGAATACAGT 1622 CCACCTGAGT 4347 G GT A TG G CGC C
 AGCT -- TT
 TGGGGGTAGTCCGCTGGTAT ACCCCATTGG GAGG TGAAT CAGT GGGGTA TC TGGTATT
 CC GAGGT TGCC A
 TCCAGCTGAGGTTGCCTTA TTTA ||||| ||||| ||||| || ||||| ||||| |||||
 TTTGGTAATGCTTCCGGAAT TTCC ATTTG GTTA CCCCAT AG ACCATAA GG CTTCG
 ATGG T
 TACCACCTGAGTACCCCAT G AT - - G TCC A C--- TA TT
 GGTTTATACCTTGTTT

GAM1637 GCGGGTCTAAGTGAAGCAGG 1623 TGCGACCTGC 4348 --- AAGTGAA GCA G
 TCGCGCAAGAGGTCTCTGCG ACGAAACAGA GCGG GTCT GCAGGTCGC AGA G
 ACCTGCACGAAACAGACATT CATT |||| ||| ||||| |||
 CCGC CGCC CAGA CGTCCAGCG TCT T
 TTA CAAAGCA --- C

GAM1638 GGGTCATCGTCTGGTGTATT 1624 GTGTATTATC 4349 A ----- T CT GTG-- - - -
 AA
 ATCTCCTGGTGGGCTACTGG TCCTGGTGGG C TCGTCTG GTG ATTAT CCTG GGC
 TAC TGG C T
 CAATTTGTTTCATGTGTGCTA CTAC | ||||| ||| |||| ||| ||| |||
 ACAACAGGGTAATCCACTTC G AGTAGGC CAC TAATG GGAC TCG GTG ACT
 G /
 CATTTGTCCTCGGATGACG C TCCTGCTTTACCTT C -- AACAA T T T TT
 ACCC

GAM1639 GGTAGTATAATCAGCTAGGC 1625 TAGAGTACTG 4350 C T T- ACAA
 CTCAGTATTCTATGTAACAA CGGTTTAGCT GGTAGTATAAT AGCTAGGCC CAGTATTCTA GTA
 A
 ATGAATGCCCTAGAGTACTG AGTT ||||| ||||| ||||| |||
 CGGTTTAGCTAGTTATACTG CCGTCATATTG TCGATTTGG GTCATGAGAT CGT /
 CC A C CC AAGT

GAM1640 TTGTTTTTGAACATGTGGCA 1626 TCAGTGCCAC 4351 TT CA AC GCAAT C-
 TGAAA TTC
 CACGCTGCAATGTACTGCCA AATTCATTA TTGTT TGAA TGTGGCAC GCT GTA TGCCA
 GGTGG T
 TGAAAGGTGGTTCTATATCC ACAA |||| ||| ||||| ||| ||| ||||
 ACCACTTGCGTCTGCCGAA AACAA ACTT ACACCGTG TGA CGT GCGGT
 CCACC A
 GTCAGTGCCACAATTTTCATT TT TA AC AGC-- CT TCA-- TAT
 AACAA

GAM1641 ACCGTGCCGCTGCCGTATTT 1627 TGCCGTATTT 4352 C C TT --- TT G
 TGAGTGTGTTCTGGAACA TGAGTGTGTT ACCGTGC GCTG CGTATT GAG TGTG CGTG A
 TGGCCACAATGTTCTGATAT CGTG ||||| ||| ||||| ||| ||| ||||
 GCCAGTCGCATGGT TGGTACG TGAC GTATAG CTT ACAC GTAC A
 C C T- GTA CG A

GAM1642 ATACGCGGTGCGTAAGTTGCG 1628 TGTAATCGTC 4353 - - TA TT CTTGA CGAA
 ATTCTTGAAGAGCCGAATAA CTGTTGACCC ATACG CGG TCG AG GCGATT AGAGC T
 AATGCTTTGTAATCGTCCTG GCCG |||| ||| || ||||| ||||
 TTGACCCGCCGTAT TATGC GCC AGT TC TGCTAA TTTCG A
 C C TG C- TG--- TAAA

GAM1643 TGTGAGCGGTATGTCGCCAA 1629 AGCGGTATGT 4354 G TC-- CAA - - T
 CCATCTGTTGTGTGTCAC TA CGCCAACCAT TGTGAGCG TATG GC CCA TCTGTT GTG G
 ACGGAGTGGAAGCTAGCCGT CTGT ||||| ||| || ||||| |||
 AACGTTTCATA ATACTTGC ATGC CG GGT AGGCAA CAC /
 A CGAT AA- G T T

GAM1644 AGAACCTGTTGATTCAACAG 1630 TGGAAATGATG 4355 A A AA C TTTTCT TC
 CACCATTCCATTTTCTGGCG CTGAGGAGAC AGA CCTGTTG TTC CAGCA CATTCCA GGCG
 C
 TCCTGTGCCTGGAATGATGC AGCA ||||| ||| ||||| ||||| |||||
 TGAGGAGACAGCAGGATCT TCT GGACGAC GAG GTCGT GTAAGGT CCGT /
 A A GA A ----- GT

GAM1645 AGCCCTGATAGCTGGAGTTT 1631 TTTGGTATCT 4356 GATA - T TATT---- TC
 GGTATCTTATTGGAAGTCCT TATTGGAAGT AGCCCT GCTGGAGTT TGGTA CT
 GGAAGTCC T
 CTAAGGGCTTCCTCCATTTT CCTC ||||| ||||| ||||| ||| |||||
 AGCTGCCACGACTCTAGTGG TCGGGG TGATCTCAG ACCGT GA CCTTCGGG /
 GGGCT G--- C C CTTTACCT AA

GAM1646 CACACTTTGTTCCAAACTGT 1632 TGTCAACATG 4357 TT A--- T- AT- TCCGT T T
 CAACATGTCTTCCGTCGTCA TCTTCCGTCG CACACT GTTCCAA CTG CAAC GTCT
 CGTCA CCA T
 TCCATTCATGGCTGGCGTGT TCAT ||||| ||||| ||| ||||| ||||| |||||
 ATGGACCAGGTTGTCCGGCT GTGTGA CAAGGTT GGC GTTG CAGG GCGGT GGT
 C
 TGTTGGAACCCAGTGTG CC GTTC CT GAC TATGT C A

GAM1647 ACACAATGGTGCGGTAGTGG 1633 TGCGGTAGTG 4358 AAT GGTAGTGG GA AG
 TCTG A
 TTTGCGATGTAGTGCTCTGG GTTTGCGATG ACAC GGTGC TTTGC TGT TGC GGCTG T
 GCTGATGTAGTCATGTGGGA TAGT ||||| ||||| ||||| ||| ||| |||||
 TAAAGTAAAGGAAGCACCCG TGTG CCACG AAATG ATA GTG CTGAT /
 GTGT GC- AAGG---- AA GG TA-- G

GAM1648 ACGGGTTGCGTGTGCGGAGG 1634 TCGTGTGCG 4359 G TG TC-- GCC - - AGT
 GCGCCGGCCTTCGCCCTCAG GAGGGCGCCG AC GGT CGTG GGGAGGGC GGC CTTC
 GCCCTC C
 TCCGGGGGGGCTGGAGCGCC GCCT ||||| ||||| ||||| ||| ||||| |||||
 GTCCTCTCATATCGCGTGAT TG CTA GCGC CTCTCCTG CCG GAGG CGGGGG /
 CGGT G GT TATA --- C T GGC

GAM1649 GCCAGCAGTGTATCCAAGTT 1635 TGGCATACT 4360 TGT - T TAAAATCGTATG A C -
 C ATT TG

TGTAAAATCGTATGGCGAGA GTCCGCATCC AG ATC CAAGT TG GCG GAC AGG
 GTGCC AGCG CC A
 CCAGGGTGCCCAGCGATTCC GTGC || ||| ||||| || ||| ||| ||| ||||| ||||| ||
 TGA CTGGCGCTGGC ATACCT TT TGG GTTCG GC CGC CTG TCC TACGG TCGC
 GG /
 GTCCGCATCCGTGCTTGTGG C-- T T CTA----- - - A - --- TC
 TCTTGTTGGT

GAM1656	CGCACTGCATCGGCGCCACA	1642	CGGCATGGTC	4367	GCCACA	A	G	TTCTTC-	---
TCCGTT	CT								
	AGACACATGGCTGTTTCTTC		TCCAGGCTGG		ATCGGC	AGAC	CATG	CTGT	CGC TGTCC
CTGAAG	A								
	CGCTGTCCTCCGTTCTGAAG		TCAG						
	CTAAGATTTTCAAGTTTTGGAC				TGGTCG	TCTG	GTAC	GGCA	GCG ACAGG
GA	CTTT A								
	ACTCGCGAGCACGTACGGCA				GACC--	-	-	TGCACGA	CTC TTTT-- AG
	TGGTCTCCAGGCTGGTCAGC								
	GTG								
GAM1657	CGCCGCGTTCACTAGCTCGG	1643	TGCCCCGTAGC	4368	-	TCAC-	-	A	- --- - - CTC
AG									
	ACAGGACATTGCAGCACTCG		TACACATACG		CGC	CGCGT	TAGCT	CGG CAGGAC	AT TGC
AG	CA GCTTGTC C								
	CTTGTCAGCGGGACGAGCAC		CGCG						
	TGACTCGCACTGGTAGTTCT				GCG	GCGCA	ATCGA	GCC GTCTTG	TG ACG TC GT
CGAGCAG	/								
	GCCCGTAGCTACACATACGC				C	TACAC	T	C	A GTC C A CA- GG
	GCGCG								
GAM1658	GCCTCGTGCTCCTCGAACTT	1644	TCCACGGAAA	4369	-	CTC	GAA	GCAG	C T -- AT
	GGCAGCCGCGGTCAGCATGC		CAAGAGAGTT		GC	CTCGTG	CTC	CTTG	CCG GG CA GC G
	GCGCGATGTCCACGGAAACA		CACG						
	AGAGAGTTCACGAGCGC				CG	GAGCAC	GAG	GAAC	GGC CC GT CG C
		C	TT-	A--	AAA-	A	T	AG	CG
GAM1659	GCTTCGTCCGCTACGCTGTG	1645	TACGCAGTGC	4370	G	----	C	CGC	- CCG---
GAAA									
	CACGCACGCGGTTGCGCCTC		CGGATGGCGG		TTC	TCCGCTA	CGCTGTG	ACGCA	
GGTTGCGC	CT CGTAC C								
	CGCGTACGAAACACAGGTAC		GGAA						
	GACAAGTAGCGCGCGGCCAT				AAG	GGGCGGT	GTGACGC	TGTGT	CCGGCGCG GA
GCATG	/								
	GTGTACGCAGTGCCGGATGG				-	AGGCC	A	A--	C TGAACA GACA
	CGGGGAAGC								
GAM1660	GTTGTGGGCACTTTTACGTT	1646	TAACTTTTGT	4371	ACTTTC	G	AGTA	-----	G G
CC AGC									
	GAGTAGTAGATAACTTTTGT		CCGAGGTTCT		ACGTT	AGT	GAT	AACTTTT	TCCGAG
TTCTT	GTGC G								
	CCGAGGTTCTTCCGTGCAGC		TCCG						
	GTGGAGCGCAGAGAACTCGG				TGCGA	TCG	CTA	TTGAAAG	AGGCTC AAGAG
CGCG	T								

AGGAAAGTTCCCAGTGATCC
GAAGCTGAGCGTCCTGGCCC
GCGGC

GAM1661 AACAACGCGTACCTTTTCCG 1647 TTCTTCGCCG 4372 CG T CTTTTC AA GTCCA C
G TCT
GTGGACAAAAGCGAGTCCAG TTGTTTACCC AACAA CG AC GGTGGACAA GCGA GG
AAATAT TCCT T
GCAAATATGTCCTTCTTAAT GCTG |||| || |||||| ||| || ||||| |||
GGGAAATATTTCTTCGCCGT TTGTT GT TG CCATTTGTT CGCT TC TTTATA AGGG
/
TGTTTACCCGCTGTCTGTAT AT C TCGC--- GC ---- - A TAA
TGTT

GAM1662 ATATTTGACCGTTCTTCCAA 1648 TAATACAGTT 4373 CTTCC- AA C ---- T--- ACT- - ---
AT
TTGTAACCGTTTGTGAGC AATATTGATG AATTGTA AC GT TTG GAGCA TAAAT C
GCATGT T
AACTTAAATCGCATGTATTT GCAC |||||| ||| ||| ||||| |||||
AACATGTTTTGTATTTGTAA TTGACAT TG CA AAC CTTGT GTTTAG TGTACA /
ATGTTCTCCCCAACCCCACT TTATAA AA T CCCC CCCT AAAT TTTT AT
GTAATACAGTTAATATTGAT
GGCACTATAT

GAM1663 CGTTTGTATACACTAAGACG 1649 TGTCGTCTAT 4374 T A CTA TT TT
TTACATGTTTTTTATGTCGT GTAAGCGTGC CGT TGT TACA AGACG ACATG T
CTATGTAAGCGTGCG G ||||| ||| ||||| |||||
GCG GCG ATGT TCTGC TGTAT /
T A A-- -- TT

GAM1664 TCCCTGCGCCTGTCTCGCGA 1650 TTGCCGATAG 4375 TG C-- TC TCCTTAC TCG
TGTCCTTACACCCGTGCAAC TCCCGTGGGG TCCC CG CTGTC GCGATG ACCCG A
CCGGGTAGCACGTATTGCCG A |||| || ||||| |||||
ATAGTCCCGTGGGGA AGGG GC GATAG CGTTAT TGGGC /
GT CCT C- GCACGA- CCA

GAM1665 CGTGTGCGTTGTGCAAGTACA 1651 TGCAAGTACA 4376 C- G C T- T CTC
ACCAG
GGCCGGCGCACTGGGCGTCG GGCCGGCGCA CGTGT GTTGT CAAGTACAGGCCGG GCAC
GGGCG CG GGC C
CTCGGCACCAGCATAAAGTC CTGG |||| ||||| ||||| ||||| |||
CACCGTGTTCTTGTGCACCG GCACG TAATA GTTTATGTTTGGCC CGTG CTTGT GC
CTG /
GTTTGTATTTGATAATCTGC TC - A TT - CAC AAATA
ACG

GAM1666 GGTCAAGAGACTCTTCAGAA 1652 TGCACAGTGA 4377 AGA- TT AA A - CC
CACAGTGCCACCACCATGTG CCTGCGGGTC GGTCA GACTC CAG CAC GTGC CA A
CACAGTGACCTGCGGGTCAG AGGC |||| ||||| ||| ||||| |||
GCTGACC CCAGT CTGGG GTC GTG CACG GT C

CGGA C- CA A T AC

GAM1667 TGGATGTCATGGACCATCGT 1653 TGTCATGGAC 4378 CA G G TG
GGCTACGGTGTACAGTGGC CATCGTGGCT TGGATGTCATGGAC TC TGGCTAC G T
CAGAATGTCCATGACATCCG ACGG ||||| || |||||
GCCTACAGTACCTG AG ACCGGTG C /
TA - AAC

GAM1668 GGA CTGTTTCGAGGCTGAGAC 1654 TGAGACAGCG 4379 CGA - ----- GG CGAA
CG-- T
AGCGGTGGGGCGAAGAGGCC GTCGGGCGAA GGA CTGTT GGCT GAG ACAGC TCGGG
GAGGCCA GCGC T
ACGGCGCTTCGGCGCAGCAT GAGG ||||| ||| ||| ||||| ||||| |||||
GGCCTCGTACTCGAAGCTGT CCTGGCGG CCGA TTC TGTG AGCTC CTCCGGT
CGCG C
AAATCTGCTTGAGCCGGCGG --- G GTCTAAA A- ATG- ACGA G
TCC

GAM1669 GGTGCCTCCAGGTGTGTCAA 1655 TGTCATAATC 4380 ---- CC - T A AAG
AGAAAGCCAAATCTATGTCA TTTAGGTTGC GGT GCCT AGGT GTG CA AGA C
TAATCTTTAGGTTGCTGCC TGCC ||| ||| ||| ||| |||
CCG TGGA TCTA TAC GT TCT C
TCGT TT A T A AAA

GAM1670 TCCTCGGTAATTCGGAACGG 1656 TATCACAGCA 4381 CGG GAACGGG- GCAG
CAAGT G
GGATGCGCAGGCGGCAAGTG CACGGATTAA TCCT TAATTCG GATGC GCGG GAGA
C
AGAGCCATCTCTCTGCAACA AGGA ||| ||||| ||||| ||| |||
GTATCACAGCACACGGATTA AGGA ATTAGGC CTATG CGTC CTCT C
AAGGA A-- ACACGACA ACAA T---- A

GAM1671 TCTATGGTCATGGTCTCGGA 1657 CCCCTGTGG 4382 -- C GT T CA AACT
ACCACTCATACTC AT
AAAGTTGCCCTCGGGCAGGG GTGTTTTCTA GT CT GGAAAA TGCCC CGGG GGGTA CAA
TAAG A
TAAACTCAAACCACTCATAC GCCA || ||||| ||||| ||||| ||| |||||
TCTAAGATATCCTTGCTTAA CA GA TCTTTT GTGGG GTCC CCCAT GTT GTTC
/
ATCTGTTGCTTCTACCCCT CC - -- T -- CTTC GTCTAAATTC--- CT
GTGGGTGTTTTCTAGCCACC
ATCACCCGCG

GAM1672 CTGCTGAGTTAATGGCAAGC 1658 TGAGTTAATG 4383 ATGGCAA -- - GTC
CCGAGCGTCCTCAGGTCTCG GCAAGCCCGA CTGCTGAGTTA GCC CGAG C C
TCGGTGGAAGTAGCTCAGCA GCGT ||||| ||| |||||
G GACGACTCGAT TGG GCTC G T

GAAGG-- CT T GAC

GAM1673 GAGAAGATGTCGGAAGTGCT 1659 TGTCGGAAGT 4384 G A - TT--- -- TT
TTCTTTTCTCTTCAGTGAGT GCTTTCTTTT GA AAGATGTCGGA GTG CT CTTT CTC C
CGAAAGTGACCGGCCACCTC CTCT || ||||| ||| || ||| |||
CGGCATCTTGTC CT TTCTACGGCCT CAC GG GAAAG GAG A
G C C CCAGT CT TG

GAM1674 TCTCGAGCTCAGTCAAGTGA 1660 TCAAGTGAAA 4385 C C CA AA----- C AT C T
AAGTTACCCATCGCGTCCTG GTTACCCATC TCT GAGCT AGT AGTGA GTTA CC CG
GTCC G
CCGGACCCGCGAGGCTAACCT GCGT ||| |||| ||| |||| ||| || ||| |||
CTCCACCCTCATTCACTAGT AGG CTTGA TCA TTA CT CAAT GG GC CAGG C
TCCGGA C - C- CCCACCTCTC C AC C C

GAM1675 AGCTGACCTGTTGTCTTTGG 1661 TGACCTGTTG 4386 TTGTCTTT GTT
GGGCGTTGTCTAGTCTCTTG TCTTTGGGGG AGCTGACCTG GGGGGC G
TCCAGGTCAGCT CGTT ||||| |||||
TCGACTGGAC TCTCTG T
CTGT---- ATC

GAM1676 CCTCGGGCTCCTTGTGGACC 1662 TGAAAGGGGT 4387 ----- CCATT ACT-- T GA ATT
T--- CC
ATTGTGGACTCCCCTTTCTG ATTCCCACCC TGTGGA GTGG CCCCTTTC GAA AGG
CCC GCGA T
AAGAAGGATTCCCTGCGACC TTTC ||||| ||| ||||| ||| ||| ||| |||
TGA CTTGCCCTCCGGGTGGCC GCACCT CACC GGGGAAAG CTT TCC GGG
CGTT G
TCATTCTGAAAGGGGTATTC TGTTT TTCC- CTTAT T AC GGT CTC CA
CCACCCTTTCCACGTTTGTG
TCTGTGCGAGG

GAM1677 GATCGGGTTCAAGGGTCTGG 1663 TCTGGCAGAT 4388 TCT --- - TG ----- T GG
TG TG
CAGATGGCCGTGAGCAGGAG GGCCGTGAGC GG GGCAGA TGGC CG AGCA
GGAGTGCTTG GCCCTTT T A A
TGCTTG TGCCCTTTGGTTGA AGGA || ||||| ||| ||| ||||| ||||| |||
TGATTTTGAAGAGGGCCAAG CC CCGTTT ACCG GT TTGT CCTCATGAAC
CGGGAGA A T /
TACTCCACATATGTTACTGC CC- CGA C CA ATACA - -- GT TT
GCCAAGCTTTGCCCCCCCCAA
GGA ACTCATTC

GAM1678 GCCTCGGACCTGTGTCAATG 1664 TTCCCAGTCT 4389 C---- CTGT ATGT CATC A G
TG T
TGGACATCCTGGAGGATGAT CCTGATTTTA GCCT GGAC GTCA GGA CTGG GGAT A
GCG C
GGCGTCTGCGTTGTGTTCCC GTCC ||| ||| ||| ||| ||| ||| |||

AGTCTCCTGATTTT TAGTCCC
CTAAGGGC

CGGG CCTG TAGT CCT GACC CTTG T TGC T
AATCC ATTT ---- CT-- - -GT G

GAM1679 GCTTTGATCAAAGAGAAATT 1665 TGAGACGGGA 4390 CA AA ATAA - TTTTTTC
CTTATAATCGTGCCGTTTTT GTGCCTTTTA GCTTTGAT AAGAG ATTCTT TCGTG CCG T
TTCTATCTGTGTTGGTTATG GTCA ||||| |||| |||| |||||
AGACGGGAGTGCCTTTTAGT TGAGACTG TTTTC TGAGGG AGTAT GGT /
CAGAGT A- CG CAG- T TGTGTCTA

GAM1680 TGGTTCCAGTGGAGTGTTGC 1666 TGAACGGAGG 4391 T TG T TCTTCTAATTGT - -
C ATTG G
TGTCTTTCTTCCTCTTCTAA TGAGGTTGCA TGT GC TCTT CTTCC GTTTAC CC TCTGGG
GA TCGG G
TTGTGTTTACCCTCTGGGCG CACG ||| || |||| |||| ||||| || ||||
AATTGTCGGGGTCCGGTCTC ACA CG GGAG GGAG CAAGTG GG AGGCC CT
GGCC /
CCGGATGGTGTGAACGGAGG - TT T ----- T T T ---- T
TGAGGTTGCACACGTTGTCC
ATTCTTGCCA

GAM1681 GAATGCCAGGTTGTAGAGTT 1667 AGAGTTATGG 4392 CCA --- G ---- C G TAT
ATGGACAGTGGGGCATATGT ACAGTGGGGC GAATG GGTG TA AGTT ATGGA AGTG
GGCA G
AATTGCTGCATTTTCCGTTG ATAT |||| |||| || |||| ||||| |||||
ATGAACTGTGAATCAACCCA CTTAC CCAAC GT TCAA TGCCT TTAC TCGT T
TTC --- TAA G GTAGT T G TAA

GAM1682 GTACAGGTTTTTCCAGGATT 1668 TGGGTTTCATC 4393 C TTCCA C AGA C
CATTGATGGAAGACCAATCG GATTAATTC GTA AGGTTT GGATT ATTGATGGA CCAAT G
GGATTGGGTTTCATCGATTAA TTCA ||| |||| |||| ||||| |||||
TTTCTTCAAACCTTTAC CAT TCCAAA TTAA TAGCTACTT GGTTA G
T CTTC- T G-- G

GAM1683 TCGGCATGAGTAGATTTTCT 1669 TAGAAAACCT 4394 -- A A CGCCAA
ATACGCCAAGTCTCCATATA ATACATCTGC TCGGCA TG GTAG TTTTCTATA G
GAAAACCTATACATCTGCCG CGA ||||| || |||| |||||
A AGCCGT AC TATC AAAAGATAT /
CT A C ACCTCT

GAM1684 TGATATGATTTTCAAATGA 1670 TTGCATATCG 4395 A TTC AG --- G AA CT-
TTCTCT
GGGAATTGTGGGACTAAAGG GTTCCACCAT TGAT TGATT AAAATG GGAATTG TG GACT
AGGC TGA T
CCTTGATTCTCTTGCTAATT TTTA |||| |||| |||| ||||| || |||| |||||
TCATCAGCTTCAAGTTGCAT ACTG ACTAA TTTTAC CCTTGGC AC TTGA TTCG ACT
G

ATCGGTTCCACCATTTTAAT
CAAGTCA

A --- CA TAT G AC ACT TTAATC

GAM1685 TGGCATCATGATTATCAGAC 1671 TGGGATTGGC 4396 ATTATCAGACA - CT -
TTTAT T
ATTAACCAACTTCCCATCCA TTGACATGAT TGGCATCATG TTAA CCAA TCCCATC CA
GCATC G
TTTATGCATCTGAGATGTTG GTTA ||||| ||| ||| ||| |||
AGATGGGATTGGCTTGACAT ATTGTAGTAC AGTT GGTT AGGGTAG GT TG TAG
/
GATGTTA ----- C -- A ---- A

GAM1686 TTTCATAGTCTACAGAGAAT 1672 TCTCAGGCCG 4397 TCTAC AA GA TC TT C
ATTTGACTCTCGCCTGATTG AGCAGGATGG TTTCATAG AGAG TATTT CTC GCCTGA
GTACAA T
TACAAC TTTTGTATCTCAG CCTC ||||| ||| ||| ||| |||
GCCGAGCAGGATGGCCTCTT AGAGTATT TCTC GTAGG GAG CGGACT TATGTT T
TATGAGA ---- CG AC C- C- T

GAM1687 CGTAGGCCACGCACGTGTTC 1673 TCAACGGTGT 4398 GC - - G C TA C
GACGTGTAGCCCAGCCCCAT TGATGTTCTG CGTAG CA CG CAC TGTT GACGTG GC C
GTCAACGGTGTTGATGTTCT CG |||| ||| ||| ||| |||
GCG GCGTC GT GT GTG GCAA CTGTAC CG /
TT A T - - CC A

GAM1688 GGACCCTCGCTGCGGTCGCA 1674 TACAGCGTGA 4399 CT- CG ACG AA G G
CGTCACGTTGAAACGCAGGA GCGACGACAG GGACC CGCTG GTCGC TCACGTTG AC
CAGGAC C
CGCAGTCCTGGTACAGCGTG CGTC |||| ||| ||| ||||| |||
AGCGACGACAGCGTCAGGTC CCTGG GCGAC CAGCG AGTGCGAC TG GTCCTG /
C ACT AG --- A - A

GAM1689 GGTAGTTGGCGTTGGTCACG 1675 TGCCAGGCGC 4400 CAC G - TGAA C A CCTC - ---
--- C
GTGCTCTTGAAGAGCCGCAG GCAGCTCGTG GGT CT CT GAGC GC GCGTCT GTAG TC
GGGCG GCGGC G
CGTCTCCTCGTAGTCGGGCG GAAG |||| ||| ||| ||| ||| |||
GCGGCCGTAGCCGCACGTGC CCG GA GG CTCG CG CGCGGA CGTC AG CTCGT
CGCCG T
TCCATGATCTGCCAGGCGCG --- G A TG-- A - C--- T TAC GCA A
CAGCTCGTGGAAGGGCCCCG
GCGCCAGCCC

GAM1690 CAAACGACGTCGTACGGTAA 1676 TTTCTTGCCA 4401 C AC AAA T CCACCAT
ATGGCAAGTGATACCACCAT CATCACACGA CAAACGA GTCGT GGT TGGCAAG GATA T
TCCCCACGTTATTTCTTGCC TTTG ||||| ||| ||| |||
ACATCACACGATTTGTTTG GTTTGTT TAGCA CTA ACCGTTC TTAT C

- CA C-- T TGCACCC

GAM1691 CAAGTGGATGGTTCTCGGGT 1677 TCAGATACTC 4402 A- GA T C C GT
ATTCGCTGTTCAAGTCAGA AAGTACCAAA CA GTG TGGT CT GGGTATTT GCT T
TACTCAAGTACCAAACATGA CATG || ||| |||| || ||||| |||
TG GT TAC ACCA GA CTCATAGA TGA /
AG AA T A C AC

GAM1692 GTGAGCTACACACCCTTTTG 1678 GCAGCACGAT 4403 - A ACCCTT CCC ----- T
TCCCGTTGCAGCACGATAAA TTAGTGAGCT GTG AGCT CAC TTGT GTTGCAGC ACGA A
TCGTATTACGTTGCAGCACG ACGC ||| |||| ||| |||| ||||| |||
ATTTAGTGAGCTACGC CGC TCGA GTG AGCA CGACGTTG TGCT A
A - ATTT-- --- CATTA A

GAM1693 GTTGCAGCACGATTTAGTGA 1679 CAGCACGATA 4404 ----- G A A ACCCTT
GCTACAAACCCTTTTGTCCC AATCGTATTA GTTGCAGC ACGATTTA TG GCT CAA T
CTTGCAGCACGATAAATCGT CGTT ||||| ||||| || ||| |||
ATTACGTTGCAGC CGACGTTG TGCTAAAT GC CGA GTT T
CATTA A A C CCCCTG

GAM1694 GTTGCAGCACGATTTAGTGA 1680 CAGCACGATA 4405 ----- G A A CACCCTT
GCTACACACCCTTTTGTCCC AATCGTATTA GTTGCAGC ACGATTTA TG GCT CA T
CTTGCAGCACGATAAATCGT CGTT ||||| ||||| || ||| |||
ATTACGTTGCAGC CGACGTTG TGCTAAAT GC CGA GT T
CATTA A A C TCCCCTG

GAM1695 GTTGCAGCACGATTTAGTGA 1681 CAGCACGATA 4406 ----- G A A CAC-- T
GCTACACACGCTTTTGTCCC AATCGTATTA GTTGCAGC ACGATTTA TG GCT CA GC T
CTTGCAGCACGATAAATCGT CGTT ||||| ||||| || ||| |||
ATTACGTTGCAGC CGACGTTG TGCTAAAT GC CGA GT TG T
CATTA A A C TCCCC T

GAM1696 GTTTGTCCCCTTGCAGCACG 1682 GCAGCACGAT 4407 A A ATTAC ----- G A C--
-- T
ATAAATCGTATTACGTTGCA TTAGTGAGCT C CG TAAATCGT GTTGCAGC ACGATTTA TG
GCTGCA ACA T
GCACGATTTAGTGAGCTGCA GCAC | || ||||| ||||| ||||| || ||||| |||
CACATTTTGTCCCCTTGCA G GT ATTTAGCA CGACGTTG TGCTAAAT GC CGACGT
TGT T
GCACGATAAATCGTATTACG A G ----- CATTA A A TCCCC T
TTGCAGCACGATTTAGTGAG
CTGCACACCC

GAM1697 TAAATCGTATTACGTTGCAG 1683 CAGCACGATA 4408 ATTAC ----- G A A
CACCCTT

CACGATTTAGTGAGCTACAC	AATCGTATTA	TAAATCGT	GTTGCAGC	ACGATTTA TG GCT
CA T				
ACCCTTTTGTCCCCTTGCAG	CGTT			
CACGATAAATCGTATTACGT		ATTAGCA	CGACGTTG	TGCTAAAT GC CGA GT T
TGCAGCACGATTTA		----	CATTA	A A C TCCCCTG

GAM1698 TAAATCGTATTACGTTGCAG 1684	ATCGTATTAC 4409	ATTAC	----	G A
CACCCTT				
CACGATTTAGTGAGCTGCAC	GTTGCAGCAC	TAAATCGT	GTTGCAGC	ACGATTTA TG
GCTGCA T				
ACCCTTTTGTCCCCTTGCAG	GATT			
CACGATAAATCGTATTACGT		GTTTAGCA	CGACGTTG	TGCTAAAT GC CGACGT C
TGCAGCACGATTG		----	CATTA	A A TCCCCTG

GAM1699 TAAATCGTGTTACGTTGCAG 1685	CAGCACGATA 4410	A T C	G A A CACCCTT
CACGATTTAGTGAGCTACAC	AATCGTGTTA	TAAATCGTGTT	CG TG AGCACGATTTA TG GCT CA
T			
ACCCTTTTGTCCCCTTGCAG	CGTT		
CACGATAAATCGTGTTACGT		ATTAGCACGA GT GC TTGTGCTAAAT GC CGA GT	T
TGCAGCACGATTTA		C T A	A A C TCCCCTG

GAM1700 TAAATCGTGTTACGTTGCAG 1686	AAGCACAATA 4411	A T C	G A A CACCTTT
CACGATTTAGTGAGCTACAC	AATCGTGTTA	TAAATCGTGTT	CG TG AGCACGATTTA TG GCT CA
T			
ACCTTTTGTCTCTGAAGC	CGTT		
ACAATAAATCGTGTTACGT		ATTAGCACGA GT GC TTGTGCTAAAT AC CGA GT	/
GCAGCACGATTTA		C T A	A A A CTCCTGT

GAM1701 TAAATCGTGTTACGTTGCAG 1687	CAGCACGATT 4412	A T C	G A CATCTTT
CACGATTTAGTGAGCTGCAC	TAGTGAGCTG	TAAATCGTGTT	CG TG AGCACGATTTA TG
GCTGCA T			
ATCTTTTGTCCCCTTGCAG	CACA		
CACGATAAATCGTGTTACGT		ATTAGCACGA GT GC TTGTGCTAAAT GC CGACGT	T
TGCAGCACGATTTA		C T A	A A TCCCCTG

GAM1702 TGAGCTACACACCCTTTTGT 1688	GCAGCACGAT 4413	- A ACCCTT	CCCC	----	T
CCCCTTGCAGCACGATAAAT	TTAGTGAGCT	TG AGCT CAC	TTGT	TTGCAGC	ACGA A
CGTATTACGTTGCAGCACGA	ACG				
TTAGTGAGCTACG		GC TCGA GTG	AGCA	GACGTTG	TGCT A
	A - ATTT--	C---	CATTA	A	

GAM1703 TGCAGCACATAAATCGTGT 1689	AAGCACGATA 4414	A A	A T C	G A A
CACCCTT				
TACGTTGCAGCACGATTAG	AATCGTGTTA	TGCAGC CA	TAAATCGTGTT	CG TG
AGCACGATTTA TG GCT CA				T

TGAGCTACACACCCTTTTGT	CGTT	
CCTCTGAAGCACGATAAATC		ACGTCG GT ATTTAGCACGA GT GC TTGTGCTAAAT GC
CGA GT /		
GTGTTACGTTGCAGCACGAT		A G C T A A A A CTCCTGT
TTAGTGAGCTGCA		
GAM1704 TGCAGCACGATAAATCGTAT 1690	GCAGCACGAT 4415	A A ATTAC ---- AAG A
C---- T		
TACGTTGCAGCACGATTAAG	TTAGTGAGCT	C CG TAAATCGT GTTGCAGC ACGATT TG
GCTGCA ACA T		
TGAGCTGCACACATTTTGT	GCA	
CCCCTTGCAGCACGATAAAT		G GT ATTTAGCA CGACGTTG TGCTAA GC CGACGT
TGT T		
CGTATTACGTTGCAGCACGA		A G ---- CATTA ATA A TCCCC T
TTAGTGAGCTGCA		
GAM1705 TGCAGCACGATAAATCGTAT 1691	GCAGCACGAT 4416	- A A ATTAC ---- G AA
CACCCTT		
TACGTTGCAGCACGATTTAG	TTAGTGAGCT	GC CG TAAATCGT GTTGCAGC ACGATTTA
TG CTGCA T		
TGAACTGCACACCCTTTTGT	ATGC	
CCCCCTGCAGCACGATAAAT		CG GT ATTTAGCA CGACGTTG TGCTAAAT GC
GACGT T		
CGTATTACGTTGCAGCACGA		T A G ---- CATTA A AC CCCCCTG
TTAGTGAGCTATGCA		
GAM1706 TGCAGCACGATAAATCGTAT 1692	GCAGCACGAT 4417	A A ATTAC ---- G A
CACCCTT		
TACGTTGCAGCACGATTTAG	TTAGTGAGCT	AGC CG TAAATCGT GTTGCAGC ACGATTTA
TG GCTGCA T		
TGAGCTGCACACCCTTTTGT	GCA	
CCCCCTGCAGCACATAAAT		TCG GT ATTTAGCA CGACGTTG TGCTAAAT AC
CGACGT T		
CGTATTACGTTGCAGCACGA		A G ---- CATTA A A CCCCCTG
TTAGTGAGCTGCA		
GAM1707 TGTTGAGGGAAGAAGCGGGG 1693	TGAGGGAAGA 4418	GG G GCCG - T CG
CTG- ACG GCT		
CCGTGGATTTATGCTGAAAC	AGCGGGGCCG	TTGA GAA AAGCGGG TGGATTTA TGC GAAA
TAAA GA CT G		
GTAAACTGGAACGCTGCTGC	TGGA	
AAAGATGTCAAATTTTGAAT		AACT CTT TTTGTCT ACCTAGGT ACG CTTT GTTT CT
GA /		
TTCGCACTGGATCCAATCTG		GG G A--- C - AA TAAA GTA AAC
TTTGTTTCGGTCAACA		
GAM1708 GAGGGAGAGTCAGTGCCGC 1694	AGTCAGTGGC 4419	AGA - CCGCTA---- - CA A
TAAACAAAAACACAATCCT	CGCTAAACAA	GAGGG GT CAGTGG AACAAAA CA T
GCTTTTTTATGTTCTCTTTA	AAAA	
TTACCGCTGCGCGCCCCCTC		CTCCC CG GTCGCC TTGT TTTTT GT C

CCG C ATTATTTCTC A TC C

GAM1709 AGCAACTCCACAGCCGTCCT 1695 TCAATGGCTT 4420 A C-- T CTT - TTTCTTCTC-
A T C

CATGTCAATGGCTTCCTGGA CCTGGATTTT C CAGCCGTC TCATG CAATGG CC TGGAT
CCA CT TTGT T
TTTTCTTCTCCCAACTTTTG CTTC | ||||| |||| |||| || ||||
TCTCTGCAGTAGATGGTCAC G GTTGGTAG AGTGT GTTACC GG GCCTG GGT
GA GACG C
GTCAGCGTCCGTGGCGTCCA A ATA C TGC T CGACTGCACT A T T
TTGCTGTGAATAGATGGTTG
AGGGATTGCT

GAM1710 ATCTAGGACCGCCGTAGAGG 1696 AGAGGTGTAT 4421 ACCGCC -- TAACAG
TCAATTTCTTAAA AA TC

TGTATAACAGGTCCTCTCAA AACAGGTCCT GG GTAGAGG TGTA GTCCTC
CGCCTT TG C
TTTCTTAAACGCCTTAATGT CTCA || ||||| |||| ||||| ||||| ||
CCCTCGCCAAGGTGGTCATG CC CATCTCC ACGT TAGGAG GTGGAA GC
/
GCTATGAGGATACTTTTGCA ATACTC CG TTTCA- TATCGGTACTG-- CC TC
GCCCTCTACCTCATACCTAG
AT

GAM1711 GGCCCTGCATACGCCATCCC 1697 TAGGATGGTG 4422 GCATA CC TTCCA----- T TG
TAAC CC

CTACAGTTCCACGGGCGTTA CACACCCGGC CGCCATCC TACAG CGGGCGT AGC
CGT CACAG G
GCTGCGTTAACCACAGCCGC C ||||| |||| ||||| |||| ||||| |||||
TTCTGTGCACGTGGCTATGT GTGGTAGG ATGTC GTCTGTA TCG GCA
GTGTC C
CTGCTCTCTTAACTCTGTAG CACAC -- TCAATTCTCTC - GT C--- TT
GATGGTGACACCCGGCC

GAM1712 AAGTATCCTTTGTAGCTAAG 1698 TAGCTAAGCC 4423 - T-- A - CT-- T G CCT-- TG
ATCT A

CCTTCTACACGGTCCTGAGG TTCTACACGG GTATC CT TGT GCT AAGC TC ACAC GT
GAGG CTA TG T
TGCTAATCTTGATGTCATCC TCCT ||||| ||||| ||||| ||||| ||||| |||||
ATGGTGCCTTCTTTAACGGT CATGG GA ACA CGA TTCG AG TGTG CA TTCC GGT
AC G
GTGATCCTGCTTAAGCGACA C TGT G A TCCT - G ATTTC GT ACCT T
TGTAGCGGTACTT

GAM1713 CGTGGTGCCAGTTATAGAAT 1699 TGCCTCACTT 4424 TG - TAGAATCCTTC GG
CCTTCGGGGTGTTCACTGGT CTCATGTTGA CG GT GCCAGTTA GGGGTGTTCACT T

GTAGGTGAATGCCTCACTTC CTGG || ||||| ||||| ||||| |||||
TCATGTTGACTGGCAACTGT GT CA CGGTCAGT CTCCGTAAGTGG G
G GT A TGTACTCTTCA AT

GAM1714 GATGGTGTACACAGGATGGC 1700 TGGTGTACAC 4425 G AG CG G
 GATGGTAGTAATGCTGTACT AGGATGGCGA GATGGT TACAC GATGG ATGGTA T
 ATTCGTGTGGCCATC TGGT ||||| ||||| ||||| |||||
 CTACCG GTGTG TTATC TGTCGT A
 - CT A- A

GAM1715 GGCGATGAGATCCTTGCTAG 1701 TGAGATCCTT 4426 CTT- TA CAA GT GCT
 TCAAGGAGGTAGCTTGAATG GCTAGTCAAG GGCGATGAGATC GC GT GGAG A T
 TCTCCAAACGCTCCTGGTTT GAGG ||||| || || ||| |
 CATCGCT TCGCTACTTTGG CG CA CCTC T /
 TCCT -- AA- TG AAG

GAM1716 GTCGTACACTGTGCAAGGAA 1702 CAAGGAATTT 4427 -- --- --- TTTTAC A-
 TAGAT
 TTTTTTTACCGTGAACGGGA TTTTACCGTG GTC GTACACTG TGCAAG GAATT CGTG
 ACGGGAGG C
 GGTAGATCATATTTTTCCCG AACG ||| ||||| ||||| ||||| ||| |||||
 TCCCACGAATTTTGTTTTA CAG CATGTGAC GCGTTC TTTGG GCAC TGCCCTTT
 /
 TCTTGCGGGCCAGTGACAT TA CGG TAT TTTTAA- CC TTATA
 GAC

GAM1717 CACGGTGTGCAGGCGGCGGC 1703 TCCCGTGCAC 4428 G AGG - - A T GTG
 CGGAGATATGCGTGACAAAG GCTGGCGCAT CACG TGTGC CGGCG GC CGG GATA GC A
 TCTATCCCGTGCACGCTGGC GTG ||||| ||||| ||||| || ||||| ||
 GCATGTG GTGT ACGCG GTCGC CG GCC CTAT TG C
 - --- A T - C AAA

GAM1718 GCCGGGCTTGAGCTTGCCGG 1704 TGGCCAGCAC 4429 - T- A T AA - GTTCT
 CCTCGAAGTAGTTGTTCTCG GCCGTGCGCG GCCG GGC TG GCT GCCGGCCTCG GT AGTT
 C
 ACCAGGCTCACGATGAGGCT T ||||| || ||||| ||||| ||||| |||||
 GGCCAGCACGCCGTCGCGGT TGGC CTG GC CGA CGGTGCGGAGT CA TCGG /
 G CC A C AG C ACCAG

GAM1719 GCCCTTGAAGATGCACACGG 1705 CGAGATCTGC 4430 -- AA CACA ---- CC - AT
 ACACC
 CGGATTTGTCGTCCGGCGAG CGGATCATCA CCT TG GATG CGGCGGATTT GTCGT
 GGCG AG GTCGC A
 ATGTGCGACACCAACGAACAG CCAG ||| || ||||| ||||| ||||| |||||
 CGGCTGCTCCGCCACGATGT GGA AC CTAC GCCGTCTAGA TAGCA CCGC TC
 CGGCG C
 CCGAGATCTGCCGGATCATC CG CA TAG- GCCTG -- C GT ACAAG
 ACCAGCAGGGC

GAM1720 GTGTCCCAGCCGCTCTTTGC 1706 TCCCAGCCGC 4431 C-- CTCC - TGT

TCCGCGCGTTGTACATCACG	TCTTTGCTCC	GTGTCCCAGC	GCTCTTTG	GCG CGT A
TCGCCCAGGGAGCCCCGCTG	GCGC			
GGACGC	CGCAGGGTCG	CGAGGGAC	CGC GCA C	
	CCC	C---	T CTA	

GAM1721 ACGTCGGTTCAGACTGTAT 1707	TCAGTCTGGC 4432	- ----	TAT T ATT
TCTGTGTATTTACCAACCCG	CCAAGACACG	ACGTCG GTT	CCAGACTG TCTG GT T
GGTCAGTCTGGCCCAAGACA	ACGT		
CGACGT	TGCAGC CAG	GGTCTGAC	GGGC CA A
	A AACCC	T--	C ACC

GAM1722 AGTACGGGTTGAGAGAAGGC 1708	TGAGAGAAGG 4433	G- A	GGCAGATAAGA AC- AC
AGATAAGAGTACGGACTTCC	CAGATAAGAG	AGTAC GGTTG GAGAA	GT GG T
CACGACGAACCATATCATT	TACG		
TCACGACCAGGTATT	TTATG CCAGC CTTT	CA CC /	
	GA A	ACTATACCAAG	GCA CT

GAM1723 CGTACACAACGTGTTTACGG 1709	TGACTTCGTA 4434	T AA T A A
AGTATGCGAAACTGTGACTT	CGCACGACGT	CG ACAC CGTGT TACGGAGT TGCG A
CGTACGCACGACGTGTGCG	GTCG	
	GC TGTG GCACG ATGCTTCA GTGT A	
	- CA C - C	

GAM1724 ACTCCCTTTGGATGCTCTCT 1710	TCCCTAGTCT 4435	T C	TCT-- CTCT TT TAAAA
A			
TCCCTCTACTATTGGTAAAA	CGGATTCTCG	AC CC TTTGGATGCTC	TCC ACTA GG
ATGTC C			
ATGTCACAAGACATCCCTAG	GGCA		
TCTCGGATTCTCGGGCATCC		TG GG AAACCTACGGG	AGG TGAT CC TACAG A
AAATGGTGT	T T	CTCTT CTC- C- ----	A

GAM1725 CCCAACATCTCAGAAGGGTG 1711	TGAGGAACTG 4436	A GA AACT C - ACCA	
TTCCCCAAG CCC			
AGGAACTGTCGTGCCTACCA	TCGTGCCTAC	TCTCAGA GGGT GG GT GTG CCT CTTTTC	
AGATCT T			
CTTTTCTTCCCCAAGAGATC	CACT		
TCCCTAAGTAGATCTGCCCT		GGAGTCT CCA CC	CA CAC GGA GAGAAG
TCTAGA A			
CTCTGAAGAGCAAGGCCACA		- AC CCC- - C AC--	TCTCTCCCG TGA
CCCCCCCCAACCCTCTGAGGT			
GTCTGGG			

GAM1726 CCCCTGAGATCAATTCAAGA 1712	TCAAGAGGTC 4437	CA CA T AT -----	TTTGTC
TCAAGA			
GGTCTATTAATATTGATATT	TATTAATATT	GAGAT ATT AGAGG CT TAA	TATTGATA
ATTCTCG A			

TGTCATTCTCGTCAAGAAGC	GATA				
AAATCGAGGATCCTATCAAT		CTCTG TAA TCTCC GA GTT	ATAACTAT	TAGGAGC	
/					
ACTCCCCTTGCGAGCCCTCT		A- AC C GC CCCCTC	CC----	TAAACG	
CAAATAGTCTCTAGGGG					

GAM1727 GAGACACAATGTTCTTAATT 1713	TAGATTCTTT 4438	-	CTAATTA TTT CAA--- ---	
CTAGTA C				
AGAGTTTGAGCCAAGTTGGA	TAACGATAGA	AC AATGTTC	GAG GAGC	GTT GGAATCT
ATGAA C				
ATCTCTAGTAATGAACCACT	GCTC			
TTATAGATTCTTTTAACGAT		TG TTACAAG CTT CTCG	CAA TCTTAGA TATTT A	
AGAGCTCTCTTCACCACATG		A TACACCA CT-	AGATAG TTT ----- G	
AACATTAGTGACTT				

GAM1728 GATTGTGTTGTGTAGGTTCC 1714	TGTCATCAGG 4439	G - A ----- - C - A CTT	
GATCGATTGACTCTTCTCCA	AAAATTATCA	GATTGT TTG TGT GGT	TCC GAT GAT TG CT C
GCATGTCATCAGGAAAATTA	ACAT		
TCAACATCAAGGCAGTC		CTGACG AAC ACA CTA	AGG CTA CTG AC GA /
	G T A TTAAA A - T - CCT		

GAM1729 GCCTTTCTGATTGCATCCTT 1715	TTTAAGGTGG 4440	CT ----- AT	GAAT- T ACT
GAGTAGAATGGTAGGACTGG	TAGGATCTTC	GCCTTT GA	TTGC CCTTGAGTA GG AGG
G			
CCCCTCCTCTGATATTTAAG	TAGA		
GTGGTAGGATCTTCTAGAAG		CGGAAG CT	GATG GGAATTTAT CC TCC /
GC	AT TCTAG GT	AGTCT - CCG	

GAM1730 GGGTTTTGATATAAGGAGTC 1716	TACCACTTGG 4441	TA GAG- G G C CTAGGA	
AAGGGGTGGTCTCGGGCTAG	AGTACTTATC	GGGTTTTGATA AG TCAAG GGTG TCT GGG	
A			
GAATCGTGAATCCAGATACC	AAAA		
ACTTGGAGTACTTATCAAAA		CCCAAACTAT TC	GGTTC CCAT AGA CCT T
CCC	-- ATGA A - - AAGTGC		

GAM1731 GGTGTTGGTGCATCCTTCGTCC 1717	GTGCATCCTT 4442	-- - - CC CT CA
TCCACTACCAAATTGTTTGG	CGTCCTCCAC	GGTTG GTGCATC CTTC GT TCCA AC A
GCAGCTGAGGTGATGTATGT	TACC	
CAATC	CTAAC TATGTAG GGAG CG GGGT TG A	
	TG T T AC T- TT	

GAM1732 TTTTCTGAGGGATAGAAAAT 1718	TGAGGGATAG 4443	GA AAA- CTAAAAGACG T
ATCTCTTCTCTAAAAGACGG	AAAATATCTC	TTTTCTGAGG TAGA TATCTCTTCT GTTC C
TTCTCTGAGCATTATGTACA	TTCT	
AGGAGGGATGGTTATCTAGC		AGAGGACTCC ATCT GTAGGGAGGA CGAG /
CTCAGGAGA	G- ATTG	ACATGTATTA T

GAM1733 ACTGTAAAACTGTCGTTGC 1719 TGTA AAAACT 4444 AACT C CCCG A
 CCCGGTTTGAATATAAGCAT GTCGTTGCC ACTGTAA GT GTTGC GTTTG A
 CTGTAATTACTTTACGGT CGGT ||||| || ||| ||||
 TGGCATT CA TAATG CGAAT T
 ---- T TCTA A

GAM1734 CGTCTGGCATAACCAAGGGC 1720 TGACCGGTAA 4445 C C ACCAAGG- TT CC G
 CTTGTTACCCAAATGGGAAC TAACAGTATC CGT TGG ATA GCC GTTA CAAATG G
 ATTTGTATGACCGGTAATAA CAAC ||| ||| ||| ||| |||||
 CAGTATCCAACG GCA ACC TAT TGG CAGT GTTTAC A
 - - GACAATAA C- AT A

GAM1735 CGTTATTTTAACATTATCAT 1721 TATTACATTG 4446 TA A C AAACGTT TTACA
 GTAAAAACGTTGCATTTACA TGAAGTTAA CGT TTTTAAC TTAT ATGTAA GCAT T
 TTCTCCCATGTTCTATATT ACCG ||| ||||| ||| ||||| |||
 ACATTGTGAAGTTAAACCG GCG AAAATTG AGTG TACATT TGTA T
 CG CC A T ATATCCT CCCTC

GAM1736 CTGTCTTTGTTTTTGCAACA 1722 TCCACAGGCA 4447 TT AACACAACA - G TTTTACG CC
 TTTT T
 CAACATCCAACGCCGTTTTA ATAAAAAAA TGC TCC AAC CCG TT TGTTGCTT
 TGGAGACGG T
 CGTTCCTGTTGCTTTTTTTG TTCG ||| ||| ||| ||| ||| ||||| |||||
 GAGACGGTTTTTCGTTTCCA ACG AGG TTG GGC AA ATAACGGA
 ACCTTTGCT T
 CAGGCAATAAAAAAATTCTG T- AAACA---- C - TTAAA-- AA C--- T
 GGTTCCGAACAAAGCATGTC
 AACCACAG

GAM1737 GGGTGTGTACGGGTAAAAGG 1723 TAAGAGCAGA 4448 - TAAAAG- A T
 TTCTAATATTGTTATAAGAG TAGTTTTGTG GGGTGT GTACGGG GTTCT ATA T
 CAGATAGTTTTGTGCGATAT CGAT ||||| ||||| ||| |||
 CC CCTATA CGTGTTT CGAGA TAT G
 G TGATAGA A T

GAM1738 TGTCGGAATGGAGGTAATCT 1724 GGAGGTAATC 4449 A -- CA TTGGTTT TG
 CTTG
 CAAGTATTGGTTTACTGAAC TCAAGTATTG TGTCGGA TGGAG GTAATCT AGTA AC AACG
 G
 GCTTGGTTTAACGTTTGGTT GTTT ||||| ||||| ||||| ||| ||| |||
 TTGCTGTGGATTATTTTCC ACAGCCT ACCTT TATTAGG TCGT TG TTGC T
 AATCCGACA A TT TG TT----- GT AATT

GAM1739 TTATCCACCCTATCTTTATA 1725 CACCCTATCT 4450 CC - TTA A AGG- C G

AGTATGCAGGGGGCCGGTAC TTATAAGTAT TTAT AC CCTATCT TAAGT TGC GGGC G T
 CGTCTATACGCACACTTAGT GCAG |||| ||||||| ||||| |||||
 GGATGGGAGTCAATAA AATA TG GGGTAGG ATTCA ACG TCTG C A
 AC A TG- C CATA - C

GAM1740 TTTAAGCCTTGTTCCTCAATC 1726 TTGGATCATT 4451 CCT TT C TTT GAA G
 GTCTTTTAATCGAAGGTTGT GGATCACTTA TTTAAG TG TCCAAT GTCT AATC GGTT T
 AAACCGGATTGGATCATTGG AA ||||| || ||||| ||||| |||||
 ATCACTTAAA AAATTC AC AGGTTA TAGG TTAG CCAA /
 --- T- C --- G-- A

GAM1741 AGATGGAAATGAGGTCAATA 1727 TGAGGTCAAT 4452 A A GT ATATCCCCAAA G T
 ATAA AGAA
 TCCCCAAAAGAGGCTCCAAT ATCCCCAAA AG TGGAAATG G CA AGA GC CCA GGC
 A
 AAGGCAGAAACAACGCTCTG GAGG || ||||| | || ||||| |||||
 GGCGTCTGTATGTGTGCGTG TC ACTTTTAC C GT TCT CG GGT TCG /
 TTCCATTTTCAACT A - TT GCGTGTGTATG G - C--- CAAC

GAM1742 GCTAGCGGTAATAAATGTTT 1728 TATCGGAAGG 4453 AG-- AA-- G T TACTTAT
 TGGTGGGTTACTTATTACAT TTTGAGTGAC GCT CGGT TAAAT TTTTGGTGGG T
 ATTTTTTATCGGAAGGTTTG TGAA || |||| ||||| |||||
 AGTGACTGAACCAGC CGA GTCA GTTTG AAGGCTATTT /
 CCAA GTGA G TTTATACA

GAM1743 GGAGGGGTATTGGCTAAAGG 1729 AGGGGTATTG 4454 TAAAG C
 TTTGCTAGCAAGCAGCGCCG GCTAAAGGTT GGAGGGGTATTGGC GTTTG T
 ATATTTTTTC TGCT ||||| |||||
 CTTTTTATAGCCG CGAAC A
 CGA-- G

GAM1744 GGATTGTGCCCTAAACTGC 1730 TCACATGCAG 4455 AT --- AAA TC- ACTA
 ATTCAGGGCTACTAATGCAC ATATAGATTG GG TGTGCC CTA CTGCAT AGGGCT A
 AGTTCTCACATGCAGATATA GCGC || ||||| ||||| |||||
 GATTGGCGCGCC CC GCGCGG GAT GACGTA TCTTGA T
 -- TTA ATA CAC CACG

GAM1745 TGTTAATGCTGGAACCGACG 1731 TTAATGCTGG 4456 GC CGA A A
 ATACTAAAGAGGTTGCACGT AACCGACGAT TGTTAAT TGGAAC CGAT CT A
 TCTAAATTGATA ACTA ||||| ||||| |||||
 ATAGTTA ATCTTG GTTG GA A
 AA CAC - G

GAM1746 TGTTTGTATATTA ACTACA 1732 TGATATTTTC 4457 AC - TTTT C--- AG C----- T
AAGGT
GCTGTTTTTAACCGAAGTGTA ACAGTTTTCC ATTA TACAG CTG AAC GAAGTGT GCGA
GTG TCC A
GGGCGACGTGTTCCAAGGTA AGTC ||| ||||| ||| ||||| ||||| ||| |||
TAAGAGGATCACTAAATTTT TAAT ATGTC GAC TTG TTTTATA TCGTT CAC AGG

/
GCTGATATTTTCACAGTTTT -- T CTT- ACAC G- TTAAAT T AGAAT
CCAGTCTGTATAATTTAAAG
CAAACA

GAM1747 ACAGATGATCTGAGTAATAT 1733 TTCACGGTCT 4458 A -- T ACCT- T- AT
ACCTCTGTTATATATTTAAT TAGTATTTT ACAG TGA TCTGAG AATAT CTGT ATAT T
GTTACGGTCTTAGTATTTT AGAT ||| ||| ||||| ||||| ||| |||
TAGATATCAATTGT TGTT ACT AGATTT TTATG GGCA TGTA /
A AT - ATTCT CT AT

GAM1748 CGACTCCATCAGAAAGAGGT 1734 TAATATTTTT 4459 CTCCA G G T A G GACCA
AAG AGA
TTAATATTTTTGTGAGACCA GTGAGACCAT CGA TCA AAAGA GTT AAT TTTTT TGA TCG
AGAGAAAG T
TCGAAGAGAGAAAGAGATAA CG ||| ||| ||||| ||| ||||| ||| |||||
AACTTTTTTTACGACTCCAT GCT AGT TTTTT TAA TTG AGAAA ACT AGC TTTTTTTC
A
CAGAAAGAGGTTTAATATTT ACCAG G A T G G ACCTC A-- AAA
TTGTGAGACCATCG

GAM1749 CTATCATGGATAATATTTGT 1735 TACAACATAC 4460 -- A - A TT
AATGGTTCTTTCCGTACAAC TGTTTAGATG CTATCAT GGATA TAT TTGTA TGG C
ATACTGTTTAGATGATAG ATAG ||||| ||||| ||| ||||| |||
GATAGTA TTTGT ATA AACAT GCC T
GA C C - TT

GAM1750 CTTTTTTACGACTCCATCAG 1736 TAATATTTTT 4461 A CTCCA G G T A G GACCA
AAG AGA
AAAGAGGTTTAATATTTTTG GTGAGACCAT CGA TCA AAAGA GTT AAT TTTTT TGA TCG
AGAGAAAG T
TGAGACCATCGAAGAGAGAA CGAA ||| ||| ||||| ||| ||||| ||| |||||
AGAGATAAACTTTTTTTAC GCT AGT TTTTT TAA TTG AGAAA ACT AGC
TTTTTTTC A
GACTCCATCAGAAAGAGGTT - ACCAG G A T G G ACCTC A-- AAA
TAATATTTTTGTGAGACCAT
CGAAGAGAG

GAM1751 CTTTTTTACGACTCCATCA 1737 TAATATTTTT 4462 A CTCCA G G T A G GACCA
AAG AGA
GAAAGAGGTTTAATATTTTT GTGAGACCAT CGA TCA AAAGA GTT AAT TTTTT TGA TCG
AGAGAAAG T
GTGAGACCATCGAAGAGAGA CGAA ||| ||| ||||| ||| ||||| ||| |||||
AAGAGATAAACTTTTTTTA GCT AGT TTTTT TAA TTG AGAAA ACT AGC
TTTTTTTC A

CGACTCCATCAGAAAGAGGT - ACCAG G A T G G ACCTC A-- AAA
TTAATATTTTTGTGAGACCA
TCGAAGAGAG

GAM1752 GCAAATCTTATCATTGGTCG 1738 ATAACATCGA 4463 CTT - --- - TTGCTTT
GTGTTTTGTCTTGCTTTGTG TTCCCATATG GCAAAT ATCAT TGG TCGGTGTT TTGTC G
ACTTTGATAATAACATCGAT ATGT ||||| ||||| ||| ||||| |||||
TCCCATATGATGTTTGT TGT TTG TAGTA ACC AGCTACAA AATAG /
--- T CTT T TTTCAGT

GAM1753 GTGTGCCTGAATCGTTCGAT 1739 TGAATAGAGT 4464 C TTCGAT C C C AA
TAACCCTACTCACCCGAATC TATCGATTCA GTGTG CTGAATCG TAAC CTA TCA CCG T
TCGGATGAATAGAGTTATCG GACA ||||| ||||| ||| ||| ||| |||
ATTCAGACACAC CACAC GACTTAGC ATTG GAT AGT GGC /
A T----- A A A TC

GAM1754 TACTGAAATCTCTCTTTGAT 1740 TCAGAGCAAG 4465 AAA---- CT GAG
TG TAGAGTATATGCAGTCAG AAACACTGCA TACTG TCT CTTTGATTGTA T
AGCAAGAAACACTGCAGTA GTA ||||| ||| ||||| |||||
ATGAC AGA GAGACTGACGT /
GTCACAA AC ATA

GAM1755 TTAGTATATCAAAGACCTTG 1741 TTCACGCCGT 4466 CC - TGATA ATCA T-- TG--
AT
TTATCGATTGATAGTGAATG TGTGTAACAA AAGA TTGTTAT CGAT GTGAATGA GATAG
GG TAGAGGA A
AATCAGATAGTGGTGTAGAG TATC ||||| ||||| ||| ||||| ||||| ||| |||||
GAATATGTCCTTTGTTATCC TTCT AACAATG GTTG CACTTATT CTATT CC
GTTTCCT /
TTGTTATCAAAGTTATTCAC AT T CCG-- GAAA GTT TATT GT
GCCGTTGTGTAACAATATCT
TTAATACAGA

GAM1756 TTATCGATGATGTAGTGGTT 1742 TGATGTAGTG 4467 -- A TATAGT C GAA
ATAGTCTCTGGAATCGTACG GTTATAGTCT TTATCGATG ATGT GTGGT CT TG T
AAGTAATACTACGCATTACG CTGG ||||| ||||| ||| |||
TCGATAA AATAGCTGC TACG CATCA GA GC C
AT - TAAT-- A ATG

GAM1757 TTATGAATATATAAAGTAGA 1743 TGACCTGTTG 4468 TA GTCCTTCTTCCTTT TTCC
TG TCG-- CAA
TGGTGTCCCTTCTTCCTTTTG CACAATCATT AAAG GATGGT TGTAAT CGTATTTT T
TGC T
TAATTTCCCGTATTTTGTGTT CTTT ||||| ||||| ||||| ||||| | |||
CGTGCCAATTGAGTAACATT TTTC TTAATA ACGTTG GTATAAGA A ATG /
ATGAGAATATGACCTGTTGC -- AC----- TCCA GT TTACA AGT
ACAATCATTCTTTATGTATT
CCATGA

GAM1758 TTTTTCACGACTCCATCAGA 1744 TAATATTTT 4469 - CTCCA G G T A G GACCA
AAG AGA
AAGAGGTTTAATATTTTTGT GTGAGACCAT CGA TCA AAAGA GTT AAT TTTT TGA TCG
AGAGAAAG T
GAGACCATCGAAGAGAGAAA CGAA ||| ||| ||||| ||| ||||| ||| ||| |||||
GAGATAAACTTTTTTTACG GCT AGT TTTTT TAA TTG AGAAA ACT AGC
TTTTTTC A
ACTCCATCAGAAAGAGGTTT A ACCAG G A T G G ACCTC A-- AAA
AATATTTTTGTGAGACCATC
GAAGAGAGAA

AATCCTGACGTTCTTATAGC	GTA						
TAGCAATGATACAATCAGTG		ATGGTGAC	TAA	ATAGT	ACGATCG	CTTG	GTCC /
GTA	----- C	A	ATATT	CA	T		

GAM1765 TAGGGGTTCTTCCGCTTGGA 1751	TGTTGTGGTT 4476	TCC	---	CT	T	TTCT	T	CTCT
TCC- AC								
ACCAATCTGGTAGTTCCTCC	TTCCTCTTAA	TCT	GCTTGG	AACCAAT	GG AG	CC	CAAC	
GGC ATTA C								
TCAACCTCTGGCTCCATTAA	TTGG							
CCTCCTGATCATTGCTGTTG		GGA	CGAATC	TTGGTTA	TC TC	GG	GTTG	TCG
TAGT T								
TGGTTTTCTCTTAATTGGT		TT-	CAT	AT -	CTTTT	T	----	TTAC CC
TTACCTAAGCTTAGGGCTTC								
TA								

GAM1766 TCATCAGTCATCTTATTGTT 1752	TGTCACACAC 4477	T	ATCTTATTG	-----	A	ACCC	
TC							
ACTATGACAGACAACCCTGG	TAGTAGATCC	TCA	CAGTC	TTACTA	TGACAG	CA	TGG C
TCCTGCCCATGCTGTCACAC	TTTC						
ACTAGTAGATCCTTTCCGGC		AGT	GTCGG	GATGAT	ACTGTC	GT	ACC T
TGTGA	-	CCTTTCCTA	CACAC	-	----	CG	

GAM1767 GATATTCCACGAAGTCATCG 1753	TATTCCACGA 4478	CCACGA	--	T	C
ACCTCCCCGGGGTGGTTGGT	AGTCATCGAC	GATATT		AGT	CATCGACC CC C
GTCGCTGTACATGATATC	CTCC				
	CTATAG	TCG	GTGGTTGG	GG	G
	TACATG	CT	T	G	

GAM1768 GTAGAAAAACACGGGGAATA 1754	TGTCATCATC 4479	AAAAC	G	ATC	G	T	GA
GCTTAAT - A							
TCGCGTCTGTGATGACACGA	GAGTAGTTCG	A	ACGG	GAAT	GC	TC	GTGATGACAC TT
TACATGC CTTG G							
TTGCTTAATTACATGCCTTG	CCGT						
AGTTTAGGCGTATGTATAGA		T	TGCC	CTTG	TG	AG	TACTACTGTG AA ATGTATG
GGAT T							
AAAGGTGTCATCATCGAGTA		CT---	G	A--	-	C	G- AAGAT-- C T
GTTCCGCCGTTCTTTAC							

GAM1769 TAGCTGTAGAGAATATGTTT 1755	TCTCCGGTAG 4480	TATG		ATGTTA	--	AACA
ACCC AT- AAG						
ACTTCTACCATGTTAGAGGT	AAGTAGAAAA	TTTACTTCTACC		GAGGT	GTAGA	CGT
GTTC TAG C						
GTAGAAACACGTACCCGTTT	TAGA					
ATTAGAAGCAGACCTACTAG		AGATGAAGATGG	CTCTA	CATCT	GCG	TAAG
ATC A						
AATCGCGTCTACTTATCTCC		TAAA	C----	TT	----	C--- ATC CAG
GGTAGAAGTAGAAAATAGAA						
ACGAGGTTA						

GAM1770 TGATGTGAGACGCACGGTAT 1756 AGATGTGACT 4481 TGT ACGCAC TCT T CT GG
 CCAA AACAG
 CTGTAGATGTGACTGTGAGG GTGAGGAACC TGA GAG GGTA GTAGA GTGA GTGA AA
 ATGAAA T
 AACCAAATGAAAAACAGTCG AAAT ||| ||| |||| |||| |||| || ||||
 CTCTTTCATCTTAATCATTA ACT CTC TCAT CATCTCACT TACT TT TACTTT /
 TCACTCTACTCTACTCTATT TT- ATTATC CT- - AT AA C--- CTCGC
 ACTCTTTCA

GAM1771 ACTTCCCCTGATCCATACTG 1757 TATCTGCCAC 4482 - CTGAATCCCTAA-- GTTC ATA
 CC GTAACCA
 AATCCCTAAGGCCTTCTGTT CCAAGAGGGC GA TCCATA GGCCTTCT TG AGA
 ATGTAT G
 CTGATAAGACCATGTATGTA TACT || ||||| ||||| || ||| |||||
 ACCAGTAACCAAAGTACATA CT AGGTAT TCGGGAGA AC TCT TACATG T
 TCTGCCACCCAAGAGGGCTA C AATCACCACCATCA ACCC CG- A-
 AAACCAA
 CTACCACCACTAATATGGAC
 TCAGCGAAGT

GAM1772 TGTAGGATTAGGTACATTAC 1758 TTAGGTACAT 4483 A TTA AT - AG GTTTCC
 GAAGT
 ACTAGCTGTTTCCGGTGCGA TACACTAGCT TGT GGA GGTAC TAC ACT CT GGTGC C
 AGTCGGACAGCACCCTAAA GTTT ||| ||| |||| |||| || ||||
 GAAAGTAGTAGTACCTCCGA ACA CCT CCATG ATG TGA GA CCACG /
 CA G --- -- A AA AATCA- ACAGG

GAM1773 ACCATATACGCGAATACAAA 1759 TACGCGAATA 4484 A - A AAACCTAG T G ACAT
 CC
 ACCTAGTGCACTACGGTACA CAAAACCTAG ACC TATA CGCGAAT CA TGCAC AC GT
 GATCC T
 TGATCCCCTTGAGGATCACG TGCA ||| |||| ||||| || ||||| |||||
 GTCGTGCAATTGTGATTCGC TGG ATGT GCGCTTA GT ACGTG TG CA CTAGG T
 GCTGTAAGGT A C - GTTA---- C G ---- AG

GAM1774 AGGGATGCCGGCCATTCCAT 1760 ACTCATGAAG 4485 AT C- A A
 GAAGTGCAACAGGAGTTGCA ATGGTTGGTC AGGG GCCGGCCATT CATGA GTGCAAC G
 CTCATGAAGATGGTTGGTCC CTT |||| ||||| ||||| |||||
 TT TTCC TGGTTGGTAG GTACT CACGTTG G
 -- AA - A

GAM1775 ATTGTAGCAGCCTAAGATAG 1761 TAGCAGCCTA 4486 - C A---- T ACA A A
 TCTGCCACACGTACACACCA AGATAGTCTG ATTGTAG CAGC TAAGAT GTC GCC CGTAC
 CACC A
 ACCGGTGGTACGGGCGACGC CCAC ||||| ||||| ||||| ||||| |||||
 GCCATCTTGCGCTGTCTACA TAACATC GTCG GTTCTA CAG CGG GCATG GTGG C
 AT T C CCGCG - --- - C

GAM1776 CATGAATAGATTATATAATG 1762 AGTCATGCCT 4487 ATATAA - C- AACA AATAAA G
A CA C G
GCCCTATCAAGAACAGTGAC TGGTAGATGC TG GC CTATCAAG GTGACTG CA CTCG
CC ATG ATT C
TGAATAAACAGCTCGACCCA GCAC ||| ||||| ||||| || ||||| |||||
ATGCATTGCGAAATACATGG AC CG GATGGTTC TACTGAC GT GAGC GG TAC
TAA G
CCGAGATGATGACAGTCATG TCC--- G TA CG-- AGTA-- A C -- A A
CCTTGGTAGATGCGCACCTT
ATCTATCATG

GAM1777 CGATGGTGTTTATACCAGGT 1763 CCAGGTAGTC 4488 TTT - TCCTTTCCC --- -
GA A
AGTCCTTTCCCGGGTTCCTT CTTTCCCGGG GATGGTG ATACCAGG TAG GGG
TTCCTTGATG TTG GACA A
GATGTTGGAGACAAAGTTGT TTCC ||||| ||||| || ||| ||||| ||||| |||||
CATAATCATCAAGGAAATTC TTACTAC TATGGTCC GTC CCC AAGGAACTAC AAT
CTGT G
CCTCTGCCCTGGTATTCCAT CT- C T----- TTA T A- T
CATTG

GAM1778 CGGTGGGGATGTCCTTCTCG 1764 TGGAACGGAG 4489 G T T T GA GCG C GG
TTCCAGAACCTCGCGTGCTG GCATCGCCAT CGGTGG GATG CCT C CGTTCCA ACCTC TG
TGTC T
TCGGTTGGACAATAGAGAGG CG ||||| ||||| ||| ||||| ||||| |||||
TTGGAACGGAGGCATCGCCA GCTACC CTAC GGA G GCAAGGT TGGAG AT ACAG /
TCG G - - - - AG- A GT

GAM1779 GACGTGACTGAGCCTTGCCG 1765 TGACCGAACC 4490 AGCCT C---- - AAAATT
GGTTGGTCAGAGATAAAATT CAGTCTGCAT GACGTGACTG TGC GGGTT GGTCAGAGAT
T
TATCGTCGTCTCTGACCGAA TAGC ||||| ||||| ||| ||||| ||||| |||||
CCCAGTCTGCATTAGCAGTC TTGCACTGAC ACG CCCAA CCAGTCTCTG /
ACGTT GATT- TCTGA G CTGCTA

GAM1780 GCGTCTCGTCTATTAACCTG 1766 TGGTATGCGT 4491 TATTAA - - - - TTCCAATTG T
TT T
GCCCAGTTGCCAGGCTTCCA TCCTTTTCGT CTTG GCCCAGTT G CCAGG C GCATG
CCAGAATC AG T
ATTCGGCATGTCCAGAATCT CCTG ||||| ||||| ||||| ||||| ||||| |||||
TAGTTCCCTTCGGTTCTGGT GAAT TGGGTCGA C GGTCC G CGTAT
GGTCTTGG TC C
ATGCGTTCCTTTTCGTCCTG GACC-- G A A T CTTTTCCTTG - CT C
GACAAGCTGGGTGTAAGCCA
GTTGACTAC

GAM1781 TCGTGGTTTCCAGCAACTTG 1767 CTGGTTGTGA 4492 TTCCA- TGA A AAT
AGGTATATGAATTTCTCCAC GTGTGCCACG TCGTGGT GCAACT GGTAT TG T
ATACTGGTTGTGAGTGTGCC G ||||| ||||| ||||| |||||

ACGG

GGCACCG TGTGG TCATA AC T
TGTGAG --- C CTC

GAM1782 TCTTGTACAGTGCGGGCTGG 1768 TGTACAGTGC 4493 ---- C T AA - A
AATGCCGTCACGAGTGCGTG GGGCTGGAAT TCTTGTACA GTG GGGC GG TGCCG TCACG G
ACCGGCACCCCGTTCACACG GCCG ||||| ||| ||| ||| |||
AGGTGTACAGGA AGGACATGT CAC CTTG CC ACGGC AGTGC T
GGAG A - CC C G

GAM1783 AGTTTTTAAGTAAGCTACAT 1769 TAAGTAAGCT 4494 --- CTACAT TTTGT TT- -
GAA
TAGAAGATGTTTTGTAAACA ACATTAGAAG AGTTTTTA AGTAAG TAGAAGATGT AAACA
ACGA TA A
TTACGATAGAACTCATACT ATGT ||||| |||| ||||| ||| ||| ||
CGTTACTGTTTCTATATCTT TCAGAAGT TCATTC ATTTTCTATA TTTGT TGCT AT
C
TTATTCTTACTCTATGAAGA ATC TT---- TC--- CAT C ACT
CT

GAM1784 CGCTGCCTTTAGAACATCAT 1770 TTCTATGATA 4495 GCCTT----- --- AATCTAT --
- TTT
AGGATATAGAATCTATTACA TAGTTCTGTA T TAGAAC ATCATAGGATATAG TACAAA
ACT T
AACTTTTTCTTGGTTTATT TCAT | |||| ||||| ||||| ||||| ||
TGTGTTATATTCTATGATAT A GTCTTG TAGTATCTTATATT GTGTTT TGG /
AGTTCTGTATCATATTCAAA AACTTATACTAT ATA ----- ATT TTC
GCG

GAM1785 CTTAATTTCAATTAGGTAAAT 1771 TAATACTTTA 4496 TTCAT T CCA G A TCA
TGTTCCAAGAGGATGTATTA CTGCTTTAT CTTAAT TAGGTAAA TGTT AGAGGAT TATT CTG
T
CTGTCATTATCTAGAAATAA TAAG ||||| ||||| ||| ||||| ||||| |||
ATCTTCTAATACTTTACTTG GAATTA GTTCATTT ATAA TCTTCTA ATAA GAT T
CTTTATTAAG TTTC- C --- A A CTA

GAM1786 GATAAAATAACAATTATTAT 1772 TAAAATAACA 4497 T C ATTAT A
ACTTGATACGAGTTTGAATT ATTATTATAC GA AAAATAA AATT ACTTG T
CTTATTTTC TTGA || ||||| ||| |||||
CT TTTTATT TTAA TGAGC /
- C GTT-- A

GAM1787 GCGTATTTGCAATTATTTAG 1773 TAAGGTAAGT 4498 CA-- T AG----- TTTCTT
TTATT
ATAAGGTAAGTTTTCTTTAT TTTCTTTATG GCGTATTTG ATTATT AGATA GTAAGT
TATGT T
GTTTATTTATATCACATATA TTTA ||||| ||||| ||||| ||||| |||||

TAGCACTTATAATTATCGGT	TGCATAGAC	TAATAA TCTGT	TATTCA	ATACA	/
GTCTAATAATGTAACAGATA	AATG	- GGCTATTAA	CGATAT	CTATA	
CGT					

GAM1788	GTCTATGTCAGTTATCCTAC 1774	TATGTCAGTT 4499	-	A--	T-	CCAAAA	CATA
	CAAAACGACATACAATATTC	ATCCTACCAA	GT	CTATGTC	GTTA	CCTA	CGA C
	GGAGAAATAGGTTTAGCATC	AACG					
	GACATGGTAC	CA	GGTACAG	CGAT	GGAT	GCT	A
	T	CTA	TT	AAAGAG	TATA		

GAM1789	TATGTAATTGTAAAACTGT 1775	TATTAGAGAA 4500	TA	TG	AAAAA	GTAT	T	-
	ACTATT							
	ATTTTTCTATTATCTTTACG	TAAGAATGAT	TATG	AT	T	CT	TTTTCTA	TATCTTT ACG A
	ACTATTAACCATAACGTAAG	CGCA						
	AGATATTAGAGAATAAGAAT		ATAC	TA	A	GA	AAGAGAT	ATAGAGA TGC A
	GATCGCATA		GC	GT	A----	AT--	T	A AATACC

GAM1790	AGAGGTTTAAGGATAGTAAA 1776	TATTATCTTA 4501	TT	A	AAAATAT	A	TA
	AATATGGATAGTAATCTTAA	ATATATAGTC	AGAGG	TAAGGAT	GTA	GGATAGTA	TCT A
	GATAGATATTATCTTAATAT	TTTA					
	ATAGTCTTTACCTCT		TCTCC	ATTCTG	TAT	TCTATTAT	AGA G
	C-	A	ATAAT--	-	TA		

GAM1791	CAGACTATTCCAGGAGGCTC 1777	CAGGAGGCTC 4502	TA-	CA-	---	C	TG	TCC
	GGCGGAGTGTGGCTCCACCA	GGCGGAGTGT	CAGAC	TTC	GGAG	GCTCGG	GGAG	TGGC
	A							
	CGCCAGGTTCCCCGAGTACG	GGCT						
	CTCCCAAGAGGTTGTTTG		GTTTG	GAG	CCTC	TGAGCC	CCTT	ACCG C
		TTG	AAC	GCA	-	GG	CAC	

GAM1792	CCCGTCTCGTACTCGGTGAC 1778	TGACGTGGTT 4503	C	C--	C	TC-	AAA	TT C
	GTGGTTCTCGAAAAAGTTTG	CTCGAAAAAG	CC	GTCTCGTACT	GGTGA	GTGGTTC	GA	AGT
	GT A							
	TCAGATCGGCTCCATCTATG	TTTG						
	AGCCATTTTACCCATGGTAT		GG	CAGGGTATGG	CCATT	TACCGAG	CT	TCG TA /
	GGGACAGG	A	TAC	T	TAT	ACC	GC	G

GAM1793	CGGACTTGCGCCGGCTACCT 1779	TGAGGTGCTG 4504	GA	T	TGACC	AGA
	CATGACCGAGGAGAGGGGAC	GCGCAAGGAC	CG	CTTGCGCCGGGC	ACCTCA	GAGG G
	CTCTGAGGTGCTGGCGCAAG	G				
	GACG	GC	GAACGCGGTCTG	TGGAGT	CTCC	G
	AG	-	----	AGG		

GAM1794	GATGAGGCACACGGCAGCCG 1780	TGAGGCACAC 4505	A	CACAC	C	CCT	AG	AAC
---------	---------------------------	-----------------	---	-------	---	-----	----	-----

TCCTGGAGTCCAGGAACCTC	GGCAGCCGTC	GATG GG	GG AGCCGT	GG TCCAGG	C
TCCCTGGAACCCTATGGCTC	CTGG				
CAACCCCATC	CTAC CC	CC TCGGTA	CC AGGTCC	T	
	- CAA--	- T--	CA	CTC	

GAM1795	GCTTTTCTGAAAGAGATATA	1781	TATATTAAGA	4506	T AAA	A-	GTA C	T
	TATATTAAGAGTACTACTAT		GTACTACTAT		GCTTT CTG	GAGAT	TATATATTAAGA	CTA TATC
T								
	CTTGCGATATTAGTCTTGAT		CTTG					
	ATGTAACATCTCCTAGAAAG				TGAAA GAT	CTCTA	ATGTATAGTTCT	GAT ATAG G
	T		- C--	CA		---	T	C

GAM1796	GTCCTGTAGTTAAAGTTGGT	1782	TAAAGTTGG	4507	----	TT	TT	C TA----	C - TC
	GGAACAGTAGGCGCACGTCA		TGGAACAGTA		GTCC	TGTAG	AAAG	GGTGGAA AG	GG
GCA CG A									
	TGTCGTTGCACCCGTCAATC		GGCG						
	TTTTCCACTCTCTTTTGGCA				CAGG	ACGTT	TTTC	TCACCTT TC	CC CGT GC T
	CTCTGGAC		TCTC	--	TC	T	TAAGTGC	A T TG	

GAM1797	GTCTCTCAAGACTATTACTA	1783	TCTCACAATA	4508	T CA	CTATC A	CTCT
	TCGTAAGATATCTCTCACAA		ATAGTTTCAG		GTC CT	AGACTATTA	GT AGATAT C
	AGTATCTCACAATAATAGTT		GAC				
	TCAGGAC		CAG GA	TTTGATAAT	CA TCTATG	A	
			- C-	AA---	C	AAAC	

GAM1798	TATCTTAAGATCTTACATCT	1784	TGAAAGAGTA	4509	-	ACAT T	TGTCCT	AA	G- --
- AAT									
	TCTTGTCTAGAAATATTCT		TCTTACTATA		TTAAGAT CTT	CT CT	AGA	TATTCTT	AGA
GTATCTT AC A									
	TGAGAGTATCTTACAATATT		GTAG						
	AGTAAAGATATCTTCTGAAA				AATTCTA GAA	GAGA	TCT	ATGAGAA	TCT TATAGAA
TG /									
	GAGTATCTTACTATAGTAGT				T AT--	T TATCAT	--	AG TC	A ATT
	AAAGTATCTTAAGATA								

GAM1799	CAGTATCCGCGTATAGTTTT	1785	TAAGACGATA	4510	G-	-----	A C	TCC
	CATTTACTCCCCCTTGATAGT		CGACACGGGC		CA	TATCCGC	GTAT GTTTT	ATTTAC C
	AAGACGATACGACACGGGCG		GGAT					
	GATAGATG		GT ATAGGCG		CATA	CAGAA	TAGATG	/
			AG		GGCACAG	G	-	TTC

GAM1800	GATTAATTGCCATAACCTAG	1786	CGACTAGTTT	4511	T A	CA C	C- C	AACA
	TCGGGTTCTCCAGAAACACG		AGCGTAGCTA		GA TA	TTGC	TAA CTAGTCGGGTT	TC AGA C
	TCCATCTCGACAGATTTCGAC		CTC					
	TAGTTTAGCGTAGCTACTC				CT AT	GATG	ATT GATCAGCTTAG	AG TCT G

C C CG T AC C ACCT

GAM1801 GCGGCACTGACGACCCACGC 1787 ACTCCGTTAG 4512 A-- CCA CAAGAC A - TCC
CT G T
AAGACCGGCACCGTTTCGGA CGGTCTTCGC TG CGAC CG CGGC CC GTTTCGGAC
GTTAGCGGT TC CTG A
CTCCGTTAGCGGTCTTCGCT TGTA || ||| || ||| || ||||| ||||| || |||
GTAACCAGGAACCGTTGGCT GC GCTG GC GTTG GG CAAGGCCTG CGGTTGCCA
AG GAC A
GTCCGGAACCTGGAGTTGAAA ATA C-- ACAAAA A T T-- -- - C
ACACGCGTCGATACGGTGCC
GT

GAM1802 GTGGTTGTAACAGTTGCTTC 1788 CGATATCGGA 4513 T A TG--- - T ATTA T TA
AATC
GAGTTGTGAATTAGAATCGT GAAAGTACCG GTGGTTG AAC GT CTCGA GTTG GA GAA
CGT CA T
TACAAATCTTACGTGCGACG TTTG ||||| ||| || |||| ||| || ||| ||
TTCAGTCCGATATCGGAGAA CACCAGT TTG CA GAGGCT TAGC CT CTT GCA GT /
AGTACCGTTTGACCAC - C TGAAA A - GA-- - GC GCAT

GAM1803 GTTCGATAAATATGGTCACA 1789 TGACGATATT 4514 ATAAA T CACC-- A A C T
CCATCGACATAAATACAGGT AACTGTCCGT GTTCG TATGG CA ATCG CATAA TA AGG A
ATACTTTTATTATGACGATA AGTC |||| |||| || ||| |||| ||||
TTAACTGTCCGTAGTCCGAA CAAGC ATGCC GT TAGC GTATT AT TTC T
C CTG-- T CAATTA A - T A

GAM1804 TGCCGCCAATCATCCGTATA 1790 CCGCCAATCA 4515 ----- CCGTATAAGT A
AGTTGACGATTCGTTATCCA TCCGTATAAG TGCCG CCAATCAT TGACG T
TGATTGGTCTTAACGGCA TTGA |||| ||||| ||||
ACGGC GGTTAGTA ATTGC /
AATTCT CCT----- T

GAM1805 TGGTTGGACACCATTTATCC 1791 ACACCATTTA 4516 ACC A- T TT TAAC CAG
TCCACTTGAATAACAGTCAG TCCTCCACTT TGGTTGGAC ATTT TCC CCAC GAA AGT A
ACTCCACTCCCCTTCCGTGG GAAT ||||| ||| ||| ||| ||| |||
TGGAGCGAATAAGTCCAACC GCCAACCTG TAAG AGG GGTG CTT TCA C
G AA- CG T C- CCCC CCT

GAM1806 TGTCTGAAATCGTTTCGTGTC 1792 TACAACAAAC 4517 GAAA T- CTACAAAA G
TACAAAAGTATGCGATGCAT ACACGACTCG TGTCT TCG TCGTGT GTATGC A
ACAACAAACACACGACTCGA AAAA |||| ||| ||||| |||||
AAAAGACA ACAGA AGC AGCACA CATACG /
AAA- TC CAAACAA- T

GAM1807 ACATTTTTAGGTCTAAAAGT 1793 TAATATCCTA 4518 TCTAAA TTTCC ATG A - GA- A
 --- AATA
 TTCCGAGATGGTAAAGACTC AGATGTCGTT AGG AG GAG GTAA GAC TCT GATA TATC
 GAGAG A
 TGAGATAATATCGAGAGAAT ACAC ||| || ||| |||| ||| |||| ||||
 AAATACCCTTTTCAGAGATAA TCC TC CTC CATT CTG AGA CTAT ATAG CTTTC
 A

TATCCTAAGATGTCGTTACA TAC--- TTA-- CA- G T ATC A AGA CCAT
 CCTCATTCTCATCCTAAAAA
 GT

GAM1808 AGTCTCTGACATCAAGGATG 1794 TGGCATCTGC 4519 CT CAA AG A
 AGCAGGTCAACGATCTGGCA CATGTTTAGG AGTCT GACAT GGATG CAGGTC A
 TCTGCCATGTTTAGGACT ACT |||| |||| |||| ||||
 TCAGG TTGTA TCTAC GTCTAG /
 AT CCG G- C

GAM1809 GAGATTTAATGCTAGTCTAA 1795 TGAGATATTT 4520 ATTT C CT- TATATTAA - AT
 ATATTTCTATATTAAGATAC TACGCTGACA GAG AATG TAGT AAATATTTT C GATA CT C
 TATCTTAAGATATCGGTA CT TTT ||| |||| ||| ||||| ||| ||
 CTGAGATATTTTACGCTGAC CTC TTAC GTCG TTTATAGAG CTAT GA T
 ATTTTACTC ATTT A CAT TCTCATGG A AT

GAM1810 CCCCACGGCACGCGGGTGTG 1796 TGAGTCCATG 4521 CAC CGCGGG G GT CC
 TTT TA
 GGCTGGCGTTGTCCATGGTT AATCATGCCA CCC GGCA TGTGGGCT GC TGT ATGG
 CATC C
 TCATCTACGTTGATGTTTCC CAGG ||| ||| ||||| || ||| |||
 GTAAGCAGTGAGTCCATGAA GGG CCGT GTACCTGA TG ACG TGCC GTAG G
 TCATGCCACAGGG ACA ACTAA- G -- AA TTT TT

GAM1811 CTGTTTACGGAAGCTGGGTA 1797 TGTGCAGACT 4522 A--- CT TATATTTAACATCCTT
 GA - A TC
 TATTTAACATCCTTAAAGGT TTTTCAGTTC GTTT CGGAAG GGG AAAGGTC
 GCGTAGG CG G A
 CGAGCGTAGGCGAGTCAAGC CTTC ||| |||| ||| ||||| ||||| |||
 CGTTCTGTGCAGACTTTTTC CGAA GCCTTC CCT TTTTCAG CGTGTCT GC C
 /
 AGTTCCTTCTTCCGACGCAA CGCA TT TGA CT----- A- T - GA
 GCAG

GAM1812 GTAGCAGTCGCAGTAGCTGT 1798 TCGCAGTAGC 4523 A GT A--- TG G T CG T
 GGTGGTTTCCGCTGATGTAG TGTGGTGGTT GT GCA CGCAGT GCTG GT GT TC C G
 ACGCGGCTGTAGTAACAGCT TCCG ||| |||| ||| ||||| |||
 GTGGTTGTAGC CG TGT GTGTCG TGAT CG CG AG G A
 A TG ACAA GT G C AT T

GAM1813 GTCGTCTACGCGGGTTGCCG 1799 TGGTACGGCT 4524 TA- ---- CGG T CG
AAAAT
GGGCTGCTGCGCTAGCAAAA GCCGCGATCT GTCGTC CGC GGGTTGC GGC GCTG
CTAGCA C
ATCGTGTCTGCTGGTACGGC CAGG ||||| || ||||| || ||||| |||||
TGCCGCGATCTCAGGAGCGA CAGCAG GCG TCTAGCG CCG CGGC GGTCGT /
GCGACGAC CGA AGGAC --- T AT CTGTG

GAM1814 TGCGATAGCTTACATCTATG 1800 TAGCTTACAT 4525 --- TAC T - - T A
GGTGGATCTAATAAAATTAG CTATGGGTGG TGCGAT AGCT ATCTA GGGT G GA CTAAT A
CTCACAACCCTTGATTGAG ATCT ||||| |||| |||| |||| |||||
CTTTAATCGCA ACGCTA TCGA TAGGT CCCA C CT GATTA /
ATT CT- T A A C A

GAM1815 TGCGCTGTTGGCCCGGACAC 1801 TCGCCGGCGA 4526 G GGA TA---- - T TT T
ATGA
GGTATTGTGGTTGATTTGGT CTAGATTCGT TGCGCTGTT GCCC CACGG TTGT GGT GAT
GGTGG AC G
GGTACATGAGTTGAGGTCCA GGGG ||||| |||| |||| |||| ||||| |||||
CCCCATCGCCGGCGACTAGA ACGCGACGA CGGG GTGCT AGCG CCG CTA CCACC
TG T
TTCGTGGGGCAAGCAGCGCA A --- TAGATC G - CC - GAGT

GAM1816 AATAACTAATGGCAAATGTA 1802 TAACTAATGG 4527 C A ---- AAAATT
TAAACAACAAAATTATACT CAAATGTATA AATAACTAATGG AAATGT TAA AACAAC A
AGAGTTGTTAAAGTTAATAT AAAC ||||| ||||| ||||| |||||
TTTCTATTAGTTGTT TTGTTGATTATC TTTATA ATT TTGTTG T
T - GAAA AGATCA

GAM1817 AGTGACATTAGTAGGGATAG 1803 TGAGCTAATT 4528 ---- TAG AT T- TTTTT AAAT
ATC AA
AATGTTGAGCTAATTTTTGT TTTGTAAATA A TTAG GGATAGA GT GAGCTAA GT AACT
TATAA A
AAATAACTATCTATAAAAAG ACTA | |||| ||||| || ||||| || ||||| |||||
ATTATACAAAGTTTTAAACT T AGTC CCTATTT CG TTTGATT CA TTGA ATATT /
CTTTAGTTTCTGCCATTTAT AAAAG TGA AC TC TCT-- AATT AAC AG
CCAGTCTGAGAAAATGTCCC
T

GAM1818 CACAGTTTTTAATTTCTTTG 1804 TTTGGTAATA 4529 C TT TT - ATTATTC AT
GTAATAAAATTATTCACAT AAATTATTCA CA AGTT TAA TCTTTGGTA ATAAA ACT A
ATCAGTATCTTCTTTATCTA CTAT || |||| || ||||| ||||| |||||
CCAGAGATTTTACTAACTTG GT TCAA ATT AGAGACCAT TATTT TGA /
- TC TT C CTTCTA- CT

GAM1819 CGTCGACCGATCAAGTATTC 1805 TGACGAGTAC 4530 - GA- AA - GC TG - AAG ----
- AA

TCAGCCTGTGATGTCTCACC CAGAAGAGGA CGA CC TC GTATTCTCA C TGATGT CTCACC
 CC GCCGC T
 AAGCCGCCGCAATCTGTGGC TCGA ||| || || ||||| || | ||||| ||||| || |||||
 TTCAAGGAGGGTGAGTACAT GCT GG AG CATGAG AGT G GCTACA GAGTGG GG
 CGGTG /
 CGTGGATGACGAGTACCAGA A AGA AC C A-GT T GA- AACTT TC
 AGAGGATCGACG

GAM1820 GCAGGTTTCAGGTATGCCATT 1806 TATGACAGCA 4531 CCA CAG A - GCAT G
 ACACGACTTAC GC
 GTCACAGGCCATGGCTCGCA AGTGCAAGCC TTGTCA GCC TGGC TC CTG GATGAACT
 GTCTCC G
 TCTGGGATGAACTACACGAC TGC ||||| || ||||| || ||||| ||||| |||||
 TTACGTCTCCGCGAAGGAGG GACAGT CGG ACCG AG GAT CTACTTGA
 CGGAGG /
 CCAGTTCATCATAGCAGATG AC- ATA A T AC-- A C----- AA
 CCAAGGCATATGACAGCAAG
 TGCAAGCCTGC

GAM1821 GCCAATTCCAATTGCTGTCC 1807 TAGAATGCGA 4532 TTCC TC G ----- TC
 GAG
 GTATTGTATTAGAGTATCGA GCAGCGATTT GCCAA AATTGCTG CGTATT TATTAGA GTA
 GATAT T
 TATGAGTAATGGTGTCTTG TGGC ||||| ||||| ||||| ||||| || |||||
 CGTTTTTCTGATAGAATGCG CGGTT TTAGCGAC GCGTAA ATAGTCT CGT CTGTG
 A
 AGCAGCGATTTTGGC ---- GA G TTTTG TC GTA

GAM1822 GCTGTAATCCAAACGAATCC 1808 TGTAATCCAA 4533 G ----- AA AA - AG - T
 TAACTGGAAGGTCAACTACT ACGAATCCTA GCT TAATCCA AACG TCCT CT GGA GTC
 AAC A
 GTTCGACTCCAAGGCAGGAA ACTG ||||| ||||| ||||| ||||| ||||| |||||
 GCGTTTTTGAAATGGATTAA CGA ATTAGGT TTGC AGGA GA CCT CAG TTG C
 GC - AAAGTTT GA CG A -- C T

GAM1823 GGTCAAGTTGTACAAGCCGAT 1809 TGTCTCATCA 4534 T- ACA C AT TGCCC
 GATGAATACATTTGCCATT TTGCCTGGAC GGTCAG TGT AG CGATGATGA ACATT A
 TGATAATGTCTCATCATTGC GTTC ||||| || ||||| ||||| |||||
 CTGGACGTTCTGACC CCAGTC GCA TC GTTACTACT TGTA T
 TT GG- C C- TAGTT

GAM1824 GTCGAGGGTGTAGCGGCCGG 1810 TAGCGGCCGG 4535 G --- GT TTCAATGT T
 TCGTTCAATGTATCCTCCGG TCGTTCAATG GTCGA GGT GTAGCGGCCG CG ATCC C
 GATTTTTGGTCGGTCGTTAC TATC ||||| ||||| ||||| ||||| |||||
 GATACCATCGAT TAGCT CCA CATTGCTGGC GT TAGG C
 A TAG TG TTT----- G

GAM1825 TGGTGAGTTAATATTCATGT 1811 TGAGTTAATA 4536 TAATATTCATG C CT
TGAACATAAACTAATATTT TTCATGTTGA TGGTGAGT TTGAA ATAAAA A
TATTTCAAATTATTTACCA ACAT ||||| |||||
ACCATTTA AACTT TATTTT A
TTAA----- - AT

GAM1826 TGTCCAAGATAGAGAGCTCC 1812 CAAGATAGAG 4537 CCA GCTCC-- TGAAT T CTA
AGTTT
TTTGGTGAATCCATCTCTAT AGCTCCTTTG TGT AGATAGAGA TTTGG CCA CT TGTTTC
A
GTTTCAGTTTAACCAAGAAA GTGA ||| ||||| |||| ||| |||||
CAGTCAGCTGGTCTAAAATT ACA TCTATCTCT AAATC GGT GA ACAAAG /
TCCATCTCTATCTAATACA TAA ACCTTTA T---- C CTG AACCA

GAM1827 CTCGAAGTCTTTGTTTTTAT 1813 TAATACAAGT 4538 - GTCT- T AC ACT
ACACGCACTAATCGCGTAAT AATGTTATTC CT CGAA TTGTTT TAT ACGC A
ACAAGTAATGTTATTCGTAG GTAG || |||| ||||| |||
GA GCTT AATGAA ATA TGCG /
T ATTGT C A- CTA

GAM1828 GCGTATGCCGATGCATTCT 1814 TAGCAGATTG 4539 T C TTT AA A---- GTG
AATAAT- TTA
CGTTTTTGCGTTAATATCTA TGTCCATATA GATGCA TCT GT TGCGTT TATCT CTCC GTCT
AGT A
CTCCGTGGTCTAATAATAGT CGTC ||||| ||| ||||| |||| ||| ||| |||
TTAATGATACTCAGCTTGGG CTGTGT AGA CG ATGTAG ATAGA GAGG TAGG
TCA T
ATAAGGAGATTTT CAGATACA T - --- AC CTTTA AA- GTTCGAC TAG
GATGTAGCAGATTGTGTCCA
TATACGTC

GAM1829 TAGAGAACACATTGATGCGT 1815 TAAGAACTTA 4540 TTG- TT TG T AT- T - A
ATCCAT A
TTTGACTTTGTTAATATAAT CATGATCCAT ATGCGT T GACTT T AAT AATG AAGAACT TAC
TG AGTG T
GTAAGAACTTACATGATCCA AGTG ||||| ||||| ||| ||| ||||| ||| |||
TAGTGATACACTTACAAGTA TATGTA ATTGAA A TTG TTAT TTCTTGA ATG AC
TCAC /
TAGTTCTTTTATTTAAGTTT AAAA T- GTT AAT T T A AT---- A
ATGAAGTTATATGTATAAAA
ATTGTTCTTTA

GAM1830 CACAGTTTTTAATTTCTTTG 1816 TTTGGTAATG 4541 C TT TT - ATTATTC AT
GTAATGAAATTATTCATAT AAATTATTCA CA AGTT TAA TCTTTGGTA ATGAA ACT A
ATCAGTATCTTCTTTATCTA CTAT || |||| ||| ||||| |||| |||
CCAGAGATTTTACTAACTTG GT TCAA ATT AGAGACCAT TATTT TGA /
- TC TT C CTTCTA- CT

GAM1831 GCCAAATCCAATTGTTGTCT 1817 TAGAATGCGA 4542 TCCA TC G TATC TG
CAAT
GTATTGTATTAGAGTATCGA GCAGCGATTT GCCAAA ATTGTTG TGTATT TATTAGAG GATA
AG G
TATGAGCAATGGTGTCTTG TGGC ||||| ||||| ||||| ||||| ||| ||
TGTTTCTCTGATAGAATGCG CGGTTT TAGCGAC GCGTAA ATAGTCTC TTGT TC G
AGCAGCGATTTTGGC --- GA G T--- GT CTGT

GAM1832 GCCGGGCGGAGCCGAACATT 1818 GGGCGGAGCC 4543 CGG- CCG--- CTCCA T T
CTCCAATATTCAATTTTTGT GAACATTCTC GC GCGGAG AACATT ATATCAAT
ATATCTATAATGTTATTAAC CAAT || ||||| ||||| ||||| |||||
CTCCGCATACGC CG CGCCTC TTGTAA TATAGTT/
CATA CAATTA TATC- T T

GAM1833 GGTGGAACGTATATTTTATT 1819 TGTAACCAC 4544 C T TTA- A TTAA
TAAGGACTTAACAATTGTCT AATTTGCTTC GGTGGAA GTA ATT TTTA GGAC C
GTAACCACAATTTGCTTCC CGCC ||||| ||||| ||||| |||||
GCC CCGCCTT CGT TAA AAAT TCTG /
- T CACC G TTAA

GAM1834 TCCAGATGTCATGATATTGA 1820 TGTCATGATA 4545 - ATAT -- TAACAAAT -
TTTGCAA TT
ATTGGAAAAATAACAAATCT TTGAATTGGA TCATG TGA ATTGGAAAAA CTATT TTGATTT
GGA G
ATTTTGATTTTTTGCAAGGA AAAA ||||| ||||| ||||| ||||| ||||| |||||
TTGGTTCCATAACTAAATTA AGTAT ACT TGACTTTTTT GATAA AATTAAA CCT
/
ACAATAGTAGTAATTTTTTT A ATCT AT TTAATGAT C TCAATA- TG
TCAGTTATCATCTATATGAA
TGTATTTGGA

GAM1835 AATCAATAGTATAGTTTTAT 1821 TAGAATATCG 4546 TA A T- TTAT ATA C C----
GT-- A
TTTTATTACGTATATTTCACT GCGTATCGTT A GTAT GTT TATTT TACGT TTCA TTTTCT
CATT CTA T
TTTCTCCATTGTCTAATAAT GATT | ||||| ||||| ||||| ||||| ||||| |||||
AGTTCAAATGTTTCTAGAAG T TATG CGG ATAAG ATGCA AAGT AGAAGA GTAA
GAT A
AATGAAAAACGTAGAATATC GC - CT --- AA- A TCTTT ACTT A
GGCGTATCGTTGATT

GAM1836 AGAGAAGCTAGTACATCTGT 1822 TAATAGCTAT 4547 A A ACA TT ----- TCC TT
ATC
TATAATAGCTTCCATATTTT TTTTATCTAT AGAGA GCT GT TCTG ATA ATAGCT ATAT
TTCTT C
TCTTATCCGCCAAGAACATA TTTA ||||| ||||| ||||| ||||| ||||| |||||
TAATAGCTATTTTTATCTAT TCTCT CGA CA AGAT TAT TATCGA TATA AAGAA /
TTAGAAAAACAAGCTCTCT - A AA- TT CTATTTT TAA C- CCG

GAM1837 AGTAAATTCGTTAAGCAAAG 1823 TAAGCAAAGA 4548 -- GTAAAATCTT---- T AGATA
 - G A TT
 AAGTAAAATCTTCGTCTTTA AGTAAAATCT GTTA AGCAAAGAA CG CTTT TTTCT G
 AT TACT A
 GATATTTCTGGATATACTTT TCGT |||| ||||||| || |||| |||| | || ||||
 AAATAGTACATGCGAGAAAA CGAT TTGTTTCTT GC GAAG AAAGA C TA ATGA
 A
 AGTGGAAGTCGTAATACCAA AA GTCTTAACCATAAT T GTGAA G G C TA
 TTCTGTTCTTTGTTAATAGC
 GGTTACAGCT

GAM1838 GATGTTCTATAAATAATTTA 1824 TCGAATAATT 4549 TT T-- T- A CA
 TTCAGATAACATATATTGTC TTATTTTATT GATG CTA AAATAA TTATTC GATAA T
 GAATAATTTTATTTTATTAG AGGC |||| || |||||| |||||| ||||
 GCCATT TTAC GAT TTTATT AATAAG CTGTT A
 CG TAT TT - AT

GAM1839 GCTGTAGATGTAACCGAGTA 1825 AGATGTAACC 4550 T- CC A CCATAAA A
 TGCGATTGCCATAAATAATC GAGTATGCGA GCTGTAGA GTAA GAGTATGCG TTG TA T
 CTAGAAAATCAACGTATATT TTGC |||||| || |||||| || ||
 TCTTTACTTTTACAGC CGACATTT CATT TTTATATGC AAC AT C
 TT TC - TAAAAG- C

GAM1840 CTGAAGAAGATTGTAGGGAC 1826 TATCATGGCA 4551 AGA AGGGA ATT G - -- CG
 TCATTCCAGGATCAGCGACG GGAGGAACAC CTGA AGATTGT CTC CCA GAT CA
 GCGACGA C
 ACGCTTTCGTTGCTTTGTAT AATC |||| |||||| || || || || || |||||
 CATGGCAGGAGGAACACAAT GACT TCTAACA GAG GGT CTA GT CGTTGCT /
 CTATCAG A-- CAAG- GAC A T TT TT

GAM1841 GGCTTCCGCGTGTCCAATA 1827 TGACATGCTG 4552 GCG AAC G CCTAA GC
 TTTA----- C
 GGGGTGCCTAAGGCGTGTGC ATCACGCCTA C TGTCC TAGG GTG GCGTGT CAGGG
 ATA T
 CAGGGTTTAATACTAGTATA GGAC | |||| |||| || |||||| |||| ||||
 GTTCGTGGCGAACACCCTGA G ACAGG ATCC CAC TCGTACA GTCCC TAT
 A
 CATGCTGATCACGCCTAGGA --- --- G TAG-- -- ACAAGCGGTGCTTGA G
 CAGGAAGCC

GAM1842 CTGGGTATGCAGCATGAGGT 1828 TGAGGTAGTT 4553 TATGCA - T TT T AC TTTA
 AGTTGTTGATCACTCGTCTT GTTGATCACT CTGGG GC ATGAGG AG GT GATC TCGTC A
 TAAGGTGTGACGACGGATCA CGTC |||| || |||||| || || |||| ||||
 CTCTTCTCATCGCCCTTGTC GGCC CG TACTCT TC CA CTAG AGCAG G
 CCGG TGTTC C - T- - GC TGTG

GAM1843 CTGTTCCGCCACTTATCGTA 1829 TGGGATACGT 4554 CC - T G T
 CAGTTTCTGTGGGATACGTA AGGCAAAACA CTGTT GCC AC TATC TACAG T
 GGCAAAACAG G |||| |||| |||| ||||
 GACAA CGG TG ATAG GTGTC /
 AA A C G T

GAM1844 GGCGCATCTGGAGGCCGTTT 1830 TCACTGTAAA 4555 ATCT C- TC--- - TG
 TGTAGGATGTTGTACTGCAT ATTACGAATC GGCGC GGAGG CGT TGTAG GATGT T
 CACTGTAAAATTACGAATCT TCCG |||| |||| || |||| ||||
 CCGTGCC CCGTG CCTCT GCA ATGTC CTACG A
 ---- AA TTAA A TC

GAM1845 GGTGATGAGGCAGGTGAAAC 1831 TGAGGCAGGT 4556 GAG ----- AAC C- GAC---
 C GAT
 CCGTGATGCCGATGAAGGAC GAAACCCGTG TGAT GCAG GTGA CCGTGATG CGATGAAG
 ATTT TGC A
 ATTTCTGCGATAAAGGCAAA ATGC |||| |||| |||| |||| |||| |||| ||||
 GTAACGAACCTTCGTCGATCA ACTG CGTC CGCT GGCACCTAC GCTGCTTC TGAA
 ACG /
 TCACGGCCTCGCTGAAGCTG TA- GAAGT CC- TA AAGCAA - GAA
 CATGTCACC

GAM1846 GTTTTAGGCTTAGTTACCGG 1832 TTAGTTACCG 4557 -- ----- - TGT CTTT TAG
 CTCTTGTGGCCTCTTTAGAG GCTCTTGTGG GTTTTAGGCTTA GTTACCG GCT CT GGCCT
 AGAG T
 TAGTCGTCCTCTTAGGCTTT CCTC |||||||| |||| |||| |||| ||||
 GGCGGTTTAACGATGGTAAC CAAAATTTGAAT CAATGGT TGG GG TCGGA TCTC
 C
 CGTAAGTTTAAAC GC AGCAATT C TT- T--- CTG

GAM1847 AACAGGATGTGCTTCATGGT 1833 TTGAACCATC 4558 ATG C----- C C C TTATACA
 CTTAGGATCTAATCGCTTAT ACGGTGAGCA AACAGG TGCTT ATGGT TTAGGAT TAAT GC
 T
 ACATGACCTCTGCCGTTGCA AGTC |||| |||| |||| |||| |||| ||||
 TTTTGAACCATCACGGTGAG TTGTCT ACGAG TACCA AGTTTTA GTTG CG /
 CAAGTCTGTT GA- TGGCAC - C C TCTCCAG

GAM1848 AGCCTGTCCCGAGCGTTGAT 1834 TGTGACACCA 4559 CT CC A G - - TC
 GTGATTCCTCCTAGTGATGT ACGTTTGAAT AGC GT CGAGCGTTG TGT AT TC C C
 GACACCAACGTTTCAATTGC TGCT ||| || |||||| |||| ||||
 T TCG TA GCTTGCAAC ACA TG AG G /
 T- A- C G T TAT

GAM1849 ATCTCTGTTTAATATGGAAA 1835 TAACTTGGTG 4560 A T AATTAA T - TGCCATAC
 TG AGTA TT

TTAAAGTTATGGACCCAAGT	TCTGTGCCTG	ATA GGA	AG TATGGAC CCAAGTT	GTT T
AGTTTC T				
TTGCCATACGTTTGTAGTAA	ATCC			
GTTTCTTTTGTAGAACTGAAA		TAT CCT	TC GTGTCTG GGTTCAA	TAA A TCAAAG
/				
TGAATAACTTGGTGTCTGTG		- - AG----	C T	----- GT AAG- AT
CCTGATCCTATGAGAGAGAT				

GAM1850 ATTGTTTCGCTATGGCATATA 1836	TATGGCATAT 4561	TTC	---	ATT-- C--- T	TATCC
T					
TATTTAACGGTGAATTATAT	ATATTTAACG	ATTG	GCTATG	GCATATAT	TAA GG GAATTA
CAC T					
CCCACTTCCGTGCTAATTCC	GTGA				
CATATTTATTTCAATGTATG		TAAC	CGATAC	CGTATGTA	ATT CC CTTAAT GTG C
CTAACATAGCAATCAAT		TAA	AAT	ACTTT TATA -	C---- C

GAM1851 CCCCTTCTATAAACGCGATG 1837	CATCAGAGCT 4562	C--	AAAC -	TGTCT G	CT C
TTTC- TT					
TCTGCGTCTGGCTTCCCCTG	TCTTCTGCAT	CC	CTTCTAT	GC GA	GC TCTGG TCC CTG
GCTT C					
TTTCGCTTTTCCGCAAGCAT	CATA				
CATCAGTGGACATCAGAGCT		GG	GAAGATA	CG CT	CG AGACT AGG GAC CGAA
C					
TCTTCTGCATCATAGAAGAA		AAA	CTA- T	TCTT- -	AC T TACTA CG
AGG					

GAM1852 CTTGTAGCATACTATGCAGC 1838	TAGCATACTA 4563	CT- C	TCCAT -	TAT- TCC
AATTC CC				
TCTTCCATTACTGCTAGTAT	TGCAGCTCTT	TA	ATG AGCTCT	TACTG CTAGTA CA TCT
TCCATCA T				
ATCATCCTCTAATTCTCCAT	CCAT			
CACCTGCATGATGGATTGCA		GT	TAC TTGAGA	ATGAT GGTCTGT GT AGA
AGGTAGT G				
GACTTGTACTIONGCTGGTTAG		CAC -	CTCC- T	TCAT TC- CGTT- AC
TACCTCAGAGTTCATCACTG				
TGCTCTTAAG				

GAM1853 GGTGCAATTTCCGCTCGTGC 1839	TATTGCATCT 4564	A	CGCTC	T----	G
AATGTGTCGTGTGGATGGCT	TGAAATAGCA	GGTGC	ATTTC	GTGCAATG	GTCGT T
TATGGTATTGCATCTTGAAA	CC				
TAGCACC		CCACG	TAAAG	TACGTTAT	CGGTA G
	A	TTC--	GGTATT	G	

GAM1854 GGTGTGACAGTTTTGTCTGA 1840	TGATATTAAA 4565	A TTT	TAAT	CAGA	C ATG
GATTAATTTGCAGAGGTATC	CCAGTTGTCT	GGTGTGAC	GT	GTCTGAGAT	TTG GGTATCAG
AC A					
AGCACATGATAAAGTCTGAT	CGGA				
ATTAAACCAGTTGTCTCGGA		CCACATTG	CA	TAGGCTCTG	GAC TTATAGTC TG T
TACGTTACACC		- ---	TT--	CAAA	- AAA

GAM1855 GTTGTTCATCATTATATA 1841 TATATAGATC 4566 C - - CA TG TT TC TC TCA
ATT
GATCAGGTTGGTTGATTCTG AGGTTGGTTG TTTGCAT ATTA TATA GAT GGT G GAT TG
ATCTTCTA AATT C
TCATCTTCTATCAAATTATT ATTC ||||| ||||| ||| | ||| || ||||| ||||
CAAAAATTCTAGAGGATTCC GAACGTA TAAT GTAT CTA CTA T TTA AC TAGGAGAT
TTAA /
ATATTCTTTGATCATCATAT - T A -- GT TC T- CT C-- AAA
GTTAATATGCAAGCGAC

GAM1856 ATGTCATGACCCTCTTCTCG 1842 TGAGATAATA 4567 CCCTCTTCTC A CA- A
TCACAGTCCAGTGATCTCAT AATATTATGA ATGTCATGA GTC CAGTC GTG T
CAAGACTGAGATAATAAATA TAT ||||| ||||| ||||
TTATGATAT TATAGTATT TAG GTCAG TAC C
ATAAATAA-- A AAC T

GAM1857 CTCTAGATCTCTGGACATGC 1843 TTGCATGTCG 4568 ATCT G TT CAT
TTGACATCTTTTCTTGCATG AGCAAATTAG CTCTAG CT GACATGC GA C
TCGAGCAAATTAGAG AG ||||| ||||| ||
GAGATT GA CTGTACG CT /
AAAC G TT TTT

GAM1858 TAGTGGTAACATAGAAGCTC 1844 TATCCCTGCA 4569 TAAC AA TC --- T CTTC -
GG AGT A
CAGGTGTAGTGGCTTCATGA CAAATTGTTG TGG ATAG GC CAG GTGTAG GG ATG
ATCGGG GC TTCC A
TCGGGGGGCAGTTTCCAATA CAGC || ||||| || ||||| || ||||| || ||||
GGAGGTGACCTGATGCATAT ACC TATC CG GTT CACGTC CC TAC TAGTCC TG
GAGG T
CCCTGCACAAATTGTTGCAG TCCC GA TT AAA - TA-- G AG --- A
CTATCCCTCCACTA

GAM1859 TATGTGGAGTTGGGTTTTTA 1845 TAAAACATTG 4570 GA- TG - TAAA GA
AAATATGAACAATATAAAAC ATAAATACAT TATGTG GT G GTTTT ATAT A
ATTGATAAATACATA A ||||| || ||||| ||||
ATACAT TA T CAAAA TATA /
AAA GT A ---- AC

GAM1860 TCCGGTGTTAGATCCCTGGT 1846 TGAGATCTAG 4571 T GATCC T - CTA--- T- T
TCCATCAGCTATGTATAGTA AATATAGCCC TCCGG GTTA CTGG TC CATCAG TG ATAG A
TGCTGTCTCGGAAAATCTGA TGGA ||||| ||||| ||||| || ||||
TGAGATCTAGAATATAGCCC AGGTC CGAT GATC AG GTAGTC GC TGTC T
TGGA C ATAA- T A TAAAAG TC G

GAM1861 TGTCTGTCTTGATTAGATAT 1847 TTAGATATCC 4572 - TC T - CTCACCGTTA T
 CCTCACCGTTATGTGATTGT TCACCGTTAT TGTCT G TTGAT AG ATATC TGTGAT G
 TGTCACAGATATGTTCTGCA GTGA ||||| ||||| ||||| |||||
 GTCCAAGATA ATAGA C GACTG TT TATAG ACACTG T
 A CT C G ----- T

GAM1862 CACTTGAACAGAATAGCCAG 1848 TCACTGGCAG 4573 A- GAA- GAAC AGAAA GGA
 TGCA
 TGAACACAGAAAAACAGGGA AATCTCATT CACTTG ACA TAGCCAGT AC AACAG CAA
 A
 CAATGCAAAAGAGAACATCA A ||||| ||| ||||| || ||||| |||
 ACCTTGCTAGCATCACTGGC ACTTAC TAA GTCAC TAC GT TCCAA CAA A
 AGAATCTCATTCA TC GACG GATC ----- CTA GAGA

GAM1863 AGGGTCTGAGGGGACTAAGT 1849 TGAGGGGACT 4574 G ---- AA GA-- A
 GGAGGCCTGAAGCCGGGTTA AAGTGAGGC AGGGTCT AGG GGA CT GTG GGCCTG A
 TGATGCAGGGTCTCTGGGCCT CTGA ||||| ||| ||||| ||| |||||
 GAGACCCT TCCCAGA TCC CCTGG CGT TTGGGC G
 G GGGT GA AGTA C

GAM1864 CCCGGCCGCCCTTGGGGGT 1850 TCCCCAGAAC 4575 TC T AA C ACA
 CTC
 TTCGGGGACACGGTTGCTGG CCCCAGGGG GCCCCTTGGGGGTT GGGGACACGGT
 GCTGGCTGCC GACA TTAG GCC T
 CTGCCAAGACACTTAGACAG TGGC ||||| ||||| ||||| ||| ||||| |||
 CCCTCTAGTGGCCAACTAGA TGGGGAACCCCCAA CCCCTGTGCCA CGACCGACGG
 CTGT GATC CGG /
 TGTCGGGGCAGCCAGCCACC GA C GG A AAC TGA
 GTGTCCCCAGAACCCCCAAG
 GGGTGGCCGGG

GAM1865 CCTACTATGTTCTTATTGGC 1851 TGTGGAAACC 4576 CT CTT - TTATGG -- T--
 AT TT
 TTATGGCCATAGACCCCTGC TGCCCAAGTGA CCTA ATGTT ATTGG C CCATAG ACCCC
 GCCCAT CC G
 CCATATCCTTGAAGGCAGTG CGTC ||||| ||||| ||||| ||||| ||||| |||
 GGCCGTGGGGTTGCTGTGGA GGAT TGCAG TGACC G GGTGTC TGGGG
 CGGGTG GG /
 AACCTGCCCAGTGACGTCTT TC --- C TCCAAA GT TGC AC AA
 AGG

GAM1866 GGATAATGGGGGAGGTCCGA 1852 TGGGGGAGGT 4577 T- GTC-- TGG- GT GCA
 ATGGGGGTCTGTGGGCTGGC CCGAATGGGG GGATAA GGGGGAG CGAA GGGTCT
 GGGCTG G
 AGGCGCGGCCTGGGCCCAAT GTCT ||||| ||||| ||||| ||||| ||||| |||
 TTTCGCTTCACTCCCCTTCT CTTATT TCCCCTC GCTT CCCGGG TCCGGC /
 TATTC CT ACTTC TTAA -- GCG

GAM1867 GTGAGTCATGGAAGAGGGTC 1853 TGAGACCCCA 4578 ----- G ---- AA GA--
A
TGAGGGGACTAAGTGGAGGC GGCTTCTTCC TCAT GGAAGA GGGTCT AGG GGA
GTG GGCCTG A
CTGAAGCCGGGTTATGATGC CTTA ||| |||| |||| || ||||
AGGGTCCTGGGCCTGAGACC AGTG CCTTCT CCCAGA TCC CCTGG CGT
TTGGGC G
CCAGGCTTCTTCCCTTAGGT TGGATTC TCGGAC G GGGT GA AGTA C
GTGAGTCAT

GAM1868 TTTTITAGCTGATGACAGAC 1854 TAGCTGATGA 4579 - ACA- A - G GTCAA TG
GC GAA
AAAGCATGTTTACAGATGGTCA CAGACAAAGC TTTTIT GCTGATG GACAA GC AT TTCAGATG
TA T AGTTA T
ATATGTGCAGTTAGAATACA ATGT |||| |||| |||| || |||| || || ||||
TGACTAGTGTGCGTCTGGAG AAGAAT TACTAT TTGTT CG TG AGGTCTGC GT G
TCAGT /
GTAGCATTGTTAAACTATCA A CAAA A A G ----- GT A- ACA
GTATAAGAAA

GAM1869 GGGGCGGAAGACCCTCATCG 1855 TGGCCGGGCG 4580 - TCATC-- - T T --- C C
- GCT
CCCTCTGCCTGGCTGTTCCG AGGCGCCCCG CC GC CCTC GCCTGGCTGT CGGG CCG
TGA CGCCTGCT GT T
GCCGCTGACCGCCTGCTGTG CCCG || || |||| |||| |||| || |||| || || ||||
CTTGAGACGAGCGGGCGCTC GG CG GGAG CGGGCCGGTA GCCC GGC ACT
GCGGGCGA CA /
ACGGGTACCCGATGGCCGGG C CCCGCC C - - ATG - C G GAG
CGAGGCGCCCCGCCGGCGT
CCTCCGCCCC

GAM1870 AATAATACTATTTAGATGAA 1856 TTCATCGTTC 4581 ACT TA-- AATT- TTATC
AAAAATTAGCTTATCAACTT GATTCATTAT AATAAT ATT GATGAAAA AGC A
CTGTTTCCAATTTTTCATCG T |||| || |||| || ||||
TTCGATTCATTATT TTATTA TAG CTACTTTTT TTG A
CT- CTTG AACCT TCTTC

GAM1871 ATTACCGTGTATATAAAATC 1857 TATAACAGCT 4582 T A TC T TTGG TCTGAATT
CTTTATGTCATTGGAGGTC TTTACATATT ATTACCG GTAT TAAAA CT TTATGTCA AGGTC
A
TCTGAATTATAAATCTGA TGGT |||| |||| |||| || |||| ||||
TCTAACTGATATAACAGCTT TGATGGT TATA ATTTT GA AATATAGT TCTAG T
TTACATATTTGGTAGT T C C- C CAA- TCTAATAA

GAM1872 CGTTAGATGGTTGATAATCA 1858 TTTGATATTT 4583 T TCAC TGTGT-- ATCTT
AT
CCGTGTGTTTTTGTATCTTT AACAAAGTAA CGTTAGATGG TGATAA CG TTTTGT
TATCAGATA G

ATCAGATAATGACATATTTG	AAAT		
ATATTTAACAAAGTAAAAAT		GCAATCTATT ATTATT GC	GAAACA ATAGTTTAT A
CGACCTTTATTATTTATCTA		T TCCA TAAAAAT ATTT-	AC
ACG			

GAM1873	GATAGGCCAAAAAATATGTTT	1859	TAGGCCAAAAA	4584	AC- -----	AG
	ACAACCTTGGGAGAATTCCAA		ATATGTTTAC		GATAGGCCAAAAAATATGTTT	AAC TTGGG A
	AATACTGTTTCGGAAATATGT		AACT			
	TTTTTGTTTATT		TTATTTGTTTTTTGTATAAA	TTG AACCT /		
			GGC TCATAA TA			

GAM1874	GATTCTGGCATATGTCGAGG	1860	TCTGGCATAT	4585	C A TC - GC G T
	CTGGGTTTCTTTATAAGGAA		GTCGAGGCTG		GATT TGGC TATG GA G TG GTTTCTT A
	CACAATCATCATCGTAGTCA		GGTT		
	TAGTC		CTGA ACTG ATGC CT C AC CAAGGAA /		
			T - TA A TA A T		

GAM1875	GTTAATATCGGTAGGGTGTA	1861	TGTAGTATAT	4586	A C -- - TAGAC A T AC
	GTATATATAGACCACAGATA		ATAGACCACA		GTTA TAT GGTAGG GTGTA GTATATA CAC GA
ATC A					
	TCACATTGATCTCCGTGTAT		GATA		
	ATACTTACATTTTTTACCAT			CGAT ATA CCATTT TACAT CATATAT	GTG CT TAG /
	AATAGC		A - TT T -----	C C TT	

GAM1876	TTATATTTAAGTTCTATAGG	1862	TATTACTCAG	4587	AA ATA AG- C TAA
	TAAAGCATTCCAGTAACCAT		AATAGATATA		TTATATTT GTTCT GGTA CATT CAG C
	CTGTAGTGATATTACTCAGA		G		
	ATAGATATAG		GATATAGA TAAGA TCATT	GTGA GTC /	
			-- C-- ATA T TAC		

GAM1877	TTATATTTTCATGTAGTGTC	1863	ACGCTACCCT	4588	TT --- C CA T
	TGAACAACTTGTGTATTTTA		ATGATGTATA		TTATAT TCAT GTAGTGT TGAA AC T
	ACGCTACCCTATGATGTATA		A		
A			AATATG AGTA CATCGCA ATTT TG G		
			T- TCC - TA T		

GAM1878	AATGCAGGTCTTGGCGGATA	1864	TGGCGGATAG	4589	----- TG GGA C T - T
AAA					
	GAACCTTTGAATGTATTAGT		AACTTTTGAA		AATGCA GGTCT GC TAGAA TT TGAATGT AT
AGT T					
	AAATTTAGCTCATCACATTT		TGTA		
	ATGATTCTGAGGTTTAGATT		TTACGT		TTAGA TG GTCTT AG ATTTACA TA TCG /
	GTAACATTATGCATT		ATTACAAATG	TT GA- - T C C ATT	

GAM1879 AATTAGTGAATTATACATAT 1865 TATTATATGG 4590 G T TTT ATA A- A-- T
 CTTTTTAAATAACTATATAT AGGTGTGTTG AATTAGT AATTATACA ATCT TAA ACT TATATGA
 CA A
 GAACATAATTGATATTATAT TTAG ||||| ||||| ||| ||| ||||| ||
 GGAGGTGTGTTGTTAGATCT TTAGTTA TTGATGTGT TAGA GTT TGG GTATATT GT A
 GTGTAGTTGATTGATT G C TT- GTG AG ATA T

GAM1880 ACAACTATATAGATAATGTG 1866 TATTACATTA 4591 ---- GA - TT AAT
 AGTTTTTAAATAACTATATT CATATAATCA ACAACTA TATA TAATGTGA GTT TA A
 GATATTACATTACATATAAT TGGT ||||| ||| ||||| ||| ||
 CATGGTTGT TGTGTTGT ATAT ATTACATT TAG AT A
 ACTA AC A TT ATC

GAM1881 CATGTGGAGGCCATTCAAAG 1867 TATGACTAAA 4592 T - ATTCAAA T CTAAAAT- T
 CC
 TAATTATGACTAAAATGACA ATGACATTTT CATG GGAGG CC GTAA TATGA GACATT
 TTTA A
 TTTTTTACCATTTAAGCAAT TTAC ||| ||||| || ||| ||||| ||||| |||||
 GTCCCCTAATCTCATATTTG GTGC TCTTT GG CGTT ATACT CTGTAA GAAT /
 CAGGGATTTCTTCGTG T A GA----- T CTAATCCC C TT

GAM1882 GATAATTGATTTGAATATTT 1868 TAATTGATTT 4593 ATT TATT TAA TCACT
 AGCTAATTCTGAATCACTTA GAATATTTAG GATAATTG TGAA TAGC TTCTGAA T
 ACCTTTTGTAGAAAATGTTATT CTAA ||||| ||| ||| |||||
 TCACAATTATC CTATTAAC ACTT ATTG AAGATTT /
 --- T--- TAA TCCAA

GAM1883 GCTTGCAGGATAGTATACAC 1869 CATAAATTGC 4594 TA- CACCAT GAAT TTTAC
 GCATATC - T
 CATTATGCTGAATGGTTTTA ATATCACGGG GTATA TATGCT GGT TCATAAATT
 ACGG GATA A
 CTCATAAATTGCATATCACG ATAT ||||| ||||| ||| ||||| ||||| |||||
 GGATATATATGTCTCCGTAC CATAT ATACGA TCA AGTATTTGA TGCC CTGT
 T
 CTTTAAGTTTATGACCTATA CAA TTCTT- ---- TATCC ATTTCCA T A
 CTAGCATATTCTTTATACAA
 CAACTTAAGGC

GAM1884 TGATTTTGAGAATACATATT 1870 ATAACATCAT 4595 ATT- ACATATTAC GA AA TA A
 A
 ACATGGATATTGAAACTGTA TTTCATTCTT TG TTGAGAAT ATG TATTG ACTG AGT
 GTCAAGA C
 AGTAGTCAAGAACATTTTGA AATT || ||||| ||| ||||| ||| ||||| |||||
 TGACTTAGTACAATAACATC AC AATTCTTA TAC ATAAC TGAT TCA TAGTTTT /
 ATTTTCATTCTTAATTAGCA GATT CTTTTAC-- A- A- -- G A

GAM1885 CACGGCCAATGTGGCTTCAT 1871 CAATGTGGCT 4596 CC T CT TTC T TG
TCTGTTTCCCTGCAAGGGCA TCATTCTGTT CACGG AATG GG TCA TGTT CCC C
ACATGGTTCCTCATTACCTG TCCC ||||| ||| ||| ||| |||
TG GTGTC TTAC CC GGT ACAA GGG /
CA T TT --- C AA

GAM1886 CGGGATGTGCTATCGAATAC 1872 TTGCTTGTTT 4597 - ATCGAATACT AC TT
TGCAGACGCAGGGTTAAGTC ACCATCAAGC CGGGATG TGCT GCAG GCAGGG A
TTGCTTGTTACCATCAAGC ATTG ||||| ||| ||| |||||
ATTGTCCCG GCCCTGT ACGA TGTT CGTTCT /
T ACTACCACT- -- GA

GAM1887 CTTAGTAGAGGTAACCTCGT 1873 AGAGGTAACC 4598 T AG A T- -- A T
GGTCAGCGGTCACTGCGACA TCGTGGTCAG CT AGT AGGTA CC CGTG GTC GCGG C
GCGCGTTGGGTACCTGCTTG CGGT || ||| ||||| || ||| |||||
G GG TCG TCCAT GG GCGC CAG CGTC /
T -- G TT GA - A

GAM1888 GAAAGTAGAATTCCTGGCAT 1874 TATAAGACAA 4599 A - ATT - - -- AATC
ATTCTTGATATAAATCACCCA TATTGTCTAG GA AGTA GA CCTGG CA TAT TCTTGATA A
TATATAAGACAATATTGTCT GCCT || |||| || |||| || ||| |||||
AGGCCTCTTACTCTC CT TCAT CT GGATC GT ATA AGAATATAT /
C T CC- T T AC ACCC

GAM1889 GAAGACATGTTGGCAGAAGG 1875 TCGCACTCGA 4600 A-- TT C CTTC--- T T TT
CTTCCTCGAGTTTGTGCTTC GATTACACACC GAAG CATG GG AGAAGG CTCGAGT TG GC
C GGGCTCGCACTCGAGATTCA TTCT |||| ||| || ||||| ||||| |||
CACCTTCTACCCGTGCGACT CTTC GTGC CC TCTTCC GAGCTCA GC CG /
TC AGC -- A ACACTTA C T GG

GAM1890 GCTTCAATCAGCGCAGTGTC 1876 TAGGATGTCT 4601 AT - ---- - - TCA A A
AATATTCTTCCTCAAGTACT GTCACACGCT GCTTCA CAGCG CAGTGT CA ATATTCT TCC
AGT CTTTATTA T
TTATTAATCTTGGTAAAGGA GCCG ||||| ||||| ||||| || ||||| ||| |||||
CTGGATAGGATGTCTGTCAC TGGAGT GTCGC GTCGCA GT TGTAAGGA AGG TCA
GAAATGGT C
ACGCTGCCGCTGTGAGGT -- C CACT C T --- G T

GAM1891 GGTAAGGATAATCTGATGCTC 1877 TAGGATAATC 4602 ATC T C- TT
TGCCCTTTCAAGACCGGAGC TGATGCTCTG GGTAAGGATA TGA GCTCTG CC T
TCGCCATGTCCTACC CCCT ||||| ||| ||||| ||
CCATCCTGT GCT CGAGGC GG /
ACC - CA AC

GAM1892 GTATAAGGAGTTCCCGTGTC 1878 TACAGAAAGG 4603 AGT G GCACA - T
 TTGCACATCTTACCTCGGGT AGATGGGATG GTATAAGG TCCCGT TCTT TCT TACC C
 ACAGAAAGGAGATGGGATGC CCTT ||||| ||||| ||| |||
 CTTATAC CATATTCC AGGGTA AGGA AGA ATGG /
 GT- G A---- C G

GAM1893 TGGAAATGATCCGCAGAAAC 1879 TGGCTCTGCT 4604 AAA- C-- AA GT
 AGGGGTATTGTTTTGGCTCT TTGATCGGAG TGG TGATC GCAGA CAGGG A
 GCTTTGATCGGAGACCA ACCA ||| |||| |||| ||||
 ACC GCTAG CGTCT GTTTT T
 AGAG TTT CG GT

GAM1894 ATGATAGAGTAACTTTGCTG 1880 TAGAGTAACT 4605 - TAACT C TATTT
 TCTAACTATTTGAACATTGT TTGCTGTCTA ATGAT AGAG TTG TGTCTAAC G
 TGGACATTAACTTTTTCTGA ACTA ||||| ||||| ||| |||||
 TCAT TACTA TCTT AAT ACAGGTTG A
 G TTTC- T TTACA

GAM1895 CACAGCGATGATGAGGAACT 1881 TGAGGAACTC 4606 TGA ---- - AA- A AA
 CTTTGAGAAAAATAGTAAAA TTTGAGAAAA CACAGCGA TGAGG AA CTCTTTGAG AAAT
 GTAA T
 TTCTTACCATTTGCATTCAA ATAG ||||| ||||| || ||||| ||| |||||
 GGAGATTGTGAATTTTCGATT GTGTCGCT GCTTT TT GAGGAACTT TTTA CATT /
 TCGCTGTG TTA AAGTG A ACG C CT

GAM1896 CAGATTGGTGAATGCTATGT 1882 TTGGTGAATG 4607 G- CT ----- C-- CT
 ATTGACTCGAGCTCTTGTA CTATGTATTG CAGATT GTGAATG ATGTATT GACT GAGCT
 T
 GCTCAAAGGTTTTGTTATGG ACTC ||||| ||||| ||||| ||| |||||
 AATACGTTATATTCACAGAG GTTTGA CACTTAT TGCATAA TTGG CTCGA G
 TTTG GA AT GGTATTGTT AAA TG

GAM1897 CCCTGGCTAACATGCTTTTC 1883 TAACATGCTT 4608 TG T- -- AC - A
 ACGTTTTTGAGGTATGATCT TTCACGTTTT CCC GC AACA TGCTTTTC GTTT TTGAGGT T
 CAATGGGCAGGAAAGCATTT TGAG ||| || |||| ||||| ||||| |||||
 GTTTTGCTGGGG GGG CG TTGT ACGAAAGG CGGG AACTCTA /
 GT TT TT A- T G

GAM1898 GCACTAAATGGGACAATCGC 1884 TAAATGGGAC 4609 A GGACAATC TTT ----- A
 TTTCGATCGGCAAAAGCCGC AATCGCTTTC GCACT AATG GC CGAT CGGC A
 CCAAACAATCGTCTGCTTTC GATC ||||| ||||| || ||||| |||||
 AACATTCAAGTGT TGTGA TTAC CG GCTA GCCG A

C AACTTT-- TCT ACAAACCC A

GAM1899 GTCCAACGGCAATTAATGAT 1885 TATCATGATA 4610 A GC TA- AATAT CAC
AACAAATATTACTATAATCAC TTTATGGTGG GTCCA CG AAT ATGATAAC TACTATAAT T
TATAATTATAGTAGTTATCA AT ||||| || ||| ||||| |||||
TGATATTTATGGTGGAT TAGGT GT TTA TACTATTG ATGATATTA /
G AT TAG ---- ATA

GAM1900 TCCAAGTAATTCAGATAATT 1886 TTGAATCACT 4611 T C ATAAT T TG
GATTCATATAATTGGTCATT TAGTTTTTTG TCCAAG AATT AG TGATTCA ATAAT G
GTTGAATCACTTAGTTTTTT GA ||||| ||| || ||||| |||||
GGA AGGTTT TTGA TC ACTAAGT TGTTA /
T T ---- - CT

GAM1901 TCTATTGAGTTGACAGATAT 1887 CTAGGAATTT 4612 T TT -- TGATA- TTTT TT ---
TG TGT
GATACTATCTTTTTTCTTGG GGTAGCTCTG T GAG GA CAGATA CTATC TTCTTGGGATC
TA GG A G
GATCTTTAGGTGATGTGAAT TTGT ||| || ||||| ||||| ||||| || |||
TTGCCCTTTATTGATTCTAG A CTC CT GTTTGT GATGG AAGGATCTTAG AT CC T
/
GAATTTGGTAGCTCTGTTGT C TT AC TGTCTC TTT- TT TTC GT TAA
TTGCATCTTCTCCATGGA

GAM1902 TCTTGTATGTCATAAGTAAT 1888 TAAGTAATGA 4613 T A -- C-- AT- T
GACTGAAAATAAGTAGGTTT CTGAAAATAA TCTTG ATGTC TAAGTA ATGA TGAAA
AAGTAGG T
TTCTATTTTTATTTCACCTT GTAG ||||| ||||| ||||| ||||| |||||
TATGATACTTAGACATTAAG GGAAT TACAG ATTCAT TATT ACTTT TTTATCT C
G - - AG TCC ATT T

GAM1903 TTACATGCTTGCTCCACTCT 1889 TCACAGACAA 4614 C----- CC T TAATTTTAC CAG A
TACAG AA
ATTATAATTTTACTCCAGTT AAAGACTGAT ACATG TTGCT AC CTATTA TC TTG CTGT
GC T
GACTGTTACAGGCAATTCAG AGGT ||||| ||||| ||||| || ||||| ||
CATCACAGACAAAAGACTG TGTAT AACGA TG GATAGT AG AAC GACA CG
T
ATAGGTTTACAGCAAACCTTTAT ATTTCA CT - C----- AAA A CTA-- AC
ATGTAA

GAM1904 TTGATGATGTGGTAAGCATT 1890 TGTGGTAAGC 4615 GTAA T GG- TG- T
AGGATTGAGTGTTATGACAC ATTAGGATTG TTGATGATGTG GCA TA AT AGTGT A
TAATATATATATTGTGTATA AGTG ||||| ||||| ||||| |||||
TATCATCAG GACTACTATAT TGT AT TA TCACA T
ATG- T ATA TAA G

GCCACTCCCATTGCATAGCT CAAC ||||| II ||||| III ||||| ||||| II
CCATATGGCAGGATAGTTGC GTA TGTA AC AGCGTG CCG GATAG GACGGT

CG /
CTGGTGCGAACTCACCATGT - CC TCA GT TT ----- ATACCT-- A
ATGGGA

GAM1912 TGAGACTATCTAGTGTA AAA 1898 TATCTCATCA 4623 C TC TAAAATT C-- TGCTATCT
CT CAT
TTTGCACGTGTTTTGTGCTAT TTACCAAATG TGAGA TA TAGTG TGCA GTGTTTG
GTGAGG TC C
CTGTGAGGCTTCCATCCAAG CCCA ||||| II ||||| III ||||| ||||| II
ATATCTCATCATTACCAAAT ATTCT AT GTTAC ATGT CGTAAAC TACTCT AG /
GCCCATGTATATATCATTGC T C- TATAT-- ACC CATTAC-- AT AAC
TATTCTTA

GAM1913 TGTTATACATCCATTTGGAC 1899 TTCATCGTTT 4624 ACAT- TTT - C
ATGAATGTCCCCATGGACAT CCTGGTCTTG TGTTAT CCA GGAC ATGAATGTCC C
TCATCGTTTCCTGGTCTTGA ATAG ||||| III ||||| |||||
TAGCA ACGATA GGT TTTG TACTTACAGG A
GTTCT CC- C T

GAM1914 TGTTGAATTGGGATTCCCAT 1900 AAGAATCTGT 4625 TT TTCCCAT - TAC C
TGAACAGTACTTTAACCCCTG GTCACATTC TG GAATTGGGA TGA ACAG TTAAAC C
TTAAGAATCTGTGTCACATT CTAA II ||||| ||||| III ||||| |||||
TCCTAATTTTTTA AT TTAAATCCT ACT TGTC GAATTG /
TT TTAC--- G TAA T

GAM1915 TTGGCATAAGCCATTGATAA 1901 TGAGATAAAA 4626 CAT A CACCAG ACCCT C
GTGCATG -- A
TAAGGACACCAGGAACCCTG AAAGAAGAGC C TGATAAT AGGA GA GC CTTT
TTGTTTC TCATT T
CCCTTTGTGCATGTTGTTTC TAAT I ||||| ||||| II ||||| ||||| |||||
TCATTATCCAGTGAATGAGA G ACTATTA TCTT CT CG GAAG AATAGAG
AGTGA C
TAAAAAAGAAGAGCTAATG ACT C TTA--- GTAAT A AAAAA-- TA C
TCATTTTCTCATTATCATCA
GTTATTGTCGG

GAM1916 AGAGCTAATGGGTGTCATTA 1902 TATCCTCCTG 4627 TAA T-- TTATT G G
TTGAGGAGTGTAGACTTATA ATTTCCCGA AGAGC TGGG GTCA GAGGA TGTA A
TCCTCCTGATTTTCCCGATG TGCT ||||| ||||| ||||| |||||
CTTT TTTG GCCC TAGT CTCCT ATAT C
TA- TTT C---- - T

GAM1917 TTCTTATCTGCGTCTTTTAT 1903 TAATACAATT 4628 T TT- CCG TC TC
CTCTTAATACTC A
CCGAGTCCACTCAAAGATTG TTTTGTGTCT TATCTGCG CT TAT AG CAC AAAGATTGTAT
TATCA A

TATCTCTTAATACTCTATCA ACTA ||||| || || || ||||| ||||
 AATGTGATAATACAATTTTT ATAGATGT GA ATA TC GTG TTTTAAACATA
 ATAGT T
 TGTGTCTACTATATTTAGTG - TTT TCA T- T- ----- G
 TAGATAAGAA

GAM1918 TTGTCTGATTAATTCTGTGA 1904 TTTGGCACTT 4629 - T CTT TTT---- TC TC AT-
 TGTC

TTGTCTCTTTGATTATTTTG TCGTTCATGG TGTG ATTG CT TGATTAT GGCACCTT GT
 ATGGAGG AC A
 GCACTTTCGTTTCATGGAGGA AGGA ||| ||| || ||||| ||||| || ||||| ||
 TACTGTCATGATGTTTGTCT ATAC TAAC GG ATTAATA CTGTGAA CA TACTTCT
 TG /
 TCATACAAGTGTCTTGTTTT G T --- TTTTGTT -- -- GTT TAGT
 ATAATTAGGTCAATGCATAG
 GATCATGATAA

GAM1919 AGATCTCCCCCATGCAAATG 1905 TGAATAGGT 4630 TCT T AAA---- GG GG
 TTTTAGGGTAGGCTGTACAT AAACGCTTGG AGA CCCCCA GC TGTTTGA GTA C
 GGAATAGGTAAACGCTTGGG GGGT ||| ||||| || ||||| |||
 GGTCTTCT TCT GGGGGT CG ATAAGGT CAT /
 TCT T CAAATGG A- GT

GAM1920 AGTGGAATTGGGGTAATCA 1906 TCAAGTGAGA 4631 GG A TCGTAATT CAA - TC
 CTCTCT C TCC
 TTCGTAATTCCTCAAGTGAG TGTCCGCTCT GTA TCA T CCT GTGA GATG CG GTTTTG
 CAAGG A
 ATGTCCGCTCTCTGTTTTGC CTGT ||| ||| || ||| ||| || ||||| |||||
 CAAGGTCCAAGCCTCTTGCC CAT AGTA GGA CACT CTAC GC TAGAAC GTTCT
 A
 AAGATTCGTCATCATCACCA A- G CCC----- TAC A T- T----- C CCG
 TAGGCCCATGAGTACACAGT
 TGCTATT

GAM1921 GATACCTGATCCTGACATGC 1907 TACCTGATCC 4632 AC C AC CAA GTAA
 AAAGTTGAGTAACGTTGATC TGACATGCAA GAT CTGAT CTG ATG AGTTGA C
 AATTGCCATAGCAGTATCAG AGTT ||| ||||| ||| ||| |||||
 TCATT TTA GACTA GAC TAC TTAAC T G
 CT T GA CG- AGTT

GAM1922 GGTGCGGGGAGAATTGCCAT 1908 TAAGAGGGGT 4633 TG ----- G A GT GAC
 CTTGGTCAAGAGACAGTGAT TCTATCACAT GG CGGGG AGAATT CC TCTTG CAAGA A
 CTTGTAAGAGGGGTTCTATC CCCG || ||||| ||||| ||||| |||||
 ACATCCCGTGTC CT GCCCT TCTTGG GG AGAAT GTTCT G
 GT AACTA - - -- AGT

GAM1923 GTCTGATAGTCGAGTGATGC 1909 TAGTCGAGTG 4634 ---- G- T --- C CCTGA
 TCATATATACCACCCTGAAT ATGCTCATAT GTCTG ATAGTCGA TGATGC CAT ATATA CAC
 A

GAM1924 GTGCAGAAAAGTGATTGGG 1910 AAAAGTGATT 4635 - - G TG T TT AGTA TCG
ATTGCTTAGGACCAGTAGCT TGGGATTGCT GTG CAGAAA AGT ATT GGAT GC AGGACC GC
A
CGAATTGTCCGGTCCTCTGT TAGG ||| ||||| ||| ||| ||| || ||||| ||
TGTCTTGGATGCTATTTCTG CAC GTCTTT TCG TAG TCTG TG TCCTGG TG /
ACAC A A - GT T TC CC-- TTA

GAM1925 TGCAGTGATTGTGCAGCTG 1911 CACCTGCAAG 4636 T TTTG---- C CACT
TAGCCACTCCTAAAGCTACA TACCACTCCT TGCAG GA TGCAG TGTAGC C
CCTGCAAGTACCACTCCTGC GCA ||||| || ||||| |||||
A ACGTC CT ACGTC ACATCG C
- CACCATGA C AAAT

GAM1926 TGGTAAGCCATCCGGAGTTC 1912 TATGTTAAGT 4637 GTTCAA -- --- - ---- CATC
ATTCAG
AAAAGTGGGCTTTCATAATA TGAAGGTCAA GA AAGTG GGCTTTCA TAATA ATC CATAC
TCC T
ATCCATACCATCTCCATTCA CACT || |||| ||||| ||||| || |||| |||
GTATAACCGGACCGTATGTG CT TTCAC CTGGAAGT ATTGT TAG GTATG AGG
/
AACGATATGTTAAGTTGAAG ACG--- AA TGA A CAAGT CC-- CCAATA
GTCAACACTTGCATCTAGAG
GTAATGTCA

GAM1927 TGTGACTGGTGAGGTCAATA 1913 TGAGGTCAAT 4638 CT G ATAATACATACAA CC
 ATACATACAAGGTCCCTAGA AATACATACA TGTGA GGTGAG TCA GGTC T
 GACTAACACATTCAATGATT AGGT |||| ||||| ||| ||||
 CACCTTTTACA ACATT CCACTT AGT TCAG A
 TT - AACTTACACAA-- AG

GAM1928 TTCTCTATAAGTGAAACATT 1914 TGACTGGGCC 4639 TC TGAAAC A TTATG AG
AGGCATCAGTTTTATGACCA TAGTCATGAT TTC TATAAG ATTAGGC TCAGTT ACCA T
AGTACTGGTGACTGGGCCTA CTTG ||| ||||| ||||| ||||| |||
GTCATGATCTTGTAATGGA AGG ATGTTC TGATCCG GGTCAG TGGT /
TA TAGTAC - ---- CA

GAM1929 GGTGAAAGGTTAAGGCAGCT 1915 AAGGTTAAGG 4640 T CAG A AGAG AGACG----

G A A

ATGAAGAGGGCATAGACGTG CAGCTATGAA GG GAAAGGTTAAGG CT TGA GGCAT

TGCTGAT AG TTC G

CTGATGAGATTCAGCGAGCT GAGG || ||||| || ||| ||| ||||| || |||

GATCAGTGAAATTAAAGATG CC CTTTCCGGTTCC GA ATT CCGTA GTGACTA TC

GAG /

CCAGTTACAGACCTTGGCCT - A-- C GA-- GAAATTAAA G - C
TTCCC

GAM1930 ATGTAGGCAATTGCGTGCCT 1916 TAGGCAATTG 4641 T ATTGCGT AA TGC
AGAACATTGCTAATGTGCCCG CGTGCCTAGA ATG AGGCA GCCTAG CAT T
TGGGTTTCCTGCCTTCAT ACAT ||| |||| ||||| |||
TAC TCCGT TGGGTC GTG /
T CCTT--- CC TAA

GAM1931 CCCGTGGGGGGTCTTAGTGG 1917 TAGCACCGCT 4642 T G TCT - AC A A
AAGTGACGTGCTGTGAATAC ATCCACTATG CCCG GG GGG TAGTGGA AGTG GTGCTGTG AT
C
AGGTCCATAGCACCGCTATC TCTC ||||| ||| ||||| ||| ||||| ||
CACTATGTCTCGCCCGGG GGGC CC CTC ATCACCT TCGC CACGATAC TG A
- G TGT A -- C G

GAM1932 CCGAGACGAAGGCCCGTCTG 1918 AGGAAGTGGT 4643 GAAG- ---- TAGA A GC A
C CC
TAGAGGAAGTGGTTGCGCAT TCGCATGCG CCGAGAC GCC CGTCTG GGA GTGGTT
GC TG GGG A
GCGGGCCAGCTCCCAGTAGA GGCC ||||| ||| ||||| ||| ||||| ||| |||
CCACGTCCCCCAGACGCGC GGCTCTG CGG GCAGAC CCT CACCAG TG AC
CCT /
AGGCACAGGGTCTCGG GGACA ACGC CCC- G A- - - CG

GAM1933 CGCGTGGCATCCACGTTGGC 1919 TTGCAGCCAC 4644 ATC T CTCA CCGA C
CTCAAAGATCCGACACCCGT GTGGCCACGT CGCGTGGC CACGT GGC AAGAT CA C
GCTTGTCTTGCA GCCACGTG G ||||| ||||| ||| ||| ||
GCCACGTG GTGCACCG GTGCA CCG TTCTG GT C
--- - ACG- TTC- G

GAM1934 GCGATGTTTTGCGCCTGGAA 1920 AGTTGTACTC 4645 A - G-- A C AA- T-- --- -
A
GTTGTACTCCCGGAAGATGC CCGGAAGATG TG TTTTGC CCTGGA GTTGTACTC CGG GA
GC CCTCCAG GTC A
CCTCCAGGTCAAAGACGTTG CCCT ||||| ||||| ||||| ||| ||| ||||| |||
GAGGCACGCTGTTCTGTCCTG AC GAAACG GGACCT CGACATGAG GCC CT CG
GGAGGTT CAG /
TGAGTACAGCTCCAGGGAGG A T GAG - T CTG TGT CAC G A
CAAAGTCAATGT

GAM1935 GCTGTAGATGTGCCTGGCTC 1921 AGATGTGCCT 4646 - T - C CTGTCCAG AG TC
TGTCCAGAATGTAGGGCCAG GGCTCTGTCC GC TG AGAT GTG CTGGCT AATGT
GGCCAG A
TCAAAGTTGGCCACGTTGTA AGAA ||| |||| ||| ||||| ||||| |||||
GCCGGTCACAATCTCCACGC CG AC TCTA CAC GGCCGA TTGCA CCGGTT A

C C A T TG----- -- GA

GAM1936 GGCAGGTGGAGTGGGACACA 1922 AGGTGGAGTG 4647 A T-- ACAGT A A
GTTAGAGAACATTAGTCCTC GGACACAGTT GGC GGTGGAG GGGAC TAGAG AC T
TGGTCCCTATCTCCACCCGC AGAG ||| ||||| |||| ||||| ||
C CCG CCACCTC CCCTG GTCTC TG T
C TAT ---- C A

GAM1937 TCTGGTTGTTGCCGTTGACC 1923 TCACTGGCAG 4648 TG C A CCC T TGT
CCCGTGTACTTGTGATGGT CGTGACAACC TCTGGTTGT C GTTG CC GTG ACT T
CACTGGCAGCGTGACAACCG GGA ||||| || ||||| || |||||
GA AGGCCAACA G CGAC GG CAC TGG /
GT - - T-- - TAG

GAM1938 TGTGCCGCTTGGAGGGAAAC 1924 TCAGTGGTTT 4649 CCG TGG T C AG TT
ATGACCACCTGAAGTCTGTT TGTTTCCTTG TGTG CT AGGGAAACA GACCAC TGA TCTG A
AACCAGGTCAGTGGTTTTGT ATAG |||| || ||||| ||||| || |||||
TTCCTTGATAGAGACACA ACAC GA TTCCTTTGT TTGGTG ACT GGAC /
AGA TAG T - -- CA

GAM1939 ACAGATGATTCAATTATCTG 1925 TGAGATCTGT 4650 ATGA AT CTT TT----- A
TT CG
CTGCTTGATCTTTTCAGGAT CATAACTAAA AG TTCA TATCTGCTG GATCTT CAGG
TTCA AGC G
TCATTAGCCGGTTAGCTTTG TAAG || |||| ||||| ||||| ||||| ||||| |||||
AGATCTGTCATAACTAAATA TC AAGT ATAGATGAC TTAGAA GTCT GAGT TCG
T
AGATTCAGTAGATATGAAGT GTTG -- --- TAAATCAATACT A T- AT
TGCTGT

GAM1940 ACGATGAATGAGTAATAAGA 1926 TTAGTGTTTA 4651 TA A AATCTA ----- A
TTCTATCAA
AATATGAAATCTATCTTATA ATAAAAATAT TAA AGAAAT TGA TCTTATAT ACAC TAATTA
T
TACACATAATTATTCTATCA GGGA ||| ||||| ||| ||||| ||||| ||||| |||||
ATTTTACCAATTAGTTAGTG ATT TTTTAA ATT AGGGTATA TGTG ATTGAT /
TTTAATAAAAAATATGGGAAT CC - AATCTA AAAATAATT - TAACCATT
CTAATTAATTTTTCCTTACA
CAATCGACGT

GAM1941 ACTTAGAGTTATGATAAAGA 1927 TTTGTTGGAT 4652 TTA---- ATTT GG TG
TATTTATCCTTAGGGTGCAG CAGTCTCTAA ACTTAGAG TGATAAAGAT ATCCTTA G C
GTAATGGGGATTAATCTTTG GT ||||| ||||| ||||| |||||
TTGGATCAGTCTCTAAGT TGAATCTC GTTGTCTTCTA TAGGGGT T A
TGACTAG AT-- AA GG

GAM1942 ATGATGATTTATGGTGAATT 1928 GTGAATTGAT 4653 T-- --- ATT-- G C T
 GATTCCGGAAGATCGCTATT TCCGGAAGAT ATGATGAT TATGG TGAATTG CCG AAGAT
 GC A
 GTATTTTGTGGTTCCACAAT CGCT ||||| ||| ||||| || |||||
 TCATTTCCATACATGTTATT TATTATTG ATACC ACTTAAC GGT TTTTA TG T
 AT TAC TTT ACCTT G - T

GAM1943 CATTTTTGGATTTTCATATAG 1929 TGAATATATT 4654 T -- T A A TTT--- T TAAATCCA
 CT
 TTGAATATATTAAGTTATT AAAGTTATTT CAT ATAGT GA TAT TTAAAGTTA ATGT GC
 GTGGCTT A
 TATGTTGCTAAATCCAGTGG ATGT || |||| || || ||||| ||| || |||||
 CTTCTAGTAGAGCCATCGCT GTG TATCA CT GTA AATTTCAAT TATA CG
 TACCGAG G
 ATATCCTTATTAACTTTAAC T TT T - C TATTCC T C----- AT
 ATGTCTACTATTTGTGTATT
 CTTCTAATG

GAM1944 GAAACGCCATTTAGCGTAGT 1930 TAGCGTAGTG 4655 A A GT GACACAA - TA---
 C
 GAGGACACAAGTGAACCTAT AGGACACAAG GAA CGCCATTT GCGTA GAG GTG AACC
 TAATGAG A
 AATGAGCAAATTTATTAGTA TGAA || ||||| |||| || || |||| |||||
 TCGGTTACATGAAGGACTTT CTT GTGGTGAG TGCAT TTC TAC TTGG ATTATTT A
 ACGTAGAGTGGTGATTC A A -- AGGAAG- A CTATG A

GAM1945 GTCAATATTATCAGATTCTA 1931 TATTATCAGA 4656 A A AGA ATATTC- T AG
 TATATTCGAATATATCAAAG TTCTATATAT GTCA TATT TC TTCTAT GAA ATATCAA T
 TCATTGATATTTTTATAATT TCGA ||| |||| || ||||| ||| |||||
 GGTAGAAGACAATAATGAC CAGT ATAA AG AAGATG TTT TATAGTT /
 A C --- GTTAATA T AC

GAM1946 TATATCAACGGACACAAAGT 1932 TCAACGGACA 4657 -- - CA--- ---- - ---- C
 TGTAT
 AGCTAACATAAACCATTGTA CAAAGTAGCT TATAT CAAC GGA CAAA GTA GCTA
 ACATAAA CAT A
 TAATTTTTATGTTTTATGTT AACA |||| |||| || ||| || ||||| |||||
 TATTAGCGTACACATTTTGG ATGTA GTTG CCT GTTT CAT CGAT TGTATTT GTA
 A
 AAGTTCCGGTTGCCATGTA CC G TGAAG TACA G TATT T TTTTT

GAM1947 TCTGTTCCCGAAAGATAATA 1933 TAATATAGAG 4658 TTCCCG A --- AG TTTT TAT
 - TTG
 TAGAGGCGTTTTATGCTGTT GCGTTTTATG CTG AA GATAATA TAG GCG ATGCTGTT
 CGCACG CGT G
 TATCGCACGCGTTTGGATCT CTGT || || ||||| || ||| ||||| ||||| |||||
 GCGCCGTGCGTCAATAGCAT GAT TT TTATTAT ATC CGC TACGATAA GCGTGC
 GCG A

CGCAACTATTCTATTATTAT
TAATTTTAGA

TTTAA- A CTT AA ---- CT- C TCT

GAM1948 ACATATGCCAGTGGGTCCAC 1934 TCAGTGGAGA 4659 T ----- --- TT-
ACTACTTTG G- TT

TGATGAGATTCAGATGACTA TGGCTCCCTT GCCAG GGG TCCACTGAT GAGA CAGATG
CC TC G

CTTTGCCGTCTTGATGAAGG GGCT ||||| ||| ||||| || ||
GATTGAATCCATCTGTTTTT CGGTT CCC AGGTGACTG TTCT GTCTAC GG

AG /

TTTTTGTCACTGGAGATGGC - TCGGTAG TTT TTT CTAAGTTA- GA TA
TCCCTTGGCTTCTATGT

GAM1949 AGATTAGTGATGAACGGATT 1935 TTAGTGATGA 4660 A - A-- T--- TGAA---- A-- T
TAATTTGGGTGAATCAAATA ACGGATTTAA AGATT GTG ATG ACGGATT AATTTGGG

TCA ATATC G

TCTGAGATATCCCTGAACAA TTTG ||||| ||| ||||| ||| |||||
CATTCCCGAGTTCTGTGATC TTAA CAC TAC TGTCTAG TTGAGCCC AGT

TATAG /

TGTCGCCATCCACAATTT - C CGC TGTC TTACAACA CCC A

GAM1950 CTTATAATTTGGGACTATGA 1936 TGTGCAGTAT 4661 ATT AC TC - - CATC
TTTCTAATTCATAACCATCT ATTGGTCATA CTTATA TGGG TATGATT TA ATT CATAAC T

AGTAGTTGTGCAGTATATTG ACCC ||||| ||| ||||| ||| |||||
GTCATAACCCCATAGTATGA GAGTAT ACCC ATACTGG AT TGA GTGTTG /
G GAT CA TT A C ATGA

GAM1951 GCAGTGGTGTCACTGAGTGT 1937 TGGCCAGATT 4662 -- GAG- CATGC G- CAA
CT

GCATGCCTGGGTGTCAATCT CCACAACAAA GCAGTGGTG TCAGT TGTG CTGG TGT TCT
T

CTTCAAGAAGCTGGCCAGAT CTGA ||||| ||| ||| ||| ||| |||
TCCACAACAACTGAGGTAC CGTCATCAT AGTCA ACAC GACC G CG AGA /
TACTGC GG AACA CTTA- GT A-- AC

GAM1952 TCACTGTCTCCATACGCCCA 1938 TGACATCCCT 4663 TCTC TACGCCCA AAAC
CCTCTTAAT

GATGTAAACACTCGCTCCTC TTGATTGTTG TCACTG CA GATGT ACTCGCT G
TTAATGCCGCCCTAAGGTGA TCAG ||||| || ||||| |||||
GTTGACATCCCTTTGATTGT AGTGAC GT CTACA TGAGTGG /
TGTCAGTGA TGTT TAGTTTCC GT-- AATCCCGCC

GAM1953 TCATTGACAGCACCGTACGG 1939 TGCGATGTAA 4664 A---- C - AACTT
CTAACTTTGAAAAGGCTGCT GAAGGTCAAT TCATTGAC GCA CGTA CGGCT T

GCGATGTAAGAAGGTCAATG GA ||||| ||| ||||| |||||
A AGTAACTG TGT GCGT GTCGG /

GAAGAA A C AAAAG

GAM1954 TTGTGGCTGAGTGTTAGTGC 1940 TTAGTGCCAT 4665 G G- ---- CCATTA -
ATATA
CATTAGTGTTCTTGCTTGGA TAGTGTTCTT TTGTG CTGA TGTT AGTG GTGTTCTT
GCTTGG A
TATAATGCAACCAGGCTAAG GCTT ||||| ||| ||| ||||| |||||
AACGCACCCACTTATTGAGC AACGC GACT ACGA TCAC CGCAAGAA CGGACC /
AAGTCAGCGCAA - GA GTTAT CCA--- T AACGT

GAM1955 CCGGTTCTATAAACTGCGTG 1941 TATAAACTGC 4666 TC TA- C TACCCAA AG C
TACCCAAAGAGAGCCCTGGC GTGTACCCAA CCGGT TA AACTG GTG AG AGC C
TTCCTCGCATAGTTCGTAA AGAG ||||| || ||||| || || |||
GACCGG GGCCA AT TTGAT CGC TC TCG T
GA TGC A ----- CT G

GAM1956 CCTGAAGAGTTCGCCGGTGG 1942 AGAGTTCGCC 4667 A TT - T C----- A
CCGAGGCGCTGCACACGCGA GGTGGCCGAG CCTGA GAG CGCC GG GGCCGAGGCG
TGC C
AACTTAAACGCCTCGGCCCT GCGC ||||| ||| ||||| || ||||| |||
AGGTGGGTTCTCGGG GGGCT CTT GTGG TC CCGGCTCCGC GCG A
- GG A - AAATTCAAA C

GAM1957 GAACTAACACGACATGCCTT 1943 CACGACATGC 4668 A G TGCCTTT ---- AT
TTCCATTTACTCATTGGGGG CTTTTCATT GAACTA CAC ACA TCCATT TACTC T
TGCTATTGGTGGATTTTGTG TACT ||||| ||| ||||| |||||
GTGGTGGTTT TTTGGT GTG TGT AGGTGG GTGGG /
G G TTT---- TTATC GG

GAM1958 GACCGTGCGGCCGACATCGC 1944 GGGCCAGGCG 4669 G C AC CA ATCT
CCAGGTCCGCGACTATCTCG GTCGCGGTTC GACC TG GGCCG ATCGCC GGTCCGCGACT
C
GACAGGTCGCGGGCCAGGCG AGGT ||||| ||||| ||||| |||||
GTCGCGGTTTCAGGTC CTGG AC TTGGC TGGCGG CCGGGCGCTGG G
- - GC A- ACAG

GAM1959 GCCGTGACGGGCGGTACCT 1945 TTCGCAGGTC 4670 G G TC- C C AG
CGCGACCGAGACGCGTTTCGC TTCCGTCGTC GCC TGACGG CGG ACCT GCGA CG A
AGGTCTTCCGTCGTCAGGGC AGGG ||| ||||| ||| ||||| |||
CGG ACTGCT GCC TGGA CGCT GC /
G - TTC - T GC

GAM1960 GGATGCTATTGAGTCTGGTG 1946 TTGAAAGAAC 4671 T T T ACA - TT CG TA TT
TA

AACAGCTCGTTTTGTTTTCG GTCACGGAGC GGATGC ATTGAG CTGG GA GCTC GT TGT TTT
CA ACG GGTA G
CATAACGTTGGTATAGTTTG AATC ||||| ||||| ||| || ||||| || ||| ||||
CCTGTTGAAAGAACGTCACG TTTGCG TGA CTC GGCC CT CGAG CA GCAAGA GT
TGT CCGT /
GAGCAATCCCGGCTCAGTGC - - - AA- G CT AA -- -- TT
GTTT

GAM1961 ACATGTGTACTTATAGTCTA 1947 TTAACGATTT 4672 CTTAT TAC T ACCTG
CTAATATGAAGTACCTGATA ATTATATATG ACATGTGTA AGTC TAATA GAAGT A
CACATTTCTATTAACGATTT T ||||| ||||| ||||| |||||
ATTATATATGT TGTATATAT TTAG ATTAT CTTTA /
TAT-- CA- - CACAT

GAM1962 GGTCTTGGATAGAATATTTG 1948 TTAACAATA 4673 T- GAATATTT C CTCGTA
TATCGTTTAATACTCGTATA CTAAATATC GGTCT GGATA GTAT GTTTAATA T
TATTATATTAACAATACTA TTTA ||||| ||||| ||||| |||||
AAATATCTTTAGACC CCAGA TCTAT CATA CAAATTAT /
TT AAAAT--- A ATTATA

GAM1963 GTCGATATTATCAGATTCTA 1949 TATTATCAGA 4674 A A AGA ATATTC- T AG
TATATTGGAATATATCAAAG TTCTATATAT GTCG TATT TC TTCTAT GAA ATATCAA T
TCATTGATATTTTTATAATT TCGA ||||| ||||| ||||| |||||
GGTAGAAGACAATAATGAC CAGT ATAA AG AAGATG TTT TATAGTT /
A C --- GTTAATA T AC

GAM1964 AGCTGATCTGTAAACTTTA 1950 TGATCTGTAA 4675 - TC AA ACT----- CT
GGATAAGACTATATCTTGTC AACTTTAGGA AG CTGA TGTA TTAGGATAAGA A
CTAATCTCTAGCAACAATAC TAAG || |||| ||||| ||||| |||||
ATTCAGACT TC GACT ACAT AATCCTGTTCT /
A TT AAC AACGATCTCT AT

GAM1965 CCCGAAATGGTGTATAGTTT 1951 TAGTTTCATG 4676 GG - ATG G TAA
CATGTTGGGGTCCATTTAAA TTGGGGTCCA CCCGAAAT TGTATAGT TTC TT GGGTCCATT A
ATGCAATGGATCCAGAAGGA TTTA ||||| ||||| ||||| |||||
ATGCTGTACGGTTTCGGG GGGCTTTG GCATGTCG AAG AG CCTAGGTAA A
-- T GA- A CGT

GAM1966 GACATCTTAAGATTCTTTCT 1952 CATCTTAAGA 4677 -- ----- A CG TAA
ATATCACGGTAATAGTTCTA TTCTTTCTAT GAC ATCTTAAGAT TCTTTCT TATCA G T
TGATAAGAAGGAAATGTAAC ATCA || ||||| ||||| ||||| |||||
ATCTTAAGATACGTC CTG TAGAATTCTA AGGAAGA ATAGT C A
CA CAATGTAA - AT TTG

GAM1967 GCGCTTGGCCTCTGGCATGG 1953 TGCCGTGTTA 4678 TG - C C-- TCC
 TGTACTCACTCCAGGCGTCC AAGGACTGGG GCGCT G CCT TGGCATGGTGTACT AC A
 AGGTATGCCGTGTTAAAGGA CGC ||||| | ||| ||||| ||||| ||
 CTGGGCGC CGCGG C GGA ATTGTGCCGTATGG TG /
 GT A A ACC CGG

GAM1968 GTTGACGAAGGCTCTCTTGA 1954 TGACGAAGGC 4679 G T A T GG
 AGCTGCCGGGAGAGGCGCTC TCTCTTGAAG GTTGAC AAGGC CTCTTG AGC GCC G
 CAAGAGGCCTTGTCGAT CTGC ||||| ||||| ||||| ||| |||
 TAGCTG TTCCG GAGAAC TCG CGG A
 - - C - AG

GAM1969 TACATGAGCGTCTCCCAGGG 1955 CTAGCCCGGT 4680 ----- T CA GT AAAC
 TGTGGACAAACTCTCCCGGT GACGTGAGCC TACATGA GCGTC CC GGGT GGAC C
 TCTAGCCCGGTGACGTGAGC ATCA ||||| ||||| ||| |||
 CATCATGTA ATGTACT TGCAG GG CCCG CTTG /
 ACCGAG T -- AT GCCCT

GAM1970 TCAATCATGGTCTCTCGGT 1956 TCAGATCGAG 4681 TCTCG - G- CA CGTA AT ATC
 CTT AT
 TCCGGGTCTGCAACCGCGTA GTAGCACTGG GTCC GTT CC GGTCTG ACCG CA CTCT
 AGCCTC GTC C
 CAATCTCTATCAGCCTCCTT ACTA ||||| ||||| ||||| ||| ||| ||||| |||
 GTCATCCAGACCTGAGGCTC CAGG CGA GG CTAGAC TGGC GT GAGA TCGGAG
 CAG /
 AGAGTCTGGATCGGTCAGAT TCA-- T AG -- TAG- CT C-- TC- AC
 CGAGGTAGCACTGGACTATC
 CTCTCCCTGA

GAM1971 TCTGGGTGAGCATAATCTTG 1957 TGAGCTGGCT 4682 TG A- A C-- C AGAAAACT
 CC
 AGCTGGCTAGAAAACTTCCA AGAAAACTTC TC GGTG GC TAAT TTGAG TGGCT TCCA T
 CCTGTTTGGATCCTCCAGGG CACC || ||||| ||||| ||||| ||||| |||||
 CCATCTCAAACAGTTGGCCC AG CTAC CG GTTG AACTC ACCGG AGGT G
 CATCTGGA GT CC - ACA T GACCTCCT TT

GAM1972 AATAGATGAGGTTTGAGATC 1958 TGAGGTTTGA 4683 CTCTA AT A CTTTCA
 TATGCTG C
 TCTAAGATATGCTGGGAAAC GATCTCTAAG TTGAGAT AG ATGCTGGGA AC AAAATGT
 GTCTATGG T
 CTTTTCAAAAATGTTATGCT ATAT ||||| || ||||| || ||||| |||||
 GGTCTATGGCTTCTATAGAT AACTTTG TC TATGATCCT TG TTTTACG
 TAGATATC /
 GCATTTTGTATCCTAGTATC C---- AC A ----- T
 ACTCGTTTCAAGTTGTACCT
 TGTTATCTGTT

GAM1973 CCCCATAGAATTGACAATAT 1959 TATTGTCTTA 4684 A--- ATT TCATA

TTTCATATAGTTTTGGATAT TCACAAGTGG CCCCAT GA GACAATATTT T
 TGTCTTATCACAAGTGGGG GG ||||| || |||||
 GGGGTG CT CTGTTATAGG A
 AACA ATT TTTTG

GAM1974 GGGAATGTACAGACTTTATG 1960 TGTCTTCTAA 4685 TGT CTT-- ---- A C GG
 TAGAAAGACCAGAGGGAATC AAAACATATT GGGAA ACAGA TATGT AGAA GAC AGA G
 TGTCTTCTAAAAACATATT TTAT |||| |||| |||| |||| ||||
 TTATTTGTTTCCT TCCTT TGTTT ATACA TCTT CTG TCT /
 --- ATTTT AAAAA - - AA

GAM1975 GGTAGAGGGATGGGAGATAT 1961 AGAGGGATGG 4686 TA AT-- - --- CAAT
 ATTCCTCAATGTTTCCTAGGA GAGATATATT GG GAGGG GGGAGAT ATA TTCCT G
 AGTTTATAGTCTCCTCCAAC CCTC || |||| ||||| || ||||
 CCTTC CC TTCC TCCTCTG TAT AAGGA T
 -- AACC A TTG TCCT

GAM1976 GTTCTCCTGCTCAGAGGCTT 1962 TAAAAACAAC 4687 GA---- C- CAA GG ATCA T
 TCGTTC
 TGTCAATGTTTGGATAGATC AAAAACCACA CTCA GG TTTGT TGTTT ATAG TTTTA
 GGGGGCC A
 ATTTTATGGGGCCTCGTT ACTA |||| || |||| |||| |||| ||||
 CATGTTATTGGTTCTCCTGG GAGT CC AAACA ACAA TATC AGAGGT CTCTTG
 T
 AGACTATAAAAAACAACAAAA ATCAACA AA --- AA ---- C TTATTG
 ACCACAACATGAGAAGGAG
 GAT

GAM1977 TCTTATAAGGTATGAAATTT 1963 TAAGGTATGA 4688 A GG AA T
 TATATATTTTATATAGAGT AATTTTATAT TCTT TAA TATG ATTTTATATA T
 CCATGTTTTAAGGA ATTT |||| || |||| ||||
 AGGA ATT GTAC TGAGATATAT T
 - TT C- T

GAM1978 TGTCTTAACCTATGTGTATG 1964 TAGCACATCC 4689 CTA TGT G TT-- C- TCCTA
 TGTGGTTTTTGTGTTCTACG GGCCTTAAGG TGTCTTAA TG ATGTGT GTTT GTGTT TACG
 A
 TCCTAAAACCTTGTATTGGC ACA ||||| || |||| || |||| ||||
 ACCCATGAATAGCACATCCG ACAGGAATT GC TACACG TAAG CACGG ATGT /
 GCCTTAAGGACA CCG C-- A TACC TT TCCAA

GAM1979 TGTTTTTTATCTTTTGTATC 1965 TGAATAGTTC 4690 TTT--- GTA CATGT A A C
 TGGACATGTCTGATCAAGGT TCCAGAGGAA TGT TTATCTTTT TCTGGA CTG TCA GGT A
 CAAATCTGAATAGTTCTCCA GATG || ||||| |||| |||| ||||
 GAGGAAGATGATGCACTGCA ACG AGTAGAAGG AGACCT GAT AGT CTA /
 TCACGT --- CTT-- A - A

GAM1980 TTCAAGTTCTAGGGAGAGAC 1966 TAGAGCATCA 4691 TTC- AG A- TG TTC ---
A
AGGAACACTCTGTTCTGTTC ATGAGAAGTT TTCAAG TAGGGAGAGAC GAAC CTC
TGTTCTGT TCCAC A
TGTTCCACAAGGTGGGAGTA TAAG ||||| ||||| ||| || ||||| |||||
TAGAGCATCAATGAGAAGTT AAGTTT ATTCTTCTCTG TTTG GAG ACGAGATA
GGGTG /
TAAGTCTCTTCTTATTTCTT CTTT AA AA TAACT TGA G
TGAA

GAM1981 AGTGTACAGGGTAGCAAGTT 1967 TACAAAGAGT 4692 G TAG AGTT C A TTAGG
A
TATCGCTCTTTGATATTTAG CATATGATCT AGT TACAGGG CA TAT GCTCTTTG TAT
AGTTCT T
GAGTTCTATAAAGAATTATA CTGT ||| ||||| || ||| ||||| ||| |||||
CAAAGAGTCATATGATCTCT TCA ATGTCTC GT ATA TGAGAAAC ATA TTAAGA A
GTAAACT A TA- ---- C - ---- A

GAM1982 ATCGTAATCATTGAGATGGT 1968 TAATTTAACC 4693 CATT C TTAACCTATCA G
AA AAAG T
CTGCATGATAATTTAACCTA TATCAGTGTC GAGATGGTCTG ATGATAAT GTGTCAT
GGGT GA TG T
TCAGTGT CATGGGGTAAGAA ATGG ||||| ||||| ||||| ||| || ||
AAGTGTTAGCAAAATCATCT TTCTATCAGAC TACTGTTA TACGGTA TCTA CT
AC A
GATGGCATAATATATTGTCA C--- C TATAA----- G -- AAA- G
TCCAGACTATCTTCGTTGCT
GGT

GAM1983 ATCTGCATCGATTTTGAGGT 1969 TGAGGTATAC 4694 C TG - TA- GATT -- A
ATACTAGAAGATTGAAAGCA TAGAAGATTG ATCTGCAT GATT AGG TA CTAGAA GAA
AGCAAT G
ATAGCGTTGTTCTTCTGAA AAAG ||||| ||||| ||| ||| ||| ||| |||||
TTCTAGCATTGTCCTTGGA TAGATGTA CTAGG TCC GT GATCTT CTT TTGTTG /
TCATGTAGAT - GT T TAC AAGT CC C

GAM1984 GCCCAACAGCAATGCTCTCA 1970 TGATTATGTT 4695 C CAA C CA TT TAT T
CAAATA
GAATTGTAATTTATTGATCC TCCTAGAACA GC CAACAG TG TCT GAA GTAATT TGA CC T
CAAATATTTCCAAGGCTTA ACTG || ||||| || ||| ||| ||||| ||| ||
TGATTATGTTTCCTAGAACA CG GTTGTC AC AGA CTT TATTAG ATT GG T
ACTGTTGTGC T A-- A TC TG T-- C AACCTT

GAM1985 GGAGTCTATTTTGTTGATGA 1971 ACGATGCCCA 4696 TGATCT TCTTTCATCT CCTC
TG T C TA A
TCTTGGGTATCTCTTTCATC TCAATACTGA TTGA TGGGTATC GTT AATG AT CAA
CTCA TCA T

TGTTCTCAATGTGATTCAA CTCC ||| ||||| || ||| ||||| ||
 CCTCATATCAATGTTGATGA AACT ACCCGTAG CAA TTGC TA GTT GAGT AGT
 G
 GTTTGATTGCGTTAACGATG ----- ----- --- GT - T -- T
 CCCATCAATACTGACTCC

GAM1986 GGGAAACACTGACGGTTTAT 1972 TAAGACACTG 4697 - - - TA A- T ATTA A CT TT G
 ACC
 GAATGGTTGAGATTAAGACA GCCATTATGA A CTGA CG GTT TGA TGGT GAG AG CA
 GGCCA AT ATGTGT T
 CTGGCCATTATGATGTGTAC TGTG | ||| ||| ||| ||| ||| || || ||| || |||||
 CTCTAATATATGATCTTGGT T GATT GT CAG ATT ACTA CTC TC GT CTGGT TA
 TATATA /
 CTGACTGCTACTCTATCAAA A T A TC AA T ATCG A -- TC G ATC
 TTA CTGACATGTTTAGATGT
 TCCC

GAM1987 GGTTATGTCTCAACTGCGCA 1973 TATCAGAGAT 4698 - G AT---- AG A A TC TA-----
 ---- TA
 TATTCTATAGCTGAAATCAA AGATAATTCA GC CAT TCTAT CTGA ATCA TT CCTGA
 C T
 TTTCCCTGATACTATAGGAC TGAG || ||| |||| ||| ||| || ||||| |
 TGTCAAGGTGACATTCAGGA CG GTA AGATA GACT TAGT GA GGA CT G /
 TAGATGATATCAGAGATAGA C A CTTAAT GA A A TA TACAGTGGA ACTGTCA
 GA
 TAATTCATGAGCCATGTTGT
 TATATCC

GAM1988 TGAGATAGATTGTTGGAAGT 1974 TAGATTGTTG 4699 G - A A
 TGAGACAGGAGTTATAGCTT GAAGTTGAGA TGA ATAGAT TGTTGGAAGTTG GAC G
 TTAACACATCTATATCA CAGG ||| ||||| ||||| ||||| |||
 ACT TATCTA ACAATTTTCGAT TTG G
 A C A A

GAM1989 TGTGCAGTACTCTCTTTGAT 1975 TAGCCTTTGC 4700 TTT --- TT CTA----- TC-- --
 TAG
 AGCCTTTGCAGCTAATCTGG AGCTAATCTG GATAG CCT GCAG ATCTGGA
 TGAGATT CAA A
 ATCTGAGATTCAATAGAGAA GATC ||||| ||| ||| ||||| ||||| |||
 TTTGTCAATCTCGTTCCTCC CTGTC GGG CGTC TAGGCCT GCTCTAA GTT
 G
 GGATGTACTCACTGAACTGC CGT ACA TT AAGTCACTCATG CCTT CT TAA
 TTGGGACACTGTCTGCGAGA
 GATGACA

GAM1990 CAATGTTCTTAGCAGTGTTT 1976 TGAGATATAG 4701 TT TA ---- TAAT C
 CATAATTTCCACCGAATGCC CCTGTATAGT CAATG CT GCAG TGTTTCA TTC A
 TGAGATATAGCCTGTATAGT CATT ||||| || ||| ||||| |||
 CATTG GTTAC GA TGTC ATAGAGT AAG C
 T- TA CGAT CCGT C

GAM1991 CCTGATGTGTAATCACTCCA 1977 TGATGTGTAA 4702 T TAATC C -- CT
 CCCTCTCTCAGGGCTTGAAG TCACTCCACC CC GATGTG ACT CA CCCT C
 TAAATCCATATCCGG CTCT || ||||| ||| ||||
 GG CTATAC TGA GT GGGA /
 C CTAAA A TC CT

GAM1992 CGGGTGTAAGATAATAACAC 1978 TAAGATTCCGG 4703 G TA TAAC ----- --- - - T
 TTCTTTCCAGTTTGTCTGA ATTTAGGATT CG GTG AGATAA ACT TCTT TCC
 AGTTTTGTCTG ATT G
 TTTGAAAATGCAGATAAGAT ATTT ||| ||||| ||| ||| ||| ||||| |||
 TCGGATTTAGGATTATTTCA GT TAC TCTGTT TGA AGGA AGG TTAGAATAGAC
 TAA A
 GTACTTTTGTCTCGCATGTG G GC TTCA CTTTATT TTT C G A

GAM1993 GAGTCTTTGTCATGAGCTTC 1979 TGTTATTTTT 4704 T GAGCTTCG T TC G CT
 GATCTGAAATCTAAGATTAG GATGTGATAA GAG CTTTGTGAT ATC GAAA TAA ATTAGAA T
 AACTTTTCTTCTGATGTTAT AGTT ||| ||||| ||| ||| ||| |||||
 TTTTGATGTGATAAAGTTC CTT GAAATAGTG TAG TTTT ATT TAGTCTT T
 - ----- T -- G CT

GAM1994 GATTGGGAATCCAGGGGTGT 1980 TATTAGATGG 4705 C- TGCTATCTT A TC CT
 A C C
 ATGCTATCTTGGATACTAAT GAATGTTCTA CAGGGGTGTA GGATACTA TAG CGT C
 CCATC TAA ATTTAT G
 AGTCCGTCCTCCATCATAAC CTAG ||||| ||||| ||| ||| ||| |||||
 ATTTATCGCGATAGATATTA GTTTTTACAT TCTATGAT ATC GTA G GG TAG ATT
 TAGATA C
 GATGGGAATGTTCTACTAGT CT CTCC----- C TT A - - A G
 ATCTCCTCTACATTTTTGTG
 AATCCCAGAC

GAM1995 GGATTTGGTGGGGTCCAGAC 1981 TCACCTCTGT 4706 T T CC- TT C AAATAAA G
 ATTGGTCATAAATAAAGAAG CTAGTACCTC GGA TTGG GGGGT AGACA GGT AT GAAG A
 GAACTTCATCACCTCTGTCT TCCA ||| ||| |||| |||| ||| |||
 AGTACCTCTCCAACCTCC CCT AACC CTCCA TCTGT CCA TA CTTC /
 C T TGA CT C ----- A

GAM1996 GTATAATTGTAAGGATATTT 1982 TATCATAATC 4707 T---- A TTC TCGAA CTAT
 AT
 TCTTGGTCGAAATGCTATTG CAATTTGAAT GTATAAT GTAAGGAT TT TTGG ATG
 TG TAGT G
 TAGTATGAACTATATCATA CCTT ||||| ||||| || ||| ||| |||||
 ATCCAATTTGAATCCTTATT TATATTA TATTCCTA AG AACC TAC ATATCA /
 TGTCATTATAT CTGTT - TTT TAA-- T--- AA

GAM1997 GTGTCGTATTATGATAGTGT 1983 TAGAATATTG 4708 T A GA- A AAAGATT

ACTATAGAAAGATTTTTGGA	GAAATAGACG	GTG CGT TTAT TAGTGT CTATAG	T
TACTGTAGAATATTGGAAAT	TCAC		
AGACGTCAC	CAC GCA GATA	GTTATA GATGTC	/
	T - AAG	A ATAGGTT	

GAM1998 TAGAAATTCTGTGATTAAGC 1984 TCAGCCTTTG 4709 T- GA- AG --- T CGT T ATT - GCT

TGTTGATGTTATCGTCAGAG	TTATAATCTC	CTGT TTA CTGT TGA GTTAT CAGAG CT
GCAAGG TGTT T		
TCTATTGCAAGGTGTTGCTT	AAGA	
TAAACATCCTTGTGAGCCT		GACA AGT GGCA ACT TAATA GTTTC GA TGTTCC
ACAA /		

TTGTTATAATCTCAAGAACG	CT ACG CT AGA C TT- C C-- T AAT
GTCTGAGCAACAGTCTTAGC	
TA	

GAM1999 TCCCAATTACTTTCTTACTA 1985 TATCAAGTTT 4710 TTACTTTCTTACTA ATT T T A TTTT

ATGATATTGTATGCTTTGAA	GCTAGTCATG	TCCCAA	ATGAT GTA GCTT GA TGAC C
TGACTTTTTCATGATGTTAT	CCTT		
CAAGTTTGCTAGTCATGCCT		AGGGTT	TACTG CGT TGAA CT ATTG /
TGGGA	CCG-----	AT- T - - TAGTA	

GAM2000 TCTAAAGTGTACATATAAAG 1986 TAAAGTGTAC 4711 - G TACAT GAA-- ---- AC T TAT A

AATTGATTATCACTTGATGA	ATATAAAGAA	TCT AAA TG ATAAA TTGATT ATC TTGA
GAAC ATG T		
ACTATATGATATCATTGTTC	TTGA	
TCAAAGATCACCGATCAAGA		AGA TTT AC TATTT AACTAG TAG AACT CTTG TAC
A		
TTATTTATTAACCCAGTTTC	C G CCAAT	ATTAG CCAC A- - T-- T
AGA		

GAM2001 TGA CTGCTAAGCTTAATAGG 1987 TTGGATCCTA 4712 - G A ----- T TA

AGATCCTAGAGTAAATCTCT	AGTTTTTCTT	TG ACTGCTAA CTTA TAGGA	GATCC AGAG A
TGGATCCTAAGTTTTTCTTA	AATG		
ATGAGTTAGTAGTACA		AC TGATGATT GAGT ATTCT	CTAGG TCTC /
	A - A	TTTTGAATC	T TA

GAM2002 TGCAGCCAGTCTTGATCTGA 1988 CAGCCAGTCT 4713 CA TC T AG G

GGTTTAGTAATGAATTAGTC	TGATCTGAGG	TG GCCAG TTGA CTG GTTTA T
AATCTGGTCCCA	TTTA	
	AC TGGTC	AACT GAT TAAGT A
	CC T- - -- A	

GAM2003 TTGGGGATGAGAGGCACTCT 1989 TGAGAGGCAC 4714 --- CACTCTTACCA A --- T A TTGTCC

TACCAACACCCAGAGGGTAG TCTTACCAAC TGGGGA TGAGAGG AC CCCAGAG GG
AGGC GCAA T
GCAGCAATTGTCCTGATCTT ACCC ||||| ||||| || ||||| || |||||
CTTGCGTTTCCCTGTCTCTG ACTTCT ACTCTCT TG GGGTCTC CC TTTG CGTT
G
GGGTTCTCTCAACATCTTCA ACA ----- - TGT C - CTTCTA
A

GAM2004 ATGGTAGCGGTCTGGTTATTG 1990 TTGCACACGT 4715 AGCG TT TTTTCTAT AT
CCC
GTTTTCTATTGCAGCATGTA CCAGTCTCCG ATGGT GTCGG ATTGG TGCAGC GTAG A
GCCAGCTCTGCGTTGCACA GCGG ||||| ||||| ||||| ||||| |||||
CGTCCAGTCTCCGGCGGGCC TACCG CGGCC TGACC ACGTTG CGTC /
AT GG-- TC TGCAC--- -- TCG

GAM2005 GTATTCCAGGCTGATCCAGC 1991 TACGGTACGC 4716 - CCAG--- T C CC G CC AT
ACT CTG
GGTACGGTACGCTGCCCGTG TGCCCGTGGC GCTG AT CGG ACGGTA GCTGC GT GCGC
AAG GT GGGG T
GCGCCCAAGATGTACTGGGG GCCC ||||| ||||| ||||| ||||| ||||| ||||| |||||
CTGTTCTTCCTTGACCTTAG CGAC TG GTC TGCCAT CGACG CG CGCG TTC CA
TCCT /
CGCAGCGCAGCTTACCGTCT A AACCTTA - T -- A A- -- GT- TCT
GATTCCAAGTACAGCCTGCG
GTAC

GAM2006 GTGAGCAGAAGCGCGCAGAC 1992 TGGAGGACCA 4717 CA C - C TG CC CTCAT
TGTCCTT
GGCGTGAGGACCAGGCTCA GGCTCATGGG GTGAG GAAGCG GC AGA GGCG GAGGA AGG
GGGATAG A
TGGGATAGTGTCCCTTATCT ATAG ||||| ||||| ||||| ||||| ||||| ||||| |||||
TCCTCCTGTCTCTCTCCCTC CACTC CTTCGC TG TCT TTGC TTCCT TCC CTCTGTC
/
TCCTTTGCGTTTCTCGTCCG -- C C - GT C- CTCT- CTCCTTCT
CTTCCTCAC

GAM2007 CCATGTTGTATAGGTAATTT 1993 TAGGTAATTT 4718 T- TG ----- T TG G- AAAT
GGGGAGGTAAGAAATAGCAG GGGGAGGTAA CCA GT TATAGG TAA T GGGG GTAAG A
CTTACAATCCCTGATTTGAA GAAA ||| || ||||| ||||| ||||| |||||
TGTGTCCTTGTATGACTTTG GGT CA ATGTTT GTT A CCCT CATTC /
G TT GT CTGTGTAA T GT AA GACG

GAM2008 CTAAATAGTCTATCGGCAGT 1994 CGGCAGTGTT 4719 TATC-- ---- --- G - AAT G
T
GTTGCTACAGGTGTATCACT GCTACAGGTG TC GGCAGTGT TGCT ACA GTGTATC
ACTTAGG TT GATAC A
TAGGAATTTGGATACTATTG TATC || ||||| ||||| ||||| ||||| ||||| |||||
TGTCGAACTTAAGTCGATAT AG CCGTTACA ATGG TGT TATATAG TGAATTC AA
CTGTG T

ATATGTTTTGGTAATTTACA TTGATT TTTA TTT A C --- G T
 TTGCCTTAGTTGAGGATTTA
 G
 GAM2009 GAACAGAGAATAATTCACAA 1995 TATTTTGTGA 4720 AC ATAA C AGGAG T
 AACTGTTGAGGAGATAATTG AAATCTCTAA GA AGAGA TTCACAAAA TGTTG ATAAT G
 CAATTGTAATAATATTTTGT TC || ||||| ||||| ||||| |||||
 GAAAATCTCTAATC CT TCTCT AAGTGT TTT ATAAT TGTTA C
 AA AA-- - AA--- A

 GAM2010 GGAGATTCTTTGTAGCATAC 1996 TAGCATACTG 4721 T - CTGT-- -- - CA
 TGTGCGATGTGACTCAACCA TGCGATGTGA GGAGAT CTTTGTA GCATA GCGA TGTG ACT
 A
 GTACACGCCTCGCTGGACTT CTCA ||||| ||||| ||||| ||||| ||||| |||||
 GTGCTTGCAAAGCATCTCT TCTCTA GAAACGT CGTGT CGCT GCAC TGA /
 C T TCAGGT CC A CC

 GAM2011 GTCTGGCTGAGGTTCCATCT 1997 TGAGGTTCCA 4722 C GC TCCATC T CT C
 TTAAATAA TGA
 AAGGTTGTGGCTTGCCTTGT TCTAAGGTTG GT TG TGAGGT TAAGGT GTGG TGC TTG
 ATCT T
 TAAATAAATCTTGATTCTTA TGGC || || ||||| ||||| ||||| ||||| |||||
 GATCTTAAGTCCAAGCGTTT CA AC ATTCTA GTTCTA CATT GCG AAC TAGA T
 TACCATCTTGCATCTTAAAC A AA C----- C TT - CTGAATTC TTC
 AAAC

 GAM2012 GTGAATCTACAATATATAGT 1998 TACTGTTTAA 4723 TAC AT TG T A - ACC
 GGTGTCCAACATAGACCTTA TATTTTGATT GTGAATC AATAT AG GTG CC ACAT AG T
 GCTGATGTAGGTAAGTGTTA CAT ||||| ||||| || ||||| ||||| |||||
 ATATTTTGATTCAT TACTTAG TTATA TT CAT GG TGTA TC /
 TT- AT GT - A G GAT

 GAM2013 TCCTTGGCTGTGCGAAATAGT 1999 AATAGTGCTT 4724 -- G - AA ---- --- A ACTT
 GCTTGGCAATATTGTACTTG GGCAATATTG TCCTT GGCT TC GA TAGTG CTT GGCA
 TATTGT G
 AATACACAATATGTCTCAAA TACT ||||| ||||| || ||||| ||||| ||||| |||||
 GATGACATTAGGTCTGAGAG AGGAA CCGA AG CT ATTAC GAA CTGT ATAACA A
 CCTTAAGGA TT G T GG AGTA ACT - CATA

 GAM2014 TGTTTGGAGGATTGTAACCT 2000 TTCAAAGACT 4725 T GGA----- T C
 AGCACATTGGGTTCAAAGAC GCATCCCAAC TGTT GGA TTG AACCTAG A
 TGCATCCCAACA A ||||| ||||| ||||| ||||| |||||
 ACAA CCT AAC TTGGGTT C
 C ACGTCAGA - A

 GAM2015 AACTTCGACTTCTCTGACTT 2001 TATGATCAAG 4726 CTC A T C C- G A

GCCGCCGGTCGATATGTATA	CGACAGCCAA	AACTTCGACTT	TG CT G CGC	GGTC ATATGT T
CGCATATGATCAAGCGACAG	AGTC			
CCAAAGTCGAAGTT		TTGAAGCTGAA	AC GA C GCG	CTAG TATACG A
	---	C - A	AA -	C

GAM2016 AGGGACTTTTAGAGCGACTC 2002 TGAAGCATTG 4727 - G CCCAAAAA G AA GC-
A AT

GCCAAAAAGTGTCTGAAGC	GAAGGATGCA	TTA GA CGACTCG	GTGTCTGAA CATTG
GGAT AATGCG CG T			
ATTCGAAGGATGCAATGCGA	ATGC		
CGATTCACGCCGCGTTAATG		GAT CT GTTGAGC	CGTAGATTT GTGGGC CCTG
TTGCGC GC /			
TCCACCGGGTGGTTTAGATG		G G	AGTCGGAC G CA TAA C AC
CCAGGCTGACGAGTTGGTCG			
TAGAAGCCCCT			

GAM2017 ATCCAATGTAGATGTGTATG 2003 GTGAGCACGA 4728 A -- G AAAT-- CTG- TC
TTAAATACTGAGCTGGTACT TTATATTGGA ATCCAATGTAG TGTGT AT TT ACTGAG
GTACT C

TCCCGGGTGCAACACTTAGT	T		
TAGATGAAGGTGAGCACGAT		TAGGTTATATT GCACG TG AA	TGATTG CGTGG /
TATATTGGAT		A AG G GTAGAT ACAA GC	

GAM2018 CGATTCTCCAGTGTGAGGTT 2004 TGACATGCAT 4729 TC GAG - - G T
ATGTGGTGGATTATAATAAT ATAACACTGT CGATTG CAGTGT GT TATGT GGTG ATTA A
CACTGACATGCATATAACAC GGGA ||||| ||||| || ||||| ||||| |||||
TGTGGGATTG GTTAGG GTCACA TA GTACA TCAC TAAT /
GT ATA C G - A

GAM2019 GACTCTGTGACCATGCGGTT 2005 TAGCTGACAA 4730 T TG AT C TA --- AC TAAC
A

AGCTGACAACGAGTTTAACC	CGAGTTTAAC	GACTC G ACC G GGT GCT	GACA GAGTT
CTGCA C			
TGCAACCTTGCAGATTGACT	CTGC		
CTGTCTAAGGCCGACCCGGT		CTGAG C TGG C CCA CGG	CTGT CTCAG GACGT C
TGCCGAGTC		C GT --- GC AAT -- TTA-	T

GAM2020 GAGATAACTAGATTGATGTC 2006 AAGCTCCAGT 4731 A T TCAAACCTTGTT TA T -
GG- AAT

AAACCTTGTTTATGATTAAC	GTATTATATT	CT GAT GATG	TATGAT ACTG GAGTTT AAA
AGTTAG C			
TGTGAGTTTAAAGGAGTTAG	ATCA		
AATCACATTGGCTATGTTTA		GA CTG TTAC	ATATTA TGAC CTCGAA TTT
TCGGTT /			
AAGCTCCAGTGTATTATATT		A T TATT-----	TG - A GTA ACA
ATCATTTGTCAAGTAATCTT			

GAM2021 GAGCATCTTGCATTGTGTAC 2007 TAAGAACTGT 4732 ATCT- ATTGT A - A
 TTAATGATTTCATCTAAGAA TGGCACCGCG GAGC TGC GTCTTAATG T
 CTGTTGGCACCGCGGCTC GCTC |||| || |||||
 CTCG ACG CA GAATTAC T
 GCGCC GTTGT A C T

GAM2022 GATGAAGGTTAATGAAAAA 2008 TTAATGAAAA 4733 T A A CT A
 CACTCTCTCAGCCGAGGTAG AACACTCTCT GATGAAGGTTAA GAAAAA C CT CTC G
 GTTTTCTTAATCTTCATC CAGC ||||| ||||| || ||||
 CTAATTCTAATT CTTTTT G GA GAG C
 - -- TG C

GAM2023 GCTGGCTTACAGTGAGGATT 2009 TGGCTTACAG 4734 C- GAG--- TTA GG AACAAATT A
 A TTAT
 TATCTGTGGTTAAACAAATT TGAGGATTTA A AGT GAT TCTGT TTA ATCA GA
 ATATGAGTAT T
 ATCAAGAAATATGAGTATTT TCTG | ||| ||| |||| ||| ||||| |||||
 ATTTATTATGCTTATATATC T TCA CTG AGACG AGT TAGTCTTATATTCGTA /
 TGATTATGAAAGCAGAGATG TA ATAGAA TAG AA AT----- - A TTAT
 TCAAGATAACTATTGAGTCA
 GC

GAM2024 GGGAATACCTCATGATGCAA 2010 TGATATCGGA 4735 ---- A CAA CC T
 GTGCCGTACGGTTCGCCGTG GGAACTATT GGGAATA CCTC TGATG GTG GTACGG T
 CTATGATATCGGAGGAACT CCC ||||| ||| |||| ||| |||||
 ATCCC CCCTTAT GGAG GCTAT TAT CGTGCC C
 CAAA - AG- -- G

GAM2025 GTTAGACGTGTCTAAATACG 2011 TGAGATGTTA 4736 CG-- TA AAG C - T AA
 ATAAGTCTCAGACTGACTTT ATCTGGGAAA GTTAGA TGTCTAAA CGAT TCTCAGA TGAC
 TTTCA C G
 CATCAAGCTGTTGAGATGTT GATT ||||| ||||| ||| ||||| ||| |||||
 AATCTGGGAAAGATTGGGTT CGATCT GCAGATTT GTTA AGGGTCT ATTG AGAGT G
 /
 TAGACGACATTCTAGC TACA GG GAA A T TTC

GAM2026 GTTGTTTATTGAGATTAGAT 2012 TAATCTGTAT 4737 T G - CAATATGA T AATT
 CAATATGATGTATGAGAGCA GTTAATAACC GTTG TTATTGA AT TAGAT TGTA GAGAGC T
 ATTTATGAGTTTTTTATAAT AAC ||| ||||| || |||| ||| |||||
 CTGTATGTTAATAACCAAC CAAC AATAATT TA GTCTA ATAT TTTTGT /
 C G T ----- - AGTA

GAM2027 GTTTATCATTCTAAGTTAGT 2013 TAAGTTAGTT 4738 T TTAGTTA GC TTC - T
 TAATGCGGTTTTCGGTCCTG AATGCGGTTT GTTTATCAT CTAAG AT GGTT GGT CCTG T
 TTTTAGGTA CTTAACTAGT TCGG ||||| |||| || ||| ||| |||
 GAGTTTCTTAGCATGGTAGA TAGATGGTA GATTC TG TCAA TCA GGAT T

GAM2028 TAACGCTTGCATGTTTGAAT 2014 TGGCTTAAGT 4739 - TG GA G G C GAGC
GTG
GTTGGCTTAAGTATTCGCAA ATTCGCAATG TAACGCTTG CA TTT ATGTTG CTTAA TATTCG
AAT GAT G
TGAGCGATGTGGTAGATTAT AGCG ||||| || || |||| |||| |||| || ||
GAATTTGAGTAGTTAAGTAA ATTGTGAAC GT AAA TATAAT GAATT ATGAGT TTA TTA
/
TATAAAAAATTGTCAAGTGT T TA AA - G - AGTA GAT
TA

GAM2029 TATGGTGTAAAGATCAATTTA 2015 TGTAAGATCA 4740 - - T T----- T CT TAC
TATACAGCTTCGTACAATTT ATTTATATAC TATGG TGTA AGA CAAT TATA ACAG TCG A
CGATCTGTTTATATTCTCTG AGCT ||||| ||||| ||||| ||||| |||||
TTGTCTCTGCATCCATG GTACC ACGT TCT GTTG ATAT TGTC AGC A
T C - TCTCTT T T- TTT

GAM2030 TCGAAAATCACTATAGGGCG 2016 TATAGGGCGT 4741 T ATA AA-- TT- CACCGT T
TT C
TAATGCTTTTAGCACCGTAG AATGCTTTTA TCGAAAA CACT GGGCGT TGCT TAG AGCA
GT TTTAA T
CATGTTTTTTAACTTTTTGG GCAC ||||| ||| ||| ||| || |||||
ATTGCTGTTTCACTATGTAG AGTTTTT GTGA CCCGTA ACGA ATC TTGT CG
AGGTT T
CACAGGATGCCCCAGTGTT - CC- GGAC TGT ACT--- - TT T
TTTGA

GAM2031 TGCTAAAAGGAGATGAAGAA 2017 TGAAGAATGC 4742 AG - --- CTCTT C A CT
TA
TGCCTCTTGGGGCCTAATCT CTCTTGGGGC TGCTAAA GA GATGAAGA ATGC GGGG CT
AT GAATAA A
GAATAATAAGGTTTATTCTT CTAA ||||| || ||||| ||| ||| || |||||
ATCAGACCTCCGCATTAATC ACGATTT TT CTACTTCT TACG CTCC GA TA CTTATT
G
TTCATCATTAGTTTAGCA GA A AAT C---- A C TT TG

GAM2032 TGGCAAAC TACTTGGATTAC 2018 TACGATAGGT 4743 A TA - T C T
TTGTCTGCTAGCTTAACGGC AATCTCGAGC TGGCAA C CTTG GATTACTTGTG C TAGCT A
TACGATAGGTAATCTCGAGC GGAT ||||| | ||| ||||| |||||
GGATTGTCA ACTGTT G GAGC CTAATGGATAG C ATCGG A
A GC T - - C

GAM2033 TGGGTGATAGTGTATGAAGC 2019 TAGTGTATGA 4744 -- --- TGA GG G- TTGA AAA
TAG T
AAGCATGATGGCGCCGTAG AGCAAGCATG GTGT ATGAAGCAAG CA TGGC CC TAG
GTC GCTG GTC T

TTGAGTCAAAGCTGTAGGTC ATGG ||| ||||| || ||| || ||| |||
TTTTGATCAGCGACACCTAG CACG TACTTCGTTT GT ACCG GG ATC CAG CGAC
TAG T
AGGAAGCCAAATTGGAATTT AT AAG TAA AA AG CA-- --- --- T
GCTTCATTAGCACTTTGGGG
CCCG
GAM2034 TGTGAGAAGCGGTACACAA 2020 TCGAGAAGCG 4745 T AG - A -- AA C A- GA
CAT A
GCAAACGGTGTCTCTCGCGAC GTACACAAGC CGAGA CG GT CACA AGCA CGGTGTC TCGCG
CGT CG TACCTC A
GTGACGCATTACCTCAATGA AAAC ||| || ||| ||| ||||| ||| || |||
GGTATACGCTGCGCCTGTGA GCTCT GC CA GTGT TCGT GCTACAG AGTGT GCG GC
ATGGAG /
CGACATCGAGTGCTGTTGTG - G- T C TG GA C CC TC AT- T
CACTCGGTCTCGCA
GAM2035 TTTTGATATAAGAATTAAGA 2021 AACACTGTAC 4746 -- A AAGACC GA CT
CCCGGTGTTAGATTCTATC CAAGATCCTT TTTTGATA TAAG ATT CGGTGTTA TTC A
TGAAGTAACACTGTACCAAG GACT ||||| ||| ||| ||||| |||
ATCCTTGACTATCAAAA AAAACTAT GTTC TAG GTCACAAT AAG T
CA C AACCAT G- TC
GAM2036 ACCTTTGACTGTTGGTTCAT 2022 TATGTCAATT 4747 TT CT TG TTATACGCA T
AATTAT TCTAAA G
TATACGCAGATATGTCAATT ATTGCCTCTA ACCT GA GT GTTCA GA ATGTC TGCC
GT A
ATTGCCTCTAAAGTGAAAGC AAGT ||| || ||| || ||||| ||| ||
ATGGCAGACATTCCCTTTGA TGGA CT TA CAAGT CT TACAG ACGG CG A
ACTGATCATCTAGGT T- AC GT TTCC----- - ----- TA---- A
GAM2037 AGTGGACTTGTAATATCTGT 2023 TGTAATATCT 4748 TT ----- T - T CAATATT
TT
AATTTGGATAGTTAGGTTGT GTAATTTGGA GTAATATC TGTAAT TGGATAG TTAGGT GTT
AATC C
TCAATATTAATCTTCTTGAT TAGT ||||| ||||| ||||| ||| |||
TCAAGCAAAGCATTTAACCT CATTATGG ATATTG ATCTATC AATTTA CGA
TTAG /
ATCTATGTTATATAACATTC CC CTCTTACAAT T C - AACGAAC TT
TCGGTATTACCCGGCCACT
GAM2038 CACTGGCCCCATCCGCGTCA 2024 TACGATAGGT 4749 GG AT- TC CAGA A TA -
T C T
GGCAGATGGCAAACACTTG AATCTCGAGC CCCC CCGCG AGG TGGCAA C CTTG
GATTACTTGTC G TAGCT A
GATTACTTGTCTGCTAGCTT GGAT ||| |||| ||| ||||| ||| ||||| ||| |||
AACGGCTACGATAGGTAATC GGGG GGTGC TCC ACTGTT G GAGC
CTAATGGATAG C ATCGG A
TCGAGCGGATTGTCAGATCC GA CCT -- TAG- A GC T -- C

TCGTGGTCCGGGGAGAATG

GAM2039 CTCTCTGAATCAAGTCATGT 2025 ATCAGATGGC 4750 GAA --- TT
TTATTAAGTTAAATCAGATG TTGAAGGAGA CTCTCT TCAAGTCAT GTTTA A
GCTTGAAGGAGAG G ||||| ||||| ||||
GAGAGG AGTTCGGTA TAAAT A
A-- GAC TG

GAM2040 GATATATGTTAGTAAATCAA 2026 TATGTTAGTA 4751 - TT T CAA AAC---- G
AGTAAACTAAGCAAGAATT AATCAAAGTA GAT ATATG AG AAAT AGTAA TAAGCAA A
GTTTATAAAACATTACTATT AAAC ||| |||| || |||| |||||
TCTTTTATATAATC CTA TATAT TC TTTA TCATT ATTTGTT /
A TT - --- ACAAAAT A

GAM2041 TCAAGTTTAAGATAGCTTAA 2027 TAGCTTAAGA 4752 A- TA TAA AT TT AG AC
GAATATTTTAATCGAGTAAT ATATTTTAAT TCAAGTTTA GA GCT GA AT TAATCG TAATTT A
TTACAATGAATTGGTGATTA CGAG ||||| || || || || ||||| |||||
TTATCGTCGTCAGTCTTCAGT AGTTCAAAT CT TGA CT TA ATTAGT GTTAAG /
AAACTTGA GA TC TG- GC TT G- TA

GAM2042 CCATGAGCAGCTTAAAGCGT 2028 TGCGATGGAG 4753 CA TAAA TT A GAAGA G -
CA
TTCAACCATTGGAAGAGCTG CGGCACGATG CCATGAG GCT GCG TCA CCATTG GCT
CTGTT CGGCCAC G
CTGTTCGGCCACCAGCGCGT GTGA ||||| || || || ||||| ||||| |||||
GGCTGCGATGGAGCGGCACG GGTACTC CGG TGC AGT GGTAGC CGA GGTAG
GTCGGTG C
ATGGTGACCGTCGGCGACTC AG C--- C- - ACGG- - C CG
ATGG

GAM2043 CCCTGTCTAGACTCAAAAGC 2029 TAGCATGTAG 4754 CT----- - AAA GC
TGTAAGGCTGTCTTATAGCA TCTTGACGT CCCTGT AGACT CA GCTGTAAG T
TGTAGTCTTGACGTCACGG CACG ||||| ||||| || |||||
GG GGGGCA TCTGA GT CGATATTC /
CTGCACGT T A-- TG

GAM2044 CGCCGCTGTGGAACATGGTA 2030 TCGAACATGG 4755 T AAAG AGA C TC CCA
TGT C
AAGTGCAGACGCGCCGCCTC TAAAGTGCAG CGCCGCTG CGAACATGGT TGC CGCGC GCC
GC TG ACGCAGC T
GCCCATGTGTACGCAGCCTC ACGC ||||| ||||| || || ||||| |||||
CGTTGCGTTCCAGCCTGGCC GCGGCGAT GCTTGTGCCA ATG GCGCG CGG CG AC
TGCGTTG C
GCGCGCCGTAGACCGTGTTG - G--- CC- C TC --- CT- C
GTAGCGGCG

GAM2051 GCAGCAGGTTGAAGAGTTAG 2037 AGAGTTAGCA 4762 A- AG CA- AAT---
TTAAAA AG

CAGAGTGTTAATGCTGGGGT	GAGTGTTAAT	GCAGC GGTGA AGTTAG GAGTGTT
GCTGGGG GAAG C		
TAAAAGAAGAGCGGCTTCCT	GCTG	
CCAGCTAGCTGAAACACTCG		TGTTG CCAACT TCGGTC CTCACAA CGACCTC
CTTC /		
TTCTGGCTTCAACCGCGTTG	CG -- TTG	AGTCGAT ----- GG
T		

GAM2052 TCACCGCTAGACGTGCGGAG 2038	TTTGCAAGGT 4763	- AG G- TC- AT G
CTCGTGATCCGAAGGGCACC	GGAGATGGTG	TCACCG CT AC TCGCGAGC GTG CC A
CCGCTTTGCAAGGTGGAGAT	A	
GGTGA	AGTGGT GA TG ACGTTTCG	CAC GG A
	A GG GA	CCC -- G

GAM2053 TGCTGTAATGCTGCAATTTA 2039	TGTAATGCTG 4764	- ATTTAA AAC
ATTCAACGTTAGAACCTTGT	CAATTTAATT	TGCTGTA ATGCTGCA TTC G
GCAGCATATACAGTA	CAAC	
	ATGACAT TACGACGT	AAG /
	A	GTTCC- ATT

GAM2054 AGCTTGGTTATGATATTGCG 2040	TTGAGTGCTT 4765	GTTAT TT A TTCC- GCAA-- A
A TA		
CATAATTTCCGGAGGCAAAT	TGTCTACGAG	AGCTTG GATA GCGC TAAT GGAG AT
CGAT GTC G		
ACGATAGTCTAGATTGACCA	TT	
TCGATGATAGACTCTAATTT		TTGAGC CTGT CGTG GTTA TCTC TAGCTA CAG A
ATTGAGTGCTTTGTCTACGA		AT--- TT A TTAA AGATAG - C TT
GTT		

GAM2055 AGGCAAAGTGAAGTCCATTA 2041	CAAAGTGAAG 4766	A AG CA AAAACAG
CATCAAAACAGATGAACAAG	TCCATTACAT	AGGCA AGTGA TC TTACATC A
ATGTGAGAGGTTACTATGTT	CAAA	
T	TTTGT TCATT AG AGTGTAG	/
	A GG --	AACAAGT

GAM2056 AGTTCCAGTCTATGATAACA 2042	TTCCAGTCTA 4767	C-- CT AA-- AAATC A
CAAATCATAAAGTTACCAAG	TGATAACACA	AGTTC AGT ATGAT CAC ATAAAGTT C
CTTTGTTAGTGAAGGATCAT	AATC	
TACTCAAGAATT	TTAAG TCA TACTA	GTG TGTTTCGA C
	AAC T- GGAA AT---	A

GAM2057 ATTTATATCTAAGATAACAC 2043	TATCAAAGAT 4768	- TAA- CAGCAAT GGA T
AG-- C		
AGCAATAGATCGGATGATTT	CTTGTTATCG	ATTTAT ATC GATAACA AGATC TGAT
TACTAA TCAT A		
ACTAAAGTCATCAATGTGGT	ATTG	

CCGTTAGTATATCAAAGATC TAAGTG TAG CTATTGT TCTAG ACTA ATGATT
GGTG A
TTGTTATCGATTGATAGTGA A TTAG ----- AA- T GCCT T
AT

GAM2058 GAAGAGGGAAATCCCTATAT 2044 AGAGGGGAAAT 4769 G AAT TAT T T G CAT
GTGCTGGTGGTTGGATGCAT CCCTATATGT GAAGA GGA CCC ATG GC GGTGGTT GATG G
GCCCCTATTGAACTACTGTC GCTG ||||| ||| ||| || ||||| |||||
TATCCTGGGTCCGTCTTC CTTCT CCT GGG TAT TG TCATCAA TTAT C
G --- TCC C - G CCC

GAM2059 GACGTTTTCGCATACTGCGTT 2045 TAATCGCACA 4770 TTCG AC TT TC
ATTATATCTTTCTATAATCG ATGATATACG GACGT CAT TGCG ATTATA T
CACAAATGATATACGTC TC ||||| ||| ||||| |||||
CTGCA GTA ACGC TAATAT T
TATA AC -- CT

GAM2060 GGTAGAGATACTTTTCAGTCT 2046 AGAGATACTT 4771 A CT- AGT G GA TGT T
CGCAT
GTGGTGGATGATGTCGTGAA TCAGTCTGTG GGT GAGATA TTC CT TGGTG TGA CG
GAATATC T
TATCCGCATTGTATAAGATG GTGG ||| ||||| ||| || ||||| ||| || |||||
TTTCTGTTTTCAAACACCAA CCA TTCTGT AAG GA ACCAC ACT GT TTTGTAG G
GTGCAATACTGTCTTACC - CAT CT- - AA TTT C AATAT

GAM2061 GGTTTAATATTTTCTTAGTA 2047 TAAAACTGT 4772 ATA-- A- G- AT-- AAAA
TG AG
CAAAAGTCAATGTTTTAAAA GTGAAATTTT TTTA TTTTCTT GTACAAAA TCA GTTTT
TATATGGA AG A
TATATGGATGAGAGAATATT GTAC ||||| ||||| ||||| ||| ||||| ||||| ||
TGTCTGTATAAAAACTGTGT GAGT AAAAGAA CATGTTTT AGT CAAAA ATATGTCT
TT A
GAAATTTTGTACCAAAGAAA GCAAA AC AA GTGT ---- GT AT
AAAACGTGAGCC

GAM2062 GTCCTTGCTGGGAGAAGATT 2048 TCCGATGTTT 4773 GC G C - AC
GCATTTTGCACCCAAGCATA TCTTAAAGGA GTCCTT TGGGAGAA ATTG ATTT TGC C
GATCCGATGTTTTCTTAAAG C ||||| ||||| ||||| ||||| |||
GAC CAGGAA ATTCTTTT TAGC TAGA ACG C
-- G C T AA

GAM2063 TATAGCTTATTATCTGTTTG 2049 TAGCTTATTA 4774 T- GCTA ATCAAATATAC A TA--
AGATTA
TGCTAATATAATATCAAATA TCTGTTTGTG TGT TGT ATATAAT TCTTGTT TCGT
GTTGGG A
TACTCTTGTTATCGTTAGTT CTAA ||| ||| ||||| ||||| ||||| |||||

	GGGAGATTAATATTACATCC		ACG GCA TATATTA		AGAATAG AGCA TAACCT	
T	AATATATACGAGATAAGACA		TT AC-- C-----	-	TATA ACATTA	
	TTATATCAACGTTGCACGCT					
	ATAAGCATTAA					
GAM2064	TATGACTTGATCAAAGAATT 2050	TGGAATCTCT 4775		CAAAGAA AATA AA AA		
	CAATAAGATAACAGAAAATTG	AGAAAAATTA TATGACTTGAT	TTC AGAT CAGA T			
	ATCTGGAATCTCTAGAAAAA	GGTC				
	TTAGGTCTGTG	GTGCTGGATTA AAG TCTA GTCT T				
		AA---- ATC- AG AG				
GAM2065	TCTATATAGTATTTTTCTGA 2051	TATCAGAATT 4776	AT- T TT TT			
	TATTTTCTATAATATCAGAA	GTCTTCCATA TCTAT AG AT TTCTGATATT C				
	TTGTCTTCCATAGG GG					
		GGATA TC TG AAGACTATAA T				
		CCT - TT TA				
GAM2066	TGATATTAAACATGGAATCA 2052	TATTAAACAT 4777	- --- -----	TT AT		
	GTTGAAATTAATTCTTTGAA	GGAATCAGTT TGATATT AAACA TGGAA	TCAG GAA T			
	TCTAGTATCCTTCCACAATG	GAAA				
	TTTCAATATCA	ACTATAA TTTGT ACCTT AGTT CTT /				
		C AAC CCTATGATCTA T- AA				
GAM2067	TTACTTTATTAATATCAGCT 2053	TAAGTGGACA 4778	TA A - C TTTA A CTT			
	ATTTCTTTTTCAC A-- TT					
	CCATATTTTACCAACTCTTT	TATAGACGCA TC GC TC ATAT CCA CT TAATAA	GATGC			
TC A						
	AATAAATTTCTTTTTCACGAT	GAAG				
	GCATCTTATTGAATGGCATC	AG CG AG TATA GGT GA ATTATT	CTACG AG /			
	TTATTATAAGTGGACATATA	A- A C A CA-- - AT- -----	GTA TT			
	GACGCAGAAGTAATGAAGAA					
GAM2068	CGGCTGCCATGTATTTCTCTG 2054	CTTGCACTTA 4779	C TTTCTG A GAT AG CA			
	GAGAGCAAGTAGATGATGAG	AAGTCTACAT CGGCTGC ATGTA	GAG GCAAGTA GATG			
GAAC G						
	GAACCAGATAGTTTATATCC	TGTA				
	ATACTTGCACCTAAAGTCTA	GTTGATG TACAT TTC CGTTTCAT	CTAT TTTG A			
	CATTGTAGTTG	T CTGAAA- A AC- A- AT				
GAM2069	GATAAGATAGTGGTCAGTTC 2055	TAAGATAGTG 4780	A- TAG TC C C			
	ATCCTTTGATAATTTTCCAA	GTCAGTTCAT GAT AGA TGG AGTT ATC T				
	ATTCTGGATC CCTT					
		CTA TCT ACC TTAA TAG T				
		GG TAA TT - T				

AATCTAATAACTGGATGTTT AATC ||||| ||||| ||||| ||||| |||||
GGATAGTAGCGTTGCCATTC TATGT CAAAT GTTGCGATGAT GGTTTG TAGGT

TGATAAACTTGTAT

T AGTCTTACC A ----- CA

GAM2076 GTGTCGGATGAACTAGTCCC 2062 TGAAC TAGTC 4787 AA CCCTGT- T-- -- T
TGTTAGCATTATAACAATTT CCTGTTAGCA GTGTCGGATG CTAGT TAGCATT AACAAT
TTC T

CTTCAGAAGTATTGTTTACT TTAT ||||||| |||| |||||| ||||| |||
AATGTTATTCTAAAAGTAGC CATAGTTTAC GATCA ATTGTAAT TTGTTA AAG C
ATTTGATAC -- AAATCTT CAT TG A

GAM2077 TACTTCCTTAGCCTTCAAAT 2063 TTTACAGATT 4788 TC TA C C A- AACT
CTAAAATAGATTCACACTCA TAAATGTATA TACT CT GC TT AAATCT AAATAGATT C
TGATCGGATCTATTTACAGA GTTG ||| || ||| ||||| |||||||
TTTAAATGTATAGTTGGTA ATGG GA TG AA TTTAGA TTTATCTAGG A
TT TA T A CA CTAGT

GAM2078 TAGGATTTGATATTTTACAC 2064 TATTTTACAC 4789 - A ACAACTGTTTA TCT T
AACTGTTTAATAGAGTCTAC AACTGTTTAA TAGG ATTTG TATTTTAC ATAGAG ACAT T
ATTTATATGTTCTCTATCGG TAGA ||| |||| |||||| ||||| |||
TGAGATACAAATACCTA ATCC TAAAC ATAGAGTG TATCTC TGTA A
A - GC----- T-- T

GAM2079 TATATTTGACTATTGGAATA 2065 ATTAACCTAT 4790 T-- - T AAT AC
TGAACCATCTCATTAACCTA GGTACATACA TATAT TG ACTAT GG ATGA C
TGGTACATACATATG TATG |||| || |||| || |||
GTATA AC TGGTA CC TACT A
CAT A T AAT CT

GAM2080 TCAATTTTTGGTAGTTGAAG 2066 TACCACATAC 4791 T AAGAA AA - C TTT
AAGTGAATATGTATCATCGT GACTCCAGAG TCAATTTTTGG AGTTG GTG TATG TAT ATCG
G
TTGGTCTTGATTGTATCATA GTTG ||||||| |||| || ||||| |||||
CCACATACGACTCCAGAGGT AGTTGGAGACC TCAGC CAC ATAC ATG TAGT G
TGA - ATA-- C- T T TCT

GAM2081 TGTTCTTATGTCAGATACAA 2067 TGTGATGTCT 4792 --- T-- - A T AG - A
AGTTTAGGAATGTAGGATTC GTTCCATTTA TGTTCTT ATG CAGATA CA AG TT GA ATGTAGG
T
TTTGCATATCTCAGTCTGTG AAGA |||||| || ||||| || || || |||||
ATGTCTGTTCCATTAAAGA ATAAGAA TAC GTCTGT GT TC GA CT TGCGTTT T
ATA ATT CTT A G T CT A C

GAM2082 TTGGTGATGGAGTCACTTTT 2068 TGATGGAGTC 4793 AGT T T TC
AGTTCTTCAGTAGTACTAAC ACTTTTAGTT TTGGTGATGG CACT TTAGT CT A

AGTGCTATTATCGA CTTC ||||||| ||| ||||| ||
AGCTATTATC GTGA AATCA GA /
--- C T TG

GAM2083 TTAAACTTTGGCATATACA 2069 TAACTTACCA 4794 CTT CATATAC C TTT
AGTCTATACTTTTAGTGTAT CACCATTTTT TTTAAA TGG AAGT TATAC T
AACTTACCACACCATTTTTT TAAA ||||| ||| ||| |||||
AAA AAATTT ACC TTCA ATATG /
TTT ACACCA- - TGA

GAM2084 TTTTTTAATAACTTTTTTCGA 2070 TATTGGAATT 4795 TTTT AG CAT- - TG A A
TAATTA TT
TAAGATCATGATATATATTG TACTGTATTA CGATA AT GATA TATAT GA TTT CTGTAT
ATTGTTTG G
GAATTTACTGTATTAATTAA ATTA ||||| || ||| ||||| ||||| |||||
TTGTTTGTTGTTTAGACGAT GCTGT TA TTAT ATGTA CT AAA GACATG
TAGCAGAT /
GTACAGGAAACTCTGATGTA TAT- GA ACAT T GT C G ----- TT
TTATTTACAATAGTGTCTGTA
TAGTGTTACA

GAM2085 GATATTCTACAGCGGGTGTA 2071 TATTCTACAG 4796 AG-- ----- TT
ATTTTTGTAGTTACTGATAA CGGGTGTAAT GATATTCTAC CGGGT GTAATT T
ACCTGGAAGGTAGAATATC TTTT ||||| ||||| |||||
CTATAAGATG GTCCA CATTGA /
GAAG AATAGT TG

GAM2086 GGAAATAGAGTAGCTGATTT 2072 TGTTATCATA 4797 - CTGATTT TTTTGTAAG T
GTT
ATTTATGTTTTGTAAAGTAA AGTTCTGAAC GGAAATAGA GTAG ATTTATG GTAATAG
AGAAG C
TAGTAGAAGGTTTCGTATTTT CTAC ||||| ||||| ||||| ||||| |||||
TCTGTTATCATAAGTTCTGA TCTTTGTCT CATC TGAATAC TATTGTC TCTTT /
ACCTACGTCTGTTTCT G CAAGTCT ----- - ATG

GAM2087 GGAGGAAGTACTGGTTTATT 2073 GGAAGTACTG 4798 - T- TTC A T
TCCTAAATGTTTTCTAGCAT GTTTATTTCC GGAGGAAG TAC GGTTTAT CTAA TGTT T
TAGCTGTAAATCCTGTATCT TAAA ||||| ||| ||||| ||| |||||
TTTTCC CCTTTTTC ATG CTAAATG GATT ACGA C
T TC TC- - T

GAM2088 GTTTGGTATATCATTTGAGA 2074 TTCTATGTCT 4799 TCATTT AACATA T TAT
TCAAAT - A
AACATATGTAGAATTTATTT CTTCTTATAT GGTATA GAGA TGTAGAATTTAT TTCA CA
CT CTTT C
TCATATCATCAAATCTCTTT CAAA ||||| ||| ||||| ||||| ||| ||| |||

ACTAAAGTAGCGTCTGTTCT CTATAT CTCT GTATCTTAGATA AAGT GT GA
 GAAA /
 GAATATAGATTCTATGTCTC TCTT-- ----- T CTT CTGC-- T T
 TTCTTATATCAAAC

GAM2089 TAGACTATGTTCTAATCTAT 2075 TAATACTACT 4800 T TTCTA T--- CT AA ATC
 TTCTATCTGTAGTGAAATCA GTAGTACTAA TAGAC ATG ATCTATT CTAT GTAGTG ATC T
 TCTTTAGATAAATACTACTGT TAGA ||||| || ||||| ||| ||||| |||
 AGTACTAATAGATGATTCGT ATCTG TGC TAGATAA GATG CATCAT TAG /
 GTCTA - TTAG- TCAT T- AA ATT

GAM2090 TATTCTTGTATTTTCGTAGTT 2076 TACAGTAATT 4801 T A G C A AAAT- ACA
 AAAC TATTAGTAAAATACCT TAACTAGAAA TATTCT GT TTTC TAGTTAAA TATT GTA ACCT T
 ACATCTTAGGGTTAATCTAC AGCT ||||| || |||| ||||| |||| ||| ||||
 AGTAATTTAACTAGAAAAGC ATAAGA CG AAAG ATCAATTT ATGA CAT TGGG C
 TAGAATA T A - A - CTAAT ATT

GAM2091 TCCTGGTGTAACCACCGT 2077 CATTATGCTA 4802 G TAAA TCAGAATT T TT- TT
 CAGAATTTATTATATTTTTA TTTGGTGGTG TCCTG TG ACCACCG TA TATA TTTAC A
 CTTATTGTAGACATTATGCT TTTC ||||| || ||||| || |||| |||||
 ATTTGGTGGTGTTTCAACAG AGGAC AC TGGTGGT AT GTAT AGATG /
 GA A TTTG TT----- C TAC TT

GAM2092 TTCTAGAACCTATAGTCTCA 2078 TCGGATCTTA 4803 -- -- C TAT CAG
 TATATGTGGTCAGAACTATC TAGGAATTCT TTCTAGAA CCTATA GTCT ATA GTGGT A
 GCTACTATCGGATCTTATAG AGGA ||||| ||||| |||| ||| |||||
 GAATTCTAGGA AGGATCTT GGATAT TAGG TAT CGCTA /
 AA TC C CAT TCA

GAM2093 AGACATTTATGTAAGTCAAA 2079 TGTTTTGTAT 4804 A - C CT
 ATCTAGACTTTGTTTTATGT TTACGTGAAC AGAC TTTATGTAAGT CAAAAT TAGA T
 TTTGTATTTACGTGAACGTT GTTT |||| ||||| ||||| ||||| |||||
 T TTTG AAGTGCATTTA GTTTTG ATTT T
 C T T TG

GAM2094 ATAATCAGAACTGTACACA 2080 ATCACATGTA 4805 CATTTTC - TC- -----
 TTTAT TC
 TTTTCTTACATGGATTTTCG AATGTAAC TT TACA TTACATG GATTT GTATT TCCA
 CTGTT G
 TATTTCCATTTATCTGTTTC TCTG |||| ||||| ||||| ||||| |||| |||||
 GCAGACAGCATTGGATCCA ATGT AATGTAC CTAAG TATAA AGGT GACAG
 /
 AAGAATAATATCCCGAATCA A----- A CCC TAAGAAACCT TTAC- AC
 CATGTAAATGTAAC TTTCTG
 TTTAT

GAM2095 ATCATACTTTCTACAAATAT 2081 CATCATATGC 4806 ----- AA-- T ATCCCAA T
 TGGTGCATATCCCAAGATCA AGGTGGATAA ATCATACTT TCTAC ATAT GGTGCAT
 GATCA C
 TCACTGATCCACATGCATCA TTCC ||||| ||| ||| ||||| ||||
 TATGCAGGTGGATAATTCCA TAGTATGGA AGGTG TATA CTACGTA CTAGT A
 GGTATGAT CCTTAAT GACG - CAC---- C

GAM2096 ATTATGCCATTAAGTGTATC 2082 TATGCCATTA 4807 TTA T TATCACC T
 TATCACCCATTGTTGAACAC AGTGTATCTA ATTATGCCA AGTG ATC CA T
 ATGATTCACTTGGCATAAT TCAC ||||| ||| ||| ||
 TAATACGGT TTAC TAG GT G
 --- T TACACAA T

GAM2097 ATTTCCATTCCATATCGGTC 2083 TAACCGGTAG 4808 CATTCCA- CAACCAT A A
 AACCATTGAGGTGAGAGATA TATATCTGAA ATTTT TATCGGT TCAGGTG GAG T
 ATTCCATCTGATAACCGGTA AT |||| ||||| ||||| |||
 GTATATCTGAAAT TAAAG ATGGCCA AGTCTAC CTT A
 TCTATATG AT----- - A

GAM2098 GCGTTAGAAGTCATTTCCAT 2084 CATCAATCTA 4809 A TCATTTCC ATCT TACTC A
 CAATCTATCATACTCGTTAT TCATACTCGT GCGTTAG AG ATCA ATCA GTT T
 ATAACCTTCTTGATTTTCTGA TATA ||||| || ||| ||| |||
 TACATAGTTCTACTAGCGT TGCGATC TC TAGT TAGT CAA A
 A TTGATACA CTTT TCTT- T

GAM2099 GGATAATATTTGTATACATC 2085 TAATATTTGT 4810 ATAC-- T ATT
 TAGTATTTATAGCTGATCTA ATACATCTAG GGATAATATTTGT ATC AGT T
 AAGACAGATGTTATCT TATT ||||| ||| ||| |||
 TCTATTGTAGACA TAG TCG /
 GAAATC - ATA

GAM2100 GTAAATCTATAATAATGTAT 2086 TTAGGCAAAT 4811 A TA TTT AAA AAAATC
 CCT ATT
 TTAGGCAAATATATAAAATC ATATAAAATC GTA ATCTATAA ATGTA AGGC TATAT TGGAT
 TATAT A
 TGGATCCTTATATATTAATA TGGA ||| ||||| |||| ||| |||| |||| ||||
 GTATATTATCCAATATGAAG CAT TAGATGTT TACAT TTTG GTATA ACCTA ATATG
 /
 TTTCTTACATCGTTGTAGAT A GC TC- AA- ----- TT- ATA
 ATAC

GAM2101 GTCGCCTTGTTCAAATTTAA 2087 CTGGTACATT 4812 C CT---- T-- T AC --- G AAT
 TC A
 CCCAGAAAGATACGAAATCA TGTATACATT GT GC TGT CAAAT TA CCAGAA A ATACGA
 CAT TTTGG A

TTCTTTGGAAATCCGGATAT GTTT ||| ||| ||||| || ||||| || |||||
 GTCGTATGTTCTTCTGGTA CA CG ACA GTTTA AT GGTCTT T TATGCT GTA
 AGGCC A
 CATTTGTATACATTGTTTGC C TTTGTT TAT C -- CCT G --- T- T
 CAC

GAM2102 TGTATTATGTTGTTTATGTT 2088 TATCATAGAC 4813 T TT A
 TAGTAATTGCTATCATAGAC AGTATCATAT TGTAT ATGTTGTTTATG TAGT A
 AGTATCATATA A ||||| ||||| |||||
 ATATA TATGACAGATAC ATCG T
 C T- T

GAM2103 TGTTAGTGTAAGTAATTAAA 2089 TAAGTAATTA 4814 TT ATTAAA ATAAAAC G A
 GCAATAAACTATAGGGGTG AAGCAATAAA TG AGTGTAAGTA GCA TATAG GGTG G
 AGATACCGCTATATGTAAAA ACTA || ||||| ||| |||||
 ACTATTTATATTTTCA AC TTATATTTAT TGT ATATC CCAT /
 TT CAAAAA ----- G A

GAM2104 TTGAAAGAATATATTTACAG 2090 TGGTATCCCA 4815 AA A CAC- - TT
 ATATCGTTAGTTAGGCTCAA TAAATGTAAT TTGA GA TATATTT GATATCGTT AG A
 TGGTATCCCATAAATGTAAT CGAT ||| || ||||| ||||| ||
 CGATCAA AACT CT ATGTAAA CTATGGTAA TC /
 AG A TACC C GG

GAM2105 CAACGGTCACGAACCTATGTG 2091 TGAATGCGTT 4816 GT C CT - G T C
 AATGCGTTTGCCATCATGTG TGCCATCATG CAACG CA GAA ATGT GAATGCGTTT CCA
 CATGTGTGCCA T
 TGCCACTACTGGCATGCATG TGTG ||||| || ||| ||||| ||||| ||| ||||| |||||
 CTGGGAAATGCATTCTACAT GTTGC GT CTT TACA CTTACGTAAA GGT GTACGTACGGT
 A
 TTTTCCTGGACGTTG AG C TT T G C C

GAM2106 CACTGGGATTGGTTAACCTC 2092 TTGGTTAACC 4817 C TT CTCTAAC TATC
 TCTAACGGTAGATATCCAAG TCTCTAACGG CA TGGGATTGG AACCT GGTAGA C
 TTCTACCAGGTTTCCGATTC TAGA || ||||| ||||| |||||
 TATG GT ATCTTAGCC TTGGA CCATCT /
 - T- ----- TGAA

GAM2107 CTTGTGTCCACATGTTTCATG 2093 GTCAAAGTCT 4818 TCA T GC T AAAA T--- T A
 TTT G
 TGTTGCGAGATTCCAAAACC TAATTTTCT TGT TG GTT GAGA TCC CCAG GTT GGA
 TTGAT CACAA A
 AGTGTGTTGGACTATTGATTT GGGC ||| || ||| ||||| ||||| ||||| ||||| |||||
 TCACAAGATTTGTGGTCAAA ACA AC CAA CTCT AGG GGTC TAA TCTGA AACTG
 GTGTT /

GTCTTAATTTTTCTGGGCGA --- - AA T AGCG TTTT T - --- T
 GGATTCTCAAAACCAACATT
 GTGGGTTATTG

GAM2108 GAAAGACATTGAGATAATGC 2094 TGGCTCAATA 4819 ----- ATAAT - CCTC A
 TTCCCCCTCGCCAAATGGCA AATTTTCCAC GAAAGACA TTGAG GC TTCCC GCC A
 ATTGGGAATGCTGGCTCAAT TGTC ||||| ||| ||||| ||
 AAATTTTCCACTGTCTTTC CTTTCTGT AACTC CG AAGGG CGG A
 CACCTTTTAAAT GGT-- T TTAA T

GAM2109 GCAATAGTTTCTACATATTT 2095 TATCAAATAA 4820 A TTCTAC---- T A A
 TTATTTGATAATATATAGAT CGATATTAAG GC ATAGT ATATT TTATTTGATA TAT T
 GTATCAAATAACGATATTAA CTTG || |||| |||| ||||| ||
 ACTTGTTACTATAGC CG TATCA TATAG AATAAACTAT GTA A
 A TTGTTCAAAT C - G

GAM2110 GGAACCGAGTTCTTCTCTTA 2096 TGGCTCCACC 4821 A C- AT --- TG
 ATATAG
 TGGATTTCAGCGGAATCGC TTGGAAGCCA GTTCTTCTCTTATGG TTTCAAG GGA
 CGCATGGG TCCT CCTC T
 ATGGGTCCTTGCCTTCATAT TGGG ||||| ||||| ||| ||||| ||| |||||
 AGTTGAAAAGAGGGTGAGGA TAGGAGGGGGGTACC AAGGTTT CCT GTGTATCC
 AGGA GGGAG /
 ATTCCTATGTGGCTCCACCT G CA CG TTA GT AAAAGT
 TGGAAGCCATGGGGGGGAGGA
 TATTGATATTC

GAM2111 TAAAAACAATACTGAACAGA 2097 TTCTTTGTTT 4822 A T TAACAAT A CA C
 TAACAATTAACACCATC GTGATGTTTT TAAAAACA TAC GAACAGA TAA AA CCAT T
 TTTATGGCTTTCTTATTCTT TA ||||| ||| ||||| ||| || |||||
 TGTTTGTGATGTTTTTA ATTTTGT GTG TTTGTTT ATT TT GGTA T
 A - CTT---- C TC T

GAM2112 TGGATAGTCTAAGTTCCCAA 2098 TAGTCTAAGT 4823 A- CCCAAC TT ATG TAT-
 C
 CTAGAGGATTTTCTAGATGT TCCCAACTAG TGGATAGTCTA GTT TAGAGGA TTCTAG
 TCTTC GATTGTG T
 CTTCTATGATTGTGCTGCAC AGGA ||||| ||| ||||| ||||| ||||| |||||
 AATTTGATGGAGAGCTAGAA ACCTATCAGAT TAA ATCTCTT AAGATC AGAGG
 TTAACAC /
 TTTTCTCTATCCAATGATAG AG CCT--- TT G-- TAGT G
 ACTATCCA

GAM2113 TGTACTAATAATTGTAGTAG 2099 TTAGTGCTAC 4824 AAT-- TG- TA G
 CTATAGTGGAATATTACTG TAACTGTTCT TGTACT AAT TAGTAGC TAGTG T
 CTACTAACTGTTCTAAGAGT AAGA ||||| ||| ||||| |||||
 ATA ATATGA TTG ATCATCG ATTAT A
 GAATC TCA TC A

GAM2114 ACGAAGTTCTTTGGCGGTTT 2100 CGAGAACTCC 4825 C----- ATT A AA TAA
CCCCA
TCATTGATTCATTTCTGATG TTCAACTCGC GGTTTTC GATTCATTTCTG TG ACAGT
TGAT C
AAACAGTTAATGATCCCCAC TACC ||||| ||||||||| || ||||| |||||
GCAATTGTCGATATTGTCCC TCAAGAG CTAAGTGAAGGC AC TGTTA GCTG
G
ACGGAAGTGAATCCGAGAAC ATCGCTCAACTTCC C-- - CC TA- TTAAC
TCCTTCAACTCGCTACCAAA
GAGCTCCGTT

GAM2115 ATAATTAATACAATATTTAG 2101 TAATACACGT 4826 --- AATAT G ATT
AAGACTTATTCGGAAAGTAT ATCATTGATT ATAATTA ATAC TTAGAA ACTT C
TCTAATACACGTATCATTGA AT ||||| ||||| ||||| |||||
TTAT TATTAGT TATG AATCTT TGAA /
TAC CACAT A AGG

GAM2116 CAATGTTGCTGCTAGACCAC 2102 TTGCTGCTAG 4827 - CACATGTCA AT
ATGTCAATCTAATAACTGGA ACCACATGTC CAATGTTGCTG CTAGAC ATCTA A
TGTTTGATAGTAGCGTTG AATC ||||||| ||||| |||||
GTTGCGATGAT GGTTTG TAGGT /
A ----- CA

GAM2117 GAATAACGGATGTCATCAAA 2103 TGTTACATTC 4828 ACG-- ----- C TCAT- - TCA
TTCATTGAACATTTATCACA ATATTTTGTG GAATA GATGT CAT AAAT TG AACATTTA
C
ATTAGATGTTACATTCATAT TTAT ||||| ||||| ||||| ||||| |||||
TTTGTGTTATACTTACATCA CTTAT CTACA GTG TTTA AC TTGTAGAT /
CTAATATTC AATCA TTCATATT T TACTT A TAA

GAM2118 GATTTTGTAAATATGCCATGG 2104 TGAAACACAT 4829 T ATG A-- A- C A C
GATAAA
AAACAAATGAAACACATTAT TATCACTCCA GATTTTG AAT CCATGGA ACAA TGAAA AC TTAT
ACTCCAT T
CACTCCATGATAAATTATTT TGAT ||||||| ||||| ||||| ||||| ||||| ||||| |||||
AATGGAGTAATAAAGTATTT CTAAGC TTA GGTACCT TGTT GCTTT TG AATA
TGAGGTA /
CGCGTTGTATCTCCATGGGT T ATG CTA GC A A A ATTTAT
AATTCGAAATC

GAM2119 GTGTCGGATGAACTAGTCCC 2105 TGAAGTATGTC 4830 AA CCCTGT- -- A-- T
TGTTAGCATTAGAACAAATTT CCTGTTAGCA GTGTCGGATG CTAGT TAGCATTAG AAC
ATTTCT T
CTTCAGAAGTATCGTTTACT TTAG ||||||| ||||| ||||||| ||||| |||||
AATGTTATTCTAAAAGTATG CATAGTTTAC GATCA ATTGTAATC TTG TGAAG C
ATTTGATAC -- AAATCTT AT CTA A

GAM2120 GTTTCCAAATAGCTTAAGAA 2106 TAGCTTAAGA 4831 AAAT AA A CAT----- A AC
 GGCATTTACGTATGACGGAG AGGCATTTAC GTTTC AGCTT GA GG TTACGT TG G
 CACATGTAACACAGTTACCA GTAT ||||| |||| || ||||| ||
 TCAGAAGCTTTAAGGAGAC CAGAGG TCGAA CT CC AATGTA AC G
 AATT GA A ATTGACAC C GA

GAM2121 TATCTAAGATAACACAGCAA 2107 TATCAAAGAT 4832 TAA- CAGCAAT GA T AGT-
 TCG
 TAGATCTGATGATTTACTAA CTTGTTATCG TATC GATAACA AGATCT TGAT TACTAA CA
 A
 AGTCATCGATGTTGTCCGTT ATTG ||| ||||| ||||| ||| ||||| ||
 AGTATATCAAAGATCTTGTT ATAG CTATTGT TCTAGA ACTAATGATT GT /
 ATCGATTGATA TTAG ----- A- T GCCT TGT

GAM2122 TATGTTTTATGAATAGATAA 2108 TGACAGGCGA 4833 G TA- G CTTCTT T TG AT C
 T TGC
 AGTAGATGGTGTCTTCTTC CACAATCGTT AATAAAG GATGTGTC CCT T TA TTC
 CGTATT TTGTTCCG C
 CTTTTGTAATTTCCCGTATT CTTT | ||||| || ||||| ||| | || ||||| |||||
 TTTGTTTCGTGCCAATTGAGT T TATTTC CTA CACAG GGA A AT AAG GTATGA
 AATGAGT /
 AACAGTATGAGAATATGACA G TTG A C----- CGT -- A C TAA
 GGCGACACAATCGTTCTTTA
 TGTATTCCATG

GAM2123 TCAATTTTTGGTCGTTGAAG 2109 TATCATACCA 4834 -- TGAAGAA - TCGTT
 AAGTGAATAATCATCGTTTG CATACGACTC TCAATTTTTGG TCGT GTGAATAATCA T
 GTCTTGATTGTATCATACCA CAGA ||||| |||| ||| |||||
 CATACGACTCCAGAGGTTGA AGTTGGAGACC AGCA TACT TGTTAGT /
 TC TACACCA A TCTGG

GAM2124 TGTTGTATATGGAGTAACTG 2110 TCAATAGTCA 4835 ATA A A AG TT
 TTGGTAGTTCTTCCGTGGAA TACTAACAGC TGTTGT TGG GT ACTGTTGGT TTC C
 TCAATAGTCATACTAACAGC A ||||| ||| || ||||| |||
 A ACGACA ATC TA TGATAACTA AGG C
 --- A C -- TG

GAM2125 AAGCACCTTCGTGTTGGA 2111 TTCAGAAATT 4836 CCTTC GG C TT
 TTTTGGCAAGTTTGGCTATT TCAACATGTG AAGCAC GTGTTG ATTTTGG AAGT G
 TCAGAAATTTCAACATGTGT TTT ||||| ||||| ||||| |||||
 TT TTTGTG TACAAC TAAAGAC TTTA G
 ----- TT - TC

GAM2126 ACTGTTGTTTTTAACGCATG 2112 TACCCTATTG 4837 TAACG TCAT- T C GG
 TCATATAGGTGTCTGATGGT TTTTATGATA ACTGTTGTTTT CATG ATAGG GT TGAT T

TTGTTATACCCTATTGTTTT AAAC ||||| ||| ||||| |||
 ATGATAAAACAACAGT TGACAACAAAA GTAT TATCC CA ATTG /
 TA--- TTTGT - T TT

GAM2127 ATCGCTTATATGAAAATCTG 2113 TGTGATGTTA 4838 GCT AAAATCTG TGTC GTG
 GACATGTCTCACAGTTAGTG GCATATGTAG ATC TATATG GACA TCACAGTTA A
 ATCATAGCTGTGATGTTAGC AT ||| ||||| ||| |||||
 ATATGTAGAT TAG GTATAC TTGT AGTGTCGAT /
 AT- GA----- ---- ACT

GAM2128 ATGAGAGCTTTATTTGTCAT 2114 GAGCTTTATT 4839 A A TCATAGTTA AATA
 AGTTAAGCCAATAATAACCG TGTCATAGTT ATG GAGCTTT TTTG AGCC A
 GCTCAAAAAAGTTCACAT AAGC ||| ||||| ||| |||
 TAC CTTGAAA AAAC TCGG T
 A - ----- CCAA

GAM2129 CCTCACTGAAAGAGTAGTCA 2115 TGGACTGCTT 4840 CAC- A - TCAA
 TGTC AATCTTTTTATGGACT TTACATTA AAA CCT TG AAGAGTAGTC ATG T
 GCTTTTACATTAAAGG GG ||| ||||| ||| |||
 GGA AC TTTTCGTCAG TAT C
 AATT A G TTTT

GAM2130 CTTTATAAACTCTTTATTCA 2116 TATAAACTCT 4841 T TCAAA- TGT
 AAGCATGTATTTTGTCCCAA TTATTCAAAG CTTTATAAACTCT TAT GCA A
 TATGTGGAGTTTATAAGG CATG ||||| ||| |||
 GGAATATTTGAGG GTA TGT /
 T TAACCC TTT

GAM2131 GACTGACATAAAACAACAT 2117 TGACATAAAA 4842 C CAA CTTTT AAA
 CTTTTGTGTAAAATGGGGCA CAACTATCTT GA TGACATAAAA CTAT GTGT A
 TATAGGTCTTTTATGTCAAT TTGT ||||| ||| |||
 C CT ACTGTATTTT GATA TACG T
 A CTG ---- GGG

GAM2132 GAGATAGTAACTTTAAAGAC 2118 TGGTAAGAGC 4843 TAA - CCTCAT-- CTGGA A T
 AG TTCTT
 CTCATGTTTCATCTGGATCAT ATCGTGGGCC TAG CTTTAAA GA GTTCAT TC TACC
 GGATA ATT T
 ACCTGGATAAGATTTTCTTT CAAT ||| ||||| || ||| ||||| |||
 TTAAC TAATTCTGTCTGGTA GTC GAAATTT CT CGGGTG AG ATGG TCTGT TAA
 T
 AGAGCATCGTGGGCCCAATT C-- G CTTTAACC CTACG A - CT TCAAT
 TCTCGTTTAAAGCCTGTTTC

GAM2133 GTGTCTGTTATATGTATAAA 2119 TTTTCTCTC 4844 CT AT-- AAAAA CCC TT A
 AATTGCCCAGTTGAAATAAA AAAGATGCTT GTGT GTTAT GTAT TTG AG GAAATA A
 TATGTTTTTCTCTCAAAGA CGGT |||| |||| ||| || |||||
 TGCTTCGGTGGCCGCAC CACG CGGTG CGTA AAC TC TTTGT T
 C- GCTT GA--- TC- TT A

GAM2134 TGGCCTGGCAACTGGAGTGG 2120 TGTTGCTTAT 4845 GCAACTG- TG - TGC
 CAGGAGGTGCTATTTCTTCG TGAGAACAGG TGGCCTG GAG GCAG GAGG T
 TTGTTGCTTATTGAGAACAG CCA ||||| ||| ||| |||
 GCCA ACCGGAC TTC TGTT CTTC A
 AAGAGTTA GT G TTT

GAM2135 TGTGTGCGGTGTTCCAACCT 2121 TTGGCACATG 4846 C ----- ACT ACACAA A
 A
 GCCAAAAGACACAAGAAATT GAAATCCTTT TGTGT GGGTG TTCCA TGCCAAAAG GA
 ATTTGA T
 TGAATTATTAAATCTCCTTC TTCG |||| |||| |||| ||||| || |||||
 ATTTTGGCACATGGAAATC ACATA TCCGC AAGGT ACGGTTTT CT TAAATT T
 CTTTTCGCCTATACA - TTTTCCTA AC- ACTTC- C A

GAM2136 ACTGTGCGAGTACTAAAAGGA 2122 AAAGGAAACA 4847 GA- - ----- ATAATGT T-
 TCC
 AACATAATGTAGTGTGATT ATAATGTAGT ACTGTC GTA CTAAAAGG AAACA
 AGTGTGA TTTA T
 TTATCCTACTTAGATTTTAT GTGA |||| ||| ||||| |||| ||||| |||
 ATTTTAATAGTGTTTATAAG TGACAG TAT GATTTTTT TTTGT TTATATT AGAT /
 ATTTTATAGATATGTGGACA GTG A AGAATA GATAATT TT TCA
 GT

GAM2137 GGTATAGGATGTTGATTAGA 2123 TAGGATGTTG 4848 T ATTAG AA A
 TGAATGCATATGCACATAAC ATTAGATGAA GGTA AGGATGTTG ATG TGC T
 AGCGTTCCTTGCC TGCA |||| ||||| ||| |||
 CCGT TCTTGCAC TAC ACG A
 T AA--- -- T

GAM2138 GTAGCTATATAATGTATGGT 2124 TAATGTATGG 4849 - AT- TGG C- AATC T
 AACATGATAATCATATTATA TAACATGATA GTAG CTAT AATGTA TAA ATGAT ATA T
 TCAAGATCATAATTAATTAC ATCA |||| |||| ||| |||| |||
 ATTTAGATAGTTTAC CATT GATA TTACAT ATT TACTA TAT /
 T GAT TA- AA GAAC A

GAM2139 TAGTTATTGTAGCATTTATA 2125 TCATGGTGTT 4850 T - TTTATACTAT TG A ATT
 CTATTAATGAACAAAACCTGT GTTTGTTATT TAGT ATTGTAG CA TAA AACAA ACTGTGAGA
 A
 GAGAATTATAGCTCTCATGG TGAC |||| ||||| || ||| ||||| |||||

TGTTGTTTGTATTGACTA
CGGTCACTG

GTCA TGGCATC GT
C A TT----- GT G

ATT TTGTT TGGTACTCT T
CGA

GAM2140 TCAAGTATTATATCTTAATT 2126 TAATACGGTC 4851 AG T-- TA -- TA
AGTGTTAAAATACATTCTAA CTGTAGTATC TCA TATTATA CT ATTAG TGT A
TACGGTCCTGTAGTATCTGA TGA ||| ||||| || ||||| |||
AGT ATGATGT GG TAATC ACA A
CT CCT CA TT TA

GAM2141 TCATATAGATAATATTATCC 2127 TAGCAGTTTA 4852 A CAGCC GAAACTACACC TCCA
TAT-- TT

ATGACAGCCACTGCGAAACT TGGAAATCTT ATT TCCATGA ACTGC TATA
CGTGAAGA CAT C
ACACCTATATCCACGTGAAG ATCA ||| ||||| |||| ||||| |||
ATATCATTTCCCATGTATTT TAA AGGTATT TGACG ATGT GCATTTTT GTA /
TTTTTACGATTGTAGCAGTT - ---- - - - - - TA-- TTTAT CC
TATGGAAATCTTATCACGTG
A

GAM2142 TCCTTTTTTGGTATACAATCT 2128 TTTGGTATAC 4853 TT ACAAT-- C CAA GT
CGACAATCTTCAGTCTGTGA AATCTCGACA TCCT TTGGTAT CT GA TCTTCA C
AGAATCAGTAGCGCAATACC ATCT |||| ||||| || |||||
AACCAGGA AGGA AACCATA GA CT AGAAGT /
CC ACGCGAT - A-- GT

GAM2143 TGAGAGAGTACTGGTTTCAT 2129 GAGAGTACTG 4854 T T TTTCTACT AG AA
GTTTCTACTAAAGAAGGCAA GTTTCATGTT TGAGAGAGTAC GGTT CATG AAAGA GC A
ACTCGTTATTTTTTTTATGA TCTA ||||| ||||| |||| |||
ACTTGTA CTCTTTCA ACTTTCTCATG TCAA GTAT TTTTT TG C
T - TT----- AT CT

GAM2144 TGGGGATTGTGGTATATGTA 2130 TGTGGTATAT 4855 -- --- AT- ATGA A CGTT-- AT
TGAGGTAGGCAGCGTTCACA GTATGAGGTA TGGGGA TTGT GGT ATGT GGT GGCAG
CAC T
TTTTGTGTTATCACTGCCAC GGCA ||||| |||| ||| |||| ||||| |||
TACATCTGACCTTGGCAAAT ACCTCT AACG CCA TACA TCA CCGTC GTG /
TCTCCA TA GTT GTC ---- - ACTATT TT

GAM2145 TTCAGCAGTGGATCCGTTAG 2131 AGTGGATCCG 4856 A G - CTCC- C
CTCCATAATACAATATTGTC TTAGCTCCAT TTCAGC GT GATC CGTTAG ATAATA A
AATACTGACGAGATTGACGC AATA ||||| || ||||| |||||
TGAA AAGTCG CA TTAG GCAGTC TGTTAT /
- G A ATAAC A

GAM2146 AAGTGGACCGGGAGGACCGA 2132 TTAGATCTGG 4857 T C A A G AAG TT A ----
ATG

GGAAGAGTCTTTCCTGATCT GCCCCCGTCC AAG GGAC GGG GG CC AGG AGTCT CCTG TC
TCTGAC A
CTGACATGATGGGTCAGATC TCTT ||| ||| ||| ||| ||| ||| ||| |||
AAGACAGGTTGGATTAGATC TTC CCTG CCC CC GG TCT TTAGG GGAC AG AGACTG
/
TGGGCCCCCGTCCTCTT T - - - G AGA TT - AACT GGT

GAM2147 AGGTCCCTGACTGCCGAGGA 2133 TCCCTGACTG 4858 GAC AGCA - AGA- G
GCAGGCCGAGGAGAGGGCGG CCGAGGAGCA AGGTCCCT TGCCGAGG GG CCGAGG GG
C
CCATGGCCTTGGACCCTTCG GGCC ||||| ||||| || ||||| ||
GCGATGGGGGCCT TCCGGGGG GCGGCTTC CC GGTTCC CC G
TA- --- A GGTA G

GAM2148 AGTGAGATACTTTCTGAGAG 2134 TGAGAGATAA 4859 AC---- G TAATAC
CCACATT CT
ATAATACATCTTACTCCACA TACATCTTAC AGTGAGAT TTTCT AGAGA ATCTTACT
TTTA C
TTTTTACTCTCCTAAACCAT T ||||| ||| ||||| ||||| |||
TATAGTGAGATACTTTCTGA TCATTCTA AGAGA TCTTT TAGAGTGA AAAT T
GAGATAATACATCTTACT CATAAT G CA---- TATTACC CC

GAM2149 CTATGGGTCCCCTCCCTCCG 2135 ACAGTGCCCA 4860 TG TC TCCCTC T A- TAG
TCTGTCACGTAGAAACCGAG TTGGGTTCTT CTA GG CCC CG CTGTC CG A
GACAGTGCCCATTTGGGTTCT GTAG ||| || ||| || ||||| ||
TG TAG GAT TC GGG GT GACAG GC /
GT TT TTACCC - GA CAA

GAM2150 GACAATGATCCTGTCAGATT 2136 TGACATTGTA 4861 A - G - G C AA - T ACT
A
CAGGGTCGCAGACAAACCTG GTCTGAAGGA GAC AT GATCCT TCAGATT CAG GTCG AGAC
AC CTG CC GCGT A
TCCACTGGCGTAAACATGCC TCTA ||| || ||||| ||||| ||| ||||| ||| ||| ||| |||
TGCGGTAGAGTCGTCTCTGA CTG TA CTAGGA AGTCTGA GTT CAGT TCTG TG GAT GG
CCGTA A
CATTGTAGTCTGAAGGATCT A T - T A C C- A - CGT C
ATAGTC

GAM2151 GCCTGAGGGCCATGGTCAAG 2137 GCCACAGCCG 4862 GA CC CAA T GAAAC TCC
GCGTCTGGAAACTGGCCATC CCGTCGCCAT GCCT GGG ATGGT GGCG CTG TGGCCA A
CACTTTGGCCACAGCCGCCG CCCC ||| || ||||| ||||| ||| |||||
TCGCCATCCCCGAGGC CGGA CCC TACCG CCGC GAC ACCGGT /
GC -- CTG C ---- TTC

GAM2152 GCTTTGGTGTCCCAGACGCC 2138 TCACCGGCGA 4863 --- A AGCT-- TT

AGCTGGCTTACTGCTCTCAC TTGGCCCGAC GCTTTGGTGTG C CAG CGCC GGC A
CGGCGATTGGCCCGACGCCA GCCA ||||| ||| |||
AGGT TGGAACCGCAG GGTT GCGG TCG /
 CCC A CCACTC TC

GAM2153 GTAAACGGCCTCCCTGTTCT 2139 TCAGAACTCC 4864 AA CCCT T- T
TGGAATGCTTCCTCAGAACT CAGGTCGTCC GT ACGGCCT GTTCT GGAA G
CCCAGGTCGTCCAC AC || ||||| |||| |||
 CA TGCTGGA CAAGA CCTT /
 CC CCCT CT C

GAM2154 GTGGACTTGTCTGAAACTT 2140 TAGAATGTCT 4865 G - CT A T AG TAG
TCTGAGAGATTAGACAACAT TGAGATATAG GTG ACT TGTC GA AC TTCTG AGAT A
TTATAGAATGTCTTGAGATA TACA ||| ||| ||| ||| ||||| |||
TAGTACAC CAC TGA ATAG TT TG AAGAT TTTA C
 A T AG C T A- CAA

GAM2155 GAATTTTGTGTTGGTGCAAG 2141 TCTGTGTATC 4866 T ----- - TA A
ACTTAAGATATTTATTTATA AATTCTGACA GAATT TGTGT TGGTGCA AGACT AGAT T
GTCTGTGTATCAATTCTGAC CATG ||||| ||||| ||||| ||||| |||
ACATGATTC CTTAG ACACA ACTATGT TCTGA TTTA T
 T GTCTTA G TA T

GAM2156 GGTCGTGTAGCGCGATAGAG 2142 TTAGATATCA 4867 C A C GA- G AAT
ATAGTCTAATATTAATATTA GATATCCGTA GGT GTGT GCG GATA GATA TCTAATATT A
GATATTAGATATCAGATATC ACAC ||| ||||| ||| ||| ||||| |||||
CGTAACACTACC CCA CACA TGC CTAT CTAT AGATTATAG /
 T A - AGA - ATT

GAM2157 GTCGAGGTAGTCTCATCACC 2143 CGAGGTAGTC 4868 - AG- TC CC TT
AGGTTTATACACCTTGATGA TCATCACCAG GT CG GTAG TCATCA AGGT A
ATCTACATGCGTAC GTTT ||| ||||| ||||| |||
 CA GC CATC AGTAGT TCCA T
 T GTA TA -- CA

GAM2158 GTGATTCATTTGGCATAGTA 2144 TATTATGTAA 4869 - TTG CG TA-- CAT AC A
CGTACTATATCATCGAACTG TATGGTGTTA GTGAT TCAT GCATAGTA TAC TAT CGA
TGTAT A
TATAACGGTGCACTTTGTAA C ||||| ||||| ||||| ||| ||| ||| |||||
ATAGCCTGTATATATTATGT CATTG GGTA TGTATTAT ATG ATA GTT ACGTG C
AATATGGTGTTAC T TAA AT TCCG AAT CT G

GAM2159 TGAGAGAGTACTGGTTTCAT 2145 GAGAGTACTG 4870 T T TTTCTACTAAA ATG

GTTTCTACTAAAGAATGCAA GTTTCATGTT TGAGAGAGTAC GGTT CATG GA C
 ACTCGTTATTTTTTTTATGA TCTA ||||| ||| ||| ||
 ACTTGTA CTCTTTCA ACTTTCTCATG TCAA GTAT CT A
 T - TTTTTTTATTG CAA

GAM2160 TGTTACTGAATTTAATATAT 2146 T TACTGAATT 4871 - -- AT-- GA
 GTATGAGATGATCCAAGACG TAATATATGT TGTTACTGA ATTTAAT ATATGT GA T
 TGTTTGTTGAGTATCGGTGA ATGA ||||| ||||| ||||| ||
 TA ATAGTGGCT TGAGTTG TGTGCA CT /
 A TT GAAC AG

GAM2161 AATAGGTAATATATATCTTT 2147 TAGGTAATAT 4872 ATATA TTTT C- TATT
 TGCCGTATCTATTATACCTG ATATCTTTTG AATAGGTA TATC GC GTATC A
 ATATAAGCGATATACCTATT CCGT ||||| ||| || |||||
 TTATCCAT ATAG CG TATAG T
 ---- AA TCCA

GAM2162 AATGTTGCTGCTAAACCACA 2148 TTGCTGCTAA 4873 - CACATGTCA AT
 TGTCATCTAATAACTGGAT ACCACATGTC AATGTTGCTG CTAAAC ATCTA A
 GTTTGGATAGTAGCGTT AATC ||||| ||||| |||||
 TTGCGATGAT GGTTTG TAGGT /
 A ----- CA

GAM2163 ACTATACTTTGGTAGGTGGA 2149 TTTTCATATAA 4874 A TG T GG C T AA---- CGT
 TACGATATATTATAAAGATC TTTCTGAAGG ACTAT CTT G AGGT ATA GA ATATTATA GAT
 A GTAAATTGTCAACATGTATA TAGT ||||| ||| ||||| ||||| ||||| |||
 ATATTTTCATATAATTTCTGA TGATG GAA C TTTA TAT CT TATAATAT CTG A
 AGGTAGT - GT - A- A T GTACAA TTA

GAM2164 CATAGGACAAACGGCAGTGA 2150 CGGCAGTGAA 4875 AC--- GAA----- G - ---- C
 CTT-- G
 AATGTGATGATCTTGGGCAG ATGTGATGAT GGCAGT AT TG ATGATCT TGGG
 AGGA GTC A
 GACTTGTCGAAAGGCTTTTC CTTG ||||| ||||| ||||| ||||| ||||| |||||
 TCCTACCTATAACCAGATCA TTGTCA TA AC TACTAGA ATCC TCCT CGG A
 TACAGATGAAGACCAACAAC ATATT ACAACCAGAAG G A CCAAT A CTTTT A
 TGTTTTATAGTGCCCTATG

GAM2165 CGAATGTATAAGGAGGTTGC 2151 TATCCATATG 4876 AA -- T CAACA TTA CT- AT--
 TC TA
 TGCAACACTTTAGATTCTAT TCTCTATATT AT GGA GGT GCTG CT GATT ATCCAT GTC
 TATATTC T
 CCATATGTCTCTATATTCTA CTAT || ||| ||||| || ||||| ||||| ||||| |||||
 TATGAATATATGACTTACAT TA CCT TCG TGAC GA CTGA TAGGTA CAG
 ATATAAG /

GGATCATAGTCAGGCCAGTC
GCTTTTCCAAATATCTTCG

AA TT C CG--- --- TAC CATT T- TA

GAM2166 GGATACATTTCCATGTATCT 2152 TACATTTCCA 4877 -- ----- CT- TCT- TTT
ATCTAACTCTGATTCTTTT TGTATCTATC GGATACA TTTCC ATGTATCTAT AAC GA
C

CCCATGTTTGTGTAGATACA TAAC ||||| |||| ||||| ||| ||
TCATTAGTTATCGGAGACAT CTTGTGT AGAGG TACATAGATG TTG CT /
GTGTTG AC CTATTGATTAC TGT TACC TTT

GAM2167 GGTGTTGAGTATTATGAGCC 2153 TGAGTATTAT 4878 -- T-- - ATTGA A T
ATTGAATATGTCCACAAGTG GAGCCATTGA GGT GTTGAGTATTA GA GCC AT TG C
AAGGGTATCCTTTGATACTC ATAT ||| ||||| || ||| |||
AACAGGCC CCG CAACTCATAGT CT TGG TG AC C
GA TTC A GAAG- A A

GAM2168 GTCAAACTCTATGTGAATT 2154 TGTGAAAGTT 4879 CTAT AT AG ATA GG T--
GGGG
CAAGGATTATATTTACAGGA TCTGGTCTTA GTCAAACT GTGA TCA GATT TTTACA ATGA
AGTTGG A
TGATAGTTGGGGGGATAACA CTGG ||||| ||| || ||| ||||| ||| |||||
CCAACCTCTTCATATGTGAA CAGTTTTGG CATT GGT TTGA AAGTGT TACT
TCAACC T
AGTTTCTGGTCTTACTGGTT T--- CT CT --- A- TCT ACAA
TTGAC

GAM2169 TATATCGAAGATAGGTAGAT 2155 TATCACATTC 4880 A TA--- T A- AT
ATGGAAGTTGATCCACCAAC TTATCTACGA TATATCG AGATAGG GATA GGA GTTG C
GATCTTATCACATTCTTATC TATA ||||| ||||| ||| ||| |||
TACGATATA ATATAGC TCTATTC CTAT TCT CAAC C
A TTACA - AG CA

GAM2170 TCTCCCTAGCCATGTAGGTT 2156 TTGCTTAAAG 4881 TAG- - AG G -
ACCAAGAACCA TG
TGCTTAAAGAAGCCACCAAG AAGCCACCAA CCC CCAT GT GTTT CTAAAGA AGCC
TTTTTCTGCTT A
AACCATTTTCTGCTTTGAC GAAC ||| ||| || ||| ||||| ||| |||||
AGGGCAGGAAGAAATAAAGG GGG GGTA CA TAGA GAGTTTTT TCGG
AGAAGGACGGG /
CTATTTTGTAGGAGATTGAC TAAG A GT G A AAATAA----- AC
AATGGGAATGGGGGA

GAM2171 TGATACCAGGAAGCACGAAT 2157 TGAGGTTTAC 4882 A T T-- AT AA CC AATCC
AAAGAA
CACATGAGGTTTACATTGCT ATTGCTAAAT AGCACGAA CACA GAGGTTTAC TGCT AT TTTG
GGATG T
AAATCCTTTGAATCCGGATG CCTT ||||| ||| ||||| ||| || ||| |||||

AAAGAATAATGAAATATCCA
CCTAT A
GCAAGAATGAAGTACGTGGA
TTTCCTTTGTGTTTGTGTTG
CCGAGGCCCG
GAM2172 TGATGAGGAAATAATGGCCA 2158 TGAGGAAATA 4883 ATG- -- AA ACCA G
CCACTTTTGAGCCATTAAAA ATGGCCACCA TG AGGA AAT TGGCC CTTTGA C
GATAGGGCTGAGATTACTCC CTTT || ||| ||| |||||
TACCGCA AC TCCT TTA GTCGG GAAAATT C
GCCA CA GA GATA A
GAM2173 TGTCAACCAAGCTAATAGAG 2159 GGGAAAGTGA 4884 - CT- TA G - CAA CAAT G
C CAAT
GCTTCCACTTCAATCTTATC GGGGTGTCCT CCA AG AA GA GCTTC CACTT TCTTATC GCA
CAA AAGAG T
CAATGCAGCAACAAGAGCAA TTCT ||| || || ||||| ||||| ||| ||| |||||
TTTCAACTCTTTTGTGTT GGT TC TT CT TGGGG GTGAA GGGATAG TGT GTT
TTCTC /
ATGATAGGGAAAGTGAGGGG C TTC TC G A A-- TAT- A T AACT
TGTCCTTTCTTCTCTGGTAG
ACA
GAM2174 AGATGGAATCCCCACCTAGG 2160 TCACCGGATT 4885 ATCCCCACC T- TTA
TATGATTCT - ATT
TGTTATAAAACATATTATTG GTGTTTTCTT TAGGTGTTA AAAACATA TTGGT GGATA
GTT T
GTTATGATTTCTGGATAGTT AATA ||||| ||||| |||| |||||
ATTTTGTAACATGTTTTAC ATTCATAAT TTTGTGT GGCCA TTTGT CAA T
TCTTTTCACCGGATTGTGTT ACAACAA-- TC TA- CTTTCTCAT A ATG
TTCTTAATACTTAAACAACA
TCCGTACT
GAM2175 GAGGTTTCATGACAAAATTCC 2161 CATGACAAAA 4886 T AAAT - TGTATTAT- -----
TTAACT
TACTGTATTATGTACGATGG TTCCTACTGT GAGGT CATGACA TC CTAC GTACGA
TGGATT A
ATTTAACTAGCACATGATT ATTA |||| ||||| ||||| ||||| |||||
CATTAGTATCGTACTCGTTT TTCCA GTATTGT AG GATG CATGCT ACTTAG /
TTCGTAGAGACATGTTATGT T AC-- A CTTTTTGCT ATGATT TACACG
ACCTT
GAM2176 GATGTGTGGCGGAGGTTGCG 2162 CACGGGGAAC 4887 GCGGA - GTCATTTCA- TC
GTCATTC GT
GGTCATTTCACTTTGTGTCA TTATTCATCG TGTGTG GGTTG CGG CTTTGTG ATTGTC
GTTT T
TTGTCGTCATTCGTTTCGTTT TCAA |||| ||||| ||||| ||||| |||||
GGAACACACAGATAGTTCAC GCACAT CTAAC GCT GGGGCAC TGATAG
CAAG /
GGGGAAC TTATTCATCGTCA AG--- T ACTTATTCAA T- ACACA-- GT
ATCGATACACGTC

GAM2177 GGAACATCTTAAACTGATAA 2163 AACACGGTTA 4888 TTAAACTG--- - AT
TCTGTTAGATTTTCTAACAC TAATTACACC GGAACATC ATAATC TGTTAG T
GGTTATAATTACACCTCGGT TCGG ||||| ||||| |||||
GTTCC CCTTGTGG TATTGG ACAATC /
CTCCACATTAA C TT

GAM2178 TACCTGAAAAAGAGTGAGTG 2164 TGAGTGATTT 4889 T AA T T TTTATTAAA TG
ATTTATTAAAGAGACGTGTA ATTAAGAGA TACC GAA AGAG GAG GA GAGACG T
TCCGTTTTTCTTTCTTCTGG CGTG ||||| ||||| ||||| |||||
TTCTGGTA ATGG CTT TCTT CTT CT TTTTGC A
T GG - T ----- CT

GAM2179 TCGTTTTTCATTTTGT TTTTGT 2165 TGATGAATTC 4890 TT TTTT T CCCATTT
ATTCCAATAT CC
TTTTTATATCTTGCCCATTT CAATATAACG TTTG TTG TATA CTTG GATGATGA
AACGTCTT T
GATGATGAATTCCAATATAA TCTT ||||| ||||| ||||| ||||| |||||
CGTCTTCCTTAGAGACGTTT AAGC GAC GTAT GAAT CTGCTGCT
TTGCAGAG /
ACCTCGTCGTCTTTAAGTAT TT TTATT - TT----- CCAT----- AT
GTTATTCAAGTTCGAAATACG
A

GAM2180 AGAATCTGAATAAGTAACGT 2166 TAAGTAACGT 4891 TCT T GT- T CCCT TCCAC
TGTTTATACCTTTACATAT TGTTTATACC AGAA GAA AAGTAAC TG TTATA TTACATA C
CCACCTAAGTTTGTGTAATA CTTT ||||| ||||| ||||| ||||| |||||
TTTATAGTTATTAGTTATTT TCTT TTT TTTATTG AT GATAT AATGTGT T
CTTTTCCTTCT CCT C ATT T TTAT TTCAA

GAM2181 GAAACTATAGCAGTTGCCTC 2167 TCACAGAGGT 4892 ACTA C TT TTT G
TTTTTGAGATGCAAATCTCA TCTTCTAGTG GAA TAG AG GCCTCT TGAGAT C
CAGAGGTTCTTCTAGTGTTT TTC ||||| ||||| ||||| |||||
CTT ATC TC TGGAGA ACTCTA A
GTG- T T- C-- A

GAM2182 GAGTGTGAGATACCCAACCA 2168 TGAGATACCC 4893 A- ACCCAACCA T TAG
TGTTTTGATAGACTTTCAAC AACCATGTTT GAGTGTG GAT TGT TTGA A
ACAATCAACACATTC TGAT ||||| ||||| ||||| |||||
CTTACAC CTA ACA AACT /
AA ----- C TTC

GAM2183 GCTATTAAACCTAATACAAA 2169 TTATAGTGAT 4894 T ACC AAT A- A A A
TATAAAACAAATTATTGATA GATGTTTTGT GC ATTAA TAATACA ATAAACA ATTATTG
TAGTA A
GTAAAATTATTATAGTGATG TGTG ||||| ||||| ||||| ||||| |||||
ATGTTTTGTTGTGTGTTATA TG TGATT ATTGTGT TGT TTTTGT TAGTGAT ATTAT A

T GAT GT- AG - T

A

TGTA || ||| ||| ||||| ||||| ||||| ||| |||
 TA TAA TGT TTAAG AAC.
 A TTA- ---- C - CTT AC TT

GTTGCGATGAT GGTTTG TAGGT /
A ----- CA

GTGG TCTGG T
GGATTCTGGTTCACCAGGCG CCTC
TCGCCATTTTATAGTAGTTGC
GGACC C
ATATCACTGATGGGTACCTC
CTCC ATGGG TAGT CT TA GTT AT AT TTTA CGCT
- CA A C G G T C-- GC A

TC |||| ||||| || |||| |||||
CTAT TTTGC TT ACGA TATTA T
T- A C TAA TTTTCT

ATCTATATTAACACTTGCTA TGCTAATCTG GCG TAT AACAGATTA CA TATT ACTT C
 TTTCTCTACCCTCTGAAGTC TTTA ||| ||| ||||| || ||| |||
 AATGCCTTTGCTAATCTGTT CGC ATA TTGTCTAAT GT GTAA TGAA /
 TATAGACGC AG T- C TTCC C-- GTCTCCCAT

TTATATCTTTTACAATACTA ATAGTCGATT GGATATGT ACA AATAG GATTA A
 TTAGTCCCTATTGTGTTATC ATAT ||||| ||| |||| ||||
 TATATATCC CCTATATA TGT TTATC CTGAT C
 TCTAT G C- TATCATAA

AA CCTGT- C ---- T

TGTTAGCATTAGCAAAATTT	CCTGTTAGCA	GTGTCGGATG	CTAGTT	TAGCATTAG AAA
ATTTC T				
CTTCAGAAGTATCGTTTACT	TTAG			
AATGTTATTCTAAAACTAGC		CACAGTCTAC	GATCAA	ATTGTAATC TTT TGAAG C
ATCTGACAC	--	AATCTT	A GCTA	A

GAM2191 GTGTCTGAATCGTTTCGATTA 2177	TGAATAGAGT 4902	TTCGATTAACCC	- C T
ACCCAATCATCCATTTTCA	TATCGATTCA	GTGTCTGAATCG	AACTC AT CATT T
GATGAATAGAGTTATCGATT	GACA		
CAGACAC	CACAGACTTAGC	TTGAG TA GTAG C	
	TA-----	A A A	

GAM2192 TACCTGATTACTATCACATC 2178	TATCACATCT 4903	GA TA-	TCT- CG A- A
TTCCGTTACAACCTTAGACAA	TCCGTTACAA	TACCT TTAC TCACA	TC TTACA CTT G
GCCTGTAAATGATTATTGTG	CTTA		
AGATGTAAAGGTA	ATGGA AATG AGTGT	AG AATGT GAA A	
	-- TAG	TATT TA CC C	

GAM2193 TCTAATGGAAGTTTTGATAG 2179	TAATGGAAGT 4904	AGTTT	A - TC
GAGATTGTCATCAGTTGATA	TTTGATAGGA	TCTAATGGA	TGATAGG GAT TGTCA A
CATTGTTTATTATCTCATCT	GATT		
ATTAGA	AGATTATCT	ATTATTT TTA ATAGT /	
	ACTCT	G C TG	

GAM2194 TTTTTCTTAGTACAAAAGTC 2180	TAAAACTTG 4905	- AAAG-	AT--- AAAA AA
AATGTTTTTAAATATATGGA	TGTGAAATTA	TTTTTCTT AGTACA	TCA GTTTT
TATATGGACGAG T			
CGAGAATTAATTTGTCTGTA	TGTA		
TAAAACTTGTGTGAAATTA		AAAAAGAG TCATGT	AGT CAAAA ATATGTCTGTTT T
TGTACTAGAGAAAAA		A ATTAA GTGTT	---- AA

GAM2195 GCAGTATTTGTAACTTTGT 2181	TTAGGTCTGT 4906	A TT-	TGT- AAAT A G
TTAACGAAATGATCATGGTA	TAATTATAAG	GCAGT TTTG AACTT	TTAACG GATC TGGTA A
GAAATATTAGGTCTGTTAAT	TTCG		
TATAAGTTCGTTAAAAATTG		CGTTA AAAT TTGAA	AATTGT CTGG ATTAT A
C	A TGC	TATT	---- - A

GAM2196 TAGGCACGTTTGGGTAACCTT 2182	TTGGGTAACCT 4907	C--- - T -	AAATATTA
TGTATT			
TTTTTAAAAATATTAACGTG	TTTTTTAAAA	TAGG	ACG TT GG GTAACCTTTTTTTAA ACGTGC
A			
CTGTATTACATCTTGTATGT	ATAT		
AAACGTTAAAAGAAAGTTACA		GTCC	TGC GA TC CATTGAAGAAAATT TGTATG /
CTTAGCCGTTTTCCCTG		CTTT C T A	GCAAA--- TTCTAC

GAM2197 TATTGTAATTTTTTAATTGA 2183 TCAACTCCTT 4908 G A TAT- ACGCC TT TAA
TATGGAGTTACGCCATATTT CTTCAATCAA TATT TAATTTTTT ATTGA GGAGTT ATAT GT
C
GTTAACGTTATTTATATCAA AAAG ||| ||||| |||| |||| ||| ||
CTCCTTCTTCAATCAAAAAG ATAG ATTGAAAAA TAACT CCTCAA TATA TA /
TTAGATA - C TCTT C---- TT TTG

GAM2198 TCCAAGAAGAAATTAATAAT 2184 TAACCTTAAC 4909 ----- AAT TC CTTAACA TC- A
TGCACAA
CTAACCTTAACACCTCTATT ACCTCTATTA A AGAAGA TAATAA TAAC CC TATT
ATAGT A
AATAGTTGCACAAATAATCT ATAG | ||||| ||||| ||| || |||||
CATTATAAATATCTGGCCAA T TCTTCT ATTATT GTTG GG ATAA TATTA /
TACGTTGTTTTATTATCTTC ATTATTC --- TT CATAACC TCT A CTCTAAT
TCTTATTATGGG

GAM2199 TGATCATTTTACAAACTTTT 2185 TTGATACTAT 4910 TTTTA C T -- TGCT ATCATA
AA TACAT
GTTGATACTATGCTTATTAT GCTTATTATA CA CAAA TTTTG TGA TACTA TATTAT AATT
ACG T
ATCATAAATTAACGTACAT TCAT || ||||| ||| |||| ||||| ||| |||
TGCACCCGTAAAATTCTTCG GT GTTT AGAAT GCT ATGAT ATAATG TTAA TGC
/
CGTAATATCTTTAGTAATTC TGCTG - T TA TTCT CGCTTC AA CCACG
GTTAAGATTTGGTCGTTGAT
CA

GAM2200 AAATAGATGTTTCGTTGTAT 2186 TTAAATGACG 4911 TTTCGTTG A A G TCAATA- T T
AA- AT
ATAGTACGATAGTTAATATC AACTATATGT TG TATATAGT CG TA TTAATA AC CC
TTGGAT TAG A
AATAACTCCTTTGGATAATA TCAT || ||||| ||| ||||| || ||||| |||
GATAATCTAAAGATTCAACG AT GTATATCA GC GT AATTAT TG GG AACTTA
ATC /
GCGTCAAAAATTATTAATG TACTT--- A A A TAAAAAC C C GAA TA
ACGAACCTATATGTTTCATTAT
CTATTT

GAM2201 AAATGAGTATTTTCTTTAA 2187 TAGGACACGT 4912 -- CTTTAAC T- C GATC- -
AA GTT
CTGGTTGACACGATCCGTGT AACAGTATCA TG AGTATTTTT TGG TGA AC
CGTGTTCTAAT CG GAG G
TCTAATCGAAGAGGTTGGCA TTCC || ||||| ||| ||| ||||| || |||
TTCCGCATTAGGACACGTAA AC TTATGAAGA ACC ACT TG GCACAGGATTA GC
CTT /
CAGTATCATTCOAAGAAGTA CT ----- TT A ACAAT C -- ACG
TTTCCATTT

GAM2202 GGATATTTTAGCTCTGGTAT 2188 TATTTTAGCT 4913 T- CT G TCATATA C AATT---
TG

ATCATATATCCAAGAATTTG	CTGGTATATC	GGATAT TTAG CT GTATA	TC AAG	TGTACA
T				
TACATGTATTGTACGCTATA	ATAT			
ACCTTTGAACTTCTATACGG		CCTATA AGTC GG CATAT	AG TTC	GCATGT /
GGA CTGATCATATCC		CT AG G	CTTCA-- T	CAATATC TA

GAM2203 TGAGAGAGTACTGGTTTCAT 2189	GAGAGTACTG 4914	T T TTTC C A A GC
GTTTCTACTAAAGAAGGCAA	GTTTCATGTT	TGAGAGAGTAC GGTT CATG TA TAA GA G A
ACTCGTTATTATTTTTATGA	TCTA	
ACTTG TACTCTTTCA		ACTTTCTCATG TCAA GTAT AT ATT CT C /
	T -	TTTT T G - AA

GAM2204 TTGTCTATATGATACACAAA 2190	TATGATACAC 4915	T T C-- - T T- TT TA
TTGTTAGTTATTGTATATAG	AAATTGTTAG	TTG CTATA GATA AC AAAT GTTAG TA GTA T
TTACCTTACCCTAATTGTTT	TTAT	
AGTCATTGTCTATAGTTAA		AAT GATAT CTGT TG TTTG TAATC AT CAT A
	T -	TAC A T CC TC TG

GAM2205 TTTGATTCTACATATTTCAA 2191	TCTACATATT 4916	- AC ---- T-- -- AAT
TGTGTGGAAATCTAGTCCAC	TCAATGTGTG	TTTGATT CT ATATT TCAA GT GTGGA C
TTGCCTCTTGATCACAATAT	GAAA	
ACAGAAATCAAA		AAACTAA GA TATAA AGTT CG CACCT /
	A CA	CACT CTC TT GAT

GAM2206 TTTTTTTACGATTGTAGCAG 2192	TGCTATGGTA 4917	T G A AATCTT GCGAATTA T- G A AA
TTTATGGAAATCTTATCATG	TCTAGGAAAT	AT GTAGCA TTT TGGA ATCAT CT ATACC
ATAG TATC C		
CGAATTACTTATACCGATAG	GATT	
ATATCAACTCGATGCTATGG		TA TATCGT AAG ACCT TAGTA GA TATGG TATC
GTAG /		
TATCTAGGAAATGATTCATC		- - A ACT--- AAG----- TC - - CT
CAAGAATGCTATATTGTTTA		
AGAA		

GAM2207 ACCGATCCAACGTGTCTTGC 2193	TATCTCGTCG 4918	--- ACGTGTCT T TT- TCATA
CTGACGACTTGTATATCATA	TTGGTATAAA	ACCG ATCCA TGCC GACGAC GTATA C
CTCGTTTTATATCTCGTCGT	AAAA	
TGGTATAAAAAAATGGATAC		TGGC TAGGT ATGG TTGCTG TATAT T
GCGGT	GCA	AAAAAAT - CTC TTTGC

GAM2208 CGGCGCGGCTTTTCCAATGC 2194	TGTCACGTAC 4919	TT-- CAA TGAA - AT
TGAAGATAGTCCATTGTGGA	GAATTTTGCC	CGGCGCGGC TTC TGC GATA GTCC T
CATGTCACGTACGAATTTTG	GCGT	
CCGCGTCG		GCTGCGCCG AAG ATG CTGT CAGG /
	TTTT C--	CA-- A TG

GAM2209 GACGGAGAGTCCTCCTCCGA 2195 TGTGGTAAGT 4920 TCCTCC --- G GT---- CTT AT
AAA-- GGT

CGATCGTGTGGTAAGTACTT ACTTCCGATC G TCCGACGAT CGT TG AAGTA CCG
CACG CC T
CCGATCACGAAACCGGTTAG ACGA | ||||| ||| || |||| ||| ||| ||
AAACGATTCGTCGTTTTCGT G GCTGCTAGA GCT CT CATGC CTT GCTG CA
A
CGTACTCGTATTCCTCGCTA ----- ATC C TATGCT TG- TT CTTAG AAG
AGATCGTCGGGCTGCTCCG

GAM2210 GATCGCCTATGGCGCGTTTA 2196 TCGCCTATGG 4921 CG ----- TT A
CGTATGTACGTCACGCGTTT CGCGTTTACG GAT CCTATGG CGCGT ACGT T
ACTCCATAGGGTGTC TATG ||| ||||| |||| ||||
CTG GGATACC GCGCA TGCA G
TG TCATTT C- T

GAM2211 GATTCCGACTCGTACGCCGA 2197 ATCACCTGGT 4922 C CGT GC GT A C GTA
GTCAGGAGACTCGTATTAG TCGTAGTAGT GATTC GACT AC CGA CAGG GA TC T
AATCACCTGGTTCGTAGTAG CAGA ||||| ||| ||| ||||| |||
TCAGAATC CTAAG CTGA TG GCT GTCC CT AG /
A --- AT TG A A ACT

GAM2212 GTTGTGCGTTTCGTTGTAGA 2198 CGATATCTCG 4923 - TTTC T CG A GTC
CGTATCGGAACGTCCATAGT ACACGCGCAC GTTGT CGC GTTG AGA TATCGGA C C
CCGATATCTCGACACGCGCA GAC ||||| ||| ||||| ||||| |
CGAC CAGCA GCG CAGC TCT ATAGCCT G /
C CA-- - - -ATA

GAM2213 TCGGGCGAGGTAAAGTCTCC 2199 CGAGGTAAAG 4924 -- AAA--- -- AAACAG GAT
ATTAAACAGACGATAGAAGT TCTCCATTAA TCGGGC GAGGT GTCTC CATT AC A
AATCCGAGTGAAGAGATAAA ACAG ||||| ||||| ||||| ||| ||
ATAACTTTATGCCCGA AGCCCG TTTCA TAGAG GTGA TG /
TA ATAAAA AA GCCTAA AAG

GAM2214 TCGTCCGTACACGGAAACAG 2200 CACGGAAACA 4925 C AC- ACA C-- A TC- TA
TCGATCGCAGTAATCGACGT GTCGATCGCA TCGTC GT ACGGAA GTCGAT GC GTAA
GACG A
AATCCGTTTTCTTATCGTTC GTAA ||||| ||| ||||| ||| ||||| |||
AGTCGATGTATTCCGTTAAA AGTAG TA TGCCTT TAGCTG TG TATT TTGC /
TCGATGA C AAT ATG ACT C CTT CT

GAM2215 AACAGATTACCATCTATATT 2201 TCAATGCCTT 4926 C TCTA AAC GCTATTTCT
AACACTTGCTATTTCTCTAC TGCTAATCTG AACAGATTA CA TATT ACTT C

CCTCTGAAGTCAATGCCTTT TT ||||| || ||| |||
GCTAATCTGTT TTGTCTAAT GT GTAA TGAA /
C TTCC C-- GTCTCCCAT

GAM2216 ACCTATAATGTATATGTATT 2202 TATTGCATCG 4927 ATA AT- TTG A- ACAC
GATCGAATACACACATGCCG GGCATATCAG ACCT ATGT ATGTA ATCGA TAC A
TAGCTCGATATTGCATCGGG GT ||| ||| |||| |||| |||
CATATCAGGT TGGA TACG TACGT TAGCT ATG /
CTA GGC TA- CG CCGT

GAM2217 CGCAGTTGATCTAACCTGTT 2203 TGACCAGTTA 4928 TGAT CTGT AG
GGTTAATAGCCTGTTGACCA GTAACATTGC CGCAGT CTAAC TGGTTAAT C
GTTAGTAACATTGCG G |||| ||| |||||
GCGTTA GATTG ACCAGTTG /
CAAT ---- TC

GAM2218 GATGACTGTCGTTAGATGTA 2204 TCACCGTTTT 4929 G GT-- ----- TA T ATC
TAGTTGGCTATCCATAAGTC TAACACGTCT GATGACT TC TAGATGT A GT GGCT C
ACCGTTTTTAAACACGTCTAT ATTA ||||| || ||||| | |||||
TAAGAGGTCGTC CTGCTGG AG ATCTGCA T CA CTGA /
- AATT CAATTTT GC - ATA

GAM2219 GTACTTATTAATCATTTGAC 2205 TTATATGGTT 4930 ACT TAA T CT A CTAT G
TCTGCCAAATAATAGGTCTA AGTCAGTGAG GT TAT TCATT GACT GCCA ATAATAGGT
TGTTCT T
TTGTTTCGTAAGAACATAATC CATA || ||| |||| ||| ||| ||||| |||||
TATTATATGGTTAGTCAGTG CA ATA AGTGA CTGA TGGT TATTATCTA ACAAG A
AGCATATGAC GT- CG- - T- A AT-- A

GAM2220 GTGTCGGATGAACTAGTCCC 2206 TGAAGTATGTC 4931 AA CCCTGT- -- A -- T
TGTTAGCATTAGAACAATTT CCTGTTAGCA GTGTCGGATG CTAGT TAGCATTAG AAC AT
TTC T
CTTCAGAACTATCGTTTACT TTAG ||||| |||| ||||| ||| ||| |||
AATGTTATTCTAAACTAGC CATAGTCTAC GATCA ATTGTAATC TTG TA AAG C
ATCTGATAC -- AAATCTT AT C TC A

GAM2221 ACAGATTACCGACCCATAAA 2207 TTTCACACTG 4932 C AT- TTTTAAT G C
CA- AC
GTTTTTAATTATGCCACTCT TAAAGAATGG CGACCC AAAGT TAT CCA
TCTTTACAGTGTGAAATCATG GA T
TTACAGTGTGAAATCATGCA GGTA |||| |||| || ||| ||||| ||||| |||
GAACATAACACATGATTT GTTGGG TTTCA ATG GGT
AGAAATGTCACACTTTAGTAC CT /
CACACTGTAAAGAATGGGGT T ATC ----- G A ACA AA

AACCTTCTAGGGTTGTTAAG
CTGT
GAM2222 CACCCGCTTGCGCAGTTAAG 2208 TTAATCCATA 4933 TG -- AG AGA GT G --- CA TAA
G AA GTA
AGGTAGTGGTGTTAATCCAT AATAAATTAT C GC TTA G A TGGTGT TAATC TAAA ATTAT
TA CA G
AAATAAATTATGTAAACAGT GTAA | || ||| | ||||| |||| |||| |||| ||
AGTAGTGGGTGAGTAGTGTT G TG AGT C T ATTACA ATTGG ATTT TGATG GT GT
/
TTAGAGGTTATTTACATTAG GT TA G- GGA TG G TTT AG TG- A GG GAT
TGTCAGGTGAGGTATGTGAG
TCGATTGGTG
GAM2223 GGGGGGTGCAGTACTATTAC 2209 TGCAGTACTA 4934 GG ATTA TTT TTTG
TCTTTACTTTGTTGTTGTTT TTA CTCTTTA GGG GTGCAGTACT CTC AC T
GAGGAGTATTGCACAACCC CTTT ||| ||||| ||| ||
CCC CACGTTATGA GAG TG /
AA G--- TT- TTGT
GAM2224 GG TAGGATTAGTGGGGGGTG 2210 TTGCACAACC 4935 AG TT - -- TT TAT TG
CAGTACTATTACTTATTATG CTCATCTTTT GGT GA AG TGGGGG GTGCAGTACTA ACT TA C
CTATTATTTAGTTAGTATTG TAGG ||| || ||||| ||||| ||| ||
CACAACCCTCATCTTTTATG CCG TT TC ACTCCC CACGTTATGAT TGA AT T
GCC GA TT T AA -- TTT TA
GAM2225 GTTAAAAGAAATAGCAAGTC 2211 AAAGAAATAG 4936 A A GC - TATT AAGT GT
AGATATTGCCAAGTTTAACA CAAGTCAGAT GTTA AAGA ATA AAG TCAGA GCC TTAACA A
GTAACATGTTAGTGAGGTTT ATTG ||| ||| || ||||| ||| |||||
TTGATCTTCATGTATCTTAT CAGT TTCT TGT TTC AGTTT TGG GATTGT A
GAC A A AC T T--- AGT- AC
GAM2226 TTAACAACATTAGGAACGAA 2212 CTTGCACAGT 4937 A TT TC-
TTAATTG
AAGATTTAAGTCTGCAAGGA TTATTCTTTT TTAACA CATTAGGAACGAAAAGA TAAG
TGCAAGGATACTACAAA T
TACTACAAATTAATTGTGGT TGTT ||||| ||||| ||||| ||| ||||| ||||| |||||
GACCTTTTGTAGTATCCTTG AATTGT GTAATTCTTGTTTTTCT ATTT
ACGTTCCCTATGATGTTT G
CACAGTTTATTCTTTTGT T A T- GAC TCCAGTG
CTTAATGATGTAA
GAM2227 TTGTGTGTTGTGTTTGGGGT 2213 TATTCCAAAA 4938 T-- GG T G AC
GATAGACACATTGTATATTC ACACATTCCA TTGTGTG TGTGTTT GG GATA AC A
CAAAAACACATTCCACACAA CACA ||||| ||||| || ||| ||
AACACAC ACACAAA CC TTAT TG /
CTT AA - A TT

GAM2228 TTTTGTCTCTTACATTAGTT 2214 TAAGAATAAT 4939 C CATT C AATA CT -- AA
 ACTTCAATATAGACTTACTT TCCTAAAAGA TTTTGTCT TTA AGTTA TTC TAGA TACT TCA T
 CAAATCCTGAAAAGTACCTC CAAG ||||| ||| ||||| ||| ||||| |||
 TAAGAATAATTCCTAAAAGA AGAACAGA AAT TTAAT AAG ATCT ATGA AGT /
 CAAGA A CC-- - A--- CC AA CC

GAM2229 GAATCGCTAGGCGCAAACCA 2215 TTAGATCCTT 4940 GCT C C T T A CAA A
 ACT
 CTTGTTTATCATTTCOAAGA TAAGAAAGAT GAATC AGGCG AAA CAC TG TTATC TTTC GAAG
 ATCTGATC C
 AGAATCTGATCACTCCAAAG AGTC |||| ||||| ||| ||| ||||| ||| ||||| |||
 ATTAGATCCTTTAAGAAAGA TTTAG TCCGT TTT GTG AC GATAG AAAG TTTC
 TAGATTAG C
 TAGTCATGTGCTTTTGCCTC AC- - C T T - AA- C AAA
 AGATTT

GAM2230 GTGGAGCCTGAGAAGGTGTC 2216 TTGCTAGACA 4941 A TG GAAG A- T - GT
 TGAAATATGCTAACTGTAGA TTTGGGTACC GTGG GCC A GTGTCTG AATA GCTA ACT A
 AGTGTAGCTATTGCTAGACA AC ||||| ||| ||||| ||| ||||| |||
 TTTGGGTACCAC CACC TGG T TACAGAT TTAT CGAT TGA /
 A GT ---- CG - G AG

GAM2231 TTGTATGATCCTGATGAACT 2217 TGAGTTGTGT 4942 T C- GA T CAT C - TT
 AACTCACATTGCGAACTACT CAATGATCAT TTG ATGATC TGAT AC AACTCA TG GA ACTAC
 C
 TCTATGTAGTATCCCATCTG CAA ||||| ||| ||||| ||| ||||| |||
 AGTTGTGTCAATGATCATCA AAC TACTAG ACTG TG TTGAGT AC CT TGATG T
 A - TA -- - CT- C A TA

GAM2232 AAAATTAACAGCATCCTCCA 2218 TCACCTCTCA 4943 A - CCACAT GT T AAC TA
 C- AT
 CATAACTTGGTGCTTTGAAC CTACGCAGCT AAATTA CAGCA TCCT AACTTG GCT TG TG
 AGGTG AAGTG G
 TGTAAGGTGCAAGTGATGCA GTAA ||||| ||||| ||| ||||| ||| ||| ||||| |||||
 ACACCTTATCACCTCTCACTA TTTAAT GTTGT AGGA TTGAAT CGA GC AC TCCAC
 TTCAC C
 CGCAGCTGTAAGTTTTATAA - G ATATT- GT C ATC TC TA AA
 GGAGTGTTGTAATTTT

GAM2233 ACCCAACCAACCTCTAACAT 2219 TGTGCAAAAG 4944 -- - AACA G AA
 TGCGCATGGCAAAGTCGCGT AGAGTGTGGT ACCCAACCA AC CTCT TTGCGCATG C A
 GTGCAAAAGAGAGTGTGGTG GGTT ||||| ||| ||||| |||
 GTTGGGT TGGGTTGGT TG GAGA AACGTGTGC G G
 GG T GAA- - CT

GAM2234 AGATGCTTAACCCAATCCAA 2220 TTCATGCTTA 4945 A A-- CAA CAT A TCTT

AAGCACATAAAACACCTTCT	GATAACGGGT	AGATGCTTA CCC ATC AAGCA AAAAC CCT A
TATATTCAGGGTTTTTCATGC	AGGC	
TTAGATAACGGGTAGGCATC		TCTACGGAT GGG TAG TTCGT TTTTG GGA T
T	- CAA A-- AC-	- CTTA

GAM2235 CGAGGGCTAAAATCAGCGGT 2221	TAAAATAGCC 4946	AAA AGC-- C T
TGTTCTACCTTGGGTAAAT	ATCAGGATAG	CGAGGGCTA TC GGTTGTT TACC T
AGCCATCAGGATAGTCCTCG	TCCT	
	GCTCCTGAT AG	CCGATAA ATGG /
	--- GACTA A G	

GAM2236 CTCATAACATTTGCGAACCA 2222	TGCCAAGCAA 4947	CGAACCA ACCA - AGCACTAAAA
C - AG T A		
TTGGACCAACTCTACCAGCA	TTGTAGCTGC	TG TTGG ACT CTACC AGTT CA TTGC
GG CATC A		
CTAAAAAGTTCCATTGCAGG	ACCA	
GTCATCAACGATGCCAAGCA		AC AACC TGA GATGG TCGA GT AACG CC
GTAG /		
ATTGTAGCTGCACCAAGGTA	----- CAA- A	AACCACG--- T T AA - C
GAAGTAACCCAACAATTGTT		
ATGAG		

GAM2237 GACCTATTGTTGCCATTGCC 2223	AAGCAGGAGG 4948	CCT CCA C A A AAT
ACGACTCCTGCTACGCGAAT	TGTGTTAGGT	GA ATTGTTG TTG CACG CTCCTGCT CGCG T
TTGCACGTGAAGCAGGAGGT	TCAA	
GTGTTAGGTTCAACAATCTC		CT TAACAAC GAT GTGT GAGGACGA GTGC T
	C-- TTG T G A	ACG

GAM2238 GCAACAGCAGCATTAAAGGT 2224	TCAAAACCCA 4949	C G AAA ATCCA T
ATCCAATGGTACATCATCAA	ATGTGCTCTT	GCAA AGCA CATT GGT ATGG A
AACCCAATGTGCTCTTGC	GC	
	CGTT TCGT GTAA CCA	TACT C
	C - C-- AAAC-	A

GAM2239 GCCATCATTGTCCTTGATAT 2225	TATCAGAGGT 4950	CAT- -- - A ATATTCCA G - -
T C		
CAATTATATTCCAAATGGTA	AACAATGTTA	CATTGT CCT TGATATC ATT AAT GTA
CCAGCGT AG GGA A		
CCAGCGTAGTGGACACATCC	AGC	
CTCACGCTGGATACGATTAT		GTAACA GGA ACTATAG TAA TTA CAT GGTCGCA
TC CCT C		
AAGAATCGATATCAGAGGTA	AATT AT G C	GAATA--- G A C - A
ACAATGTTAAGC		

GAM2240 GCTAGCTCACGAACAGCCAC 2226	TAGCTCACGA 4951	- C ACA CA C GA-- A
ATTACCACCAAAGAGCAATG	ACAGCCACAT	GCTA GCTCA GA GCCA TTA CACCAAA GCA T
CTGCAACATTTGGTGCTAAA	TACC	

CTGGCGATCTGAGCATAGC

CGAT CGAGT CT CGGT AAT GTGGTTT CGT G

A - AG- CA C ACAA C

GAM2241 GCTTAGAGCCTAAGATCATG 2227 TAAGACACGG 4952 AAGATC C-- TC G A A T C-----
---- TC

GCTGAAATCATGCGTATCAT ATTTTCAACA ATGG TGAAA AT CGT TC TAT GGG
AGTGC T

ATTGGGCAGTGCTCTATCGC CCAT |||| |||| || |||| |||| ||||
ACTTTGGGTAATCCCAACCC TACC ACTTT TA GCA AG ATA CCC TCACG A
ATAAGACACGGATTTTCAAC ATAAC- ACA -- G C A - AACCCCTAATGGGTT CT
ACCATCAATAAGGTTCTTAA
GC

GAM2242 GCTTGCAAAAATCCCACATT 2228 TTCAAGCACT 4953 AAA T ATTA AC ATAA
CCGCCAT CTA

GTATTAAGACCAAGTGATAAA GCTGGGACACT GCTTGCA ATCCCACA TGT AG CAGTG AAGA
ATG C

AGACCGCCATATGCTACCAC GTGG ||||| ||||| || || |||| |||| ||||
CATCAATCTCTTCAAGCACT CGGATGT TAGGGTGT ACA TC GTCAC TTCT TAC

/ GCTGGGACACTGTGGGATTGT --- C GG-- -- GAAC CTAAC-- CAC
AGGC

GAM2243 GGCTTGAAGTTGTGGATAAA 2229 TGAAGTTGTG 4954 CT-- A----- CT TTT-
ATCCTTA

ATGTCTGGAGTTTATGATCC GATAAAATGT GG TGAAGTTGTGG TAAATGT GGAG ATG
C

TTACACCACAACATCCACCT CTGG || ||||| ||||| |||| ||||
CCACATTTTACAATCAACCA CC ACTTCAATACC ATTTTACA CCTC TAC /
TAAC TTCATGAACC AAGT AACTAAC -- CACC AACACCA

GAM2244 GTAAGCATAGAGTTAACTTC 2230 TGAGTTGTAA 4955 -- ACTTCAACA A CT
AACAGACTCAAGCCTAGCGC TGCTGACTCT GTAAG CATAGAGTTA GACTCA GC A
TGAGTTGTAATGCTGACTCT ATGG |||| ||||| ||||| ||||
ATGGTCTTAC CATTG GTATCTCAGT TTGAGT CG /

TG CGTAATG-- - CG

GAM2245 TCCAACATATGCCATCTCCTT 2231 ATGGAGCGCT 4956 CCAT TCTG AA- - C-- C C TA
G C

CTGCCTTAATGGAGCGCTGC GCTTCAGCTT ATG CTCCT CCTT TG GAGCG TG TT AGCT
CCAG AATAAT T

TTCAGCTTACCAGGAATAAT ACCA || |||| |||| || |||| |||| |||| ||||
CTCATTATTCTGGAGCTTAA TAC GGGGA GGAA AC CTCGC AC AA TCGA GGTC
TTATTA /

CAATACGCTCACACCCAAGG C--- CCA- CCC A ATA - T -- - C
ACCAGGGGCCATGACAGGGA

GAM2246 TGCCCTTGGTATAAACATCA 2232 GTCACATGGA 4957 C GTA A A GC- CT---- C
CACC CA

ATGGCCTTTGCTATGCCGCC	AGTTTAACAA	TG CCTTG	TAAAC TC	ATG CTTTG	ATGC GC
ATGAGA A					
ACCATGAGACAACTTCTCAT	GGTC				
TTGCAGCATTAACAACAAAG		AC GGAAC	ATTG AG	TAC GAAAC	TACG CG
TACTCT /					
TCACATGGAAGTTTAACAAG		T A--	A G ACT	AACAAT A TT--	TC
GTCA					

GAM2247 ACATTCAACTTTTGTGACTT 2233	ATCACGTACA 4958	ACT	TTC- - A	ATC- C -
AG				
CTTGATGAGATCTATCAGTG	ATTTCGTCAC	ACATTCA	TTTGTGAC	TTG ATG GATCT
AGTGG GT AAAC T				
GCGTAAACAGTTTGTTTAAC	AGAT			
ACTATTACTGAGATCACGTA		TGTAAGT	AGACACTG	AAC TGC CTAGA TTATC CA
TTTG /				
CAATTTTCGTACAGATGAAT		---	CTTT A A	GTCA A A TT
GT				

GAM2248 CAATCAATTTAGCACTAAGA 2234	TGCGTTCTTA 4959	AA A - - GC
ATCATAGCGTCATATGCGTT	GGTGCAGAAA	CAATC TTT GCAC TAAGAAT CATA G
CTTAGGTGCAGAAAGGTTG	GGTT	
	GTTGG AGA CGTG ATTCTTG GTAT T	
	AA - G C AC	

GAM2249 CATTGTTGACAGCCATTTCA 2235	AAATGTAGAA 4960	T CAGCCA -	A-- AACATT
GA AG			
AATGTAGAAAATGAAACATT	AATGAAACAT	CA TGTTGA	TTTCA AATGTAGAAA TGA AA
TTGCA C			
AAGATTGCAAGCCCTGTAAC	TAAG		
ATTCGTCAAGATTTTTCAT		GT ACAACT	AGAGT TTACGTTTTT ACT TT AATGT /
TCTGAGACATCAACATTG		T AC----	C AGA GC---- AC CC

GAM2250 CTATCATTATGTGTACAACA 2236	TAAAGCACGG 4961	A T ACAACA AACA AGA C-
----- A		
ACCAACATGCTTAGAACCTA	TCACACTTAG	CTATC TTA GTGT ACC TGCTT ACCTAATAT
ATGGC G		
ATATCATGGCAGAAGCCATT	GATA	
CTAATCATATTAGGTAAAGC		GATAG GAT CACA TGG ACGAA TGGATTATA
TACCG A		
ACGGTCACACTTAGGATAG		- T C----- C--- A-- CTAATCT A

GAM2251 GTAACATTGACAGGGATAGA 2237	AACATTGACA 4962	- - - TA- AA-- G
ACAAGAGAAGAAATTCTCAA	GGGATAGAAC	GTA ACATTGAC AGG GA GAAC GAGAA A
TAGTTTGCCTCTCCTGGTCA	AAGA	
GTGTATAC		CAT TGTGACTG TCC CT TTTG CTCTT A
	A G T CCG ATAA A	

GAM2252 GTGAAGTCTCACACTAGACA 2238 TCACTAGCAA 4963 TCACA-- TTCATTTTCA T A
 C
 TTTCATTTTCATAGTTGATA TAACATGTCT GTGAAGTC CTAGACAT TAGT GATA CA G
 ACACGTGTGGTATCACTAGC AGGG ||||| ||||| ||| ||| ||
 AATAACATGTCTAGGGCAAA TACTTCAG GATCTGTA ATCA CTAT GT T
 TGACTTCAT TAAACGG CAATAACG-- - G G

GAM2253 GTTCAAGAACACCAGTTACA 2239 TAACAGGTGC 4964 ---- A ATTTTCAT C CGA
 ATTTTCATTGTCAAATTCGAA AATTTCTTGA GTTCAAGAA CACC GTTACA TGT AAATT A
 TTCAAGTTTAACACGTGTAA AC ||||| ||| ||||| ||| |||||
 CAGGTGCAATTTCTTGAAC CAAGTTCTT GTGG CAATGT ACA TTTGA T
 TAAC A GC----- A ACT

GAM2254 TGCAGTCATAATAGGGTAGA 2240 CAGTCATAAT 4965 C ATA AGAAAGATTTTA-- CC
 AGAAAGATTTTACTTTACCA AGGGTAGAAG TG AGTCATA GGGTAGA CTTTA A
 GCCTGAAGATTTACACCATA AAAG || ||||| ||||| |||||
 CATTGTCCTTATGACTTCA AC TCAGTAT TCCGTTT GAAGT G
 T --- ACATACCACATTTA CC

GAM2255 TGGACATATCAAGTTTCTTA 2241 TGCATAGCAG 4966 TA--- ----- -- A - AAA
 AGCATACCAAAAAGTAGGCT AAACAATCTT TGGACA TCAA GTTTCT TA GCATA CC A
 ATGCATAGCAGAAACAATCT TGAC ||||| ||| ||||| || ||||| ||
 TTGACTTTCTGTCCA ACCTGT AGTT CAAAGA AT CGTAT GG A
 CTTTC TCTAA CG A C ATG

GAM2256 AGTTTTGTCAGTGCAGGCCG 2242 TCAGTGCAGG 4967 TT T A ---- TG TTG TA
 GTGTTTGATGGTGTAAATA CCGGTGTTTG AGT TG CAGTGC GG CCGG T ATGGTGT A
 CACCATGTGCCGGAACCCCC ATGG ||| || ||||| || ||||| || ||||| ||
 GCACTGCCATTGCT TCG AC GTCACG CC GGCC G TACCACA /
 TT C C CCAA GT --- TA

GAM2257 CTGTTAGTACCTTTTCTTCC 2243 TAGCACGCCG 4968 A C CCT ACC -- A CAC
 AA
 CTCGACCGCTCCGATGTCAC AGCCGCAAGA CTGTT GTAC TTTTCTTC CG GCTC CG TGT
 ATCAGC T
 ATCAGCAATTTGTTGATAGC GGAA ||||| ||| ||||| || ||||| || ||||| ||
 ACGCCGAGCCGCAAGAGGAA GACAA CATG GGAAGGAG GC CGAG GC ACG
 TAGTTG /
 GGTGTACCAACAG C T AAC --- CC - A-- TT

GAM2258 CTTCTCAGAAGGCTTGTTTG 2244 TTCAACATGG 4969 A A - T TGGT G
 AATGGTTCCTAGAAATGGGA CCATCGAGGA CTTCTC GA GGCT TGTT GAA TCCTA A
 TTCAACATGGCCATCGAGGA G ||||| || ||||| ||| |||||

G GAGGAG CT CCGG ACAA CTT AGGGT A
- A T - ---- A

GAM2259 AACCATGCGTTTTTTTGA CT 2245 CGAGAGCTCC 4970 GTTTTTT-- - T AA A A C-- C
TTGTAAT

CAGTAGCTCAATCGAGAAAG TGAGTTCATA TGA CTCAG AGCTC TCG GAA GGC ACT
CTCAC GG A
GCACTCCTCACCGGTTGTAA TTCA ||| |||| |||| ||| ||| |||| |||| ||
TATATTTTTCTGTGGGTCT ACT GAGTC TCGAG AGC CTT CTGTGA GGGTG CC
/
AGTGTCTTCCGAGAGCTCC ACTACTTAT T C -- - C TCT T TTTTAT
TGAGTTCATATTCATCAGCA
TGGTT

GAM2260 AGTTGCTTGTTGGAAAAGCT 2246 AAAGCTATGT 4971 TG T G TGTA
ATGTTTCAAATACGTTTGTA TTCAAATACG AGT CTTGT GGAAAAGCTAT TTTCAAATACGTT T
ATTAAATAATGTATTTGAAA TTTG ||| |||| |||| |||| |||| |||| |||| ||||
ATAGCTTTTCCGCAAGAGAC TCA GAACG CCTTTTCGATA AAAGTTTATGTAA /
T GA - - TAAAT

GAM2261 CAGTATAACAGCAGGCCAAC 2247 TAACAGCAGG 4972 - A A---- - GGT
TGCCACTGGTTCACAGGTGC CCAACTGCCA CAGTATAA CAGC GGCCA CTGC CACT T
GCAGCTTCACTGGCTGGTTG CTGG |||| ||| ||| ||| ||| ||| |||
CTTATATTG GTTATATT GTTG TCGGT GACG GTGG C
C G CACTTC C ACA

GAM2262 CCAGTGGTTGCCATACCAGT 2248 AGTGGTTGCC 4973 - TT A C AAA - CA
AAAAGTCCACCATTTGTGAG ATACCAGTAA CCAG TGG GCC TAC AGTA GTC CAC T
ATAGTATTGTGCGTTCCAT AAGT ||| ||| ||| ||| ||| ||| ||| |||
TTGG GGTT ACC TGG GTG TTAT TAG GTG /
T T- C - GA- A TT

GAM2263 CTCATAGTAAGGTAGCTTGT 2249 TAGCTTGTGT 4974 AG - T GGACAT
GTGTTGTGTCTGTGGACATA GTTGTGTCTG CTCAT TAAGGTAGCTTGT G GTTGTGTCTGT A
AAGAAGAATAGACACAGCCC TGGA |||| |||| |||| ||| |||| |||| ||||
GACAAGCTATTTTAAAATGA GAGTA ATTTTATCGAACA C CGACACAGATA A
G AA G C AGAAGA

GAM2264 GACACTCAATATCAAATGAG 2250 TCTCTCAGCA 4975 C AA- ATG T T
AGAATGTTGTATTGTGGCCA TGGTATTGAA GACA TCAATATCA TGAGAGA TTG ATTG G
GTCTAGTCTCTCAGCATGGT TGTC ||| |||| |||| |||| ||| |||
ATTGAATGTC CTGT AGTTATGGT ACTCTCT GAT TGAC G
A ACG --- C C

GAM2265 GATAGTTTGGGGGAGGCCTT 2251 TAGTTTGGGG 4976 GG G T TTT

TGTTTTACATATAATGGCTC GAGGCCTTTG GATAGTTTGG GAG CC TTGT A
 AGCCAAACTATC TTTT ||||| ||| |||
 CTATCAAACC CTC GG AATA /
 GA - T TAC

GAM2266 GCAGATTTTGTGTGTCAGT 2252 TCAGTTACAG 4977 TG- C A- T AATTA
 TACAGCAGGAATTGTTAATT CAGGAATTGT GCAGATTTTGT TGTCAGTTA AGC GGAAT GTT
 A
 AAAAAAAAAACATTCCGGGCT TAAT ||||| ||||| ||| ||| |||
 TTAAGTACAAGCATAAGAT CGTCTAGAATA ACAGTCAAT TCG CCTTA CAA /
 CTGC CGA T GG - AAAAA

GAM2267 GGCAAACATCATATTAGTTAC 2253 TTACCAGTTT 4978 A-- A A T TT TA
 ATTGACTGGTAATAATGTAA TTGTACCAGT GGCA ACTC TATT GT ACA GACTGGTAATAATG
 A
 TTGTATTGTTACCAGTTTTT ACGA ||| ||| ||| ||| ||| |||||
 GTACCAGTACGAGTCAATGC CCGT TGAG ATGA CA TGT TTGACCATTGTTAT T
 C AAC C C - TT GT

GAM2268 GGCGCACGCATGTTGAGCAC 2254 TGACAGTGCA 4979 G--- GA CA - GGTG
 CATCAGTAGTTATGTGTTGG AGTATGCGTG GGC CACGCATGTT GCAC TCAGTAGTTAT
 GTGTT T
 TGTTAGGAATACAATAACTG AAAA ||| ||||| ||| ||||| |||||
 CTGACAGTGCAAGTATGCGT CCG GTGCGTATGA CGTG AGTCGTCAATA CATAA /
 GAAAAGCC AAAA A- AC A GGAT

GAM2269 GGGTGGGAAAATGTGAAAGC 2255 TGAAAGCGTG 4980 - G ----- T GAAAA TT TA T
 TTTTT A
 GTGCGAACTGAGGGAAAAGT CGAACTGAGG AAA GC TGCGA AC GAGG GTGG GGT
 AGG GGC GAA G
 GGTTGGTTAAGGTGGCTTTT GAAA ||| ||||| ||| ||| ||| ||| |||
 TGAAAGTTTTCTGCCCCCT TTT TG ACGTT TG CTCC CACC CCG TCC CCG
 CTT T
 GCCCCACAGTGCCTCTGTT G - CCCAAAT T GTGA- C- -- C TC--- T
 AAACCCTTGCAAGTGTTCAT
 GGGTCCTGCTT

GAM2270 GTACCTCAAGCTGGATGTGA 2256 GTTGGCACCT 4981 T TG CCA T TCTA T C -
 TATATA
 CCATGTTGCGTCTATTATGT GGGTTATTAC CTGGA G A TGT GCG TTATGT GGCAC TGG
 GTTATTACATG A
 TGGCACCTGGGTTATTACAT ATGT ||||| ||| ||| ||||| ||||| |||||
 GTATATAAGTGATTCCATGT GATCT C T ACA CGC AGTACA TCGTG GTC
 CGATAATGTAC G
 AATAGCACTGTGTGCTACAT T GT C-- - TTAA - T A CTTAGT
 GAAATTCGCACACTTGCTTC
 TAGAGAGGTAT

GAM2271 GTGGGATATGTGTTAAAGCA 2257 TTAAAGCAGG 4982 ATA AAA T CT C TGG
GGCTATCTCTCACCTGCATT CTATCTCTCA GTGGG TGTGTT GCAGGCTA CT CAC TGCATT
A
TGGAAGGCAATGCAAGTGCA CCTG |||| |||| |||||| || |||||
AGTGGCCTGCCTCAACACAA CACTC ACACAA CGTCCGGT GA GTG ACGTAA A
AACTCAC AAA CTC - AC A CGG

GAM2272 GTTCTCGTGGCAGATCTCAA 2258 TTGACACCCA 4983 - - -- A --- -- TA G AT
CAGCTGTGGTAGTGAGCAAT ATTGGCCCTT GTTC TCG TGGCAG ATCTC ACA GCTG TGG
GT AGCAAT T
ATTTCAATTGTTGACACCCAA GTAG |||| |||| |||| || |||| || |||||
TTGGCCCTTGTAGAGGTGGC CAAG AGT ACTGTC TGGAG TGT CGGT ACC CA
TTGTTA /
TGTCATTGATGAAC T T GG A TCC TA CA G CT

GAM2273 GTTCTGTGTAAGATAGATTG 2259 TAGATTGGGT 4984 TG T G GTG
GGTTAGGATCTGTGTGTGGT TAGGATCTGT GTTCTG TAAGATAGATTGGGT AGGATCT TGT G
AAAACGGAGATCCTTGCTCA GTGT |||| |||||||| |||| ||
ATCTGTCTTGTGCAGAAT TAAGAC GTTCTGTCTAACTCG TCCTAGA GCA T
GT T G AAA

GAM2274 GTTTTCCCGCCAGTTGAAAA 2260 TTAAGTGTCA 4985 TT ----- T TTA-- CC T
CTCT- T
AATGTTAGGACCACTACCCT TTTTAAAGGG T TCCC GCCAGT GAAAAAATG GGA AC
ACC CTTT T
CTCTTTT TAGAAGTTGTTGG ACTG | ||| |||| |||||| || || ||| |||
TTGTTATCCAAGTTTATTTT G AGGG TGGTCA TTTTTTTAT CCT TG TGG GAAG
/
TTTTACTGGTCATTTTAAAG TC AATTTTAC T TTGAA AT T TTGTT A
GGACTGC

GAM2275 TATGTAGTCTGTAGACAGAC 2261 TG TAGACAGA 4986 A - A T C - GGAGTT
AGTGAGCGGGTGCGGGAGTT CAGTGAGCGG TATGT GTCT GT GACAGACAG GAG GGGT GCG
T
TAAGGAGCGCAATCCACTCC GTGC |||| |||| || |||||| || |||| |||
CTGTCTGTCACTAGACACGT ATGCA CAGA CA CTGTCTGTC CTC CCTA CGC /
A - T - C A A GAGGAA

GAM2276 TCCTAATCAGACGGCTTGTG 2262 TGCACGGCTA 4987 A AC T TTTAT
CATAAGCTTTTTATTAATTT CCTGGTAGGG TCCT ATCAG GGCT GTGCATAAGCTT T
TAAGCTTATGCACGGCTACC A |||| |||| || ||||||||
TGGTAGGGA AGGG TGGTC TCGG CACGTATTCGAA A
A CA - TTTTA

GAM2277 TGCTCATCTCGTGCTAAGAG 2263 TGCCAAGTAC 4988 CA G A CT C GTGTA

CTCTTGGCGAAGGCTCTGTG	TCTGGTAGGA	TGCT TCTC TGCTA GAG CTTGGCGAAGG TCT
C		
TACTAAAAAGATCTTTGCCA	GACT	
AGTACTCTGGTAGGAGACTG		ACGG AGAG ATGGT CTC GAACCGTTTCT AGA /
GCA	TC G - AT	- AAAAT

GAM2278 TGTTTTGAGTGGGCCTGCTC 2264	TATAACGGAA 4989	TT- --- C- T TCA TAA-- A
TAAT		
ATTCACGGTGCAGTAACTGA	CACCTGCATC	GT TGA GTGGGC TGC CAT CGGTGCAG
CTG TATAGAAG A		
TATAGAAGTAATAAATGTCT	GGCA	
TCTATAACGGAACACCTGCA		CA ACT TACCCG ACG GTA GCTACGTC GGC
ATATCTTC A		
TCGGCATGCGCACTGCCCAT	TCC AGG	TC C CG- CACAA A TGTA
GGATCACCTACA		

GAM2279 TTACCCAAAACCCACCAGGT 2265	TGTAGACAAC 4990	----- - A- A A ---- AC---- AG-
A		
AGCTTTATGCATGTAGACAA	TTCTTGAGAT	CCAG GT GCTTT TGC TGT AGACA
TTCTTG ATTCTT T		
CTTCTTGAGATTCTTATCTG	TCTT	
AGAGTATACGAGAAAAAAA		GGTT CG TGAAA ACG GCG TCTGT AAGAGC
TGAGAG C		
TGTCTTTTCAGCGAGCAAAAA	ATAAC	A AG A A ACTT AAAAAA ATA T
GTGAGCATTGGCAATATGGG		
TCCAGGGGGCG		

GAM2280 TTCGTGTTAGGCTAGTCTGG 2266	TAGGCTAGTC 4991	G C G CT ACAT
ACAAAACACTGTTTTACATT	TGGACAAAAC	TTC TGTTAGG TAGTCTG ACAAACA GTTTT T
AAAAAAGGACTGTTTTGTAC	ACTG	
AGGCTACCTAGCAAGAG		GAG ACGATCC ATCGGAC TGTTTTGT CAGGA A
	A - A --	AAAA

GAM2281 AGAATTGCATTCCTTTTGTT 2267	CGTGCAACCC 4992	TT-- TCTCT CAAATT CCACAG
GT --- T		
TCTCTTTCTTCGTCAAATTG	CTTCTGCGGA	TTGTT TTCTTCGT GGG TGCA GCGGA
ATCCAG G		
GGCCACAGTGCAGTGCGGAA	GAAT	
TCCAGTGTCTGGATTGATCT		AACAA AAGAGGCG CCC ACGT CGTCT
TAGGTC /		
GCCGTGCAACCCCTTCTGCG	CTAT	CTTT- TCTT-- CA---- GC AGT T
GAGAATTTCAACAATATCTT		
CATGCAACTCT		

GAM2282 AGTAGCACCGGTTGTGTAGC 2268	TGACAACACA 4993	GC GG AGC TC
CAGAGATCTGACTCTCTGAC	GGAGGTAATA	AGTA ACC TTGTGT CAGAGA T
AACACAGGAGGTAATACT	CT	
	TCAT TGG GACACA GTCTCT G	
	AA AG ACA CA	

GAM2283 ATGTCCCCAGGCCTTGTGAA 2269 GCACCGTTTG 4994 CC GC AC - CTCAGT C
A
ACTTCAACGGTCTCAGTGCT AATTCACAAG ATGT CCAG CTTGTGAA TTCAA CGGT
GCTAATG TTGG G
AATGCTTGGAGCACTAACAT CTGG |||| ||| ||||| |||| ||| ||||| ||||
TAGCACCGTTTGAATTCACA TACA GGTC GAACACTT AAGTT GCCA CGATTAC
AATC C
AGCTGGATACAT TA -- -- T ----- - A

GAM2284 CAAATCAACACATACAACCC 2270 TTATCGTGCA 4995 TC A AACC TTCT CACG A
A
TTCATTCTACACACGGTACG CATGTCTGAA CAAA AACAC TAC CTTCA ACA GTACGA
AATAG T
AAAATAGATGCTATTATCGT GAAG |||| |||| ||| |||| ||| ||||| ||||
GCACATGTCTGAAGAAGTAG GTTT TTGTG ATG GAAGT TGT CGTGCT TTATC /
GTGTTTCTTTG CT G AA-- C--- ACA- A G

GAM2285 GACAGTATTGCAGAGTTGGA 2271 CAGTATTGCA 4996 --- A T A-- TAC
GGCATACTCAGTTGCCGTAC GAGTTGGAGG GACAGT ATTGCAG GT GG GGCA T
CCGCCTGCAATCTCACTGTC CATA ||||| ||||| || |||
CTGTCA TAACGTC CG CC CCGT C
CTC - C ATG TGA

GAM2286 GCAGACAGTCCATATTAGCC 2272 TGTGCGCAGCG 4997 AC CCATATT - ACAA C GCAT
TCAT
TGCACAAAGACACGAGCATC CTTCAACTTC GCAG AGT AGC CTGC GACA GA CA C
ATCATCCAATTGTATATCAT CTGC |||| ||| ||||| |||| || ||
GTGCGCAGCGCTTCAACTTCC CGTC TCA TCG GACG CTGT CT GT /
TGC CT ACT---- C ----- A ATAT TAAC

GAM2287 GGATAATAGACTTGGGCACG 2273 TTGGGCACGC 4998 TAAT-- ---- C-- TAACTAGT C-
A AT C
CTCTTAACTAGTTTGTCCAC TCTTAACTAG A GACTTGG GCA GCTCT TTGTC ACAA
GC TGGT A
AAAGCATTGGTCATAGCCGG TTTG ||||| ||| |||| |||| |||| ||| ||||
CCTTGTAAGACAACCAGAGC TCTGAACC CGT CGAGA AACAG TGTT CG
GCCG T
TTTTGCATCTCCAAGTCTTT TAAATT TCTA TTT CC----- AA C -- A
AAATTCC

GAM2288 GTTAAAGTATTGTCTTTGCA 2274 TAAAGTATTG 4999 A ATT - AA CG - T
AATGGAGGCGGGCTTTGCAT TCTTTGCAAA GTTAA GT GTCTT TGC ATGGAGG G GC T
TACCTCCATAGGCATAAGAC TGGA ||||| || ||||| ||| |||
ACATTAAC CAATT CA CAGAA ACG TACCTCC T CG /
A --- T GA AT A T

GAM2289 GTTTGTAAGAGCTAAATCAG 2275 TGA-- A C CGTTCCA TT - A
 CCATACGTTCCAGCTTACGA ATATTACAG GT TGTA GCTAA TCAGC ATA GC AC GAGC
 A

GCAACAGCTCTGTCGCGCTC C || |||| |||| |||| || || ||||
 ATATGCTGACTTAGCAATAT CG ACATT CGATT AGTCG TAT CG TG CTCG C
 TACACGC C ATAA C - ACTCG-- C- T A

GAM2290 TCTTTATATATTCTAAATAT 2276 TGGGTTCTCA 5001 - CTAAATAT ACACAT
 ACCCGGAACACATTTTGATA TGGTATACTA TCTTTA TATATT ACCCGGA T
 CTCTGGGTTCTCATGGTATA AAGG ||||| ||||| |||||
 CTAAAGG GGAAAT ATATGG TGGGTCT T
 C TACTCT-- CATAGT

GAM2291 TGATAATGCCTCATAATAGA 2277 ATAATGCCTC 5002 GCCTCATAAT C- CTT AATTT
 GCCTGGCCTTTCCAAATTTA ATAATAGAGC TGATAAT AGAG CTGGC TCCA A
 TTAAATGGATAGCCAGCACT CTGG ||||| |||| |||| ||||
 CTTATCATAATTATTA ATTATTA TCTC GACCG AGGT /
 ATACTAT--- AC AT- AAATT

GAM2292 TGGTACGTAAATTGGGTGC 2278 TACGTAAAT 5003 AAATT- CAA- - CAA - C C
 CG
 AATGCACAAGTTTACTACCG TGGGTGCAAT TGGTACGTT GGGTG TG CA GTT TA TA
 CGCA T
 CACGTACATGCGATATTATA GCAC ||||| |||| || |||| ||||
 ACCCCTGACAAGATCACCTT ACCATGCAA TCCAC AC GT CAA AT AT GCGT A
 TATCCAACGTACCA CCTATT TAGA A CCC T T A AC

GAM2293 TTAGCAAAAATTTGGCAGCG 2279 TTTGGCAGCG 5004 AAA- - -- - ATTAAC CAG A A
 TC AA
 ATCATTAACAAGGCAGGTAT ATCATTAACA AATT TGGCA GC GATC AAGG GTATC TGTG
 CCA CAAT A
 CATGTGACCATCCAATAAAT AGGC ||||| |||| |||| |||| |||| ||||
 GAATTGTTGGCACAGATACA TTAA ACCGT CG CTAG TTCC CATAG ACAC GGT
 GTTA T
 ACCCTTATGTGGATCAGCAT TCTA C TA A GTGTA- CAA - - T- AG
 TGCCACAATTATCTTCTAA

GAM2294 TTGGTCTCCCTCACCCGTAT 2280 AATTACACAA 5005 TC- - TATAAT AAA T T AAAC -
 AGAG
 AATTGTA AAAATCAGTGAAG CTTTGGGTCTG CCTC ACCCG TGTA TCAG GAAG GA TCC
 TAAAGAG T
 TGAAACTCCTAAAGAGAGA AGGT ||||| |||| |||| |||| |||| ||||
 GTTACCACTCTTTGCGGAAA GGAG TGGGT ACATT AGTC CTTT CT AGG
 GTTTCTC T

TCTTTCCTGAATTACACAAC
TTTGGGTTCGAGGTCAAGCCA
A

ACT C TTCAAC A-- - - AA-- C ACCA

GAM2295 AAATTTAGAAATATACAGAC 2281 TCCAATGTAT 5006 TT T A TCTATC -TC TCTT
TCTATCGCGTGTCTATATCT TTATGTCTGA AAAT AGAAA AT CAGAC GCGT G TATA C
TCTTTTTATATCCAATGTAT TTTT |||| |||| |||| ||||
TTATGTCTGATTTTTCTTCA TTTA TCTTT TA GTCTG TGTA C ATAT /
TTT CT T - TATTTA ACT TTTT

GAM2296 AAGTCATGCTATTGTAGGAA 2282 TTGCTCAAAA 5007 - ---- G TTTT
TTTTTTTTTACAGTTGCTCA ACGATGGTAG AAGTCA TGCTATTGT AG AATT T
AAAACGATGGTAGTGACTT TGAC ||||| ||||| || ||||
TTCAGT ATGGTAGCA TC TTGA /
G AAAAC G CACT

GAM2297 ATCCCAACAATGCTATAGCA 2283 TAGCATTAGT 5008 ----- - A AT
TTGCGCATAGCATTAGTCAT CATAAACTTG ATCCCA AC AATGCTAT GC T
AAACTTGGGAT GGAT ||||| || ||||| ||
TAGGGT TG TTACGATA CG /
TCAAATAC A - CG

GAM2298 CGCAGCATATTCTAAATAC 2284 TGATATAATT 5009 TCCT CATCTA-- C CT -
TAAAG - AAT
ATCTAAATTTTACTATTAT TTGTCCATTG AAATA AATTTTTA TATTATA TGG CA ATAT
AGAT A
ACTTGGCATAAAGATATAGA TAGT |||| ||||| ||||| |||| ||||
TAATACTCGTCTGATATAAT TTTAT TTAAAAAT ATGATGT ACC GT TATA TCTG
/
TTTGTCCATTGTAGTATAAA TGTC CTTTATAA - T- T TTAA G CTC
AATTAATATTTCTATTTCTG
TATATTTGCG

GAM2299 GAATGTTTCGCGGAGTATAGC 2285 TCGCGGAGTA 5010 TCGC T CCTA T
CTATTATTTTCTAAATAACA TAGCCTATTA GAATGT GGAG ATAG TTATTT C
AACTGTTTCTTTATATATT TTTT ||||| ||||| |||||
C CTTATA TCTT TGTC AATAAA /
TATT T AAAC T

GAM2300 GGAAGTGGATATACATAGTT 2286 TCGCTAGCCT 5011 --- T TACA T C
GTGATCATCATTATCGCTAG TATCCTCTAT GGA AG GGATA TAGT GTGAT A
CCTTATCCTCTATATCC ATCC ||| ||||| |||||
CCT TC CCTAT ATCG TATTA T
ATA T TCCG C C

GAM2301 GGACGTTCTCGTACAGGACG 2287 ATCCGATAAC 5012 CGT C GA AACTATAA-- - A
C

TATCATCTGAATAATAACTA
TATGTAGT

G ATAA- -- CT- GTAAA GAC

GAM2308 CTATTGTTTCATAATCACTA 2294 TAAGTGATTG 5019 TTTC- - TGAA
GATGAATACCTTCTAAGTGA TTTTTTTAAT CTATTG ATAATCACT AGA T
TTGTTTTTTTAATGG GG ||||| ||||| ||
GGTAAT TGTTAGTGA TCT /
TTTTT A TCCA

GAM2309 GGAAGTTGATTCAGAGTATG 2295 TATGATAATG 5020 TTC ---- AT TATC- A TA
ATAATGTATCGACGTAAATA TATCGACGTA GGAAGTTGA AGAGT ATG AATG GACGT AA
T
TTATTTAATGTTTCTTCTAT AATA ||||| |||| || |||| |||| ||
TTCCATTTTAACCTTCTCAG CTTTCGACT TTTCA TAC TTAT TTGTA TT T
CTTTC C-- ATTT CT CTTCT A TA

GAM2310 GTATCAAAGTATTTAGATGA 2296 ATCACATCAT 5021 A A A ATT - TTTTA
ATTTGATAAAATTATTTTAT TAAACATAT GTATCAA GT TTT GATGA TGAT AAAATTA T
GACCTTTAATTTTAATCACA TGAT ||||| || |||| |||| |||||
TCATTAACACATATTGATAC CATAGTT TA AAA TTACT ACTA TTTTAAT G
A C A AC- A TTCCA

GAM2311 TGGCTTATACACAACAAACA 2297 TGAAAGATTA 5022 CT C- AACAAACAT TACTCT
CCTC GAC
TATGAAAGATTACTCTAATA CTCTAATATC TGG TATA AC ATGAAAGAT AATATC AAC
A
TCCCTCAACGACATACAGTT CCTC || |||| || ||||| |||| ||
AAAGATATTGTCTTTTATTT ACC ATAT TG TATTTTCTG TTATAG TTG T
CTTCAGGTAATATATCCCA CT AA GACTTCTT- ----- AAA- ACA

GAM2312 TTATTTTCTTCTTCTGTGCA 2298 TGAATAGTTG 5023 CTTCTG T C GA CCGCTT
TCTCTTTATTGATATTCCGC CAAAAAGAAA TTATTTTCTT TGCA CT TTTATT TATT A
TTACACTACTAGTAAAAATG ATGA ||||| |||| ||||| ||||
AATAGTTGCAAAAAGAAAAT AGTAAAAGAA ACGT GA AAGTAA ATGA C
GA AA---- T T AA TCATCA

GAM2313 TTGGAAATATAAGAGGTGGA 2299 AGAGGTGGAG 5024 AAT GCATCT CATTTTGAT
AATCC
GCATCTTCCCATTTTGATGA CATCTTCCCA TTGGA ATAAGAGGTGGA TCC GATGTTA
C
TGTTAAATCCCAAAAACATAA TTTT |||| ||||| || |||||
CATCTGATACAACGGATCCA AACCT TATTTTACCT AGG CTACAAT A
TTTTTTATTCTCCAA CCT ----- CAACATAGT CAAAA

GAM2314 TTGTAAATGAACGGGAAAA 2300 AAATGAACGG 5025 T -- A--- C TTTT
 AAGTCTCTTTTAACCCGAAC GAAAAAAGTC TTG AAAATGA ACGGGAAA AAGT TC A
 TTGTTATTTCTGTGCTTAT TCTT ||| ||||| ||||| |||||
 TTTTCAA AAC TTTTATT TGTCTTT TTCA AG /
 T CG ATTG - CCCA

GAM2315 TTTTAAACCGTTTAACTTAT 2301 TAGTAATAGT 5026 T TTATAAC T TT- AT A C-
 G G
 AACAATTTTTATTTCTATAT ACATAGATAT CGTT AAC AAT TTTAT CTAT CTAGAGAG CG
 ACAATG ATTG T
 CTAGAGAGACGCACAATGGA TTAC ||||| ||| ||||| ||| ||||| || ||||| |||||
 TTGGTCGCAATCATTGTCTC GCAA TTG TTA AGATA GATA GATCTTTT GC TGTTAC
 TAAC C
 GTTTTCTAGTAATAGTACAT T TCAT--- T CAT AT - TC - G
 AGATATTTACTGTTTAACGT
 ATTAAGA

GAM2316 CACTCTGCGTCGTTGTCCCT 2302 TATCCTCTTT 5027 T- G T-- C - C TTTTCC
 TCC C
 GCACCACTCTATCCTCTTTT TCCAGGTCCG CACTC GCGTC TTG CCCTG AC CACT TATCCTC
 AGG GA A
 CCAGGTCCGACAAGTCTCCC ACAA ||||| ||||| ||| ||||| ||||| ||| ||
 CTCACGGGGATGTAGTGCGT GTGAG CGCAG GAC GGGAC TG GTGA GTAGGGG
 TCC CT A
 CCAGGGCTTCAGGACGCTCG CT - TTC C C T CAC--- CCT G
 AGTG

GAM2317 CCACAGGCAAAAGCCCACGT 2303 TGAGCCAAGT 5028 A CCC--- TT - AGT - - T
 AG
 TGAGCCAAGTCTGCCTGTGCG CTGCCTGTGCG CCACAGGC AAAG ACG GAGC CA CTGCC
 TG TCG CGGCG G
 TCGGCGAGGTCCGCCGTGAG TCGG ||||| ||||| ||| ||||| ||||| ||| |||||
 CATGGCAGTGAGCTCCGTCA GGTGTCCG TTTC TGC CTCG GT GACGG AC AGT
 GCCGC /
 CCCTCTTTAGCCTGTGG A TCCCAC -- A --- T G - CT

GAM2318 CCAGGGCCTCTGTCCAGTCC 2304 GTCCAGTCCC 5029 TCC - GA AAGAA GT
 CCGAGGCAAGAAGGGTCGAA CGAGGCAAGA CCAGGGCCTCTG AGT CCCC GGC GG C
 CCAGCTGGGGAACCTCTCCGG AGGG ||||| ||||| ||| ||||| ||||| ||| ||
 GGGTCCTGG GGTCTGGGGGC TCA GGGG TCG CC G
 CTC A -- A---- AA

GAM2319 CCTATGACAACGAGCTTAGT 2305 TATGACAACG 5030 T C T TT- -C
 TCCGCCTAGGTCGGTGTCTA AGCTTAGTTC CC ATGACAA GAGC TAG CCG C T
 TGCTCTTGTCGTTGG CGCC || ||||| ||||| ||| |||
 GG TGCTGTT CTCG ATC GGC G A
 T - T TGT TG

GAM2320 CTAAAAATGTTGTGATAGAA 2306 ATTACATCTC 5031 ATGT- T AG TA
TCTTTAGACTAAGATTACAT ATTCTCTTTT CTAAAA TG GAT AATCTT G
CTCATTCTCTTTTGG GG ||||| ||||| |||||
GGTTTT AC CTA TTAGAA A
CTCTT T CA TC

GAM2321 GACCAGGGTGCCCTCGGTGA 2307 TCCAGCACTC 5032 CA CCT T AAC- TC TT
AACTGTTGGGCCTCATCTGG GTCCTCGTCG GAC GGGTGC CGG GA TGTTGGGCC
ATCTGG G
TTGTTCCAGATGGTCCAGCA CACT ||| ||||| ||| || ||||| |||||
CTCGTCCTCGTCGCACTTGT CTG TTCACG GCT CT ACGACCTGG TAGACC /
C -- CT- C GCTC -- TT

GAM2322 GAGGCTGCACCAGCAGTGAC 2308 TGA CTGCAA 5033 CA- A-- G ACCAAC
TGCACCAACTGTACCAGCAG GGCACCAGCC GAGGCTG CC GCAGT ACTGC T
TGA CTGCAAAGGCACCAGCC TT ||||| || ||||| |||||
TT TTCCGAC GG CGTCA TGACG /
CAC AAA G ACCATG

GAM2323 GCCAGATCGTTGACCTGCTC 2309 CGTCAGGGTG 5034 ATCGT CT T - A
ATCCTTGATGTCAGAGACTT GGCGTCATAT GCCAG TGAC GCTCATCCT GATG TCAGAG C
TTTTGGCCGTCAGGGTGGGC CCTG ||||| ||| ||||| ||||| |||||
GTCATATCCTGGT TGGTC ACTG CGGGTGGGA CTGC GGTTTT T
CTAT- -- - C T

GAM2324 TAATAATATCGAGATGGTAA 2310 GATGGTAATA 5035 A - GT---- A AG TG
TATCTTAAGATATTTAGTCT TCTTAAGATA TAATA TATC GAGATG AATATCTT AGATATTT TC
A
GAAAGAGAATGTCTAAAGAT TTTA ||||| ||||| ||||| ||||| ||||| ||||| |||||
ATTTCTCTACATCTCGGATA ATTGT ATAG CTCTAC TTATAGAA TCTGTAAG AG /
ATGTTA A G ATCTCT A -- AA

GAM2325 TGCCACCAGCCCGGTCACTG 2311 TTGACAGTAG 5036 C CC - CGC TC TCC
CGCTCTCCACTCCCATCGTG GCTTGTTGTG TGCCAC AGC GGTC ACTG TC CAC C
TTGACAGTAGGCTTGTTGTG GCA ||||| ||| ||||| ||||| ||||| |||||
GCA ACGGTG TTG TCGG TGAC AG GTG /
- T- A --- TT CTA

GAM2326 TGGGAGACTTTCTGGGAGAC 2312 TGGGAGACTT 5037 ACTTT C-- G C G A
TTTCTGGGAGACTTTCTGGG TCTGGGAGAC TGGGAG CTGGGAGA TTTCT GGAGA TTTCT
GGAG C
AGACTTTCTGGGAGACTTTC TTTC ||||| ||||| ||||| ||||| ||||| |||||
TGGGAGACTTTCTCCAGCG ACCCTC GACCCTCT AGAGG TCTTT AGAGG TCTT /

CCTCCCA

CGC-- TTC G C G T

GAM2327 TTGTCTTGGGAGTATCTCGC 2313 TATAACAGGC 5038 CTT TCTC G ----- CCAT
TGTA AACCTGTTGTGTGCC AGTAGTTTA TTGT GGGAGTA GCT TAAAA
CCTGTTGTGTG A
ATATTTCCATATAACAGGCA GAGT ||| ||||| || ||||| |||||
GTAGTTTTAGAGTAATTTAC AACG TCCTCAT TGA ATTTT GGACAATATAC /
TCCTTGCAA T-- TTAA G GATGAC CTTT

GAM2328 TTTTATAGGATGAGAATGAGG 2314 TCAGAGTCTT 5039 AT--- AA-- - C A TA T TCT
A TA
TGTAACGACATCTTAGGATA TACCATCTCG AGG GAG TGAGGTG TAA GAC TCT GGATA
TATC GA AGGG T
TTATCTCTGAAAGGGTATTT GAAA ||| ||| ||||| ||| ||| ||||| ||| |||
ATTCTCTCGATATTATCTCA TCC TTC GCTCTAC ATT CTG AGA TCTAT ATAG CT
TCTT T
GAGTCTTTACCATCTCGGAA AGATT AAAG C T - C- T --- C AT
ACTTTTAGACCTAAAAA

GAM2329 AAACACTGCACAAGATCTCA 2315 TGAGATCTTG 5040 CA- AG GA- CAC
CAGCACTGGATTGTCACAGG ATTCAGTGTT AAACACTG CAAGATCTCAC CACTG TTGT A
CACA ACTACAGTGAGGTGAG T ||||| ||||| ||||| |||||
ATCTTGATTCAGTGTT TTTGTGAC GTTCTAGAGTG GTGAC AACA /
TTA GA ATC CGG

GAM2330 AATAGGGTTGTGAGGTAGGC 2316 TGAGGTAGGC 5041 T- G GC - AG-- -- T TAAT
GG CG
GGTTGCCAGGCAGATTAGGT GGTGCCAGG GGGT GTGAG TAG GGT TGCC GCA GAT
AGGT GTGGG GTG G
TAATGTGGGGGGTGC GG TAC CAGA ||| ||||| ||| ||||| ||| ||||| ||||| |||
TATTACTTACTTTTGT TTCA CATTCA TT TCA ATGG TGT TTG TTCA CATT
TAT T
ATTGTTGGGGGTATACTATT TT - A- T GGGT TA T TT-- AT CA
ACTTACTTACTTTGT

GAM2331 ACGTGTGTCGCCTGGTGCGG 2317 GATCACTACC 5042 T G----- - A CA A ACCAAA
A- C C
TGTCCACACGAGCAGTAATG TCGGGTGTGA GGTGCG TGTC CAC CGAG GTA TGGTCTG
GCT GGT CT A
GTCTGACCAAAGCTAGGTCC CGGT ||||| ||||| ||||| ||||| ||||| ||||| |||||
TCAAGAGCACCCAGCCTTC CCGCGC GCAG GTG GCTC CAT ACTAGAC CGA
CCA GA A
AGCAGATCACTACCTCGGGT - GGGCCTG T G -- C GACTTC CC C G
GTGACGGTCCGGGCGCGCCG
GTGGCCACCT

GAM2332 ACTTGAGGTCAGGCCTCTCC 2318 TGAGGTCAGG 5043 A -- G CCC G
CCGGGGTCCCCGAGGGGCGT CCTCTCCCCG ACTTG GGT CA GCCTCTC GG G

GAAGCCCAGGT GGGT ||||| ||| || ||||| ||
TGGAC CCG GT CGGGGAG CC T
- AA G C-- C

GAM2333 AGTTGGAGATGTTGTAGCCC 2319 TGTGTAGCC 5044 GA G G CG---- AAAC- C--- T
GTCACAAACTCCACGTCCGC CGTCACAAAC AGTTGGA TGTT TA CC TCAC TC ACG C
GTCCCTGATCATGGTGAAAA TCCA ||||| ||| ||| ||| ||
AGAGGTAGAGCAGGTCCAGC TCGACCT ACGA AT GG AGTG AG TGC C
T GG G - AGAAAA GTACT TCCC G

GAM2334 CCATGCAGCTGTGTAGTTGC 2320 AACACAGCAC 5045 ----- - T GA TG AA
CTAGGAGCTGGTTTAACAGA TTGAAGTCCT CCATGCA GCTGTGT AGT GCCTAG GC
GTTT C
AACGCCTCTAGGCTACTAAC GTGT ||||| ||||| ||| ||||| || |||
ACAGCACTTGAAGTCCTGTG GGTGTGT CGACACA TCA CGGATC CG CAAA /
TGG CCTGAAGTTCA A T TC -- GA

GAM2335 CCCCCAGACTCTCGAAGATT 2321 TTGAATGAGG 5046 AGA C CA GT A --- A C
G-- CTCT
CTTCAAAACACCGGTCTAGA TTGGAGTCGG CGA TT TTCAAAA CCG CT GAGTTCT GGG
GAAG GAG GGT C
GTTCTGGGAGAAGCGAGGGG GGG ||| || ||||| ||| || ||||| ||||| |||
TCTCTCAAATCGCCAGACTC GTT AG AAGTTTT GGC GA CTCAAGG CCC CTTC CTC
CCG A
ACTTCCCCTACGGAAGTCAA GG- T AG -- A CAT - A AGA CTAA
GCGGGATTTTGAATGAGGTT
GGAGTCGGGGG

GAM2336 CCCCCATCTTCCAAGTGTTT 2322 TTCACTACA 5047 T AAGT TCATA A C -- T
ATTAC
ATAAGGCGCCGATGCGCTGC GAACAGCACG ATC TCC GT AGGCGCCG TG GCTG
CTGTAGTGAAATT TGC A
TGTAGTGAAATTTTGCATTA CGGC ||| ||| || ||||| || ||| ||||| ||||| |||
CATAACCAGCATAATTTAC TAG AGG CG TCCGCGGC GC CGAC
GACATCACTTTAA ACG T
TACAGAACAGCACGCGGCGC C AGGT TC--- - A AA T ACCAA
CTCTGCTGGAGGACGATGGG
GG

GAM2337 CCCCGGGTAGAGTTCGCTGC 2323 CTGGCAGAGA 5048 - G - TTTTTT
AGAGCCAGGGTTTTTTTTTA ACTCTGCCAC CCCC GGTAGAGTTC CTGC AGAGCCAGGG T
CCATCCTGGTTCTGGCAGAG GGGG |||| ||||| ||| ||||| |||
AACTCTGCCACGGGG GGGGC CCGTCTCAAG GACG TCTTGGTCCT /
A A G ACCATT

GAM2338 CGTGTCCAGCTTGTAGTTGG 2324 TCCCTGCACA 5049 - CT- TT T
ACAGGCTCAGCTTGTCCCTG CCTGGTACAT CGTGT CCAG TGTA GACAGGC C
CACACCTGGTACATG G ||||| ||| ||||| |||||

GTACA GGTG ACGTC CCTGTTG /

T CAC -- A

GAM2339 CTAGCACGAGGGGTTGGCAT 2325 TGAAAACACC 5050 G TTGG TT A C- C GA -
AA AAT

TTGAAAACACCGTCCGGAGA GTCCGGAGAC AGGGG CAT GAAAAC CCGT CGGAGA TTCT
AGTATT AGG TC T

CTTCTGAAGTATTAGGAATC TTCT ||||| ||| ||||| ||| ||||| ||| ||| ||
AATTACACGAACCTAAGTAC TCCCC GTG CTTTGT GGCG GCCTCT AAGA TCATGA
TCC AG A

TAGAGAAATCTCCGAAGCGG - TA-- GT G AA A GA A A- CAC
GGTTTTCTGGTGATCCCCTA
TCCTAG

GAM2340 CTCTCAACACCATCTTGAGT 2326 TGAGTTCTCT 5051 A A TCT - A A GTTTTTT
TCTCTAGGGAAACAGGTGTT AGGGAAACAG CTCTC AC CCA TGAG TTCTCT GGGA ACAGGT
A

TTTTAAATCACAATCTGTGT GTGT ||||| ||| ||| ||||| ||| |||||
CCCGGGGGAACCTCATGCTG GAGAG TG GGT ACTC AAGGGG CCCT TGTCTA /
GGGTCGAGAG C G CGT C G G AACTAA

GAM2341 GACAGTTTAAGCACTGAATG 2327 CAGTTTAAGC 5052 C AA - A TA- A
TATCAAGGGGCCTCACTCAG ACTGAATGTA GA AGTTT GCA CTGA TG TC A
TTGCCAAAACATC TCAA || ||||| ||| ||||| ||
CT TCAA CGT GACT AC GG G
A AC T C TCC G

GAM2342 GACGCTGCGAAGCAGTGCAT 2328 AAGCAGTGCA 5053 C CGAA C G A CCTCC
AGAGTGCCTGGAGATCCCTC TAGAGTGCCT GA GCTG GCAGTGCATAGAGTG CTG AG TC
A

CATTACCAGAACTCAGACAC GGAG || ||||| ||||| ||||| ||| ||| ||
TCTATGCGCTGTCCCACAGC CT CGAC TGTCGCGTATCTCAC GAC TC AG T
ATC A ACCC A - A ACCAT

GAM2343 GAGAGTCTGCTCGTGGATTT 2329 GTAAACCTTA 5054 -- -TG TTT - G TTTA- ATCC
TA GTTTTA

TGCCAGGCGCCGTTTAAAGA CACTCGGGGC TC G GA TGCCAG GC CCG AAG
ACGAGGAGC GGT G

TCCACGAGGAGCTAGGTGTT TCTG || | || ||||| || ||| ||||| |||
TTAGAAACAAAACACGTTT AG C CT ACGGTC CG GGC TTC TGCTCCTTG CCA
A

CTCGTAAACCTTACACTCGG CC A GT T-- T G TCACA CAAA CA AAACAA
GGCTCTGGCATTCTGCAGAC
CCTAGACCTC

GAM2344 GATAGTTTAAGCACCTTTTC 2330 TAGTTTAAGC 5055 A CTT-- A ACC
ATGACCTAGGCAGAAATTCAA ACCTTTTCAT GATAGTTTA GCAC TTC TG T
GTGCCTAAACTATC GACC ||||| ||||| ||| ||

GAM2345 GCAAGACCTCGAGGGGGCCG 2331 TGGCATCTAT 5056 AAG GG A - - ----- T
 TGCAAATAGTGCCGGTGCTT CTGTACGGTT GC ACCTCGAG GGCCGTGCA ATAG TGCC GGT
 GCTT T
 TTATGAGCTACACACACCTG ACTC || ||||| ||||| ||| ||| ||| |||
 GCATCTATCTGTACGGTTAC CG TGGAGCTC TTGGCATGT TATC ACGG CCA CGAG
 A
 TCGAGGTGTCGC CTG A- C T T CACACAT T

GAM2347 GCAGACACCGTGAGAGACTC 2333 TCACAACTAA 5058 - CA A A A --- A A
TCTAAGCTAGTTAGTGATAA CGGCTCAGAG GCA GA CCGTG GAG CTCTCT AGCT AGTT
GTGATA G
GTATATCACAATAACGGCT GGAC ||| || |||| || |||| |||| |||| ||||
CAGAGGGACTCATGCGGGAT CGT CT GCGCT CTC GGGAGA TCGG TCAA CACTAT T
CTTGC T AG A A C CAA - A

GAM2349 GCCCTTCCTTACAGCGACCA 2335 TGACTCCTGA 5060 - - A C CCA A
CAGAAAACTCTGACTCCTGA GAGGACAGAG GCC CT TCCTT CAG GA CAGA A
GAGGACAGAGGC GC ||| || |||| || || ||||
CGG GA AGGAG GTC CT GTCT A
A C A - CA- C

GAM2350 GCCTGTAGGTAAGCCCCCA 2336 TGGCAGCGTC 5061 -- TAA-- CC C- CA TT
TCCTCACCTTTTTCAGGGCC CCCCTCAGCA GCCTGT AGG GC CC ATCCT CCT T
AGGGTCTGGCAGCGTCCCCC GGC ||||| ||| || || ||||| |||
TCAGCAGGC CGGACG TCC CG GG TGGGA GGG T
AC CCCTG AC TC CC AC

GAM2351 GGCCCCCGGAAGAGCTGCG 2337 AGTGGTAGGT 5062 ---- AG GA GCTTA AA
CA
AGTGGTAGGTGCTTAGGAAC GCTTAGGAAC GGCCCC GGA AGCTGC GTGGTAGGT
GG CCT T
CTCATGTAGGGGCGCTTAC CTC A ||||| ||| ||||| ||||| || |||
CACGCAGCTGTCCCCCTTGG CTGGGGG CCCT TCGACG CACCATTG CC GGA /
GGGTC TTCC G- -- ---- GG TG

GAM2352 GGCGGGGTTGGGCAACACTC 2338 TGCCCAGTGG 5063 AA C TATATA C GT T G
AATTA G
GGGCATTTATATAGACTAAG GGTCTCTCTG GGC CACT GGGCATT GA TAA CCCACA
GGCCTCT GTT GGC G
TCCACATGGCCTCTGGTTA GT ||| ||| ||||| || ||| ||||| ||||| ||| |||
ATTAGGCGGGGGCCAATGGG CTG GTGA CCCGTAA CT ATT GGGTGT CCGGGGG
TAA CCG G
GGGCCTGTGGGTATTACTCA GG - ----- C AT - G ---- G
ATGCCAGTGGGGTCTCTCT
GGT

GAM2353 GGGTCTGTAAAGAGGAAGCG 2339 AGAGGAAGCG 5064 - ----- --- G G CCCTTC
GGCGGGGCCGTCCCTTCCCC GGCGGGGCGG GGGT CTGT AAAGAGGAA GC GGCGGG
CCGT C
CCCAGCGGCCCGCTGGCATC TCCC ||||| ||| ||||| || ||||| |||
TTCCTCTTTTTTTTGACAGC CCCA GACA TTTCTCCTT CG TCGCCC GGCG /
ACCC C GTTTTT CTA G - ACCCCC

GAM2354 GGTAAGGTGTGTGAGAGCG 2340 AAGGTGCTTA 5065 AAA GT- A C T TT----
CCCA
AGAGTAGAGATTACCTTTA TTTCTCTCTC GGT GGT GTG GAG GAGAG AGAGA
CACCTTTATC A
TCCCCAAAAAAGGTAAAGGT TCCT ||| ||| ||| ||||| ||||| ||||| |||||
GCTTATTTCTCTCTCTCCTC CCA CCG CAC CTC CTCTC TCTCT GTGGAAATGG /
CACTCTGCCAGACC GA- TCT - - - TTATTC AAAA

GAM2355 GGTGGTCCTAAGAGTCTGTG 2341 TGTCACAGAC 5066 CC - - ATTATTTTT
AACTTAAATTATTTTTTATA TGCTTAAGCC GGTGGT TAAG AGTCTGTGA ACTTAA T
CAAACTTAAGTGTACAGA ATC ||||| ||| ||||| ||||| |||||
CTGCTTAAGCCATC CTACCG ATTC TCAGACACT TGAATT /
A- G G CAAAACATA

GAM2356 GGTGTCTCTGTTGATAGGGC 2342 TCTCCCGTAC 5067 - GT A G C TG TTAA C TCA
AT TTCT
GAGATGTGGTTTTAACAGCC GCAAGGGGCA GTCTCT TG TA GG GAGATG GT CAG CTG
ACTTAA TCT T
TGTCAACTTAAATTCTTTCT ACC ||||| ||| ||| ||||| || ||| ||| ||||| |||

TTAAACAGACTTAAGTCTCC CGGGGA GC AT CC CTCTAC TA GTC GAC TGAATT
 AGA T A AC - G - CT TAC-- A CTC C- CAAA
 AGACTGCATATTCCATCTCC
 CGTACGCAAGGGGCAACC

GAM2357 GTTGAATAGAGTGTGGTCTT 2343 TAGAGTGTGG 5068 A----- - G CA TTTTCTC TC
 TTCAAGATTTTCTCTGGCTC TCTTTTCAAG GTTG ATAGAG TGT GTCTTTT AGA TGGC
 T
 TGTGCCATTTTCTTTTAAAA ATTT ||| ||||| ||| |||
 AGGGCGACATCTCTATAGTG CAAC TATCTC ACA CGGGAAA TTT ACCG /
 TCACCAAC CACTGTGA T G AA TCTTTT- TG

GAM2358 TACAGACCCTGCAGCGCTCC 2344 AAAAAGCGTT 5069 GAC--- ---- CCA- T- - C AGG -
 G TCC
 AGATGTGACACAGGTAGCCC AACAAGCAGG A CCTGC AGCGCT GA GT GA AC
 TAGCC CT GATC A
 TGGATCTCCAGGTGATTGAG AGAA | |||| |||| || |||| |||| ||||
 AGGCTAAGGTATCGGCTTTC T GGACG TTGCGA CT CG CT TG ATCGG GA
 TTAG /
 AAAAAGCGTTAACAAGCAGG AGAAGA AACAA AAAA TT G A GA- A G TGG
 AGAAGATGTA

GAM2359 TAGAGCATTCTAATGGGGGC 2345 TGAGCAGCAT 5070 --- AA GA ATA C A G
 AACA- CACC
 AGAGTATATGCTCCTGGACC GCCCCCAAAG ATTCT TGGGGGCA GT TGCTC TGG CCT
 GTCATA GGTA A
 TGGTCATAAACAGGTACACC GGAT |||| ||||| || ||||| ||||| ||||
 ACCACTACCCCGGCTATGAT TAGGG ACCCCCGT CG ACGAG ATC GGA TAGTAT
 CCAT /
 GAGGACTATGAGCAGCATGC TTT AA A- --- T A G CGGCC CACC
 CCCCAAAGGGATTTTGA
 AAGCTTATCA

GAM2360 TCAAAACACTGTGCATCGTC 2346 TGA CTCCACT 5071 CA C A T TC -- A TG
 AGGGTTGATCCAGGTGAGTA CGGACGATTC TCAAAA CTGTG ATCGTC GGGT GA CAG GTG
 GTA G
 TGGCTTACACACAACTGACT ACAG ||||| ||||| ||||| ||| ||| |||
 CCACTCGGACGATTCACAGG AGTTTT GACAC TAGCAG CTCA CT GTC CAC CAT /
 ATTTTGA AG T G C CA AA A TC

GAM2361 TCTATCCTGGCTATGGGGGC 2347 TATCCTGGCT 5072 -- ATG --- - A
 CAGGGCCAGGCTGAGGACGC ATGGGGGCCA TCTATCCT GGCT GGGGCCAG GGCCA
 GGCTGAGG C
 TCTCGGCTATGGCCATCTTG GGGC ||||| ||| ||||| ||||| |||||
 GCCCCGGCCTCGGGGTAGA AGATGGGG CCGG CCCCAGTT CCGGT TCGGCTCT G
 CT --- CTA A C

GAM2362 TCTGTGGGATTGGCGGGGTA 2348 TGGCCACGTC 5073 TTG G A TG G

GAM2363 TGGGACTCGGTGTGGAGGAG 2349 AGAGGGGGTAG 5074 AC G TAGTTA C C
AGGGGTAGTTACGATTACTC TTACGATTAC TGGG TC GTGTGGAGGAGAGGGG CGATTA TC
A
CATGACTAATCGCAAGTCCT TCCA ||||| || ||||| ||||| ||||| ||
CCTCTCCTCTACACAGACGC ACCC AG CACATCTCCTCTCCTC GCTAAT AG /
CCA GC A CTGAAC C T

GAM2365 AGACGGCTCGACCTTCTGGG 2351 TCTCCAGACA 5076 - C CCTT- G C TTC AAAC
TCTCGGATTCGAGAGAAACT CGGTATTTTT AGA CGG TCGA CTG GTCT GGA GAGAG T
TAACCTCTCTCCAGACACGG GAAC ||| ||| ||| ||| ||| ||| |||
TATTTTGAACCGATCT TCT GCC AGTT GGC CAGA CCT CTCTC /
A A TTTAT A - --- CAAT

GAM2367 ATCGTAATTGTCTTCGATAA 2353 TATTATAAGC 5078 - CG ATT TAG
ATTACTAGGGCTGTTATTAT GCAATTACGA ATCGTAATTGTCTT ATAA AC G
AAGCGCAATTACGAT T ||||||||| ||| ||| ||
TAGCATTAACG GAA TATT TG /
C -- AT- TCG

GATCATCGAGTAGTTTCGTA ATCGAGTAGT CC GAGAAGG CGTAGAATTGAT GTAG
 ACGAG ATGT C
 CGAGAATGTAACCCGCGTAC TTCG || ||||| ||||| ||| |||||
 TTGTTACATCTACATCGGTT GG CTCTTTC GCGTTTTGGCTA CATC TGTT
 TGCG /
 TTGCGTAAACCTTTCTCAG A CAAAAT ----- TACAT- A CC
 G

GAM2369 CGATATAAAAACGATAATAC 2355 ATCATAGGCA 5080 TAAAAAC CGGA CG C -----
 ---- TA
 CACGGAGCCTCGGATTCTAT TTGGTATTGT GATA GATAATACCA GCCT GATT TATA
 ACGCA C
 AACGCATACAACGTGTGCAT TATT ||| ||||| ||| ||| ||| ||||
 TCTGAATGTATAAATCATAG CTAT TTGTTATGGT CGGA CTAA ATAT TGTGT
 A
 GCATTGGTATTGTTATTATC TA----- TA-- TA - GTAAGTCTTAC CA
 G

GAM2370 GATGACGGCCGATAAGACAA 2356 TCGAAGTCAA 5081 -- AAGACAATGA A C GA
 GATTATCA
 TGATGACTACGACGAGGAGT ATCGGTCGAT GATGA CGGCCGAT TGA CTG A GAG
 GTAT C
 ATGATTATCACATAACAACA TCAT ||||| ||||| ||||| ||| ||| |||
 GTACACTCTCGAAGTCAAAT TTACT GCTGGCTA ACTGA GCT CTC CATG A
 CGGTCGATTCATT TA A----- A - A- ACAACAAT

GAM2371 GCACGTCTGTCTGTGTACAG 2357 TGACACATGA 5082 - - --- - A CTTGT
 TCTTGTGAAACCACTGACAC CACAAGAACG GC ACGT CT GTC TGTGT CAGT G
 ATGACACAAGAACGTCGC TCGC || ||||| ||| ||||| ||||
 CG TGCA GA CAG ACACA GTCA /
 C A ACA T - CAAA

GAM2372 GCAGTACTTTTCGGTGGATA 2358 TACGATACAG 5083 T TTT G CA A - AT
 CGATACAGCGAAATCAAAAA CGAAATCAAA GCAG AC TCGGTG ATACGATA GCGA AT
 CAAAAAG G
 GATGAGTTTTTTGCATCTCG AAGA ||||| || ||||| ||||| ||| ||| |||||
 CATATTGTGTGTGCTGGTAC TGTC TG GGTCGT TGTGTTAT CGCT TA GTTTTTT /
 GTCTGT - CAT G A- C C GA

GAM2373 GCCGGTACTGACATCTAACG 2359 TAACGTGACA 5084 - GACATCTAA T CC TT - G
 GTG TTA
 TGACACCGTTTCTCGGTCCG CCGTTTCTCG GCCGGTA CT CG GACA GT CTCGG TCC
 ATA GTTCCAT T
 ATAGTGTTCCATTTATCGC GTCC ||||| || || ||||| ||||| |||||
 GTGGAGCAAATGTGGACCCG CGGCCGT GA GC CTGT CA GAGCC AGG TGT
 CGAGGTG /
 AGGGACCTGTCTCGCCAACC C ACCAACC-- T C- GG C - AAA CGC

GAM2374 GCTGCGTTCGGTCCCAATAG 2360 TATCATAGAC 5085 - - C AA---- T- G ----- - - T
ATATGTGCACTGGATTTAAC AACTTGACAT GC TGC GTT CGTCCC TAGA ATGT CA CTG
GAT TTAACG C
GTCGTGTTGATATCATAGA TTTC ||||| ||||| ||||| |||||
CAACTTGACATTTTCTGAGA CG ACG TAA GCAGGG GTCT TACA GT GAT CTA
AGTTGC G
CACGGGACGAAATGGCACGC C G A CACAGA TT - TCAACA A T T

GAM2375 GTATATCTAAATAGAAATAA 2361 TAAATAGAAA 5086 A A - A AA- ---- CTA AAA
AGAGTGTTAATGCTAAAACA TAAAGAGTGT GTAT TCT AATA GA AT AGAGT GTTAATG C
TTGAAACATTA ACTAGAATT TAAT ||||| ||||| ||||| |||||
CTATCATATCATATTCAGAC CATA AGA TTAT CT TA TCTTA CAATTAC A
ATAC C C A A CTA AGAT AAAGTT

GAM2376 GTCTTCCTTCCGCAAGGACG 2362 TTCGTTCTTC 5087 - TT C CCAT CCT
CCATATCCCTGCTCCGATTC GGTTGGTAAG GTCTT CC CCG AAGGACG ATC G
GTTCTTCGGTTGGTAAGAT AT ||||| ||||| ||||| |||||
TAGAA GG GGC TTCTTGC TAG C
T TT - T--- CCT

GAM2377 GTGTAAAAGTCGACGTTCCA 2363 AAAAGTCGAC 5088 --- C--- TT GC AAACCTAA TT
CATCA C
CGTTCACGTGCGGAAACTTA GTTCCACGTT CGA CGTTC ACG CACGT GG CGTCT
AGA AATTT T
ACGCTTTTAGACATCAAATT CACG ||||| ||||| ||||| |||||
TCTGTAAATTAACAATCTAG GCT GCAAG TGT GTGCG CC GCAGA TCT
TTAAA G
ACGAGCAACCCCAAGCGTGT ACA TTAT GT AA CCAACGA- -- AACAA T
GTGTTATTGAACGACATCGA
TTAACAT

GAM2378 TAGACTATATATTCTAAGAA 2364 TCAGATCTCT 5089 T AC- - CGT-- ACGAT AG A
ATC CTC
ATTGTACGAGGCCGTGTCTG CGCTCTCCTG AAGAAAT GT GAG GC GTCTGACG GA
ACG CG AGAAT A
ACGACGATGAAGACGACGAT ACAT ||||| ||||| ||||| |||||
CAGAATCTCATGTATTCTAC TTCTTTA CA CTC CG TAGACTGT CT TGC GC
TCTTA /
GCCGTTCTCTGTCAGATCTC - GTC T CTCTC ---- CT C A-- TGT
TCGCTCTCCTGACATTTCTT
TCTCCGTCTA

GAM2379 TTTGCTTAACAGTGGCATGT 2365 TACCACACAA 5090 AACA----- C AAT TA
GACAATTCTACGTCGATCGT GGATCAAAGC TTTGCTT GTGG ATGTGAC TC C
TACATACCACACAAGGATCA AGA ||||| ||||| ||||| |||||
AAGCAGA AGACGAA CACC TACATTG AG G
ACTAGGAACA A CT- CT

GAM2380 CAAATATCTGGATAGCATAT 2366 TAGCATATGC 5091 T---- TA C T CT A
 TAATC
 GCTATCCTAATCTATATCTG TATCCTAATC GGATAGCATATGCTATCC AT TA AT GGGTAGC
 TATGCTATCC T
 GGTAGCATATGCTATCCTAA TATA ||||| ||||| ||||| ||||| |||||
 TCTATATCTGGGTAGCATAG CCTATCGTATACGATGGG TA AT TA CCTATCG
 ATACGATGGG A
 GCTATCCTAATCTATATCTG CTAAT TC T C AT G TCTAT
 GGTAGCATATGCTATCCTAA
 TCTATATCTG

GAM2381 CCCGTGTTTTCCCAACAAA 2367 TGACAGTTGT 5092 G TT -- ACAA TGGA AA
 GATTGTTAGTGGAATTAATG TCCTGGTAGG CCC TG TTCC CCA GATTGTTAG ATT T
 GAGTGTCTGACAGTTGTTCC GATT ||| ||| ||| ||||| |||
 TGGTAGGGATTCTGAGGG GGG GC AGGG GGT TTGACAGTC TGA /
 A TT AT CTTG TG-- GG

GAM2382 CCTTCTGGATCCAGGAATGT 2368 TGTAGACCAG 5093 TCCA ATGT -- AATTA - -- CGC-
 - TT AAT
 TGTCTTCAATTAATGTAGAC CCGCCCTGTT GGA TGTC TTC ATGT AGA CCAGC
 CCTG GATG C
 CAGCCGCCCTGTTGATGAAT GATG ||| ||| ||| ||||| ||||| ||||| |||||
 CCAACCATCCAGGCCTTCGC CCT ACAG AAG TACA TCT GGTCG GGAC CTAC
 C
 TGGCTTCTAACATCCCACGA AACA GG-- TC CACCC A TC CTTCC -- CAA
 ACTGACAGGTCCACAACATA
 GTAAGG

GAM2383 GACGAAACCTTGACCCTTCT 2369 TAATAAGGAG 5094 - AACCTT- C- C CT G A
 GA A
 TGTCAACCTCTTCAGGCCCG CCGTCCTTAT GA CGA GAC CTTCTTGT AACCT TCAG
 CCCGGGGTT GT TG A
 GGGTTAGTGATGAAACAGGC TCTT ||| ||| ||| ||||| ||||| ||||| ||||| |||
 AACTCCGGGGCTGATCAGGT CT GTT CTG GAGGAATA TTGGA AGTC GGGCCTCAA
 CG AC /
 TAATAAGGAGCCGTCCTTAT C CTTATTC CC A CT G - G- A
 TCTTGCTC

GAM2384 GCGTTGGGGGCCAGAATCA 2370 TCTCTGGACA 5095 T ----- - G
 GAGGTGATCTCTGGACATTA TTAACCTCCA GCGT GGGGG CCAGA ATCA A
 ACTCCACGCC CGCC ||||| ||||| ||||| |||||
 CCGCA CCTTC GGTCT TAGT G
 - AATTACA C G

GAM2385 GTAGCATATACTACCCAAAT 2371 TAGCATATGC 5096 A CT---- TA C T CT
 A
 ATCTGGATAGCATATGCTAT TATCCTAATC TACTACCCA ATAT GGATAGCATATGCTATCC
 AT TA AT GGGTAGC T

CCTAATCTATATCTGGGTAG TATA ||||| ||| ||||| ||||| || || || |||||
 CATAGGCTATCCTAATCTAT ATGATGGGT TATA CCTATCGTATACGATGGG TA AT TA
 CCTATCG A
 ATCTGGGTAGCATATGCTAT C TCTAAT TC T C AT G
 CCTAATCTATATCTGGGTAG
 TATATGCTAT
 GAM2386 TAGGCGGGGTTAAGCGTGCA 2372 TGCAACGTTA 5097 A - T
 TCTTCTGGGATGCAACGTTA AGCCCCGTTT TAGGCGGGGTT AGCGT GCATCT C
 AGCCCCGTTTA A ||||| ||||| |||||
 A T T G C C C C G A T T G C A C G T A G G T
 A A G

GAM2387 TCCCAGAGGGATTAGAGAAT 2373 AGAGGGATTA 5098 A--- - TT AA- A --- A
 CCTGACTTGCAAATGCTCTA GAGAATCCTG TCCC GAGG GA AGAG TCCTG CTT GC A
 GGCGGGAAGCCTCTCTTCTC ACTT ||| ||||| || ||||| ||||| ||| ||
 CTCCCCCGGGA AGGG CTCC CT TCTC AGGGC GGA CG A
 CCCC T TC CGA - TCT T

GAM2388 TGTGTTATTTTAACGAAGAG 2374 TTTTAACGAA 5099 TTA AA C - - TTGCA
 CGTGAAGCACCGCTTGCAAA GAGCGTGAAG TGTG TTTTAACG GAG GTG AAGCAC CGC A
 TTACGTGTGTGCTTACACAC CACC ||| ||||| || ||||| ||||| |||
 TTCCCGTTAGAACACCACA ACAC AAGATTGC TTC CAC TTCGTG GTG /
 CAC CC A A T CATT A

GAM2389 AAACATAATATTAATTCTTT 2375 TAAATTGATG 5100 A T T A AA-- A- TTACC
 TGAGTTAAAATTTATAAATG GACCTAATGG AAAC TAATA TAATTCT TTG GTT AATTTATA
 ATGAT A
 ATTTACCAAACTTGTCTATC AGTT ||| ||||| ||||| || ||||| ||||| |||||
 ATATAAATTGATGGACCTAA TTTG GTTAT ATTGAGG AAT CAG TTAAATAT TACTG A
 TGGAGTTATTATTGAGTTT A T T C GTAG AC TTCAA

GAM2390 AAAC TAGAGGCAGTAATGTT 2376 AGGCAGTAAT 5101 C AC-- AG- TCCCTTAAC ---
 ACCATT
 ACCTTAGGTTCCCTCCCTTAA GTTACCTTAG AGTAATGTT CTT GTTCC GCTATAT
 GAGATTTT G
 CGCTATATGAGATTTTACCA GTTC ||||| ||| ||||| ||||| |||||
 TTGATGCAAAGAATCTCTG TTATTACAA GAA CAAGG TGATATA CTCTAAGA
 A
 CATATAGTGGAACAAAAAGT T CCCT AAA ----- CGT AAACGT
 CCCAACATTATTTCTTTTA
 TGGTTT

GAM2391 AAATTGCAATAGTTTCTACA 2377 TATCAAATAA 5102 T --- TTCTAC---- T A A
 TATTTTATTTGATAATATA CGATATTA A AAA TGCA ATAGT ATATT TTATTTGATA TAT T
 TAGATGTATCAAATAACGAT CTTG ||||| ||||| ||||| ||||| ||||| |||
 ATTAACTTGTTACTATAGC TTT ACGT TATCA TATAG AATAAACTAT GTA A
 TGCATTTT T CGA TTGTTCAAAT C - G

GAM2392 AACAGATGAAGTAAAATAAT 2378 TGAAGTAAAA 5103 TAA-- AA TA TA TA CAT-----
TCCA TC
ATGTTAAGTTATGTACATTA TAATATGTTA TAAAA TATGTT GT TG CAT CATG ATAT
GAA A
CATGCATATATTCCAGAATC AGTT |||| |||| || || |||| |||| ||
ATTTTTCGTTATATTATTTA ATTTT ATATAA CA AC GTA GTAC TATA CTT T
TCCACATGCTATGCCCAACA TAGGA GA -- CC TC ACCTATTTAT TTG- TT
GAATATAAGGATTTTTACAT
CTCCTGTT

GAM2393 AACTTATTATTGTTAGATGA 2379 TGAAATAACT 5104 ---- TG TG-- CCTACTTT A T
TCG
TGAAATAACTGATAGACCTA GATAGACCTA TGTTAG ATGA AAATAAC ATAGA TGG
TATA GTGCA A
CTTTTGGATATATGTGCATC CTTT ||||| ||| ||||| |||| ||| ||| |||||
GACATTGTATCTGTAACAT GCAATT TATT TTTATTG TATCT ATC ATGT TATGT
/
AAATTCTATACCCGTTATTT ATTAA GT CCCA TAAAT--- A C TAC
TGTATAATTATTAACGAAC
ATTAGTT

GAM2394 ACCGAAACAACTTTTCAGAT 2380 TCTCTGATTA 5105 CTTT T A ATAT
GATGACGATATCACAACCGC TTTGTTTTGG ACCGAAACAA TCAGA GATG CG C
CATCTCTGATTATTTGTTTT T ||||| |||| ||| ||
GGT TGGTTTTGTT AGTCT CTAC GC A
TATT - C CAAC

GAM2395 ACTCTAGCACTTGTTTATTT 2381 TAATATCAAT 5106 A TG- T TGT TT GTAAGT----
TT
GTCTTTGATTGTTTATTTTA GAAATAAAAA TGTTT TT TC TTGAT TTATT ACAATAAT
TTAATAAGT A
CAATAATGTAAGTTTAATAA ATAA |||| || || |||| |||| ||||| |||||
GTTTACCATTGTGTAATAGG ATAAA AA AG AACTA AATAG TGTTATTA
AATTGTTA /
AGAAAAATTATTGTTGATAA A TAA T T-- T- AAAAGAGGAT CC
TATCAATGAAATAAAAAATA
AGGTTATGGT

GAM2396 AGGTTATAATGTAACAAATT 2382 TATTATTCTA 5107 TA CAAATTATC C T
ATCATACATATGATTTTGAA CTTTGCATT AGGTTA ATGTAA ATA ATATGATT T
TCATATTATTCTACTTTTGC AACC |||| |||| || |||||
ATTAACCT TCCAAT TACGTT TAT TATACTAA /
-- TTCATCT-- - G

GAM2397 AGTGTTGGTATTGCTTCGAG 2383 TATTCGCTA 5108 ATT T- CC TC
ACCTCGTTTCTGACAACGAT GTTAAATCAG AGTGTTGGT GCT CGAGA TCGTT T
ATTCGCTAGTTAAATCAGC CACT ||||| ||| |||| ||||
ACT TCACGACTA TGA GCTTT AGCAA G
AAT TC AT CA

GAM2398 ATAAAATCAATCCAATCAAT 2384 TATCACTTCT 5109 CAATCCA TGCTCT CTCA
AG

GCTCTAATATCACTTCTCAT CATGAGAATA ATAAAAT ATCAA AATATCACTT
TGAGAATATT G
GAGAATATTAGGAAAAATAT TTAG ||||| |||| ||||| |||||
TTTTAAATGAGTGATGTTTT TATTTTA TAGTT TTGTAGTGAG ATTTTATAA A
GATATTTTAT ----- TAA- AA

GAM2399 ATAAACTAAACATTTTTTTGA 2385 TATTTTTTCT 5110 TTTT TG TG TT - A-- - ----- G
TA

ATGGGAAATTGTAATTGCTA TGTTTGATTA A T AA GGAAA GTAAT TGCT GTAT CA ACA
TGATAA C
GTATCAACAGTGATAATACG CTGA | | || |||| |||| |||| |||| ||||
TTTATCAATGTCTATAACTG T A TT TCTTT TATTG ACGG CATA GT TGT ACTATT

/
AATACATAGGCATGTTATTT CATT GT GT TT T ATA A CAATATC A TG
TTTCTTGTTTGATTACTGAT
AAAGTTTAT

GAM2400 ATATTTTGCAATATCTCTAT 2386 TAATATAGAC 5111 TT TCTCTATTATT TTCCC- A
AT T

TATTTCTTCTTCCCGTTTAA TTATACGAAG ATATT GCAATA TCTTC GTTTA TAT TC T
TATATTCTTCTGATAATATA ATTT |||| |||| |||| |||| ||||
GACTTATACGAAGATTTGTT TATAG TGTTGT AGAAG CAGAT ATA AG C
GTCTGATAT TC TT----- CATATT - AT T

GAM2401 ATCGCACACGGTGCAGCAAA 2387 CAGCAAACAC 5112 GCA GCA- CAATA
GAAGTATTAAGA G

CACAATAACAGAAGTATTAA AATAACAGAA ATC CACGGT GCAAACA ACA TTC G
AAGATTTCGGAAGAGGACTAT GTAT || |||| |||| |||| ||||
CAAGATGTGTATGTTTGTGA TAG GTGTCA TGTTTGT TGT GAG A
AAACTGTGGAGAT AG- AAAG ATG-- AGAACTATCAG--- A

GAM2402 ATCTAATACAGTTAATGACA 2388 AATGACAGAT 5113 T TAAT T T TTCTTT TC
GATCATTATTTATTTCTTTA CATTATTTAT ATCTAA ACAGT GACAGA CATTATTAT ACTT T
CTTCTATAAGTTTGTGATT TTCT |||| |||| |||| |||| ||||
AGTGTGTTGTTTATATTGTT TAGGTT TGTTA TTGTTT GTGAT AGTG TGAA /
TGGAT T TAT- - T TT---- TA

GAM2403 ATTTATTTTTTGATGAAGGA 2389 TGAAGGATCT 5114 A A - TC-- ---- C A TTG
TCTAGTGACGTATGTCTTG AGTGACGTA ATTT TTTTTTG TGA AGGA TAG TGTA GT TGTC

C
CAACGACAAATTTACAAAAT TGTC |||| |||| |||| |||| |||| ||||
CTAATTTTCCTATTAATAAA TGAA AAGAAAT ATT TCCT ATC ACAT TA ACAG /
GAAAAAGT A A A TTTA TAAA T A CAA

GAM2404 ATTTTAAATGCGTTGGAAA 2390 TGTTATCTTT 5115 TT AAT--- T ----- - TC--
TATCTAAT
AATAACTAATTTAGTAGCGT TTAAATTGTT G GGAAA AAC AATTTA GTAGCGTTTG TG
GTTG C
TTGTGTCGTTGTATCTAATC CCCA I ||||| ||| ||||| ||||| || ||||
AAAAC TTTTAATTCATCATC C CTTT TTG TTAAAT TATTGTAGAC AC TAAT /
AGATGTTATCTTTTAAATT TT ACACCC - TTTTC T TACT TTTCAAAA
GTTCCACATTTCTTCGTA
TCGTTTAAAAT

GAM2405 CCACTTTTATTAAAATGTCC 2391 TGGAAAAGGA 5116 C AAAAT CA- AAACGA - AA
ACTTTTAAACGAATATAGGT TGATTATGAA CCA TTTTATT GTC CTTT ATATA GGTT A
TAAAATGGCCATATATGGAA ATAA ||| ||||| ||| ||||| ||||| ||||
AAGGATGATTATGAAATAAA GGT AAAATAA TAG GAAAA TATAT CCGG /
ATGG - AGTAT TAG GG---- A TA

GAM2406 CTGTTTTAATCATATTAAAT 2392 TTAGGAAATA 5117 TAT A ----- T A AAACAG -
AG
GATTAGGAAATATTATGAAT TTATGAATTT TAA TGATTAGGA AATATTATGAA TT ATA
TTTCAAAA GC T
TTAATAAAACAGTTTCAAAA AATA ||| ||||| ||||| ||| ||||| ||||
GCAGTCTGTGTTTTGAAAGG ATT ACTAGTTTT TTGTGGTACTT AA TAT
AAAGTTTT TG /
ATATAAACTTCATGGTGTTA C-- G AATTA C A AGG-- G TC
TTAATTTTGATCAGTTACAA
AATGGAATAG

GAM2407 GAGTGGCAGAGAAATCATT 2393 ATTAGATTCA 5118 CA AATCATTAC AG----- AT
CAATCTGATTTAGTTGATAA TCTATATCTT GAGTGG GAGA AATCTGATTT TTGATAA T
ATTTGTTATTAAATGAATAA CTC ||||| ||| ||||| ||||| |||||
AATTAGATTCATCTATATCT CTCCT TTCT TTAGATTAAA AATTATT /
TCTTCACTC TC ATATCTAC- ATAAGTA GT

GAM2408 GATACGTAATTAATAATATC 2394 TTTGTTGGTG 5119 AA AA TTA C A TTT
TAGCCTTTT
ATCATTAGGATACTTTTTTA GTACGTTAAG GATACGT TTAAT TATCATCA GGATA TTTTTT
TTA CTA T
TTATTTCTATAGCCTTTTTC CGTA ||||| ||||| ||||| ||||| ||||| ||| |||
ATATTATTTAGTTTTAACAA CTATGCG AATTG ATGGTGGT TTTAT AAGAAA AAT GAT
/
AGAAATATTTGTTGGTGGTA -- C- TG- A C TTT TTATTATAC
CGTTAAGCGTATC

GAM2409 GATGATATAAATGATAAAAT 2395 TGATATAAAT 5120 T ATGATAAAA C A ATT
GTTTTGCGATACAATTTTAT GATAAAATGT GATGA ATAA TGTTTTG GAT CA T
ATGATCCCGAAACAGATAAA TTTG ||||| ||||| ||||| ||| |||
CCTTATTCGTC CTGCT TATT ACAAAGC CTA GT T
- CCAAATAG- C - ATA

GAM2410 GATGGTAAGATCTCTCTTGT 2396 TAAGATCTCT 5121 - - C TGG T
 TGGAGATTATTCTATTATAG CTTGTTGGAG GATGG TAA GATCT TCTTGT AGA T
 GAAGATCGTTAGTTATT ATTA ||||| ||| ||||| ||||| |||
 TTATT ATT CTAGA AGGATA TCT A
 G G - TTA T

GAM2411 GATTTTCATATTAAATGTTAC 2397 TAGTACAAAT 5122 TAAATGT A----- T TT
 AAAATTTGTATCTATATTTT CAAAATATTG GATTTTCATAT TACAA ATTTGTA CTATATTTTC
 C
 CTTCTCGAGAATGTAGTACA TGTT ||||| ||| ||||| ||||| |||||
 AATCAAAATATTGTGTTAAA CTAGAGTATG GTGTT TAAACAT GATGTAAGAG /
 ATGTATGAGATC TAAATT ATAAAAC - CT

GAM2412 GCATATGTTCCAGGATTGAT 2398 TAATACTGTG 5123 C GA A C A CCA
 GACAGCGGCATTAAATATCC GTTAAAGATT GCATATGTT CAGGATT TGAC GCGG ATTA TAT
 A
 AAACAAGTGTTAATACTGTG TTGA ||||| ||||| ||| ||| ||||| |||
 GTTAAAGATTTTGAAACGTA TGTATGCAA GTTTTAG ATTG TGTC TAATT GTG A
 TGT A AA G A - AAC

GAM2413 GCGTCTAGATTTAAAAAAGT 2399 TTTAAAAAAG 5124 GAT----- AG - A CC
 TTATATATTAGTACCAAATA TTTATATATT GCGTCTA TTAAAAA TTTA TATATT GTA A
 TAAATATACTAAAGATTTTT AGTA ||||| ||||| ||| ||||| |||
 AATTATAGTATGGACGT TGCAGGT AATTTTT AAAT ATATAA TAT /
 ATGATATT AG C A AA

GAM2414 GCTATATCAATCAAAAATAG 2400 GGAAATGAAC 5125 AT C AA--- TTC GATGTTAGA
 AA
 TTCTTATTTCTGATGTTAGA CTAGTACATT GCT AT AATCAAA TAG TTATTTCT TCC A
 TCCAAAAGAGGAGGAAATGA TGAT ||| || ||||| ||| ||||| |||
 ACCTAGTACATTTGATTTAT CGA TA TTAGTTT ATC AGTAAAGG AGG A
 TAAGC AT T ACATG CA- ----- AG

GAM2415 GGAACGCTATTCAGTACATA 2401 TTCGTTAGAA 5126 AT----- ATAA CCATTA T-
 TAGC
 ATCTCCATTAAATGTTACGT AAGTACTGAT GGAACGCT TCAGTAC TCT AATG
 TAGG T
 AGCTGTTTTTCGTATTCGTTA AATA ||||| ||||| ||| ||| |||
 GAAAGTACTGATAATAAAT CTTTGTGA AGTCATG AGA TTGC ATGC G
 AATAAAGTGTTTC AATAATAATAAT AAA- ----- TT TTTT

GAM2416 GGTAATATATTTACATGGG 2402 TCTGATGATA 5127 ----- A-- G - A

ATCAAAAGATTTTGCATCTG	AAATATATTT	GGTA	AATATATTT	CAT GGAT CAAA G
ATGATAAAATATATTTCAAA	CAAA			
TTTATACC	CCAT	TTATATAAA	GTA TCTA GTTT A	
	ATTTAAACT	ATA G C T		

GAM2417	GTA	ACTGCGTTAATGGGCAT 2403	AATGACAACT 5128	C TA	GCA	TTT
	CATTTATTTAGTATTAATG	ATACCGGTTA	GTA	ACTG GT	ATGG	TCATTTA A
	ACAACTATACCGGTTAC	C				
	CATTGGC CA	TATC	AGTAAAT G			
	- -	AAC	TAT			

GAM2418	GTATTA	AAAATATTGTTTGTG 2404	ATCAGAGTTA 5129	AA TT	GTT TC - - T
	TTTAATCCTATCATGTATTG	TAACAAATCC	GTATTA	ATA GTTTGT	TAA CT ATCATGT ATTG C
	TCCTAGTAACATGATCAGAG	TATG			
	TTATAACAAATCCTATGTAA		TATAAT TAT TAAACA	ATT GA	TAGTACA TGAT /
	TAT	G- CC	AT- GA C	A C	

GAM2419	GTTAGAAAATATAAATTGTT 2405	TCTGCAGTAT 5130	AAA-- A TT	ATCC
	TAGATAATCCAAATATATCT	ATGGTAACTT	GTTAGA	TATA ATTGT AGATA A
	GCAGTATATGGTAACTTTAA	TAAT		
	T	TAATTT	GTAT TGACG TCTAT /	
	CAATG A	--	ATAA	

GAM2420	GTTGAATGCATATATTGGAA 2406	TTCTTCATGT 5131	G A TG A CTAATAT	G CT
	TTC A			
	GTGCTAATATGGATTGGAGG	TTGGTAATGG	GTTGAAT CAT TAT GA GTG	GGATTG AGGT
	CT TCAAGTT A			
	TCTCTTTCTCAAGTTAAAGA	ATTT		
	ACTTGGTATAGGTATTTACA		TAATTTA GTA ATG TT TAC	CTTAAC TTTA GA
	GGTTCAA A			
	ATTCTTCATGTTTGGTAATG		G - GT G TT----	A TG TAT G
	GATTTAAT			

GAM2421	GTTTAGGAATCGAAACAAGT 2407	TTATTTGTTC 5132	AT-----	-- T	TTAAATCCTA
	TGA				
	GTTGGTTTAAATCCTACTAT	TTCGTCCGAC	GTTTAGGA	CGAA ACAAGTG TGGT	
	CTAT T				
	TGATAATATAGATGCTATTA	ATAA			
	TTTGTTCTTCGTCCGACATA		CAAGTCTT	GCTT TGTTTAT ATCG	GATA /
	ACTTCTGAAC		CAATACAGCCT	CT T TA-----	TAA

GAM2422	TAAAGTTAAGTTTAAATCTG 2408	TAAGTTTAAA 5133	TTA- AA- GCAAA G
	GCAAATGTTTGTAACGGC	TCTGGCAAAT	TAAAG AGTTTA TCTG TGTTT T
	AACAGAAATGTAAATTCCTTC	GTTT	
	TTTA	ATTC	TAAAT AGAC GCAAA /

TTCC GTA AACG- A

GAM2423 TAATACATTGGGAAGAAGGA 2409 AGAAGGATTT 5134 T GA A- TG TT T
TTTTGTTATTAGGTTTAAGC TGTTATTAGG TAATACAT GG AG AGGATTT TTA AGGT T
TTTAGTGAAATTTTAACTAA TTTA ||||| || || ||||| || ||||
CTTGTGTATTA ATTATGTG TC TC TTTTAAA GAT TTCG A
T AA AA GT -- A

GAM2424 TACTGCGATGTATCAATATG 2410 TTTATCAAAT 5135 -- AT TA TA TG- T AAGGC
TTTTAATGATGTGATTAAAA TCATCCAAAT TACT GCG GTATCAA TGTTT ATGA TGAT
AAAATTA C
TTAAAGGCCATAAAATAATT ACTT |||| || ||||| |||| |||| |||||
TTATCAAATTCATCCAAATA ATGA TGT CATAGTT ATAAA TACT ACTA TTTAAT A
CTTTGATACCATGTTTAGTA TT AC TC CC TAA - AAAAT

GAM2425 TAGATTGCTCAGCTGTAAAA 2411 TTGCTCAGCT 5136 G -- AAA- TGAACAT
TTTAGTGAACATGTAAATTA GTAAATTTA TAGATT CTCA GCTGTA TTTAG G
TTTAAAAACGTGCAGTGTTG GTGA ||||| |||| ||||| |||||
GGAAATTTG GTTTAA GGGT TGACGT AAATT T
A TG GCAA TATTAA

GAM2426 TATCATGTTGTAAGCGTTGA 2412 TTAATGCCTA 5137 TG A-- GTAA
TTGTAATAAAGAATTAATGC TACGAACTGA TATCA TTGTA GCGTTGATT T
CTATACGAACTGATA TA |||| |||| |||||
ATAGT AGCAT CGTAATTAA /
CA ATC GAAA

GAM2427 TCATATACTGTGACGGCGTT 2413 TGTCAAGAAG 5138 -- GACG--- G-- GAAT
GATGCAGAATTTGTGATGTG CAAAAAAAT TCATATA CTGT GC TTGATGCA T
TCAAGAAGCAAAAAAATAG AGCA ||||| |||| || |||||
CATATATGA AGTATAT GATA CG AACTGTGT T
AC AAAAAA AAG AGTG

GAM2428 TCATATCTCCCTCTAAAGAA 2414 TCTAAAGAAG 5139 ATCTCCCT- AA GATG- - TTC-
TGTTTT
GAGACGATGACTGGCTTTCT AGACGATGAC TCAT CTAAAG GAGAC ACTGG CT
TATGTT G
ATGTTTGT TTTTGGTGT TTT TGGC |||| ||||| |||| ||||| |||||
GACATATCCTAGACCAGTAT AGTA GATTTC CTTTG TGACC GA ATACAG /
ACGGTTTCAACTTTAGTAAA GACTAAAAT AA GCATA A TCCT TTTTGTG
ATCAGATGA

GAM2429 TCCATACGCTATAATAAGTA 2415 TAATACAACT 5140 CGC ATAA AAG TT
AAGATGTTGTTTTACGATAT ATAAATATG TCCATA TATA GTA ATGTTG T

AATACAACTATAAAATATGG GA ||||| ||| ||| |||||
 A AGGTAT ATAT CAT TATAGC /
 AAA CAA- AA- AT

GAM2430 TCCATATAACAATCCTAAAT 2416 TATAACAATC 5141 A - - A-- TG AGAAGA A AA
 TGTCGAGAAGAAATGCTATT CTAAATTGTC TCC TATAAC AAT CCT AAT TCG AATGCT TT
 A
 AAAAAAAAAAGTATTAAACGA GAGA ||| ||||| ||| ||| ||||| ||
 TGGTTATGAGGAATTCGTTA AGG ATATTG TTA GGA TTG AGC TTATGA AA /
 TAAGGA A C A GTA GT AAA--- A AA

GAM2431 TCTGAGTTAAATGTTTATAG 2417 TGAGTTAAAT 5142 T TTATAGATCAT A - TT
 ATCATGTAAAGGTATTGTTT GTTTATAGAT TCTGAGTTAAA GT GTAA GGTATT GT A
 ATAGCGGATACTGTTACACT CATG ||||| || ||| ||||| ||
 TTTAACTTAGA AGATTCAATTT CA CATT TCATAG CG /
 T ----- G G AT

GAM2432 TGAAAATTCAAAAAAATTAC 2418 TATCACATTC 5143 A---- A ATGCATTTT A A TAAA-
 -- A
 TTTAGGTATGCATTTTAA CTACAATGAG AAA AATT CTTTAGGT TAA CTTATT GT
 TGGTATC A
 CTTATTAGTTAAATGGTATC ATTA ||| ||| ||||| ||| ||||| || |||||
 AAAGATATCACATTCCTACA TTT TTAA GAAGTCCA ATT GAGTAA CA
 ACTATAG /
 ATGAGATTATTTCTACACC AGACC C CATCCTTT- A - TCCTTAC A
 TGAAGCAATTCCAGATTTTG
 TATTTCA

GAM2433 TGAAGAAACAGAATATTTCA 2419 TGGAATGTTA 5144 AGAAACAG-- A-- ATA--- A
 AT
 TTAAAGAATATAATACTTAT ACAAATATAT TGA AATATTTTCATTA AGAATATA CTT
 TCTTT T
 CTTTATTTAAAGGAAAAGGA CA ||| ||||| ||||| ||| |||||
 TCCATATATTTTGTATAATG ACT TTGTAAGGTAAT TTTTATAT GAA AGGAA /
 GAATGTTAACAAATATATCA ATATAAACAA ATG ACCTAG A AT

GAM2434 TGGTCAAGGTGGGTTTCGGTT 2420 TTGAACCTAA 5145 AAG- ---- CA TTTA
 ACAAAA
 TCATATTTTTCATATTCA GAGCAATGGA TGGTC GT GGGTTTCGGTTT TATT GCATATTC
 T
 CAAAATAATGAAGAATATGT CCA ||||| || ||||| ||| |||||
 AGTAAAAATTGAACCTAAGA ACCAG CG TCCAAGTTAAA ATGA TGTATAAG /
 GCAATGGACCA GTAA AGAA A- ---- AAGTAA

GAM2435 TGTAATGGAACAAATGACG 2421 AATGGAACAA 5146 ACAA GA TG TG
 ATAATGGTGTCTTTGTTATT ATGACGATAA TGTAATGGA AT CGATAA G T

GGAATAAGTTTATTTACA TGGT ||||| || ||||| |
ACATTTATTT TA GTTATT T /
GAA- AG GT TC

GAM2436 TGTGAAGTTAACAATATTTG 2422 TTGCACAACA 5147 A--- AACAA T A T AA A
ATAAGTTGTTTGATAAAACT TGTTATATAA TGTGA GTT TAT TGATA GTTGT TGATA ACTT T
TATATAAGTTATTGCACAAC CAGA |||| || || |||| |||| ||||
ATGTTATATAACAGAAACAA ACGCT CAA ATA ATTGT CAACA GTTAT TGAA A
TATCGCA ATAA AGACA T A C -- T

GAM2437 TGTTTGTTTATTTCTGCTTC 2423 GTGATAAGTT 5148 T CTGCTTCT C AATACA
TAATTTATTATTTGCAACAA TCCAAATAAA TGT TGTTTATTT AATTTATTATTTG AACAA G
ATACAGATACTAATGTTTCA CATA || ||||| ||||| ||||
GGTGATAAGTTTCCAAATAA ACA ACAAATAAA TTGAATAGTGGAC TTGT A
ACATACA T CCT----- T AATCAT

GAM2438 TTAATTTAACTTGCCAATCA 2424 TCAATTGGCA 5149 T - ATCATTA CT
TTAGTTGATGCTACTTCATC CAGTTGTATT TTAAT TAACT TGCCA GTTGATG A
AATTGGCACAGTTGTATTGG GG |||| |||| |||| |||||
GGTTA GTTGA ACGGT TAACTAC C
T C ----- TT

GAM2439 TTCCATTGATACGTACTATA 2425 TATCTAGACA 5150 AT- AT G A TA TG
TCTAGTAATGATGTGTTTAT TAGTAGGTTG TTCC TG AC TACTAT TCTAG ATGA T
ATCTAGACATAGTAGGTTGC CATA |||| || || ||||| |||| ||||
ATAAGGAA AAGG AC TG ATGATA AGATC TATT /
AAT GT G C TA TG

GAM2440 TTGGGTATCGTAGATGAAAA 2426 TATCGTAGAT 5151 T G A AC A AGA
ACTTACTATAGAATCCATAG GAAAAACTTA TTGGG ATC TAGATGA AA TT CTAT A
AAAATTATTATTTAGATCCC CTAT ||||| || ||||| || || ||||
AA AAGG TAG ATTTATT TT AA GATA /
- - A AA - CCT

GAM2441 TTGTAAAATGAACGGGAAAA 2427 AAATGAACGG 5152 T -- ---- C TTTT
AGTCTCTTTTAACCCGAAC GAAAAAGTCT TTG AAAATGA ACGGGAAA AAGT TC A
TGTTATTTCTTGTGCTTATT CTTT || ||||| ||||| |||| ||
TTTCAA AAC TTTTATT TGTTCTTT TTCA AG /
T CG ATTG - CCA

GAM2442 TTTCTGATCCATTAGATTTA 2428 TAGTATCATA 5153 ---- CCAA --- AG TAATCAT----
- A
AACCCAAACATTGATACAGA AATGTCATCG T AGATTTAAAC ACAT TGATAC AAACA
TGTCAG

AACATAATCATTGTCAAGTT TTTG | ||||| ||| |||| |||| ||||
TGACACATCTCCACTTTTGT A TCTAGGTTTG TGTA ACTATG TTTGT ACAGT
T
TTAGTATCATAAATGTCATC TATTT CTAC AAT A- TTTCACCTCTAC T
GTTTGGATCTTTTATAGTTC
TATCAAGAGA
GAM2443 AAGGATATGGTACTACTGCT 2429 TATGGTACTA 5154 A- G T C GAG GAGTGACG
GCTGCTGAGGAGAGGAGTGA CTGCTGCTGC AAGGAT TG TACTAC GCTG TGCT GAGAG
G
CGGTCAGAGATGCTCTCGAA TGAG ||||| || ||||| ||| ||| ||||
GGTACGGCTGTGGTAGCGGG TTCCTG GC ATGGTG CGGC ATGG CTCTC T
GTCCTT GG G T - AAG GTAGAGAC

GAM2444 AAGGTAGCCAAGGTTCTGCC 2430 TCTGACACAC 5155 C---- C ----- CA- TG C T
CTTTCA T
TCTGGCCAGCATACAGGTGG CCTGTGATAT TGCCT TG GCCAG TACAGG GT TC
AGATGGT TGT A
TCTCTAGATGGTCTTTCATG TGGT ||||| || ||||| || || ||||| ||
TTATTACACATCATCTGACA ACGGA AC TGGTT GTGTCC CA AG TCTACTA
ACA T
CACCCTGTGATATTGGTGTC TGCTA T TCTCTG ATA CA C - C----- T
TCTCATAGGCAATCGTTTCC
TGCACTGCCTT
GAM2445 AATTATACCAGAGTTTGGTA 2431 TATACCAGAG 5156 - GTTTG TTT
TTTTTTTAAATCTGAGATGCG TTTGGTATTT AATTATACC AGA GTATTTT A
TCGTCTGGGTATAGTT TTTT ||||| ||| |||||
TTGATATGG TCT CGTAGAG A
G GCTG- TCT

GAM2446 ACAAAGACATTGTAATAGA 2432 TGAAATTTTA 5157 AAA -- AAT GA C A
TTTGATATTATTACTTACTA ACAGAGTGTC ACA GACAT TGT AGATTT TATTATTA TT C
GATTGATGATGAAATTTTAA CATG ||| ||||| ||| ||||| ||||| ||
CAGAGTGTCCATGT TGT CTGTG ACA TTAAA GTAGTAGT AG T
AC- AG AT- -- T A

GAM2447 ACGAGATTCGTGGCGTGTTG 2433 TACAGTATCC 5158 AGATTCG C TA CC
TATATGTATCCTCAGTACAA CAATCAAACG ACG TGG GTGTTGTA TGTAT T
CTACAGTATCCCAATCAAAC T ||| ||| ||||| |||||
GT TGC ACC TATGACAT ACATG /
AAACTA- C CA AC

GAM2448 ACGCGGATGTCATAGGGAGC 2434 TGTCATAGGG 5159 ---- C-- GA GA GAG GG GT
GTGATCGAGGGGGGTTGGTT AGCGTGATCG ACGCGG ATGT ATAGG GCGT TC GGG
TTG T
TAACAAACCCACGGAGAATG AGGG ||||| ||||| ||||| ||| ||| |||
CGATCTATTTTACGTTCAAC TGCGCC TGCA TATCT CGTA AG CCC AAC T

CGCGT

AACT TTT AG AG GCA A- AA

GAM2449 ACTCGTTCCTGGCCGCGGAC 2435 CGCCGCGGAC 5160 CC- - A ACGA
GAAGATACGAACGGCGTCTT TAAAAGATGA ACTCGTT TGG CCGCGG CGAAGAT A
CGCCGCGGACTAAAAGATGA GT ||||| ||| ||||| |||||
GT TGAGTAG ATC GGCGCC GCTTCTG /
AAA A - CGGC

GAM2450 AGAACACCACCTCCATCCTC 2436 CTCGTCTGTCT 5161 A T CCTCCC-- CA
CCCCAGT
CCCGACGGGCATATTATCCC TTATTATGGG AGA CACCACC CCAT CGACGGG TATTAT
C
CAGTCTCGTCCCAGTAATAC GTGG ||| ||||| ||| ||||| |||||
TCGTCTGTCTTTATTATGGGG TCT GTGGTGG GGTA GCTGCTC ATAATG T
TGGTGGTCT G - TTATTCT -- ACCCTGC

GAM2451 AGATGATGAATCGAGCGGAG 2437 TGATGAATCG 5162 T T C- AG CAAGA -----
- TC
GATCGCAAGAGGATGCTGTC AGCGGAGGAT AGA GATGAA CGAG GG GATCG GGAT
GCTG C
CAACCAGCTGCCTTCGTGCA CGCA ||| ||||| ||| || ||||| ||| |||||
TCAAGTCCAAGTCGATCGCC TCT CTA CTGCTC CC CTAGC CCTG CGAC
A
AACTCGTTCATCTTCT T - AA G- TGAA- AACTACGTGCTTCCGT CA

GAM2452 AGCTCCACGATGCGCTTCGT 2438 TGGCAGATCT 5163 TC C T C----- G CG GT
- TG
GTTTCATCTCGTGCCGGCTCG TCTTGTGGAT CACGATG GCT CGTGTTCAT TC TGCCGGCT
TG CACCA CCT A
TGGTCACCACCTTGATCGGG GCGC ||||| ||| ||||| || ||||| || ||||| |||
TTGGTGTTCAGCAGCTGGCA GTGTTGC CGA GCGTAGGTG AG ACGGTCGA AC
GTGGT GGG /
GATCTTCTTGTGGATGCGCA CT T C TTCTTCT - CG TT T CT
GCTCGTTGTGTCGTT

GAM2453 AGCTCGGGGTCCTCCAGCGG 2439 CGGTTACCG 5164 CCTC AAG- GA C CT-
CACG TTT CC
CGGCGAAGGCGACTCGTCGG ACGTTATCCG CAGCGGCGGCG GC CT GTCGGA CGTC
GGTGG C CGGT C
ACTCGTCCACGGGTGGTTCT ACAG ||||| || || ||||| ||| ||||| |||||
CGGTCCCACACCGGTTACC GTCGCCGCCGCG CG GA CAGCCT GCAG CCACT
G GCCA /
GACGTTATCCGACAGGGGCA CC-- ACAA GG - ATT ---- T- - CA
ACACGCCGCCGCTGCCGCCA
CCGCCACCGTT

GAM2454 AGTGTAGCTGCGGCGGATCG 2440 TAGCTGCGGC 5165 TAG ATCGA A GC

ACGAAGGACGCCGCCGGAGG GGATCGACGA AGTG CTGCGGCGG CGAAGG CGCC C
 CGCCTTCGCTGCCGCCGCAG AGGA |||| |||||| |||| ||||
 ACCGCT TCGC GACGCCGCC GCTTCC GCGG G
 CA- GTC-- - AG

GAM2455 ATCGTAATTTGTAGATGAAT 2441 TGAATAAATG 5166 - T A ATGTGT A- A
 AAATGTGTGATAAGTTAACG TGTGATAAGT AT CGTAATT GT GATGAATAA GATA GTT A
 ACCGTGTCTCTTGTTATTCG TAAC || |||||| || |||||| |||| ||||
 TCCATTAATTGCGCGT TG GCGTTAA TA CTGCTTATT CTGT CAG /
 C T C GTTCT- GC C

GAM2456 ATCGTGCAGCGGTTGGAAC 2442 AGCGGTTGGA 5167 - GGAAC TC T GCTCGC
 - T
 CGCTCCCGTTGTAGCAGCTC ACTCGCTCCC ATCGTGCAGCG GTT CGC CCGTTG AGCA
 CAGG GCC C
 GCCAGGGCCTCGCGGCACTT GTTG |||||||| || || |||| |||| |||| ||||
 GTGTTTCGACGGTGGCGTTGA TGGCGCGTCGC CGG GCG GGCAGC TTGT GTTC
 CGG G
 TGGGCTCGCTGCGCGGT T GTAGTT GT - ----- A C

GAM2457 ATGTCGACGAGCCGGACCGA 2443 GACGAGCCGG 5168 GA - GA AA - GT- CCA
 AACCCCGTCCGGCCAGCTGA ACCGAAACCC ATGTC CGAGC CG CCG ACC CC CCGG G
 CCGGCAAGGAGGTACCGGCG CGTC |||| |||||| || || |||| ||||
 CGCTCGGAGACAT TACAG GCTCG GC GGC TGG GG GGCC C
 AG C -- CA A AAC AGT

GAM2458 CAATGTACTTGGCTCCAATG 2444 TGGAAAGTCC 5169 T - C - T ACTCACC
 TATTG CT
 GGACTTTCCTGTTGACTCAC CTATTGAGTC CAA GTAC TTGGCTC AAT GGGACTTTCC GTTG
 CCC AC T
 CCCCTATTGACCTTATGTAC AGTG ||| ||| |||||| || |||||| |||| ||| ||
 TGGGCAAAACCCAATGGAAA GTT CATG GACTGAG TTA CCCTGAAAGG TAAC GGG
 TG /
 GTCCCTATTGAGTCAGTGTA - T - T - CCAAAC TCA-- TA
 CTTG

GAM2459 CACGTCCAGGCTCACCGAGG 2445 AGGCCGTCAG 5170 CCA CACCGA- -- - T CC
 G
 CCGTCAGCCTGTTGCCGCGG CCTGTTGCCG CACGT GGCT GGC CGTC AGCCTG TG
 GCGGCT A
 CTGAACGGCCGCCACGCCAG CGGC |||| ||| || ||| |||| || ||||
 GTTCGACGCCGCCACCTCTA GTGCG CTGG CCG GCAG TTGGAC GC CGCCGG A
 GGTCCAGCGTG AC- ATCTCCA CC C C AC C

GAM2460 CAGGAAAAGTAGCGGCGGAC 2446 AGACTGTCGC 5171 AAA- A C AGA- - C T
 TGGA GG

GGACGCCCGTCGAGAGACTG	CTCCTGGATA	GA	GT	GCGGCGGACGGACG	CCGTCG	GAC
TGT GCC CC TATC G						
TCGCCTCCTGGATATCGGGG	TCGG					
CAGGTACGATGGGGTTCGAG		CT	CG	CGCCGTCTGCCTGC	GGCAGT	CTG ACG TGG
GG ATGG G						
GTCGCCGTGACGGTCGTCCG	CCAG -	T	GCCG	G C -	TAGC	AC
TCTGCCGCGCGACCTCTTG						

GAM2461 CAGGCAACTTTATCTTCTCC 2447	TAGCGTGTTA 5172	AACTT	TTC	TGA	--	--
GAAGAC C						
AGCCATTTGAGTTAGCGTGT	TTAGGAAGAC	AGGC	TATC	TCCAGCCATT	GT	TAGC
GTGTTATTAG TC C						
TATTAGGAAGACTCCCAGGA	TCCC					
ATACTAATAGCATCTGTTGC	TCCG	G TAG	AGGTCGGTAG	CA	GTTG	TACGATAATC
AG A						
CACGATGATGGCTGGATGCG	-----	CGT	TAG	CC	TC	ATA--- G
ATGGCCTG						

GAM2462 CCAAGAAGATGTTCTGTGCCA 2448	TGGGAAGATT 5173	AT---	G	A	CG	G
AAGCGTTCCGAGAAGTTCCC	CTGGCGGGAA	CCAAGAAG	GTTC	TGCCA	AG	TTCC AGAAG
C						
CTTTTCTGGAAGATTCTGG	CTTC					
CGGGAACTTCCCCTTTTGG		GGTTTTTC	CAAG	GCGGT	TT	AAGG TCTTT /
	CCCTT	G	C	AG	G	TCC

GAM2463 CCAGAGGCAGAGGAGGACAG 2449	AGAGGCAGAG 5174	GGACAGAGAAG	C	ACGTA	-	-
C A T GA- AA						
AGAAGCTGGCCGCACGTAGC	GAGGACAGAG	A	CTGGC	GC	GC	CTGGCGA CTGG GAT
GC GTT GG T						
CTGGCGACTGGCGATAGCTG	AAGC					
TTGAGGAATTGCTGGAAGCG	T	GGCCG	CG	TG	GATTGCT	GGCC CTA CG CGA
TC /						
CCATCCCGGATCGTTAGTGT	GA-----	C	CC---	T	A	- C - AGG GT
CCGCCGCCGGAGTCCTCTGT						
CTCTGG						

GAM2464 CCAGGAGAACTGGATCACGT 2450	TGGGCTCGGG 5175	GA	ACT	TCA	T	-
TCTGGTCTTGGGTATCGTAC	ACGCGGACGC	CCAGGA	GGA	CGT	CTG	GTCTTGGGT TCGT
CAGG G						
AGGAAGATCTTGATGGGCTC	TCCT					
GGGACGCGGACGCTCCTCCT		GGTCCT	CCT	GCA	GGC	CAGGGCTCG GGTA GTTC /
GG	-----	C--	-	G	-	- TA

GAM2465 CCCTGCCGTGATGTGTTTTT 2451	GTAAAGCAGT 5176	-	-	-	----	GAT
GTTTGATCTTTAAGTGTTAT	ACGAGGCGGC	CCCTGC	CGT	GATGT	GTTTT	TGTTT CTT AG
T						
TCTCTAAGTAAAGCAGTACG	ATCG					
AGGCGGCATCGACGTGCAGG		GGGACG	GCA	CTACG	CGGAG	ACGAA GAA TC /
G	T	G	G	CATG	AT-	TC TTA

GAM2477 CGGGGTTTATTTTATTGCA 2463 TACAGTGAGA 5188 --- C CATCTG -- C C C -
- A

TTGGCCATCTGACTCTTACA	ATAAATAACA	GTTTATTTTATTG ATTGGC	ACTC TTACA
GCA ACG AAG GC T			
CGCACACGCAAGGCATTGGC	AACC		
GACTTTCGTTGCATGTAGAT		TAAATAAGAGTGAC TGACCG	TGAG GATGT CGT TGC
TTC CG T			
GAGTGCCAGTACAGTGAGAA	CAA	A ----- TA A - T AG G	
TAAATAACAAACCTG			

GAM2478 CGTCCAGGCCGATGCCGCAC 2464	GTGAGCAGGT 5189	AGG A C - G C CG----	A
CTCTCACGGAGTCCGCGCCG	GCAGCACGGG	CGTCC CCG TGC GCACCT CTCAC GAGT CG	
CCGGC G			
GCAGAAGTCGGAGAAGCCGC	GACG		
ACTTGGTGAGCAGGTGCAGC		GCAGG GGC ACG CGTGGA GAGTG TTCA GC	GGCTG
A			
ACGGGGACG	---	- A C G C CGAAGA A	

GAM2479 CGTCTGATGTGGGTGCTGGC 2465	TGATGTGGGT 5190	T	GGTGCTG	GCTG TT TG	-
A GGA C					
GGGGCTGTCGTTAGTGTGGT	GCTGGCGGGG	CG CTGATGTG	GCGGG	TCG AG TGGTCA	
GGT CG TGCT G					
CAGGTACGGGATGCTCGTCG	CTGT				
GCGGGACGGCCGTGACCGTG		GT GACTGCGC	CGCCC	GGC TC GCCAGT CCG	
GC GCGG T					
CTCGGAACCCGCGACGCGTC		- AG-----	AA-- -- GT	G - AGG C	
AGTG					

GAM2480 CGTCTGGATATGACCGACCC 2466	TGTCGGGGTC 5191	- T	CC	-----	CG A
CCTGACATCGGCGGCGCGAG	TCGGTCGTCT	CGTC TGGA ATGACCGA	CCCTGACATCG		
GCGGCG AG T					
ATTTTATGCCGCAGAAGTC	CCGT				
GATGTCGGGGTCTCGGTCGT		GCGG GCCT TGCTGGCT	GGGGCTGTAGC	CGCCGT	
TT /					
CTCCGTGGCG	T C	CT	TGAAGA	AT T	

GAM2481 CGTGGTGGAGCTCACGGTCG 2467	TGGTGGAGCT 5192	TG - - C	AA-- AT
AAGGCGATTTGCTGCTGTGG	CACGGTCGAA	CG GTG GAG CT ACGGTCG	GGCG T
TGACCGTTAGACTCGCGCTG	GGCG		
CG	GC CGC CTC GA TGCCAGT	TCGT T	
	GT G A T	GGTG CG	

GAM2482 CTGCGTTCTACGGTGGTCAG 2468	TACGGTGGTC 5193	GT C-- CCGAA - A G
ACCGAAGACTGCGACGGTAC	AGACCGAAGA	CTGCGTTCTACG GGT AGA GACT GCG CG T
CGACGCTGGTTCGCGCCTCTT	CTGC	
ATACCCACGTAGAACGCAG		GACGCAAGATGC CCA TCT CTGG CGC GC A
	AC TAT CCGCG	T A C

GAM2483 CTTGGTGTGGTTGTTACGTA 2469 TAGCAGCACG 5194 -- TA A- ACGAG C AC---
GG C
GCAGCACGAGCACGGACAGC AGCACGGACA CTTGGTGTGGTTG TTACG GC GC CACGGA
AGC GGGC TGA A
ACGGGCGGTGACACGTCGAG GCAC ||||| |||| || |||| |||| |||| ||||
GCCCAACACGTTCTCCGTGA GGACTACGCCAAC GATGT TG TG GTGCCT TTG
CCCG GCT C
ACAGGTCGGTCGTGTAGTTC TT GC GC GACAA C CACAA GA G
AACCGCATCAGG

GAM2484 GAATACAATGGAAAGTCCCT 2470 TCAGTGTACT 5195 A TC AC- CCC CTT T--
GCCAA AA
ATTGACTCACCACATTGAC TGGCAGCAAT GG AAG CCTATTG TCA ACATTGAC ATA
GCTT CAATGG A
CTTATATGCTTGCCAACAAT GGGT ||||| ||||| ||||| ||||| ||||| ||||| |||||
GGAAAAACCCATTGGAAAGT CC TTT GGGTAAC GGT TGTGACTG TAT TGAA
GTTACC A
CCCTATTGAGTCAGTGTACT C TT GAC TCA AGT CCC AG--- CA
TGGCAGCAATGGGTTTTTCC
CATTGGCTC

GAM2485 GACAATCGTAGTCATATCAC 2471 TGTCAGGACA 5196 A T CATAT T TC --- ACTA
ATGATTTCTCGACAGATCGA TCATGTGTTT GACA TCG AGT CACATGAT TC GACAGA TCG
C
CTACACCACGATAATCTGTC AACT ||||| ||||| ||||| ||||| ||||| ||||| |||||
AGGACATCATGTGTTTAACT TTGT AGC TCA GTGTACTA AG CTGTCT AGC /
CGATGTT - - ATTT- C GA AAT ACCA

GAM2486 GACGAGGATACGGAGATGGA 2472 AGATGGAGAT 5197 GATA - - TG - TC AA
GATGGAGTTCTCTCCGCGTA GGAGTTCTCT GACGAG CGGAGA TG GAGA G AGT
TCTCCGCGT C
ACGCGGCGCGGAGACTGCTG CCGC ||||| ||||| ||||| ||||| ||||| ||||| |||||
TTGTCTCGCGCTCTCCGCTC CTGCTC GCCTCT GC CTCT T TCG AGAGGCGCG G
GTC ---- C G GT G TC GC

GAM2487 GACTGAGTTGACCGTGAATG 2473 TGAGTTGACC 5198 CT TT - TG ATG AT
AGAGATAGTCTTTGGCTTGC GTGAATGAGA GA GAG GAC CG A AGAG A
GTGTTCTCTTTTTC GATA ||||| ||||| ||||| ||||| ||||| ||||| |||||
CT TTC TTG GC T TTTC /
TT TC T GT CGG TG

GAM2488 GAGGGCTCGTTCGCGCGGGT 2474 AAGAGCAAGG 5199 G CG - GGG AC TG CA
AAC A TC
GCTCTTCTACATCTGGTCGG CGCTGAAGGC GAG GCT TTC GCGC TGCTCTTCT ATC
GTCGGG CG GTG TGT A
GCACGAACGTGATGTTCAAC GCTC ||||| ||||| ||||| ||||| ||||| ||||| |||||
ACGACGCTGACGGACCTGGC CTC CGG AAG CGCG ACGAGAAGA TAG CGGTCC GC
CGC GCA /

GATCAAGAAGAGCAAGGCGC
TGAAGGCGCTC

G -- T GA- AC -- AG AGT A CA

GAM2489 GAGTTGGCGGGTGTGTGTG 2475 TTAGATCGGT 5200 - GG - GA -- T- CC--- - -
G

TGAGTGAGTGAGTCCCTTCG TTGAAGTTGA TGGC GTGT TGTGTGT GT GAG GAGT
CTTCGA TCGATC GATC A
ATCGATCGATCGATTGATTA AACT |||| ||| ||||| || ||| ||| ||||| ||||| ||||
GATCGGTTTGAAGTTGAAAC ACCG CACA GTACACG CG CTC CTCA GAAGTT
GGCTAG TTAG T
TCCTCTCCGGCGAGCACATG T G- T AG GC TC AAGTT T A T
TACACGGCCATGATC

GAM2490 GATCCCGATGGTGGTCAGGC 2476 ACGCTGCGCA 5201 A --- G ----- T T C AATC
TC

TGGTGTGCGCAGTCGTCGTCG TCCCCTCGAG TCCCG TGGT GGTCA GCT GGTG CGCAG
CGTCGT GG GTCG C
GAATCGTCGTCCACCGACCT CGTG |||| ||| |||| ||| ||||| ||||| || |||
CATGACGCTGCGCATCCCCT GGGGC ACTA CCGGT CGA CTAC GCGTC GCAGTA
TC CAGC /
CGAGCGTGGCCTTGATCACG - GTT G GCTCCC - - C --- CA
GGGTC

GAM2491 GCACCCCGATCAACGACCAC 2477 CCAGCACCGC 5202 - TCAACGACCA A --- TCC
GAGCAGTGCAACGCGTCCGA TTGAACTCGG GC ACCCCGA CGAGC GTGC AACGCG G
CACCGCGTTCCAGCACCGCT GGTC || ||||| |||| ||| |||||
TGAAGTCGGGGTTCG CG TGGGGCT GTTCG CACG TTGCGC A
C CAA----- C ACC CAC

GAM2492 GCACGTCGTCGCCCCGTACC 2478 TGGCTCACGT 5203 TC CG C ACC CC TC AC
CCAGGCCCATCTCCACCGTG GGAACACCGT GCACG GT CC CGT CCAGG CATC C C
TTGATGTTCTGGCTCACGTG GT |||| || || ||| |||| ||| |
GAACACCGTGT TGTGC CA GG GCA GGTCT GTAG G /
CA A- T CTC T- TT TG

GAM2493 GCATATAAGATATACAGAGA 2479 CATCAGATAG 5204 A AGATA- GAA - TCTAA T T
A TAG

AAGGATTTTGCTGTCTAACG AGTTCTGTCT C TATA TACAGA AGGATTTTG CTG CG CC
ATACAG TGT T
TCCTATACAGATGTTAGTCG GTAA | ||| |||| ||||| ||| || ||||| |||
TACTGTATCGGCGCATCA G ATAT ATGTCT TCTTGAGAT GAC GC GG TATGTC
ACA /
GATAGAGTTCTGTCTGTAAG C ATAGGA G-- A TAC-- - C - TGC
GATATATACGC

GAM2494 GCGGTGTGTACAACGAGGCA 2480 TGTCACGTTG 5205 - G A CCGACCAACT - A
TCCGACCAACTGCGGTGCGA TGAACAGCCG GCGG TGT TACAACG GGCAT GCG GTGCG
A

AATCGCACTCGTATGTCACG C |||| ||| ||||| ||||| ||| |||||
 TTGTGAACAGCCGC CGCC ACA GTGTTGC CTGTA TGC CACGC A
 G A A ----- T T

GAM2495 GCTGGCGCAGAACTCGCACC 2481 TCACCGATCC 5206 G A T CACCGT A TT
 GTTCGGTGAACGTGATGTTA GCGTTCGCGG GCTG CGC GAAC CG TCGGTGA CGTGATG A
 TTCATCACGATCACCGATCC TAGC |||| ||| ||| ||| ||||| |||||
 GCGTTCGCGGTAGC CGAT GCG CTTG GC AGCCACT GCACTAC /
 G - C CT---- A TT

GAM2496 GCTGGGTTATCTCGACGTGG 2482 TGGGTTATCT 5207 TT CGT C GAAGC A AA
 CGGAGAAGCTGCGCAAGGAA CGACGTGGCG GCTGGG ATCTCGA GG GGA TGC GCA GG
 T
 TACCCCATGTGCAACGGTCC GAGA ||||| ||||| || ||| ||||| ||
 CCTCGAGGTTCTCGGC CGGCTC TGGAGCT CC CCT ACGTGT CC A
 T- --- - GGCA- A CC

GAM2497 GGAAGCCACTTCGATGTCCG 2483 TCGCACGGGA 5208 A- A- TC GT TA T GCG
 TG TAGTAGTCCGCGGACAAG GTCCCGGCCG GGA GCC CT GAT CCGTG GTAG CC G
 GCTATCGCACGGGAGTCCCG GCGC ||| ||| || ||| ||||| ||||| ||
 GCCGGCGCTCC CCT CGG GG CTG GGCAC TATC GG A
 CG CC CC AG GC - AAC

GAM2498 GGACATGAATCCGTGCGGTT 2484 GGAGAACCGA 5209 ATGAA G-- A C----
 TTTT CTG
 CTACGGGGAGCAGCGGCCTC AGACGGACCG GGAC TCCGT CGGTTCT CGGGGAG
 AGCGGCCTC GAGC C
 TTTTGAGCCTGCCTCGCTTT TCC |||| |||| ||||| ||||| ||||| ||||| |||||
 CGAGGCCGCTACCATCTCCT CCTG AGGCA GCCAAGA GCTCCTC TCGCCGGAG
 TTCG /
 CGGAGAACCGAAGACGGACC CC--- GAA G TACCA CT-- CTC
 GTCC

GAM2499 GGAGAAGGAGTCGAGGGGGC 2485 TGGGAAGTTC 5210 A A GA - A G GTCC A- -
 C A
 GGGGAGGTCCCGAATACTCA GAACTCGTCG GG GA G GT CG GGGGGCGG GAG CGAAT
 CTCA CAA CG G
 CAACCGAGACCGTTTGCTGG TCCC || ||| || ||| ||||| ||| ||||| ||||| |||||
 GAAGTTCGAACTCGTCGTCC CC CT C CA GC CCCCTGCT CTC GCTTG GGGT GTT
 GC A
 CCCCGCACGTGTCGCGC G GTG C C G AA-- AA C T C

GAM2500 GGAGGTCGGTCGATCACGTC 2486 TGGCACGAAT 5211 C T TC --- T AA
 GTTTCGTTAAATAGATGGCA TCGTCCTCGT GGAGGT GG CGA ACG TCGT TCGTT A
 CGAATTCGTCCTCGTCCACC CCAC ||||| || ||| ||| |||||

TCC

CCTCCA CC GCT TGC AGCA GG TAG /

- T CC TTA C AT

GAM2501 GGCGACGCATGCCCTGGAGG 2487 CACCCGGAGT 5212 - A C AG G - GACT TCG
TGAGCCTGCTGGACTTCTCG ACGTGTACGC GGCG ACGC TGC CTGG GT AGC CTGCTG TC

A

ACGCTGATGGCGGCGCTGCA C ||||| ||||| ||||| ||||| ||||| ||||| |||||
CCCGGAGTACGTGTACGCC CCGC TGTG ATG GGCC CG TCG GGCGGT AG C
A C A CA - C ---- TCG

GAM2502 GGCTATCAGTGCCGTCGTGG 2488 TCGCCGCGAT 5213 C A-- CG CC
TGACGGCCGCGACTATCGCC GGCGCCCCGA GG TATC GTGCCGTCGTGGTGA G G
GCGATGGCGCCCCGATACC TACC ||||| ||||| ||||| ||||| ||||| ||||| |||||
CC ATAG CGCGGTAGCGCCGCT C C
- CCC AT AG

GAM2503 GGGCAGCTGGTTCTCGGCCG 2489 AGCTGGTTCT 5214 CT C- ---TC AG A-- T CT - -
TA- C

TGTCCACCAGTTTGATCTTG CGGCCGTGTC CGG CGT G CACC TTG TCT GTT CC GC
CGTGCTG GGC C
TTCTCCGCCGTGCTGTAGGC CACC ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
CCGGCCGCTCGGCACGTGCA GCC GCA C GTGG AGAT AGG CAG GG CG
GCACGGC CCG /
GGCCGACCGGAAAGTAGAAG -- CT GCT GA A- GAA C CC A T TCG G
GTGAGCTCGACGTCCCGCTC
CAGCGGGTCC

GAM2504 GGGGTGTTTGGTCTTCTGAT 2490 TGACATGGAG 5215 TT-- TCTTCTGAT - G- G
CAGTA

TGGCAGGGCGCTGTGTGAGG GCCGCTGCTG GGGGTG TGG TGGCAG GGC CTGTGT
AGG G
CAGTAGTTATACCTGACATG TAAC ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
GAGGCCGCTGCTGTAAACAAT CTCTAC ATC GTCGTC CCG GGTACA TCC /
ATCTATGTTTATCTC TTGT TATAACAAT G GA G ATATT

GAM2505 GGTCTGATCCCGCGAGGGA 2491 GGAGGTGGAA 5216 TGA C A C CGGGG AA GA
C G G

GCCGCCGGGGAGGAGGTGGA GTGGAGGTGTC TC CGCGAGGG GC GC AGGAGGTGG
GTG GGTCGG GAG CGGCC C
AGTGGAGGTCGGCGAGGCGG GCGA ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
CCGCGGGCTGATTCTTGCC AG GCGCTTCT TG CG TCCTCCACC CGC CCGGTT
CTT GTCGG /
GCGCCCCACCTCCTGCGTA --- T A - ---- CC G- - A G
TCTTCGCGTGAGAACC

GAM2506 GTATGGATGATATACTTACT 2492 TGATATACTT 5217 T- TT T GTTG CTTACTAT
CCT A

GTTGTTGTTCACTTACTATT ACTGTTGTTG GTATGGA GATATAC AC GTT TTCA TATCA
 ATATAA A
 ATCACCTATATAAACTTGT TTCA ||||| ||||| || ||| ||| ||||| |||||
 ATTCATGATACTTACCACTG CATATTT CTGTATG TG TAA AAGT ATAGT TATGTT
 /
 AAAAAATTGTGTATGTCTTT TT -- T AA-- CACCATTC ACT C
 TTATAC

GAM2507 GTCGCTGTCACCGGAGTTGA 2493 TCACCGGAGT 5218 - C - AG TG T C G
 TGCCCAGCATGATCGTGCTG TGATGCCAG GTCG CTGT AC CGG T A GC CAGCAT A
 CGCTTTGAACTGTGTAACAG CATG ||||| ||||| || ||| || |||||
 TCGAC CAGC GACA TG GTC A T CG GTCGTG T
 T A T A- GT T C C

GAM2508 GTGCTAGCTGCGGAGGCAGA 2494 GGAGGCAGAA 5219 TG T G ---- GA T T- C -
 -- G
 AGCGGCTGCTGGCGCTGGTG GCGGCTGCTG G C AGCTGCG A GGCA AGCGGC GC GGCG
 TGGT GCCGCG GGC G
 CCGCGGGCGGAGCCGGCGCG GCGC | | ||||| | ||| ||||| || ||||| ||||| |||
 GCGACCGTCGTCTCGTTGCC C G TTGGCGT T CCGT TTGCCG TG CTGC GCCA
 CGGCGC CCG /
 GTTCTTGCCCGCTTGTGCGG GT T G TCGC TC T CT T G GG A
 TTTGTGC

GAM2509 GTTCGGTTGCGTGTATGTGT 2495 ACACCGGAAG 5220 GG GTAT- T CA
 TGTGATCAAAGGTCCCAACA CGCGGAAGAA GTTC TTGCGT GTGTTG GAT A
 CCGGAAGCGCGGAAGAAC C ||||| ||||| ||||| |||
 CAAG GGCGCG CACAAC CTG /
 AA AAGGC C GA

GAM2510 GTTCTACCGCCCCGAAACGA 2496 TCTACCGCCC 5221 CCCC-- CG--- TA
 CGTTGTTATATACGGAACCT CGAAACGACG GTTCTACCG GAAACGA TTGT T
 TTGTTTCCACCCACGGTGGA TTGT ||||| ||||| ||||| |||
 AC CAAGGTGGC CTTTGTT GGCA /
 ACCCAC TCCAA TA

GAM2511 GTTTCATAACCGTACGCGA 2497 GGCGATCGCG 5222 T C ACC A AACA CCCCC C
 AACACGCCCCCAGATCAAC CATATATAGA GT TC ATA GT CGCGA CGCC GAT A
 GTCGGCGATCGCGCATATAT CAC || ||| || ||||| ||| |||
 AGACAC CA AG TAT TA GCGCT GCGG CTG A
 C A A-- C A--- ---- C

GAM2512 TACTGGCCACAAAAGTAGCA 2498 TAGCTAGTAT 5223 CA AAG A AACTC G
 GTTAAACTCTTGAAACAAA TGGTGTCAGT TACTGGC CAA TAGC GTTA TTG A
 ATGATAGCTAGTATTGGTGT A ||||| || ||||| ||| |||
 CAGTA ATGACTG GTT ATCG TAGT AAC A

TG ATG A AA--- A

GAM2513 TCAACGTGTTCTTTTCTCGT 2499 TGAAATGGTG 5224 CTTTTC TTCT GATG AA-
GATCTG TG A
TCTTCTACGATGATGCCGTT TGTATAGGAT TT TCGTTC ACGAT CCGTTCTG ACATTA
T TCGC A
CTGAAACATTAGATCTGTTG GGGT || ||||| |||| ||||| ||||| | ||||
TCGCAAAGTGATGAAATGGT AA AGCGAG TGCTG GGTTAGGAT TGTGGT A
AGTG /
GTGTATAGGATGGGTCGTTT TT---- TTT- ---- ATG AA---- GT A
TGAGCGATTAACACGTTGA

GAM2514 TCGAAGCTCAGGTTGTACCG 2500 TAGTACAGGC 5225 - CAG - CGTT T
TTCGGGGTCGTCCCCGTAGT GAAAGTTGTT TCGA AGCT GT TGTAC CGGGG C
ACAGGCGAAAGTTGTTGA GA ||||| ||||| ||||| |||||
AGTT TTGA CG ACATG GCCCC G
G AAG G AT-- T

GAM2515 TCGGTGTCCTGGCTGTGCAC 2501 TCAGATCGCC 5226 CT CT G TAGCAA C-- C G
GTAGCAACGATCTCCGCCGG GTGACTCCTG TCGGTGTC GG GT CACG CGATCT CGC
GGT T
TGTACACCGCGATCAGATCG GCAC ||||| || ||||| ||||| |||||
CCGTGACTCCTGGCACCGA AGCCACGG CC CA GTGC GCTAGA GCG CCA A
T- T- - C----- CTA - C

GAM2516 TCGTAGGTAAATTGCAGTTG 2502 TAAATTGCAG 5227 A T T -- GC-- A AG
AGCATAGGTGATATCAGTCA TTGAGCATAG TCGT GG AAAT GCAGTT GA ATAGGTGAT TC T
CGACATCATCTATATGATCC GTGA ||||| ||||| ||||| |||||
AAGCTGCGTTTCCGACGA AGCA CC TTTG CGTCGA CT TATCTACTA AG C
G - - AC AGTA C CA

GAM2517 TCTCTTACACCCCTATTGCC 2503 CACCCCTATT 5228 TTAC CTATTG TAAAT GA
TAAAATTATGGAAAATCGTA GCCTAAAATT TCTC ACCC CC TATG A
TATGGAAAAGGGTAGATGAG ATGG ||||| ||||| ||||| |||||
A AGAG TGGG GG ATGC A
TAGA AAAA-- TAT--- TA

GAM2518 TCTGACCCCTCCAAGACGGG 2504 TGAGTCACCA 5229 CCA-- - T- A TT CC T CAAA
ATC CC
ATGAATTTTACACCAAGAAT AACACGATCG AG ACGGGA GA TT ACA AAGAA GAGTCAC
CACG GTGA A
GAGTCACCAAACACGATCGT TGAC ||||| ||||| ||||| |||||
GACCACGCTCACCGTGATAG TC TGCTCT CT AG TGT TTCTT CTCAGTG GTGC
CACT C
TGACTCTTCTTTTTGTCGGA TTTAG A TC C GC TT - ATA- --- CG

CTCCTTCTCGTACTGATTTA
CTTGTACGGA
GAM2519 TCTTGACGGAGCGCACGCAC 2505 TGACGGAGCG 5230 - G A AC C GCATC TC
TCATCGAGCATCTGATCCTT CACGCACTCA TCTTGA CGGA CGC CGC TCAT GA TGATCCT
G
CGTCGGGGTCATCATGAGCG TCGA ||||| ||||| ||||| ||||| |||||
GCGTCTGCTCGAGA AGAGCT GTCT GCG GCG AGTA CT ACTGGGG /
C - - - - - CT

GAM2520 TGACGGCTCCTTAAATAGCC 2506 GGAAATCGGA 5231 AATA TA C--- A- CGA
AAACT GGA
TAGTTTTTCGACGATCCGGT GACGTTTCTC CTTA GCC GTTTTT GACG TCCGGT
CCGAGGG GCCTA T
CGACCGAGGGAAACTGCCTA GAAA |||| ||||| ||||| ||||| ||||| |||||
GGATCCTATGGGTTTCTCGG GAGT TGG CAAAAG TTGC AGGCTA GGCTCTT
TGGGT C
AAATCGGAGACGTTTCTCGA AGAA CA CTCT AG AA- ---- ATC
AAACACGGTAAGATGAGGCG
CCGTCA

GAM2521 TGGGCAACAGTCCAGACAGA 2507 TTCAACGGCA 5232 CA CC AG CAA--- ACC C
CCAACCGTTGAAACCGAGCC TCTCGTGCGT TGGGCAA GT AGAC AC CCGTTGAA GAG C
TCTCCGTTCAACGGCATCTC CTTA ||||| ||||| ||||| ||||| |||||
GTGCGTCTTAATTTGCCA ACCCGTT TA TCTG TG GGCAACTT CTC /
-- AT CG CTCTAC GC- T

GAM2522 TGGTCCTCGGGTAGCTGCTC 2508 TAGCTGCTCG 5233 T A T--- G CA- GGG
GTCGGCCGAGCTCATCCGGC TCGGCCGAGC TGGTCC CGGGT GCTGC CGTCGGCC AGCT
TCCGGCGA G
GAGGGGTGGTCGCCGGAGGT TCAT ||||| ||||| ||||| ||||| ||||| |||||
AGCTGGTCGGCGTCTGCGG GCCGGG GCTCG CGGCG GCGGCTGG TCGA
AGGCCGCT /
CGGCTCGGGGCCG - G TCCT - TGG GGT

GAM2523 TGTTGAGCTCCTCGGTGGGG 2509 TGTTGTAGTT 5234 G GGT G - CC A- --
GT TTC
GTGATGTTGTAGTTGGTCCT GGTCTCGAG TCCTCGGT GG GATGTT TAG TTGGT TCG
GCGGGC CGGCGG CG C
CGAGCGGGCCGGCGGGTCTG CGGG ||||| ||||| ||||| ||||| ||||| ||||| |||||
TCCTGTGCGCGCTGCTGCCC AGGAGCCG CC CTACGG GTC AGCCA AGC CGCCCC
GTCGCC GC /
GCGCCGACACCGACCTGGGG G GC- G C C- CG TC -- TGT
CATCCGCCGCGCGAGGATCT
CCTGACA

GAM2524 TGTTGGTGTCTCTGAAGACT 2510 TCAGTGGCTT 5235 T G CTCA T AC T-- T- TCC
ACTC
CAGGTACCACCTGGTTGTCA CACCAGCAGG GTGTC CT AAGA GG ACC CTGGT GTCACT
GG AGGCTGGG A

CTTGGTCCAGGCTGGGACTC TTCC ||||| || ||| ||||| || |||||
 ATCTTCTTCAGCTTCCTCAG CACAG GA TTCT CC TGG GACCA CCGTGA CC
 TTCGACTT T
 TGGCTTCACCAGCAGGTTCC T G ---- T AC CTT CT --- CTTT
 TCTTGAGTGACACCACCA

GAM2525 TTCATGCTAGTCGTGTATCC 2511 TGTCGTGCTA 5236 TAG- TGTAT CT T TA- G G
 GC GA
 CTGCGTGGTCACCGTAGTGG GGTTCGAAG TTCATGC TCG CC GCGTGG CACCG GT
 GC TTGGG TG G
 CGTTGGGGCTGGAGCTCATA ATGT ||||| || || ||||| ||||| || ||||| ||
 CTCGAAGTGATCATCGGTGT AAGTATG AGC GG CGTGCT GTGGC TA TG AGCTC
 AC /
 CGTGCTAGGTTTCGAAGATG TAGA TTT-- AT - TAC G A AT TC
 TATGAA

GAM2526 TTCCCGAACCGAACGAGATC 2512 GTCAACAGAA 5237 GAACC CAGT CACAG
 CACAC AAG TT
 AGTAGACACAGACATGCACA ACCATGTTCT TTCCC GAACGAGAT AGA ACATG TCTGT
 GATAT A
 CTCTGTAAGGATATTTATCT CCGT ||||| ||||| || ||||| ||||| ||||| |||||
 ATGTCAACAGAAACCATGTT AAGGG CTTGCTCTG TCT TGTAC AGACA CTGTA
 T
 CTCCGTCTCGTTCACGAAGG AAGCA CC-- ---- CAA-- A-- TC
 GAA

GAM2527 TTTTGGTGGATGACTCGGTT 2513 TTGCTGATTG 5238 TG---- TG - GATG T - A GT
 GA A
 ATGGATTGCTGATTGATGTT ATGTTCTTCC CGGTTA GAT CT GATT TTC TCC CGACGTG
 TGG TA ACTG C
 CTTCCCGACGTGATGGGTTA CGAC ||||| || || ||||| ||||| ||||| || |||||
 GAACTGACTCGGTTGGTCTA GCCGGT TTA GA CTAG AAG AGG GCTGTGC ATC
 GT TGGC /
 CGTGTCGCGGACGAAAAGAT TGGCTA GT G AA-- C C - TG -- T
 CGAGTGATTATCGGTTGGCC
 GGCCGCGGAGG

GAM2528 CCGATAACGATATAAGACTA 2514 TATAACAGCC 5239 GAT ATAA TAGA - TG GCTA
 GATGTTATTCAAGTGTCTGCT GTCAATTGTT CC AACGAT GAC TGTTAT TCAG TCT T
 ATCCTTGGGTGCTGATATAA TAGG || ||||| || ||||| ||||| ||||| |||||
 CAGCCGTCAATTGTTTAGG GG TTGTTA CTG ACAATA AGTC GGG /
 AT- A--- CCG- T GT TTCC

GAM2529 CGAAGATCATCAGCGATGTG 2515 TTATATGTTC 5240 A-- C G - ACT- TG
 AGAGAACTTCATGAGATTGA ATGATCAAGT CGA GATCAT AGC ATGTGAGA GA TCA A
 TTA CTGCTTATATGTTCA CG || ||||| || ||||| ||||| ||||| |||||
 TGATCAAGTCG GCT CTAGTA TTG TATATTCT CT AGT G
 GAA C - G CATT TA

GAM2530 GCGAACAATGTTATTAAC 2516 TCAAAGGTGC 5241 TA AAGTA AGAA CAAA - AA
 AA A CC TG
 GAAGTATGAGAATTTCCAAA AAAGAAAGAC AT AAACG TG TTTC GC CC TTGATG CTTA
 GACT TC A
 GCCCAATTGATGAACCTAAG AGAA || |||| || ||| || |||| |||| |||| ||
 ACTCCTCTGATCCGAAAGTC TG TTTGC AC AAAG CG GG AACTAT GAGT CTGA
 AG T
 TGAGAATATCAAAGGTGCAA -- GAAG- AG-- AAA- T A- AA - A- CC
 AGAAAGACAGAAGCGTTTGT
 AACTTGTTTCGT
 GAM2531 TTCGTGCTGGGGGAAGAGGT 2517 AGAGGTTATC 5242 G G ATCC A T TGT GA-----
 ----- A
 TATCCGAATGGTTTAGATGT CGAATGGTTT GGG AAGAG TT GA TGGTT AGA TTGG
 TCTTA G
 TTGGGATCTTAAGTTAAGA AGAT ||||| || ||||| || ||| ||||
 AATGGGTGATTGAACCTCCA CTT TTTT GA CT ACCAA TCT AACC AGAAT T
 ATTCTCAACCACTCAAAGGT G G AA-- C C T-- TCCAAGTTAGTGGGTAA T
 TTTTGTTCCAGATTTGAA
 GAM2532 AACAGTGTCAATGATCGAAT 2518 TCAATGATCG 5243 T GGCAA GAAGAG ATA
 TGGCAAGAGTGAAGAGTGGA AATTGGCAAG AACAGTG CAATGATCGAATT GAGT TGG G
 TAGTTACCAATGCTTGGAAG AGTG ||||| ||||| ||| |||
 AGTTTGCTCATTGCTATTGT TTGTTAT GTTACTGGTTTGA TTCG ACC /
 T C AAAGG TA---- ATT
 GAM2533 ATTAGGACCCTGGAAAAATG 2519 TGGAACAAAA 5244 G - - AAATG C TGAAAG
 GA
 GGGCTCTTGTCTTGAAAGA GTCCAAATTC ATTA GA CC CTGGAA GGGCT TTGTTCT
 AGGA G
 GGAGAGTGTCTTGGAACAAA TAGA ||| || |||| |||| |||| |||
 AGTCCAAATTCTAGAGGATT TAGT TT GG GATCTT CCTGA AACAAGG TCCT /
 GTGAT G A A AAA-- A ----- GT
 GAM2534 GATTGAACCAAAGGGAAC 2520 TCACTGGTCC 5245 TG GG A ACA CTTCC TA
 GG
 CATTTTGGACCCTTCCAGTG GAGGAGATTT GAT AACCAAAG A CT TTTTGGACC AGTGGT
 GT A
 GTTAGTGGATTAACATCACT CTTT ||| ||||| || ||||| |||| ||
 GGTCCGAGGAGATTTCTTTG TTA TTGGTTTC T GA GGAGCCTGG TCACTA CA T
 GTTTGATT GT TT A --- ----- -- AT
 GAM2535 TCACCACTGACATTTTCGGAG 2521 TTAAACCAAT 5246 A A GA GG AA-- GAT GAT
 AAT A C
 ATGGGTGCCAATTTAGATGT GGAAAAAGGC ACC CTGAC TTTCG GATG TGCC TTTA GTT
 AGGGT TG TC A
 TGATAGGGTAATTGATCCAA AATA ||| ||||| |||| ||| ||| ||| ||| ||| |||
 GGACAACCTCTTAAACCAATG TGG GATTG GAGGT TTAT ACGG AGGT CAA TCTCA
 AC AG A

C - G- A- AAAA AAC AT- --- - G

GAM2536 CCGCTACTGAAGGCTATCTT 2522 TATTATCTCC 5247 CTGAAGG CTTAATAAG T - AA
ATG TTT TCCT

ATAAAGTTGTGTGAGTAGTA	ATAAAAAAAT	A	CTAT	TTGTG	GAG	TAGTA	TGGCA	CT
ACC G								
AATGGCAATGCTTTTACCTC	AATA							
CTGTATCTGGTCATAGAACT		T	GATA	AATAC	CTC	ATTAT	ACTGT	GA TGG T
GTCATATTATCTCCATAAAA		AAAAAA-	ATAAAAAA--	-	T	--	CAA TAC	TCTA
AAATAATAGAAAAAATAGCG								
G								

GAM2537 GTGTTAATCTTGCCCACATA 2523 TGGAAAGAAA 5248 - A G CATATGAACTG GCTGTA-
AAAAGGAG

T

TGA	A	C	T	G	A	C	C	A	A	G	C	T	G	T	A	C	T
A	T	C	T	A	A	A	G	G	A	G	T	A	A	A	C	A	A
G	G	G	A	T	G	G	A	A	A	G	A	A	T	T	G	G	T
G	G	G	G	A	A	G	T	A	A	G	C	T	A	C			

 TTGGTTGGGG GT GTT ATCTT CCCA ACCAA CTATCT

 || ||| ||||| |||| |||| |||||

 CA CGA TGGAA GGGT TGGTT GGTAGG /

 T A G ----- AAAGAAA GAACAAAA

GAM2538 TACTCAACGGTAGTGCATTC 2524 GTGCATTCCA 5249 A ATTA GT- T
CAATTAGTGTGCCCATTTGG ATTAGTGTGC TACTCA CGGTAGTGCATTCCA GT GCCCAT T
GTGGGTTGGACGAGTGGAAT CCAT ||||| ||||| || |||||
GCACTGCTGTGAGTA ATGAGT GTCGTCACGTAAGGT CA TGGGTG G
- GAG- GGT G

GAM2539 CTTGTTCCAGCCAGTAGCCG 2525 TATCTCAGAG 5250 GTAG GG- AACA--- AGTGGAA
TG A ACGTCAGG
GGGAGAACATCACCCAGTGG GGGTGAACAG A CCG GAG TCACCC TTTGAG ACA
TGGC C
AATTTGAGTGACAATGGCAC GAGC | ||| ||| ||||| ||||| ||| ||||
GTCAGGCATACAACACGCCA T GGC TTC AGTGGG AGACTC TGT ACCG A
TGTATCTCAGAGGGGTGAAC ATAA ACA GAGGACA G----- TA - CACAACAT
AGGAGCTTACACGGAATATG
GCCAGAAAAG

GAM2540 TTGTGTGAGCAGTTACTGGC 2526 TAATGTACCT 5251 ACT- - CCTTTTA AA - AG- A
- ATATTA
AGACCTTTTATCTAATGTAC AGCTATAGAT AGTT GGC AGA TCT TGT ACCT CTAT
GATCT CCT T
CTAGCTATAGATCTCCTATA CTCC ||| ||| ||| ||| |||| |||
TTATGTCCACAGGAAGATTA TCAG CCG TCT GGG ACG TGGG GATA TTAGA GGA
/
TAGAAGAGGTAGCAGGGGGG ATCT G AATCAG- GG A GAA - A CACCTG
ACTAATCTGGCCTCTAGACT
GTTAGCAGCA

GAM2541 AGTTTGGGACGCCTCATGCA 2527 TCACTGGCTG 5252 T-- G TCATG AAATGGAT TG
AA- G
GTGAAAATGGATGTGTTCAA GGGTCCCTGT AGTT GGGAC CC CAGTGA G TTC
TCTGG A

TCTGGGAGACCAGACGGGAG AGCT |||| |||| || |||| | ||| ||||
 TGTTGTTGAAGTCACTGGCT TCGA CCCTG GG GTCACT T GAG AGACC G
 GGGGTCCCTGTAGCT TGT G TCG-- GAAGTTGT GT GGC A

GAM2542 ATCTGGTACATGTGGCTGGG 2528 TCACTGGGCG 5253 T GCAG----- T--- GA C
 T- A
 CAGTCGGTTCCTGGAGTTTG TCCAGGGCTT G GGCTGG TCGGTTCC GGAGTTT GGC
 CTCGGT TCCTC A
 AGGCCCTCGGTTTCCTCAAT CTAG | ||||| ||||| ||||| ||| ||||| |||||
 GAGGATCACTGGGCGTCCAG C CCGACT GGTCTGAGG CTTCGGG CTG GGGTCA
 AGGAG /
 GGCTTCTAGTGAGCTGGAG T AAGGAAGGTGA TGAT AC C CT T
 TGAAGGAATCAGCCTCAAC
 TACCTGGGGT

GAM2543 ATGCACCCACCTGGAAAACA 2529 CCTCACATTG 5254 - A TG AAAACA CT TCAC
 GCA GA
 GAGACTTCGTCACTGGGGTG GTTCTCGAGC ATGCA CCC CC G GAGA TCG TGGGGT
 GGG C
 CAGGGGACGACCCGCCTCAC TGGG ||||| ||| | |||| ||| ||||| |||
 ATGGTTCTCGAGCTGGGGG TCGT GGG GG C CTCT GGT ACTCCG CCC /
 GCTGCGT C - GT GAG--- T- TAC- --- AG

GAM2544 ATGCCAAGGTGGTGAGAGTG 2530 TGTCATGGAC 5255 CAAG AGA TA AG G
 GCTAGGCCAGCCGTGAGGG ATCATAACGC ATGC GTGGTG GTGGC GGCCC CC T
 GGGCTGTGTCATGGACATCA GT |||| ||||| ||||| ||||| ||
 TAACGCGT TGCG TACTAC TACTG TCGGG GG G
 CAA- AGG TG G- A

GAM2545 CCATTCTGGCTCTTTTGGTG 2531 TCTGGCTCTT 5256 TT - TTT- GG T T G
 ACGGGACTAGTCTCTGTGGA TTGGTGACGG CCA CTGGCT CT GGTGACG AC AG CTCT T
 GAGTCTGTTTCGTTACCTTG GACT ||| ||||| || ||||| || |||||
 TAGCAGTCGGTCTGG GGT GGCTGA GA CCATTGC TG TC GAGA G
 CT C TGTT TT - T G

GAM2546 CGGTACATATCGCACTGGG 2532 TGACAACGGG 5257 G A----- A TG A-- ---
 GTACAC
 ACTGATTGTTGGTATGCCAT GCTCTACTCA CACTGGG CTG TTGT GT TGCCATGGA
 GATTAGGCCG A
 GGAGATTAGGCCGGTACACA GTGA ||||| ||| |||| || ||||| |||||
 CTCAGGGTGGCCTGGTCAGA GTGACTC GGC AACA CG ATGGTACCT
 CTGGTCCGGT C
 TCCATGGTAGTGGCTGACAA - ATCTCGG - GT GTG AGA GGGACT
 CGGGGCTCTACTCAGTGAAG
 GTGGAGTTCCG

GAM2547 GTCAGTAGGATGGTGTTGGG 2533 GCACTGGTGT 5258 ATG TG C TCTC - G C
 G AG

GACCCTAGTTCTCGCCACCT	TTTACACCCT	GG GTGT GGGAC CTAGT	GCCACCTCA CT AT
TTCTGTGG CCGG G			
CACTGATCTTCTGTGGGCC	ACTG		
GGAGGTGTTGGCTACGGGAA		CC CACA TTTTG GGTCA	CGGTGGGGT GG TA
AAGGGCATC GGTT /			
CATGGCTGGGGTGGCACTGG		--- -- T ---	C - C - GT
TGTTTTACACCCTACTGAC			

GAM2548 ACAGCGATAAAAGAACAAC	2534	TTCGGAGTTG	5259	ATAAAAGAA	- CAAAC	AC
CGACAAACGTGTCACTAAGA		GTGATGACGT		ACAGCG	CAACTC GA	GTGTC T
TATTCGGAGTTGGTGATGAC		TGT				
GTTGT		TGTTGC		GTTGAG CT	TATAG /	
		AGTAGTG--		G -----	AA	

GAM2549 ATGTGTGTAGTTGAGCTGCT	2535	AGCAGCAGTA	5260	T-- TG	C GAA A TA
CGCGAACTTACAAGTAGATC		GCTACTATTC		ATGTG GTAGT	AGCTGCT GC CTT CAAG G
TTGAAGCAGCAGTAGCTACT		TCGC			
ATTCTCGCAT		TACGC		TATCA TCGATGA CG	GAA GTTC /
		TCT --		- AC-	- TA

GAM2550 GGCAGTCTCATACTATGCTA	2536	TATGCTAACC	5261	A CT- C - A AG	TGA ATA C
ACCTGAGCAAATTCATGAGT		TGAGCAAATT		GGC GT	CATA TATG CTA CCTG CAAATTCA GT
CCA C					
ATACCACCAATGGCGAACAT		CATG			
TGAATTTGGGCAGGCTAGAT				CCG CG GTAT GTAT GAT GGAC GTTTAAGT	CA GGT A
ATGCTATGCAAGCAGCC				A AAC C A C GG	TA- AGC A

GAM2551 AGCACCTTTCCGAGCTGTGA	2537	ATCACAGAAG	5262	- --- CGAG	CGGA TGA-
CAAAGAATG AA					
CGGACATTGATCCTCAAAGA		AAAGATGGAT		AGCA CC TTTC	CTGTGA CAT TCCT
GTGC G					
ATGGTGCAAGAGAGTACAGT		GCT			
AACAAAGGGAGACTATGATC				TCGT GG AAAG	GACACT GTA AGGG CATG A
ACAGAAGAAAGATGGATGCT				A TAG AA--	A--- TCAG AAACAATGA AG

GAM2552 GTTCGCACAAGAGAGTGCTG	2538	TCATCGCATG	5263	A GA CT	AAA- C T --- CC --
A AG					
TCAGATAAAGCGATCATATC		GATTTGATTA		C AGA GTG GTCAGAT	GCGAT ATA CA AC
CAAT TTCTT TG A					
AACCCCAATTTCTTATGAGA		CAAT			
GACAGAGAGCCATTGAGTAT				G TTT CAT TAGTTA	CGCTA TAT GT TG GTTA
GAGAG AC /					
ATGTTATCATCGCATGGATT				A AA --	GGTA C T ATA A- CC - AG
TGATTACAATTTAGTGCTGA					
AT					

GAM2553 TGGCTATTCCAAGATATCCA	2539	ATTTAGCTGT	5264	ATTCCAA	ATC CTTT TT G
GAT					

CTTTACAGCTATTATGGTAA	TGTTAATCGT	TGGCT	GAT CA	ACAGCTA ATGGTAAT AT A
TGATGATATTGATGATTATC	AAGC			
ATTTAGCTGTTGTTAATCGT		ACCGA	CTA GT	TGTCGAT TACTATTA TA /
AAGCCA	ATG----	ATT ----	T-	G GTT

GAM2554 ACGTTAGCTGATATGGATGG 2540	TGATATGGAT 5265	G -	ATG A	TTCTT	TAT
TAAAGATTCTTATTCTTATT	GGTAAAGATT	ACGTTA CT	GATATGG	GT AAGATTCTTA	
ATTATTC C					
ATTCTATCGAACGAATGATT	CTTA				
TTTGAGGATCTTCACAACCC		TGTAAT GA	CTATACC	CA TTCTAGGAGT	TAGTAAG G
ATATCTAGGTAATGT		G T	CAA C	TTT--	CAA

GAM2555 ATTTAGCAACTTTTGGGCTT 2541	TTTAATGGTG 5266	C ----	TG--	TAACG	TTA	TGG A
A T T						
GTGGTAACGGCCTTAGGTGT	AGACTACACC	A TTTTGG	GCT	TGG	GCC	GGTGT CT
CACTAT TA AGA G						
TGGCTACACTATATATAGAT	ACTG					
GTTTCTTTAATGGTGAGACT		T AAAACC	TGA	GTC	CGG	CCACA GA GTGGTA AT
TCT T						
ACACCACTGGCAAAATCTGA		T	ATTA	TAAA	TAAAA	TCA TCA - - T T
AATAGTATTACCAAAATTTCTGAAT						

GAM2556 TTGCAGACTGCGTCAGGTAC 2542	TCAGGTACAT 5267	C -	ACA	GGT C	T
ATGTGGTGCCCTGTTATTT	GTGGTGCCCC	TTGCAGA	TGCG	TCAGGT	TGT GC CCTGTTA T
TAATAGGAGCCAAACAAGGA	TGTT				
CCTGGTCGCATCTGCGG		GCGTCT	ACGC	GGTCCA	ACA CG GGATAAT /
	- T	GGA	AAC A	T	

GAM2557 ACATGATATTAGATCTGATT 2543	TCTCATCGAA 5268	T TTA	CTGAT--	AA	A----	A A
AA AT						
ATTTAGAAGATAAGATAGAA	TATATCCCTA	ACA	GATA	GAT	TATTTAG	GATA GAT GA
ATT AG A						
ATTAAAGATATAACTGGAAT	AATA					
CTCATCGAATATATCCCTAA		TGT	CTAT	CTA	ATAAATC	CTAT CTA CT TAA TC T
ATACTGAAAAATCCTTATCC		C	TC-	AAAAGTC	C-	ATAAG - C GG AA
TGT						

GAM2558 AGGTTCTGATATCTTGGGTA 2544	TATCTTGGGT 5269	A T --	TT C	ACTAA-	C
C					
ATGTTTTACCGCAGACTAAG	AATGTTTTAC	AGGTTCTG	TATC	TGG	GTAATGTT AC GCAG
GAGTTTTA CAAC C					
AGTTTTACCAACCCAGTTGC	CGCA				
TAAATTTTCAGATGCTGCGT		TTTAGGAC	ATAG	ACC	TATTACAG TG CGTC
TTTAAAT GTTG /					
TTGACATTATTTCCATGATA		C T TT	TT -	GTAGAC	C A
CCAGGATTT					

GAM2559 AGTGCCCTAACAGCACCGGC 2545 T TACTCCAGC 5270 - A CAC TGCC A
 TGGATGCCAATACATAGTAT CGCTACTGGT AGTG CCCTA CAG CGGCTGGA AATAC T
 TACTCCAGCCGCTACTGGTA AGGG |||| |||| || |||| ||||
 GGGACACT TCAC GGGAT GTC GCCGACCT TTATG /
 A G ATC CA-- A

GAM2560 GCCTTATGCTGGGACTACCC 2546 TACCCCTTTC 5271 TG C C T A CCTGAA C
 CT TC
 CTTTCAAACGCATTAGACCT AAACGCATTA CTTATGC GGA TACCC TT CAAACGCATT GA
 ATCAAC CT TTCC T
 GAAATCAACCCTCTTTCCTC GACC |||| || |||| || |||| || |||| || ||||
 TTCTGGAATTAGTGTTGATG GAATGTG TCT GTGGG AA GTTTGTGTAA CT TAGTTG
 GA AAGG T
 ATTTCAATGTGTTTGCAACG GT T C C - TTAG-- T TT TC
 GGTGTTCTTGGTGTAAGAGC

GAM2561 TCGTGATTTGATTAAGCGAT 2547 TCAATCGGTT 5272 A ATT T T
 TTGGTTGGTTTAAGAATCAA GCTTTTACAA TCGTG TTTG AAGCGATT GGTTGGTT A
 TCGGTTGCTTTTACAAATAC ATAC |||| || |||| |||| ||||
 GA AGCAT AAAC TTCGTTGG CTAATAA A
 - ATT - G

GAM2562 TGATTTGCTGGTAGTAAGA 2548 ATTACATTGA 5273 T CT T GA C AT TA
 TGGATGAAATGTCATTTGAT TTCATTTTCC TGA TTCG GG TAG AAGATGGAT AATGT ATTTG
 TATGT A
 TATGTTAAACGCATACCAAA TATT |||| || |||| |||| |||| |||| ||||
 TTACATTGATTCATTTTCCT ACT AAGC TTATC TTTTACTTA TTACA TAAAC ATACG /
 ATTCGAATTCA T -- C G- T C- CA

GAM2563 TTCCGATCTAGTGAATCCCA 2549 TGGCTGCTGC 5274 -AT A C T- A - C C G C
 C T
 CAACGTATGCACGCATCACA TGATGATTTT AGTG A CCC CAA GTA GC CGCA TCA AA
 CATCAGT AGTA GCTA AGC T
 ACCATCAGTGAGTACGCTAC GATT |||| || |||| || |||| || |||| || ||||
 AGCTTATGCTATGGCTGCTG TTAC T GGG GTT CAT TG GCGT AGT TT GTAGTCG TCGT
 CGGT TCG A
 CTGATGATTTTGATTGCGGG C CG - - TT G T T A - - A T
 TTTTACTTGGGGGCTCCATT
 ATCTTGAA

GAM2564 AATCTCTATGCGATGTATAT 2550 TTGCAGCCTT 5275 TC TA A- T- C TGTT G
 TT
 GCCTGGTGTTAGGTTGGGAC TCCCACGCAT AA TC TGCG TGTA ATGC TGG AGGTTG
 GACATGCTCTTT A
 ATGCTCTTTTTATTAAAGGG TTTA || || |||| |||| |||| |||| |||| ||||
 TGTGTTGCAGCCTTTCCAC TT AG ACGT ATAT TACG ACC TCCGAC
 TTGTGTGGGAAA /
 GCATTTTATAGCTGCAATGA GA TA CG TT C CTT- G TT

GAM2565 AATGGGAAAAGTTCTGATT C 2551 TGTTCACGA 5276 A TT A ATCG TT T T TT
C AGT
AAGCTATCGTTATTTTG TGTT TTTTGCCTAT AATGGG AAAGTTCTGA CA GCT TTA TG GT
AGTG TTAT TGC T
AGTGT TTTATCTGCAGTTTT T ||||| ||||||| || ||| ||| ||| ||||
AGCATATAATTACTTACCAT TTATCC TTTTAGGACT GT CGG AAT AC CA TCAT AATA
ACG /
TTAAGGCTGTTTCAGGATTT G TT - ---- TT - T T- T ATT
TGCCTATT

GAM2566 AGAAATTTTAAGCTTAAAAG C 2552 TAGCGAATTT 5277 A--- T A G T TAT - A
C
TCTTAGCGAATTTGCTCGCT GCTCGCTTTA T AGCTTAAAAG CTT GC AATT GCTCGCTT
TGCAATTG TTCCT GAG T
TTATTGCAATTGTT CCTAGA TTGC | ||||||| ||| || ||| ||||||| ||||||| ||||| |||
GCTATTCAGGGAATTGATTG A TTGAGTTTTC GAA CG TTAG TGAGCGGA ATGTTAGT
AAGGG CTT /
TATAGGCGAGTTGATTAGCA ACGC - A A T T-- T A A
AAGCTTTTGAGTTCGCAAGA
ATCTCT

GAM2567 CATTAGCACCTATTAGGGTA T 2553 TAGGGTAGCA 5278 CT- - CTCATA---- A CG -
T
GCATGGTCTCATAATGATAT TGGTCTCATA GCAC ATTAG GGTAGCATGGT ATGAT TTAC
ACCT ATTTGT T
TACCGACCTATTTGTTTCGG ATGA ||||| ||||||| ||||| ||||| ||||| |||||
CAAGTGAGGTTAGTAGAGTT TGTG TAATC CCATTGTGTCG TATTG GATG TGGA
TGAACG C
ATAGAATCTCCTGCTGTGTT TAT T TCCTCTAAGA A AT G G
ACCTCTAATTATGTGTGATA
ATG

GAM2568 CCTCTCAATGAACCAATAAC 2554 TCAATGAACC 5279 - - TA-- T - A
TTGGAATGATAATTTATCTA AATAACTTGG CCT CTCAA TGAACCAA ACT GGAAT GATA T
TTCCTGGTGAATTTGGTTTA AATG ||||| ||||||| ||| ||||| ||||
GTTGGGAAGG GGA GGGTT ATTTGGTT TGG CCTTA CTAT /
A G TAAG T T T

GAM2569 GGAACGGTACAAGAATGGGC 2555 AACGGTACAA 5280 A GCC- - TGCAT- T
CCTTCTATGCTTGCATCTAA GAATGGGCCC GGAACGGTACAAG ATGG CTTC TATGCT
CTAAATTCT T
ATTCTTTAAAGAATTTGGTT TTCT ||||||| ||||| ||||| |||||||
TTGTGGCATATGGAGATGAC CCTTGCCGTGTTT TACC GAGG ATACGG
GGTTTAAGA A
CATATTTGTGCCGTTCC A AGTA T TGTTTT A

GAM2570 GGAGATGTTGTAATGTGGGG 2556 TGTTGTAATG 5281 T TGT - TGCAT TT
TCATGCATTGCCTTCTGGGC TGGGGTTCATG GGAGA GTTGTA GG GGTCA TGCC C

ATTATTTGACCGCTCCTTAT CATT ||||| ||||| ||||| |||||
 AACTCTCT TCTCT CAATATT TC CCAGT ACGG /
 - CC- G TTATT GT

GAM2571 GTAGGACTACTATATTTTCAT 2557 TATTTTCATGA 5282 CTA GATT A-- GG T
 GATTGGGCAGATACTAGGGC TTGGGCAGAT GTAGGA CTATATTTTCAT GGGCAGAT CTAG
 C T
 TTTTGTACTAGATGATCTGT ACTA ||||| ||||| ||||| |||||
 CTCCAGATGAGATATGGAAT CATCCT GGTATAGAGTA TCTGTCTA GATC G T
 CCTAC AA- GACC GTA AT T

GAM2572 GTCGTTTTGAAGACTTGGA 2558 ACAGGTAGGG 5283 - AAA--- TG A - GTATT
 GA- C
 AATGAAGAAGTGGTAGCACA TATTTACCTG TG GA TGAAGAAG GT GCA CAGGTAGG
 TACCTGGC TGATT A
 GGTAGGGTATTTACCTGGCG GCGA || || ||||| ||||| ||||| |||||
 ATGATTCAAAATCAAAAGTT AC CT ATTTCTTC TA CGT GTCTATCC ATGGATTG
 ACTAA /
 AGGTACCTATCTGTTGCAAT T AAGATA CT A T ---- AAA A
 TCCTTCTTTAATAGAATCTC
 ATGTTTCCGAC

GAM2573 GTCTTGTAAGAAAGTGGAA 2559 AAAAGTGGAA 5284 T AAA GGA AC TAAAA A
 GT
 AACGACCTGTGGTAAATGT CAACGACCTG GTCT GTG AAGT ACAACG CTGTGG TGTG
 ATCTT G
 GAATCTTGTAAGAAAGGATAC TGGT ||||| ||||| ||||| |||||
 ACAAAGACCCACAGTACGTT TAGA TAC TTCA TGTTGC GACACC ACAC TAGGA A
 GTGAAACTTCTACATTAGAT T ATC AAG AT CAGAA A AA

GAM2574 GTGAAGTACAAAAATATTAC 2560 TATTACATGA 5285 T - GA T G CT AA T TG AA
 TTC
 ATGAAATATTTGGAATCTCA AATATTTGGA CAAAAATAT AC AT AATATT G AAT C CTTG ATA
 ATGA TTAAT A
 ACTTGATATGATGAAATTA ATCT ||||| ||||| ||||| |||||
 ATTTCAATTTATTAGGATCA GTTTTTATA TG TA TTGTAA T TTA G GAAC TAT TACT
 GATTA A
 TTGTATCAAGAAGGTATTGT C A AA -G TG AA - GT AG TTT
 AATGTTAAATAGTCATATTT
 TTGTAACAGC

GAM2575 TATTGATGGGGATGAACTA 2561 TGGTAAGAAA 5286 GAA A T CGTAAA C GT
 C TTTT
 TCAATTCTATAAACGTAAA CAGATTTTGT GGAT ACTATCA TTCTA AAAA TCTT GCCAG
 TTCC TTGGG A
 TCTTCGCCAGGTTTCCCTTG GAAA ||||| ||||| ||||| |||||
 GGTTTTTAAACTTCTAGTG CTTA TGGTAGT AAGGT TTTT AGAA TGGTC AAGG
 GATCT /
 GAAGTGGTAAGAAACAGATT AG- A - AGACAA - -- T TCAAA

TTTGGAAATGATGGTGAATT
 CCTATTTGATA
 GAM2576 TGGCTAGATATCTTAAATCC 2562 TATCTTAAAT 5287 A - TC AG TG GG C-- ATT-
 - TT
 AAGTCTGATGGTTTTGTAGC CCAAGTCTGA GATATC TTAAA CA TC AT TTTTGTAG AGGTG
 TTGAG GGA T
 AGGTGATTTTGAGGGATTTG TGGT ||||| ||||| || || || ||||| |||| |||||
 ATTCCTCTCAATTGGTGCCT TTATGG AATTT GT AG TA AGAGCATC TCCGT
 AACTC CCT G
 ATACTACGAGAAATTGGAAA - T TT AA GT A- ATA GGTT T TA
 TGTTTTTAATGGTATTGCCA

GAM2577 TTGTTATTGATCGTTATGAA 2563 TGAAAGATTG 5288 TATT AT TT TC A- TG TAA
 TT
 AGATTGAGAGGATATCCATG AGAGGATATC T GATCGTT GAAAGA GAGAGGATA CATGGG
 AAG A AATTAG A
 GGAAAGTGATAAAATTAGTT CATG | ||||| ||||| ||||| ||||| ||| | |||||
 ATACTAATTCTTTGCTTGAT A CTAGCGA CTTTCT TTCTTTTAT GTATCT TTC T
 TTAATC /
 CTATGTTTATTTTCTTCTCT TTT- GT C- TT AG GT TC- AT
 TTCTGAGCGATCTTTACAA

GAM2578 TTTTATAAGGTGCCTTTTTTC 2564 TGATTTCGGAA 5289 G C A G A -- TTA
 TGAAATGATGTACTGTTCTT AGAGTATATT TTTTATAA GTGC TTTTCTGAA T ATGT CTGT
 TCTTGC A
 GCTTAAATTGCGAGAAGACA ATGA ||||| ||||| ||||| ||||| ||||| |||||
 GAATATGATTTCGGAAAGAGT AAAGTATT TATG AGAAAGGCTT A TATA GACA AGAGCG
 /
 ATATTATGAAA A - -G A GA TTA

GAM2579 ATACGTTTAGATTTGTCAAA 2565 TGTTATGGAT 5290 TTG- AAA ATT GAA AATT -
 - TT
 ACTAACTATCATTCTGGAAG TCGGATGGTA GAT TCA CTAACATC CTG GAGTCCA
 ACATT TCAT CCC T
 AGTCCAAATTACATTTTCATC AGAT ||| ||| ||||| ||| ||||| ||||| |||||
 CCTTTGTTGGGTATGATGAT CTG AGT GATTGATAG GGT CTTAGGT TGTA
 AGTA GGG G
 GTTATGGATTTCGGATGGTAA CATA AGA AAT AGG AT-- T T TT
 GATAGTTAGAGATGAATACG
 TCTATCGTGT

GAM2580 CAGGTAATCGTGATATCCGT 2566 TAACTGGAAT 5291 AC A ---- TC GA AT
 TCTTCTTATGTTGAGGGGAA GTCTAGAAAT CAGGT TCGTGAT TC CGTTCT TTATGTT
 GGGGAA T
 ATTTATTCCTCAGGATATAA CATG ||||| ||||| || ||||| ||||| |||||
 CTGGAATGTCTAGAAATCAT GTTCA AGTACTA AG GTAAGG AATATAG CTCCTT /
 GAACTTG -- A ATCT TC GA AT

GAM2581 TAGAGAAAAATTATCTGGTT 2567 TACCTGTTCC 5292 TTTT TCTTT - T -
 ACAAGT CT

TTACATCTTTTAGTGCTAGT	AGATATTTTA	TATCTGG	ACA	TAGT GCTAG ACCG
TCTTTCATAT AAATG C				
ACCGTCTTTCATATACAAGT	CCTC			
AAATGCTCATCCATTTCAAT		ATAGACC	TGT	GTCG CGATT TGGT AGAAGGTGTA
TTTAC A				
GTGGAAGATTGGTTTTAGCT		T---	CCAT-	T T T AC---- CT
GCTGTACCTGTTCCAGATAT				
TTTACCTCTA				
GAM2582 TCAAGAATGTATTGGTGAAA 2568	TGAAAGAATC 5293	AG	GTGA	CTTA TT TG
GAATCTTATCTTTTTCTGAA	TTATCTTTTT	TCA	AATGTATTG	AAGAAT TCTT TC A
TTGATTAAGAGAAATTCTTG	CTGA			
GCGATACGTTTCTGA		AGT TTGCATAGC	TTCTTA	AGAA AG A
	CT	GG--	AAG-	TT TT
GAM2583 TTTGAGTCTTAAATATGGAA 2569	TATGGAAATG 5294	A	TG-----	T G CCTTTTG AA-
CT				
ATGAGGTTATTTTGAAAACA	AGGTTATTTT	TAAAT	TGAAA	AGGT ATTTT AAAACA
CCGG CATCTT G				
CCTTTTGCCGGAACATCTTC	GAAA			
TGATGAGGTGGCGCTGGAGT		ATTTA ATCTTT	TCCA TAAAA	TTTTGT GGTC
GTGGAG /				
ATGTTTTAAAAATACCTAAT		G	TCATTAA	- A ATGA--- GCG TA
TACTTTTCTAGATTTAAATA				
CTCGAG				
GAM2584 AGCTTATTGAAACGGGCGAT 2570	TTGAAACGGG 5295	T	G TACT	- C
ACTATTAGTGACTTGTTATC	CGATACTATT	AGCTTA	TGAAACGG	CGA ATTAG TGA T
TAATTCGACCGTTTCGTTGA	AGTG			
GCT		TCGAGT GCTTTGCC	GCT	TAATC ATT T
	T	A	----	T G
GAM2585 GAGCTTAATATAGCTACTGC 2571	TATGTGAGGC 5296	AT	--	A A-- ----- A T
TA				
TCTATGTGAGGCTTTCTTTC	TTTCTTTCAT	AGCTAC	TGCTCT TGTG	GGCT TTCTTTC
TGG AAGGAG T				
ATGGTAAGGAGTATTTTTCC	GGTA			
TTTCTAGAGGGGAAAATTAT		TCGATG GCGAGA	ACGC CCGA	AGGGGAG ATC
TTCCTT /				
AGAAGCCATGCGCAAGAGCG		--	CG	- GTA AGATATTAAA - T TT
GCGTAGCTCTC				
GAM2586 GATTTTTTTGAAGAGGCAATT 2572	AGAGGCAATT 5297	GA	- TTT	ACTC G
TGTTGCAGACTCTGGATCCA	TGTTGCAGAC	GATTTTTT	AGAGG CAA	GTTGCAG TG A
CTGCAATTCTTTGTCCTCTG	TCTG			
AAGAAAATC		CTAAAGA	TCTCC GTT	TAACGTC AC T
	AG	T TCT	----	C
GAM2587 GGTGCTGAGCTTGATGCGGC 2573	TCAGTGAATG 5298	C	C GA	T - TTT

TATTCTTGATAGGTTTTC	TCGTAAAGAA	GGTG TGAG TT	TGCGGC ATTC TTGATAGGT	C
TACCTATCAGTGAATGTCGT	CTCA			
AAAGAACTCACGCC		CCGC ACTC AG	ATGCTG TAAG GACTATCCA	/
	- A AA	- T	TAA	

GAM2588 TACGAAAGGCAAGGTTTATA 2574	TTAAAGCCAA 5299	A ---	ATAT TG GTT
TTATGGAGTGTTTAGAACTT	ATTGCCTTCG	TACGAA GGCAA	GGTTT TA GAGT T
GTAAAGCCAAATTGCCTTC	TA		
GTA	ATGCTT CCGTT	CCGAA AT TTCA	/
	- AAA	---	TG AGA

GAM2589 ATTGATCTGTGGTGGCATGT 2575	TGGCATGTTA 5300	A G	A ATC A CG
TATGGATCGTTATGTGCGTA	TGGATCGTTA	ATTG TCT TGGTGGCATGTT	TGG GTT TGTG T
ATTACAGAGCTACCAAATAT	TGTG		
GTCACTAAAGACAAT		TAAC AGA ATCACTGTATAA ACC	CGA ACAT A
	- A	- AT-	G TA

GAM2590 ATTGCCACAGTGCACCTTCT 2576	TTCAGAGAAT 5301	CAG C	CGA C-	T	GAGT
TCC					
CGAGCTGCCCTCTTTGATAT	GGCGGCACAG	ATTGCCA TG	ACTTTCT	GCTGCC	TCTTTGA
ATGCAAA TCC C					
GCAAAGAGTTCCTCCCTTTT	GAAA				
GGATACATTTGTATTTCAGAG		TAACGGT AC	TGAAAGG	CGGCGG	AGAGACT TATGTTT
AGG T					
AATGGCGGCACAGGAAAGTC		--- C	ACA	TA	- ACAT TTT
CATGGCAAT					

GAM2591 CGAGTCTAGGAGCAGTTCTA 2577	TAGGAGCAGT 5302	CTA-	CTA ---	T
GGGGTCTTTTCACTCTTAAG	TCTAGGGGTC	CGAGT	GGAGCAGTT	GGGGTCT TTTCACCTC T
GGTGAAGGTTGGACTCCAGC	TTTT			
TGCTTTGAAAGCTCG		GCTCG TTTCGTCGA	CCTCAGG	GAAGTGGG A
	AAAG	---	TTG	A

GAM2592 GAATGCGTTTCAAATCTCAA 2578	AAATGTGTTG 5303	TT AA T	T	TT ATGAT	TCA
- TT					
AGATAAATGTGTTGGTATGA	GTATGATAAA	CG TCA TC	CAAAGA	AAATGTG GGT	AAACGA
TTGG CTTGCT T					
TAAACGATCATTGGCTTGCT	CGAT				
TTTGCAGCAGGTTCAACACT		GT AGT AG	GTTTTT TTTATAC	CCA	TTTGTT AACT
GGACGA /					
TGTTTTGACCCTCATATTTT		TT -- C	C	TC GT---	CAC T CG
TTTTTGCGATGATTTGCATT					
T					

GAM2593 GGATGAGAAAGTTGATTCTT 2579	TGAGAAAGTT 5304	--	TTCTTCTAAAG	ACA
CTAAAGTGATACATAAAACAA	GATTCTTCTA	GGATG	AGAAAGTTGA	TGT T
AAAACTCGACTTTTTACTAT	AAGT			

CC

CCTAT TTTTTCAGCT ACA /
CA CAAAAA----- AAA

GAM2594 TATAGATTGGGTGAAGGCTG 2580 TGATAACACC 5305 G T CTG AAT AA
GTTATCGTAAATGTAAAGAA TTCTCCAAAT TATAGATT GG GAAGG GTTATCGTA GTA G
TACTATGATAACACCTTCTC TTGT ||||| || ||||| ||||| ||
CAAATTTGTA ATGTTTAA CC CTTCC CAATAGTAT CAT /
A T A-- --- AA

GAM2595 TGGTTTAAACCGGAGTCAAA 2581 CAAATTGCAA 5306 TA CC- TC CA AAT T T
T
TTGCAAAAATTCTTAATGCA AAATTCTTAA TGGTT AC GGAG AAATTG AAAATTCTT GCAG
TTTTGG GG A
GTTTTTGGTGGTAACCCCGA TGCA |||| || ||| ||||| ||||| ||| ||||| ||
AGTCTGCCAAAGAATTTTCC ACCGA TG TCTC TTTAAC TTTTAAGAA CGTC GAAGCC
CC /
AATTTTTCTCTCAAGTCGAG GC AAC TT C- AC- T - A
CCA

GAM2596 AGAACACATAACGCGACTGC 2582 TGAGGAAGAT 5307 G G AA GAT GGT A - AA
AA- T
TAATTCGATGACGGTGAGGA TGTGTCTAAA AC C GACT CT TTC GAC GAGGAAG TTGTGT CT
AG CAGGTTTC T
AGATTGTGTCTAAAGAACAG GAAC || |||| || ||| ||||| ||||| || || |||||
GTTTCTTTGAAGCCTGGTGC TG GTTGA GA AAG CTG TTCCTTT AATACA GA TC
GTCCGAAG /
TCAGTACATAACTTTCCTTC - G AG AGT AC- C T C- GTG T
AGTCTGAGAAGAAGGAGTTG
GTAAATTTGTT

GAM2597 ATGGACTGGTGAAAAAACTA 2583 TCAACGATTT 5308 G AAACTATGT T GT AACG G
CCATG- A
TGTGATATGTTTGATATCAA CTTTAGCAGT ACTG TGAA GA AT TTGATATCA GG GGC
TCTTAG C
ACGGGGGGGCCCATGTCTTAG CTGT ||| ||| || || ||||| || ||| |||||
ACGTTGAGAATCCGTGCCGC TGAC ATTT CT TA AACTATAGT TC CCG
AGAGTT /
TATTATGATATCAACGATTT G ----- T GC ATTA G TGCCTA G
CTTTAGCAGTCTGT

GAM2598 CCTGTTTGTAGAGAAACAAT 2584 ATCATATTTG 5309 AA CA- -- TTG -- A A-- T
AC
TCATGGACAAGTGTTTGGAT AGTTCAAATA GAGA CAATT TGGAC AAGTGT GATT ACAT
GCT GGTTA CTG C
TACATAGCTAGGTTATCTGA ATTG ||| |||| |||| ||||| ||| ||||| ||||| ||
CCAGCAGCTGACCATAAGCA TTCT GTTAA ACTTG TTTATA CTAA TGTA CGA
CCAGT GAC /
ATGTTAAATCATATTTGAGT GG TAA AG --- AT A ATA C GA
TCAAATAATTGGGTCTTATT

CATAAACGGG
 GAM2599 CGGTGGATGTGACCCATTTC 2585 TGTAATGAAT 5310 CAT TTAAATCAAT AT TG TG ACG
 A A - A
 TTAAATCAATGTTACGATGG CCGGTCACCTA CC TTC GTTACG GG C TC AC
 ACTTCTAAA CT CAG G
 TGCTGTCACGACAACCTTCTA AGCC || ||| ||||| || | || || ||||| || |||
 AAACCTCAGAGATCTGTAGGT GG AAG TAATGT TC G GG TG TGAAGGTTT GA
 GTC A
 TTGGAAGTGGTAGGTGGTGC CCT ----- CG GT GT A- G G T T
 TGCTGTAATGAATCCGGTCA
 CTAAGCCGCTG
 GAM2600 CTGAATCACATCAGAACATA 2586 TTAATGGAGT 5311 AGAA A CTAAC C ATA A TT
 C GAAT
 TCAGGCTAAAGCACTAACAT TACTGCGAGA ATC CAT TCAGG GCA TAAC CA TAATG
 TTATCCTT GTC C
 ACAATAATGTTTTATCCTTC TCTG ||| ||| |||| ||| ||| ||| ||||| |||
 GTCGAATCAATTAGATCGAG TAG GTA AGTCT CGT ATTG GT ATTAC AATGGGAG
 TAG A
 GGTAATCATTAAATGGAGTTA G--- - AGAG- C AG- A T- C ATTA
 CTGCGAGATCTGAATGGGAT
 GTAGATAAAG
 GAM2601 GCGATGAGGTAGTATGCAAT 2587 TGAGGTAGTA 5312 T C AA CAAT AAAGC
 AATACTTTCCAATGCTGTGA TGCAATAATA GCGA GAGGTAGTATG AAT TACTTTC GCTGTG
 A
 AAGCAACAGGTACAGTTCAG CTTT |||| ||||| ||| ||||| |||||
 GAGGTAGAGTTTATGCTATT CGTT CTTTATCGTAT TTG ATGGAGG TGACAT /
 TCCTTGC C - AG ACT- GGACA

 GAM2602 GCTGAATCAGTTATTAGTAA 2588 TAGTATACTC 5313 T A A AT T- A C - CG- - ---
 AC
 CAAGATGGCATCGATAGTAT CGGACCGCTA TTAG AACA G TGGC CGATAG AT CT CG GAC
 CTACA AGT GCA A
 ACTCCGGACCGCTACAAGTG CAAG |||| ||||| |||| ||| ||||| ||||| |||
 CAACAAATGCAAACTATGT AATC TTGT C ACCG GCTATC TA GA GC CTG GATGT
 TCA CGT /
 AGACAGTCTCGCAGCATCTC T -- -- TC C C T ACA A AAA AA
 TATCGGCCACTGTTTCTAAT
 CTGAAAAAGC
 GAM2603 CTGCTGCGTGAGGTTTATTC 2589 TGAGGTTTAT 5314 ---- TA AATTCAA TC
 TTAAAAATTCAAACTTCTT TCTTAAAAAT CTGCTGCGTGAG GTT TTCTTAAA
 AACTTCTTCGC T
 CGCTCTGATGTGAAGAAGTT TCAA ||||| ||| ||||| |||||
 CTTTAAGGACGGGCTCCAGC GATGACGCATTC CGG AGGAATTT TTGAAGAAGTG
 G
 TTACGCAGTAG GACCT GC C----- TA

 GAM2604 GACTGGAGAGTTTGATGACT 2590 TGAAGTCCAG 5315 -- CT- AC A GA- AGGAAAATG
 CAA-- AT

TTCTTCAACATAGGGGCTGA GAAAATGGTC TGA TTCTTCA AT GGGGCT AGTCC
 GTCA GTTT T
 AGTCCAGGAAAATGGTCACA ACAA ||| ||||| ||||| |||| ||| |||
 AGTTTATTTTGAACGAGAAT ACT AAGAGGT TA CTTCGA TCGGG CGGT
 CAAG /
 GGCAGTAGGGCTCGAAGCTT AT AAT CT - AGC ATGA----- AAGAG TT
 CATTCTGGAGAATAATCATA
 TTGAATTTGTT

GAM2605 TCGTTGATGTGTATGACGCT 2591 TGATGTGTAT 5316 - G CTC CG T
 CTGCCGATTTCTGTAGAGAT GACGCTCTGC TCGTTG ATGT TATGACG TGC ATTC G
 TAGCACCGTCGTAACATGCA CGAT ||||| ||| ||||| ||| ||||
 GCGA AGCGAC TACA ATGCTGC ACG TAGAG T
 G - C-- AT A

GAM2606 TGGTGCCGTCCCATGTCCA 2592 TACCCGCAA 5317 T- AACATT GA-- AA- -
 AATTAA AT AA
 TCAACATTCCGGACGCGAAG TTAAAGGATC GTCCATC CCG CGCG GTTTACC CGCA
 AGG CCGA C
 TTTACCCGCAAATTAAGGA CGAA ||||| ||| ||| ||||| ||| ||| |||
 TCCGAAACCATCGGCCCTGA CAGGTGG GGC GCGT CAGGTGG GCGT TCC
 GGCT /
 AATGCGTGGTGGACAGCTGC AT ----- ATGA CGA T AAAG-- C- AC
 GAGTACGGGGTGGACTACGG
 GGGCGCCGCCA

GAM2607 AATCAATGGCGAGTGTGCAT 2593 TCGCATGCTA 5318 ---- - - A G
 GCAGGACTATGAAGTGGCCC CGCTATGTTT AATCA ATGGCG AGTGTGC ATGCAGG CTAT A
 TGCATCGCATGCTACGCTAT TTGA |||| ||||| ||||| ||||| |||
 GTTTTTGATT TTAGT TATCGC TCGTACG TACGTCC GGTG /
 TTTTG A C C A

GAM2608 CAGCCTTTCTGAACAACTGA 2594 TGAGATATGG 5319 C- A ----- TGGAAA TT A
 TCATG
 TGAGATATGGAGTGGAAATA AGTGGAAATA CAA TG TGAGA TATGGAG TAC GCCT
 CTG A
 CTTGCCTACTGTCATGAACA CTTG ||| ||||| ||||| ||| ||| |||
 ACCAGAGGCTGTAATGATTC GTT AC ACTCT GTA CTTC ATG CGGA GAC /
 TTCATGAACCTGTTATAAAC CC A CAAATATTGTCCAA TTAGTA T- - CAACA
 TCTCAACACCTTGTGATGGA
 TGAAATCTG

GAM2609 GAGCAAATGACACTTTGTGT 2595 AATGACACTT 5320 AAA TTT--- T- C TT
 ACCCTATTATTCTGAGGTTT TGTGTACCCT GAGC TGACAC GTG ACC TA A
 CATTAAGATGTGTAAAGGT ATTA ||| ||||| ||| ||| ||
 TC CTTG ATTGTG TAC TGG GT T
 GAA TAGAAT CT A CT

GAM2610 TTTCTGTTTCATCCCCTTTG 2596 CAGCCCAAAA 5321 TCCCC AT AA GG
 GATGCTGAATACTTGGTTCA TTTTGGAATG TTTCTGTTTCA TTTGG GCTG TACTT T

GAGTGCAGCCCCAAAATTTTG	GAAG				
GAATGGAAG	GAAGGTAAGGT	AAACC	CGAC	GTGAG	T
	TTTA-	--	--	AC	

GAM2611	CTGTTTCCGCCGGGCCTGAC	2597	GGTCACAAAT	5322	C	C	A	TC	G	G	CC	T
CTG	TTCTCGCTCCGACATCCTGT		GTGGGAGAGG		CTGTTTC	GCCGGGC	TG	CT	TC	CTCC	ACAT	
TGT	GACTTGC	A										
	TGACTTGCCTGACAAGCAGG		ATGG									
	TCACAAATGTGGGAGAGGAT				GACAGAG	TGGCCCG	GC	GG	GG	GAGG	TGTA	ACA
CTGGACG	/											
	GGCGAGCCCGGTGAGACAG				-	A	-	TA	A	G	A-	-
											AAC	

GAM2612	GTACAGAGGATCATTAATTAATT	2598	TACCAAGGCA	5323	--	TT	AA	TTATTTTCAC	-	T
	TTAACTTTATTTTCACTGGA		AAATTTTGG		GTACAGAGG	ATCA	AAATTTT	CT		TGG
	GCTGCAGCTACCAAGGCAAA		TTGC							
	ATTTTGGTTGCTTTTGTGC				CGTGTTC	TGGT	TTTAAA	GA		ACC
			GT	T-	CG	-----	A	A		

GAM2613	TTCATTGATTGTTATTTTTT	2599	TATCAGATTT	5324	GATT	ATTTTTT		CT
	GTCTGGTGTACTCAATGTAT		TTAAAACCCC		TTCATT	GTT	GTCTGGTGTA	C
	CAGATTTTAAAACCCCAGA		AGAT					
	TGAA		AAGTAG	CAA	TAGACTATGT	/		
			ACCC	AATTTT-	AA			

GAM2614	CTCGGGAGTGAAAACCTTATC	2600	TACAACGCGT	5325	-	AA	AA-	AAACACAAACC
A	AGGAATTCTCGCGCAAACAC		GGGAAGACTT		CTCGGGAGTG	AA	CTTATCAGG	TTCTCGCGC
TGTGCGCC	A							
	AAACCTGTGCGCCAACCGGT		TGAT					
	GTACAACGCGTGGAAGACT				GAGTTTTTAC	TT	GAGTAGTTT	AAGGGTGCG
ACATGTGG	C							
	TTGATGAGGATTGCATTTTT				G	AG	CAG	CA-----
	GAG							C

GAM2615	GAAGATTCAGGTGCAGTGCA	2601	GTGCAGTGCA	5326	AG--	AATGCCA	-	TTCCACA
T	T							
	ATGCCAGCCAGTTCCACAGT		ATGCCAGCCA		GAAGATTC	GTGCAGTGC		GC
GTGGC	GCC	T						
	GGCTGCCTTTTGGTTGCCAT		GTTC					
	GATTCCTGAGTACCTTAGCA				CTTTTAGG	CACGTCACG	TG	GTC
	CTGCACAACAGGATTTTC				ACAA	ATTCCA-	A	CTTAG--
								T
								T

GAM2616	GCAGTATGAGAGTAGTCAGA	2602	TGGGATACTC	5327	ATGAGA	C-	A	CGC	CC
	CATCCCATGACAGCGCGACG		TGATTATGAA		GCAGT	GTAGTCAGA	ATCCCATG	CAG	
GACGCG	C								

CGCCCAACGCGTCATTGACA	ACCG					
TGGGATACTCTGATTATGAA		TGTCG	TATTAGTCT	TAGGGTAC	GTT	CTGCGC /
ACCGCTGT	CCAAAG	CA	A	A--	AA	

GAM2617	GCTGCGTGCCGCGCAGCGTATG 2603	CCGCAGCGTA 5328	CG	C	C	TG	T	AT	-	-	A
	ATGTCTTCACCAATTACGAA	TGATGTCTTC	GCTG	TG	CGCAG	GTA	ATGTC	TCACCA	TACG		
AAGAGG	GCG T										
	GAGGGCGATCTCGCTTTTCT	ACCA									
	TACGTATGGTGATGATGTAC		CGAC	AT	GTGTC	CAT	TGTAG	AGTGGT	ATGC	TTCTTT	
CGC	C										
	TACTCTGTGCTAATCAGC		TA	C	T	CA	T	--	A	T	T

GAM2618	GTGTTGCATTCCTTTCTGGC 2604	TTGCATTCCT 5329	-	-----	T	G	AAA	AAT			
AAGA											
	ATTCATGGTCGAAAGCAATC	TTCTGGCATT	TGTTGCAT	TCC	TTTCTGGCAT	CATG	TCG	GC			
	CCATTCTT A										
	CATTCTTAAGAAAATCAAGG	CATG									
	AGTGGTTCGCGGACGGCGTG		ACGACGTA	AGG	AAAGACTGTG	GTGC	GGC	CG			
GGTGAGGA	A										
	CGTGTCAGAAATCTTCTTGG		G	TTCTTCT	C	-	AGG	CTT	ACTA		
	AGATGCAGCAT										

GAM2619	TTTGGCTCAACTTTCTTACA 2605	TGGCTCAACT 5330	TG	ACTT	TA	CTT	-	T
	AAACTTTTTGGCAATATTTG	TTCTTACAAA	TT	GCTCA	TCT	CAAAA	TTTG	CAA A
	ACCAAACCTTTTGCAGATGC	ACTT						
	TGGGCTGAA	AA	CGGGT	AGA	GTTTT	AAACC	GTT /	
		GT	CGT-	C-	CC-	A	T	

GAM2620	GGCAAGTCAGGAAGTGATAT 2606	TATTACAAAG 5331	CAA	AGGA	A---	A	GCTT-	A
T								
	TACAAAGTTTAAAGCTTTTA	TTTAAAGCTT	GG	GTC	AGTG	TATTACAA	GTTTAA	TTCC A
	CCTATTGGAGATTTGATTTG	TTAC						
	GATGTTGTAGTAATGATACT		CC	TAG	TCAT	ATGATGTT	TAGGTTT	AGGG T
	GGAAGATAAACC		AAA	AAGG	AGTA	G	AGTTT	A T

GAM2621	GTTGATTTGCATGAAGCCAT 2607	TTATAGCAAT 5332	---	CAT	----	-	AAAA	C	AATG-
ATGCC									
	CTTTGCAAAATACAAGGGCA	AGACCATTG	GATTTG	GAAGCCA	TCT	TTGC	TA	AAGGGC	
TTG	A								
	ATGTTGATGCCACACTTCCA	GTTT							
	GAAGAGGCCCTTATAGCAAT		TAAAC	CTTTGGT	AGA	AACG	AT	TTCCCG	
C								GAC	
	AGACCATTTGGTTTCCAAAT		AAT	---	TTACC	T	----	A	
	TTAAGGC							GAGAA	
								CTTCA	

GAM2622	TGGTTTCTGTGGAGCTGGAT 2608	TATAGTTACA 5333	G	T	GG-	-	A	TAA-	GT
---------	---------------------------	-----------------	---	---	-----	---	---	------	----

TAATATCTAAAGGTAAACTG	GCTAAGACTG	TG TTTC GT	AGCTG GATTA TATC	AG A
TATGGTATAGTTACAGCTAA	AAAG			
GA CTGAAAGCA		AC AAAG CA	TCGAC TTGAT ATGG	TC /
	G T GAA	A -	TATG AA	

GAM2623 ACATGCCAGAGGCAGCAAGG 2609	AGGCAGCAAG 5334	A -	AGGCCATGTG-- TG	AGT
CCATGTGATGAGGAGTGCTA	GCCATGTGAT	ACATGCCAG GG	CAGCA	A AGG G
CCCTTGTAATTTTAAGAGAT	GAGG			
GTTGTCCACTGGTATGT		TGTATGGTC CC	GTTGT	T TCC C
	A T	AGAGAATTTTAA GT	CAT	

GAM2624 CAGTAGTCAATGCAGTAAAC 2610	TCAATCTTGA 5335	A	A	ACTT--	- A
TTGGTTGACCCAGAAGGAGT	AATTACCGTA	CAGT GTCAATGC GTAA	GGTTGAC CC	G	
CAATCTTGAAATTACCGTAT	TTGA				
TGACACTG		GTCA CAGTTATG CATT	CTAACTG GG	A	
	- C	AAAGTT	A A		

GAM2625 TCAGTATATGGCAGAAGCAA 2611	TATGGCAGAA 5336	A	AGAAGCA	TGATTATGC	A
A A					
TTGATGATTATGCCAGTAAT	GCAATTGATG	TC GTATATGGC	ATTGA	CAGTA TTTATT	
TC T					
TTATTATCATTAGGAATAAA	ATTA				
TACTGAACCAAATTCAATGG		AG TATATGTCG	TAACT	GTCAT AAATAA GG	T
AGCAGGCTGTATATGGA		G	GACGAGG	TAAACCAA-	- - A

GAM2626 AGATGAGTTTCCTAAAGAGA 2612	TAAAGAGAAC 5337	G	AA	ACATTC	G TC
ACATTCTATGTGGATGAGTG	ATTCTATGTG	AGAT AGTTTCCT	AGAGA	TATGTGGATGA TGG	
C					
GTCCATCTGTCATCCGCGTA	GATG				
TTTCTGAGGAGACTGTTT		TTTG TCAGAGGA TCTTT	ATGCGCCTACT GTC	/	
	- G-	-----	- TA		

GAM2627 CAATGTAGTAGGATATGGAA 2613	TCCACAGGAG 5338	A	GG -	GAGT	A G- CTGT
T AAAACGA					
GACTGAGTTTGTGGAAGAGA	GTTATTAAAT	T GGATAT AA	GA CT	TTGTGGA GAGAA ATAT	
GGGG CT	A				
AGATATCTGTGGGGTCTAAA	GTCC				
ACGAAGTACCACAAGTCCCC		A CCTGTA TT TTGG	GACACCT TTTT	TATA CCCC	
GA	G				
TTTATATGATTTTTGTCCAC		C	AA A	AG--	G AG TTT- T ACACCAT
AGGAGGTTATTAAATGTCCC					
ACTAAGTTG					

GAM2628 CATTGAGAGAGCAGGGACCA 2614	ATGGTCCAAG 5339	TT G	AG	AC	ACC
TTTACTCGACCAACATGAAG	TTTTGTTCTT	CA GA	AGAGC	GGACCATTT	TCG A
ATGGTCCAAGTTTTGTTCTT	G				

GAM2629 TCACTGACACATCTAGCAA 2615 TGGCTTGATG 5340 - TG A--- TAG AA A A
ACAGTGATGAATACATATTG ATGACGAGTT TC AC AC CATC CAA CAGTG TG A
GCTTGATGATGACGAGTTGG GGTA ||| | |||| ||| |||||
TAGA AGTG TG GTAG GTT GTTAT ACT
A GT AGCA TA- CG - A

GAM2630 ATAAACAGGGGCCTGTAGGG 2616 TGACAAGTAT 5341 C AGGGAA - TG - TA T
TAC T
AACATCATGTTGGCATTGGG GTTCTAATGG C TGT CATCA TGT GC ATTGGGAT ATTTGTT
GCT CTATTACT T
ATTAATTTGTTTGCTTACCT TTGA | ||| ||||| || ||||| ||||| |||||
ATTACTTTGAAGTGGTAGCA G ACA GTAGT ATA TG TAATCTTG TGAACAG CGA
GATGGTGA G
GCTGACAAGTATGTTCTAAT T ----- C GT G TA T C-- A
GGTTGATACTGATGACATGT
CCTTGAGTGT

GAM2631 ATTATGGCATGTTGCCAGGA 2617 TATGGCATGT 5342 G- - GAA- CC TGGG A
AGGCCTCGTTCCGATGGGGA TGCCAGGAAG ATTATG CATGTTG CCAG GG TCGTTCCGA
GAAGGTT A
AGGTTAAAGAGCCTTTGATT GCCT ||||| ||||| ||| || ||||| |||||
TGGGGCGAACCATGGCTGGA TGATAC GTACGAC GGTC CC AGCGGGGTT
TTTCCGA A
CAGCATGGACATAGT AG A GGTA A- TAG- G

GAM2632 GACTTTTTGCCATATTGAGC 2618 TCACCTGTGTC 5343 A TG TTGAT GG AT G T
TT AGG
ATGTTGATAGGGGTTGGGAT AGCAGTAACT GCCAT T AGCATG AGG TTGGG AGT GCTGTT
TATA TGGCAA A
AGTGGCTGTTTTATATTTGG TACT ||||| ||||| || ||||| || ||||| |||||
CAAAGGAGAAGTTGTCACTT TGGTA G TCGTAT TCC AGCTC TCA TGACGA GTGT
ACTGTT G
GTGCAGCAGTAACTTACTCG - GT TTT-- AA AT A C TC GAA
AAACCTTTTTATGCTTGGAT
GGTTGATTG

GAM2633 GTCAATTGTCTCAATAACAG 2619 TACGTTGGTA 5344 AA CTCAA- A - G
TGTTCTTTTGC GGGAGCATG ACTGCAACAG GTC TTGT TAAC GTGTTCTTT TGC G
AAGAATACGTTGGTAACTGC AC ||| |||| |||| ||||| |||
AACAGAC CAG AACG GTTG CATAAGAAG ACG G
AC TCAATG - T A

GAM2634 TGGGTTGATTGTAACACTCA 2620 AGTTATGAAC 5345 --- CACTC A A AA GGAC--
- AG
TGATTATGAATTAAGCTTTT ATAAACCTTG TGGGTTGA TTGTAA ATG TTATGA TT GCTTTT
ATG C

GGACATCAGCATTGATCACA CAAA ||||| |||| | ||||| || ||||| |||
ACAAAAAGCCGAAGTTATGA ATCCAAC T AACGTT TAC AGTATT AA CGAAAA TAG
A
ACATAAACCTTGCAAAATTC TAA CCAAA A G GC ACAACAC TT
AACCTA
GAM2635 TTAAGGATGTGACTGAAAAT 2621 TCCAGTAGTG 5346 GAC AAT ATGA A A ATT A
A AAA
GTCATGATACATGAGAGTGG GGCTTCTTCA TAAGGATGT TGAA GTC TAC TG GAGTGG
TGAG CATTT AG G
ATTTGAGACATTTAAGAAAG AGAG ||||| ||| || ||| ||||| ||||| |||
TGGCTAAAATGCTCACCCT GTTCCTACG ACTT CGG ATG AC CTCACC ACTC
GTAAA TC /
CCAGTAGTGGGCTTCTTCAA AGA CTT GTG- - - --- - A GGT
GAGCATCCTTGG
GAM2636 TATAATTGATATAATAAAAG 2622 TAATTGATAT 5347 A T AAA- ---- A TATTC A C--
AAA
GATCTAAATATTCACACCCT AATAAAAGGA TATA TTGATA AAT AGG ATCT AA AC CC
TTC G
TCAAAGATAGAACATGGCGT TCTA ||| ||||| ||| ||| || ||| ||| |||
TATTTTAAAGATATCACCTG ATAT AGCTAT TTA TCC TAGA TT TG GG AAG /
TAGATTTTATCGAATATA A T GATG ACTA A TTTAT C TAC ATA
GAM2637 TATTCTAGTAGAGGAACTAA 2623 AGAGGAACTA 5348 A C ATGTT TCT
TGTTTTTATATCTTTACTTA ATGTTTTTAT TATTCT GTAGAGGAA TA TTTATA T
TAAGTAATTTCTTTACAGGA ATCT ||||| ||||| || |||||
ATG GTAAGG CATTTCTTT AT GAATAT T
A A ----- TCA
GAM2638 CGGGAAAGCCGACGGTGACG 2624 TGGCAAAGAC 5349 AAAGC - - CCT---- G- T
CCCTGGTCGTGCTAGCTAGT TTTGACTTGC CGGG CGAC GGT GACGC GGTC TGCTAGC
A
GCTGGCAAAGACTTTGACTT GTCT ||| ||||| ||||| ||| |||||
GCGTCTGCCGGTCGACGCCC GCCC GCTG CCG CTGCG TCAG ACGGTCG G
G GCA-- G T TTCAGTT AA T
GAM2639 GCCCCACCAATGTTACGT 2625 TGGCATGCAG 5350 - C-- A - C TG C T
CGCGGGTGAGCTCCCCTCTA CGATGGTTAC GCC CC ACCA TGTT CA GTCGCGGG AG
TCCCCTC A
AAGAGGGGATTTTCCCCGTG GGTG ||| ||| ||||| || ||||| || |||||
GCATGCAGCGATGGTTACGG CGG GG TGGT GCGA GT CGGTGCCC TT AGGGGAG A
TGGC T CAT A C A CT T A
GAM2640 GGCCGCTGTGGCAGCACGGT 2626 TGTGGCAGCA 5351 C - - C--- - C
CCAAGGACCCAGTCCTTGTG CGGTCCAAGG GGCCG TGT GGC AGCA GGTC CAAGGAC C

GAM2646 GGGTGAGGGTGTGGCAAGAA 2632 TGAGGGTGTG 5357 --- GTGG-- AA ACT AAA
AACCCTGACAAAAGCATGT GCAAGAAAAC GGGTGAG GGT CAAGA ACC GACA G
GTTTCGTTCTTGAGAAAAA CACT ||||| || ||||| || ||||

CTTTGTTTACCC

CCCATT TCA GTTCT TGG TTGT C
GTT AAAAGA -- CT- GTA

GAM2647 TCAGGAGAGGTTAGTTTTCT 2633 GAGGTTAGTT 5358 AG T ----- G G
TTGCTAATGGTGATGATATC TTCTTTGCTA TCAGGAG GTTAGT TTCTTT GCTAATG TGAT
A
ATATTAGCCGCACAAGAAAA ATGG ||||| ||||| ||||| ||||| |||||
GGACATTGGCATTCTTGA AGTTCTT CGGTTA AGGAAA CGATTAT ACTA /
A- C AGAACACGC - T

GAM2648 TCTTAGAATGTTCTTTATGG 2634 TTCACACCCA 5359 AAT-- TTA AAGATT -
AGAGA-- TTGAAA
AAGATTGGTGGGTTGGACAA TCCTTACACC TCTTAG GTTCT TGG GGTGGGT TGGACA
TGC A
GAGATGCTTGAAAATCTATA AGAT ||||| ||||| ||||| ||||| |||||
TGCAGAGATAGTGTTACACAC AGAATT CAAGG ACC CTACCCA ACTTGT ACG
T
CCATCCTTACACCAGATGGA GTTGT TAG ACATTC C GATAGAG TATATC
ACTGTTGTTAAGA

GAM2649 TTGTTGGAAAAATTTTCAGT 2635 TGTTACGGAA 5360 TG AAA A GGCAA A
AACATGGCAATTGAAGAGAT AATACTTTGA TTGT GA ATTTTC GTAACAT TTGAAG G
TTTCAGATGTTACGGAAAAAT CAA ||||| ||||| ||||| ||||| |||||
ACTTTGACAA AACA TT TAAAAG CATTGTA GACTTT A
GT CA- G ---- T

GAM2650 GAACAAGGAAATGGAGCTCG 2636 TTAAAGTGAA 5361 - AATGGA T - TCTTCC - A-
CCC
AACTCTTCCCACTTAAGAAG CTGTTACGCG GAA CAAGGA GC CG AAC CACTT AAGA
GGC A
GCCCCACAAGCCGATCTTAA CGAA ||||| ||||| ||||| ||||| |||||
AGTGAACGTGTACGCGCGAA CTT GTTCCT CG GC TTG GTGAA TTCT CCG /
ACGTCCTTGCTTC C GCAAAG C A TCAA-- A AG AAC

GAM2651 GATACCCTACCCTATGAATT 2637 TACCCTACCC 5362 - - TGAATTA A CAA T GGA
AAACAAGAGCAAACAGAGCT TATGAATTAA GATAC CCT ACCCTA AACA GAG ACAGAGC
TT C
TTGGACCTAATGCCGAGTTC ACAA ||||| ||||| ||||| ||||| |||||
TTGCGCTTGCATAGGCGTGC GGGCG GCG ATACGT TCGC TTC TTGAGCC GT C
GGG T G ----- G --- - AAT

GAM2652 AACCAATTGTGCATCATTGA 2638 GTGCATCATT 5363 A -- - AGAA - G
GAATCACTCGAACGATGTGA GAGAATCACT AACC ATTGT GCAT CATTG TCAC TC A
GACAATGTATGTATGCGATA CGAA ||||| ||||| ||||| ||||| |||||
GGTT TTGG TAGCG TGTA GTAAC AGTG AG A

A TA T AG-- T C

GAM2653 CTTCAATTTAGCACGTTATG 2639 TACAACAGCC 5364 AA TTAT T ATTTC A C
CTTTTGATTTCTACGAGATC CGTGCTAAGG CTTC TTTAGCACG GCT TTG TACG GAT A
ACATCACGTACAACAGCCCG AGG |||| |||||| |||| ||||
TGCTAAGGAGG GGAG GAATCGTGC CGA AAC ATGC CTA /
-- C--- C ---- A C

GAM2654 GCAGAGTTAATCGTACAGCA 2640 AGAGTTAATC 5365 A T ACA AAAT --- - A--
CTCA
AATGTCCATACTGGAGAAGG GTACAGCAAA GCAG GTTAA CGT GC GTCC ATACTG GAG
AGGC A
CCTCAACACAGCTTAGATTG TGTC |||| |||| || || |||| || ||||
GCAGTATCAGGGATTAGCCA CGTC CAGTT GTA CG TAGG TATGAC CTT TTCG /
TGTTGACCCTGC C - C-- AT-- GAC G AGA ACAC

GAM2655 GCAGCCGTACAAAAAGAATA 2641 TGAGCGGACT 5366 G AAAA AATA AA G C AAA
TGAAC TTGATGACACACAAA AATGGTATGG GCA CCGTAC AG TG CTT ATGACA AC T
TGACAGTTGTTATGAGCGGA TGC |||| || || || |||| ||
CTAATGGTATGGTGC CGT GGTATG TC GC GAG TATTGT TG G
- GTAA AG-- -- - - ACA

GAM2656 CAAGTGTCAAACTTCTTAGG 2642 AATCACAAAG 5367 G AC-- AG- AA ACTG
ATTAGAAGGACACTGGAAGA GACTTGTTGA CAA TGTCAA TTCTT GATTAG GGAC G
AGTCCCTAATCACAAAGGAC TAGT |||| || || || |||| ||
TTGTTGATAGTTG GTT ATAGTT AGGAA CTAATC CCTG A
G GTTC ACA -- AAGA

GAM2657 CACTGGAGGAGCAAGACAGC 2643 GAGGAGCAAG 5368 - AA CAG- T ATACG GTTAA---
GA C TA
GTCTGTGCATACGGCGTTAA ACAGCGTCTG TGA GGAGC GA CGTCTG GC GC TGGT
TGAT TGC A
TGGTGATGATCTGCTAATTG TGCA |||| || || || || || || || || || || || ||
CAATTAGGCCAGATATGGAG ATTT TCTCG CT GTAGAT CG CG ACCG ATTA
ACG /
CATAAGCTAGATGGATTTC A AA TTAG - AATA- AGGTATAG G- - TT
AGCTCTATTTAGTG

GAM2658 GACTTGTCAAATGCTAGAGC 2644 TCAAATGCTA 5369 - GA-- CCCAC- C
CACCCACGAACAATTCCAAA GAGCCACCCA GACTTGTC AATGCTA GCCA GAA A
ACTGGTATGATGGCGTTATG CGAA |||| || || || || || || || || || || || ||
GCAAGTT TTGAACGGT TTGCGGT TGGT CTT /
A AGTA CAAAC A

GAM2659 GAGAGTATTGTGCAGAAGTG 2645 AGAAGTGGTT 5370 AT--- A- GGT CAA- A
 GTTCTGTTTCAAGCAAAGGC CTGTTTCAAG GAGAGT TGTGC GAAGT TCTGTTT GC A
 GTCTGAGCAGGTTAATTTTG CAAA ||||| |||| |||| || ||
 AGCGCATCATAGCTTTC CTTTCG ACGCG TTTTA GGACGAG CG A
 ATACT AG ATT TCTG G

GAM2660 GAGATTCGAGTTGAGGACCA 2646 AAGCTCAAGG 5371 GTTGAGGA AAG CAG T
 AGTGAGTTTTCAAGGACTTCG GAATGGATCG GAGATTCGA CC TGAGTTTT GAC T
 TCAAAGCTCAAGGGAATGGA AATC ||||| || ||||| ||
 TCGAATCTC CTCTAAGCT GG ACTCGAAA CTG /
 AGGTAA-- GA- --- C

GAM2661 GCGAACTTCTAGAAAAAACT 2647 TGGCAAGAGT 5372 -- -- AAAA - GA - TTGG
 TACTTGAGCCTGTTGGAGGA TAAGCTATTT GC GAA CTTCTAGAA CTTA CTT GCC TG A
 TTCATGGCAAGAGTTAAGCT TGGA || || ||||| |||| || || ||
 ATTTTGAAGATTTCAAGC CG CTT GAAGGTTTT GAAT GAG CGG AC G
 AA TA ATC- T AA T TTAG

GAM2662 TGCTGCTGGAGAGGCACTTC 2648 TGAGATCATC 5373 GC- GAGA -- TACTAAAGTG
 GATCTATGA G
 TTGGTTACTAAAGTGGATGG ACCAAGGGCA CT TG GGC ACT TCTTGGT GATGGTC
 AGCTT G
 TCGATCTATGAAGCTTGGAC GTGC || || ||||| ||||| ||||| ||||
 AAGTTGAGATCATCACCAAG GA AC TCGTGA GGAACCA CTACTAG TTGAA
 A
 GGCAGTGCTAACAAAAAGCA AAA AA-- CG ----- AG----- C

GAM2663 TGGTAAAGTTCATCAATACA 2649 TAAAGTTCAT 5374 - CATCAA - TA- A
 ATGTTAGCTATAACAGTGGC CAATACAATG TGGTAAA GTT TACAAT GT GCTAT A
 ACTACAATTGTACATAGCAT TTAG ||||| || ||||| || ||||
 TTGCCA ACCGTTT CGA ATGTTA CA CGGTG C
 A TAC--- A TCA A

GAM2664 GTAAATCTGTTATCTCAAGT 2650 TCAAGTGAAT 5375 C A - T- TT AAA AGTT -
 T
 GAATTTACTGAATTTGCAAA TTA CTGAATT AT TGTT TCTCAA GTGAAT TACTGAAT GC GA
 GAAAG GTCGAAA A
 GAAGTTGAAAGGTCGAAATA TGCA || ||||| ||||| ||||| || || ||||| |||||
 ATTCGACATTTTCTATCGG TA ACAA AGAGTT CACTTA ATGATTTG CG CT CTTT
 CAGCTTT /
 AGCTGGTTTAGTATTATTCA A - T TT GT AGG AT-- A A
 CTTTGAGAAACAAATATTAC

GAM2665 TCATGGCGTTCCTTATTACG 2651 TGA CT TATGC 5376 C - TA T A - CA
 TATTAAGTACAAAAGCCAC GGTAGGGCAA TCATGG GTT CTTAT CGTAT AAGT CA AAAGCC
 C

AAGGCTTTCTGACTTATGCG CCCA ||||| ||| ||||| ||||| ||||| || |||||
 GTAGGGCAACCCATGG GGTACC CAA GGGATG GCGTA TTCA GT TTTCGG /
 - C -- - - C AA

GAM2666 TTCGGTTCATAGAGTATTGC 2652 TTCAAAGACT 5377 - - CTA- T C - A A TT
 T
 CTACTAAGGTAGTTCCTGAT ATAGATCAGA TAGA GTATTGC CTAAGG AGTT CTGATT ATAGT
 CT TTG GATCCCT T
 TATAGTACTATTGTTGATCC AGCT |||| ||||| ||||| ||| ||||| ||||| || ||| |||||
 CTTTACAGGGGTTTCAAAGA ATCT CATAACG GATTCT TCGA GACTAG TATCA GA AAC
 TTGGGGA A
 CTATAGATCAGAAGCTTCTT T A AAAG - A A - - T- C
 AGGAAAGCAATACATCTATT
 GAATATCAAA

GAM2667 GAGATGAGGAATTCTGAAGG 2653 TGAGGAATTC 5378 AT ----- T TA C
 GTTCTACATGCCTAGGTATG TGAAGGGTTC GAG GAG GAATTCTGAAGGG TC CATGC T
 GACTTCTTCGGAATTTGAGG TACA ||| ||| ||||| ||||| || |||||
 GATAAAAGCTTGGCTC CTC TTC TTTAAGGCTTCTT AG GTATG A
 GG GAAAATAGGGAG C -- G

GAM2668 GGGTTTAAAAGGAAAATGGG 2654 TGTTATGGGA 5379 AAAGGAAA - GA TTA G
 TG T- AC
 ATGGAAAGAAGTTCTTTAAT TTATTTCCGT ATGG GATGGAAA AGTTCT ATGATGTC
 TGGT CCATC TC A
 GATGTCGTGGTTGCCATCTT CACT |||| ||||| ||||| ||||| ||||| || |||||
 CACATTGATTGGTGGTGGCT TATC CTGCCTTT TTAGGG TATTGTAG GTCG
 GGTGG AG /
 GGATGTTATGGGATTATTTT ACGTA--- A A- --- - GT TT TT
 CGTCACTATATGCAAGAACC
 T

GAM2669 GGTGAATCGATTAAGAGAGA 2655 AGAGAGAAGA 5380 A - GA- ACGCTTG AT A
 G A TT
 AGATCTGACGCTTGCTTGCG TCTGACGCTT TCGATT AGAG AGAA TCTG CTTGCGT CA
 AGCAG ATGGG AT T
 TATCAAAGCAGGATGGGAAT GCTT ||||| ||||| ||||| ||||| ||||| || ||||| ||||| ||
 TTTGTATACCCGTGCTGTTG AGTTGA TCTT TCTT AGAC GGACGCA GT TTGTC
 TGCCC TA /
 TGTCACGCAGGATGATGGCA G A GCC GG TAGTA CT G G A TG
 GACCGTTCTATTCTGAGTTG
 AAGAGCC

GAM2670 GTCCGCCTTGCCAAGGACTA 2656 TCACAGGGCA 5381 GACTATT TTT---- CCA AATA ---
 CA AA AA
 TTGCCATTTTGGACCACTTA TTCATTTTCA GCCA TGG A CTT AGTGAGGA AAT TG
 GAAA T
 ATAAGTGAGGAAATCATGAA TTGG |||| |||| ||| ||||| ||| || |||||
 GAAAAATCATTTTGACACAA CGGT ACTT GGA TCACTCCT TTA AC TTTT /
 TTAGCTCCTCACTCACAGGG ----- TACTTTT ACG CAC- CGA AC AG AC
 CATTCATTTTCATTGGCTGG

CATCGCAGAT

GAM2671 AATGCCTTGTGTACTTAAGT 2657 TGATACTCTT 5382 C- TGT ATT CA C T
TAGAGTCAATCACAGATCCT CCTAAGTCCG AATG CTTG ACTTA G AGAGT ATCA AGATCCTT
T

TTTAAAGGGATTTCTGATAC AGAT |||| ||| ||||| ||||| ||||| |||||
TCTTCCTAAGTCCGAGATCA TTAC GAGC TGAAT C TCTCA TAGT TTTAGGGA A
TT TA C-- -CT -- C A

GAM2672 CTGAATAGTTGAGTCTTTAG 2658 TGAGTCTTTA 5383 AA T T TA AA GG- T A
TAAATTAAAGGACCTTCCAA GTAAATTAAA CTG TAGT GAG CTT GT ATTAAA ACC TCC A
TGGATGGTACATTTAATCAA GGAC ||| ||||| ||||| || ||||| |||||
CAAGCTCCACTAAACAG GAC ATCA CTC GAA CA TAATTT TGG AGG /
AA C - -- AC ACA T T

GAM2673 CTTACGAATAATGATTTATC 2659 TTCCTCATTG 5384 ACGAA - C TT TAT A
TAATGTTGGATATATACTA AATAAGATTA CTT TAATGATTT AT TAATG GGA ATA ACT A
AACAGTTATTTCTCATTGA TTAG ||| ||||| || ||||| ||| |||||
ATAAGATTATTAGTATGAAG GAA ATTATTAGA TA GTTAC CCT TATTGA A
GTATG A A T- T-- C

GAM2674 CTTCTTCACCGTTATACTCT 2660 TGTGCAAGAT 5385 T TTATAC T - C- G
TTCATAAGAGGGCAGTTTGG AAACCGGTGA CTTCT CACCG TCTT CATAAGAG GG AGTTTG
A
AAACAAACTTTCCGCTCTTG GAAG ||||| ||||| ||||| ||||| || |||||
TGCAAGATAAACCGGTGAGA GAAGA GTGGC AGAA GTGTTCTC CC TCAAAC A
AG - CAAAT- C G TT A

GAM2675 GACTCCCTACTATAATACCG 2661 AGGATTCTAG 5386 AC A CG A A A T
GGAACCTTAAGAACTCTTTT TACTATAAGG GACTCCCT TATA TAC GGA CCTTA GA CTC T
GAGATCTAAGGATTCTAGTA GGAG ||||| ||||| ||||| ||||| |||||
CTATAAGGGGAGTC CTGAGGGG ATAT ATG CTT GGAAT CT GAG T
A- C AT A - A T

GAM2676 GTAAGTCCGTTATTCCCTAC 2662 TGAATAGAGG 5387 TC TT - C T T
TCTTCTTTCTTTTATAGGAA TAACGTTCTT GTAAG CGTTA CC CTA TC TCTTTCTT T
GGATGAATAGAGGTAACGTT AT ||||| ||||| ||||| ||||| |||||
CTTAT TATTC GCAAT GG GAT AG AGGAAGGA A
TT -- A A T T

GAM2677 TCATCATGTAATTGTACAAA 2663 CTCCCATTCA 5388 T T C A C C A G
TAGCTGCAATGAGAGTTGGT CTAATTATGC TCATCA GTAAT GTA AA TAG TG AATG GAGTT G
AAACTCCCATTCACTAATTA GTTA ||||| ||||| ||||| ||||| |||||
TGCGTTACTTGGTGA AGTGGT CATTG CGT TT ATC AC TTAC CTCAA T
T - A A - - C A

GAM2678 AAGGAATCTTAACTAATATT 2664 TGAATATATT 5389 - AACT - C TG
 AGACATATTCATGTTGTATA TACATATTTA AAGGAAT CTT AATAT TAGA ATATTCATGT T
 TATGAATATATTTACATATT CAAA ||||| || |||| |||| |||||
 TACAAAGAATTCCTT TTCCTTA GAA TTATA ATTT TATAAGTATA /
 A ACAT C A TA

GAM2679 ACTGATAATGATCATTATCT 2665 ATAATGATCA 5390 - TC TAT AG AA G C A
 AAGCATAAAAGGTTCTCCAA TTATCTAAGC ACTGATAAT GA AT CTA CAT AAG TT TCC A
 ATGGAAGGCTTCAATGTCT ATAA ||||| || || || || || || ||
 AGTCTATATTCAATTATCAG TGACTATTA CT TA GAT GTA TTC AA AGG A
 T A TA TCT CT AC G A T

GAM2680 AGAAAAAGTAATGGTTTATT 2666 TATAACAAGA 5391 AAA C- AAG- A G
 ATACACTATCAAGTATATGA TATATGTGTG AGAA GTAATGGTTTATTATACA TATC
 TATATGAA GCT C
 AAGCTGCAAAGCTTCATATA GTAA ||| ||||| |||| ||||| ||||
 ACAAGATATATGTGTGGTAA TCTT TATTACCAAATGGTGTGT ATAG ATATACTT CGA
 A
 ACCATTATATTCT A-- AT AACA - A

GAM2681 AGTCTAATATGATGTCTAGA 2667 TGTCATATTC 5392 AAT AT- C T G A C T
 ATTTGAGATATGGCCTTGTC TACACTAACA AGTCT ATG GT TAGAAT TGA AT TGG CTTGTCT
 A
 TTATAGGACGAGTCCAATGT TTCG |||| || || |||| || || || |||||
 CATATTCTACACTAACATTC TCAGA TAC CA ATCTTA ACT TA ACC GAGCAGG T
 GAGACT GCT AAT C T G - T A

GAM2682 GATAGATTTCCAATATTCTT 2668 TAGATTTCCA 5393 -- ATTC AACAA - T
 ACAACAAAACTTATATCAT ATATTCTTAC GATAGATT TCCAAT TTAC AAACCTTATA
 TCATTAA A
 TAATATTTAATGATTATGAG AACAA ||||| |||| || ||||| |||||
 TTTGGTAAAAATTGGAGAAA TTATCTAA AGGTTA AATG TTTGAGTAT AGTAATT /
 TCTATT AG AA-- G---- T T

GAM2683 GTTTTATATGATGCCTAGTA 2669 TATGATGCCT 5394 AT A C- TT AGATA C CTT
 TTTGAGATATGGCCTCGTCT AGTATTTGAG GTTTT ATG TGC TAGTA TG TGG CTCGT C
 TCAACAACGGGACCAAAGCC ATAT |||| |||| |||| || |||||
 ATTTACTACTGCAACATTCA CAAAA TAC ACG ATCAT AC ACC GGGCA A
 AAAC CT A TC TT CGAA- A ACA

GAM2684 ATAATCCAGAATTACAATGA 2670 TGAAGTAGAG 5395 GAA A - - GA TT T
 AGTAGAGATGATCATTATTT ATGATCATTATA ATAATCCA TTAC ATG AA GTAGA TGATCATTATA
 TGAGTTT A

GAGTTTTAAAAGCTCGCCTA	TTTG	
ATGGTCAATCTACATTACAT		TATTAGGT GATG TAC TT CATCT ACTGGTAAT GCTCGAA
/		
AGTAGCTATGGATTAT		ATC A A A A- CC A

GAM2685 GTTAAGAGGTATTTTAAATA 2671	AGAGGTATTT 5396	A--- - AT- C -- A T
ATCTAAATAACTATGGAATT	TAAATAATCT	GTTAAG GGTATTT TAA AAT TAAATAA CT
TGGAAT G		
GTATTCCAAGAATTATTTAA	AAAT	
ATTCATTATAAATACCCAC		CAATTT CCATAAA ATT TTA ATTTATT GA ACCTTA /
ATTTAAC	ACAC	T ACT A AA - T

GAM2686 TGAGAAAGATAAATGGTCTT 2672	TATTACTAAA 5397	AA A AA CA TA---- - A G
AAATTCACAATTAAGTATAT	TATATTGCAA	TGAGA GATAA TGGTCTT ATT CAAT AGTA
TATGAA GCT T		
GAAAGCTGTTAAGCTTCATA	ATGA	
TTACTAAATATATTGCAAAT		ACTTT CTATT ATTAGAA TAA GTTA TCAT ATACTT CGA
T		
GAAAGATTATTATCGATTTC		AG - AG AC TATAAA T - A
A		

GAM2687 CATAGAAGTTCAAGTAAACC 2673	TTCAAGTAAA 5398	TTC-- AAA CT AT C - T - -
AAGA		
CCTCATGGATTAGCCTCTTA	CCCCTCATGG	AGAAG AAGT CCC CATGG TAG CTC TTAGG
GGC TC TCTC T		
GGTGGCTCTCTCAAGATAAA	ATTA	
CGGAGATGACGCCTCTAATG		TCTTC TTCG GGG GTGTC GTC GAG AATCT CCG AG
AGAG A		
AGTCTGCTGTGTTGGAAGC		TTATT AA- TT -- T T - C T GCAA
TTTTATTCTTCTGTG		

GAM2688 CTGGGAGTTGTGGGCTGATG 2674	TGATGTAGAG 5399	T- ---- T G - G
TA		
TAGAGATGAGAATTGTTCTG	ATGAGAATTG	AGTTG GGGCTGA TG AGA ATGAGAAT
TGTTCTGGG GGCTTTGGCCA A		
GGGGGCTTTGGCCATAAACT	TTCT	
GGCTAAAGCCGCCAGAATA		TCGAC TCTGACT AC TTT TGCTTTTG ATAAGACCC
CCGAAATCGGT /		
GGTTTTCGTGTTTCATGAAC		CT CAAGT - G G G CA
TCAGTCTTCCAGCTCTCGG		

GAM2689 TCTGCTCTGGTTGAGCGCGT 2675	TGAGAACTCG 5400	G TT C A-- G G CTT
CATTGCGACATACCTTTAT	GCTGCTCCCA	TCT CTCTGG GAGCG GTC TTC C ACATAC T
AAGTATGTGAGAACTCGGCT	GAGG	
GCTCCCAGAGGAGA		AGA GAGACC CTCGT CGG AAG G TGTATG A
G	-- - CTC A- AAT	

GAM2690 ATTTTATATTGTATTGAAT 2676 TATTGTATTG 5401 T AT----- GTGG T
 AGCGTGTGGGTATATTGTTA AATAGCGTGT ATTTTATATTGTAT GA AGCGT GTATA T
 TACGGCGCTTAACATGAAAT GGGT ||||| ||| |||
 CCATACAATATGAAGAT TAGAAGTATAACATA CT TCGCG CATAT G
 C AAAGTACAAT G--- T

GAM2691 GAATTTGAATTTGTAAATAC 2677 TCGGATGGAT 5402 ----- G AATG C GCAA A
 AG TAC
 ATTGGGTGAGAGAATGAGTC GTTATATTTG GTAAATA CATT GGTGAGAG AGT GTTC
 ATAT TGG AT A
 GTTCGCAAATATATGGAGAT CGTT ||||| ||| ||||| ||| ||| ||| |||
 TACATTGTATGGCCAGATAT CGTTTAT GTAG CTATTTTC TCA CGAG TATA ACC
 TA T
 GAGCACTACTTTTATCGGAT ATTGTAG G A--- - ---- G GG TGT
 GGATGTTATATTTGCGTTTA
 AATTT

GAM2692 GAGTATGATCGATTAAACAA 2678 TCGATTAAAC 5403 T - AA AAT - AAATAA- C -----
 GA
 ATTGGTACAAAATAATCCGT AAATTGGTAC TA GATC GATTA CA TG GTACA TC
 GTCTGTGT GGCAA T
 CTGTGTGGCAAGATTTATTG AAAA || ||||| || ||||| || ||||| |||||
 TTGGTGTGCACAGATCGAGA AT TTAG CTGGT GT AC CATGT AG TAGACACG
 TTGTT T
 CAATATGTACACATGGATGG T A AG --- A ATAACAG C TGTGG AT
 TCAGATTTTATTT

GAM2693 GCGATTTGTTGTTAATTGTT 2679 TTTACAGTTG 5404 A TT TTT AAAGA
 TTGCGCAAAGAACAGACGTG ATTCAAAATG GCG TTTG GTTAATTGT GCGC A
 TTTACAGTTGATTCAAAATG T || ||||| ||||| |||||
 T TGT AAAC TAGTTGACA TGTG /
 A T- TT- CAGAC

GAM2694 GCGTGAGGGAGTTTTTGGCA 2680 TTTGGCAAAC 5405 A A- T- TG T-- TTA
 CGACGA
 AACGTTTTGCGTTACAATTG GTTTTGCGTT GCGTG GGG GTT T GCAAACGTTT GCG
 CAATTG T
 CGACGATGAGGGACAATTGC ACAA ||||| ||| | ||||| ||| |||||
 GCTACAAACGTTTGCTGATC TGCAC CCC CAG A CGTTTGCAA CGC GTTAAC /
 GACGACCCACGT - AG CT GT CAT --- AGGGAG

GAM2695 GCTCTATAGCTTACCATTAT 2681 TAGCTTACCA 5406 T- AC GC ACA T
 GCTATACATGCTGAGCAAGA TTATGCTATA GC CTATAGCTT CATTAT TAT TGC G
 TAATAATGCCAAGCTATGGT CATG || ||||| ||||| ||| |||
 TGC CG GGTATCGAA GTAATA ATA ACG /
 TT CC -- GA- A

GATTGGAATCTGGGAATTTA ATTG ||||| |||| || ||||| || |||| || | |||
 TACTTCTTGATAAAGTTGTT CCATATAA ACGAG GT AATAGTT CT TCAT TT G CTA
 G
 GAGCAAATATACC --- TT TGA - - A TAAG GT A

GAM2702 TTCTAGATGCAGAGATGGAC 2688 AGAGATGGAC 5413 A CA - AGTGATA G- GAG
 CCTAGTGATATTATGGGTGA CCTAGTGATA TTCTAG TG GAGATGGACC CT TTATG GT A
 GACAAGCGACATGAGAGGGA TTAT ||||| || ||||| || ||||| ||
 GGTCTATTTTGACACCTAGA AAGATC AC TTTTATCTGG GG AGTAC CG /
 A C AG A GAG--- AG AAC

GAM2703 CTGAGCTATAGTAAAAACGA 2689 TATAGTAAAA 5414 A - AAAACGAAA G T A
 GAGCCAT
 AACACCCGTTGTCAAATACA ACGAAACACC CTG GCTATA GTA CACCC TTG CAAATACA
 CAA A
 ACAAGAGCCATAACAACAAT CGTT || ||||| || ||||| || ||||| ||
 TGTGTGTTTGTGCGAGGGTGG GGC CGGTAT CAT GTGGG AGC GTTTGTGT GTT /
 CAATATGCTACATATGGCCG - A CGTATAACG - T - AACAAACA
 G

GAM2704 TTTTTCGTATACCGTACATG 2690 TTAAAGGCAA 5415 ATA CA-- T C C CG- CAA
 TTCTTCAATAAACTCCGGA CTATACGGGA TTTTTCGT CCGTA TGT CTT AATAA ACTC GA
 C
 CAACATTTTCAAAGAGTTTA CACG ||||| |||| || || ||||| || || ||
 TTAAAGGCAACTATACGGGA AAAAAGCA GGCAT ACG GAA TTATT TGAG CT A
 CACGAAAAA CAG ATCA - A - AAA TTT

GAM2705 GATTCGTAATGTTCAAGGCT 2691 ACAAGTGCAT 5416 AA CT GC A - - - CCGAC C
 - AT
 GTGCTGTACAAGTGCATTCA TCAACTGGAC GTTC GG GT TGT CAAG TGCATTCAA CT GGA
 AGA TGC ATCG T
 ACTGGACCGACAGACTGCAT CGAC |||| || || ||||| ||||| || ||||| ||||
 CGATTGACGATCGCATTCTC CGAG CC CG GCA GTTC ACGTGAGTT GA CCT TCT
 ACG TAGC /
 TCCAAGTTTGAGTGCATCTT AG AC TA G T T A C--- T C AG
 GGACGATGCCACCGAGAGCT
 ACGATTC

GAM2706 ATGCCGCGTACCACTGTCTA 2692 TCTAAACTCT 5417 C A CT - --- AAAAG
 GCCTTTC
 AACTCTAGTCAAAAGGTGGC AGTCAAAAGG ATGCCG GT CCA GTCTAAA CT CTAGTC
 GTG A
 CTTTCAGATTATACACAAAC TGGC ||||| || ||||| || ||||| ||
 AGATTAGCGATAGCTTTAGA TACGGC CA GGT TAGATTT GA GATTAG CAC /
 TTGGACACGGCAT A - - C TAGC ACAA ATATTAG

GAM2707 GTACTGTAGACGTAAAGCGG 2693 AGCGGTAGCG 5418 GTA C AAA A CTT- A- - T
 CTCA TA

GAGGCTCCTTTGAAGCGGTA TTGCCTCAAA ACT GA GT GCGGG GGCTC TGA GCG
 GTAGCG TGC AAAC C
 GCGTTGCCTCAAACTACAA ACTA ||| ||| |||| |||| ||| ||||| ||| |||
 GTTTGCACCGCTACTCGTAC TGA CT CA TGCTC TCGGG ACT TGC CATCGC ACG
 TTTG /
 TCATACAGGGCTACTCGTAC A-- A --- A ACAT CA T C ---- AA
 ATCAAGTAC

GAM2708 CGAGTCCAATACTATTGTTG 2694 TGGTGTAGAG 5419 A GAA TG---- GA
 TGATTTTAACA AAT
 AAAATGTTGGTGTAGAGGGT GGTGATTTTA TCCAAT CTATTGTT AATGTTGG TA GGG
 AGGAG C
 GATTTTAACAAGGAGAATCT ACAA ||||| ||||| ||||| || ||| |||||
 TGCTCCTTCCGGTAAAGAGT GGGTTA GATGGCAA TTACAACC AT CCT
 TCCTC /
 CCAACATTGAAACGGTAGCA C AG- TGAGAA GG ----- GTT
 TTGGGCTCG

GAM2709 GAGCACGGTACCATCAAGAC 2695 TATTACATCG 5420 GTA - CGA AA A CAT
 CG TGTG
 TCCATCCGATGGTAAACTGA GTGGACCAAG G CCATCAAGAC TCCATC TGGT ACTGA
 TGTAAT TTGT CAA T
 ATGTAATCATTTGTGCGCAAT TGAT | ||||| ||||| ||| |||| ||||| ||| |||
 GTGTTGGATTTGAACAATAT C GGTAGTTCTG AGGTAG ACCA TGGCT ACATTA AACA
 GTT T
 TACATCGGTGGACCAAGTGA A-- T TGA GG - T-- A- TAGG
 TGGATGTCTTGATGGACGAG
 TTT

GAM2710 GTTGTTCCTTGTTACGATAAT 2696 TAATGTAGAG 5421 - TTG-- A - G CCC- - AC
 GTAGAGTCCCCGGAGCTTAC TCCCCGGAGC GTTG TTC TTACG TA ATGTAGA TC GGAG
 CTT A
 AGTAGAGACTCCATCCGAGT TTAC ||||| ||||| ||||| || ||||| ||| |||
 CTACATCTAATGTAAATGCT CAGC GAG AATGT AT TACATCT AG CCTC GAG G
 GAGTCGAC T TCGTA A C G CCTA A AT

GAM2711 GATCGTCTGACAAAATCCGC 2697 TCCGATGAAT 5422 AA--- C - ----- C AA
 AA
 GTGCGCAGCCTTCATCGGCG TGATGGCAGC CA ATCCG GTG CGCA GCC TTCATCGG
 GACGAC CAT T
 ACGACAACATAATACATGGA CAGA || ||||| ||||| ||| ||||| ||||| |||
 GTCGTCTCCGATGAATTGAT GT TAGGT CAC GCGT CGG AAGTAGCC CTGCTG
 GTA /
 GGCAGCCAGATGCGCCACTT ACAAG T C AGACCGA TAGTT T AG CA
 GGATGAACATGGAAGTGAAG
 ATC

GAM2712 TCTGGCAAGTCAGCTATTAT 2698 TGACTAGCGG 5423 - A CAG ATTA AAGAAC CA
 CAAGAACCTAGTTACCAGGC AAAGAAAGAA TCT GGCA GT CT TC CTAGTTACCAGG A
 AAGACCTGGTGAAGTAGCGGA AACT ||||| || || || ||||| |||||
 AAGAAAGAAAACCTGCCAAGA AGA CCGT CA GA AG GATCAGTGGTCC /

A - AAA A--- AAAGGC AG

GAM2713 CCTCACGATGAGCGACTCGG 2699 TGAGCGACTC 5424 CG ----- C AAGTT TC CT
CA
GAAGTTGTATCAATCTTTCC GGAAGTTGT CCTCA A TGAGCGACT GGG GTA
AATCTTTC GC C
TGCCACTTGCGAAGGATTTA ATCA |||| | ||||| || || ||||| ||
CTGGCCCCAGTTGCTCGGCA GGAGT T GCTCGTTGA CCC CAT TTAGGAAG CG /
TTTTTATGAGG ATTTTACG C GGT-- -- -- TT

GAM2714 GATAGGTGCAGTGCTTCCAA 2700 TGAGATGGAA 5425 G TG ---- TG AAAGGA - AT- A
AT
AAGGATCTTTCAAATCGACG GTGCTTGGTG GATA G CA G CTTCCA TCTT TCAA CG CG
T
ATTATGCGCGTGCTTGATGA TGCG |||| | || |||| |||| |||| ||||
GATGGAAGTGCTTGGTGTGC TTAT C GT C GAAGGT AGAG AGTT GC GC A
GTATT G GT GGTT GT ----- T CGT - GT

GAM2715 TTTGATGCAAGATGGGTGGT 2701 TGCAAGATGG 5426 G ----- G --- G- T G
GATTTA
GCGGGTGTGAGGACGGATTT GTGGTGCGGG TTT ATGCA AGAT GGT GGTGC GG GTGA
GACG T
ATCACGTACGTTGTTATCCG TGTG ||||| ||||| |||| ||||| |||||
AGCGCCGAAGCTGGTCTTAG AGA TGCGT TCTG TCG CCGCG CC TATT TTGC /
AGGAGTTGCGTGAGA G TGAGGAGAT G AAG AG - G ATGCAC

GAM2716 TTTCTGATGATGAGATGACA 2702 TGAGATGACA 5427 AT - - C- A G AAAAGGG
AT
GGCTTCATTAGAAGCTGTGC GGCTTCATTA TTCTG GATGAGA TGA CAGG TTC TTAGAAGCT
TGCT TTTTGA G
TAAAAGGGTTTTTAATGATA GAAG |||| ||||| |||| ||||| ||||| |||||
TAAAAAGAGGCAAAGTTTTT GAGAT TTATTCT ACT GTCC AAG AGTTTTTGA ACGG
AAAAAT A
GAGGAAAACCTGATCAGTCT GG G A AA G A AG----- AT
TATTGGTAGAGA

GAM2717 GATCCGGCTTTCAACAGAAA 2703 TTTGGAAACG 5428 T AA GAAA ATGACG - A A T
GCAACAA C GA
TTTAAATGACGAGCGATTCC ACTAAAATTA TTC CA TTAA AG CG TTCCAAA CT GAG
TA GAC A
AAAACCTTGAGGCAACAATAC AAGA ||| || |||| ||||| ||||| |||||
GACGAAATGTCTAGTAAATA AAG GT AAATT TC GC AAGGTTT GA CTT AT CTG
/
TTCAGCTTTGGAAACGACTA T AG AGAG AAAA-- A A C - ATAAATG - TA
AAATTAAGAGATGGAGAAT
ATCGCAGATC

GAM2718 GCAGAATTGTTAGAAAATGT 2704 TACAGCAATA 5429 AGAA TTAGAAA C -- TG
 TGCTGTCACAAGCGCTGTAA TGAACGATCA GC TTG ATGTTGCTGT AC AAGCGC T
 GCGCTTTAGTACAGCAATAT GAAA || ||| ||||| || |||||
 GAACGATCAGAAAAGC CG GAC TATAACGACA TG TTCGCG /
 AAAA TAGCAAG - AT AA

GAM2719 ACACATCGCAAACCACTCTG 2705 TTGAACAGTA 5430 - C TC C T C T C C AC A
 CC
 ACTTAAGTGGTGCTGCTTTA TCGTTAATCA A AC AC TGA TTAAC GGTGCTG TTTAATATA TA
 GTT GCA GG ATCC T
 ATATATTACGTTTCGCAACGG TTGT | || ||| ||||| ||||| || ||| || |||||
 AATCCCCTCAGGATGCCCTG T TG TG ACT AATTG CTATGAC AAGTTATAT GT CAA CGT
 CC TAGG /
 CAACTGCTATATTGAACAGT C T TT - - - C - - C- G AC
 ATCGTTAATCATTGTTGTCT
 TGCTGATTCTG

GAM2720 CACTTTGTGTTGGAGAATTG 2706 ACATTGCCAT 5431 AG ---- CTA AC TT CAT TC
 A G
 TAGTAATGCTATCTCACCGT TGTACAATTA GG AATTGTA GTAATG TCTC CG GATCC GC
 GTT TTCTT A
 TGATCCCATGCTCGGTTATT CCCA || ||||| ||||| ||| || ||||| || ||||| |||||
 CTTGAACAAGAAAACCATGT CC TTAACAT CGTTAC AGAG GC CTAGG TG CCAA
 AAGAA A
 TAAGGATCCTCGTAGAGACA CA GTTAC --- AT TC AAT TA - C
 TTGCCATTGTACAATTACCC
 ACAAATATTG

GAM2721 CGTGTGTCTGTTGACTCGTT 2707 ATCAAGAATC 5432 - TATCAA TTAAAACAGCCGA T
 T CTAA T G
 TCTATCAAGGATTTAAAACA CCGAACTGAA TCGTTTC GGAT TCTT ATGATA GA
 GCAAA TA T
 GCCGATCTTTATGATATGAC ACGA ||||| ||| ||| ||||| || ||||| ||
 TAAGCAAATTAGTAATACTT AGCAAAG CCTA AGAA TACTAT CT CGTTT AT A
 TGCCTTCTATCATCAAGAAT C TCAAGC ----- C - TC-- C A
 CCCGAACTGAAACGACTAAT
 CGACTCACACG

GAM2722 CGTGTGATGCTGTTTATGA 2708 TTGATGCTGT 5433 - T A-- AT- ---- T C
 AGCAATGAGTGTATTCTACC TTATGAAGCA CGTGTGATG C GTTTATGA GCA GAGT
 GTATTC AC A
 AACGTGAATATATTAAGTCT ATGA ||||| ||||| ||| ||| ||||| ||
 CCTGCACATTATAAACTGCC GCGCAATTAC GCAAATATT CGT CTCA TATAAG TG A
 ATTAACGCG C T ACA CCT ATTA - C

GAM2723 CTCGAATGGTGACAAAAATA 2709 TTAGCTGCAC 5434 GA AAATAGGA C CCC TAC
 AACC ACAA AGAA
 GGAGCACAGGCCCGGTATA AGAATCTATT T CAA GCA AGGC GGTA GAT GTGTA
 TTAAGA C
 CGATAACCGTGTAACAATTA ACCC | || ||||| ||||| ||| ||||| |||||
 AGAAGAACACAATCTTAGCT A GTT CGT TTCG CCAT CTA CACGT GATTCT /

GCACAGAATCTATTACCCGC A- AAAAC--- T C-- TAT AGA- C--- AACA
TTTTGCCAAAATTGAACCAA
TCGAG

GAM2724 GCTCTTGGATCCGCAGGTAT 2710 TTAGAGCATA 5435 C AT TAT CT CT ACA
TGCTTCTAGTCTTGTTGCAC TTTTGTGGCA GCT TTGG CCGCAGG TGCTT AGT TGTTGC A
AACTCGTAACATCGCTTAGA CCAA ||| ||| ||||| |||| ||| |||||
GCATATTTTGTGGCACCAAT CGA AACC GGTGTTT ACGAG TCG ACAATG /
AGC T AC TAT AT CT CTC

GAM2725 TACCCGCATGTAAAGGATGT 2711 TGTGATAACT 5436 T - AT- - C T CT - - C
GA
GATAACTGCTCTCCTATCGA GCTCTCCTAT TG AAAGGAT GTG AACTGC TCTC TA CGATG
CAA CGA TCTTTG CT A
TGCTCAACGATCTTTGCCTG CGAT || ||||| ||| ||||| ||| ||| ||||| ||
AACAAGACAAAGGTTTCGATT AC TTTTCTA CGC TTGATG AGAG AT GCTAC GTT GCT
GGAAAC GA /
GTCATCGCTAGAGACGTAGT - A CAT C - C T- A T A AC
TTACCGCAATCTTTTCAGAT
TCACGGTG

GAM2726 TATGGTGATCAACGTGTATC 2712 AGTCGCAGAT 5437 TG A CTA GCTA ATCA
A C AA
TAACAATCACGAGCTATCTG TGTGATTGTA TATGG ATCA CGTGTAT ACAATCACGA TCTGT
GAT TGG TGA T
TATCAGATATGGCTGAAATT ATAC |||| ||| ||||| ||||| |||| ||| ||||| ||
ATCAACCAAGTCGCAGATTG ATGTC TAGT GTACATA TGTTAGTGTT AGACG CTG
ACC ACT /
TGATTGTAATACATGTGATT GT - A-- ---- ---- A A AT
GCTGTA

GAM2727 TCAGAATCGTGGTTCTTATA 2713 TTGCAGGAAT 5438 A C - - C TC T A--
ACTT
CATATCATGCTGTAACCTTC TACGCATATG GGTTCTT TA ATAT CATGCT GTAA TTTCT
GGTGAT GCGG TCGAT A
TTCGGTGATTGCGGATCGAT A ||||| || ||||| ||||| ||||| ||||| ||||| |||||
ACTTATTGCATCGAACGCTG TTAAGGA GT TATA GTACGG TATT AAAGA TCATTA CGTC
AGCTA /
CTATTACTCAGAAAATTATG C - C G A C- T GCA CGTT
GGCATGCATATTGCAGGAAT
TACGCATATGA

GAM2728 CATATAGCACGAACGCCATG 2714 AAGCTGGCGA 5439 C AA T AAAAAT- A
TTTTATCAAAAAATTCCAAT CGTACTATAT CATATAG ACG CGCCA GTTTTATCA TCC A
GGACTTCTAATGGTAAAGCT G ||||| ||| ||||| ||||| |||
GGCGACGTACTATATG GTATATC TGC GCGGT CGAAATGGT AGG /
A A- - AATCTTC T

GAM2729 TTGGTATTAGTGCTATTAAT 2715 TTAGTGCTAT 5440 A TA- AGTT AG
GAGTTGGAAGTAAATCCTGC TAATGAGTTG TTGGT TTAGTG TTAATG GGA T
ATTAACTCGCACTGACATCG GAAG ||||| ||||| ||||| |||

GAM2736 TCTTGAGTATACGACTGATG 2722 TGAGTATACG 5447 G TACGA - CT AA AT G TG A

C
 ACTTTGAAGAAAATGCTGCT ACTGATGACT TCTT AGTA CTGA TGA TTG GAAA GCT C ATA
 GATAACTTTGTTGGAGCTTT TTGA |||| ||| |||| ||| ||| ||| ||| |||
 TGATAATATTATTCAGCTTG AGAA TCGT GACT ATT AAT TTTT CGA G TGT T
 CTGAAGA G TC--- T AT AG -- -GT T

GAM2737 TGTATATGAAGATTACGACA 2723 TATCAAAGTT 5448 TGAA A--- ATTG AAATT
 GTGTGGAGATTGATTTTAGA GTGATTGAAT TGTATA GATTACGAC GTGTGGAG
 ATTTTAGA T
 AAATTTGACAAATCTAAGGT TGTA ||||| ||||| ||||| |||||
 GTCCCTCCATATCAAAGTTG ACATGT TTAGTGTTG TATACCTC TGGAATCT G
 TGATTGAATTGTACA TAAG AAAC CCTG AAACA

GAM2738 TTCTCCGATTAGTAATATTG 2724 TGAGCAGGCG 5449 C AATATTGAA - GG GG
 AAGCCTCTCAGAGGTGGTGG AAGAAACAAT TTCT CGATTAGT GCCT CTCAGA TGGT C
 CAGAATCAATCTGAGCAGGC TGAT |||| ||||| |||| ||||| |||
 GAAGAAACAATTGATCGCAG AAGA GCTAGTTA CGGA GAGTCT ACTA A
 AA C ACAAAGAAG C A- AG

GAM2739 GTTTTTGAATGATCTTGAGT 2725 TGAGTATACG 5450 GAATGA G TACGA - CT AA
 AT G TG A
 ATACGACTGATGACTTTGAA ACTGATGACT GTTTTT TCTT AGTA CTGA TGA TTG GAAA
 GCT C ATA C
 GAAAATGCTGCTGATAACTT TTGA ||||| ||||| |||| ||| ||| ||| ||| |||
 TGTTGGAGCTTTTGATAATA CGAAAA AGAA TCGT GACT ATT AAT TTTT CGA G
 TGT T
 TTATTCAGCTTGCTGAAGAA AGAAGA G TC--- T AT AG -- -GT T
 GAAGAAAAAGC

GENE	TARGET	UTR SEQUENCE	SEQID	BINDING-SITE
GAM15	DKFZp761D221	3' GTAAATTGTACTCTCATTCCA	26056	AAT AATCCG
		TGGAATGA GTA TTAC		
		ACCTTACT CAT AATG		
		CT_ GTTA__		
GAM15	KIAA0217	3' GTAACCATACACTTTTATTCCA	33284	A AATCC
		TGGAATGAA TGTA GTTAC		
		ACCTTATTT ACAT CAATG		
		C AC__		
GAM15	SRPK2	3' TAACAGTGATCACATTCATTCC	9111	A AA C__
	A	TGGAATGAA TGT ATC GTTA		
		ACCTTACTT ACA TAG CAAT		
		_ C_ TGA		
GAM15	TCL6	3' AACAGATTTACATCCCAGACA	14839	GAA AA C
		TG TG ATGTAAATC GTT		
		AC AC TACATTTAG CAA		
		AG_ CC A		
GAM15	TCL6	3' AACAGATTTACATCCCAGACA	21756	GAA AA C
		TG TG ATGTAAATC GTT		
		AC AC TACATTTAG CAA		
		AG_ CC A		
GAM15	TTYH2	3' AACAGATTTGCAGCTCATTCC	26376	AA C
		GGAATGA TGTAATC GTT		
		CCTTACT ACGTTTAG CAA		
		CG A		
GAM15	LOC220776	3' GATGGTGTCCACATTTTACCCC	33933	AA AAAT_
	A	TGG TGAAATGT CCGTT		
		ACC ATTTTACA GGTAG		
		CC CCTGT		
GAM16	PRKG2	3' CTTCTCGTTTGAGTACTACTAA	12940	ATACAT A
		TTAGTAGTA CGA AAG		
		AATCATCAT GCT TTC		
		GAGTTT C		
GAM16	DKFZp761P1010	3' CTTTTCTGGTTTATACTACTA	20478	A C _
	A	TTAGTAGT ATA ATC GAAAAG		
		AATCATCA TAT TGG CTTTTC		
		A T T		
GAM16	FLJ11996	3' TTTGAAAGTGTATTATTACTAA	24534	___
		TTAGTAGTAATACA TCGAA		

AATCATTATTATGT AGTTT
 GAA
 GAM16 LOC200269 3' TCAGGTGCCTACTACTAA 42761 ATA _
 TTAGTAGTA CATC GA
 ||||| ||| ||
 AATCATCAT GTGG CT
 CC_ A
 GAM17 AKAP13 3' AAGGCATCTTTCCAAGTACTCA 43174 T CG GG
 TGA GTACT GG GGATGCCTT
 ||| ||| || |||||
 ACT CATGA CC TCTACGGAA
 _ A_ TT
 GAM17 DKFZP434N014 3' AAGACATCCCCCCTCCATC 30388 TACTC C
 GATG GGGGGGGATG CTT
 ||| ||||| |||
 CTAC TCCCCCCTAC GAA
 C_ A
 GAM17 FLJ23598 3' AAGACACCCCCCTGGACCCATC 24152 TAC A C
 A TGATG TCGGGGGGG TG CTT
 ||| ||||| |||
 ACTAC GGTCCCCC AC GAA
 CCA _ A
 GAM17 LOC149086 3' AAGAGCTATTCGCCGAGTCCA 40945 A T AT _
 CCA TG TG ACTCGGGGGGG GC CTT
 || ||||| |||
 AC AC TGAGCCCCCTT CG GAA
 C C AT A
 GAM17 LOC92568 3' AAGGCATCCACATTTAAGTCAC 34572 A T CG GG_
 CA TG TG ACT GG GGATGCCTT
 || ||| || |||||
 AC AC TGA TT CCTACGGAA
 C _ AT ACA
 GAM18 AKAP2 3' GTATACAGTTATTTTCTCA 14063 G AGA
 TGAG AAAATGA TGTATAC
 ||| ||||| |||||
 ACTC TTTTATT ACATATG
 _ G_
 GAM18 CRIM1 3' GCATTCCCACCTTTTCCTCA 18561 _ AA
 TGAGGAAAA TG GATGT
 ||||| || |||
 ACTCCTTTT AC TTACG
 C CC
 GAM18 CYP27B1 3' GGTATACATCTTCCCCT 6433 AAAAT
 AGG GAAGATGTATACC
 || |||||
 TCC CTTCTACATATGG
 C_
 GAM18 ICOS 3' ACGTTGGCCAGTTTTCCTCA 14383 GAA_
 TGAGGAAAAT GATGT
 ||||| |||

			ACTCCTTTTG TTGCA		
			ACCGG		
GAM18	MTMR2	3'	ATGCATCTGCCATTTTCCTCA 18243	A_	
			TGAGGAAAATG AGATGTAT		
			ACTCCTTTTAC TCTACGTA		
			CG		
GAM18	MYD88	3'	ATCTTCACCCTCAGTTTCCTCA 8296	A_____	
			TGAGGAAA TGAAGAT		
			ACTCCTTT ACTTCTA		
			GACTCCC		
GAM18	PDK4	3'	GCATTTTCTATTTTCCCCA 46442	A	__
			TG GGAAAAT GAAGATGT		
			AC CCTTTTA TTTTACG		
			C TC		
GAM18	RB1CC1	3'	ACTACTTCATTTTCTCA 16629	G	AT
			TGAG AAAATGAAG GT		
			ACTC TTTTACTTC CA		
			_ AT		
GAM18	SLC18A1	3'	AGAGTGTTACCCTCTTTTCCTC 9016	T	AGATGT _
	A		TGAGGAAAA GA ATAC CT		
			ACTCCTTTT CT TGTG GA		
			_ CCCAT_ A		
GAM18	AGTRL2	5'	AGGGCTTCCCTCATCTTCCTCA 11644	A	A_ T ATA
			TGAGGAA ATGA GA GT CCT		
			ACTCCTT TACT CT CG GGA		
			C CC T _		
GAM18	BAG5	3'	GCATCTGCATTTTCCCCA 11306	A	A
			TG GGAAAATG AGATGT		
			AC CCTTTTAC TCTACG		
			C G		
GAM18	DKFZP564I122	3'	AGGCAGCTCTCCTCATTTTCCC 31645	A	_ T ATA
	CA		TG GGAAAATGA AGA GT CCT		
			AC CCTTTTACT TCT CG GGA		
			C CC _ AC_		
GAM18	FLJ20511	3'	GGTGTTCAATTTTCCCCA 19529	A	AGATGT
			TG GGAAAATGA ATACC		
			AC CCTTTTACT TGTGG		
			C _		
GAM18	FLJ20813	3'	ATATCTTCATCCTTCTCA 19678	AA	
			TGAGGA ATGAAGATGT		

			ACTCTT TACTTCTATA		
			CC		
GAM18	FLJ21140	3'	ACATCTTCACCTTCTTCA	24139	AA
			TGAGGAA TGAAGATGT		
			ACTTCTT ACTTCTACA		
			CC		
GAM18	KCNV1	3'	ACATCTTCATTCTCCCA	15709	A A
			TG GGA AATGAAGATGT		
			AC CCT TTACTTCTACA		
			— C		
GAM18	KIAA0022	3'	ATGTATCTCATTCTCCTCA	17026	A A
			TGAGGA AATGA GATGTAT		
			ACTCCT TTACT CTATGTA		
			C —		
GAM18	KIAA0161	3'	GCATGCCTCAGTTTCCTCA	16432	A AG_
			TGAGGAAA TGA ATGT		
			ACTCCTTT ACT TACG		
			G CCG		
GAM18	KIAA0410	3'	AGGTGGTGCATTCTCATTTTCC	16614	AG —
			TCA TGAGGAAAATGA ATGTAT ACCT		
			ACTCCTTTTACT TACGTG TGGA		
			CT G		
GAM18	KIAA1443	3'	ATATTTCTTTTCCTCA	31930	T A
			TGAGGAAAA GA GATGT		
			ACTCCTTTT CT TTATA		
			C —		
GAM18	KIAA1737	3'	GCATCTTACCCATTTTCTTCA	33447	—
			TGAGGAAAATG AAGATGT		
			ACTTCTTTTAC TTCTACG		
			CCA		
GAM18	LZIC	5'	ATAATTTCAATTTTCCTCA	26156	A
			TGAGGAAAATGAAG TGT		
			ACTCCTTTTACTTT ATA		
			A		
GAM18	MGC2452	5'	GGTTTTTCATTTTCTCA	26373	G TGTAT
			TGAG AAAATGAAGA ACC		
			ACTC TTTTACTTTT TGG		
			— ———		
GAM18	OS4	3'	GGTAAGTCCATTTTCC	12290	AA GTA
			GGAAAATG GAT TACC		

			CCTTTTAC CTG ATGG		
			__ A__		
GAM18	PCDH19	3'	ACATCTTCATTTTCTCTCA 31859		—
			TGAGGAAAA TGAAGATGT		
			ACTCCTTTT ACTTCTACA		
			T		
GAM18	PRO0456	5'	ACATTTTCATCTCCCCA 15392	A AA	
			TG GGA ATGAAGATGT		
			AC CCT TACTTTTACA		
			C C_		
GAM18	PRSC	3'	ACATTTTGTAATTTTCTCTCA 13347	G__	
			TGAGGAAAAT AAGATGT		
			ACTCCTTTTA TTTTACA		
			ATG		
GAM18	LOC148758	5'	AGGTATGCCCTCTCCTCTTCCT 38587	AAT A T_	
	CA		TGAGGAA GA GA GTATACCT		
			ACTCCTT CT CT CGTATGGA		
			CTC _ CC		
GAM18	LOC154007	3'	ATATTTTCATTGCCCCCA 39451	A AA	
			TG GG AATGAAGATGT		
			AC CC TTACTTTTATA		
			C CG		
GAM18	LOC90494	5'	ACACTAACATTTTCTCTTA 31575	A_ A	
			TGAGGAAAATG AG TGT		
			ATTCCTTTTAC TC ACA		
			AA _		
GAM18	LOC92379	3'	GGCATACATCTCACACTCA 34268	GAAAA A A	
			TGAG TGA GATGTAT CC		
			ACTC ACT CTACATA GG		
			AC__ _ C		
GAM19	COL19A1	3'	TACCGTTTTTTATTTTCATAACA 7599	TTT	
			TGTTATGAAAATGAAA GTA		
			ACAATACTTTTATTTT CAT		
			TGC		
GAM19	SLC26A4	3'	ATGCTGCCTCATTTTCACAGCA 6026	A AATT	
			TGTT TGAAAATGA GTAT		
			ACGA ACTTTTACT CGTA		
			C CCGT_		
GAM19	CRSP3	3'	TACATGTTGTTTCATATTCATAA 30412	A ATT__	
	CA		TGTTATGAA ATGAA TGTA		

			ACAATACTT TACTT ACAT		
			A GTTGT		
GAM19	FLJ11320	3'	ACAAATTTTCGGGGCCATACCA 20423	T	AAAA
			TG TATG TGAAATTTGT		
			AC ATAC GCTTTAAACA		
			C CGGG		
GAM19	FLJ20045	3'	GATTTCACTTTTCATGACA 19144	A	
			TGTTATGAAA TGAAATT		
			ACAGTACTTT ACTTTAG		
			C		
GAM19	KIAA0410	3'	TATACAAACCTCATTCTTCAT 16622	_	AA
			ATGAA AATGA TTTGTATA		
			TACTT TTACT AAACATAT		
			C CC		
GAM19	PABPC5	3'	TATACAAATCTTCATTTTCATA 28098	T	_
	CA		TGT ATGAAAATGAA ATTTGTATA		
			ACA TACTTTTACTT TAAACATAT		
			_ C		
GAM19	LOC157292	3'	ATACAAATGTTTCATAGCA 41774		AATGAA
			TGTTATGAA ATTTGTAT		
			ACGATACTT TAAACATA		
			G_____		
GAM19	LOC202460	5'	TATGCTGCTCCAATTTTCATAAC 42985		A AAATTT
	A		TGTTATGAAA TG GTATA		
			ACAATACTTT AC CGTAT		
			A CTCGT_		
GAM20	ITGAV	3'	CACAAAATGAGAATTATATTG 7974	G	ATAG_
	TCA		TGA AAATATAATTT TTGTG		
			ACT TTTATATTAAG AACAC		
			G AGTAA		
GAM20	THBS1	3'	TTATAAATTATTTTCTCA 9257	T	
			TGAGAAA ATAATTTATAG		
			ACTCTTT TATTAAATATT		
			_		
GAM20	DKFZP564O123	3'	CACAGAGAAATTATATTCCTTA 29905	A	ATAG
			TGAG AATATAATTT TTGTG		
			ATTC TTATATTAAA GACAC		
			C GA__		
GAM20	KIAA0336	3'	CACAACAGTGACTATATCACTC 16010	AA	AT A
	A		TGAG ATATA TTAT GTTGTG		

			ACTC TATAT AGTG CAACAC		
			AC C_ A		
GAM20	KIAA1494	5'	CACAACTATGAACATTTCT 33961	ATAA	
			AGAAAT TTTATAGTTGTG		
			TCTTTA AAGTATCAACAC		
			C__		
GAM20	RYK	3'	CATTTGTAAATTATATTTTCA 40204	A T	
			TGAGAA TATAATTTATAG TG		
			ACTTTT ATATTAAATGTT AC		
			- T		
GAM20	LOC123047	5'	ACAACTCTTAATTTCTCA 37237	A TTTAT	
			TGAGAAAT TAA AGTTGT		
			ACTCTTTA ATT TCAACA		
			- C__		
GAM21	XT3	3'	CATTTCTCAAGAATCCTC 21443	A AT	
			GAG ATTCTTGA AATG		
			CTC TAAGAACT TTAC		
			C CT		
GAM21	COE2	3'	TATTCCAACGAATTCTCA 32131	- -	
			TGAGAATTC TTG AATA		
			ACTCTTAAG AAC TTAT		
			C C		
GAM21	POLD3	3'	CAGTTTTTCAGAATTCTCA 44052	T TAA	
			TGAGAATTCT GAA TG		
			ACTCTTAAGA CTT AC		
			- TTG		
GAM21	RI58	3'	ATCTTTACTCAAGAATTTCA 14794	A A T	
			TGAGA TTCTTGA TAA GAT		
			ACTTT AAGAACT ATT CTA		
			- C T		
GAM22	ADCY6	3'	GGCTGTTCCCTCTCCAA 17589	T AA	
			TTGGA GA GAACAGCT		
			AACCT CT CTTGTCGG		
			- CC		
GAM22	ADCY6	3'	GGCTGTTCCCTCTCCAA 21977	T AA	
			TTGGA GA GAACAGCT		
			AACCT CT CTTGTCGG		
			- CC		
GAM22	DRD1	3'	TAAATTAATGAGTTTTATCCAA 6466	GAA GC	
			TTGGATGAAA CA TAATTTA		

				AACCTATTTT GT ATTAAAT		
				GA_ A_		
GAM22	MORF	5'	AGATGTTCTTTCACCCGA	14720	A	G
			TTGG TGAAAGAACA CT			
			AGCC ACTTTCTTGT GA			
			C A			
GAM22	FLJ13111	3'	TGGCTGCCTCCTTCATCCAA	24685	A	A_
			TTGGATGAA GA CAGCTA			
			AACCTACTT CT GTCGGT			
			C CC			
GAM22	KIAA0495	3'	TGGCTGTTTTCCACCCAA	31366	A	AA
			TTGG TG AGAACAGCTA			
			AACC AC TTTTGTTCGGT			
			C C_			
GAM22	LOC145988	5'	AATTAGCTGCAGCCAA	38034	A	AAAGAA
			TTGG TG CAGCTAATT			
			AACC AC GTCGATTAA			
			G _____			
GAM23	ED1	3'	GTGACTCTTAGCCCTCA	7099	A A	A
			TGA GG CTAAGAGT GC			
			ACT CC GATTCTCA TG			
			C _ G			
GAM23	EFNB2	3'	CTCTAGAGTTTAGTCCTT	10296	AGTAG	A
			AAGGACTAAG CTA AG			
			TTCCTGATTT GAT TC			
			GA__ C			
GAM23	PCDHGA1	3'	CTGAAGCCTCAGTCCTTCA	20981	AA TA	AA
			TGAAGGACT GAG GCT AG			
			ACTTCCTGA CTC CGA TC			
			_ _ AG			
GAM23	PCDHGA10	3'	CTGAAGCCTCAGTCCTTCA	20982	AA TA	AA
			TGAAGGACT GAG GCT AG			
			ACTTCCTGA CTC CGA TC			
			_ _ AG			
GAM23	PCDHGA11	3'	CTGAAGCCTCAGTCCTTCA	20984	AA TA	AA
			TGAAGGACT GAG GCT AG			
			ACTTCCTGA CTC CGA TC			
			_ _ AG			
GAM23	PCDHGA11	3'	CTGAAGCCTCAGTCCTTCA	25790	AA TA	AA
			TGAAGGACT GAG GCT AG			

			ACTTCCTGA CTC CGA TC	
			— — AG	
GAM23	PCDHGA12	3'	CTGAAGCCTCAGTCCTTCA 9826	AA TA AA
			TGAAGGACT GAG GCT AG	
			ACTTCCTGA CTC CGA TC	
			— — AG	
GAM23	PCDHGA2	3'	CTGAAGCCTCAGTCCTTCA 20985	AA TA AA
			TGAAGGACT GAG GCT AG	
			ACTTCCTGA CTC CGA TC	
			— — AG	
GAM23	PCDHGA3	3'	CTGAAGCCTCAGTCCTTCA 20986	AA TA AA
			TGAAGGACT GAG GCT AG	
			ACTTCCTGA CTC CGA TC	
			— — AG	
GAM23	PCDHGA4	3'	CTGAAGCCTCAGTCCTTCA 20987	AA TA AA
			TGAAGGACT GAG GCT AG	
			ACTTCCTGA CTC CGA TC	
			— — AG	
GAM23	PCDHGA5	3'	CTGAAGCCTCAGTCCTTCA 20988	AA TA AA
			TGAAGGACT GAG GCT AG	
			ACTTCCTGA CTC CGA TC	
			— — AG	
GAM23	PCDHGA6	3'	CTGAAGCCTCAGTCCTTCA 20989	AA TA AA
			TGAAGGACT GAG GCT AG	
			ACTTCCTGA CTC CGA TC	
			— — AG	
GAM23	PCDHGA7	3'	CTGAAGCCTCAGTCCTTCA 20990	AA TA AA
			TGAAGGACT GAG GCT AG	
			ACTTCCTGA CTC CGA TC	
			— — AG	
GAM23	PCDHGA8	3'	CTGAAGCCTCAGTCCTTCA 25787	AA TA AA
			TGAAGGACT GAG GCT AG	
			ACTTCCTGA CTC CGA TC	
			— — AG	
GAM23	PCDHGA9	3'	CTGAAGCCTCAGTCCTTCA 20991	AA TA AA
			TGAAGGACT GAG GCT AG	
			ACTTCCTGA CTC CGA TC	
			— — AG	
GAM23	PCDHGB1	3'	CTGAAGCCTCAGTCCTTCA 20992	AA TA AA
			TGAAGGACT GAG GCT AG	

			ACTTCCTGA CTC CGA TC	
			— — AG	
GAM23	PCDHGB2	3'	CTGAAGCCTCAGTCCTTCA 20993	AA TA AA
			TGAAGGACT GAG GCT AG	
			ACTTCCTGA CTC CGA TC	
			— — AG	
GAM23	PCDHGB3	3'	CTGAAGCCTCAGTCCTTCA 20994	AA TA AA
			TGAAGGACT GAG GCT AG	
			ACTTCCTGA CTC CGA TC	
			— — AG	
GAM23	PCDHGB4	3'	CTGAAGCCTCAGTCCTTCA 9827	AA TA AA
			TGAAGGACT GAG GCT AG	
			ACTTCCTGA CTC CGA TC	
			— — AG	
GAM23	PCDHGB5	3'	CTGAAGCCTCAGTCCTTCA 20995	AA TA AA
			TGAAGGACT GAG GCT AG	
			ACTTCCTGA CTC CGA TC	
			— — AG	
GAM23	PCDHGB6	3'	CTGAAGCCTCAGTCCTTCA 20996	AA TA AA
			TGAAGGACT GAG GCT AG	
			ACTTCCTGA CTC CGA TC	
			— — AG	
GAM23	PCDHGB7	3'	CTGAAGCCTCAGTCCTTCA 20997	AA TA AA
			TGAAGGACT GAG GCT AG	
			ACTTCCTGA CTC CGA TC	
			— — AG	
GAM23	PCDHGC3	3'	CTGAAGCCTCAGTCCTTCA 26188	AA TA AA
			TGAAGGACT GAG GCT AG	
			ACTTCCTGA CTC CGA TC	
			— — AG	
GAM23	PCDHGC3	3'	CTGAAGCCTCAGTCCTTCA 8450	AA TA AA
			TGAAGGACT GAG GCT AG	
			ACTTCCTGA CTC CGA TC	
			— — AG	
GAM23	PCDHGC4	3'	CTGAAGCCTCAGTCCTTCA 20998	AA TA AA
			TGAAGGACT GAG GCT AG	
			ACTTCCTGA CTC CGA TC	
			— — AG	
GAM23	PCDHGC5	3'	CTGAAGCCTCAGTCCTTCA 20999	AA TA AA
			TGAAGGACT GAG GCT AG	

			ACTTCCTGA CTC CGA TC		
			— — AG		
GAM23	TACC1	3'	CTTTAGGGTTAGTCCTCA 12963	A	GAGTAG
			TGA GGA CTAAAG		
			ACT CCTGATT GATTTC		
			— GG—		
GAM23	TEM7	3'	TCTTTAGGACATTAGTCC 21674	GA	AG
			GGA CTAAAGA		
			CCTGATT CA GATTCT		
			A_ G_		
GAM23	EIF4B	3'	TCTTCATGCTACTCTTAACCTC 37402	C__	TA_
	C		GGA TAAGAGTAGC AAGA		
			CCT ATTCTCATCG TTCT		
			CCA TAC		
GAM23	FLJ13150	3'	TCTCCCATCTCCCAGTCCTTCA 24201	AA	TAGCTAA
			TGAAGGACT GAG AGA		
			ACTTCCTGA CTC TCT		
			CC TACCC_		
GAM23	FLJ14327	3'	CTTTGGGTCGTTAGTCCTCCA 24425	A	_ GTAG
			TG AGGACTAA GA CTAAAG		
			AC TCCTGATT CT GGTTTC		
			C G G_		
GAM23	FYCO1	3'	CTCCAGTCATGCTCTTGTCCT 23708	A T	_ AA
	CA		TGA GGAC AAGAGTA GCT AG		
			ACT CCTG TTCTCGT TGA TC		
			C _ AC CC		
GAM23	KIAA0125	3'	CTTCCTGGGCCCTGGTCCTTCA 30346	A A	AGCTA
			TGAAGGACTA G GT AAG		
			ACTTCCTGGT C CG TTC		
			_ C GGTCC		
GAM23	KIAA0202	3'	TCTTTAGTAATTTAATCTTCA 32180	ACTAA	A
			TGAAGG GAGT GCTAAAGA		
			ACTTCT TTTA TGATTCT		
			AA_ A		
GAM23	KIAA0748	3'	CTACTCCTTGGTCCTCCA 16703	A	_
			TG AGGACTAAG AGTAG		
			AC TCCTGGTTC TCATC		
			C C		
GAM23	N4BP3	3'	TCTGGGGCCTCCAGTCCTTCA 32939	AA	TA AA
			TGAAGGACT GAG GCT AGA		

			ACTTCCTGA CTC CGG TCT		
			C_ _ GG		
GAM23	PRO1770	3'	AGCTACTCCTGGTCCCTCA 15325	A	A
			TGA GGACTA GAGTAGCT		
			ACT CCTGGT CTCATCGA		
			C C		
GAM23	UBE2G1	3'	CTTCTCCTTAGTCCTTCA 9347	_	T
			TGAAGGACTAAG AG AG		
			ACTTCCTGATTC TC TC		
			C T		
GAM23	UNC5D	3'	TCTTCAATTTCTTAGTCCCTC 28117	A	TAGCTA
			GA GGACTAAGAG AAGA		
			CT CCTGATTCTT TTCT		
			C TAAC_		
GAM23	VDAC3	3'	TCTTTAGCTACTCCTTTTCCTA 12204	A	CTAA
	CA		TG AGGA GAGTAGCTAAAGA		
			AC TCCT CTCATCGATTTCT		
			A TTTC		
GAM23	LOC145980	5'	TCCTTAGCTACCCTGTTTT 40651	TA A	A
			AGGAC AG GTAGCTAA GA		
			TTTTG TC CATCGATT CT		
			_ C C		
GAM23	LOC150372	3'	CTTCAAGACTCGTCCTTCA 38939	TAA	AGCTA
			TGAAGGAC GAGT AAG		
			ACTTCCTG CTCA TTC		
			_ GAAC_		
GAM23	LOC157860	3'	TCCTTAGCTTTTGAAGCTCCTC 41862	A _ AA T	A
	A		TGA GGA CT GAG AGCTAA GA		
			ACT CCT GA TTT TCGATT CT		
			_ C AG _ C		
GAM23	LOC167147	5'	TTTAATCTGTCCTTCA 40228	TA	GTAGC
			TGAAGGAC AGA TAAA		
			ACTTCCTG TCT ATTT		
			_ A_		
GAM23	LOC201626	5'	TCTTCAGGTTTCAGTTCTTCA 42891	AA	TAG A
			TGAAGGACT GAG CT AAGA		
			ACTTCTTGA CTT GA TTCT		
			_ TG_ C		
GAM23	LOC90249	3'	CTTAATGCTGGTCCTTCA 31010	AAG	GCTA
			TGAAGGACT AGTA AAG		

			ACTTCCTGG TCGT TTC	
			___ AA___	
GAM24	DPYSL3	3'	ATTACTAACTCTCCAAGCATAG 7070	AA_____
	AA		TTCTATGCTTG AGTAAT	
			AAGATACGAAC TCATTA	
			CTCTCAA	
GAM24	FGF23	3'	TTATCACTTTTAAGCATA 21796	A
			TATGCTTGAAAAGT ATAA	
			ATACGAATTTTCA TATT	
			C	
GAM24	GATM	3'	CTATTTGGCTTCAAGTATA 7224	A AAT
			TATGCTTGAA GT AATAG	
			ATATGAACTT CG TTATC	
			_ GT_	
GAM24	IPT	3'	CTATTATTAAGCAGCACAGA 19152	A T AAAG
			TCT TGCT G TAATAATAG	
			AGA ACGA C ATTATTATC	
			C _GAAA	
GAM24	ShrmL	3'	CTATTATTACTTTGTAGTAGAA 21912	GCTTG
			TTCTAT AAAGTAATAATAG	
			AAGATG TTTCATTATTATC	
			ATG___	
GAM25	CX3CR1	3'	TCAAATGCTTGGCTTCT 34979	_ TT
			AGAA TCAA GCATTTGA	
			TCTT GGTT CGTAAACT	
			C _	
GAM25	FBXW1B	3'	TTCAAATGTAAATTGTTC 27370	T _
			GAA CAATT GCATTTGAA	
			CTT GTTAA TGTAAACTT	
			_ A	
GAM25	FBXW1B	3'	TTCAAATGTAAATTGTTC 27380	T _
			GAA CAATT GCATTTGAA	
			CTT GTTAA TGTAAACTT	
			_ A	
GAM25	FBXW1B	3'	TTCAAATGTAAATTGTTC 14668	T _
			GAA CAATT GCATTTGAA	
			CTT GTTAA TGTAAACTT	
			_ A	
GAM25	NCOA6	5'	TGCAATTATTCTTTATA 15295	C
			TATAAAGAAT AATTGCA	

ATATTTCTTA TTAACGT

GAM25 TRPC6 3' TCAAATGCAAATCTTTA 10978 ATCAA
TAAAGA TTGCATTTGA
||||| |||||
ATTTCT AACGTAACT
A____

GAM25 ZNF135 3' TGCAATTAATCTTTATA 9490 ATC
TATAAAGA AATTGCA
||||| |||||
ATATTTCT TTAACGT
AA_

GAM25 BAG2 3' TCAAATGCATCAATTCTCTA 43753 A CAAT
TA AGAAT TGCATTTGA
|| ||||| |||||
AT TCTTA ACGTAACT
C ACT_

GAM25 FLJ12649 3' TTCAAATGCAGATTAATTCT 23835 C _
AGAAT AAT TGCATTTGAA
||||| |||||
TCTTA TTA ACGTAACTT
A G

GAM25 GFR 3' TCCAATGCTTTTTGACATCTTT 14642 A_ TT_ T
ATA TATAAAGA TCAA GCATT GA
||||| ||| |||||
ATATTTCT AGTT CGTAA CT
AC TTT C

GAM25 KIAA0626 3' CAAATAAAGACTGATTCTTTA 22313 A GC_
TAAAGAATCA TT ATTTG
||||||| || |||||
ATTTCTTAGT AG TAAAC
C AAA

GAM25 PRO0902 5' CAAATGCCTATTCTTTA 27608 CAATT
TAAAGAAT GCATTTG
||||| |||||
ATTTCTTA CGTAAAC
TC____

GAM25 STX12 3' CAAATGCATAAGTTTCTTTG 32983 TCAAT
TAAAGAA TGCATTTG
||||| |||||
GTTTCTT ACGTAAAC
TGAAT

GAM25 SZF1 3' CAAATCCAAGATTCTTTA 18173 AA C
TAAAGAATC TTG ATTTG
||||||| || |||||
ATTTCTTAG AAC TAAAC
_ C

GAM25 LOC143879 3' TCAAATGTGCACATTCTTTA 37662 CAATT
TAAAGAAT GCATTTGA
||||||| |||||

			ATTTCTTA	TGTAAACT	
			CACG_		
GAM25	LOC158954	3'	TGCAATTAATCTTTATA	30313	ATC
			TATAAAGA	AATTGCA	
			ATATTTCT	TTAACGT	
			AA_		
GAM25	LOC200609	5'	TCAAATCAAGATTCTTT	43333	AA C
			AAAGAATC	TTG ATTTGA	
			TTTCTTAG	AAC TAAACT	
			— —		
GAM25	LOC50999	3'	TCAAATGAAAATTCTTTAT	18118	CAATTG
			ATAAAGAAT	CATTGCA	
			TATTTCTTA	GTAAACT	
			AAA_		
GAM26	CRACC	3'	CCAGAACCCATCCCAATA	22154	A A
			TATTGG	AT GGTTTTGG	
			ATAACC	TA CCAAGACC	
			C C		
GAM26	FLJ14351	5'	TTAATTCCAAAGGCTCTTCCAA	24073	T G
			TTGGAA	AG TTTTGGGAATTAA	
			AACCTT	TC GAAACCTTAATT	
			C G		
GAM26	KIAA0102	3'	TTAATTCCTATTTCAATA	16477	TT
			TATTGGAATAGG	TTGG	
			ATAACTTTATCC	AATT	
			TT		
GAM26	OBSCN	3'	AATTCCAACAACCTCCAA	34987	ATAG _
			TTGGA	GTT TTGGAATT	
			AACCT	CAA AACCTTAA	
			— C		
GAM27	FLJ14600	3'	ATCTTTATTTCATGTGTCA	26573	AAAC AT
			TGACACA	GAA TAAAGAT	
			ACTGTGT	CTT ATTTCTA	
			A_ _		
GAM27	KIAA0215	3'	TAATTTAGCTTTGTGTCA	16385	ACG
			TGACACAAA	AAATTA	
			ACTGTGTTT	TTTAAT	
			CGA		
GAM27	NFASC	3'	TTAATTTGCTTTGTGTCA	34833	A A
			TG CACAAA	CGAAATTAA	

			AC GTGTTT GCTTTAATT		
			— C		
GAM27	PDE10A	3'	TATTTTCACTTTGTGTCA 13464	AC T	
			TGACACAAA GAAA TA		
			ACTGTGTTT CTTT AT		
			CA T		
GAM28	CKTSF1B1	3'	AGAGTCTTTTATCTGGT 15022	ATTT	
			ACCAGATAAAA TTCT		
			TGGTCTATTTT GAGA		
			CT__		
GAM28	CPNE3	3'	AGAAAAATTTGAAGTCTG 9992	AA_	
			CAGAT AAATTTTCT		
			GTCTG TTAAAAAGA		
			AAG		
GAM28	MYO10	3'	AGAAAAATAATCTGGT 14730	AAAA	
			ACCAGAT ATTTTCT		
			TGGTCTA TAAAAAGA		
			A__		
GAM28	PRKCN	3'	AGAAAAGTTTTACCTGGTTG 12396	ATA	
			TAACCAG AAAATTTTCT		
			GTTGGTC TTTGAAAAGA		
			CA_		
GAM28	EIF2C2	3'	AGAAAAATATATATCTGGTT 35613	AAA__	
			AACCAGATA ATTTTCT		
			TTGGTCTAT TAAAAAGA		
			ATATA		
GAM28	FLJ12934	3'	AGAAAACAATTTTATTTGG 23174	—	
			CCAGATAAAAATT TTTCT		
			GGTTTATTTTAA AAAGA		
			CA		
GAM28	KIAA1701	3'	AGATGGATTTTATCTGG 33683	A TT	
			CCAGATAAAA TT TCT		
			GGTCTATTTT AG AGA		
			_ GT		
GAM28	OSBPL10	3'	AAAAATGAAATATCTGGTT 19414	AAA_	
			AACCAGATA ATTTT		
			TTGGTCTAT TAAAAA		
			AAAG		
GAM28	SYPL	3'	AGAAAAACCTTTATTTGG 44643	AA	
			CCAGATAAA TTTTCT		

			GGTTTATTT AAAAAGA		
			CC		
GAM28	LOC120114	3'	AGAATGTGATTATCTGGTTG 37210	AA	TT
			TAACCAGATAA AT TTCT		
			GTTGGTCTATT TG AAGA		
			AG T_		
GAM28	LOC150848	5'	AGAAATAATTATTTGGTTA 41251	AAATT	
			TAACCAGATAA TTTCT		
			ATTGGTTTATT AAAGA		
			AAT__		
GAM28	LOC202454	5'	AGAAAAATTTTTGATGGT 43433	GA	
			ACCA TAAAAATTTTCT		
			TGGT GTTTTTAAAAAGA		
			A_		
GAM29	PKHD1	3'	AGATCGTTAACATGGGTAA 28938	AC	AA
			TTACCCAT TAA GATCT		
			AATGGGTA ATT CTAGA		
			CA G_		
GAM29	PLAG1	3'	AGATCTTTTAAATGTTTAGTA 8515	CC	AC
			TATTA CAT TAAAAGATCT		
			ATGAT GTA ATTTTCTAGA		
			TT A_		
GAM29	DKFZP434O125	3'	TCTTCTGTAATGGGTAATG 32406	_	TAA
			TATTACCCAT AC AAGA		
			GTAATGGGTA TG TTCT		
			A TC_		
GAM29	KIAA0419	3'	AGATCTTTCTGTGACAGGTAA 16258	CA_	TA
			TTACC TAC AAAGATCT		
			AATGG GTG TTTCTAGA		
			ACA TC		
GAM29	KIAA0940	3'	AGATCTTTTAGTATTATGTAA 17146	CC_	
			TTAC ATACTAAAAGATCT		
			AATG TATGATTTTCTAGA		
			TAT		
GAM29	MGC12217	3'	AGATCTTTGCATGAGGTAA 26515	_	ACTA
			TTACC CAT AAAGATCT		
			AATGG GTA TTTCTAGA		
			A CG_		
GAM29	OSBPL3	3'	AGACCTTTTAGTTATGAGTA 17813	C	_ A
			TAC CATA CTAAAAG TCT		

			ATG GTAT GATTTTC AGA		
			A T C		
GAM30	FCMD	3'	GGAACCATCAGCACCA 13574	C	ACTGG
			TTGGTGCTG TGGT TCCT		
			AACCACGAC ACCA AGGG		
			T _____		
GAM30	P3	5'	CAGGACAACCCAACAGCACCAG 21254	C	TACTG
			TTGGTGCTG TGG GTCCTG		
			GACCACGAC ACC CAGGAC		
			A CAA__		
GAM30	FLJ14146	3'	CAGGACCAGTGACAGCACC 24032	CTGG	
			GGTGCTG TACTGGTCCTG		
			CCACGAC GTGACCAGGAC		
			A__		
GAM30	KIAA0935	3'	GA CTCACAGCAGCACCGA 36011	GTACT	
			TTGGTGCTGCTG GGTC		
			AGCCACGACGAC TCAG		
			AC__		
GAM30	P15-2	3'	CAGCTTCAGCAGCAACAA 20782	G TA	
			TTG TGCTGCTGG CTG		
			AAC ACGACGACT GAC		
			A TC		
GAM30	TOR2A	3'	AGGAACCCAGAGCACCA 28216	G TACTGG	
			TTGGTGCT CTGG TCCT		
			AACCACGA GACC AGGA		
			_ CA__		
GAM30	LOC144848	3'	ACTTCCAGCAGCACCA 36419	TACT	
			TTGGTGCTGCTGG GGT		
			AACCACGACGACC TCA		
			T__		
GAM30	LOC150372	5'	GATCTGCCAGCAGCCCCAA 38940	T CT	
			TTGG GCTGCTGGTA GGTC		
			AACC CGACGACCGT CTAG		
			C _		
GAM30	LOC163682	5'	CAGGAAAGGGCCAGCAGCCCCA 42087	T TA GG	
	A		TTGG GCTGCTGG CT TCCTG		
			AACC CGACGACC GA AGGAC		
			C GG A_		
GAM31	FLJ20209	3'	AACTGATGTCAAAACCAGA 41400	G C TTAA	
			TC GGT TTG ACATCAGTT		

			AG CCA AAC TGTAGTCAA		
			A A _		
GAM31	MMD	3'	AACTGATGTTTACAAACCAGA 30074	G C T	
			TC GGT TTGT AAACATCAGTT		
			AG CCA AACA TTTGTAGTCAA		
			A _ _		
GAM31	LOC143920	3'	GAAGTTTAACAAAACCCGA 37641	C A	
			TCCGGT TTGTTAAAC TC		
			AGCCCA AACAATTTG AG		
			A A		
GAM31	LOC145858	3'	TAAAGGATTTTAACAAGACCC 38002	C AG	
			GGGTCTTGTTAAA ATC TTA		
			CCCAGAACAATTT TAG AAT		
			_ GA		
GAM32	MAP3K8	3'	AACTTGAAGATTGTAG 11704	CC	
			TTACAATCTTTA GGTT		
			GATGTTAGAAGT TCAA		
			_		
GAM32	KIAA1795	3'	ACCTGAAGATTGTAATA 35698	CC	
			TATTACAATCTTTA GGT		
			ATAATGTTAGAAGT CCA		
			_		
GAM32	LOC143666	3'	ACCAGAGATTGTAATA 40368	ACC	
			TATTACAATCTTT GGT		
			ATAATGTTAGAGA CCA		
			_		
GAM32	LOC253258	3'	ACCAGAGATTGTAATA 46146	ACC	
			TATTACAATCTTT GGT		
			ATAATGTTAGAGA CCA		
			_		
GAM32	LOC96573	3'	ATAACTTCAATAAAGATTGTAA 31642	CC_	
			TTACAATCTTTA GGTTAT		
			AATGTTAGAAAT TCAATA		
			AACT		
GAM33	PCDH10	5'	AAATGTCAAGAAGACATCCA 21881	GGATA CTA	
			TGGATG TTC ACATTT		
			ACCTAC AAG TGTAAG		
			AAG_ AAC		
GAM33	PCDH10	5'	AAATGTCAAGAAGACATCCA 26765	GGATA CTA	
			TGGATG TTC ACATTT		

			ACCTAC	AAG	TGTA	AAA	
			AAG_	AAC			
GAM33	LOC149684	3'	GTTATCAAATCTCATCCAA	41050		ATTCC	
			TTGGATGGGAT	TAAC			
			AACCTACTCTA	ATTG			
			AACT_				
GAM34	C22orf19	3'	TTTATTATCCCAAGTTCCTGCT	9777	T	CGA	
		G	TAGCA	GGATT	GATAATAAA		
			GTCGT	CTTGA	CTATTATTT		
			C	ACC			
GAM34	FLJ10545	3'	TTTATTATCTCCTGATATGC	19930		GATTC	
			GCATG	GAGATAATAAA			
			CGTAT	CTCTATTATTT			
			AGTC_				
GAM34	PCDH20	3'	GTTTATTACCTCATAAGTGC	23138	GG	TC	A
			GCAT	AT	GAG	TAATAAAC	
			CGTG	TA	CTC	ATTATTTG	
			AA	_	C		
GAM34	LOC144866	5'	TTACTTGGAATCCATGC	40480	_	A	
			GCATGGA	TTCGAG	TAA		
			CGTACCT	AGGTTC	ATT		
			AA	_			
GAM35	ADAMTS5	3'	TTTCTATCATGTCCAACACATT	13919	_	GT	
		CAA	TTGAATGTGTTG	ATG	ATAGAAA		
			AACTTACACAAC	TGT	TATCTTT		
			C	AC			
GAM35	HEPH	5'	CTATACCATCCACCCTCA	16717	AT	TT	
			TGA	GTG	GATGGTATAG		
			ACT	CAC	CTACCATATC		
			CC	_			
GAM35	LPIN1	3'	TTTCTATACCACTGTCATT	33471		TGTTGA	
			AATG	TGGTATAGAAA			
			TTAC	ACCATATCTTT			
			TGTC_				
GAM35	RAB7	5'	TGCCCCCAACACATTCAA	11013		AT	
			TTGAATGTGTTG	GGTA			
			AACTTACACAAC	CCGT			
			CC				
GAM35	RELN	3'	TTCTACAATACAACACATTGAA	45284	G	A	GTA
			TT	AATGTGTTG	TG	TAGAA	

			AA TTACACAAC AT ATCTT		
			G _ AAC		
GAM35	SLC10A2	3'	TCTTGTAATTTCAACACACCCA 6067	AA	TGG _
	A		TTG TGTGTTGA TATA GA		
			AAC ACACAACT ATGT CT		
			CC TTA T		
GAM35	COTL1	3'	TCTGCACCACACATTCAA 42469	TGAT	A
			TTGAATGTGT GGT TAGA		
			AACTTACACA CCA GTCT		
			_____ C		
GAM35	KIAA0326	3'	ACCACACAGTTACACATTCA 32156	_____	A
			TGAATGTGT TG TGGT		
			ACTTACACA AC ACCA		
			TTGAC _		
GAM35	LOC255328	3'	TTCTTACCCAACACATCAA 46182	A	AT T
			TTGA TGTGTTG GGTA AGAA		
			AACT ACACAAC CCAT TCTT		

GAM36	SLC6A6	3'	CAACACCCAGTCCTATTCCA 9004	GATCA	
			TGGAATGGGAT TGTTG		
			ACCTTATCCTG ACAAC		
			ACCC_		
GAM36	SMURF1	3'	AGTTTAATCCCCCATTCCA 44410	AT	CATGTT
			TGGAATGGG GAT GCT		
			ACCTTACCC CTA TGA		
			C_ ATT_		
GAM36	TEM7	3'	AGCTATGATCATCCCA 21668	TT	
			TGGGATGATCATG GCT		
			ACCCTACTAGTAT CGA		

GAM36	ZNF10	3'	CAACACATCTCCACTACCA 17693	AA_ _	ATCA
			TGG TGG GATG TGTTG		
			ACC ACC CTAC ACAAC		
			ATC T _		
GAM36	DKFZp547H025	3'	GCACAATGCATCCCATCCCA 21371	A	ATCA T
			TGG ATGGGATG TGT GC		
			ACC TACCCTAC ACA CG		
			C GTA_ _		
GAM36	FLJ12704	3'	AAGCAACCCATGCCCATTTCCA 24561	_	ATCAT
			TGGAATGGG ATG GTTGCTT		

			ACCTTACCC TAC CAACGAA		
			G C_____		
GAM36	KDEL3	3'	AACCTGATCATCCCACCCA 13723	AA	T
			TGG TGGGATGATCA GTT		
			ACC ACCCTACTAGT CAA		
			C_ C		
GAM36	KIAA1817	3'	AAGCATCTGGGATCACCCCACT 33859	A A	ATGT_
	C		GA TGGG TGATC TGCTT		
			CT ACCC ACTAG ACGAA		
			C C GGTCT		
GAM36	LOC153727	5'	AAGCAACATGATTTCCCATCC 41679	A	AT
	A		TGGA TGGG GATCATGTTGCTT		
			ACCT ACCC TTAGTACAACGAA		
			_ CT		
GAM36	LOC158382	5'	AATATAATCATTCCATCCCA 41962	A	C
			TGG ATGGGATGAT ATGTT		
			ACC TACCTTACTA TATAA		
			C A		
GAM36	LOC196264	3'	GACAGGAAACATCCCATTCCA 42336		A_ A
			TGGAATGGGATG TC TGTT		
			ACCTTACCCTAC AG ACAG		
			AA G		
GAM37	EIF5A2	3'	GTTTTGGTAAATCTCTTA 21661	A	TT
			TAAGAGATTTA CT AAT		
			ATTCTCTAAAT GG TTG		
			_ TT		
GAM37	FEZ1	3'	CAAATTAAAGAAGGATGTCTTA 22875	G	AA
			TAAGA ATTT CTTTAATTTG		
			ATTCT TAGG GAAATTAAAC		
			G AA		
GAM37	IL18R1	3'	TGCATTTCAAGTTAAATGTCTT 9951	G	T TT
	A		TAAGA ATTTAACTT AA TGCA		
			ATTCT TAAATTGAA TT ACGT		
			G C T_		
GAM37	ROBO1	3'	TGCAAATTAAAACATATTTTC 28589		TTAAC
			GAGAT TTTAATTTGCA		
			CTTTA AAATTAAACGT		
			TACA_		
GAM37	ROBO1	3'	TGCAAATTAAAACATATTTTC 8852		TTAAC
			GAGAT TTTAATTTGCA		

			CTTTA AAATTAAACGT		
			TACA_		
GAM37	KIAA0441	3'	TGCAGACTAGTTAAATC 16713	TTAA	
			GATTTAACT TTTGCA		
			CTAAATTGA AGACGT		
			TC__		
GAM37	KIAA0923	3'	TTAAAGTAAATCTCTTA 15246	A	
			TAAGAGATTTA CTTTAA		
			ATTCTCTAAAT GAAATT		
			-		
GAM37	KIAA1432	3'	TGCAAATTAACATAGTCTCTTA 33155	TAAC	
			TAAGAGATT TTAATTTGCA		
			ATTCTCTGA AATTAAACGT		
			TAC__		
GAM37	LOC152559	3'	GCATTAGTTAAATCCCTTA 39285	A	TTAATT
			TAAG GATTTAACT TGC		
			ATTC CTAAATTGA ACG		
			C TT__		
GAM37	LOC197131	3'	CAAAATTAAGTCAATCTCT 42445	TAAC	
			AGAGATT TTTAATTTG		
			TCTCTAA AAATTAAAC		
			CTC_		
GAM38	CLIPR-59	3'	TATTAACAGATACTCCCATAAT 17791	_ C C	
			GTTATGGGAG ATC GT AATA		
			TAATACCCTC TAG CA TTAT		
			A A A		
GAM38	DKFZp547I014	5'	TATTAACAGTTAATCCCATAAC 21468	GATCC_ C	
			GTTATGGGA GT AATA		
			CAATACCCT CA TTAT		
			AATTGA A		
GAM38	FLJ11184	3'	TGTTGATCTCCCACAATT 20366	A	CGT
			AGTT TGGGAGATC CA		
			TTAA ACCCTCTAG GT		
			C TT_		
GAM38	KIAA0426	3'	ATTGACAGATAATGACTGA 16307	GGGAG C	
			TCAGTTAT ATC GTCAAT		
			AGTCAGTA TAG CAGTTA		
			A__ A		
GAM38	KIAA1354	3'	ATTGACAATCCCATAAT 30541	GATCC	
			GTTATGGGA GTCAAT		

			TAATACCCT CAGTTA	
			AA____	
GAM38	LOC257058	5'	GAGGACTCATAATTGA 46560	AGA G
			TCAGTTATGGG TCC TC	
			AGTTAATACTC AGG AG	
GAM39	FMOD	3'	CACTTAATTCTTCCCATTT 7769	TT_ GA
			AAATGGGA GT AAGTG	
			TTTACCCT TA TTCAC	
			TCT A_	
GAM39	KAL1	3'	CACTTTTGTTCACCATCTGA 5715	A _ TT TG
			TCA ATGG GA G AAAGTG	
			AGT TACC CT T TTTCAC	
			C A T_ GT	
GAM39	MAB21L1	5'	CACTTTTCCTCCATTTGA 12111	ATTGT
			TCAAATGGG GAAAGTG	
			AGTTTACCT TTTTCAC	
			CC____	
GAM39	MMP14	5'	CACTTTGAGGAACAATCCCCTT 11434	T G_____
	T		AAA GGGATTGT AAAGTG	
			TTT CCCTAACA TTTCAC	
			C AGGAG	
GAM39	OPA1	3'	CACTCTCTATATCCATTTGA 28321	ATTGT A
			TCAAATGGG GA AGTG	
			AGTTTACCT CT TCAC	
			ATAT_ C	
GAM39	OPA1	3'	CACTCTCTATATCCATTTGA 28329	ATTGT A
			TCAAATGGG GA AGTG	
			AGTTTACCT CT TCAC	
			ATAT_ C	
GAM39	OPA1	3'	CACTCTCTATATCCATTTGA 28337	ATTGT A
			TCAAATGGG GA AGTG	
			AGTTTACCT CT TCAC	
			ATAT_ C	
GAM39	OPA1	3'	CACTCTCTATATCCATTTGA 28345	ATTGT A
			TCAAATGGG GA AGTG	
			AGTTTACCT CT TCAC	
			ATAT_ C	
GAM39	OPA1	3'	CACTCTCTATATCCATTTGA 28353	ATTGT A
			TCAAATGGG GA AGTG	

			AGTTTACCT	CT TCAC		
			ATAT_ C			
GAM39	SLC16A2	3'	CACTCTCACCAAGTCACCA	13267	_ _	A
			TGG GATT GTGA AGTG			
			ACC CTGA CACT TCAC			
			A AC C			
GAM39	ZNF192	3'	CACTCTTAGAATTCCCATT	12986	_ G	A
			AAATGGGA TT TGA AGTG			
			TTTACCCT AA ATT TCAC			
			T G C			
GAM39	ALS2CR3	3'	CACTTTTAAAAAATACCATT	17410	GATTG_	
	A		TCAAATGG TGAAAGTG			
			AGTTTACC ATTTTCAC			
			ATAAAAA			
GAM39	C3IP1	3'	CACTTCCACACTATTTATTTGG	22273	AT_ A	
			TCAAATGGG TGTG AAGTG			
			GGTTTATTT ACAC TTCAC			
			ATC C			
GAM39	DKFZp761J139	3'	CATGTAACAATCCCATTGGA	26035	A	GAAA
			TC AATGGGATTGT GTG			
			AG TTACCCTAACA TAC			
			G ATG_			
GAM39	FLJ10468	3'	CACCCTCCCATCCAGCTGA	19873	AA	T T AA
			TCA TGGGAT G GA GTG			
			AGT ACCCTA C CT CAC			
			CG _C CC			
GAM39	FLJ10781	3'	CACTTTGATTCCCATT	20133	TT G	
			TCAAATGGGA GT AAAGTG			
			GGTTTACCCT TA TTTAC			
			_ G			
GAM39	FLJ11175	3'	CACCCCAGAGTCCTCAT	20361	_ G	AAA
			TCAAATG GGATT TG GTG			
			AGTTTAC CCTGA AC CAC			
			T G CC_			
GAM39	FLJ20972	3'	CACCCTTATATCCTCAT	24625	AT	AA
			TCAAATGGG TGTGA GTG			
			AGTTTACTC ATATT CAC			
			CT CC			
GAM39	FLJ23233	3'	CACCTCCAGTCTCATT	23999	T	AA
			AATGGGATTG GA GTG			

			TTACTCTGAC CT CAC		
			_ C_		
GAM39	HRIHFB2122	3'	CACTTCCTGCCCCATTTGG	13897	ATT A_
			TCAAATGGG GTG AAGTG		
			GGTTTACCC CGT TTCAC		
			_ CC		
GAM39	KIAA0016	3'	CACTTTCCTCCATTTG	16529	ATTGT
			CAAATGGG GAAAGTG		
			GTTTACCT CTTTCAC		
			CC_		
GAM39	KIAA0459	3'	CACTTCCAATGCCAGTTTGA	30572	_ G T A
			TCAA TGG ATTG GAA GTG		
			AGTTT ACC TAAC CTT CAC		
			G G _ _		
GAM39	KIAA0712	3'	CACTTCATTCTCCCCGTCTGA	16263	A ATT_ A
			TCA ATGGG GTGAA GTG		
			AGT TGCCC TACTT CAC		
			C CTCT _		
GAM39	KIAA0773	3'	CACTTTCATTTTCAATTGA	16194	A GG TT
			TCAA TG A GTGAAAGTG		
			AGTT AC T TACTTTCAC		
			A TT_		
GAM39	KIAA0930	3'	CATGGTCCAGCCCCATTTGA	34912	AT T AA
			TCAAATGGG TG GA GTG		
			AGTTTACCC AC CT TAC		
			CG _ GG		
GAM39	KIAA0976	3'	CACTCGACATCCCATTTCGG	17164	A T GAA
			TC AATGGGAT GT AGTG		
			GG TTACCCTA CA TCAC		
			C _ GC_		
GAM39	KIAA1046	3'	CACTTTCACTTTACACTTG	17219	A GG TT
			CAA TG A GTGAAAGTG		
			GTT AC T CACTTTCAC		
			C AT T_		
GAM39	KIAA1143	3'	CACTTTCATTTTTCATCTG	34072	A GG TT
			CA ATG A GTGAAAGTG		
			GT TAC T TACTTTCAC		
			C TT T_		
GAM39	KIAA1580	5'	CACTTCGCCCTCCCCATTTGA	34410	ATT_ A
			TCAAATGGG GTGAA GTG		

			AGTTTACCC CGCTT CAC	
			CTCC _	
GAM39	KIAA1715	3'	ACTTGACCCTATTTGA 33788	ATT GA
			TCAAATGGG GT AAGT	
			AGTTTATCC CA TTCA	
			_ G _	
GAM39	PLSCR4	3'	CACCTTTGTATCTCATTTGA 21621	T TG A
			TCAAATGGGAT G AA GTG	
			AGTTTACTCTA T TT CAC	
			_ GT C	
GAM39	PSTPIP2	3'	CACTTTCACAAATATTTGG 23679	GGA
			TCAAATG TTGTGAAAGTG	
			GGTTTAT AACACTTTCAC	
			A _	
GAM39	RAI15	3'	CACCCACACCCCCATTTGG 33116	AT AAA
			TCAAATGGG TGTG GTG	
			GGTTTACCC ACAC CAC	
			CC C _	
GAM39	RNAH	3'	CTGAACAATCCATTTGA 31037	G GAA
			TCAAATGG ATTGT AG	
			AGTTTACC TAACA TC	
			_ AG _	
GAM39	SSH1	3'	CACTTTCACTGTGGATTTGG 21054	GGGATT
			TCAAAT GTGAAAGTG	
			GGTTTA CACTTTCAC	
			GGTGT _	
GAM39	TUBB5	3'	CACCCTCTATGAGTCCCATT 12728	GT _ AA
			AAATGGGATT GA GTG	
			TTTACCCTGA CT CAC	
			GTAT CC	
GAM39	LOC112687	3'	CACTTTCACACTTGCCAT 36065	_ AT _
			ATG GG TGTGAAAGTG	
			TAC CC ACACTTTCAC	
			T GTTC	
GAM39	LOC127602	5'	CACCTTCACCCACCATGTGA 36903	A GATT A
			TCA ATGG GTGAA GTG	
			AGT TACC CACTT CAC	
			G ACC _ C	
GAM39	LOC143425	3'	CACTTTCACACCACTTGG 42350	A GAT
			TCAA TGG TGTGAAAGTG	

		GGTT ACC ACAC TTTCAC		
		C _ _		
GAM39	LOC145725 5'	CACTCTCCAGCCATTTGG 37946	GA	T A
		TCAAATGG TTG GA AGTG		
		GGTTTACC GAC CT TCAC		
		_ _ C		
GAM39	LOC145732 5'	CACTCTCCAGCCATTTGG 37955	GA	T A
		TCAAATGG TTG GA AGTG		
		GGTTTACC GAC CT TCAC		
		_ _ C		
GAM39	LOC151623 5'	CACTCCCCGCAGTCCCCCTGA 41378	AAT	AA_
		TCA GGGATTGTG AGTG		
		AGT CCCTGACGC TCAC		
		CC_ CCC		
GAM39	LOC196957 5'	CACTCTCCAGCCATTTGG 42428	GA	T A
		TCAAATGG TTG GA AGTG		
		GGTTTACC GAC CT TCAC		
		_ _ C		
GAM39	LOC196961 5'	CACTCTCCAGCCATTTGG 42437	GA	T A
		TCAAATGG TTG GA AGTG		
		GGTTTACC GAC CT TCAC		
		_ _ C		
GAM39	LOC197138 5'	CACTCTCCAGCCATTTGG 42455	GA	T A
		TCAAATGG TTG GA AGTG		
		GGTTTACC GAC CT TCAC		
		_ _ C		
GAM39	LOC197414 3'	CACCTTCATAGTCACATTCGA 42513	A G	A
		TC AATG GATTGTGAA GTG		
		AG TTAC CTGATACTT CAC		
		C A C		
GAM39	LOC219406 5'	GCTCCAAAATCCCATTTGA 44939	G	AA
		TCAAATGGGATT TG AGT		
		AGTTTACCCTAA AC TCG		
		A C_		
GAM39	LOC222486 5'	CACTTTCACAATTAGCAT 45299	G_	
		ATG GATTGTGAAAGTG		
		TAC TTAACACTTTCAC		
		GA		
GAM39	LOC253731 5'	CACTCTCCCTATCCCATTAGA 46562	A	TGT A
		TC AATGGGAT GA AGTG		

			AG TTACCCTA CT TCAC		
			A TCC C		
GAM39	LOC255461	5'	CACTCCCCGCAGTCCCCCTGA 46464	AAT	AA_
			TCA GGGATTGTG AGTG		
			AGT CCCTGACGC TCAC		
			CC_ CCC		
GAM39	LOC255516	5'	CACTCCCCGCAGTCCCCCTGA 46470	AAT	AA_
			TCA GGGATTGTG AGTG		
			AGT CCCTGACGC TCAC		
			CC_ CCC		
GAM39	LOC92095	3'	CACTTTCACAAAAACGTT 33773	GGA_	
			AATG TTGTGAAAGTG		
			TTGC AACACTTTCAC		
			AAAA		
GAM39	LOC92096	3'	CACTTTCACAAAAACGTT 33776	GGA_	
			AATG TTGTGAAAGTG		
			TTGC AACACTTTCAC		
			AAAA		
GAM40	ALDH1B1	3'	CAAACATCCCAAATGTCCA 6348	ATGGC GC	A
			TGGA TT GGGAT TTTG		
			ACCT AA CCCTA AAAC		
			GT__ A_ C		
GAM40	MEL	3'	CAAGACACAAGGCATTCCA 11842	G	CGGGATA
			TGGAATG CTTG TTTG		
			ACCTTAC GAAC GAAC		
			G ACA__		
GAM40	UBE4B	3'	CCAAATGTGGCAAACCAACCCC 12681	AA_ C	GGG
	A		TGG TGG TTGC ATATTTGG		
			ACC ACC AACG TGTAACCC		
			CCA A G_		
GAM40	LOC146517	3'	ATCCCAAAGCCATTCCA 38181	GC	
			TGGAATGGCTT GGGAT		
			ACCTTACCGAA CCCTA		
			A_		
GAM40	LOC158230	3'	CCAAATTCGGCAAGCCATCCA 39765	A	G AT
			TGGA TGGCTTGC GGAT TTGG		
			ACCT ACCGAACG CTTA AACC		
			_ G _		
GAM40	LOC204970	5'	CCGAGGCCCCCAAGCCATCCCA 43067	A	C ATA
			TGG ATGGCTTG GGG TTTGG		

ACC TACCGAAC CCC GAGCC
C _ CG_
GAM40 LOC254065 5' CAAATATTCAACAACTCCA 46521 ATG C CG
TGGA G TTG GGATATTTG
|||| | ||| |||||
ACCT C AAC CTTATAAAC
_ _ _ AA
GAM41 ERMAP 3' CCATCACCATCCAGCCCAGCA 20607 A A TCTTCTC
TG TGG CT GGTGATGG
|| ||| || |||||
AC ACC GA CCACTACC
G C CCTA _
GAM41 Rab11-FIP3 3' CCATCACCAAGACTGGCCA 16226 A TCT C
TGG CT TCT GGTGATGG
||| || ||| |||||
ACC GG AGA CCACTACC
_ TC_ A
GAM41 LOC85028 5' CCATCAAGACTGAGAAAAAGCA 27584 A GA C _
CACCA TG TG CTT TTCTCGGT GATGG
|| || ||| ||||| |||||
AC AC GAA AAGAGTCA CTACC
C AC A GAA
GAM42 CLTCL1 3' CAGAGCCACAACAACA 31835 T AA G
TGTT GT TG GGTCTG
|||| || ||| |||||
ACAA CA AC CCGAGAC
_ _ _ A
GAM42 DYRK1A 5' TCAGAACTTAATTTACAAATAA 28188 TG_
TTGTTTGTA GGGTTCTGA
||||||| |||||
AATAAACATT TTCAAGACT
TAA
GAM42 LPIN2 3' TTCAAAACAAAATGTTACAACA 16063 T GG_ C
ATA TATTGTT GTAATG GTT TGAA
||||| ||||| ||| |||
ATAACAA CATTGT CAA ACTT
_ AAAA A
GAM42 OMD 3' TCAGAATACCAAAACAA 11455 GTAA GG
TTGTTT TGG TTCTGA
||||| ||| |||||
AACAAA ACC AAGACT
_ _ AT
GAM42 ZNF304 3' CAGAACCCCATAGGCAAG 21828 A_
TTTGT ATGGGGTTCTG
||||| |||||
GAACG TACCCCAAGAC
GA
GAM42 LOC150622 5' TTCAGAACCATCCTAACAATA 38998 TGTAATGG
TATTGTT GGTCTGAA
||||| |||||

			ATAACAA CCAAGACTT		
			TCCTA__		
GAM42	LOC152925	3'	CAGTGGCACATTACAAACAGTA 39330	GG	_
			TATTGTTTGTAAATG GTT CTG		
			ATGACAAACATTAC CGG GAC		
			A_ T		
GAM42	LOC205355	5'	TTCAGAACCCCTAGAGCAAT 43596	GTAAT	
			ATTGTTT GGGGTTCTGAA		
			TAACGAG CCCCAAGACTT		
			AT__		
GAM42	LOC220766	5'	CAGCAACCATCACAAATAA 43648	A	GGTT
			TTGTTTGT ATGG CTG		
			AATAAACA TACC GAC		
			C AAC_		
GAM42	LOC92270	5'	CAGAATTCACAACAATA 34062	T AAT	GG
			TATTGTT GT G GTTCTG		
			ATAACAA CA C TAAGAC		
			_ __ TT		
GAM43	MGAT5	5'	CATGTGCAGGGTTTATGGTAAT 8237	C	GAC
	G		TATTACCA AGATT GCACATG		
			GTAATGGT TTTGG CGTGTAC		
			A GA_		
GAM43	YWHAZ	3'	ATGTATATCTGTGGAATA 9443	A	TGACGC
			TATT CCACAGAT ACAT		
			ATAA GGTGTCTA TGTA		
			_ TA__		
GAM43	LRRN3	5'	CATGTGTGCATATCTATAGTA 34399	CAC	_ A
			TAC AGAT TG CGCACATG		
			ATG TCTA AC GTGTGTAC		
			ATA T _		
GAM43	SCDGF-B	3'	GTTGTCAATTGTGGTAA 24881	A	C
			TTACCACAG TTGACG AC		
			AATGGTGTT AACTGT TG		
			_ _		
GAM43	SCDGF-B	3'	GTTGTCAATTGTGGTAA 26983	A	C
			TTACCACAG TTGACG AC		
			AATGGTGTT AACTGT TG		
			_ _		
GAM43	LOC151248	3'	GCGTATCTATGGTAATA 39089	C	TG
			TATTACCA AGAT ACGC		

			ATAATGGT TCTA TGCG		
			A _		
GAM44	LOC132671	3'	TCTAATAATAACATTTAAA 29778		
			TTTAAATGTTATTATTGGA		
			AAATTTACAATAATAATCT		
GAM45	GNAI3	3'	AAACAATCTTAACTATGCACA 13237	ACA	ATG
			TGT CATG AAGATTGTTT		
			ACA GTAT TTCTAACAAA		
			C_ CAA		
GAM45	AKAP6	3'	GTCTTCATCATCATACA 10490	CAC	
			TGTA ATGATGAAGAT		
			ACAT TACTACTTCTG		
			AC_		
GAM45	ARGBP2	5'	TAAACAATCTCTACATGT 9658	A	A
			ACATG TG AGATTGTTTA		
			TGTAC AT TCTAACAAAT		
			_ C		
GAM45	ARGBP2	5'	TAAACAATCTCTACATGT 22042	A	A
			ACATG TG AGATTGTTTA		
			TGTAC AT TCTAACAAAT		
			_ C		
GAM45	FLJ10922	3'	AAACTGCCCATCATGTGCAC 20251	A	AAGATT
			GT CACATGATG GTTT		
			CA GTGTACTAC CAAA		
			C CCGT_		
GAM45	FLJ20666	3'	CAACTTCATCATCTACA 19580	CAC	A
			TGTA ATGATGAAG TTG		
			ACAT TACTACTTC AAC		
			C_ _		
GAM45	HRMT1L3	5'	GTCCATCATGTGTCCA 21259	T	AA
			TG ACACATGATG GAT		
			AC TGTGTACTAC CTG		
			C _		
GAM45	KIAA0373	5'	GTTTCCATCATGTGTACA 16185		A
			TGTACACATGATG AGAT		
			ACATGTGTACTAC TTTG		
			C		
GAM45	ZFR	3'	AAAGAACTTCATCATTGTACA 18186	C	A G
			TGTACA ATGATGAAG TT TTT		

ACATGT TACTACTTC AA AAA
 _ _ G
 GAM45 LOC221271 3' AAATGGTCTCATACACGTACA 44122 ACATG A TG
 TGTAC ATGA GAT TTT
 |||| ||| ||| |||
 ACATG TACT CTG AAA
 CACA_ _ GT
 GAM45 LOC221876 5' TAAATTTTACTCCAACCATGTG 45079 A_ A ATT_
 TACA TGTACACATG TG AG GTTTA
 ||||| || || ||||
 ACATGTGTAC AC TC TAAAT
 CA C ATTT
 GAM46 COX15 3' TTGGATATACCTAGATT 10600 A GA
 GATCTA GTA TATCCAA
 |||| || |||||
 TTAGAT CAT ATAGGTT
 C _
 GAM46 CXCL6 3' GATATCTATTGTGGATCTT 8884 _
 AAGATCTA AGTAGATATC
 ||||| |||||
 TTCTAGGT TTATCTATAG
 G
 GAM46 EFNB2 3' TGGACAGCTTACCTAGTCTTGT 10298 T A _ATA
 A TACAAGA CTA GTA G TCCA
 ||||| || ||| |||
 ATGTTCT GAT CAT C AGGT
 _ C T GAC
 GAM46 GBP1 3' GATAATAATTAGATCTTG 7810 G GA
 CAAGATCTAA TA TATC
 ||||| || |||
 GTTCTAGATT AT ATAG
 A A_
 GAM46 MEF2A 5' TGGACCTCAGATCTTGTA 12119 AAGTA TA
 TACAAGATCT GA TCCA
 ||||| || |||
 ATGTTCTAGA CT AGGT
 _ CC
 GAM46 PPP1CB 3' GATATCTGTTTAATCTT 8559 C
 AAGAT TAAGTAGATATC
 |||| |||||
 TTCTA ATTTGTCTATAG
 _
 GAM46 BIVM 3' GGAGCAGATCTTGTG 19256 AA AGATA
 TACAAGATCT GT TCC
 ||||| || |||
 GTGTTCTAGA CG AGG
 _ _
 GAM46 CDH26 3' TTGGATATCTAAAAGTCT 22373 T AAG
 AGA CT TAGATATCCAA
 || || |||||

			TCT GA ATCTATAGGTT		
			_ AA_		
GAM46	FLJ10961	3'	GATAATAATTAGATCTTG 31777	G GA	
			CAAGATCTAA TA TATC		
			GTTCTAGATT AT ATAG		
			A A_		
GAM46	HTMP10	3'	TGGGGTCCTTAGATC 27051	TA A	
			GATCTAAG GAT TCCA		
			CTAGATTC CTG GGGT		
			— —		
GAM46	KIAA0471	5'	TGGATACCTACTTAGTGCT 16916	AT A	
			AG CTAAGTAG TATCCA		
			TC GATTCATC ATAGGT		
			GT C		
GAM46	KIAA1493	3'	GACATCTACTTGGGAGCTGT 32090	AGA A	
			ACA TCTAAGTAGAT TC		
			TGT GGGTTCATCTA AG		
			CGA C		
GAM46	KIAA1634	3'	ATCTGCTTAACTTGTA 31749	ATC	
			TACAAG TAAGTAGAT		
			ATGTTC ATTCGTCTA		
			A_		
GAM46	KIAA1877	3'	TTGGATCTTTCTAGATCTT 32888	A T T	
			AAGATCTA G AGA ATCCAA		
			TTCTAGAT C TTT TAGGTT		
			— — C		
GAM46	MAL2	3'	GTGAATACTTAGATTTGTA 27470	A GA	
			TACA GATCTAAGTA TAT		
			ATGT TTAGATTCAT GTG		
			— AA		
GAM46	SB52	3'	TGAATATTTATATCTTGTA 28735	CTAA C	
			TACAAGAT GTAGATAT CA		
			ATGTTCTA TATTTATA GT		
			— — A		
GAM46	LOC150848	5'	TTGGACCTCACAAATCTTGTA 41262	CTAA A TA	
			TACAAGAT GT GA TCCAA		
			ATGTTCTA CA CT AGGTT		
			AA_ _ CC		
GAM47	ASPH	3'	GCTATTAAGAGTACTTTGTGTT 26223	A _ CC	
	A		TAATACAAA TAC CT AATAGC		

			ATTGTGTTT ATG GA TTATCG	
			C A A_	
GAM47	EIF5A2	3'	CTTTTGGACTTTGTATTA 21659	ATACC T
			TAATACAAA TCCAA AG	
			ATTATGTTT AGGTT TC	
			C____ T	
GAM47	RP42	3'	GCTACAGGGAATATTTTGTA 21801	CC AA_
			TACAAAATA TCC TAGC	
			ATGTTTTAT AGG ATCG	
			A_ GAC	
GAM47	SFRS2	3'	GCTATTGAAAAGGTTATTTTGT 32504	_ C__
	A		TACAAAATA CCT CAATAGC	
			ATGTTTTAT GGA GTTATCG	
			T AAA	
GAM47	TSG	3'	GCTCTTGGACACATTTTGTATT 21811	ACC T
	A		TAATACAAAAT TCCAA AGC	
			ATTATGTTTTA AGGTT TCG	
			CAC C	
GAM47	KIAA1332	3'	GCTATTGCTGTACCTTGTGTTA 35258	AA CTC
			TAATACAA TAC CAATAGC	
			ATTGTGTT ATG GTTATCG	
			CC TC_	
GAM47	KIAA1912	3'	GCTATGATAGGTATTTTGTGTT 36313	CCA
	A		TAATACAAAATACCT ATAGC	
			ATTGTGTTTTATGGA TATCG	
			TAG	
GAM47	LOC127534	3'	GCTACTGGGGATTTTGTAT 37172	A T A
			ATACAAAAT CC CCA TAGC	
			TATGTTTTA GG GGT ATCG	
			_ _ C	
GAM47	LOC146880	3'	CTATGTTTGGTATTTTGTCTTA 38259	T TCCA
			TAA ACAAATACC ATAG	
			ATT TGTTTTATGG TATC	
			C TTTG	
GAM47	LOC221656	3'	GCTTCTAGGTATTTTGTATTG 44294	CCAAT
			TAATACAAAATACCT AGC	
			GTTATGTTTTATGGA TCG	
			TCT__	
GAM48	CLCN5	5'	CATAAACTGAAATACCTAA 5535	ACATTAGG
			TTAGGTATTTTA ATG	

			AATCCATAAAGT	TAC		
			CAA_			
GAM48	ATP9A	3'	CCATCCTACTTAAACACCTA	31079	AT	CAT
			TAGGT TTAA TAGGATGG			
			ATCCA AAATT ATCCTACC			
			C_ C_			
GAM48	KIAA1383	3'	CCAGGCATTTAAATACCTAA	34583		CATTAGGA
			TTAGGTATTTTAA	TGG		
			AATCCATAAAATT	ACC		
			TACGG_			
GAM48	LOC219722	3'	CCATCCTAGGCAAAAACCTCC	44708	TA	AACA
			GG TTTT TTAGGATGG			
			CC AAAA GATCCTACC			
			TC ACG_			
GAM49	IGJ	3'	GTGAAAATCAGGAGGTGTAATA	29472	CG	CAATATA
			TAT CACC ATTTTCAC			
			ATA GTGG TAAAAGTG			
			AT AGGAC_			
GAM49	ATP6M8-9	3'	GTGAAAATCATATTTGGGC	12327	A C	A
			GC CC AATAT ATTTTCAC			
			CG GG TTATA TAAAAGTG			
			_ T C			
GAM49	KIAA0447	3'	AAAATTAGCTGGGTGCGATG	35490		ATA
			TATCGCACCCA TAATTTT			
			GTAGCGTGGGT ATTAAAA			
			CG_			
GAM49	MGC11352	3'	TGAAAATTAATGGATGC	32356	C	ATA
			GCA CCA TAATTTTCA			
			CGT GGT ATTAAAAGT			
			A A_			
GAM49	LOC136015	3'	GTGAAAATTATTGCGTGC	37500	C	TA
			GCAC CAATA ATTTTCAC			
			CGTG GTTAT TAAAAGTG			
			C _			
GAM49	LOC154788	3'	GTGAAAATTATTGCGTGC	41725	C	TA
			GCAC CAATA ATTTTCAC			
			CGTG GTTAT TAAAAGTG			
			C _			
GAM50	INPP5B	3'	CACAAAAATGTCTTCC	45733	AAGT	
			GGA GGATATTTTGTG			

CCT TCTGTAAAAACAC

GAM50 ZNF18 3' CACAAAAATACTCAGCTCC 38249 AAG GA
GGA TG TATTTTTGTG
||| || |||||
CCT AC ATAAAAACAC
CG_ TC

GAM50 CAMKK2 3' CACAAACCCTCCATCCACTTCC 13310 A ATT____
C GG AAGTGGAT TTTGTG
|| ||||| |||||
CC TTCACCTA AAACAC
C CCTCCC

GAM50 DKFZp547H025 3' CACAAAAATGGTCTTTCT 21368 TGGA
GGAAAG TATTTTTGTG
||||| |||||
TCTTTC GTAAAAACAC
TG_

GAM51 DES 3' AGGGTGGACTTAGAAAGCA 35692 C A
TGC TTCTAA TCTATTTT
||| ||||| |||||
ACG AAGATT AGGTGGGA
A C

GAM51 FGF2 3' GCTTGAAAATAAATTATGGGG 7741 TC ATC
CCT TAA TATTTTCAAGC
||| ||| |||||
GGG ATT ATAAAAGTTCG
GT AA_

GAM51 PDE4B 3' CTTGAGTTTGGAGTCAGAAAGC 8467 C AAA TT
A TGC TTCT TCTA TTCAAG
||| ||| ||| |||||
ACG AAGA AGGT GAGTTC
A CTG TT

GAM51 RERE 3' GCTTGAAAACCGTCCGAAGGCA 14407 TAAATCTA
TGCCTTC TTTTCAAGC
||||| |||||
ACGGAAG AAAAGTTCG
CCTGCC_

GAM51 ARG99 3' GCTTGAAATGCTATGAAGGCA 25670 TAAATCTAT
TGCCTTC TTTCAAGC
||||| |||||
ACGGAAG AAAGTTCG
TATCGT_

GAM51 FLJ12592 3' CTCGAAAAGTTGTGATTAGAA 25872 C TA____ A
GACA TG CTTCTAAATC TTTTC AG
|| ||||| |||||
AC GAAGATTTAG AAAAG TC
A TGTTG C

GAM51 KIAA0266 3' TTGAAACTGGAAGGCA 22312 AATCTAT
TGCCTTCTA TTTCAA
||||| |||||

		ACGGAAGGT	AAAGTT		
		C_____			
GAM51	KIAA0478	3' CTTGAAGCGCAGAAGGCA	16979	AAATCTAT	
		TGCCTTCT	TTTCAAG		
		ACGGAAGA	GAAGTTC		
		CGC_____			
GAM51	KIAA0493	5' GGGACAGACTTGAAGGCA	32143	T A A	
		TGCCTTC	AA TCT TTTT		
		ACGGAAG	TT AGA AGGG		
		_ C C			
GAM51	LOC127428	3' GCTTTGGAGATTTGGAAAGCA	36900	C	ATTTTC
		TGC	TTCTAAATCT AAGC		
		ACG	AAGGTTTAGA TTCG		
		A	GGT_____		
GAM51	LOC152313	3' AATGGATGACTTAGAAGG	41470	_____	
		CCTTCTAA	ATCTATT		
		GGAAGATT	TAGGTAA		
		CAG			
GAM51	LOC201952	5' TTGAAAGCTAAAGGCA	43397	CTAAATC	_
		TGCCTT	TA TTTTCAA		
		ACGGAA	AT GAAAGTT		
		_____ C			
GAM51	LOC220672	3' GCTTGAAATTACATTCAGAAG	30308	A C T	
		CTTCT	AAT TA TTTCAAGC		
		GAAGA	TTA AT AAAGTTCG		
		C C T			
GAM51	LOC221395	3' GCTCAAAAATGGAAACTGAAAG	44184	C TAAA	CA
	CA	TGC	TTC TCTATTTT AGC		
		ACG	AAG AGGTAAAA TCG		
		A	TCAA AC		
GAM51	LOC256529	5' CTTGAAAGCGGATTCAGAGGAC	46588	C A TA	
	A	TG	CTTCT AATC TTTTCAAG		
		AC	GGAGA TTAG GAAAGTTC		
		A	C GC		
GAM52	KIAA0205	3' CAAAAATAAATGCGAACAT	17002	A GA	
		ATGTTC	GTA TATTTTTG		
		TACAAG	CGT ATAAAAAC		
		_ AA			
GAM52	SLC5A7	3' CAAAATCTTCACTGAATATC	22389	A TAT	
		GATGTT	CAGT GA TTTTG		

			CTATAAGTCA CT AAAAC		
			_ TCT		
GAM53	ACO1	3'	CTGAGGGTCTGGTGCCA 7954 A	GAGA	
			TG CACCAGACCT CAG		
			AC GTGGTCTGGG GTC		
			C A__		
GAM53	ATRN	3'	CTGTCTCAACTGTGCA 29300 A C ACC		
			TG CAC AG TGAGACAG		
			AC GTG TC ACTCTGTC		
			_ _ A__		
GAM53	DTX1	5'	GCTGTTTCCTCCGGCATAAGA 10679	GACA A CCT	
			TCT CC GA GAGACAGC		
			AGA GG CT CTTTGTCTG		
			ATAC C C__		
GAM53	FBXW1B	3'	GTCATCTCTGGTGTCAG 14664	CCT _	
			CTGACACCAGA GA GAC		
			GA CTGTGGTCT CT CTG		
			_ A		
GAM53	FBXW1B	3'	GTCATCTCTGGTGTCAG 27366	CCT _	
			CTGACACCAGA GA GAC		
			GA CTGTGGTCT CT CTG		
			_ A		
GAM53	FBXW1B	3'	GTCATCTCTGGTGTCAG 27376	CCT _	
			CTGACACCAGA GA GAC		
			GA CTGTGGTCT CT CTG		
			_ A		
GAM53	GAB2	3'	CTTAGGGAGGTTGGTGTCAGA 14651	GA__	
			TCTGACACCA CCTGAG		
			AGACTGTGGT GGATTC		
			TGGAG		
GAM53	GAB2	3'	CTTAGGGAGGTTGGTGTCAGA 27846	GA__	
			TCTGACACCA CCTGAG		
			AGACTGTGGT GGATTC		
			TGGAG		
GAM53	GRINL1A	3'	GTATCAAGATCAGTGTCAGA 34445	CA C _ G	
			TCTGACAC GA CT GA AC		
			AGACTGTG CT GA CT TG		
			A_ A A A		
GAM53	NFRKB	5'	GTTCCAGAACTGATGTCAGA 12822	C AC AG	
			TCTGACA CAG CTG AC		

			AGACTGT GTC GAC TG			
			A AA CT			
GAM53	SH3BP2	3'	GCTGCCTCAGGTCAGGCCAGG 8949	ACA A	A	
			TCTG CC GACCTGAG CAGC			
			GGAC GG CTGGA CTC GTCG			
			C__ A C			
GAM53	SHC1	3'	CTTGGCCTTGTGTCAGA 8971	C A T		
			TCTGACAC AG CC GAG			
			AGACTGTG TC GG TTC			
			T C _			
GAM53	SLC19A1	3'	GCCATCTCAGGTTGGCGGCAGA 9022	ACA A	CA	
			TCTG CCAG CCTGAGA GC			
			AGAC GGTT GGA CTC CG			
			GGC _ AC			
GAM53	ABLIM	3'	GCTGTCTCTCTGACACCAG 8116	ACAC	CCT	
			CTG CAGA GAGACAGC			
			GAC GTCT CTCTGTCG			
			CACA ____			
GAM53	ABLIM	3'	GCTGTCTCTCTGACACCAG 13549	ACAC	CCT	
			CTG CAGA GAGACAGC			
			GAC GTCT CTCTGTCG			
			CACA ____			
GAM53	APOL6	3'	CTCCAGTCTGGGTGTCAGA 24969	_	CT	
			TCTGACACC AGAC GAG			
			AGACTGTGG TCTG CTC			
			G AC			
GAM53	BICD2	3'	GTGTTTGTCTGGTGTGTCAG 34852	CT G		
			CTGACACCAGAC GA AC			
			GACTGTGGTCTG TT TG			
			T_ G			
GAM53	CHST4	3'	CTGCCACCTGGTGTGTCAG 12337	ACC AGA		
			CTGACACCAG TG CAG			
			GACTGTGGTC AC GTC			
			C__ C__			
GAM53	DKFZP434I0714	5'	CTGTTTCAGGTCTGACTCA 41530	CAC		
			TGA CAGACCTGAGACAG			
			ACT GTCTGGA CTTTGTC			
			CA_			
GAM53	EIF5	3'	TGTTTCAGTCTGGTGCCA 7701	A C A		
			TG CACCAGAC TGAG CA			

			AC GTGGTCTG ACTT GT		
			C _ _		
GAM53	FLJ00001	3'	GCTGCCTCACTCTGTGGTGTCA 39783	GACC_	A
		GG	TCTGACACCA TGAG CAGC		
			GGACTGTGGT ACTC GTCG		
			GTCTC C		
GAM53	FLJ10101	3'	GCTGTGCGTCCTGGTGTGAGA 24048	_	CTGA
			TCTGACACCAG AC GACAGC		
			AGACTGTGGTC TG CTGTGCG		
			C ____		
GAM53	FLJ10209	5'	GCTCAATCAGATCCTGGTGTCA 19769	AC_	GAC
		GA	TCTGACACCAG CTGA AGC		
			AGACTGTGGTC GACT TCG		
			CTA AAC		
GAM53	FLJ20344	3'	CTGTCTCAGTTGTCAGA 19404	CCAGAC	
			TCTGACA CTGAGACAG		
			AGACTGT GACTCTGTC		
			T ____		
GAM53	GIT2	3'	TCTGAGATCTGGTGTGAGA 27687	C	G
			TCTGACACCAGA CT AGA		
			AGACTGTGGTCT GA TCT		
			A G		
GAM53	GIT2	3'	TCTGAGATCTGGTGTGAGA 27700	C	G
			TCTGACACCAGA CT AGA		
			AGACTGTGGTCT GA TCT		
			A G		
GAM53	GIT2	3'	TCTGAGATCTGGTGTGAGA 16605	C	G
			TCTGACACCAGA CT AGA		
			AGACTGTGGTCT GA TCT		
			A G		
GAM53	GL004	3'	GTCATGGTCTGGTGCCAGA 32829	A	TGA
			TCTG CACCAGACC GAC		
			AGAC GTGGTCTGG CTG		
			C TA_		
GAM53	KIAA0174	3'	GCTGTTTCCCTTGTAACAGA 38432	AC C	ACCT
			TCTG AC AG GAGACAGC		
			AGAC TG TC CTTTGTGCG		
			CA T C ____		
GAM53	KIAA0562	3'	GCTGTCTCAGGCCTTCCTTAGA 16243	CACC	A
			TCTGA AG CCTGAGACAGC		

AGATT TC GGACTCTGTCG
 CCT_ C
 GAM53 KIAA0652 3' GCTGTTTGTCTCCAGGTGTCAG 16409 ____ CTG
 A TCTGACACC AGAC AGACAGC
 ||||| ||| |||||
 AGACTGTGG TCTG TTTGTCG
 ACC ____
 GAM53 KIAA0876 3' GCTTTGATGGTCTGGTGCCAG 32299 A TGA C
 CTG CACCAGACC GA AGC
 || ||||| || |||
 GAC GTGGTCTGG TT TCG
 C TAG _
 GAM53 KIAA0960 5' GCTATTGTTCCCTGGTGTTAGA 44520 ACCTGA C
 TCTGACACCAG GA AGC
 ||||| || |||
 AGATTGTGGTC TT TCG
 CCTTG_ A
 GAM53 KIAA1303 3' GCTGTCTTCACAGGTCTGATGT 32834 C ____
 ACA CAGACCTG AGACAGC
 || ||||| |||||
 TGT GTCTGGAC TCTGTCG
 A ACT
 GAM53 KIAA1423 3' CTGCACTCCAGCCTGGGTGTCA 30920 AGAC _ A_
 GA TCTGACACC CTG AG CAG
 ||||| ||| || |||
 AGACTGTGG GAC TC GTC
 GTCC C AC
 GAM53 KIAA1701 3' GCTGTTTTGTCTGACACCAGA 33685 ACAC CT
 TCTG CAGAC GAGACAGC
 ||| ||| |||||
 AGAC GTCTG TTTGTCG
 CACA ____
 GAM53 MGC16179 3' TGAGACAGCACTGTTTGGTGCC 26514 A _____ AGA
 AGA CTG CACCAGAC CTG CA
 || ||||| || |||
 GAC GTGGTTTG GAC GT
 C TC|||C AGA
 GAM53 MKP-7 3' GCTGGTTCACTAGTGTGTCAGA 33008 C ACC A
 TCTGACAC AG TGAG CAGC
 ||||| || ||| |||
 AGACTGTG TC ACTT GTCG
 A ____ G
 GAM53 PRO1770 3' GCTATTTGTGTTTAGTGTGTCAGA 15326 C CTG C
 TCTGACAC AGAC AGA AGC
 ||||| ||| || |||
 AGACTGTG TTTG TTT TCG
 A TG_ A
 GAM53 Rab11-FIP2 3' CTCAAAGTCTGGTGTAGA 17097 A C_
 TCTG CACCAGAC TGAG
 ||| ||||| |||

			AGAT GTGGTCTG ACTC		
			— AA		
GAM53	UBXD2	3'	CTTGACTCGGTGTCAGA 33913	A CC	
			TCTGACACC GA TGAG		
			AGACTGTGG CT GTTC		
			— CA		
GAM53	LOC147054	5'	CTGTCTCATCACTGCCAGA 40792	ACAC ACC	
			TCTG CAG TGAGACAG		
			AGAC GTC ACTCTGTC		
			C__ ACT		
GAM53	LOC154881	3'	CTATCTCATGTGTTAGA 39497	CAGACC C	
			TCTGACAC TGAGA AG		
			AGATTGTG ACTCT TC		
			T_____ A		
GAM53	LOC157858	5'	CTGCCTCAGGTTGACAGA 41867	ACACCA A	
			TCTG GACCTGAG CAG		
			AGAC TTGGACTC GTC		
			AG_____ C		
GAM53	LOC196047	5'	GCTGCAGGGTCTGGCATCAG 43146	CA GAGA	
			CTGA CCAGACCT CAGC		
			GA CT GGTCTGGG GTCG		
			AC AC__		
GAM53	LOC253286	5'	GCTGGCAGAATCCTGGTGTCA 46585	AC__ AGA	
			TGACACCAG CTG CAGC		
			ACTGTGGTC GAC GTCG		
			CTAA G__		
GAM54	PRRG1	3'	CCCATAAATGGGTAACATATTC 6653	T TATG__	
			CTAA TTAGGAAT TGTT TTATGGG		
			AATCCTTA ACAA AATACCC		
			T TGGGTA		
GAM55	ALX3	3'	CCACCTCTTTTCCATTCC 13221	CA ATTAT	
			GGAA GAAAAAGA TGG		
			CCTT CTTTTTCT ACC		
			AC CC__		
GAM55	ARHGAP6	5'	TCCACAGCGTCTTCTCCTGTTC 6848	AAA ATTAT	
			CT AGGAACAG AAGA TGGG		
			TCCTTGTC TTCT ACCT		
			CTC GCGAC		
GAM55	ARHGEF6	3'	AGTTCCTTTTCTGTCCT 33842	A A	
			AGGA CAGAAAA GAATT		

			TCCT GTCTTTT CTTGA		
			— C		
GAM55	ATF7	3'	TCTTTGGTCATTTTTCTGCTCC 13726	A	GA TT
	T		AGGA CAGAAAAA ATTA GGA		
			TCCT GTCTTTT TGGT TCT		
			C AC T_		
GAM55	BAT1	5'	TCTTTGTTTTCTTTGCTGTTT 11015	A A	TTATT
	CT		AGGAACAG AAA GAA GGA		
			TCCTTGTC TTT CTT TCT		
			G C TTGTT		
GAM55	CD34	3'	CCAACAGATGCTTTTCTGTCTC 7532	GA	AGA A_
	T		AG ACAGAAAA ATT TTGG		
			TC TGTCTTTT TAG AACCC		
			TC CG_ AC		
GAM55	DYRK2	3'	TCTGCTTTTCTCCTCTCTGTTT 13210	AAA_	TTATT
	CT		AGGAACAGA AGAA GGA		
			TCCTTGTC TCTT TCT		
			CTCC TTCG_		
GAM55	DYRK2	3'	TCTGCTTTTCTCCTCTCTGTTT 9635	AAA_	TTATT
	CT		AGGAACAGA AGAA GGA		
			TCCTTGTC TCTT TCT		
			CTCC TTCG_		
GAM55	FGF23	3'	CCAGAATGGCCCCACTCTGTTT 21791	AAAAGA__	A
	C		GGAACAGA ATT TTGG		
			CCTTGTC TAA GACC		
			CACCCCGG _		
GAM55	FOX E1	3'	TCCAATAACTCTCCCCCTTTTCC 10785	C AAAA	A
			GGAA AG AGA TTATTGGA		
			CCTT TC TCT AATAACCT		
			_ CCCC C		
GAM55	GRINL1A	3'	TAATTCTCCCTCTGTCCT 34446	A AAA	
			AGGA CAGA AGAATTA		
			TCCT GTCT TCTTAAT		
			_ CCC		
GAM55	GRLF1	3'	TCCAGTGCCCTCCCTCTGTTCC 38416	AAA AAT	
			GGAACAGA AG TATTGGA		
			CCTTGTC TC GTGACCT		
			CCC CC_		
GAM55	LPL	3'	TCCAGTGCGTCTCTTTTGTTC 5752	AA AT	
	T		AGGAACAGAA AGA TATTGGA		

			TCCTTGTTTT TCT GTGACCT		
			C_ GC		
GAM55	MAGEB4	3'	CCTGCTGCTTTCTCTGTTCT 8175	A	AATTATT
			AGGAACAGA AAAG GG		
			TCCTTGTCT TTTC CC		
			C GTCGT__		
GAM55	MAP3K14	3'	CAGGGATCTTTTTCTGCCCCT 10090	AA	ATTA
			AGG CAGAAAAAGA TTG		
			TCC GTCTTTTCT GAC		
			CC AGG_		
GAM55	MPP2	3'	CCAGTGCGCTTCCTCTGTTCC 30081	AA	AAT
			GGAACAGA AAG TATTGG		
			CCTTGTCT TTC GTGACC		
			CC GC_		
GAM55	MUC3B	3'	TCGGTGTTCTGCCCCTACTCC 45258	AC	AAAA
			GGA AG AGAATTATTGG		
			CCT TC TCTTGGTGGCT		
			CA CCCG		
GAM55	NUP98	3'	CCAGGGTATTCTTTTTCCATCC 18441	ACA	TA_
			GGA GAAAAAGAAT TTGG		
			CCT CTTTTCTTA GACC		
			AC_ TGG		
GAM55	PAFAH1B1	3'	CCGTTGCGCTCTTTCTGTTTCT 6009	A	AATTAT
			AGGAACAGAAA AG TGG		
			TCTTTGTCTTT TC GCC		
			C CGCTT_		
GAM55	PMP2	3'	CCAATCAGTGTCTTTTCTGTT 8544	A	_ _
	CC		GGAACAGAAAA GA ATT ATTGG		
			CCTTGTCTTTT CT TGA TAACC		
			C G C		
GAM55	RFX5	3'	CCTTCCTTTTCCTGTTTCT 6046	A	AATTATT
			AGGAACAG AAAAG GG		
			TCTTTGTC TTTC CC		
			C CTT_____		
GAM55	RNF4	3'	CCAGGCCATCTCTGTTCT 8839	AAAA	ATTA
			AGGAACAGA GA TTGG		
			TCCTTGTCT CT GACC		
			_____ ACCG		
GAM55	SALL1	3'	CCGCCCCTTCCTTCTGTTCC 8878	AAA	TTAT
			GGAACAGAA GAA TGG		

			CCTTGTCTT CTT GCC		
			C__ CCCC		
GAM55	TAP2	3'	TCCTATATCCTTCCTTGTTCCT 6142	AAA AAT T	
			AGGAACAG AAG TAT GGA		
			TCCTTGTT TTC ATA CCT		
			CC_ CT_ T		
GAM55	USH3A	3'	CCAATCGTTCTCTGTTCC 27560	AAAA T	
			GGAACAGA GAAT ATTGG		
			CCTTGTCT CTTG TAACC		
			_____ C		
GAM55	24432	5'	CCAGCCCTTGTTCTGTTCC 23225	A AATTA	
			GGAACAGAA AAG TTGG		
			CCTTGTCTT TTC GACC		
			G CC__		
GAM55	BOP	5'	TCGCTGGTCCTTTTTCTTTCC 41210	C A T	
			GGAA AGAAAAAG ATTA TGG		
			CCTT TCTTTTTC TGGT GCT		
			_ C C		
GAM55	C5orf7	3'	GATTCTTTTTCTCCCCCT 31942	AAC	
			AGG AGAAAAAGAATT		
			TCC TCTTTTCTTAG		
			CCC		
GAM55	C6orf26	3'	CCAGGCTCCTTTTTCTGTTTCT 24928	AATTA	
			AGGAACAGAAAAAG TTGG		
			TCTTTGTCTTTTTC GACC		
			CTCG_		
GAM55	CHRA1	3'	CCAGGACATTCCCCTCTGTTCC 18902	AAAA TA_	
	T		AGGAACAGA GAAT TTGG		
			TCCTTGTCT CTTA GACC		
			CCC_ CAG		
GAM55	CHRA1	3'	CCTCTGTTCTCTGTTCCCT 18903	AAAA TATT	
			AGGAACAGA GAAT GG		
			TCCTTGTCT CTTG CC		
			C__ TCT_		
GAM55	DKFZP434C171	3'	CCACTTAGTTTCTTTTTCATTTC 17883	CA _ T_	
	CT		AGGAA GAAAAAGAA TTA TGG		
			TCCTT CTTTTTCTT GAT ACC		
			A_ T TC		
GAM55	DT1P1A10	3'	TCCACCCTCTCCCCTGTTCCCT 30859	AAAA ATTAT	
			AGGAACAG AGA TGGA		

				TCCTTGTC	TCT	ACCT		
				CCC_	CCC_			
GAM55	FKBP4	3'	CCATTTCTTCTCTCTGTTCC	7754	AAA	TTAT		
			GGAACAGA	AGAA	TGG			
			CCTTGTCT	TCTT	ACC			
			C_	CTTT				
GAM55	FLJ11539	3'	CCGGCTTCCTTTTCTGTCC	24086	A	A	TTA	
			GGA	CAGAAAA	GAA	TTGG		
			CCT	GTCTTTT	CTT	GGCC		
			_	C	C_			
GAM55	FLJ14735	3'	CCAGTATTCTTTTTCTTTTCC	26607	C	T		
			GGAA	AGAAAAAGAAT	ATTGG			
			CCTT	TCTTTTCTTA	TGACC			
			T	_				
GAM55	FLJ14950	3'	TCCATATCTGTTCTCTGTTC	26677	AAAA	TAT_		
		T	AGGAACAGA	GAAT	TGGA			
			TCCTTGTC	CTTG	ACCT			
			C_	TCTAT				
GAM55	FLJ20079	3'	TCCAAGTTCTCTCTGTTC	19177	AA	A		
			GGAACAGAA	AGAATT	TTGGA			
			CCTTGTC	TCTTGG	AACCT			
			C_	_				
GAM55	FLJ21596	3'	TCTGTGATTCTTTTCCCTCC	24214	ACA	T		
			GGA	GAAAAAGAATTAT	GG			
			CCT	CTTTTCTTAGTG	CT			
			CCC	T				
GAM55	FLJ22195	3'	CCAATAGTCCCTGCTCCT	22997	A	AAAAA	A	
			AGGA	CAG	GA	TTATTGG		
			TCCT	GTC	CT	GATAACC		
			C	C_	_			
GAM55	GOLPH3	3'	TTGAGTTTCTTTTCTGTCC	22689	A	TTA	TG	
			GGA	CAGAAAAAGAA	T	G		
			CCT	GTCTTTTCTT	A	T		
			_	TG_	GT			
GAM55	KIAA0295	3'	CCAAGGTTCCCTCTGTTCCT	33779	AAAA	A		
			AGGAACAGA	GAATT	TTGG			
			TCCTTGTC	CTTGG	AACC			
			CTCC	_				
GAM55	KIAA0599	3'	CCAGATTCTTTTATCC	37855	ACA	AT		
			GGA	GAAAAAGAATT	TGG			

CCT TTTTCTTAG ACC
 A__ __
 GAM55 KIAA0825 3' TCCAAAGGTTCTTTCATTCC 30594 CAGAA TA
 GGAA AAAGAAT TTGGA
 ||| ||||| ||||
 CCTT TTTCTTG AACCT
 AC__ GA
 GAM55 KIAA1030 3' TCAGTTCCTCTCCTGTTCT 44822 AAAA ATT
 AGGAACAG AGA ATTGG
 ||||| || ||||
 TCCTTGTC TCT TGA CT
 C__ CCT
 GAM55 KIAA1126 3' TCCTTGTGTCTGTTTCTCTGTT 35610 AAA__ ATTATT
 CCT AGGAACAGA AGA GGA
 ||||| || ||
 TCCTTGTCT TCT CCT
 CTTTG GTGTT_
 GAM55 KIAA1464 3' TCCAAGTTGTTTACTCTGTTCC 33887 AAAA TA_
 T AGGAACAGA GAAT TTGGA
 ||||| || ||||
 TCCTTGTCT TTTG AACCT
 CA__ TTG
 GAM55 KIAA1535 3' TCTGGTTATCTTCCTGTTCT 38767 AAA ATT TG
 AGGAACAG AAGA AT GA
 ||||| ||| || ||
 TCCTTGTC TTCT TG CT
 C__ AT_ GT
 GAM55 KIAA1536 3' TCATTGGTTCCTCTTTCTGTTTC 21923 AA_ T
 C GGAACAGAAA GAATTA TGG
 ||||| ||||| ||
 CCTTGTCTTT CTTGGT ACT
 CTC T
 GAM55 KIAA1655 5' CCAAATCTCTTCTGTTCC 33084 AA ATTA
 GGAACAGAA AGA TTGG
 ||||| || ||||
 CCTTGTCTT TCT AACC
 C_ A__
 GAM55 KIAA1805 3' AATTCTTTTCTGTACCT 38999 A
 AGG ACAGAAAAAGAATT
 || ||||| |||||
 TCC TGTCTTTTCTTAA
 A
 GAM55 MAP2K6 3' CCAATTTTCTTTTACTCC 25701 ACAG TT
 GGA AAAAAGAA ATTGG
 || ||||| ||||
 CCT TTTTCTT TAACC
 CA__ T_
 GAM55 MAP2K6 3' CCAATTTTCTTTTACTCC 8642 ACAG TT
 GGA AAAAAGAA ATTGG
 || ||||| ||||

			CCT TTTTCTT TAACC		
			CA__ T_		
GAM55	MY014	3'	CCAATAACTCTTTTTTTTTTCC	25190	C A
	T		AGGAA AGAAAAAGA TTATTGG		
			TCCTT TTTTTTCT AATAACC		
			T C		
GAM55	NCOA2	3'	CCATGCTCTTGTCTGTTCCCT	13294	A ATTAT
			AGGAACAGAA AAGA TGG		
			TCCTTGTCTT TTCT ACC		
			G CGT__		
GAM55	SLC38A5	5'	CCATCTGTCTTTCTGTCCCT	27296	A AA ATTAT
			AGG ACAGAA AGA TGG		
			TCC TGTCTT TCT ACC		
			C __ GTCT_		
GAM55	TOM1	3'	CCATCCTTCCTCTGTTCCCT	11985	AA AATTAT
			AGGAACAGA AAG TGG		
			TCCTTGTCT TTC ACC		
			CC CT__		
GAM55	TTYH2	3'	TCCTGCCTCCTTTTTCCGTTCT	26379	A AATTATT
			GGAAC GAAAAAG GGA		
			TCTTG CTTTTTC CCT		
			C CTCCGT_		
GAM55	UGT2B10	3'	CCAATAAAGCTCGGTTCCCT	6736	AGAAAA AA
			AGGAAC AG TTATTGG		
			TCCTTG TC AATAACC		
			GC__ GA		
GAM55	ZNF238	3'	CCTTTTTCTTTTTCTCCCCT	13043	AAC TTATT
			AGG AGAAAAAGAA GG		
			TCC TCTTTTTCTT CC		
			CC_ TTT__		
GAM55	LOC144893	3'	TAATTCCTTCTGTTCCCT	40462	AAA
			AGGAACAGAA GAATTA		
			TCCTTGTCTT TTTAAT		
			CC_		
GAM55	LOC147042	3'	TCCAGTGAGCCTCCTTCAACTC	40787	ACA AA AA
	CT		AGGA GAA AG TTATTGGA		
			TCCT CTT TC AGTGACCT		
			CAA CC CG		
GAM55	LOC147093	5'	TCAGTTCCTTTCTCTGTTCCCT	40805	A AATT
			AGGAACAGA AAAG ATTGG		

		TCCTTGTCT TTTC TGACT			
		C CT__			
GAM55	LOC147645 3'	TCCCAATTCTTTCTCTGCCCC 38360	AA	A	ATT
		GG CAGA AAAGAATT GGA			
		CC GTCT TTTCTTAA CCT			
		CC C C__			
GAM55	LOC150299 3'	CCAATAATCTTATCCACTCC 41181	ACA	AA	A
		GGA GA AAGA TTATTGG			
		CCT CT TTCT AATAACC			
		CAC A_ _			
GAM55	LOC151647 3'	TCCAAAGGGTCCTCATTCTGTT 39157	AA	A	A_
	CCT	AGGAACAGAA AG ATT TTGGA			
		TCCTTGTCTT TC TGG AACCT			
		AC C GA			
GAM55	LOC152274 3'	TCTGGACTTTCTTTCTGTTCC 39236	AA	TTA	TG
	T	AGGAACAGAAA GAA T GA			
		TCCTTGTCTTT CTT G CT			
		C_ TCA GT			
GAM55	LOC152275 3'	TCTATTTTCTTCTTCTGTTCC 41459	A	TTAT	
		GGAACAGAA AAGAA TGGA			
		CCTTGTCTT TTCTT ATCT			
		C TT__			
GAM55	LOC152313 5'	CAATCCTTCTTTGTTCCCT 41473	GAAA	TT	
		AGGAACA AAGAA ATTG			
		TCCTTGT TTCTT TAAC			
		____ CC			
GAM55	LOC153196 5'	TCCACGAGACTCTTTTCTGTCC 41592	A	A A	AT_
	CT	AGG ACAGAAAA GA TT TGGA			
		TCC TGTCTTTT CT AG ACCT			
		C _ C AGC			
GAM55	LOC157909 5'	TCCAATCCTTTTCTGTACCT 39679	A	AATT	
		AGG ACAGAAAAAG ATTGGA			
		TCC TGTCTTTTTC TAACCT			
		A C__			
GAM55	LOC158450 5'	TCTACTGCTTTTCTACTCCT 39844	AC	AATTAT	
		AGGA AGAAAAAG TGGA			
		TCCT TCTTTTTC ATCT			
		CA GTC__			
GAM55	LOC158504 5'	TCTACTGCTTTTCTACTCCT 39855	AC	AATTAT	
		AGGA AGAAAAAG TGGA			

		TCCT TCTTTTTC ATCT		
		CA GTC__		
GAM55	LOC200205 3'	CCATGTTTCCCCACCTCTGTTC 42735	AAAA__	TTAT
	CT	AGGAACAGA GAA TGG		
		TCCTTGTCT CTT ACC		
		CCACCC TGT_		
GAM55	LOC200261 3'	CCGACTTCCTTTTTTTGCTCCT 42749	A	AATTA
		AGGA CAGAAAAAG TTGG		
		TCCT GTTTTTTTC AGCC		
		C CTC_		
GAM55	LOC222662 3'	CCAAGTTTCCTTGTTTCCT 44602	AAAAA	TTA
		AGGAACAG GAA TTGG		
		TCCTTGTT CTT AACC		
		C__ TG_		
GAM55	LOC254556 3'	CCAGGCCATCTCTGTTTCCT 45392	AAAA	ATTA
		AGGAACAGA GA TTGG		
		TCCTTGTCT CT GACC		
		__ ACCG		
GAM55	LOC254707 5'	TCCATGCAACTTCCTGTTCCT 46554	AAA	AATTAT
		AGGAACAG AAG TGG		
		TCCTTGTC TTC ACCT		
		CC_ AACGT_		
GAM55	LOC257612 5'	CCGGAACCCCTTCCTGTTCCT 46740	AAA	AATTA_
		AGGAACAG AAG TTGG		
		TCCTTGTC TTC GGCC		
		C_ CCCCA		
GAM55	LOC51652 3'	CCAATAGTTACTTTTCTGGTCC 18152	A	AG
	T	AGGA CAGAAAA AATTATTGG		
		TCCT GTCTTTT TTGATAACC		
		G CA		
GAM55	LOC90520 3'	CCTGCTTTCTTTCTGTTCC 31631	AA	TTATT
		GGAACAGAA AGAA GG		
		CCTTGTCTT TCTT CC		
		__ TCGT_		
GAM55	LOC91050 3'	TCCAACATGGTTCTTCTGTTCC 32339	AAA	__
		GGAACAGA AGAATTAT TGGA		
		CCTTGTCT TCTTGGTA ACCT		
		__ CA		
GAM56	C9orf14 5'	AATCAAGACCTCATTAC 41908	AT	ATAC
		GTAATGA GT CTTGATT		

			CATTACT CA GAACTAA		
			C_ _ _ _		
GAM56	LOC143187	3'	TAATCAAGGGAGAAACCCATTA	29745	AATGTATA
		C	GTAATG CCTTGATTA		
			CATTAC GGAACATAAT		
			CCAAAGAG		
GAM56	LOC158332	3'	TAATCAAGGCATGGGTATTGC	39824	GA G A
			GTAAT AT TAT CCTTGATTA		
			CGTTA TG GTA GGAACATAAT		
			_ G C		
GAM57	CKN1	3'	TTTTATTCTTTCTTCTTCA	5533	A T
			TGAA AAGAAAGA ATAGAG		
			ACTT TTCTTTCT TATTTT		
			C _		
GAM57	DVL3	3'	GCTCTCTTTATCTTTCTCTCTC	10699	AAA T T
	A		TGA AGAAAGATA AGAGG GC		
			ACT TCTTTCTAT TCTCT CG		
			CTC T _		
GAM57	EGF	3'	CACAGTATCTTTTCTTTCA	7688	AA AGAG
			TGAAA GAAAGATAT GTG		
			ACTTT TTTTCTATG CAC		
			C_ A_		
GAM57	EVC	3'	GCACCTCTGCCTTCTTCCT	15885	A TA_
			AG AAGA TAGAGGTGC		
			TC TTCT GTCTCCACG		
			C TCC		
GAM57	EVX1	5'	GCACCCGGCCTTTCTTTCTC	7713	A ATATAGA
			GA AAAGAAAG GGTGC		
			CT TTTCTTTC CCACG		
			C CGGC_		
GAM57	FANCE	3'	CTATATTTTCTTTTCA	22447	A
			TGAAAAAGAA GATATAG		
			ACTTTTCTT TTATATC		
			_		
GAM57	FKBP1A	3'	CACCTCTGTTTCCTCTT	6472	AA T
			AAGA GA ATAGAGGTG		
			TTCT CT TGTCTCCAC		
			C_ T		
GAM57	GNAI1	3'	TTATATCATTTCTTTTCA	7843	_
			TGAAAAAGAAA GATATAG		

A

GAM57	GOCAP1	3'	CACCTCAGAGATTTTTCTTTCTTCA	22938	A	ATA_
			A AAGAAAGAT GAGGTG			
			A TTCTTTTCTA CTCCAC			
			C GAGA			
GAM57	MLLT2	3'	CACAGATTTTTCTTTTCTA	12568		ATAGAG
			TGAAAAAGAAAGAT GTG			
			ACTTTTCTTTTCTA CAC			
			GA_			
GAM57	NID	3'	GCACTGATGTCCCTCCTTTTCT	8340	AA AT	GA
	A		TGAAAAAG AG ATA GGTGC			
			ACTTTTCT TC TGT TCACG			
			C_ CC AG			
GAM57	NT5E	3'	ACCATATTTTTCTTCTTCA	8364	A	AGA
			TGAA AAGAAAGATAT GGT			
			ACTT TTCTTTTCTA CCA			
			C _			
GAM57	SMARCC1	3'	GCCTAATCTCTCTCTTTTCTA	9041	A	TATAG
			TGAAAAAGA AGA AGGT			
			ACTTTTCT TCT TCCG			
			C CTAA_			
GAM57	SUFU	3'	GCCCGTATCTTTCTCTTC	18256	AA	AGA
			GAA AGAAAGATAT GGT			
			CTT TCTTTCTATG CCG			
			C_ C_			
GAM57	ATP1B4	3'	GCACCTGAATTCTTTTCTTCA	14325	AA	TATAG
			TGAA AGAAAGA AGGTGC			
			ACTT TTTTCT TCCACG			
			C_ TAAG_			
GAM57	COE2	3'	GCACTCAGCATCTTTGTTCTTC	32128	A G	ATA G
	A		TGAA AA AAAGAT GAG TGC			
			ACTT TT TTTCTA CTC ACG			
			C G CGA _			
GAM57	DKFZP564O0423	3'	GCACCTCTATAGCCTTACTCA	44066	A A	A_
			A AG AAG TATAGAGGTGC			
			A TC TTC ATATCTCCACG			
			C A CG			
GAM57	FLJ10420	3'	GCACCTCTGACATTCCTTTT	19856	A	GATA
			AAAAG AA TAGAGGTGC			

TTTTC TT GTCTCCACG
 C ACA_
 GAM57 FLJ11117 3' GCACCTCTATACCTCAGCT 20327 AA_ A
 AG AG TATAGAGGTGC
 || || |||||
 TC TC ATATCTCCACG
 GAC C
 GAM57 FLJ14457 3' CACCTCTATGCACTTCTTTCT 26542 ____
 AGAAAGA TATAGAGGTG
 ||||| |||||
 TCTTTCT GTATCTCCAC
 TCAC
 GAM57 FLJ23231 3' GCACCTCTAGCTGTCTGCCTCA 24679 A AA ____
 A AG AGATA TAGAGGTGC
 || ||||| |||||
 A TC TCTGT ATCTCCACG
 C CG CG
 GAM57 FLJ31978 3' GCACCCCTTGTGTTTTCCCTCT 29490 ____ A_
 AGA AAGATATAG GGTGC
 || ||||| |||||
 TCT TTTGTGTT CCACG
 CCC CC
 GAM57 FLJ32334 3' GCACCTCTTGTTCCTTTTC 29367 A T
 GAAAAAG AAGATA AGAGGTGC
 ||||| ||||| |||||
 CTTTTTC TTTTGT TCTCCACG
 C _
 GAM57 GBTS1 3' GCACCTCTCTCCTCTGTCTTCA 29729 A A TAT_
 A AAGA AGA AGAGGTGC
 ||||| ||||| |||||
 A TTCT TCT TCTCCACG
 C G CCTC
 GAM57 ITM3 3' GCACCTTTTTCCCTTTTCCTTCT 25195 A A ATAT
 CA TGA AA GAAAG AGAGGTGC
 ||||| ||||| |||||
 ACT TT CTTTC TTTCCACG
 C C CCTT
 GAM57 KIAA0350 3' GCACCTCTTTCTTCCTCTGTCA 30671 AAA A TAT
 TGA AG AAGA AGAGGTGC
 ||||| ||||| |||||
 ACT TC TTCT TCTCCACG
 GTC C T__
 GAM57 KIAA0663 3' CACCTCTACCAATCCATCTTCA 16811 A AA A__
 A AAGA GAT TAGAGGTG
 ||||| ||||| |||||
 A TTCT CTA ATCTCCAC
 C AC ACC
 GAM57 KIAA0795 3' GCACCTCTTAATTCATTTTCA 24585 A AGATAT
 TGAAAA GAA AGAGGTGC
 ||||| ||||| |||||

			ACTTTT CTT TCTCCACG		
			A AAT__		
GAM57	KIAA1010	3'	ACTGGATGTCTTTCTTCTTCA 35668	A	AGA
			TGAA AAGAAAGATAT GGT		
			ACTT TTCTTTCTGTA TCA		
			C GG_		
GAM57	KIAA1210	3'	CACCTCCCTTCCCTTTTTC 46085	AAA	TATA
			TGAAAAAG GA GAGGTG		
			ATTTTTTC CT CTCCAC		
			C_ TCC_		
GAM57	KIAA1210	3'	CACCTCCCTTCCCTTTTTC 46086	AA	TATA
			TGAAAAAGA GA GAGGTG		
			ACTTTTTTT CT CTCCAC		
			C_ TCC_		
GAM57	KIAA1508	5'	GCACCTCTCTGGTCTTCCCTTT 30994	A_	AT_
			AAAG AAGAT AGAGGTGC		
			TTTC TTCTG TCTCCACG		
			CC GTC		
GAM57	KIAA1775	3'	CACCTCTACTTCTGTTCTTCCC 26941	AA_	_ TA
			TCA TGA AAGAA AGA TAGAGGTG		
			ACT TTCTT TCT ATCTCCAC		
			CCC G TC		
GAM57	KIAA1829	3'	CACCATCACCATCCTTTTTC 31029	AAA	ATA _
			TGAAAAAG GAT GA GGTG		
			ACTTTTTC CTA CT CCAC		
			_ CCA A		
GAM57	PCDH10	3'	GCACTATCTATCTTTCT 26769	TA	_
			AGAAAGA TAGA GGTGC		
			TCTTTCT ATCT TCACG		
			_ A		
GAM57	TRIP-Br2	3'	GCACCCTTGCTTGCCTTTTTC 16491	A_	ATAT A
			TGAAAAAG AAG AG GGTGC		
			ACTTTTTC TTC TC CCACG		
			CG GT_ _		
GAM57	LOC115073	3'	ACAAATGCATCTTTCTTTTGTG 36236	_	A GAG
			A TGA AAAAGAAAGAT TA GT		
			ACT TTTCTTTCTA GT CA		
			G C AAA		
GAM57	LOC128344	3'	CACCTCCCTCCTTTTTC 36922	AAA	TATA
			GAAAAAG GA GAGGTG		

		CTTTTTC CT CTCCAC	
		___ CC___	
GAM57	LOC143452 5'	GCACCTCTGTTTTCCCTTCT 37622	A_ T_
		AGAA GA ATAGAGGTGC	
		TCTT CT TGTCTCCACG	
		CC TT	
GAM57	LOC144308 3'	GCACCATGTTCCGTTCCCTTTTT 40407	_ AGAT GA
	CA	TGAAAAAG AA ATA GGTGC	
		ACTTTTTC TT TGT CCACG	
		C GCCT A_	
GAM57	LOC152573 3'	CTACATGTTTCTTTTTCA 39288	G A
		TGAAAAAGAAA AT TAG	
		ACTTTTCTTT TA ATC	
		G C	
GAM57	LOC201194 3'	CACCTCCATTGGGCCCTTTTTTC 43217	AAAGAT A
	A	TGAAAAAG AT GAGGTG	
		ACTTTTTC TA CTCCAC	
		CCGGGT C	
GAM57	LOC219899 3'	TCATATCTTTCTTTTTCA 43993	A
		TGAAAAAGAAAGATAT GA	
		ACTTTTCTTTCTATA CT	
		-	
GAM57	LOC253019 3'	CACCTCTACCAATCCATCTTCA 45666	A AA A_
		A AAGA GAT TAGAGGTG	
		A TTCT CTA ATCTCCAC	
		C AC ACC	
GAM57	LOC253975 3'	CACCTCTACCAATCCATCTTCA 45933	A AA A_
		A AAGA GAT TAGAGGTG	
		A TTCT CTA ATCTCCAC	
		C AC ACC	
GAM57	LOC257486 3'	CACCTCCCTTCCCTTTTTTA 34323	AAA TATA
		TGAAAAAG GA GAGGTG	
		ATTTTTC CT CTCCAC	
		C_ TCC_	
GAM57	LOC257486 3'	CACCTCCCTTCCCTTTTTTCA 34324	AA TATA
		TGAAAAAGA GA GAGGTG	
		ACTTTTTT CT CTCCAC	
		C_ TCC_	
GAM57	LOC51644 3'	CACCCTTCCTATTCTTTTTCA 18130	_ ATAT A
		TGAAAAAGAA AG AG GGTG	

ACTTTTTCTT TC TC CCAC
 A CT__ _
 GAM57 LOC90170 5' GCACCATTCATCTTTCTCA 30909 A AT _
 A AGAAAGAT AGA GGTGC
 | ||||| ||| ||||
 A TCTTTCTA TCT CCACG
 C C_ TA
 GAM57 LOC91208 5' CACCTCTGCAGTCCTCTTCA 32521 A AA A_
 A AAGA GAT TAGAGGTG
 | ||| ||| |||||
 A TTCT CTG GTCTCCAC
 C C_ AC
 GAM58 ETR101 3' CAGCCGAGAAGTTCCTGG 35829 T
 TCAGGAACTTCTCG GTTG
 ||||| ||||| ||||
 GGCCTTGAAGAGC CGAC
 -
 GAM59 DMRT1 3' CCTCCCAATCCAAAACGTA ACT 22481 GGA_ C
 G CAGTTACG GGAT GGGAGG
 ||||| ||| |||||
 GTCAATGC CCTA CCCTCC
 AAAA A
 GAM59 CAPN6 3' CCTCCCAATCCAAGTAGC 15567 GGGA C
 GTTAC GGAT GGGAGG
 |||| ||| |||||
 CGATG CCTA CCCTCC
 AA_ A
 GAM59 FLJ13769 3' CCTCCTGGATTCTGCAACT 24592 A GA
 AGTT CGGGAG TCGGGAGG
 ||| ||||| |||||
 TCAA GTCCTT GGCCTCC
 C A_
 GAM59 FLJ22167 5' CCCCCAATCCCCCAGATCCTG 23740 TTAC_ A C A
 TG TACAG GGG GGAT GGG GG
 |||| ||| ||||| ||| ||
 GTGTC CCC CCTA CCC CC
 CTAGA C A _
 GAM59 H-plk 5' CCTCCTGGTTCCCAACAAC 17983 ACG A
 GTT GG GGATCGGGAGG
 ||| ||| ||||| |||||
 CAA CC CTTGGTCCTCC
 CA_ _
 GAM60 CDH6 3' GACATCTGGAAACCTCTACATA 11373 _ A CAT
 TATGT GA GTTTCC TGTT
 |||| ||| ||||| ||||
 ATACA CT CAAAGG ACAG
 T C TCT
 GAM60 PMCHL1 3' TGAACAATGCTTAACATA 25632 G TTTCC
 TATGT AAG CATTGTCA
 |||| ||| ||||| ||||

			ATACA TTC	GTAACAAGT	
			A	_____	
GAM60	SERPINB9	3'	TGAGGTAACTTCACATA	10368	--
			TATGTGAAGTTT CC CA		
			ATACACTTCAAA GG GT		
			T A		
GAM60	SMCX	3'	GGAGGAGGAACTTCACATA	10397	CA G
			TATGTGAAGTTTCC TT TTC		
			ATACACTTCAAAGG AG AGG		
			___ G		
GAM60	UBE4A	3'	ACAGAGTAACTTCACATA	11193	TCCCA
			TATGTGAAGTT TTGT		
			ATACACTTCAA GACA		
			TGA___		
GAM60	ZNF141	3'	TGGAGAGAACTTCACATG	9497	___
			TATGTGAAGTTTC CCA		
			GTACACTTCAAAG GGT		
			AGA		
GAM60	ABCA9	3'	TGAACAATGAGAATACATG	27828	AAGT C
			TATGTG TTC CATTGTTCA		
			GTACAT AAG GTAACAAGT		
			___ A		
GAM60	KIAA0534	3'	CAGTAGGAAAACTTCAAATA	35382	G _ C
			TAT TGAAGTTT CC ATTG		
			ATA ACTTCAAA GG TGAC		
			A A A		
GAM60	KIAA1229	3'	TGAACAATGAGAATACATG	31102	AAGT C
			TATGTG TTC CATTGTTCA		
			GTACAT AAG GTAACAAGT		
			___ A		
GAM60	LOC129831	3'	TGAACAAGCACTTCACA	36982	TTCCCA
			TGTGAAGT TTGTTCA		
			ACACTTCA AACAAAGT		
			CG___		
GAM60	LOC151040	3'	TGAACAATGAGCACACATG	39045	AA TCC
			TATGTG GTT CATTGTTCA		
			GTACAC CGA GTAACAAGT		
			A_ ___		
GAM60	LOC254672	3'	TGAACAATGCTTAACATA	45399	G TTTCC
			TATGT AAG CATTGTTCA		

			ATACA TTC	GTAACAAGT		
			A	_____		
GAM60	LOC90843	3'	CAATTG	GAAACTTTTCACA	32116	_ C
			TGTGAA	GTTTCC ATTG		
			ACACTT	CAAAGG TAAC		
			T	T		
GAM60	LOC92568	3'	TGAACAATGAGATCACATG	34582		AGTT C
			TATGTGA	TC CATTGTTCA		
			GTAACT	AG GTAACAAGT		
			_____	A		
GAM61	FBXL5	5'	TTGGTTTGCTTCAACAA	27305		A GT
			TTGTTGAA	CAAA CCGA		
			AACA	ACTT GTTT GGTT		
			C	_____		
GAM61	GNAI1	3'	TCTGACCTTGTTTCAGCAAA	7841		A C
			TTTGTGAAACAA	GTC GA		
			AAACGACTTTGTT	CAG CT		
			C	T		
GAM61	GTF2F1	3'	TGAGACTCTGTCTCAATAAA	7885		A A _
			TTTGTGAA	ACA AGTC CG		
			AAATAACT	TGT TCAG GT		
			C	C A		
GAM61	KIAA0527	3'	TTGGATTATACCAACAAA	45851		AAACA
			TTTGTG	AAGTCCGA		
			AAACAAC	TTTAGGTT		
			CATA	_____		
GAM61	SYPL	3'	ATATTCATTCTTGTTTCACAAA	44644		T A TCC
			TTTGT	GAAACAA G GAATAT		
			AAACA	CTTTGTT C CTTATA		
			_____	_____TTA		
GAM61	LOC145820	3'	ATTCGGA	ACTTTCAACAAA	37989	CAAAG
			TTTGTGAAA	TCCGAAT		
			AAACA	ACTTT AGGCTTA		
			CA	_____		
GAM61	LOC201627	3'	TGAGACTGTGTCTCAACAAA	42898		A A _
			TTTGTGAA	ACA AGTC CG		
			AAACA	ACT TGT TCAG GT		
			C	G A		
GAM62	EYA1	3'	TCAATGTGATATAAACAGCTTC	6117		AG C TC__
			TCCA	TGGA AGC GTTTATATT		TGA

			ACCT TCG CAAATATAG ACT	
			CT A TGTA	
GAM62	LZTR1	5'	AAATAACCAACAACCTCTTCCA 13633	CC_ TA_
			TGGAAGAG GTT TATTT	
			ACCTTCTC CAA ATAAA	
			CAA CCA	
GAM62	ERAP140	3'	TCAGAAATGTGTGACCCTTC 37089	AGCC _
			GAAG GTT TATATTTCTGA	
			CTTC CAG GTGTAAAGACT	
			C__ T	
GAM62	KIAA1557	3'	CAAAAATGTGGAAGGCCTCCCA 30639	A A G C
			TGG AG GCC TTTATATTT TG	
			ACC TC CGG AGGTGTAAA AC	
			C _ A A	
GAM62	PRDM10	5'	TCAAAAATGAAGCCAGCTCTTC 21499	C_ A C
	C		GGAAGAGC GTTT TATTT TGA	
			CCTTCTCG CGAA GTAAA ACT	
			AC _ A	
GAM62	SRF	3'	CAGAAATGGGCAGTTCTCCCA 9097	A C TA
			TGG AGAGC GTT TATTTCTG	
			ACC TCTTG CGG GTAAAGAC	
			C A _	
GAM62	LOC148709	5'	CAGAAATGTAACCTCACCCA 38580	AA CCGT
			TGG GAG TTATATTTCTG	
			ACC CTC AATGTAAAGAC	
			CA _	
GAM62	LOC164295	5'	TCAGAGGAGAACGGCTGTTCCA 40143	G ATA
			TGGAA AGCCGTTT TTTCTGA	
			ACCTT TCGGCAAG GGAGACT	
			G A_	
GAM63	KIAA0061	3'	AAATATGGGCTCCTGATGGACC 33890	TAC A_ AT_
	TCA		TGAGGTCC CA AGC TATTT	
			ACTCCAGG GT TCG ATAAA	
			TA_ CC GGT	
GAM64	ANK1	3'	CCTGGAGGATCCCAAGTGAGCT 30284	C TCAGT
			AGC CATTG TCCTCCAGG	
			TCG GTGAC AGGAGGTCC	
			A CCT_	
GAM64	ATP8B2	3'	CCCAAAGGAACTGGATGGGCT 32511	GT CCA
			AGCCCATC CAGTTCCT GG	

			TCGGGTAG GTCAAGGA CC		
			— AAC		
GAM64	BLAME	3'	CCAGGATCTGACAATGAGC 21306 C T CCA		
			GC CATTGTCAG TCCT GG		
			CG GTAACAGTC AGGA CC		
			A T —		
GAM64	CDX1	3'	TCCTGGAGAAAAGGGATGGAGC 7557 _ G AG C		
	T		AGC CCATT TC TTC TCCAGGA		
			TCG GGTAG GG AAG AGGTCCT		
			A _ AA _		
GAM64	DGAT2	3'	CCTGGAGGAACCAGCTGC 26290 CCATT CA		
			GC GT GTTCCTCCAGG		
			CG CG CAAGGAGGTCC		
			T _ AC		
GAM64	FUT3	5'	TCCTGAAGGTCAGTACAA 5647 T_ C		
			TTGTCAGT CCT CAGGA		
			AACAGTCA GGA GTCCT		
			CT A		
GAM64	FUT8	3'	GGGAACTGACATAGGCT 10796 CAT		
			AGCC TGTCAGTTCCT		
			TCGG ACAGTCAAGGG		
			AT_		
GAM64	GJA5	5'	TCCTGGAGGAAGTACACAAGC 36902 CCA CAG_		
			GC TTGT TTCCTCCAGGA		
			CG AACA AAGGAGGTCCT		
			— CATG		
GAM64	INPP5D	3'	TCCTGGAGTGAGACAAGGGCT 40306 A AGT _		
			AGCCC TTGTC TC CTCCAGGA		
			TCGGG AACAG AG GAGGTCCT		
			_ _ T		
GAM64	PYGB	3'	TCCCGGAGGAACCCATTTGTGC 8768 C TTGTCA A		
	T		AGC CA GTTCCTCC GGA		
			TCG GT CAAGGAGG CCT		
			T TTACC_ C		
GAM64	SNTB2	3'	CCGAGGGGAGAACTGACCATGG 28378 T CT A_		
			CCAT GTCAGTTC CC GG		
			GGTA CAGTCAAG GG CC		
			C AG AG		
GAM64	TIMP3	3'	TCCCAGATGATGACAATG 5933 GT C CA		
			CATTGTCA TC TC GGA		

			GTAACAGT AG AG CCT		
			___ T AC		
GAM64	AP3D1	5'	TCCCAGAACCCACAGTGGGC 10049	CA	CTCCA
			GCCCATTTGT GTTC GGA		
			CGGGTGACA CAAG CCT		
			CC AC___		
GAM64	BRD2	5'	CCTGCAGACCAACAGCGGGCT 11574	A	CA TC C
			AGCCC TTGT GT CT CAGG		
			TCGGG GACA CA GA GTCC		
			C AC __ C		
GAM64	C17orf31	3'	CCCGGAAAAACTGACACTG 19001	T	CC A
			CA TGTCAGTT TCC GG		
			GT ACAGTCAA AGG CC		
			C AA C		
GAM64	CG018	5'	TCCTGGAGGAAGCTCATGA 27403	TG C	_
			T T AGTT CCTCCAGGA		
			A A TCGA GGAGGTCCT		
			GT C A		
GAM64	DKFZp434F142	3'	CCTGCCTGACAATGGCCT 25994	C	TTCCTC
			AG CCATTGTGTCAG CAGG		
			TC GGTAACAGTC GTCC		
			C C___		
GAM64	DNAJC5	3'	CCTGGAGGAAGGACTGACTGG 30812	TT	___
			CCA GTCAGT TCCTCCAGG		
			GGT CAGTCA AGGAGGTCC		
			___ GGA		
GAM64	FLJ11506	3'	CCCAGAGGAACTGATAAGC 23967	CCA	CA
			GC TTGTCAGTTCCTC GG		
			CG AATAGTCAAGGAG CC		
			___ AC		
GAM64	FLJ12190	3'	CCTGGAGGAAGAAGGGCT 24667	A	GTCAG
			AGCCC TT TTCCTCCAGG		
			TCGGG AG AAGGAGGTCC		
			A ___		
GAM64	FLJ14816	3'	CCTGGAGGGCAGCAATGG 26638	CA	T
			CCATTGT GT CCTCCAGG		
			GGTAACG CG GGAGGTCC		
			A_ _		
GAM64	IL14	5'	TCCTGGCTTCAGCAATGGGCT 45704		CAGTTCCT
			AGCCCATTGT CCAGGA		

			TCGGGTAACG	GGTCCT		
			ACTTC__			
GAM64	KIAA0265	3'	TCCTGGAAAACTATAA	34628	C	CC
			TTGT AGTT TCCAGGA			
			AATA TCAA AGGTCCT			
			_ AA			
GAM64	KIAA0495	5'	TCCCGGACCCGACAATGGGC	31363		AGTTCC A
			GCCCATTGTC TCC GGA			
			CGGGTAACAG AGG CCT			
			CCC__ C			
GAM64	KIAA1045	3'	TCCTGGAGATCCTAATGGGC	35200		TCAGTTC
			GCCCATTG CTCCAGGA			
			CGGGTAAT GAGGTCCT			
			CCTA__			
GAM64	KIAA1529	5'	TCCCAGAGGAACTGACTAAGGC	34948	CATT	CA
	T		AGCC GTCAGTTCCTC GGA			
			TCGG CAGTCAAGGAG CCT			
			AAT_ AC			
GAM64	KIAA1719	5'	CCTGGAGAGGCGGACGATGGGC	33819	A	TC
			GCCCATTGTC GT CTCCAGG			
			CGGGTAGCAG CG GAGGTCC			
			G GA			
GAM64	LRG	3'	TCCTAGAACACACGATGGGCT	27547	CA	CTCC
			AGCCCATTGT GTTC AGGA			
			TCGGGTAGCA CAAG TCCT			
			CA A__			
GAM64	MGC23980	3'	TCCTGAAGAAATAGATATAGCT	29607	CCAT	A C C
			AGC TGTC GTT CT CAGGA			
			TCG ATAG TAA GA GTCCT			
			AT__ A A A			
GAM64	MRPS10	3'	CCTGAAAGAGGCAAGACTACAA	19939	C	__ __
	TGGGCT		CCCATTGT AGTT CCTC CAGG			
			GGGTAACA TCAG GGAG GTCC			
			_ AAC AAA			
GAM64	NEIL2	3'	CCCGGAAGGCAATGGG	29673	AG	TCCA
			CCCATTGTC TTCC GG			
			GGGTAACGG AAGG CC			
			_ C__			
GAM64	PACSIN2	3'	CCTGGAAGGCAGATGAGCT	14096	C	GTCAGTT _
			AGC CATT CCT CCAGG			

			TCG GTAG	GGA GGTCC		
			A AC_____	A		
GAM64	PTK6	3'	CCTGCGCTGACAAGGGC	12599	A	TCCTC
			GCCC TTGTCAGT	CAGG		
			CGGG AACAGTCG	GTCC		
			_____	C_____		
GAM64	TAO1	3'	CCTGGAGGGCACTGAGCT	11190	CCATTG	_____
			AGC TCAGT TCCTCCAGG			
			TCG AGTCA GGGAGGTCC			
			_____	C		
GAM64	LOC123591	3'	CCTGGAGGCTGCCAAGGGC	37251	A T TT	
			GCCC TTG CAG CCTCCAGG			
			CGGG AAC GTC GGAGGTCC			
			_____	C		
GAM64	LOC143286	5'	TCCTGAAAGAGATGATGGACT	40356	C TG AGT CTC	
			AG CCAT TC TC CAGGA			
			TC GGTA AG AG GTCCT			
			A GT _____	AAA		
GAM64	LOC150271	5'	TCCCGGGTGCTGACAGCAAGCT	41175	CCA T CCA	
			AGC TTGTCAGT CCT GGA			
			TCG GACAGTCG GGG CCT			
			AAC T C_____			
GAM64	LOC151176	5'	CCTGGAGGCCATCATGGGC	41315	T TCAGTT	
			GCCCAT G CCTCCAGG			
			CGGGTA C GGAGGTCC			
			_____	TACC_____		
GAM64	LOC196478	5'	CCTGAATGACAATGGAGT	42379	_____	G TTCCTC
			GC CCATTGTCA CAGG			
			TG GGTAACAGT GTCC			
			A AA_____			
GAM64	LOC254268	3'	TCCTGGAGAACTGCAGGG	45692	AT T C	
			CCC TG CAGTT CTCCAGGA			
			GGG AC GTCAA GAGGTCCT			
			_____	A		
GAM64	LOC56912	5'	CCTAGCGACTGACAACAGGCT	21364	CA C CC	
			AGCC TTGTCAGTT CT AGG			
			TCGG AACAGTCAG GA TCC			
			AC C_____			
GAM64	LOC92710	3'	CCTCCAGGATCCTTACTAATAA	34834	C T_____	TCCA
			TGGGC CATTGT AG TCC GG			

			GTAATA TC	AGG CC		
			A ATTCCTIII	ACCT		
GAM64	LOC93190	5'	CCTAAAGGCTGACAGTG	35488	TT CC	
			CATTGTCAG CCT AGG			
			III III			
			GTGACAGTC GGA TCC			
			__ AA			
GAM65	B3GNT3	3'	GTGCACCTGCAGTGGTTTAA	15534	AC CC _	
			TTAAACCACT GT GTG AC			
			II III II			
			AATTGTTGA CG CAC TG			
			__ TC G			
GAM65	HTR4	3'	TGATCTTGGCTGTGGTTTAA	6546	TACGT T C	
			TTAAACCAC CCG GA CA			
			III II II			
			AATTGTTG GGT CT GT			
			TC__ T A			
GAM65	PSA	3'	CATTGGAGGAGTGGTTTAA	22129	ACG _	
			TTAAACCACT TCCG TG			
			III II			
			AATTGTTGA AGGT AC			
			GG_ T			
GAM65	PSA	3'	CATTGGAGGAGTGGTTTAA	27738	ACG _	
			TTAAACCACT TCCG TG			
			III II			
			AATTGTTGA AGGT AC			
			GG_ T			
GAM65	RBMS3	5'	CAGGAATAGTGGTTTAA	15828	CG G	
			TTAAACCACTA TCC TG			
			III II			
			AATTGTTGAT AGG AC			
			A_ _			
GAM65	DKFZp761B0514	3'	TGGAGAGATGTAGTGATTTAA	26052	C CGTGA	
			TTAAA CACTACGTC CCA			
			III			
			AATTT GTGATGTAG GGT			
			A AGA__			
GAM65	FLJ10290	3'	TCATTGTAGTGGCCTAA	19798	AA TCC	
			TTA CCACTACG GTGA			
			III III			
			AAT GGTGATGT TACT			
			CC _			
GAM65	KIAA1841	3'	TGGCCAGGTGTAGTGG	39028	T G A	
			CCACTACG CC TG CCA			
			II II III			
			GGTGATGT GG AC GGT			
			_ _ C			
GAM65	UQCR	3'	CACACGTAGTGGCTTAA	13710	A CC	
			TTAA CCACTACGT GTG			
			III			

			AATT GGTGATGCA CAC		
			C —		
GAM65	ZIM3	3'	TGGCCAGGCGTGGTGG	27462	T G A
			CCACTACG CC TG CCA		
			GGTGGTGC GG AC GGT		
			— — C		
GAM65	LOC113523	3'	TGGCCAGGCGTAGTGG	36156	T G A
			CCACTACG CC TG CCA		
			GGTGATGC GG AC GGT		
			— — C		
GAM65	LOC143465	3'	TGGCCAGGTGTAGTGG	40366	T G A
			CCACTACG CC TG CCA		
			GGTGATGT GG AC GGT		
			— — C		
GAM65	LOC92539	5'	TGGTCACGGTGGTGGT	34505	CGT
			ACCACTA CCGTGACCA		
			TGGTGGT GGCAC TGGT		
			—		
GAM66	GNB1	3'	TGTCAATGATGTAAATTCAGTC	7852	A — TTA_
		CCT	AGG ATTGAATTT CGTT	ACA	
			TCC TGA CT TAAA GTAG	TGT	
			C T TAAC		
GAM66	LRAT	3'	TTAAAGCAAGATTCAATTCCT	30184	C
			AGGAATTGAATTT GTTTTAA		
			TCCTTAACTTAGA CGAAATT		
			A		
GAM66	RPE65	3'	AAATGGCTTTTAATTCCT	5871	TT
			AGGAATTGAA TCGTTT		
			TCCTTAATTT GGTAAA		
			TC		
GAM66	SLC4A7	3'	TGTTAAAATGATGGATTCAACT	9674	A —
		TCT	AGGA TTGAATT TCGTTTAAACA		
			TCTT AACTTAG AGTAAAATTGT		
			C GT		
GAM66	AMOTL2	3'	TGTTAAAGCTGCTCGATTCC	18295	ATTTC
			GGAATTGA GTTTTAACA		
			CCTTAGCT CGAAATTGT		
			CGT_		
GAM66	CG018	3'	TGTTAAAAATGCTGTCAAATCC	27406	A ATTTCG
		T	AGGA TTGA TTTTAACA		

			TCCT AACT AAAATTGT		
			A GTCGTA		
GAM66	KIAA0441	3'	TTAAAATTTAAATCCAGTTCCT 16714	A	C_
			AGGAATTG ATTT GTTTTAA		
			TCCTTGAC TAAA TAAAATT		
			C AT		
GAM66	KIAA0470	3'	TGTTAAAACAGGGTCAATCC 16778	A	A TC
			GGA TTGA TT GTTTTAACA		
			CCT AACT GG CAAAATTGT		
			— — GA		
GAM66	KIAA1712	3'	TGTTAAAACAAGTGATTTCC 33541	TTGA	C
			GGAA ATTT GTTTTAACA		
			CCTT TGAA CAAAATTGT		
			TAG_ —		
GAM66	NET-6	3'	TGTTAAGGGAAATCCAAATTCC 15742	GA_	G
			GGAATT ATTC TTTTAACA		
			CCTTAA TAAAG GGAATTGT		
			ACC —		
GAM66	RCD-8	3'	AAAGCTTTTTTCAGTTCCT 15639	TTTC	
			AGGAATTGAA GTTTT		
			TCCTTGACTT CGAAA		
			TTT_		
GAM66	LOC127281	3'	TTAAAAGTGCAGTTCCT 36891	AATTTC	
			AGGAATTG GTTTTAA		
			TCCTTGAC CAAAATT		
			GT_____		
GAM67	MLLT3	3'	GTGGTGGTTCATTCCACA 10869	A	AAC
			TGTG AAT ACCATTAC		
			ACAC TTA TGGTGGTG		
			C CT_		
GAM67	MN1	3'	AAGTATTGTTATTTTATA 8271	CCAT	
			TGTGAAATAACA TACTT		
			ATACTTTATTGT ATGAA		
			T_____		
GAM67	AKAP6	3'	TTGGGATATGGTATTATTTTAC 10492	C	TA
	A		TGTGAAATAA ACCAT CTAA		
			ACATTTTATT TGGTA GGGTT		
			A TA		
GAM67	DJ37E16.5	3'	TAAGTAATAGTGACCCTTTCAC 21579	TAA_	C
			GTGAAA CAC ATTACTTA		

			CACTTT GTG TAATGAAT		
			CCCA A		
GAM67	FLJ20694	3'	AAGTACTGTGTATTTCACA 19603	A	CAT
			TGTGAAATA CAC TACTT		
			ACACTTTAT GTG ATGAA		
			_ TC_		
GAM67	KIAA0276	3'	TAAGTAAAATTTATTTTAC 35138	CACCA	
			GTGAAATAA TTACTTA		
			CACTTTATT AATGAAT		
			TAA__		
GAM67	KIAA0993	3'	GTAGCAGTGTTATTCTACA 32082	A	CA
			TGTG AATAACAC TTAC		
			ACAT TTATTGTG GATG		
			C AC		
GAM67	KIAA1056	3'	AGGAAATGGAACCATTTTACA 17045	AACA	A
			TGTGAAAT CCATT CTT		
			ACACTTTA GGTA GGA		
			CCAA A		
GAM67	LOC257354	3'	AAGACTAGGTGTTATCCTACA 45573	AA	ATTA
			TGTG ATAACACC CTT		
			ACAT TATTGTGG GAA		
			CC ATCA		
GAM67	LOC90198	5'	AGTGGTGGTGTACCTCAC 30957	AA	
			GTGA TAACACCATTACT		
			CACT ATTGTGGTGGTGA		
			CC		
GAM67	LOC91380	5'	TTTAAGTGGTGTGCTGCTTCA 32761	A A	C
	CA		TGTGAA TA CAC ATTACTTAAA		
			ACACTT GT GTG TGGTGAATTT		
			C C T		
GAM68	ACADSB	3'	GGAAAATGCAATAAAATA 7314	A	
			TATTTTA TGCATTTTCT		
			ATAAAAT ACGTAAAAGG		
			A		
GAM68	MLLT3	3'	TAGAAAATGCACCAAATA 10870	TAA	
			TATTT TGCATTTTCTA		
			ATAAA ACGTAAAAGAT		
			CC_		
GAM68	MTAP	3'	AATTTGGTAAAATGCATCAAAA 8287	A	_
			TTTT ATGCATTTT CTAAATT		

			AAAA TACGTAAAA GGTTTAA		
			C T		
GAM68	WARS	3'	TAGAAAGTGCTTTGAAATA 33413	T	
			TATTTTAA GCATTTTCTA		
			ATAAAGTT CGTGAAAGAT		
			T		
GAM68	Di-Ras2	3'	TGGAAAATGCATTTAATA 19046	T	
			TATTT AATGCATTTTCTA		
			ATAAA TTACGTAAAAGGT		
			T		
GAM68	RAB39	3'	TAGCAAATGCATTTAATA 37646	T	_
			TATTT AATGCATTTT CTA		
			ATAAA TTACGTAAAA GAT		
			T C		
GAM68	LOC158292	5'	AGAAAATGATTAAAATA 41931	G	
			TATTTTAAT CATTTTCT		
			ATAAAATTA GTAAAAGA		
			-		
GAM68	LOC93380	3'	TAATTTAGAAATGAATTAAAA 35727	G	T
			TTTTAAT CATTT CTAAATTA		
			AAAATTA GTAAA GATTTAAT		
			A _		
GAM69	DCLRE1A	5'	GATTAAGCTGTTGAACCTA 34280	GTT	
			TAGGTTCAACAG TTTGATT		
			ATCCAAGTTGTC GAATTAG		

GAM69	LRRN3	5'	AATCAGCTCCTATTGAACCTA 34398	C	TTT
			TAGGTTCAA AGG TTGATT		
			ATTCAAGTT TCC GACTAA		
			A TC_		
GAM69	PISD	3'	AATCAATCACTGAACCTG 15652	ACAG	TT
			TAGGTTCA GT TTGATT		
			GTCCAAGT CA AACTAA		
			___ CT		
GAM69	RGPR	3'	TCATGGTAACTACTGAACCTA 26970	ACA	TT__
			TAGGTTCA GGTT TGA		
			ATCCAAGT TCAA ACT		
			CA_ TGGT		
GAM69	SLC38A1	3'	GAAAACCTATGGAACCTA 25036	AAC	
			TAGGTTT AGGTTTTT		

			ATCCAAG TCCAAAAG		
			GTA		
GAM70	C8orf1	3'	GTTGAAAGACCGTTTACA 10532	T	
			TGTAAACGGTCTTTT AC		
			ACATTTGCCAGAAAG TG		
			T		
GAM70	CROT	3'	TGTTTGATGGGAAAGACCACTA 22126	AAC	AC_
	CA		TGTA GGTCTTTTT TAAACA		
			ACAT CCAGAAAGG GTTTGT		
			CA_ GTA		
GAM70	PB1	3'	TTACTAGAAAGACCATTACA 19984	AC	C
			TGTAA GGTCTTTTTA TAA		
			ACATT CCAGAAAGAT ATT		
			A_ C		
GAM70	PLAGL2	3'	TGTCCAGCAACGGTACCGTTTA 34882	C TT A AA	
	CA		TGTAAACGGT T TT CT ACA		
			ACATTTGCCA G AA GA TGT		
			T GC C CC		
GAM71	CTF1	3'	TCTGTTTTTTCCATCCCCAC 7012	AT	AACAT
			GTG GATG GAAACAGA		
			CAC CTAC TTTTGTCT		
			CC CTT__		
GAM71	NEBL	5'	TTTCTGTTCACTCACAC 13102	A _	T
			GTG TGA TGAACA GAAA		
			CAC ACT ACTTGT CTTT		
			_ C _		
GAM71	OPCML	3'	TCTGCTTCTCTCCTCATCATCA 8397	ACAT_	A
	T		GTGATGATGA GAA CAGA		
			TACTACTACT CTT GTCT		
			CCTCT C		
GAM71	PCDHA9	5'	TTCTGTTTCAACAATCATTAC 15215	GAACA	
			GTGATGAT TGAAACAGAA		
			CATTACTA ACTTTGTCTT		
			ACA__		
GAM71	PCDHA9	5'	TTCTGTTTCAACAATCATTAC 25607	GAACA	
			GTGATGAT TGAAACAGAA		
			CATTACTA ACTTTGTCTT		
			ACA__		
GAM71	PCLO	3'	TTTCAGGACTTCATCATCAC 45215	CA__	
			GTGATGATGAA TGAAA		

CACTACTACTT ACTTT
 CAGG
 GAM71 RAB4A 3' TTCTGTTTCATATTTTTC 10926 T C
 GA GAA ATGAAACAGAA
 || ||| |||||
 CT TTT TACTTTGTCTT
 T A
 GAM71 ARFGAP3 3' TTTCTGTTTCACGTTCTTC 15926 T_ A
 GA GAAC TGAAACAGAAA
 || ||| |||||
 CT CTTG ACTTTGTCTTT
 TC C
 GAM71 BOP 5' TTTCGATGTCAATCATCAC 41211 GA _
 GTGATGAT ACAT GAAA
 ||||| ||| |||
 CACTACTA TGTA CTTT
 AC G
 GAM71 CCR1 3' TTTCTGTTCTTCCATCAC 6976 AT_ T
 GTGATG GAACA GAAA
 ||||| ||| |||
 CACTAC CTTGT CTTT
 CTT _
 GAM71 DKFZP434F1735 5' TCTGTTTCATGTGCCCATC 17856 ATGA
 GATG ACATGAAACAGA
 ||| |||||
 CTAC TGTACTTTGTCT
 CCG_
 GAM71 DKFZP434P211 3' TCCGTCTCGCTCATCATCAC 15871 ACA A A
 GTGATGATGA TGA AC GA
 ||||| ||| |||
 CACTACTACT GCT TG CT
 C_ C C
 GAM71 EK1 3' TCTGTTTCACGTTCTGTTG 20709 A
 TGATGAAC TGAAACAGA
 ||||| |||||
 GTTGCTTG ACTTTGTCT
 C
 GAM71 KCNT1 3' TTCTACTTCTGCATCGTCAC 30979 AACAT AC
 GTGATGATG GAA AGAA
 ||||| ||| |||
 CACTGCTAC CTT TCTT
 GT_ CA
 GAM71 KIAA1046 3' TTTCTGTTTCCCATATCTCAC 17222 T AACAT
 GTGA GATG GAAACAGAAA
 ||| ||| |||||
 CACT CTAT CTTTGTCTTT
 _ ACC_
 GAM71 KIAA1719 3' TTCCTGTCCCATCATTAC 33826 A_ T
 GTGATGATG ACA GAA
 ||||| ||| |||

			CATTACTAC TGT CTT		
			CC C		
GAM71	MGC20253	3'	TCTGTCTCATGTTTCGTGCA 29400	_	A
			TG ATGAACATGA ACAGA		
			AC TGCTTGTACT TGTCT		
			G C		
GAM71	MGC5566	3'	CTGCAACATATTCATCATC 23487	C	AAA
			GATGATGAA ATG CAG		
			CTACTACTT TAC GTC		
			A AAC		
GAM71	SDF1	3'	TCTGTCTCATCCATCATCAT 43692	AAC	A
			GTGATGATG ATGA ACAGA		
			TACTACTAC TACT TGTCT		
			C_ C		
GAM71	SRF	3'	TCTTGTTTCACTCCACCATCAC 9106	A	AACA _
			GTGATG TG TGAAACA GA		
			CACTAC AC ACTTTGT CT		
			C CTC_ T		
GAM71	TRIM26	3'	TCTGTCCAGGTGCCCTCATCA 9502	A__	GAA_
			TCAC GTGATGATGA CAT ACAGA		
			CACTACTACT GTG TGTCT		
			CCCC GACC		
GAM71	LOC114971	3'	TCTGTCCACACATTATCAC 36211	AACA	AA
			GTGATGATG TG ACAGA		
			CACTATTAC AC TGTCT		
			AC_ C_		
GAM71	LOC148189	3'	TTTCTAATTATTCATCATTAC 38488	AC	AAC
			GTGATGATGA ATGA AGAAA		
			CATTACTACT TATT TCTTT		
			_ AA_		
GAM71	LOC151121	5'	TCTGCATCCATCATCAC 39054	AAC	AAA
			GTGATGATG ATG CAGA		
			CACTACTAC TAC GTCT		
			C_ _		
GAM71	LOC151473	3'	TTTCTACTCACAATTTGATCAT 39124	G CA_	AAC
			CAC GTGATGAT AA TGA AGAAA		
			CACTACTA TT ACT TCTTT		
			G TAAC CA_		
GAM71	LOC200734	3'	TTTCTATCTTTAGCCCATCATC 42845	AACA	AC_
			AT GTGATGATG TGAA AGAAA		

			TACTACTAC	ATTT	TCTTT		
			CCG_	CTA			
GAM71	LOC221943	5'	CTGCTTCACTGCGTCATCAT	45117		AACA	A
			GTGATGATG	TGAA	CAG		
			TACTACTGC	ACTT	GTC		
			GTC_	C			
GAM71	LOC257494	3'	TCTGTCCAGGTGCCCTCATCA	46689		A__	GAA_
			TCAC	GTGATGATGA	CAT	ACAGA	
			CACTACTACT	GTG	TGTCT		
			CCCC	GACC			
GAM71	LOC91522	3'	TCTGTTTCCATTATCAC	32963		AACAT	
			GTGATGATG	GAAACAGA			
			CACTATTAC	CTTTGTCT			
GAM72	SOX12	3'	TGGTCATTTCAATCCA	13832		CAATG	
			TGGATTGAAA	GATTA			
			ACCTAACTTT	CTGGT			
			A__				
GAM72	C21orf55	5'	TTGATTCTATTCAATCCA	19499		ACAAT	
			TGGATTGAA	GGATTAA			
			ACCTAACTT	CTTAGTT			
			AT__				
GAM72	MGC2452	5'	GATTCATTGCTTCAACACA	26370		GA	A
			TG	TTGAA	CAATGGATT		
			AC	AACTT	GTTACTTAG		
			AC	C			
GAM72	P2RXL1	3'	AATTCACCTTCAGTCCA	11926		ACAA	
			TGGATTGAA	TGGATT			
			ACCTGACTT	ACTTAA			
			C__				
GAM72	PPP1R16B	3'	ATCCAGACTGTTTCAGCCCA	30764		AT	A__
			TGG	TGAAACA	TGGAT		
			ACC	ACTTTGT	ACCTA		
			CG	CAG			
GAM72	LOC255328	3'	AGTACCAATTTCAATCCA	46178		CAA	_
			TGGATTGAAA	TGG	ATT		
			ACCTAACTTT	ACC	TGA		
			A__	A			
GAM72	LOC90509	3'	TATTAATTATTTCAAGTCCA	31611		CAATG	
			TGGATTGAAA	GATTAATA			

			ACCTGACTTT TTAATTAT		
			A_____		
GAM73	COL19A1	3'	AGGTTATTTTATTTATTGTA 7592	___	
			TACAATAAATAAGA ATCT		
			ATGTTATTTATTTT TGGA		
			AT		
GAM73	DNC11	3'	CATTGCTGCTCCTTATTTATTG 43776	AATCTAA	
	TA		TACAATAAATAAG AATG		
			ATGTTATTTATTC TTAC		
			CTCGTCG		
GAM73	HSPC031	3'	GGACTTCTTATTTACTGTA 18185	A _	
			TACA TAAATAAGAA TCT		
			ATGT ATTTATTCTT AGG		
			C C		
GAM74	APPL	3'	CTGCAAACTCCGCCTCCCA 14400	AC _ C	
			TG AGGTG AG TTGCAG		
			AC TCCGC TC AACGTC		
			CC C A		
GAM74	BCL9	5'	ACTGCAAGCTCAGGATTTC 10522	GACAGG	
			TGAAAT TGAGCTTGCACT		
			ACTTTA ACTCGAACGTCA		
			GG_____		
GAM74	CYP1A2	3'	CTGCAACCTCTGCCTCCCA 6412	AC _ C	
			TG AGGT GAG TTGCAG		
			AC TCCG CTC AACGTC		
			CC T C		
GAM74	CYP1A2	3'	CTGCAACCTCTGCCTCCCA 34256	AC _ C	
			TG AGGT GAG TTGCAG		
			AC TCCG CTC AACGTC		
			CC T C		
GAM74	DFFB	3'	CTGCAACCTCCGCCTCTCA 42242	C _ C	
			TGA AGGTG AG TTGCAG		
			ACT TCCGC TC AACGTC		
			C C C		
GAM74	DISC1	3'	CTGCAACCTCTACCTCCCA 20736	AC _ C	
			TG AGGT GAG TTGCAG		
			AC TCCA CTC AACGTC		
			CC T C		
GAM74	DSCR3	3'	CTGCAACCTCCACCTCCCA 12685	AC _ C	
			TG AGGTG AG TTGCAG		

			AC TCCAC TC AACGTC		
			CC C C		
GAM74	FCRH1	3'	CTGCAACGCCTGCCTCTCA	27499	C GA _
			TGA AGGT GC TTGCAG		
			ACT TCCG CG AACGTC		
			C TC C		
GAM74	FEZ1	3'	CTGCAACCTCCACCTCCCA	22877	AC _ C
			TG AGGTG AG TTGCAG		
			AC TCCAC TC AACGTC		
			CC C C		
GAM74	GHR	3'	CTGCAATCTCCACCTCCCA	5673	AC _ C
			TG AGGTG AG TTGCAG		
			AC TCCAC TC AACGTC		
			CC C T		
GAM74	MEFV	3'	CTGCAACCTCCACCTCCCA	5769	AC _ C
			TG AGGTG AG TTGCAG		
			AC TCCAC TC AACGTC		
			CC C C		
GAM74	MEFV	3'	CTGCAACCTCCGCCTCCCA	5770	AC _ C
			TG AGGTG AG TTGCAG		
			AC TCCGC TC AACGTC		
			CC C C		
GAM74	MICB	3'	CTGCAACCTCTGCCTCCCA	12565	AC _ C
			TG AGGT GAG TTGCAG		
			AC TCCG CTC AACGTC		
			CC T C		
GAM74	PCDHB9	3'	CTGCAACCTCCGCCTCCCA	21205	AC _ C
			TG AGGTG AG TTGCAG		
			AC TCCGC TC AACGTC		
			CC C C		
GAM74	PDE6B	3'	CTGCAACCTCCACCTCCCA	5828	AC _ C
			TG AGGTG AG TTGCAG		
			AC TCCAC TC AACGTC		
			CC C C		
GAM74	PER2	3'	CTGCAACCTCTGCCTCCCA	23091	AC _ C
			TG AGGT GAG TTGCAG		
			AC TCCG CTC AACGTC		
			CC T C		
GAM74	PLA2G2D	3'	AGGCCACCTGTCACTCA	14767	AA A
			TGA TGACAGGTG GCTT		

			ACT ACTGTCCAC CGGA		
			C _ _		
GAM74	RHD	3'	CTGCAACCTCCGCCTCCCA 18217	AC	_ C
			TG AGGTG AG TTGCAG		
			AC TCCGC TC AACGTC		
			CC C C		
GAM74	RHD	3'	CTGCAACCTCCGCCTCCCA 18337	AC	_ C
			TG AGGTG AG TTGCAG		
			AC TCCGC TC AACGTC		
			CC C C		
GAM74	SEDL	3'	CTGCAACCTCCGCCTCCCA 15910	AC	_ C
			TG AGGTG AG TTGCAG		
			AC TCCGC TC AACGTC		
			CC C C		
GAM74	SEPN1	3'	CTGCAACCTCCACCTCCCA 32989	AC	_ C
			TG AGGTG AG TTGCAG		
			AC TCCAC TC AACGTC		
			CC C C		
GAM74	SLC13A1	3'	CTGCAAGCTCCGCCTCCCA 22775	AC	_
			TG AGGTG AGCTTGCAG		
			AC TCCGC TCGAACGTC		
			CC C		
GAM74	SLC14A2	5'	CTGCAACCTCCACCTCCCA 14009	AC	_ C
			TG AGGTG AG TTGCAG		
			AC TCCAC TC AACGTC		
			CC C C		
GAM74	SLC15A1	3'	CTGCAACCTCCGCCTCCCA 11521	AC	_ C
			TG AGGTG AG TTGCAG		
			AC TCCGC TC AACGTC		
			CC C C		
GAM74	SMAC	5'	CTGCAACCTCTGCCTCCCA 29051	AC	_ C
			TG AGGT GAG TTGCAG		
			AC TCCG CTC AACGTC		
			CC T C		
GAM74	SNX15	3'	CTGCAACCTCCACCTCCCA 36505	AC	_ C
			TG AGGTG AG TTGCAG		
			AC TCCAC TC AACGTC		
			CC C C		
GAM74	SS18	3'	CTGCAACCTCCGCCTCCCA 12164	AC	_ C
			TG AGGTG AG TTGCAG		

			AC TCCGC TC AACGTC		
			CC C C		
GAM74	TRIM9	5'	CTGCAACCTCCGCCTCCCA	17515	AC _ C
			TG AGGTG AG TTGCAG		
			AC TCCGC TC AACGTC		
			CC C C		
GAM74	UGDH	3'	CTGCAAGCTCTGCTTCCCA	9388	AC _
			TG AGGT GAGCTTGCAG		
			AC TTCG CTCGAACGTC		
			CC T		
GAM74	YES1	3'	CTGCAAGCTCTGCCTCCCA	11914	AC _
			TG AGGT GAGCTTGCAG		
			AC TCCG CTCGAACGTC		
			CC T		
GAM74	ZFP36L1	3'	ACTGCACCTTCCCTCATTTCA	11362	CA T CT
			TGAAATGA GG GAG TGCAGT		
			ACTTTACT CC CTT ACGTCA		
			_ _ CC		
GAM74	BAG5	3'	CTGCAACCTCCACCTCCCA	11303	AC _ C
			TG AGGTG AG TTGCAG		
			AC TCCAC TC AACGTC		
			CC C C		
GAM74	C9orf9	3'	CTGCAACCTCCGCCTCCCA	21028	AC _ C
			TG AGGTG AG TTGCAG		
			AC TCCGC TC AACGTC		
			CC C C		
GAM74	CHRA1	3'	CTGCAACCTCCGCCTCCCA	18904	AC _ C
			TG AGGTG AG TTGCAG		
			AC TCCGC TC AACGTC		
			CC C C		
GAM74	DKFZP564I122	3'	ACTGTGGCGCTCACCTGT	31644	_ TG
			ACAGGTGAGC T CAGT		
			TGTCCACTCG G GTCA		
			C GT		
GAM74	FLJ00024	5'	CTGCAACCTCTGCCTCCCA	31892	AC _ C
			TG AGGT GAG TTGCAG		
			AC TCCG CTC AACGTC		
			CC T C		
GAM74	FLJ10346	5'	CTGCAAGCTCCACCTCCCA	19837	AC _
			TG AGGTG AGCTTGCAG		

			AC TCCAC TCGAACGTC		
			CC C		
GAM74	FLJ10535	3'	CTGCAACCTCTGCCTCCCA	19919	AC _ C
			TG AGGT GAG TTGCAG		
			AC TCCG CTC AACGTC		
			CC T C		
GAM74	FLJ10846	3'	CTGCAAGCTCTGCCTCCCA	20199	AC _
			TG AGGT GAGCTTGCAG		
			AC TCCG CTCGAACGTC		
			CC T		
GAM74	FLJ12572	5'	CTGCAACCTCTGCCTCCCA	23198	AC _ C
			TG AGGT GAG TTGCAG		
			AC TCCG CTC AACGTC		
			CC T C		
GAM74	FLJ14950	3'	CTGCAACCTCCACCTCCCA	26673	AC _ C
			TG AGGTG AG TTGCAG		
			AC TCCAC TC AACGTC		
			CC C C		
GAM74	FLJ22002	3'	CTGCAACCTCCGCCTCCCA	24246	AC _ C
			TG AGGTG AG TTGCAG		
			AC TCCGC TC AACGTC		
			CC C C		
GAM74	FLJ22531	5'	CTGCAACCTCCACCTCCCA	23945	AC _ C
			TG AGGTG AG TTGCAG		
			AC TCCAC TC AACGTC		
			CC C C		
GAM74	FLJ22794	3'	CTGCAACTTCCACCTCCCA	44028	AC _ C
			TG AGGTG AG TTGCAG		
			AC TCCAC TT AACGTC		
			CC C C		
GAM74	FLJ23053	3'	CTGCAAGCTCCGCCTCCCA	23206	AC _
			TG AGGTG AGCTTGCAG		
			AC TCCGC TCGAACGTC		
			CC C		
GAM74	FLJ23392	3'	CTGCAACCTCTGCCTCCCA	24161	AC _ C
			TG AGGT GAG TTGCAG		
			AC TCCG CTC AACGTC		
			CC T C		
GAM74	FLJ23519	3'	CTGCAAGCTCCGCCTCCCA	25976	AC _
			TG AGGTG AGCTTGCAG		

			AC TCCGC TCGAACGTC			
			CC C			
GAM74	FLJ23563	3'	CTGCAACCTCTGCCTCCCA	33563	AC _ C	
			TG AGGT GAG TTGCAG			
			AC TCCG CTC AACGTC			
			CC T C			
GAM74	FLJ25416	3'	ACTAAGAGTTCACCTGTCCTTC	29625	AT	GC
	A		TGAA GACAGGTGAGCTT			
			ACTT CTGTCCACTTGAG			
			C_ AA			
GAM74	GAL3ST-4	3'	CTGCAACCTCTGCCTCCCA	23911	AC _ C	
			TG AGGT GAG TTGCAG			
			AC TCCG CTC AACGTC			
			CC T C			
GAM74	GOLGA3	3'	CTGCAAGCTCCGCCTCCCA	12514	AC _	
			TG AGGTG AGCTTGCAG			
			AC TCCGC TCGAACGTC			
			CC C			
GAM74	H-plk	5'	CTGCAACCTCCACCTCCCA	17985	AC _ C	
			TG AGGTG AG TTGCAG			
			AC TCCAC TC AACGTC			
			CC C C			
GAM74	KIAA0426	3'	CTGCAACCTCCGCCTCCCA	16310	AC _ C	
			TG AGGTG AG TTGCAG			
			AC TCCGC TC AACGTC			
			CC C C			
GAM74	KIAA0469	3'	CTGCAAGCTCCATCTCCCA	16891	AC _	
			TG AGGTG AGCTTGCAG			
			AC TCTAC TCGAACGTC			
			CC C			
GAM74	KIAA0527	3'	CTGCAACCTCTGCCTCCCA	45846	AC _ C	
			TG AGGT GAG TTGCAG			
			AC TCCG CTC AACGTC			
			CC T C			
GAM74	KIAA0561	3'	CTGCAACCTCCGCCTCCCA	32764	AC _ C	
			TG AGGTG AG TTGCAG			
			AC TCCGC TC AACGTC			
			CC C C			
GAM74	KIAA0599	3'	CTGCAACCTCCGCCTCCCA	37856	AC _ C	
			TG AGGTG AG TTGCAG			

			AC TCCGC TC AACGTC		
			CC C C		
GAM74	KIAA0841	3'	CTGCAACCTCCGCCTCCCA	35361	AC _ C
			TG AGGTG AG TTGCAG		
			AC TCCGC TC AACGTC		
			CC C C		
GAM74	KIAA1054	3'	CTGCAACCTCCGCCTCCCA	33953	AC _ C
			TG AGGTG AG TTGCAG		
			AC TCCGC TC AACGTC		
			CC C C		
GAM74	KIAA1198	3'	CTGCAATCTCTGCCTCCCA	31708	AC _ C
			TG AGGT GAG TTGCAG		
			AC TCCG CTC AACGTC		
			CC T T		
GAM74	KIAA1373	3'	CTGCAACCTCCACCTCCCA	35127	AC _ C
			TG AGGTG AG TTGCAG		
			AC TCCAC TC AACGTC		
			CC C C		
GAM74	KIAA1443	3'	CTGCAAGCTCCGCCTCCCA	31931	AC _
			TG AGGTG AGCTTGCAG		
			AC TCCGC TCGAACGTC		
			CC C		
GAM74	KIAA1497	5'	CTGCAACCTCTGCCTCCCA	33528	AC _ C
			TG AGGT GAG TTGCAG		
			AC TCCG CTC AACGTC		
			CC T C		
GAM74	KIAA1615	3'	CTGCAACCTCCACCTCCCA	34084	AC _ C
			TG AGGTG AG TTGCAG		
			AC TCCAC TC AACGTC		
			CC C C		
GAM74	KIAA1922	5'	CTGCAACCTCCGCCTCCCA	36455	AC _ C
			TG AGGTG AG TTGCAG		
			AC TCCGC TC AACGTC		
			CC C C		
GAM74	KIAA1924	3'	CTGCAAGCTCCGCCTCCCA	36475	AC _
			TG AGGTG AGCTTGCAG		
			AC TCCGC TCGAACGTC		
			CC C		
GAM74	KIAA1971	3'	CGCAAGCTCCGCTTCCCA	36729	AC _ A
			TG AGGTG AGCTTGC G		

			AC TTCGC TCGAACG C			
			CC C C			
GAM74	KIAA1971	3'	CTGCAACCTCCACCTCCCA	36730	AC _ C	
			TG AGGTG AG TTGCAG			
			AC TCCAC TC AACGTC			
			CC C C			
GAM74	KIAA1987	5'	CTGCAATCTCCGCCTCCCA	42497	AC _ C	
			TG AGGTG AG TTGCAG			
			AC TCCGC TC AACGTC			
			CC C T			
GAM74	LY75	3'	ACTGCAAATCTCCGCCTCCCA	8148	AC _ C_	
			TG AGGTG AG TTGCAGT			
			AC TCCGC TC AACGTCA			
			CC C TA			
GAM74	MAN1C1	3'	GCCCACTCACTTGCCATTCCA	21645	A A CTT	
			TG AATG CAGGTGAG GC			
			AC TTAC GTTCACTC CG			
			C C ACC			
GAM74	MCLC	3'	CTGCAACCTCCACCTCCCA	17491	AC _ C	
			TG AGGTG AG TTGCAG			
			AC TCCAC TC AACGTC			
			CC C C			
GAM74	MGC11115	3'	ACCCAGGGCCTCACCTGCCACT	26091	AA A _ GCA	
	CA		TGA TG CAGGTGAG CTT GT			
			ACT AC GTCCACTC GGG CA			
			C_ C C ACC			
GAM74	MGC15631	3'	ACTGGTGCACACCTGTCATCCC	26489	AA A TTG	
	A		TG ATGACAGGTG GC CAGT			
			AC TACTGTCCAC CG GTCA			
			CC A TG_			
GAM74	MGC35558	3'	ACTGCAAGCGCTGAGTCCTTC	29611	AT A_ GA	
			GAA GAC GGT GCTTGCAGT			
			CTT CTG TCG CGAACGTCA			
			C_ AG _			
GAM74	MGC5149	3'	CTGCAACCTCTGCCTCCCA	35784	AC _ C	
			TG AGGT GAG TTGCAG			
			AC TCCG CTC AACGTC			
			CC T C			
GAM74	moblak	3'	CTGCAAGCTCCGCCTCCCA	28308	AC _	
			TG AGGTG AGCTTGCAG			

			AC TCCGC TCGAACGTC		
			CC C		
GAM74	MOCS3	3'	CTGCAACCTCCGCCTCCCA	15830	AC _ C
			TG AGGTG AG TTGCAG		
			AC TCCGC TC AACGTC		
			CC C C		
GAM74	PSPH	3'	CTGCAAGCTCTGCCTCCCA	10924	AC _
			TG AGGT GAGCTTGCAG		
			AC TCCG CTCGAACGTC		
			CC T		
GAM74	RAB21	3'	CTGCAAGCTCCACCTCCCA	17367	AC _
			TG AGGTG AGCTTGCAG		
			AC TCCAC TCGAACGTC		
			CC C		
GAM74	RAB33B	3'	CTGCAACCTCCGCCTCCCA	25329	AC _ C
			TG AGGTG AG TTGCAG		
			AC TCCGC TC AACGTC		
			CC C C		
GAM74	RAP140	3'	CTGCAAGCTCTGCCTCCCA	17557	AC _
			TG AGGT GAGCTTGCAG		
			AC TCCG CTCGAACGTC		
			CC T		
GAM74	RNF9	3'	ACTACAATGCTCTGTCTATCTC	27409	A GGT _ C
			GA ATGACA GAGC TTG AGT		
			CT TACTGT CTCG AAC TCA		
			C _ _ T A		
GAM74	STAF65(gamma)	3'	CTGCAACCTCTGCCTCCCA	16924	AC _ C
			TG AGGT GAG TTGCAG		
			AC TCCG CTC AACGTC		
			CC T C		
GAM74	SYT13	3'	CTGCAACCTCCGCCTCCCA	44889	AC _ C
			TG AGGTG AG TTGCAG		
			AC TCCGC TC AACGTC		
			CC C C		
GAM74	TADA3L	3'	CTGCAAGCTCCGCCTCCCA	28547	AC _
			TG AGGTG AGCTTGCAG		
			AC TCCGC TCGAACGTC		
			CC C		
GAM74	UBF-fl	3'	CTGCAACCTCTGCCTCCCA	26602	AC _ C
			TG AGGT GAG TTGCAG		

			AC TCCG CTC AACGTC		
			CC T C		
GAM74	LOC126661 3'	CTGCAACCTCCGCCTCCCA	36851	AC	_ C
		TG AGGTG AG TTGCAG			
		AC TCCGC TC AACGTC			
		CC C C			
GAM74	LOC128989 3'	CTGCAACCTCCGCCTCCCA	36943	AC	_ C
		TG AGGTG AG TTGCAG			
		AC TCCGC TC AACGTC			
		CC C C			
GAM74	LOC135293 3'	CTGCAACCTCTGCCTCCCA	37493	AC	_ C
		TG AGGT GAG TTGCAG			
		AC TCCG CTC AACGTC			
		CC T C			
GAM74	LOC146784 5'	CTGCAACCTCCACCTCCCA	38238	AC	_ C
		TG AGGTG AG TTGCAG			
		AC TCCAC TC AACGTC			
		CC C C			
GAM74	LOC146909 3'	CTGCAAGCTCCGCCTCCCA	38266	AC	_
		TG AGGTG AGCTTGCAG			
		AC TCCGC TCGAACGTC			
		CC C			
GAM74	LOC146952 5'	CTGCAACCTCCACCTCTCA	40767	C	_ C
		TGA AGGTG AG TTGCAG			
		ACT TCCAC TC AACGTC			
		C C C			
GAM74	LOC147071 5'	CTGCAACCTCTGCCTCCCA	36136	AC	_ C
		TG AGGT GAG TTGCAG			
		AC TCCG CTC AACGTC			
		CC T C			
GAM74	LOC147694 3'	CTGCAAGCTCCGCCTCCCA	38372	AC	_
		TG AGGTG AGCTTGCAG			
		AC TCCGC TCGAACGTC			
		CC C			
GAM74	LOC147817 3'	CTGCAACCTCCACCTCCCA	38385	AC	_ C
		TG AGGTG AG TTGCAG			
		AC TCCAC TC AACGTC			
		CC C C			
GAM74	LOC149821 5'	CTGCAAGCTCCGCCTCCCA	41109	AC	_
		TG AGGTG AGCTTGCAG			

			AC TCCGC TCGAACGTC		
			CC C		
GAM74	LOC151475 5'	CTGCAACCTCCACCTCCCA	41356	AC _ C	
		TG AGGTG AG TTGCAG			
		AC TCCAC TC AACGTC			
		CC C C			
GAM74	LOC152300 3'	CTGCAAGCTCTGCCTCTCA	39251	C _	
		TGA AGGT GAGCTTGCAG			
		ACT TCCG CTCGAACGTC			
		C T			
GAM74	LOC152794 5'	CTGCAACCTCTACCTCCCA	39320	AC _ C	
		TG AGGT GAG TTGCAG			
		AC TCCA CTC AACGTC			
		CC T C			
GAM74	LOC153579 5'	CAGGACTCATCTGCCATTTCA	39404	A _	
		TGAAATG CAGGTGAG CTTG			
		ACTTTAC GTCTACTC GGAC			
		C A			
GAM74	LOC153811 3'	CTGCAAGCTCCGCCTCCCA	39416	AC _	
		TG AGGTG AGCTTGCAG			
		AC TCCGC TCGAACGTC			
		CC C			
GAM74	LOC154282 5'	CTGCAACCTCCACCTCCCA	41699	AC _ C	
		TG AGGTG AG TTGCAG			
		AC TCCAC TC AACGTC			
		CC C C			
GAM74	LOC157798 5'	CTGCAACCTCCGCCTCCCA	41848	AC _ C	
		TG AGGTG AG TTGCAG			
		AC TCCGC TC AACGTC			
		CC C C			
GAM74	LOC196047 5'	CTGCAACCTCCGCCTCCCA	43144	AC _ C	
		TG AGGTG AG TTGCAG			
		AC TCCGC TC AACGTC			
		CC C C			
GAM74	LOC200339 3'	CTGCAACCTCTGCCTCCCA	43298	AC _ C	
		TG AGGT GAG TTGCAG			
		AC TCCG CTC AACGTC			
		CC T C			
GAM74	LOC200860 3'	CTGCAACCTCCACCTCCCA	43354	AC _ C	
		TG AGGTG AG TTGCAG			

			AC TCCAC TC AACGTC		
			CC C C		
GAM74	LOC201173 5'	CTGCAACCTCTGCCTCCCA	42215	AC _ C	
		TG AGGT GAG TTGCAG			
		AC TCCG CTC AACGTC			
		CC T C			
GAM74	LOC201220 5'	CTGCAACCTCTGCCTCCCA	42222	AC _ C	
		TG AGGT GAG TTGCAG			
		AC TCCG CTC AACGTC			
		CC T C			
GAM74	LOC201411 3'	CTGCAACCTCTGCCTCCCA	31528	AC _ C	
		TG AGGT GAG TTGCAG			
		AC TCCG CTC AACGTC			
		CC T C			
GAM74	LOC202025 3'	CTGCAACCTCCGCCTCCCA	43402	AC _ C	
		TG AGGTG AG TTGCAG			
		AC TCCGC TC AACGTC			
		CC C C			
GAM74	LOC203297 5'	CTGCAACCTCTGCCTCCCA	37136	AC _ C	
		TG AGGT GAG TTGCAG			
		AC TCCG CTC AACGTC			
		CC T C			
GAM74	LOC203350 3'	CTGCAACCTCCGCCTCCCA	43534	AC _ C	
		TG AGGTG AG TTGCAG			
		AC TCCGC TC AACGTC			
		CC C C			
GAM74	LOC219735 3'	CTGCAACCTCTGCCTCCCA	44720	AC _ C	
		TG AGGT GAG TTGCAG			
		AC TCCG CTC AACGTC			
		CC T C			
GAM74	LOC221463 3'	GTTACTCACCTGTCATT	44203		CTT
		AATGACAGGTGAG GC			
		TTACTGTCCACTC TG			
		AT_			
GAM74	LOC222070 5'	CTGCAACCTCTGCCTCCCA	45181	AC _ C	
		TG AGGT GAG TTGCAG			
		AC TCCG CTC AACGTC			
		CC T C			
GAM74	LOC253666 5'	CTGCAACCTCCGCCTCCCA	45568	AC _ C	
		TG AGGTG AG TTGCAG			

			AC TCCGC TC AACGTC		
			CC C C		
GAM74	LOC256360	5'	CTGCAAGCTCCGCCTCCCA	46175	AC _
			TG AGGTG AGCTTGCAG		
			AC TCCGC TCGAACGTC		
			CC C		
GAM74	LOC90371	5'	CTGCAACCTCCACCTCCCA	31321	AC _ C
			TG AGGTG AG TTGCAG		
			AC TCCAC TC AACGTC		
			CC C C		
GAM74	LOC91115	3'	CTGCAACCTCCGCCTCCCA	32396	AC _ C
			TG AGGTG AG TTGCAG		
			AC TCCGC TC AACGTC		
			CC C C		
GAM74	LOC91115	3'	CTGCAACCTCCACCTCCCA	32395	AC _ C
			TG AGGTG AG TTGCAG		
			AC TCCAC TC AACGTC		
			CC C C		
GAM75	AKAP2	3'	CTGACTCATGGATCTGGTA	14060	AA A T
			TATCA GA CC TGAGTCAG		
			ATGGT CT GG ACTCAGTC		
			_ A T		
GAM75	CD164	3'	TGATTTGTTCTTTGA	12631	CTT
			TCAAAGAAC GAGTCA		
			AGTTTCTTG TTTAGT		
			_		
GAM75	PCTK1	5'	GACGGGTCCTTTGGTA	26909	A TGA
			TATCAAAG ACCT GTC		
			ATGGTTTC TGGG CAG		
			C _		
GAM75	RECK	3'	CTGACTTTCTTTTTTGATA	22090	CCTT
			TATCAAAGAA GAGTCAG		
			ATAGTTTTTT TTCAGTC		
			CT_		
GAM75	WRB	3'	TTTAAGTAAGTTCTTTGA	10998	_
			TCAAAGAAC CTTGAG		
			AGTTTCTTG GAATTT		
			AAT		
GAM75	ATP6V1D	3'	CTGTTCTGGTTCTTTGA	18087	TT T
			TCAAAGAACC GAG CAG		

			AGTTTCTTGG CTT GTC		
			T_ _		
GAM75	DNAM-1	3'	CTGAATTGAGTTACTTTGATA 13337	AAC TG G	
			TATCAAAG CT A TCAG		
			ATAGTTTC GA T AGTC		
			ATT GT A		
GAM75	FLJ20281	5'	CTGAATCAGGGTTCCTTGA 43727	A G	
			TCAA GAACCTTGA TCAG		
			AGTT CTTGGGACT AGTC		
			C A		
GAM75	GGA2	3'	CTGCATTCAGTCCTTTGATG 28919	A CT _	
			TATCAAAG AC TGAGT CAG		
			GTAGTTTC TG ACTTA GTC		
			C _ C		
GAM75	KIAA1388	5'	CTGACTCTTACATTTCTTTGG 44950	CCTT__	
			TCAAAGAA GAGTCAG		
			GGTTTCTT CTCAGTC		
			TACATT		
GAM75	PCDH20	3'	CTGCAGCAGATTTCTTTGATA 23136	CC AGT	
			TATCAAAGAA TTG CAG		
			ATAGTTTCTT GAC GTC		
			TA GAC		
GAM75	STK38L	3'	TGACAGATCTTTGATA 34294	AC TGA	
			TATCAAAGA CT GTCA		
			ATAGTTTCT GA CAGT		
			A_ _		
GAM75	ZER6	3'	TTTATTAGTTCTTTGATA 31748	CT_	
			TATCAAAGAAC TGAG		
			ATAGTTTCTTG ATTT		
			ATT		
GAM75	LOC144893	3'	ATTTAAGGTCCTTTGATA 40456	A	
			TATCAAAG ACCTTGAGT		
			ATAGTTTC TGGAATTTA		
			C		
GAM75	LOC146515	3'	CTGACTCAGCCTCTGAT 38193	A AACC	
			ATCA AG TTGAGTCAG		
			TAGT TC GACTCAGTC		
			C C_		
GAM75	LOC151877	3'	CTGACCCAGGGTTTTGA 41395	AA A	
			TCA GAACCTTG GTCAG		

			AGT TTTGGGAC CAGTC		
			— C		
GAM75	LOC56899	5'	CTGGCGGGCTCCTTTGATA 21335	AA_ TGA	
			TATCAAAG CCT GTCAG		
			ATAGTTTC GGG CGGTC		
			CTC —		
GAM75	LOC90161	3'	CTGACTCAGAATCTGATG 30902	AA ACC	
			TATCA GA TTGAGTCAG		
			GTAGT CT GACTCAGTC		
			— AA_		
GAM75	LOC90538	3'	CTGACATACATGGTTCTTT 31655	T A_	
			AAAGAACC TG GTCAG		
			TTTCTTGG AC CAGTC		
			T ATA		
GAM76	ITPR2	3'	CACATTCGCAATGCATCA 7989 C	C C	
			TGA GTATTGCG AA TGTG		
			ACT CGTAACGC TT ACAC		
			A — —		
GAM76	TRAF5	3'	ACGGTTGCTCAACACATCA 10964	C A C	
			TGA GT TTG GCAACTGT		
			ACT CA AAC CGTTGGCA		
			A C T		
GAM76	FLJ20296	3'	TGCACAGTTCTACACTGTCA 19356	TAT CGC	
			TGACG TG AACTGTGCA		
			ACTGT AC TTGACACGT		
			C_ ATC		
GAM76	KIAA0574	3'	GTTGCACAAATGTGAATAC 34347	G AC	
			GTATT CGCA TGTGCAAC		
			CATAA GTGT ACACGTTG		
			— AA		
GAM76	LOC145719	3'	GTTACACAGCTACAGTATGT 40578	CGCAA C	
			ACGTATTG CTGTG AAC		
			TGTATGAC GACAC TTG		
			ATC_ A		
GAM76	LOC145720	3'	GTTACACAGCTACAGTATGT 40567	CGCAA C	
			ACGTATTG CTGTG AAC		
			TGTATGAC GACAC TTG		
			ATC_ A		
GAM76	LOC197114	3'	GTTACACAGCTACAGTATGT 43190	CGCAA C	
			ACGTATTG CTGTG AAC		

			TGTATGAC GACAC TTG	
			ATC__ A	
GAM76	LOC197117	3'	GTTACACAGCTACAGTATGT 43197	CGCAA C
			ACGTATTG CTGTG AAC	
			TGTATGAC GACAC TTG	
			ATC__ A	
GAM77	POLE3	3'	TAGTCCCCCAAATAAGTAATA 18900	GC A TG
			TATTACTTAT GG GG TTG	
			ATAATGAATA CC CC GAT	
			AA _ CT	
GAM77	SLC5A7	3'	CAACACCTCCTGATAGTAGTA 22390	TATGC
			TATTACT GGAGGTGTTG	
			ATGATGA CCTCCACAAC	
			TAGT_	
GAM77	LOC120939	3'	CAACACCTCTATAGTGA 37511	TATGC
			TTACT GGAGGTGTTG	
			AGTGA TCTCCACAAC	
			TA__	
GAM78	C1D	3'	TACTTTATCATGTTTTCATGAT 13032	_ TC T
			ATCAT AA CAT GATAAAGTA	
			TAGTA TT GTA CTATTTTCAT	
			C TT _	
GAM78	C20orf142	3'	GTACCTGTTGGACAAGATTATG 36932	CA__ TG AA
	ATA		TATCATAATC T ATA GTAC	
			ATAGTATTAG G TGT CATG	
			AACA GT C_	
GAM78	RI58	3'	TACTTTATATGCATTATGATG 14797	C TG
			TATCATAAT CAT ATAAAGTA	
			GTAGTATTA GTA TATTTTCAT	
			C _	
GAM78	TNRC9	3'	TACTTTTTTATGAGTTATGATA 35322	TC TGAT
			TATCATAA CAT AAAGTA	
			ATAGTATT GTA TTTCAT	
			GA TTT_	
GAM78	LOC135293	3'	GTA CTTGATAGGATTATGATA 37494	ATTGATA
			TATCATAATCC AAGTAC	
			ATAGTATTAGG TTCATG	
			ATAG__	
GAM79	FLJ20208	3'	CGACCTTGAAGTGTGCTCA 19293	A AACCTA
			TGAGTACA TTCAG TCG	

			ACTCGTGT AAGTT	AGC	
			C CC_____		
GAM80	LTBP1	3'	CCGTTCTTAGCCAAGCTGCTA	6242	A GT A
			TAGCA GCT TGGCTAA AACGG		
			ATCGT CGA ACCGATT TTGCC		
			— — C		
GAM80	PRLR	5'	CCGTTTCGCGAAACAGCTT	6649	G_ TAAA
			AAGCTGTT GC AACGG		
			TTCGACAA CG TTGCC		
			AG C_____		
GAM80	DOCK3	3'	CCGCCCTCAGTAAGCAGCTTGC	33033	G AAAAA
			GCAAGCTGTT GCT CGG		
			CGTTCGACGA TGA GCC		
			A CTCCC		
GAM80	KIAA1483	3'	CTTTTCTAGCAGCTGC	34615	A CTA C
			GCA GCTGTTGG AAAA G		
			CGT CGACGATC TTTT C		
			— — — A		
GAM80	SARM	3'	CCGTTCTAGTGGGGCTTGCT	17457	GT G AA
			AGCAAGCT T GCTA AACGG		
			TCGTTCCG G TGAT TTGCC		
			— G CC		
GAM80	WDR7	3'	CCTTCTTTATCAACAGCT	17609	C AAC
			AGCTGTTGG TAAA GG		
			TCGACAACT ATTT CC		
			— CTT		
GAM81	ADAM22	3'	AGCAAGTTTCCTAAGGTACA	22324	A ACT
			TGTA CT GGAAACTTGCT		
			ACAT GA CCTTTGAACGA		
			G AT_		
GAM81	ADAM22	3'	AGCAAGTTTCCTAAGGTACA	22326	A ACT
			TGTA CT GGAAACTTGCT		
			ACAT GA CCTTTGAACGA		
			G AT_		
GAM81	FLJ21302	3'	AGCAAGCAGGTTCAAATACAGT	23181	ACTAC AA__
	A		TACTGTA TGGA CTTGCT		
			ATGACAT ACTT GAACGA		
			AA__ GGAC		
GAM81	KIAA0650	3'	GTTCCCAGTAATTACAGTA	42572	C A
			TACTGTAA TACTGG AAC		

			ATGACATT ATGACC TTG		
			A C		
GAM81	KIAA1155	3'	AGTTTCCAAAGTCACAG 31194	A AC	
			CTGT ACT TGGAAACT		
			GACA TGA ACCTTTGA		
			C A_		
GAM81	NXP-2	3'	CAAATTTCTTAGGATTATAGT 35229	_ ACT C	
	A		TACTGTAA CT GGAAA TTG		
			ATGATATT GG CCTTT AAC		
			A ATT A		
GAM81	SBBI31	3'	AGCAAGTTTTCGAAGTCACAGT 15265	A ACTG	
			ACTGT ACT GAAACTTGCT		
			TGACA TGA CTTTGAACGA		
			C AG_		
GAM81	LOC151248	5'	AGCAAGTTTTCACAGTTAAACA 39085	AACT _	
			TGT ACTG GAAACTTGCT		
			ACA TGAC CTTTGAACGA		
			AAT_ A		
GAM82	LOC145761	5'	ATCTCGTGTGTGTTAAGATG 40581	G_ _	
			CGTC AGCG ACACGAGAT		
			GTAG TTGT TGTGCTCTA		
			AA G		
GAM83	NPEPPS	3'	AATGGTTAAACACAAAAGGCTG 12995	TG C_ ACC	
	AT		GT GCTT GT TAACCATT		
			TA CGGA CA ATTGGTAA		
			GT AAA CAA		
GAM83	PKIA	3'	AATGATTATCATTAGAAGCTAA 13697	GTACC_ C	
	C		GTTGGCTTC TAA CATT		
			CAATCGAAG ATT GTAA		
			ATTACT A		
GAM83	SLC21A2	3'	AGAGACAGAAGCCAACGA 12155	_ AC	
			TCGTTGGCTTC GT CT		
			AGCAACCGAAG CA GA		
			A GA		
GAM83	DKFZp547M072	3'	AGGTCACAGAAGCCAACGA 30613	_ _	
			TCGTTGGCTTC GT ACCT		
			AGCAACCGAAG CA TGGA		
			A C		
GAM83	FLJ10761	3'	AATGACTAGAGGGAGCCAAGA 20104	G GTAC AC	
			TC TTGGCTTC CTA CATT		

			AG AACCGAGG	GAT GTAA	
			— GA— CA		
GAM83	P17.3	5'	AATGGTTGCCCCACGAAGCCA	21137	T AC—
			CGA		
			TCGT GGCTTCGT	CTAACCATT	
			AGCA CCGAAGCA	GGTTGGTAA	
			— CCCC		
GAM84	TM4SF6	3'	ACTACTTACTGATAGACCA	9282	AG T
			TG CTATCAGTAAGT	GT	
			AC GATAGTCATTCA	CA	
			CA	T	
GAM84	KIAA1239	3'	GTTTGCAACTGATAGCTCA	35340	AAGT
			TGAGCTATCAGT	TGTAAAT	
			ACTCGATAGTCA	ACGTTTG	
			—		
GAM84	KIAA1423	3'	AATTTACAGGTTACCAACTCA	30918	CTATCA G
			TGAG	GTAA TTGTAAATT	
			ACTC	CATT GACATTTAA	
			AAC—	G	
GAM84	MGC23980	3'	ACACTTAATAATAGCTCA	29604	CAG T
			TGAGCTAT	TAAGT GT	
			ACTCGATA	ATTCA CA	
			ATA	—	
GAM85	CNTNAP2	3'	GGAAACATCTTCTGTGTA	15420	C CA CTG
			TACACAGA	GA TG TCC	
			ATGTGTCT	CT AC AGG	
			T — AA—		
GAM85	GRLF1	3'	GGACATCGTCTGTGT	38415	CATGC
			ACACAGACGA	TGTCC	
			TGTGTCTGCT	ACAGG	
			—		
GAM85	LPIN2	3'	ATAGATGCCATCTGTGTG	16060	CGA G
			TACACAGA	CAT CTGT	
			GTGTGTCT	GTA GATA	
			ACC —		
GAM85	POU3F1	3'	GAGAGCCGCGTCTGTGTA	29831	ACAT G
			TACACAGACG	GCT TC	
			ATGTGTCTGC	CGA AG	
			GC—	G	
GAM85	AMOTL1	3'	GGGAGCGCCATCTGTGTG	36467	CGACA G
			TACACAGA	TGCT TCC	

			GTGTGTCT	GCGA GGG		
			ACC_ _			
GAM85	CSRP2BP	5'	GACAACACGAGTTTGTGTG	34736	GACA C	
			TACACAGAC	TG TGTC		
			GTGTGTTTG	AC ACAG		
			AGC_ A			
GAM85	DKFZP564O0463	3'	CAGCCATGTCTCTGCGTA	15443	A C _	
			TAC CAGA	GACATG CTG		
			ATG GTCT	CTGTAC GAC		
			C _ C			
GAM85	KIAA0227	3'	ATAGTTATGTCTGTGTA	30448	ACAT	
			TACACAGACG	GCTGT		
			ATGTGTCTGT	TGATA		
			AT_			
GAM85	KIAA0618	3'	GACTGTTACTGTGTCTGTGTA	16835	ACAT_ T	
			TACACAGACG	GC GTC		
			ATGTGTCTGT	TG CAG		
			GTCAT	T		
GAM85	KIAA0711	3'	CAGCTGTTGTGATCTGTGTA	16955	_ T	
			TACACAGA	CGACA GCTG		
			ATGTGTCT	GTTGT CGAC		
			AGT _			
GAM85	KIAA1046	3'	GGATGCTGGCATCTGTGTA	17220	CGA T T	
			TACACAGA	CA GC GTCC		
			ATGTGTCT	GT CG TAGG		
			ACG _ _			
GAM85	ZNF387	3'	CAGACGTGCCTCTGTGTA	16174	CGA _	
			TACACAGA	CATG CTG		
			ATGTGTCT	GTGC GAC		
			CC_ A			
GAM85	LOC199990	3'	GACCGTAGTCGTCTGTG	42681	A T	
			CACAGACGAC	TGC GTC		
			GTGTCTGCTG	ATG CAG		
			_ C			
GAM85	LOC91170	3'	CAGCACTGTCTGTCTGTG	32480	_ _	
			CACAGAC	GACA TGCTG		
			GTGTCTG	CTGT ACGAC		
			T C			
GAM86	HCGIV.9	5'	CGGGTAACGGCTCCTG	21056	T G	
			CAGGAGCCGTT	AC CTG		

GTCCTCGGCAA TG GGC

GAM86 LOC127534 3' AAGTAATACCAAAGGGCTCCTG 37162 G ACGC A
CAGGAGCC TTT TG TACTT
||||||| ||| || |||||
GTCCTCGG AAA AT ATGAA
G CC__ A

GAM86 LOC222171 5' AAGTATCTCATCGAAAAGGCTC 44557 G A CT__
CTG CAGGAGCC TTT CG GATACTT
||||||| ||| || |||||
GTCCTCGG AAA GC CTATGAA
A _ TACT

GAM87 PLXNB2 3' GCCCCACGTCAAAGGTCAAGTG 14778 TG__ A A
AG CTCGTTTG TGAC TGG GC
||||||| ||| ||| ||
GAGTGAAC ACTG ACC CG
TGGAA C C

GAM87 SLC7A6 3' CTCCATGTAGATAAGAGC 10128 G G_
GTTT TGT ACATGGAG
||| ||| |||||
CGAG ATA TGTACCTC
A GA

GAM87 UFD1L 3' CTCCATGGAGAAGCAAACATGT 36275 TC GTGA_
GA TCAC GTTTGT CATGGAG
||| ||||| |||||
AGTG CAAACG GTACCTC
TA AAGAG

GAM87 BANP 5' CCCTCACCACAACCGAATGA 32911 C T _ CAT
TCA TCG TTGTG TGA GG
||| ||| ||||| ||| ||
AGT AGC AACAC ACT CC
A C C C__

GAM87 C20orf59 3' CTCCATGTCAGACACACGAG 22624 T G
CTCGT TGT TGACATGGAG
||||| ||| |||||
GAGCA ACA ACTGTACCTC
C G

GAM87 CLIPR-59 3' CCATGTCACCCAGAAAG 17786 CG T
CT TTTG GTGACATGG
|| ||| |||||
GA AGAC CACTGTACC
A_ C

GAM87 FLJ10898 5' CTCCATACCAGACAAATGA 29890 G AC
TCGTTTGT TG ATGGAG
||||||| || |||||
AGTAAACA AC TACCTC
G CA

GAM87 KIAA0350 3' CTCCATGCCACACGGGTGG 30664 GTTT A
TCACTC GTGTG CATGGAG
||||| ||| |||||

			GGTGGG CACAC GTACCTC		
			_____ C		
GAM88	ACTN2	3'	GTCAGTTTAATTGCCAG 6759	C	AG
			CTGGCAAT TAAACT C		
			GACCGTTA ATTTGA G		
			_____ CT		
GAM88	C1orf22	3'	GTATGTTTAGATCCCAGG 24840	CA	TA
			CCTGG ATCTAAAC GC		
			GGACC TAGATTTG TG		
			C_ TA		
GAM88	LOC114932	3'	ATATGGATTTAGATTATCA 36004	GC	CTAG
			TG AATCTAAA CCATAT		
			AC TTAGATTT GGTATA		
			TA A_____		
GAM88	LOC119369	3'	ATATGTATCCTGATTGCCAGG 37206		TAAACTAGC
			CCTGGCAATC CATAT		
			GGACCGTTAG GTATA		
			TCCTAT_____		
GAM88	LOC255533	5'	ATATGGCTCAAGGACTGCCGG 46330	A	AAACT
			CTGGCA TCT AGCCATAT		
			GGCCGT AGG TCGGTATA		
			C AAC_____		
GAM89	INHBC	3'	CAAGATGAGTTGACACAACC 12064	ATCG	
			GGTT CAGCTTATCTTG		
			CCAA GTTGAGTAGAAC		
			CACA		
GAM89	PLAGL1	3'	TTCAAAATAAGAAAATAACCTT 8530	CGCAG	C
			GAGGTTAT CTTAT TTGAA		
			TTCCAATA GAATA AACTT		
			AAA_____ A		
GAM89	DKFZP434G1411	3'	TTCAAGATAAACTTCTGTAACC 44232	CGC	C
	T		AGGTTAT AG TTATCTTGAA		
			TCCAATG TC AATAGAACTT		
			TCT A		
GAM89	LOC91409	3'	CAAGATAGATAACACTC 32804	_____	GCAGCT
			GAG GTTATC TATCTTG		
			CTC CAATAG ATAGAAC		
			A _____		
GAM90	ALDH3A2	3'	AAAATTGGCATCAATTTTAA 34337		T TG
			TTAAAATTGAT C ATTTT		

			AATTTTAACTA G TAAAA	
			C GT	
GAM90	BMPR1A	5'	GAAAATCAGAAGTACAGTTTTA 10528	A__
			TAAAATTG TTCTGATTTTC	
			ATTTTGAC AAGACTAAAAG	
			ATG	
GAM90	ESM1	3'	AAAAGAAGAATCAATTTT 13911	GA
			AAAATTGATTCT TTTT	
			TTTAACTAAGA AAAA	
			AG	
GAM90	KIAA0408	3'	GAAAATCAGATTTTTTTT 16234	TT T
			TAAAA GAT CTGATTTTC	
			ATTTT TTA GACTAAAAG	
			TT _	
GAM90	LOC57117	5'	GAAACACAGAAGCAATTTTAA 21664	A AT
			TTAAAATTG TTCTG TTTC	
			AATTTTAAC AAGAC AAAG	
			G AC	
GAM90	LOC91585	5'	AAAATCAGACAAAAGTTTTAA 33075	GAT_
			TTAAAATT TCTGATTTT	
			AATTTTGA AGACTAAAA	
			AAAC	
GAM91	SDHD	3'	TTGTCATGCCATTAAGCTC 8898	ACAA A
			GAGCTTAA CATGA CAG	
			CTCGAATT GTACT GTT	
			ACC_ _	
GAM91	FLJ10324	5'	CAGCTGCTCCTGGAGTTTGAGC 19828	AA T A
			GCTTAAAC CA GA CAGCTG	
			CGAGTTTG GT CT GTCGAC	
			AG C C	
GAM91	LOC152876	5'	CTGTTTTGTGTTTAAACCTC 41560	C ACAT
			GAG TTAAACA GAACAG	
			CTC AATTTGT TTTGTC	
			C GT__	
GAM91	LOC221749	3'	AGCTGTTCACTGCCAGCTC 44178	TAAA ACA
			GAGCT CA TGAACAGCT	
			CTCGA GT ACTTGTCGA	
			CC_ C_	
GAM92	KIAA1045	3'	CCATTATGAAAAACACAGC 35193	C _
			GCTGTGTTT TCG GGTGG	

			CGACACAAA AGT TTACC		
			A A		
GAM93	CEACAM1	3'	CCTGGACTTGTTTTAACT 7440 C	ATTATA	
			AGT TAGAACAA TCCGGG		
			TCA ATTTTGT T AGGTCC		
			A C_____		
GAM93	EBAF	3'	CCCAAATACTGACCCATTCTGG 32607	CAAA _ CC	
	ACT		AGTCTAGAA TTA TAT GGG		
			TCAGGTCTT AGT ATA CCC		
			ACCC C AA		
GAM93	NOTCH2	3'	CCCAGATCTGAGCATTCTAGGC 23648	CAAA T C	
			GTCTAGAA TTA ATC GGG		
			CGGATCTT AGT TAG CCC		
			ACG_ C A		
GAM93	KIAA0232	3'	CCCAGGTTACATTTGTTCTAGA 36034	TAT C	
	T		GTCTAGAACAAAT ATC GGG		
			TAGATCTTGT TTA TGG CCC		
			CAT A		
GAM93	TU12B1-TY	3'	CCCGGATGACCTTTCCAGACT 18645	A CAAATTA	
			AGTCT GAA TATCCGGG		
			TCAGA CTT GTAGGCC		
			C TCCA_____		
GAM93	LOC90786	5'	CCAAGAGAATCTGTTCTAGAC 32012	A ATATCC	
			GTCTAGAACA ATT GG		
			CAGATCTTGT TAA CC		
			C GAGAA_		
GAM94	BLAME	3'	GCCATCACACCACGAGGA 21309 A	CAC	
			TC CTCGTGGTGT GTGGC		
			AG GAGCACCACA TACCG		
			_ C_		
GAM94	C10orf2	3'	GCCACGTGAACATCCGGCGA 22403 A T T _		
			TC C CG GGTGT CACGTGGC		
			AG G GC CTACA GTGCACCG		
			C _ _ A		
GAM94	CALCR	3'	CCACATGAACTACGTGA 7478 TC G C		
			TCAC GTGGT TCA GTGG		
			AGTG CATCA AGT CACC		
			_ _ A		
GAM94	CYLN2	3'	CCACGTGTGCACGCATGA 9421 _ _		
			TCGTG GTGT CACGTGG		

			AGTAC CACG GTGCACC		
			G T		
GAM94	EIF5A2	3'	GGCCACATGCAACCATGTGA 21660	TC	GT C
			TCAC GTGGT CA GTGGCC		
			AGTG TACCA GT CACCGG		
			— AC A		
GAM94	ZRF1	5'	GGCCTCCACACCACGAAAGA 45267	AC	CACGT
			TC TCGTGGTGT GGCC		
			AG AGCACCACA CCGG		
			AA CCT—		
GAM94	ARHF	3'	GCCACCCCCACCACGAGTG 21121		TCAC
			CACTCGTGGTG GTGGC		
			GTGAGCACCAC CACCG		
			CCC—		
GAM94	FLJ13110	3'	CCACGTGAGTGAGATGA 23220	—	TGGTG
			TCA CTCG TCACGTGG		
			AGT GAGT AGTGCACC		
			A G—		
GAM94	FLJ14146	3'	GCCACGTGTTTGCAGCGA 24034	G T—	
			TCGT GTG CACGTGGC		
			AGCG CGT GTGCACCG		
			A TT		
GAM94	KIAA0169	5'	GGCCACGGCGCACCACGAGT 36053		CA
			ACTCGTGGTGT CGTGGCC		
			TGAGCACCACG GCACCGG		
			CG		
GAM94	KIAA0864	5'	GCCACGTCCGACGAGGA 31684	A —	TGTC
			TC CTCGT GG ACGTGGC		
			AG GAGCA CC TGCACCG		
			— G —		
GAM94	MGC15705	5'	CCACATGAGCCATGTGA 26500	TC	G C
			TCAC GTGGT TCA GTGG		
			AGTG TACCG AGT CACC		
			— — A		
GAM94	p25	3'	GCCACAGCCACACGTGTGA 13892	T	GT CAC
			TCAC CGTG GT GTGGC		
			AGTG GCAC CG CACCG		
			T AC A—		
GAM94	PHCA	3'	GGCCACAGCCAACCAGAATGA 20376	C G	GTCAC
			TCA TC TGGT GTGGCC		

			AGT AG ACCA CACCGG		
			A _ ACCGA		
GAM94	POMT1	3'	GGCCACCTGAACCACGAG 14018	G C	
			CTCGTGGT TCA GTGGCC		
			GAGCACCA AGT CACCGG		
			_ C		
GAM94	LOC152925	3'	TATGTGCACCACGAGTGA 39335	T	
			TCACTCGTGGTG CACGTG		
			AGTGAGCACCAC GTGTAT		
			-		
GAM94	LOC221463	5'	GCCACATGTGGCAAGTGG 44201	CGTGG	_
			TCACT TGTCACT GTGGC		
			GGTGA ACGGTG CACCG		
			TA		
GAM94	LOC254266	3'	GGCCACGTTCCAACAAGTGA 46481	CG_ TGTC	
			TCACT TGG ACGTGGCC		
			AGTGA ACC TGCACCGG		
			ACA T__		
GAM95	CACNB2	5'	GTTTTGGCATGCCTGCAGGAA 6388	G A_ GA	
			TT CTGCA CA GCCAAAAC		
			AA GACGT GT CGGTTTTG		
			G CC A_		
GAM95	CD2AP	3'	GGCCTTGTTTTGCTGTAGCAA 14434	_____ A	
			TTGCTGCA ACAG GCC		
			AACGATGT TGTT CGG		
			CGTTT C		
GAM95	EXTL3	3'	GCCATCTGTGTGCAGCAA 7168	- _	
			TTGCTGCA ACAGA GC		
			AACGACGT TGTCT CG		
			G AC		
GAM95	MBNL	3'	GGTTTGGATGTTGCAGC 22029	GAG A	
			GCTGCAACA CCAAA CC		
			CGACGTTGT GGTTT GG		
			A_ _		
GAM95	MGAT4B	5'	GGCTCCTGGAAGTGCAGCAG 27621	A_ _	
			TTGCTGCA CAG AGCC		
			GACGACGT GTC TCGG		
			CAAG C		
GAM95	NONO	3'	TTGAATTTGTTGCACAA 39900	C GC	
			TTG TGCAACAGA CAA		

AAC ACGTTGTTT GTT
_ AA
GAM95 PIM1 3' GGTCCCGGCTCTGTGGGTGA 43756 TG G A AAA
T CT CA CAGAGCC ACC
| ||| ||||| |||
A GG GT GTCTCGG TGG
GT _ _ CCC
GAM95 PLAT 3' GTTTTTACTTTCTGTTGCCACA 6638 CT CC__
A TTG GCAACAGAG AAAAC
||| ||||| |||||
AAC CGTTGTCTT TTTTG
AC TCAT
GAM95 PLAT 3' GTTTTTACTTTCTGTTGCCACA 26897 CT CC__
A TTG GCAACAGAG AAAAC
||| ||||| |||||
AAC CGTTGTCTT TTTTG
AC TCAT
GAM95 PNUTL2 3' GGTTTTGGGGATGCAGTCAA 27839 _ ACAGAG
TTG CTGCA CCAAAACC
||| ||||| |||||
AAC GACGT GGT TTTGG
T AGG__
GAM95 RCN2 3' TTTTGGCTCTTTTAGGAA 8805 G CAAC
TT CTG AGAGCCAAAA
|| ||| |||||
AA GAT TCTCGGTTTT
G TT__
GAM95 TARBP2 3' GGTTTTTACTGCTGCAGCAG 28629 A AGCC
TTGCTGCA CAG AAAACC
||||||| ||| |||||
GACGACGT GTC TTTTGG
C AT__
GAM95 TJP1 3' TTTGACCTCTGCAGCAA 9268 ACA C_
TTGCTGCA GAG CAAA
||||||| ||| |||||
AACGACGT CTC GTTT
_ CA
GAM95 ARHGEF9 3' GGTTTCCCATGTTGCAGCA 17542 ____
TGCTGCAACA GAGCC
||||||| |||||
ACGACGTTGT TTTGG
ACCC
GAM95 BCMP1 3' GGTTTTGGCCCTCTTGCAG 25457 C A
CTGCAA AG GCCAAAACC
||||| || |||||
GACGTT TC CGGTTTTGG
C C
GAM95 CLGN 3' GTTTTGGTTTGTACAG 10570 CA G
CTG ACAGA CCAAAAC
||| ||||| |||||

GAC TGTTT GGTTTTG
 A_ _
 GAM95 CMG2 3' GGTTTTGGCCCCCTTTGCTGCAA 27722 T C A_
 TTGC GCAA AG GCCAAAACC
 ||| ||| || |||||
 AACG CGTT TC CGGTTTTGG
 T _ CC
 GAM95 DKFZP434E2318 3' GTTTTGGTTAGTGCCACAA 25817 CT ACAG
 TTG GCA AGCCAAAAC
 ||| ||| |||||
 AAC CGT TTGGTTTTG
 AC GA_
 GAM95 DKFZp761D112 3' TTTGACTGCTGCGGCAA 26078 A AGC
 TTGCTGCA CAG CAAA
 ||||| ||| |||
 AACGGCGT GTC GTTT
 C A_
 GAM95 FHR5 3' TTTTGTGGTTGTAGCAA 25086 AGAGC
 TTGCTGCAAC CAAAA
 ||||| |||
 AACGATGTTG GTTT
 GT_
 GAM95 FLJ22390 5' GGTTTTGGCTTGTGATCA 22959 CA_ G
 TG ACA AGCCAAAACC
 || ||| |||||
 AC TGT TCGGTTTTGG
 TAG _
 GAM95 FLJ31153 3' TTTGTTTGTACTGCGGCAA 29416 _ GC
 TTGCTGCA ACAGA CAAA
 ||||| ||| |||
 AACGGCGT TGTTT GTTT
 CA _
 GAM95 FUBP3 3' GTTTTTTCTGTTGCAACAG 31875 C CC
 TTG TGCAACAGAG AAAAC
 ||| ||||| |||
 GAC ACGTTGTCTT TTTTG
 A _
 GAM95 GTPBP1 5' GGCTTTGACTCGGACTGCAGCG 10498 A_____
 A TTGCTGCA CAGAGCC
 ||||| |||||
 AGCGACGT GTTTCGG
 CAGGCTCA
 GAM95 KIAA0237 3' GGCTCTTGGGATGCAGCAA 16452 A_ _
 TTGCTGCA CA GAGCC
 ||||| || |||
 AACGACGT GT CTCGG
 AGG T
 GAM95 KIAA0420 3' GGCTCATCTCTGCTGCAGTAA 31727 A ____
 TTGCTGCA CAGA GCC
 ||||| ||| |||

			AATGACGT GTCT CGG		
			C CTACT		
GAM95	KIAA0483	3'	GTTTTGCCATTGCAGCAA 17530	_____	
			TTGCTGCAA CAGAGC		
			AACGACGTT GTTTTG		
			ACC		
GAM95	KIAA0515	5'	GGTCTTAGTGGCTGCAGCAG 31927	ACAGA AA_____	
			TTGCTGCA GCCA ACC		
			GACGACGT CGGT TGG		
			_____ GATTC		
GAM95	KIAA0759	3'	TTGGCTCTGTCCAGCAA 33443	CA	
			TTGCTG ACAGAGCCAA		
			AACGAC TGTCTCGGTT		
			C_		
GAM95	KIAA1155	3'	GGCCTTTGAACTGCAGCAG 31196	A__ _	
			TTGCTGCA CAGAG CC		
			GACGACGT GTTTC GG		
			CAA C		
GAM95	KIAA1449	3'	TTTGCTGTTGCACAA 21900	C AGC	
			TTG TGCAACAG CAAA		
			AAC ACGTTGTC GTTT		

GAM95	KIAA1656	3'	GGTTCTGGCTCTGACACAG 32735	CAA A	
			CTG CAGAGCCA AACC		
			GAC GTCTCGGT TTGG		
			ACA C		
GAM95	KIAA1735	3'	GGCCTCAATGGTTGCAGCAA 42346	A__ _	
			TTGCTGCAAC GAG CC		
			AACGACGTTG CTC GG		
			GTAA C		
GAM95	KIAA1932	3'	GGTTTTGGCTTGTCACAGCAA 36349	CA G	
			TTGCTG ACA AGCCAAAACC		
			AACGAC TGT TCGGTTTTTG		
			AC _		
GAM95	MAN1	3'	GGCACATTGTTGCAGCAA 15618	A__	
			TTGCTGCAACAG GCC		
			AACGACGTTGTT CGG		
			ACA		
GAM95	MGC12966	3'	TTTTGGTCTGCAGCAA 26421	ACA G	
			TTGCTGCA GA CCAAAA		

AACGACGT CT GGTTTT

GAM95 MGC16063 3' GGTCTTAACCTCTGATTGTAGCA 27592 _ CC A
A TTGCTGCAA CAGAG AA ACC
||||||| |||| || |||
AACGATGTT GTCTC TT TGG
A AA C

GAM95 MKRN2 3' TTGTTGCCACATGTGCAGCAA 35858 A GA__ _
TTGCTGCA CA GC CAA
||||||| || || |||
AACGACGT GT CG GTT
_ ACAC TT

GAM95 PDE10A 3' GGTTTATTTATGTTGTAGCAA 13462 _____
TTGCTGCAACA GAGCC
||||||| |||||
AACGATGTTGT TTTGG
ATTTA

GAM95 PDE7B 5' GGTCTGGGCACTGCAGCAG 21012 ACA A AAA
TTGCTGCA G GCC ACC
||||||| | ||| |||
GACGACGT C CGG TGG
_ A GTC

GAM95 PROL2 3' TTTGCCTTGTTGCAACA 13685 C A C
TG TGCAACAG GC AAA
|| ||||| || |||
AC ACGTTGTT CG TTT
A C _

GAM95 SSH2 3' GGTTTTTGGCTTATCACAGCA 31185 CAACA _
TGCTG GAGCCAAAA CC
||||| ||||| |||
ACGAC TTCGGTTTT GG
ACTA_ T

GAM95 LOC122704 3' GTTTTGGCCAGGCAGTCAA 36693 _ AACAGA
TTG CTGC GCCAAAAC
||| ||| |||||
AAC GACG CGGTTTTG
T GAC_

GAM95 LOC124944 5' GGCTCGGGTGTGTAGCAA 36777 _____
TTGCTGCAACA GAGCC
||||||| |||||
AACGATGTTGT CTCGG
GGG

GAM95 LOC143153 3' GGTCTGACTCTGTCACCCAG 37580 CA__ C A
CTG ACAGAG CA AACC
||| ||||| || |||
GAC TGTCTC GT TTGG
CCAC A C

GAM95 LOC143154 3' GGTCTGACTCTGTCACCCAG 37587 CA__ C A
CTG ACAGAG CA AACC
||| ||||| || |||

		GAC TGTCTC GT TTGG	
		CCAC A C	
GAM95	LOC144747 5'	GGTGCTGCTGTCTGCAGCAA 37784	_ _ CAAA
		TTGCTGCA ACAG AGC ACC	
		AACGACGT TGTC TCG TGG	
		C G _	
GAM95	LOC146515 3'	GGTTTTTGAATTGCAGCAG 38194	C_
		TTGCTGCAA AGAGCC	
		GACGACGTT TTTTGG	
		AAGT	
GAM95	LOC147658 3'	GGTTTTGGCTCTACCGG 38354	CAAC
		CTG AGAGCCAAAACC	
		GGC TCTCGGTTTTGG	
		CA_	
GAM95	LOC149175 3'	GTTTTGAAGTCTGCAGCAG 38662	ACA C_
		TTGCTGCA GAG CAAAAC	
		GACGACGT CTC GTTTTG	
		_ AA	
GAM95	LOC151178 5'	GGCGTTCTGTTACAGCAG 39072	C _
		TTGCTG AACAGA GCC	
		GACGAC TTGTCT CGG	
		A TG	
GAM95	LOC158156 3'	GGTTTTGGTGCAGTTGCACAA 39743	C AGA
		TTG TGCAAC GCCAAAACC	
		AAC ACGTTG TGGTTTTGG	
		_ ACG	
GAM95	LOC158527 5'	GTTTCCACTTCTGCAGCAA 39863	ACA CCA
		TTGCTGCA GAG AAAC	
		AACGACGT TTC TTTG	
		C_ ACC	
GAM95	LOC165693 3'	GGCTCCCTCGTTCTGCAGCAA 40188	_ A_
		TTGCTGCA AC GAGCC	
		AACGACGT TG CTCGG	
		CT CTCC	
GAM95	LOC168576 5'	GGTCTTGGGAGGCCTGCAGCAG 40255	ACAGAG A
		TTGCTGCA CCAA ACC	
		GACGACGT GGTT TGG	
		CCGGAG C	
GAM95	LOC200301 5'	GGTTCACCTGTGTTGTAGCAA 42782	_
		TTGCTGCAACA GAGCC	

			AACGATGTTGT	CTTGG		
			GTCCA			
GAM95	LOC203429 3'	GGTCAGTGTCTGTTGCACAA	43051	C	_____	
		TTG TGCAACAGA	GCC			
		AAC ACGTTGTCT	TGG			
		—	GTGAC			
GAM95	LOC219294 3'	GGTTCTGACTCTGTCACCCAG	44688	CA__	C A	
		CTG ACAGAG CA	AACC			
		GAC TGTCTC GT	TTGG			
		CCAC	A C			
GAM95	LOC219295 3'	GGTTCTGACTCTGTCACCCAG	44682	CA__	C A	
		CTG ACAGAG CA	AACC			
		GAC TGTCTC GT	TTGG			
		CCAC	A C			
GAM95	LOC219401 3'	GGTCTTCAAGTTGCAGCAA	44593	A__	—	
		TTGCTGCAAC	GAG CC			
		AACGACGTTG	TTC GG			
		AAC	T			
GAM95	LOC220705 3'	GGTTTTGGTGTCTGCTACAA	43835	CT	ACAGA	
		TTG GCA	GCCAAAACC			
		AAC CGT	TGGTTTTGG			
		AT	CCTG_			
GAM95	LOC221540 3'	GGCCTCACTCTGTTGCACAA	45045	C	_____	
		TTG TGCAACAGA	GCC			
		AAC ACGTTGTCT	CGG			
		—	CACTC			
GAM95	LOC221833 3'	GTCTTGTGCGAATCGCTGCAGCA	44457	ACA GC__	A	
	G	TTGCTGCA GA	CAA AC			
		GACGACGT CT	GTT TG			
		CG_	AAGCT C			
GAM95	LOC257354 3'	GGCTCATCTCTGCTGCAGTAA	45580	A	_____	
		TTGCTGCA CAGA	GCC			
		AATGACGT GTCT	CGG			
		C	CTACT			
GAM95	LOC257545 3'	GGCCTCACTCTGTTGCACAA	46693	C	_____	
		TTG TGCAACAGA	GCC			
		AAC ACGTTGTCT	CGG			
		—	CACTC			
GAM95	LOC257598 3'	GGCCTCACTCTGTTGCACAA	46750	C	_____	
		TTG TGCAACAGA	GCC			

			AAC ACGTTGTCT CGG		
			— CACTC		
GAM95	LOC51580	3'	GGTTCTTCTGAAATTGCAGCAG 18017	—	—
			TTGCTGCAA CAGA GCC		
			GACGACGTT GTCT TGG		
			AAA TCT		
GAM95	LOC90092	3'	GTTTTGGTCGTACACAGCAG 30791	CA	A G
			TTGCTG AC GA CCAAAAC		
			GACGAC TG CT GGTTTTG		
			AC —		
GAM95	LOC90133	3'	TTTGGCTCTGGCACAG 30870	C	AA
			TTG TGC CAGAGCCAAA		
			GAC ACG GTCTCGGTTT		
			— —		
GAM96	AGTR1	3'	AGAGAACATTCTCTGCAG 25593	—	CGGG G
			CTGCAG GGAAT GTTC CT		
			GACGTC CCTTA CAAG GA		
			T — A		
GAM96	AGTR1	3'	AGAGAACATTCTCTGCAG 6341	—	CGGG G
			CTGCAG GGAAT GTTC CT		
			GACGTC CCTTA CAAG GA		
			T — A		
GAM96	AGTR1	3'	AGAGAACATTCTCTGCAG 11242	—	CGGG G
			CTGCAG GGAAT GTTC CT		
			GACGTC CCTTA CAAG GA		
			T — A		
GAM96	AGTR1	3'	AGAGAACATTCTCTGCAG 14308	—	CGGG G
			CTGCAG GGAAT GTTC CT		
			GACGTC CCTTA CAAG GA		
			T — A		
GAM96	AGTR1	3'	AGAGAACATTCTCTGCAG 25768	—	CGGG G
			CTGCAG GGAAT GTTC CT		
			GACGTC CCTTA CAAG GA		
			T — A		
GAM96	PPP2R5D	3'	GCCAACCCCCCTGCAG 12917	AATCG	C
			CTGCAGGG GGGTT GC		
			GACGTCCC CCCAA CG		
			— C		
GAM96	FLJ10853	3'	AGCAAGAATGACCTCCTGCAG 20210	AATC	G_ —
			CTGCAGGG GG GTTC GCT		

			GACGTCCT CC TAAG CGA		
			____ AG AA		
GAM96	KIAA0189	5'	AGCAACAGGATTCCCTCAGTA 16316	C	GGG C
			TACTG AGGGAATC GTT GCT		
			ATGAC TCCCTTAG CAA CGA		
			____ GA ____		
GAM96	KIAA1100	3'	GCGAGGAGTCCCTGCA 17085	A	GGGG
			TGCAGGGA TC TTCGC		
			ACGTCCCT AG GAGCG		
			G ____		
GAM96	PDE8A	3'	CCCTGCCGACCCCTGCAGTA 31378	AAT__	
			TACTGCAGGG CGGGG		
			ATGACGTCCC GTCCC		
			CAGCC		
GAM96	LOC149832	5'	AACCTTAACATCCCCTACAG 41077	C A C__	
			CTG AGGG AT GGGGTT		
			GAC TCCC TA TTCCAA		
			A C CAA		
GAM97	FLJ11618	3'	GCAAAGGTCATAACCTCACCA 22793	AG A	GAG
			TG GAG TTATGATT GT		
			AC CTC AATACTGG CG		
			CA C AAA		
GAM98	CBFB	3'	ATTGATGCAATTTGATATTTTT 7505	CATA	G
			AAAAATATCAAA GCAT AAT		
			TTTTTATAGTTT CGTA TTA		
			AA__ G		
GAM98	CBFB	3'	ATTGATGCAATTTGATATTTTT 23146	CATA	G
			AAAAATATCAAA GCAT AAT		
			TTTTTATAGTTT CGTA TTA		
			AA__ G		
GAM98	DYRK1A	5'	TTGTAGTTATGTTAGATATT 28191	A	_TG
			AATATC AACATAGC A A		
			TTATAG TTGTATTG T T		
			A A GT		
GAM98	SNX9	3'	CTATGTTTGTATATTTTT 18329	_	
			AAAAATAT CAAACATAG		
			TTTTTATA GTTTGTATC		
			T		
GAM98	TCTE1L	3'	TATGTGCATGTTTGTATTTTT 35142	A_	
			AAAAATATCAAACAT GCATG		

			TTTTATAGTTTGTA TGTAT		
			CG		
GAM98	TSN	3'	ATGTGATGCTTGATATTTT 10984	A A	
			AAAATATCAA CAT GCAT		
			TTTTATAGTT GTA TGTA		
			C G		
GAM98	NTT73	3'	ATTCATTTTGTTTGTTTGATAT 19823	T	___
			ATATCAAACA AGCA TGAAT		
			TATAGTTTGT TTGT ACTTA		
			_ TTT		
GAM98	NUDT11	3'	TGTATATGTTTGAAATTTT 30145	A	_
			AAAAT TCAAACATA GCA		
			TTTTA AGTTTGTAT TGT		
			A A		
GAM98	POPX1	3'	ATTTAGTTATATTGATATTTT 17118	C A	
			AAAATATCAAA ATAGC TGAAT		
			TTTTATAGTTT TATTG ATTTA		
			A _		
GAM98	TRIM2	3'	ATGTCATGTTTGACATTTT 17598	A	AG
			AAAAAT TCAAACAT CAT		
			TTTTTA AGTTTGTA GTA		
			C CT		
GAM99	TSN	3'	CACTTG GGGAGATTTGCCACA 10985	C	GAGTAA
			TG GGCAAATCTT AAGTG		
			AC CCGTTTAGAG TTCAC		
			A GGG___		
GAM99	KIAA1535	3'	CACTTTTACCCGCTCACTGCC 38764	AATCT	A
			GGCA TG GTAAAAGTG		
			CCGT GC CATTTTCAC		
			CACTC C		
GAM99	NECL1	3'	CACTCTTACCCAAGACTCTG 22163	CAAA	A A
			CGG TCTTG GTAA AGTG		
			GTC AGAAC CATT TCAC		
			TC___ C C		
GAM100	NFIB	3'	AGATAATAGACCAGCAATTGCA 12120	CC	TTC
			TGTAA GTT GTCTATTATCT		
			ACGTT CGA CAGATAATAGA		
			AA C___		
GAM100	DKFZp434J0617	3'	ATAATAGGAACGGCGACA 25980	AA	TCGT
			TGT CCGTTT CTATTAT		

ACA GGCAAG GATAATA
 GC _____
 GAM100 LCE 3' ATAATAGACAAAAGAAAATGGC 23532 AA _____
 ACA TGT CCGTTTTC GTCTATTAT
 ||| ||||| |||||
 ACA GGTAAAAG CAGATAATA
 C_ AAAA
 GAM100 mPA-PLA1 3' ATAATAGAAAGAAAGCTACA 29249 ACC G_
 TGTA GTTTTC TCTATTAT
 ||| ||||| |||||
 ACAT CGAAAG AGATAATA
 _____ AA
 GAM100 LOC158629 5' AGATAATAGTTGTTGAAAGC 42018 T____
 GTTTTCG CTATTATCT
 ||||| |||||
 CGAAAGT GATAATAGA
 TGTT
 GAM101 FECH 3' TAATGCAATAACTGTTATC 5636 C GA
 GATAACAGTTAT TG ATTA
 ||||| || |||
 CTATTGTCAATA AC TAAT
 _ G_
 GAM101 HS3ST2 3' TAATTCCAAGTGGCATGTATC 12680 A _ TC
 GATA CA GTTA TGAATTA
 ||| || ||| |||||
 CTAT GT CGGT ACCTTAAT
 _ A GA
 GAM101 NT5C2 3' AATTCCAGATTTCTTTGTC 14524 C TT
 GATAA AG ATCTGGAATT
 ||||| || |||||
 CTGTT TC TAGACCTTAA
 _ TT
 GAM101 NXF5 3' AATTCCAGTCTGTGCATC 27006 A_ TTAT
 GAT ACAG CTGGAATT
 ||| ||| |||||
 CTA TGTC GACCTTAA
 CG T____
 GAM101 NXF5 3' AATTCCAGTCTGTGCATC 27007 A_ TTAT
 GAT ACAG CTGGAATT
 ||| ||| |||||
 CTA TGTC GACCTTAA
 CG T____
 GAM101 PKHD1 3' TAATTCCACACTGTTA 28943 TATC
 TAACAGT TGAATTA
 ||||| |||||
 ATTGTCA ACCTTAAT
 C____
 GAM101 PPP1R8 3' TAATTCCAGAGTACTGTCCTC 8570 TA TA
 GA ACAGT TCTGGAATTA
 || ||||| |||||

			CT TGTCA AGACCTTAAT		
			CC TG		
GAM101	PPP1R8	3'	TAATTCAGAGTACTGTCCTC 15340	TA	TA
			GA ACAGT TCTGGAATTA		
			CT TGTCA AGACCTTAAT		
			CC TG		
GAM101	PPP1R8	3'	TAATTCAGAGTACTGTCCTC 28856	TA	TA
			GA ACAGT TCTGGAATTA		
			CT TGTCA AGACCTTAAT		
			CC TG		
GAM101	SLC7A6	3'	TAATTTCAACAACCGTTATC 10132	A	ATC
			GATAAC GTT TGGAATTA		
			CTATTG CAA ACTTTAAT		
			C C__		
GAM101	FLJ10178	3'	TAATTCAGTAACTGTTTTTC 19754	T	T
			GA AACAGTTA CTGGAATTA		
			CT TTGTCAAT GACTTTAAT		
			T _		
GAM101	HEYL	3'	TAATTCATCAGACTGCTGTC 15932	A	ATC
			GATA CAGTT TGGAATTA		
			CTGT GTCAG ACCTTAAT		
			C ACT		
GAM101	KIAA0173	3'	TAATCCCAGTAGCTGTTA 16042	T	A
			TAACAGTTA CTGG ATTA		
			ATTGTCGAT GACC TAAT		
			_ C		
GAM101	NSBP1	3'	TAATTCAGAGAATTTTTATC 25045	C	A
			GATAA AGTT TCTGGAATTA		
			CTATT TTAA AGACCTTAAT		
			T G		
GAM101	PRO1257	3'	ATTTTGAAAAGTGTATC 20657	A	T
			GATAACAGTT TC GGAAT		
			CTATTGTCAA AG TTTTA		
			A _		
GAM101	ZDHC2	3'	TAATTCAGCCTTTTGTTTTTC 18492	T	TTAT
			GA AACAG CTGGAATTA		
			CT TTGTT GACCTTAAT		
			T TTCC		
GAM101	LOC118851	3'	TAATTCAGACTCTGATC 37204	AA	TTA
			GAT CAG TCTGGAATTA		

CTA GTC AGACCTTAAT
 _ TC_
 GAM101 LOC145813 3' AATCCCAGATAATCATATC 40597 ACA A
 GATA GTTATCTGG ATT
 ||| ||||| |||
 CTAT TAATAGACC TAA
 AC_ C
 GAM101 LOC220565 3' AATTCCTTTAGATGTTATC 43630 G TCT
 GATAACA TTA GGAATT
 ||||| || |||||
 CTATTGT GAT CCTTAA
 A TT_
 GAM101 LOC85414 3' TAATTCCAAATGCTGTTA 26953 T C
 TAACAGT AT TGGAATTA
 ||||| || |||||
 ATTGTCG TA ACCTTAAT
 _ A
 GAM101 LOC90141 3' TAATTCCAAATACTGGTATC 30882 A TATC
 GATA CAGT TGGAATTA
 ||| ||| |||||
 CTAT GTCA ACCTTAAT
 G TAAA
 GAM102 C8orf2 3' CATGGTGTGACGGCACCTGT 14020 C AAA
 ACGGG GCCTGATA ATG
 |||| ||||| |||
 TGTCC CGGACTGT TAC
 A GG_
 GAM102 KCNK13 3' CATTTTTACCAGGGCTTGGGGA 22592 A_ G A
 TC CGGGC CCTG TAAAAATG
 || |||| ||| |||||
 AG GTTCG GGAC ATTTTTAC
 GG _ C
 GAM102 STARD7 3' CATTTTTATCAAATGTGTGA 21355 GG CC
 TCAC GCG TGATAAAAATG
 ||| || |||||
 AGTG TGT ACTATTTTAC
 _ AA
 GAM102 STARD7 3' CATTTTTATCAAATGTGTGA 29259 GG CC
 TCAC GCG TGATAAAAATG
 ||| || |||||
 AGTG TGT ACTATTTTAC
 _ AA
 GAM102 LOC220930 3' CATTTTTACAGCTACCCTGATT 44733 C CGC A
 AATCA GGG CTG TAAAAATG
 |||| || || |||||
 TTAGT CCC GAC ATTTTTAC
 _ ATC _
 GAM102 LOC57107 3' CATTTTTATCAGGGCCC 21648 G
 GGGC CCTGATAAAAATG
 ||| |||||

CCCG GGA C T A T T T T T A C

GAM102 LOC90643 3' C A T T T T T A T C A A A A G C A G G T T A 31852 C G G G C C
T T A A T A C G C T G A T A A A A A T G

||| || || |||||
T T A T G C G A C T A T T T T T A C
T G A A A

GAM103 ATP8A2 3' C A T T A G A A G A G A T G C C T T T 44918 _
A A A G G T A T C T C T C T G A T G
||||| |||||
T T T C C G T A G A G A G A T T A C

A

GAM103 GCNT3 5' T G T C A G A A A A T A C C T T T 11140 C T C
A A A G G T A T T C T G A T G
||||| |||||
T T T C C A T A A G A C T G T

A A _

GAM103 SYNGR3 3' T T C A T C A G A C A G A C A C C T C C 10409 A A C
A A G G T T C T T C T G A T G G A
| ||| || |||||
C T C C A A G A A G A C T A C T T
C C C

GAM103 VLDLR 3' C A T C A A G A T A C C T T T 34450 C T C
A A A G G T A T C T T G A T G
||||| |||||
T T T C C A T A G A A C T A C

GAM103 AP1S2 3' A A T G G T G C A G A A A G A G A T A C C T 10000 _ A T G G A
T T A A A G G T A T C T C T C T G C A T T

||||| ||| |||
T T T C C A T A G A G A G A C G T A A
A A G T G _

GAM103 BTBD3 3' A T G T A A T G A G A T A C C T T T 17336 T C T G A T G G
A A A G G T A T C T C A C A T
||||| |||
T T T C C A T A G A G T G T A

T A A _ _ _

GAM103 FLJ10290 3' A A T G T C C A G C A G A G T T A C C 19796 T C T A
G G T A C T C T G T G G A C A T T
||| |||| |||||
C C A T G A G A C A C C T G T A A

T _ G

GAM103 FLJ20079 3' T C C T A C C A G A G A G A A A C C T T T 19178 A A T _
A A A G G T T C T C T C T G G G A
||||| ||||| |||
T T T C C A A G A G A G A C C C T

A C A T

GAM103 FLJ20695 3' C A T A G A A C A G A T A C C T T T 19612 C _ A
A A A G G T A T C T T C T G T G
||||| ||||| |||

TTTCCATAGA AGAT AC
 CA _
 GAM103 HOMER-2B 3' AATGTCCACCAGACACCAGCC 11246 ATCTC A
 GGT TCTG TGGACATT
 ||| ||| |||||
 CCG AGAC ACCTGTAA
 ACCAC C
 GAM103 KIAA1871 3' TTCATACCAGAGAGAAACC 30708 A _
 GGT TCTCTCTG ATGGA
 ||| ||||| ||||
 CCA AGAGAGAC TACTT
 A CA
 GAM103 YAP1 3' GTCCAGCAAGATACTTT 12754 CTC A
 AAGGTATCT TG TGGAC
 ||||| || ||||
 TTTCCATAGA AC ACCTG
 _ G
 GAM103 LOC221477 3' ATGTCCATAAGAAACCCTT 44251 TATCTC G
 AAGG TCT ATGGACAT
 ||| ||| |||||
 TTCC AGA TACCTGTA
 CAA_ A
 GAM104 C11orf25 5' AACCCCGCTCAACGCCACCC 25397 A_ CGT T
 TCA TGAGGGGT GCGT GT GGGTT
 ||||| ||| || |||||
 ACTCCCCA CGCA CG CCCAA
 CC ACT C
 GAM104 LOC150142 5' AACCCAGAACACCACCTCTCA 38847 AGC C G
 TGAGGGGT GT GT TTGGGTT
 ||||| || || |||||
 ACTCTCCA CA CA GACCCAA
 C_ _ A
 GAM104 LOC200982 3' ACCCAAATGTCACCCCCCA 43371 A AG CGTG
 TG GGGGT CGT TTGGGT
 || |||| ||| |||||
 AC CCCC GTA AACCCA
 C CT _
 GAM105 FLJ10292 3' GTTGCTGATGGACAGTGA 19801 CGC
 TTAC CCATCAGCAAC
 ||| |||||
 AGTG GGTAGTCGTTG
 ACA
 GAM106 ITPR1 3' TCACAATACATTTGTAGCTCCC 7986 AG CTA
 GGGAGC TAAATGTA TGA
 |||| ||||| |||
 CCCTCG GTTTACAT ACT
 AT AAC
 GAM106 MMP19 3' CATTTTATTACATGCTCCCA 8267 _ A TACT
 TGGGAGCA GT AATG ATG
 ||||| || ||| |||

ACCCTCGT CA TTAT TAC
 A C TT__
 GAM106 MMP19 3' CATTTTATTACATGCTCCCA 23074 _ A TACT
 TGGGAGCA GT AATG ATG
 ||||| || ||| ||
 ACCCTCGT CA TTAT TAC
 A C TT__
 GAM106 POLS 3' GTCATTGTTTTACTGCCCTCA 13865 A TGT T
 TGGG GCAGTAAA AC ATGAC
 ||| ||||| || ||||
 ACTC CGTCATTT TG TACTG
 C _ T
 GAM106 C9orf5 3' TCAGGCCTATCCTCTGCTCCCA 25717 TAA TA A
 TGGGAGCAG ATG CT TGA
 ||||| || ||| ||
 ACCCTCGTC TAT GG ACT
 TCC CC _
 GAM106 Di-Ras2 3' AGAACATTTACTGGCCCCA 19042 AG A
 TGGG CAGTAAATGT CT
 ||| ||||| ||
 ACCC GTCATTTACA GA
 CG A
 GAM106 DKFZP434P211 3' CATAACACAGGAGACCTGCTCC 15865 TAAA__ AC
 C GGGAGCAG TGT TATG
 ||||| || ||| ||
 CCCTCGTC ACA ATAC
 CAGAGG CA
 GAM106 FLJ23017 3' CACAGTACCACTGCCACCA 23128 GA AAAT A
 TGG GCAGT GTACT TG
 || |||| |||| ||
 ACC CGTCA CATGA AC
 AC C__ C
 GAM106 KIAA0523 3' GTACATTCACTGCTGCCA 33644 G A
 TGG AGCAGT AATGTAC
 || |||| ||||| ||
 ACC TCGTCA TTACATG
 G C
 GAM106 KIAA1046 3' TCAGCCATTTACTCTCCCA 17221 C TACTA
 TGGGAG AGTAAATG TGA
 |||| ||||| ||
 ACCCTC TCATTTAC ACT
 _ CG__
 GAM106 PPP1R10 3' GTCAGTCACTCCCTGCTCCCA 8578 TAAAT ACTA
 TGGGAGCAG GT TGAC
 ||||| || ||| ||
 ACCCTCGTC CA ACTG
 CCT__ CTCG
 GAM106 SEC15B 3' GTCCATTCTGCTCCCA 33126 TA T
 TGGGAGCAG AATG AC
 ||||| ||| ||

			ACCCTCGTC TTAC TG	
			C_ C	
GAM106	TIMM9	5'	GTCACCTTGACATTACTGCTCCC 14831	A ACTA
	A		TGGGAGCAGTAA TGT TGAC	
			ACCCTCGTCATT ACA ACTG	
			_ GTTC	
GAM106	LOC150174	3'	CATAACACAGGAGACCTGCTCC 38872	TAAA__ AC
	C		GGGAGCAG TGT TATG	
			CCCTCGTC ACA ATAC	
			CAGAGG CA	
GAM106	LOC150213	3'	CATAACACAGGAGACCTGCTCC 36956	TAAA__ AC
	C		GGGAGCAG TGT TATG	
			CCCTCGTC ACA ATAC	
			CAGAGG CA	
GAM106	LOC152313	5'	AGTAGCATCCCTGCTCCCA 41472	TAA _
			TGGGAGCAG ATGT ACT	
			ACCCTCGTC TACG TGA	
			CC_ A	
GAM106	LOC201965	3'	GTCATCTGTTTAACACTCCCA 42934	CAG TACT
			TGGGAG TAAATG ATGAC	
			ACCCTC ATTTGT TACTG	
			ACA C__	
GAM107	EMP1	3'	GAGTAAACCATGTATTCCC 7134	AT C
			GGGGATG TGTGGT TACTC	
			CCCTTAT GTACCA ATGAG	
			_ A	
GAM107	MAPK14	3'	AGTAAAGGCCTCATCTCC 7000	TTGT _
			GGGGATGA GGTCT ACT	
			CCTCTACT CCGGA TGA	
			_ AA	
GAM107	MAPK14	3'	AGTAAAGGCCTCATCTCC 29111	TTGT _
			GGGGATGA GGTCT ACT	
			CCTCTACT CCGGA TGA	
			_ AA	
GAM107	MAPK14	3'	AGTAAAGGCCTCATCTCC 29104	TTGT _
			GGGGATGA GGTCT ACT	
			CCTCTACT CCGGA TGA	
			_ AA	
GAM107	ST7	3'	ATCATTCAGATCATCCCC 15098	_
			GGGGATGATT GTGGT	

			CCCCTACTAG TACTA		
			ACT		
GAM107	SYNGR1	3'	AGTAGCACCATTATCCCC 11058	ATT	_
			GGGGATG GTGGT CTACT		
			CCCCTAT TACCA GATGA		
			___ C		
GAM107	ARHGEF2	3'	TAGGCCACAACACCCC 11092	A A	
			GGGG TG TTGTGGTCTA		
			CCCC AC AACACCGGAT		

GAM107	BLCAP	3'	AGTGGCCATCATCCTC 13520	TTG T	
			GGGGATGA TGG CTACT		
			CTCCTACT ACC GGTGA		

GAM107	FLJ14800	3'	GAGTAGACAGCCCCCTCCCC 26622	TGATT G	
			GGGGA GT GTCTACTC		
			CCCCT CG CAGATGAG		
			CCCC_ A		
GAM107	HSPC019	3'	AGTAGCTTAATTACCCC 15251	A T T	
			GGGG TGATTG GG CTACT		
			CCCC ATTAAT TC GATGA		

GAM107	KIAA1729	5'	AGTAGAAGTGTTATCCCC 42947	TGTGG	
			GGGGATGAT TCTACT		
			CCCCTATTG AGATGA		
			TGA_		
GAM107	OLFM3	3'	AGTAAAGCATCATCCTC 39959	T GGTC	
			GGGGATGAT GT TACT		
			CTCCTACTA CG ATGA		
			_ AA_		
GAM107	PASK	5'	AGACATACATTTCATCCCC 17501	T _	
			GGGGATGA TGTG GTCT		
			CCCCTACT ACAT CAGA		
			T A		
GAM107	LOC253613	3'	AGAGATTGTTCATTCCC 46007	TGT A	
			GGGGATGAT GGTCT CT		
			CCCTTACTG TTAGA GA		

GAM107	LOC90092	5'	GCTGTGGCAATCGTCCCC 30789	___	
			GGGGATGATTGT GGT		

CCCCTGCTAACG TCG
 GTG
 GAM107 LOC91748 3' GAGCCCCTCATCATCCCC 33287 T T TCTA
 GGGGATGAT G GG CTC
 ||||| | || ||
 CCCCTACTA C CC GAG
 _ T CC_

GAM107 LOC92249 5' AGTCAGTCACAATCTCCCC 34019 T T _
 GGGGA GATTGTGG CT ACT
 |||| ||||| || ||
 CCCCT CTAACACT GA TGA
 _ _ C

GAM108 ADCY7 3' CATGTAAGGAGGACTACTGT 6782 C GGG
 ACAG AGTT CTTACATG
 ||| ||| |||||
 TGTC TCAG GAATGTAC
 A GAG

GAM108 RAB4A 3' CATGTAAGCTGGGGCCGCTCA 10925 C A _G
 A AGC GT T GGCTTACATG
 | ||| | |||||
 A TCG CG G TCGAATGTAC
 C C G G

GAM108 TIF1 3' CATGTAAGATGGCAACTGTATT 30276 CA GG
 A TAATACAG GTTG CTTACATG
 ||||| ||| |||||
 ATTATGTC CGGT GAATGTAC
 AA A_

GAM108 FLJ14855 3' CATGTTCTTAACTGCT 27058 CTT
 AGCAGTTGGG ACATG
 ||||| ||||
 TCGTCAATTC TGTAC
 T_

GAM108 FLJ23462 3' ATGTAAGCTGTGCTGTTTA 24263 C TG
 A AGCAGT GGCTTACAT
 | |||| |||||
 A TTGTCG TCGAATGTA
 T TG

GAM108 GOLPH3 3' ATGTAAATCTATTGTATTA 22685 CAGT GC
 TAATACAG TGG TTACAT
 ||||| || |||||
 ATTATGTT ATC AATGTA
 _ TA

GAM108 LOC145368 3' AGCCCATCTGCTGTATTA 37826 T
 TAATACAGCAG TGGGCT
 ||||| |||||
 ATTATGTCGTC ACCCGA
 T

GAM109 DKFZp547l094 3' TGCCCTTGAACACTCTTACA 25858 C A TATA
 TG AAGA GT CAAGGGCA
 || ||| || |||||

AC TTCT CA GTTCCCGT
 A _ CAA_
 GAM109 FLJ11996 5' CCCTTGTGCGTATCTCACA 24532 CA AGTTA
 TGTG AGA TACAAGGG
 |||| ||| |||||
 ACAC TCT GTGTTCCC
 _ ATGC_
 GAM109 FLJ32334 3' CCCTTGTGTTACCTCCCGCCA 29366 T AA A T
 TG GC GA GT ATACAAGGG
 || || || || |||||
 AC CG CT CA TGTGTTCCC
 _ CC C T
 GAM109 HBP1 3' GCCCCTAAATTTTGCAC 14561 AG TACAA
 GTGCAAGA TTA GGGC
 ||||| ||| |||
 CACGTTTT AAT CCCG
 A_ C____
 GAM109 KIAA0063 3' TGCCCTTGCCACTTCCCCAAAC 17018 GCAA_ TATA
 A TGT GAAGT CAAGGGCA
 ||| |||| |||||
 ACA CTTCA GTTCCCGT
 AACCC CC_
 GAM109 LOC221296 3' TGCCCTTGGAATACTCCTGCA 44172 A A TATA_
 CA TGTGCA GA GT CAAGGGCA
 ||||| ||| |||||
 ACACGT CT CA GTTCCCGT
 C _ TAAGG
 GAM110 DUSP4 3' AAAGTTGGGACTGAGCAG 7089 _ ATTC
 TTGC CAG TCCCAACTTT
 |||| ||| |||||
 GACG GTC AGGGTTGAAA
 A _____
 GAM110 DUSP4 3' AAAGTTGGGACTGAGCAG 27664 _ ATTC
 TTGC CAG TCCCAACTTT
 |||| ||| |||||
 GACG GTC AGGGTTGAAA
 A _____
 GAM110 EIF5A 3' AAAGCGGTGGATTCTGGCAA 7703 T TC AA
 TTGCCAGA TC CC CTTT
 ||||| || || |||
 AACGGTCT AG GG GAAA
 T GT C_
 GAM110 FGF13 3' AAAGTTGGGTTCTTGGCA 27361 ATTCT
 TGCCAG CCCCAACTTT
 ||||| |||||
 ACGGTT GGGTTGAAA
 CTT_
 GAM110 IQGAP2 3' AAAGTTGGGGGGTGGGAA 13427 G GAT
 TT CCA TCTCCCAACTTT
 || ||| |||||

			AA GGT GGGGGGTTGAAA		
			G ____		
GAM110	IRAK1	3'	AAAGTTGGGAGCATGGCAG 7297	GATT	
			TTGCCA CTCCCAACTTT		
			GACGGT GAGGGTTGAAA		
			AC__		
GAM110	KLHL2	3'	AAGTGA CTGAGAATCTAGCA 14111	C	CCA_
			TGC AGATTCTC ACTT		
			ACG TCTAAGAG TGAA		
			A TCAG		
GAM110	OPHN1	3'	AAGTTAGAGAATCTGGCAA 8399	CC	
			TTGCCAGATTCTC AACTT		
			AACGGTCTAAGAG TTGAA		
			A_		
GAM110	WBSCR1	3'	TGGGTCTAGAATCTGGCA 22725	____	
			TGCCAGATTCT CCCA		
			ACGGTCTAAGA GGGT		
			TCT		
GAM110	WBSCR1	3'	TGGGTCTAGAATCTGGCA 25708	____	
			TGCCAGATTCT CCCA		
			ACGGTCTAAGA GGGT		
			TCT		
GAM110	ARHGAP11A	5'	AAGTGGAGAGAATCTGGCAA 16636	_ A	
			TTGCCAGATTCTC CCA CTT		
			AACGGTCTAAGAG GGT GAA		
			A _		
GAM110	B3GNT5	3'	AAAGTTCATGAATCTGGTAA 25763	TCCC	
			TTGCCAGATTC AACTTT		
			AATGGTCTAAG TTGAAA		
			TAC_		
GAM110	FEM-2	3'	AAAGTTGAAAGTGGCAA 16005	GATT CC	
			TTGCCA CT CAACTTT		
			AACGGT GA GTTGAAA		
			____ AA		
GAM110	FLJ11259	3'	AAGTAGAGAAATCTGGCAA 20380	_ CCA	
			TTGCCAGATT CTC ACTT		
			AACGGTCTAA GAG TGAA		
			A A_		
GAM110	FLJ14437	3'	AAAGTTGGGAGAAAGGGGAA 26305	G AGA	
			TT CC TTCTCCCAACTTT		

		AA GG AAGAGGGTTGAAA	
		G GA_	
GAM110	KIAA0459	3' AAAGTTGGGAAAACCTCCAGCA	30570 CA _ C
		TGC GA TT TCCCAACTTT	
		ACG CT AA AGGGTTGAAA	
		AC C A	
GAM110	KIAA0547	3' TGGGAAGACATCTGGCAA	16697 _ _
		TTGCCAGAT TCT CCCA	
		AACGGTCTA AGA GGGT	
		C A	
GAM110	KIAA1762	3' AAAGTTGGAGCCTGGCA	31908 ATT C
		TGCCAG CTCC AACTTT	
		ACGGTC GAGG TTGAAA	
		C_ _	
GAM110	KIAA1951	3' AAAGTAGGAATCTGGCAG	36511 CCCA
		TTGCCAGATTCT ACTTT	
		GACGGTCTAAGG TGAAA	
		A_	
GAM110	LOC145900	3' AAAGTTGCCTGCTCTGGCAG	38010 TTCTCC
		TTGCCAGA CAACTTT	
		GACGGTCT GTTGAAA	
		CGTCC_	
GAM110	LOC150933	3' AAAGTTGTTTTTCTGGCAG	41269 TTCTCC
		TTGCCAGA CAACTTT	
		GACGGTCT GTTGAAA	
		TTTT_	
GAM110	LOC152876	5' AAAGCCAGAGGCTTTGGCAA	41559 TT CCAA
		TTGCCAGA CTC CTTT	
		AACGGTTT GAG GAAA	
		CG ACC_	
GAM110	LOC254936	3' AAAGTTGCCTGCTCTGGCAG	45525 TTCTCC
		TTGCCAGA CAACTTT	
		GACGGTCT GTTGAAA	
		CGTCC_	
GAM110	LOC256867	5' AAAGTCAGGAGGATTGACAG	45469 CCA CA
		TTG GATTCTCC ACTTT	
		GAC TTAGGAGG TGAAA	
		AG_ AC	
GAM110	LOC90190	3' AAAGTTGGGATTTGGCAG	30944 TTC
		TTGCCAGA TCCCAACTTT	

GACGGTTT AGGGTTGAAA

GAM110 LOC90639 5' AAAGCTGGGAGGGAGGCGA 31831 AGA A
TTGCC TTCTCCCA CTTT
||||| ||||| |||
AGCGG GGGAGGGT GAAA

A__ C

GAM111 GRIN2B 5' GAAGAAGGGACTGGACATT 6492 G AA
AATGTCCAG TC TTTCTTC
||||||| || |||||
TTACAGGTC AG GAAGAAG

_ G_

GAM111 KCNMB3 5' GAAGAAATGAAGGACA 15748 AGG A
TGTCC TCA TTTCTTC
||||| ||| |||||
ACAGG AGT AAAGAAG

GA_ _

GAM111 MS4A3 3' GAAGAAAAATGAGACATTTTT 12779 _ GGTCAA
AAAAATGTC CA TTTCTTC
||||||| || |||||
TTTTTACAG GT AAAGAAG

A AA_____

GAM111 NPTX1 3' GAAAAGCAACATGGACATTTCC 8353 A G CAA_
A AAATGTCCA GT TTTC
| ||||| || |||
C TTTACAGGT CA AAAG

C A ACGA

GAM111 PDK4 3' GAAATTTGAGCTAAACATTTTT 46441 CC G _
AAAAATGT AG TCAA TTTC
||||||| || ||| |||
TTTTTACA TC AGTT AAAG

AA G T

GAM111 SELP 3' GAAGAAATTCCTGTAGCAT 8913 C_ TC
ATGT CAGG AATTTCTTC
||| ||| |||||
TACG GTCC TTAAAGAAG

AT _

GAM111 VANGL2 3' GAGCCTTTGACTCAGACATTTT 35481 CA TTT
T AAAAATGTC GGTCAA CTT
||||||| ||||| |||
TTTTTACAG TCAGTT GAG

AC TCC

GAM111 ADMP 5' GAAGAACCAGACCTGGAC 29656 AAT
GTCCAGGTC TTCTTC
||||||| |||||
CAGGTCCAG AAGAAG

ACC

GAM111 AKT3 3' GAAAATGATTCCTGGACAT 11958 _ A
ATGTCCAGG TCA TTTC
||||||| ||| |||

TACAGGTCC AGT AAAG
 TT A
 GAM111 AQP9 3' GAAGCTACCTGGATATTTCC 21967 A CAA
 A AAATGTCCAGGT TTTC
 | ||||| ||||
 C TTTATAGGTCCA GAAG
 C TC_
 GAM111 ATP9A 3' GAAGGACCTCAGACATTTT 31084 C_ AA
 AAAATGTC AGGTC TTTC
 ||||| |||| ||||
 TTTTACAG TCCAG GAAG
 AC _
 GAM111 C5orf6 3' GAATTGAACCTGACATTTT 18703 C _
 AAAATGTC AGGT CAATTT
 ||||| |||| |||||
 TTTTACAG TCCA GTTAAG
 _ A
 GAM111 FLJ10769 3' GAAAACTGTGCCATGGACATT 20114 _ _ A_
 TTT AAAAATGTCCA GGT CA TTTC
 ||||| |||| ||||
 TTTTACAGGT CCG GT AAAG
 A T CAA
 GAM111 FLJ12572 3' GAAAAAGCCTAGGACATT 23199 _ CAA
 AATGTCC AGGT TTTC
 ||||| |||| ||||
 TTACAGG TCCG AAAG
 A AA_
 GAM111 FLJ14624 3' GAAGAAATTGACTCTTGACAGTT 35337 _ CCA
 TTT AAAAA TGT GGTCAATTTCTTC
 |||| || |||||
 TTTT AC G TCAGTTAAAGAAG
 G TTC
 GAM111 FNBP3 3' AAGTTGACTTAAACATTTT 39073 CC
 AAAATGT AGGTCAATTT
 ||||| |||||
 TTTTACA TTCAGTTGAA
 AA
 GAM111 KIAA0087 3' GAAGAGGAGGCCTGGAC 16558 AA
 GTCCAGGTC TTTCTTC
 ||||| |||||
 CAGGTCCGG GGAGAAG
 A_
 GAM111 KIAA0335 5' AAGAAATTGGGACTTTTTT 16727 T AGGT
 AAAAA GTCC CAATTTCTT
 |||| || |||||
 TTTT CAGG GTTAAAGAA
 T _
 GAM111 KIAA1671 3' GATTGACCTGGAGATTTT 32693 G
 AAAAAT TCCAGGTCAATT
 |||| |||||

TTTTTA AGGTCCAGTTAG
 G
 GAM111 MGC14836 5' GAAGAAATTGGGAACATT 27235 _ AGGT
 AATGT CC CAATTTCTTC
 ||||| || |||||
 TTACA GG GTTAAAGAAG
 A ____
 GAM111 MGC16385 5' GAAAACCGCCCCTGGACGTTT 29662 TCAA__
 AAATGTCCAGG TTTC
 ||||| |||||
 TTTGCAGGTCC AAAG
 CCGCCA
 GAM111 MGC20235 3' GAAAATCTGACCTGGCATT TT 29666 T A__
 AAAATG CCAGGTCA TTTC
 ||||| ||||| |||||
 TTTTAC GGTCCAGT AAAG
 _ CTA
 GAM111 PAK6 3' AAGAAATTGCAAGGACTTTTTT 21386 T AG T
 AAAAA GTCC G CAATTTCTT
 ||||| ||||| |||||
 TTTT CAGG C GTTAAAGAA
 T AA _
 GAM111 PDZ-GEF1 3' GAAGAAATTGCCCTGGCACTTT 15522 A T T
 T AAAA TG CCAGG CAATTTCTTC
 ||||| ||||| |||||
 TTTT AC GGTCC GTTAAAGAAG
 C _ C
 GAM111 PRO0641 3' AAGGAATGACCTGAAACATTTT 15400 C_ A
 T AAAAATGT CAGGTCA TTTCTT
 ||||| ||||| |||||
 TTTT TACA GTCCAGT AAGGAA
 AA _
 GAM111 PRO1430 5' AAGAAAATCTTGGCATT TT 20674 T TCAA
 AAAATG CCAGG TTTCTT
 ||||| ||||| |||||
 TTTTAC GGTT C AAAGAA
 _ TA__
 GAM111 RGS20 3' AAGAAATATGGGCATT TT 9802 GGTCA
 AAAATGTCCA ATTTCTT
 ||||| ||||| |||||
 TTTTACGGGT TAAAGAA
 A____
 GAM111 SKIL 5' ATTGACCCTGGACATCTTT 11883 A _
 AAA ATGTCCAGG TCAAT
 ||||| ||||| |||||
 TTT TACAGGTCC AGTTA
 C C
 GAM111 SLC2A10 3' ATTGACTTGGACATTTT 25063
 AAAAATGTCCAGGTCAAT
 ||||| ||||| |||||

TTTTTACAGGTTTCAGTTA

GAM111 LOC149134 5' GAAGAAATGTCCGGCATT TTTT 40959 T A T A
AAAAATG CC GG CA TTTCTTC
||||| || || || |||||
TTTTTAC GG CC GT AAAGAAG

_ _ T _

GAM111 LOC91549 3' GAAGAAATTATTTGACATTTT 33013 C C
AAAAATGTC AGGT AATTTCTTC
||||| ||| |||||
TTTTTACAG TTTA TTAAAGAAG

_ _

GAM112 HOXA3 3' AAATCAAAGGCGCTTTGAAA 24992 _ TATTG
TTTCAAAG GCT TGATTT
||||| ||| |||||
AAAGTTTC CGG ACTAAA
G AA_

GAM112 PMP22 3' AGAAATCAGTGACAACAAGTCT 5846 A _
TTGAAA TTCAAAGGCTT TTGT GATTTCT
||||| ||| |||||
AAGTTTCTGAA AACA CTAAAGA
C GTGA

GAM112 CDKL2 5' AGAAATCACACAGCGCTGGAA 10070 AAG TA
TTTCA GCT TTGTGATTTCT
|||| ||| |||||
AAGGT CGA AACACTAAAGA
CG_ C_

GAM112 FLJ21290 3' GAAATCATGTCCTTGAAA 24633 A TTATT
TTTCAA GGC GTGATTTCT
|||| ||| |||||
AAAGTT CTG TACTAAAG
C _

GAM112 HSPC065 3' GAAATCAACATCTTTGAAA 15453 CTTAT _
TTTCAAAGG TGT GATTTCT
||||| ||| |||||
AAAGTTTCT ACA CTAAAG
_ A

GAM112 KIAA1796 3' AGAAAACAATAAGCCTCTGAAA 43963 A GA
TTTCA AGGCTTATTGT TTTCT
|||| ||||| |||||
AAAGT TCCGAATAACA AAAGA
C _

GAM112 SPTLC2 3' AGAACTTTAATAAGCCCTTGAG 11271 A TGAT
A TTTCAA GGCTTATTG TTCT
|||| ||||| |||||
AGAGTT CCGAATAAT AAGA
C TTC_

GAM112 ZFD25 3' AGAAAATATAAGCCTTT 18320 TGTGA
AAAGGCTTAT TTTCT
||||| |||

		TTTCCGAATA AAAGA		
		TA__		
GAM112	LOC146435 3'	AAATCACAAACCTTGAAA 38152	A	CTTA
		TTTCAA GG TTGTGATTT		
		AAAGTT CC AACACTAAA		
		_ A__		
GAM112	LOC148709 3'	CAGAATAAGCCTTTCAAA 38581	C	G
		TTT AAAGGCTTATT TG		
		AAA TTTCCGAATAA AC		
		C G		
GAM112	LOC164955 3'	AAATCACCATCTGAAGCTTTTG 40111	ATT__	
	AAA	TTTCAAAGGCTT GTGATTT		
		AAAGTTTTCGAA CACTAAA		
		GTCTAC		
GAM112	LOC219627 3'	AGAAATCTTAACCTTTGAAA 44273	GC	TTGT
		TTTCAAAG TTA GATTTCT		
		AAAGTTTC AAT CTAAAGA		
		TC T__		
GAM112	LOC220906 3'	AGAAATCTTAACCTTTGAAA 43925	GC	TTGT
		TTTCAAAG TTA GATTTCT		
		AAAGTTTC AAT CTAAAGA		
		TC T__		
GAM112	LOC221312 3'	AAATCAAATTACCTTTGGAA 44137	CTT	G
		TTTCAAAGG ATT TGATTT		
		AAGGTTTCC TAA ACTAAA		
		AT_ _		
GAM113	CBFA2T1 3'	GTATCTTTCTATGCTGCTT 10545	TA	AC
		AAGCAGCAT AAA TGC		
		TTCGTCGTA TTT ATG		
		TC CT		
GAM113	GARS 5'	TCCGCGTCCAGTGCTGCTT 7798	AAAA	T C
		AAGCAGCATT AC GC GA		
		TTCGTCGTA TG CG CT		
		CC_ _ C		
GAM113	NDP 3'	TTGGCTCTCAATGCTGTTT 5811	AAAAACT	
		AAGCAGCATT GCCGA		
		TTTGTCGTAA CGGTT		
		CTCT__		
GAM113	FLJ11101 3'	TGGATTTTAATGCTGCTT 20315	ACTG	
		AAGCAGCATTAATAA CCG		

			TTCGTCGTAATTTT	GGT		
			A__			
GAM113	FLJ13072	5'	TCCAGCAGAAGATGCTGCTT	43236	AAAAA	C_
			AAGCAGCATT	CTGC GA		
			TTCGTCGTAG	GACG CT		
			AA__	AC		
GAM113	FLJ20729	3'	TGGCTTTTAAATATGCTT	19658	GC	CT
			AAGCA ATTA AAAA	GCCG		
			TTCGT TAATTTT	CGGT		
			A_	__		
GAM113	FLJ20802	5'	CAGCTTCAAATGCTGCTT	19674	AA	A
			AAGCAGCATT	AA CTG		
			TTCGTCGTAA	TT GAC		
			AC	C		
GAM113	FLJ22169	3'	CTTCCTGGGCCCTCATTGCTGC	23523	TTAAAACT	__
		TT	AAGCAGCA	GCC GAAG		
			TTCGTCGT	CGG CTTC		
			TACTCC__	GTC		
GAM113	GOLGA1	3'	TCGGCAGTTTCAGGTGTAGCT	7863	A	AA
			AGC GCATT	AAACTGCCGA		
			TCG TGTGG	TTTGACGGCT		
			A	AC		
GAM113	KIAA0014	3'	TCCAGCAGCTCAATGCTGTTT	16118	AAAAA	C_
			AAGCAGCATT	CTGC GA		
			TTTGTCGTAA	GACG CT		
			CTC__	AC		
GAM113	KIAA0494	3'	TGGCAGCTCCTACTGCTGCTT	16593	T	AAAA
			AAGCAGCA TA	CTGCCG		
			TTCGTCGT AT	GACGGT		
			C	CCTC		
GAM113	MAP	3'	CTTCAAGTTATTTTAAATGCTCT	23096	C	ACT C_
		T	AAG AGCATTA AAA	GC GAAG		
			TTC TCGTAATTTT	TG CTTC		
			_	AT_ AA		
GAM113	NIR3	3'	CTTCGGTTTTTTTAAATGC	32927	CT	
			GCATTAAAAA	GCCGAAG		
			CGTAATTTT	TGGCTTC		
			T_			
GAM113	LOC160156	5'	TTTGAGCTCATTAATGCTGCT	39992	AAACT	_
			AGCAGCATTA	GC CGAA		

TCGTCGTAATT CG GTTT
 ACT__ A
 GAM113 LOC220477 5' CAGTAACTTTCAATGCTGC 37408 A ____
 GCAGCATT AAA ACTG
 ||||| || |||
 CGTCGTAA TTT TGAC
 C CAAA
 GAM114 ADCY7 5' CCAGAGGCCCTCTCCCA 6783 TAA A TCT A_
 TGGG GA GA GG TCTGG
 ||| || || || ||||
 ACCC CT CT CC AGACC
 ____ _ C_ GG
 GAM114 CACNB1 3' CCAGATCCAAGGTCCCTCACCC 6385 A AA _
 GGGT AG GATCT GGATCTGG
 ||| || |||| |||||
 CCCA TC CTGGA CCTAGACC
 C C_ A
 GAM114 DEC1 5' TCCAGATCCAGATCCTTGTGC 18875 A A
 GTA GA GATCTGGATCTGGA
 ||| || ||||| |||||
 CGT TT CTAGACCTAGACCT
 G C
 GAM114 HPCA 3' TCAGTCAGGCCCCCTTACCCA 7919 AAGA AT
 TGGGTAAG TCTGG CTGG
 ||||| |||| |||
 ACCCATTC GGACT GACT
 CCCC ____
 GAM114 XK 3' CCACAGAAATCTCTCACCCA 22057 A A _ GATC
 TGGGT AGA GA TCTG TGG
 |||| ||| || ||| |||
 ACCCA TCT CT AGAC ACC
 C _ AA ____
 GAM114 DKFZp547I224 5' TCCAGATCATCTCCCA 21480 TA A
 TGGG AGA GATCTGGA
 ||| || |||||
 ACCC TCT CTAGACCT
 _ A
 GAM114 DKFZP564D0478 3' TCCAGATTTTTTCTCCTCACC 25810 A A TCT
 C GGGT AG AGA GGATCTGGA
 ||| || || |||||
 CCCA TC TCT TTAGACCT
 C C TTT
 GAM114 FLJ12572 3' TCCAGATCCAGACCCTCTTAT 23201 AGA
 GTAAGA TCTGGATCTGGA
 |||| ||||| |||||
 TATTCT AGACCTAGACCT
 CCC
 GAM114 HIC2 3' CCAGAAGCCCTTCTTGCCCA 32525 ATCT A_
 TGGGTAAGAAG GG TCTGG
 ||||| || ||||

ACCCGTTCTTC CC AGACC
 _____ GA
 GAM114 HSA243666 3' TCCAGACTAGAGCCTCCTTACC 19022 A A_ A
 TA TGGGTAAG AG TCTGG TCTGGA
 ||||| || |||| |||||
 ATCCATTC TC AGATC AGACCT
 C CG _
 GAM114 KIAA0296 3' CCAGATCTGGCTTCTTTCCCA 16218 T AT TG
 TGGG AAGAAG C GATCTGG
 ||| ||||| | |||||
 ACCC TTCTTC G CTAGACC
 T _ GT
 GAM114 LEAP-2 5' TCCAATCAATCTCCTTACTCA 27545 A CTG C
 TGGGTAAG AGAT GAT TGGA
 ||||| ||| ||| |||
 ACTCATTC TCTA CTA ACCT
 C A_ _
 GAM114 MGC10715 3' CCAGATCCAGAGATCCCCA 23613 TAA AGA
 TGGG GA TCTGGATCTGG
 ||| || |||||
 ACCC CT AGACCTAGACC
 _ AG_
 GAM114 SARM 3' CCAGATCCAGACCTAGGCCT 17455 AAGA A
 GGGT AG TCTGGATCTGG
 ||| || |||||
 TCCG TC AGACCTAGACC
 GA_ C
 GAM114 LOC143287 3' CCAGATTCAATCACCTTACCCA 40344 AA C
 TGGGTAAG GAT TGGATCTGG
 ||||| ||| |||||
 ACCCATTC CTA ACTTAGACC
 CA _
 GAM114 LOC150967 5' CCAGATCTTTCTAACCCA 39036 A _
 TGGGT AGAA GATCTGG
 |||| ||| |||||
 ACCCA TCTT CTAGACC
 A T
 GAM114 LOC154877 3' TCCTGATTGAGCTCTTCTTACC 41745 T T
 CA TGGGTAAGAAGA CTGGATC GGA
 ||||| ||||| |||
 ACCCATTCCTTCT GACTTAG CCT
 C T
 GAM114 LOC165904 3' CCAGAGTGTCCCTCTACCCA 40193 A A_ CTGGA
 TGGGTA GA GAT TCTGG
 ||||| || ||| |||||
 ACCCAT CT CTG AGACC
 _ CC TG_
 GAM114 LOC200325 5' CCTGAGATCTTCCTGCCCA 43288 A _
 TGGGTA GAAGATCT GG
 ||||| ||||| |||

ACCCGT CTTCTAGA CC
 C GT
 GAM114 LOC206463 5' CCAGATTGCTTCCTACTCA 43122 A ATCTG
 TGGGTA GAAG GATCTGG
 ||||| ||| |||||
 ACTCAT CTTC TTAGACC
 C GT___
 GAM114 LOC220469 3' TCCAGCAGAGGACCTCCCACCC 37555 AA A A GGAT
 A TGGGT GA G TCT CTGGA
 ||||| ||| ||| |||||
 ACCCA CT C AGG GACCT
 CC _ C AGAC
 GAM114 LOC245806 3' CCAGATCCCTTCCTGCCCA 44130 A ATCT
 TGGGTA GAAG GGATCTGG
 ||||| ||| |||||
 ACCCGT CTTC CCTAGACC
 C ____
 GAM115 GTF2I 3' CCACTTTTACTTTTCGTCCAAA 26883 C AA _
 TAA TTA TTGGACGAGAA GAAA TGG
 ||| ||||| ||| |||
 AAT AACCTGCTTTT TTTT ACC
 A CA C
 GAM115 GTF2I 3' CCACTTTTACTTTTCGTCCAAA 26887 C AA _
 TAA TTA TTGGACGAGAA GAAA TGG
 ||| ||||| ||| |||
 AAT AACCTGCTTTT TTTT ACC
 A CA C
 GAM115 LNK 3' CCAGACTGCTTCCCGTCCAAGT 11972 A A_ AAA
 ACTTGGACG GAA AG TGG
 ||||| ||| || |||
 TGAACCTGC CTT TC ACC
 C CG AG_
 GAM115 SLC18A1 3' CCATTTCTCTTCTGCTGG 9017 TG A G A
 T G C AGAA AGAAATGG
 | | ||||| |||||
 G C G TCTT TCTTTACC
 GT __ C
 GAM115 FLJ23563 3' CCATTTCCAAAGAACCCAAGTA 33560 ACGAGAAAA
 G TTA CT TGG GAAATGG
 ||||| |||||
 GATGAACC CTTTACC
 CAAGAAAC_
 GAM115 KIAA0408 5' CCATTTCTTCTCTATTTCAG 16232 C_ A
 TTGGA GAG AAAGAAATGG
 ||||| ||| |||||
 GACTT CTC TTTCTTTACC
 AT C
 GAM115 KIAA0527 3' CCATTTCTCTGAACTCCAGTAA 45844 T CGAGAAA
 TTACT GGA AGAAATGG
 ||||| ||| |||||

		AATGA CCT TCTTTACC	
		_ CAAGTC_	
GAM115	KIAA1535 3'	CCATCCCTCCCCTCCTTTTCAG 38765	C__ AAA AA
	GTAA	TTACTTGGA GAG AG ATGG	
		AATGGACTT CTC TC TACC	
		TTC CCC CC	
GAM115	MGC13007 5'	CAGTTCCTCTCGTCCAAG 26120	AAA A
		CTTGGACGAGA GAA TG	
		GAACCTGCTCT CTT AC	
		C__ G	
GAM115	RBM14 3'	CCACTTCCCCATCTCCCCAAGT 13020	AC AAA_ A
	AG	TTACTTG GAGA GAA TGG	
		GATGAACC CTCT CTT ACC	
		C_ ACCC C	
GAM115	LOC147343 5'	CACTTCCCTCCCCAAGTAA 40831	AC AAAA A
		TTACTTG GAG GAA TG	
		AATGAACC CTC CTT AC	
		C_ C__ C	
GAM115	LOC149301 3'	CCATCTCCTCCATCTAAGTAA 38690	C_ AAAA A
		TTACTTGGA GAG GA ATGG	
		AATGAATCT CTC CT TACC	
		AC ____ C	
GAM115	LOC257319 3'	CCACTTCTTTTTTCTAAATAA 45831	C AC A
		TTA TTGG GAGAAAAGAA TGG	
		AAT AATC CTTTTTCTT ACC	
		A _ C	
GAM116	CANX 3'	TTTCTCCTCTGCTATGCA 42278	_
		TGCATAGCA AGGAGAAA	
		ACGTATCGT TCCTCTTT	
		C	
GAM116	DKFZP564C196 3'	GTTCCCTCCCTGCTCTGCA 34714	T A A
		TGCA AGCA GGAG AAT	
		ACGT TCGT CCTC TTG	
		C C C	
GAM117	PDGFRA 3'	ATCTATGTTTATAATACTACTA 12879	C CAAT A
	CT	AG AGTAGTAT AACG AGAT	
		TC TCATCATA TTGT TCTA	
		A ATAT A	
GAM117	KIAA0222 3'	TCGAGTATTAATACTACTGC 16047	C A_
		GCAGTAGTAT AATA CGA	

			CGTCATCATA TTAT GCT		
			A GA		
GAM117	PRO1600	5'	GTCATTCATACTACTGCT 15315	C A	
			AGCAGTAGTAT AAT AC		
			TCGTCATCATA TTA TG		
			C C		
GAM117	TEB4	3'	TCTTCTGACATTACTGCT 30429	A ATAAC	
			AGCAGTAGT TCA GAAGA		
			TCGTCATTA AGT CTTCT		
			C _____		
GAM117	LOC125268	3'	CTTCTAGTGGACATTACTGCT 37452	A AATAAC	
			AGCAGTAGT TC GAAG		
			TCGTCATTA AG CTTC		
			C GTGAT_		
GAM117	LOC220469	3'	TTCCTATTGACATCTACTGCT 37556	TA_ AC	
			AGCAGTAG TCAATA GAA		
			TCGTCATC AGTTAT CTT		
			TAC C_		
GAM118	EIF2C1	3'	TGCTATGCAAAACAATCTA 14507	CTAGA G	
			TAGATTGT TGCA TAGCA		
			ATCTAACA ACGT ATCGT		
			AA____ _		
GAM118	TCF2	3'	CTGCTGGCACCTCAGACAATC 6075	_ A _	
			GATTGTCT AG TGC AGTAG		
			CTAACAGA TC ACG TCGTC		
			C C G		
GAM118	CNNM4	3'	CTGCTGTACCCAGAAATCTA 21425	G AGA	
			TAGATT TCT TGCAGTAG		
			ATCTAA AGA ATGTCGTC		
			_ CCC		
GAM118	HRH4	3'	GCCACCACACCTGGATAATT 22261	A CA A	
			GATTGTCTAG TG GT GC		
			TTAATAGGTC AC CA CG		
			C AC C		
GAM118	KIAA1449	3'	ACTGTTCTAACAATCTA 21897	C T	
			TAGATTGT TAGA GCAGT		
			ATCTAACA ATCT TGTC		
			_ _		
GAM118	KIAA1981	3'	CTGCTGTCCAGACAACTC 42609	_ A _	
			GA TTGTCT GAT GCAG		

		CT AACAGA CTG CGTC	
		C C T	
GAM118	RHOBTB3 3'	TGCTTTTCATCTGGACAA 17078	C T
		TTGTCTAGATG AG AGCA	
		AACAGGTCTAC TT TCGT	
		_ T	
GAM118	LOC149076 5'	TGGA CTCCATCAAGACAATC 38639	A C AG
		GATTGTCT GATG AGT CA	
		CTAACAGA CTAC TCA GT	
		A C G_	
GAM119	PLN 3'	TTACTGATAACATAAACAGTA 8538	CACT_ T
		TACTGTTTA TC GTAA	
		ATGACAAAT AG CATT	
		ACAAT T	
GAM119	SMT3H1 3'	CTTTACTACTGTAAACAGTA 30125	CTTCT
		TACTGTTTACA GTAAAG	
		ATGACAAATGT CATTTC	
		CAT__	
GAM119	EZFIT 3'	CTTCACGTGGTTGTAAACAGCA 22195	A C TC A
	GA	TCT CTGTTTACA T TGT AAG	
		AGA GACAAATGT G GCA TTC	
		C T GT C	
GAM119	FLJ13110 3'	TGCAGAATGTAAACAGCAGA 23223	A C
		TCT CTGTTTACA TTCTGTA	
		AGA GACAAATGT AAGACGT	
		C _	
GAM119	KIAA0429 3'	TTTTACAGAATATAACAACAG 16475	TACAC__
	TA	TACTGTT TTCTGTAAAG	
		ATGACAA AAGACATTTT	
		CAAATAT	
GAM119	KIAA0662 3'	CTTTACAGAAGCAAATAGTA 39802	ACA
		TACTGTTT CTCTGTAAAG	
		ATGATAAA GAAGACATTTC	
		C__	
GAM119	KIAA1371 3'	CTTCACAAGGGTTGCAAAAAGT 42907	G A _ TC A
	AGA	TCTACT TTT CA CT TGT AAG	
		AGATGA AAA GT GG ACA TTC	
		A C T GA C	
GAM119	KIAA1508 5'	CTTTACAGGGTGCAACAGCAA 30993	A_ A T
	GA	TCT CTGTTT CACT CTGTAAAG	

AGA GACAAA GTGG GACATTTC
 AC C _
 GAM119 moblak 5' TACAGAAGTCCAGGAGA 28310 A TTTAC
 TCT CTG ACTTCTGTA
 ||| ||| |||||
 AGA GAC TGAAGACAT
 G C____
 GAM119 RAB6C 3' TTACAGAAGAACCAGTGGA 25836 T ACA
 TCTACTG TT CTTCTGTAA
 ||||| || |||||
 AGGTGAC AA GAAGACATT
 C ____
 GAM119 LOC219899 3' CAGAGCAGTGCAAAAGTAGA 43990 G A _
 TCTACT TTT CACT TCTG
 ||||| ||| ||| |||
 AGATGA AAA GTGA AGAC
 _ C CG
 GAM119 LOC221773 3' CAGAAAAGACAAACAGTAGA 43762 ACAC_
 TCTACTGTTT TTCTG
 ||||| ||| |||
 AGATGACAAA AAGAC
 CAGAA
 GAM120 ADCY2 3' TCTGTGCTCACCCATTGT 32436 ATCAA
 GCAATGGGT TACAGA
 ||||| |||
 TGTTACCCA GTGTCT
 CTC____
 GAM120 AMACR 3' CTGTATTGAATCAGAATGC 34015 ATG_ A
 GCA GGT TCAATACAG
 || ||| |||||
 CGT CTA AGTTATGTC
 AAGA _
 GAM120 CASP6 3' TCTGTATTGAAAATGGCTTT 26873 AATGGGTA
 AAAGC TCAATACAGA
 |||| |||||
 TTTCG AGTTATGTCT
 GTAAA____
 GAM120 CASP6 3' TCTGTATTGAAAATGGCTTT 6894 AATGGGTA
 AAAGC TCAATACAGA
 |||| |||||
 TTTCG AGTTATGTCT
 GTAAA____
 GAM120 EIF1A 3' TCTGTATTTCCTTTCTTTT 42727 C TATC
 AAAAG AATGGG AATACAGA
 |||| ||| |||||
 TTTTC TTACCC TTATGTCT
 T T____
 GAM120 GALNT1 3' CTGATAGATAATCCCATTGC 21724 _ A A
 GCAATGGG TATC AT CAG
 ||||| ||| |||

CGTTACCC ATAG TA GTC
TA A _

GAM120 KLHL3 3' TCTGTATTGATTGTGTCTTTT 42272 _ ATGGGT
AAAAG CA ATCAATACAGA
||||| || |||||
TTTTC GT TAGTTATGTCT
T GT__

GAM120 PKHD1 3' TCTGTATTGATGGACTCATTTT 28944 C _
T AG AATGGGT ATCAATACAGA
|| ||||| |||||
TC TTA CTCA TAGTTATGTCT
T GG

GAM120 PNN 3' TCTGTATCATACATTGCTTTT 35234 GGTATCA
AAAAGCAATG ATACAGA
||||| |||||
TTTTCGTTAC TATGTCT
ATAC__

GAM120 PPT2 3' CTGTGACCACCTCATTGCT 28964 _ ATCAA
AGCAATG GGT TACAG
||||| ||| |||||
TCGTTAC CCA GTGTC
T CCA__

GAM120 PPT2 3' CTGTGACCACCTCATTGCT 11633 _ ATCAA
AGCAATG GGT TACAG
||||| ||| |||||
TCGTTAC CCA GTGTC
T CCA__

GAM120 PRDM2 3' CTGTATTGAACTTTGCT 18002 TG A
AGCAA GGT TCAATACAG
||||| ||| |||||
TCGTT TCA AGTTATGTC

GAM120 PRKAR2B 3' TCTGTATTCTTACTCACTTTT 8611 CAA TC
AAAAG TGGGTA AATACAGA
||||| ||||| |||||
TTTTC ACTCAT TTATGTCT
__ TC

GAM120 RAB18 3' TCTGTATTGACAAGACTGTTGT 22222 GTA__
TTTT AAAAGCAATGG TCAATACAGA
||||| ||||| |||||
TTTTTGTTGTC AGTTATGTCT
AGAAC

GAM120 RECQL5 3' TCTGTATTGGCTACTGTTCTT 10451 C GTA
AAG AATGG TCAATACAGA
||| ||||| |||||
TTC TTGTC GGTTATGTCT
_ ATC

GAM120 SFRS2 3' TCTGTATTATAACCATTGTTT 32505 G C
AAGCAATGG TAT AATACAGA
||||| ||| |||||

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          TTTGTTACC ATA TTATGTCT
              A _
GAM120 TRIM34 3' TCTGCAACATTACACCATTC 22253 A _ ATCAATA_
          TTCC          A AAGCAATGG GT CAGA
              | ||||| || |||
              C TTCGTTACC CA GTCT
              C A CTTACAAC
GAM120 TRIM34 3' TCTGCAACATTACACCATTC 28177 A _ ATCAATA_
          TTCC          A AAGCAATGG GT CAGA
              | ||||| || |||
              C TTCGTTACC CA GTCT
              C A CTTACAAC
GAM120 ARL5 3' TCTGTATTGTACTAACCA 14402 _ T
          TGG GTA CAATACAGA
              ||| ||| |||||
          ACC CAT GTTATGTCT
          AAT _
GAM120 CSE-C 3' CTGTATTGGACTAATTCT 43980 C G A
          AG AAT GGT TCAATACAG
              || ||| ||| |||||
          TC TTA TCA GGTTATGTC
          _ A _
GAM120 FLJ10482 3' CTGCATTGAATACCTGTTTCT 19876 C _ A
          AG AATGGGTAT CAAT CAG
              || ||||| ||| |||
          TC TTGTCCATA GTTA GTC
          T A C
GAM120 FLJ11149 3' TTGTAAATAGCCATTGCTTTT 20346 G CAAT
          AAAAGCAATGG TAT ACAG
              ||||| ||| |||
          TTTTCGTTACC ATA TGTT
          G AAT_
GAM120 FLJ11275 3' TCTGTATTAATTATTGCTTTT 20404 GTATC
          AAAAGCAATGG AATACAGA
              ||||| |||||
          TTTTCGTTATT TTATGTCT
          AA_
GAM120 FLJ14326 5' CTGTACTGCCATCCTATTGC 25904 TAT_ A
          GCAATGGG CA TACAG
              ||||| || |||
          CGTTATCC GT ATGTC
          TACC C
GAM120 FLJ20527 3' CTGTATTGTTCCATAGC 19540 A TAT
          GC ATGGG CAATACAG
              || ||| |||||
          CG TACCT GTTATGTC
          A T_
GAM120 KIAA1464 3' CTGAGATACCCATTGCT 33883 AATA
          AGCAATGGGTATC CAG
              ||||| |||

```


TCGTTACCCATAG GTC
A____
GAM120 MGC13183 3' TCTGTATTGACCGGTTTTTGT 26146 ____ G TA
TTT AAAAGCA AT GG TCAATACAGA
||||| || || |||||
TTTTTGT TG CC AGTTATGTCT
TTT G ____
GAM120 MGC16142 3' CTGCCTTTTACACATTGCTTTT 26507 G TCAATA
AAAAGCAATG GTA CAG
||||||| ||| |||
TTTTCGTTAC CAT GTC
A TTTCC____
GAM120 WNT2B 3' CTGTATTGGACAGCACTGC 23694 A G_ A
GCA TG GT TCAATACAG
||| || || |||||
CGT AC CA GGTTATGTC
C GA ____
GAM120 WNT2B 3' CTGTATTGGACAGCACTGC 10393 A G_ A
GCA TG GT TCAATACAG
||| || || |||||
CGT AC CA GGTTATGTC
C GA ____
GAM120 LOC144559 3' CTGTGTATTACCCTTGCTTTT 37765 T TCA
AAAAGCAA GGGTA ATACAG
||||| |||| |||||
TTTTCGTT CCCAT TGTGTC
____ TA____
GAM120 LOC147622 3' TCTGTACTGATTGATGTGCTT 40851 ATGGGT A
AAGCA ATCA TACAGA
|||| ||| |||||
TTCGT TAGT ATGTCT
GTAGT_ C
GAM120 LOC150630 5' TCTGTATTGAGAAGTTATTCT 41243 C GTA_
AG AATGG TCAATACAGA
|| |||| |||||
TC TTATT AGTTATGTCT
____ GAAG
GAM120 LOC155081 3' TCTGTATTATTATATGTGCT 39546 ATGG TC
AGCA GTA AATACAGA
||| || |||||
TCGT TAT TTATGTCT
GTA_ TA
GAM120 LOC196812 3' CTGTATTACATTGCTTT 43135 GGTATC
AAAGCAATG AATACAG
|||||| |||||
TTTCGTTAC TTATGTC
A____
GAM120 LOC221421 3' TCTGGAGGAACCCATTGCT 44326 A AATA
AGCAATGGGT TC CAGA
||||||| || |||

			TCGTTACCCA AG GTCT		
			_ GAG _		
GAM120	LOC222228	3'	TCTGTATTATTATATGTGCT 45277	ATGG TC	
			AGCA GTA AATACAGA		
			TCGT TAT TTATGTCT		
			GTA_ TA		
GAM120	LOC222233	3'	TCTGTATTATTACATGTGCT 45246	ATGG TC	
			AGCA GTA AATACAGA		
			TCGT CAT TTATGTCT		
			GTA_ TA		
GAM120	LOC90906	3'	CTGTGTATTACCCTTGCTTTT 32152	T TCA	
			AAAAGCAA GGGTA ATACAG		
			TTTTCGTT CCCAT TGTGTC		
			_ TA _		
GAM121	CLECSF12	5'	GATTCTCTTTTGTCCACA 37685	AG TGGTA	
			TGTGGATAAAA G AATC		
			ACACCTGTTTT C TTAG		
			CT _____		
GAM121	DGUOK	3'	ACCACCTTTCCATCCCCA 28134	T AA	
			TG GGAT AAAGGTGGT		
			AC CCTA TTTCCACCA		
			C CC		
GAM121	DGUOK	3'	ACCACCTTTCCATCCCCA 28138	T AA	
			TG GGAT AAAGGTGGT		
			AC CCTA TTTCCACCA		
			C CC		
GAM121	LIFR	3'	AGATTATTCTCCTCTATCCACA 8099	AAA T TA	
			TGTGGATA AGG GG AATCT		
			ACACCTAT TCC CT TTAGA		
			C_ T TA		
GAM121	SPAG6	3'	ATTTACTCCTCTTTATCACA 14817	G A T	
			TGTG ATAAA AGG GGTAAAT		
			ACAC TATTT TCC TCATTTA		
			_ C _		
GAM121	TNS	3'	GATCTGCCTTTATCCAC 22901	AA TG TAA	
			GTGGATAA AGG G ATC		
			CACCTATT TCC C TAG		
			_ GT _		
GAM121	FLJ10759	3'	ACCACCTTCCTGCCCACA 20099	A AA	
			TGTGG TA AAGGTGGT		

ACACC GT TTCCACCA
 C CC
 GAM121 FLJ10815 3' GATTCAGACCTTGTCCACA 20172 AAA GGTA
 TGTGGATA AGGT AATC
 ||||| ||| |||
 ACACCTGT TCCA TTAG
 ____ GAC_
 GAM121 FLJ11259 3' AGACTCCATCTTTTCACCCA 20381 ATA TAAA
 TGG AAAAGGTGG TCT
 || ||||| |||
 ACC TTTTCTACC AGA
 CAC TC_
 GAM121 FLJ30567 3' TCACCTGTGATTTATCCACA 29632 A_
 TGTGGATAAA AGGTGG
 ||||| |||||
 ACACCTATTT TCCACT
 AGTG
 GAM121 KIAA1361 3' AGATCTAAAGCCTTTTTATCCC 31164 T GG A
 A TG GGATAAAAAGGT TA ATCT
 || ||||| || |||||
 AC CCTATTTTCCG AT TAGA
 ____ AA C
 GAM121 LEAP-2 5' AGATCTTGTTACCTCCTCATCT 27544 AAAA T ____
 ACA GTGGAT AGG GGTAAT ATCT
 ||||| || ||||| |||||
 CATCTA TCC CCATT TAGA
 C__ T GTTC
 GAM121 P1P373C6 5' ATTTACCACCCTTCCAGA 21187 G TAAAAA
 T TGGA GGTGGTAAAT
 | |||| |||||
 A ACCT CCACCATTTA
 G TC_
 GAM121 PTP4A1 3' ATTTGCTTTTTATCCA 9531 AGGT
 TGGATAAAA GGTAAT
 ||||| |||||
 ACCTATTTT TCGTTTA

 GAM121 UNC5D 3' GATTTACTCATCTATCCA 28113 AAAA _
 TGGAT AGGTG GTAAATC
 |||| |||| |||||
 ACCTA TCTAC CATTAG
 ____ T
 GAM121 LOC143287 3' AGATTCAATCACCTTACCCA 40343 ATAAA A_
 TGG AAGGTGGT AATCT
 || ||||| |||||
 ACC TTCCACTA TTAGA
 CA__ AC
 GAM121 LOC145678 5' AGATTCAACTTTACCATCCACA 40553 AAA GGTA
 TGTGGAT AAGGT AATCT
 ||||| ||||| |||||

ACACCTA TTTCA TTAGA
 CCA AC__
 GAM121 LOC149506 5' ATTTGCCTCCATCCCA 41003 T AAAAA T
 TG GGAT GG GGTAAAT
 || ||| || |||||
 AC CCTA CC CCGTTTA
 _ _ _ _ T
 GAM121 LOC153020 3' ACTCCTTTTTACCCATA 39352 A T
 TGTGG TAAAAAGG GGT
 |||| ||||| ||
 ATACC ATTTTCC TCA
 C _
 GAM121 LOC255394 5' TGCTACCTTTTTACCCACA 45480 A
 TGTGG TAAAAAGGTGGTA
 |||| |||||
 ACACC ATTTTCCATCGT
 C
 GAM121 LOC84549 3' ATTTATATGTATTTTACCACA 26257 A GGTG_
 TGTGG TAAAAA GTAAAT
 |||| |||| ||||
 ACACC ATTTT TATTTA
 _ ATGTA
 GAM121 LOC92391 3' AGACCTAGTGCTGTTTCTTCCA 34272 TA A G AA
 CA TGTGGA AAA GGTG TA TCT
 |||| || |||| || ||
 ACACCT TTT TCGT AT AGA
 TC G G CC
 GAM122 CRI1 3' ATGTATCACGTGTGCTTTG 15647 TGT A
 CAAAGC ACGC TGATACAT
 |||| || |||||
 GTTTCG TGTG ACTATGTA
 _ C
 GAM122 TAPBP 3' TATCATGTAGCTTCTGAA 9182 _ GTAC
 TTCA AAGCT GCATGATA
 |||| |||| |||||
 AAGT TTCGA TGTACTAT
 C _
 GAM122 XRCC5 3' TATTACATACATGCTTTGAA 22114 _ CGCA
 TTCAAAGC TGTA TGATA
 ||||| || ||||
 AAGTTTCG ACAT ATTAT
 T AC__
 GAM122 HDAC9-PENDING 3' ATGTATCATACTATAGTCTTGA 16250 AG CGC
 A TTCAA CTGTA ATGATACAT
 |||| |||| |||||
 AAGTT GATAT TACTATGTA
 CT CA_
 GAM122 KIAA0121 3' ATGTAGACAATACAGCTTTGGA 35967 CGCATGA
 TTCAAAGCTGTA TACAT
 ||||| ||||

			AGGTTTCGACAT	ATGTA	
			AACAG__		
GAM122	KIAA0620	3'	GTATCATGCACCAACTGTGAA	31123	A C TAC
			TTCA AG TG GCATGATAC		
			AAGT TC AC CGTACTATG		
			G A CA_		
GAM122	KIAA1550	3'	GTGTGGCAGGCACACAGCTTTG	33073	AC A A
	AA		TTCAAAGCTGT GC TG TACAT		
			AAGTTTCGACA CG AC GTGTG		
			CA G G		
GAM122	PRO0461	5'	ATGTATTGATGTACAGCCTTGA	25285	A CAT
	A		TTCAA GCTGTACG GATACAT		
			AAGTT CGACATGT TTATGTA		
			C AG_		
GAM122	LOC118738	3'	ATCATGGGCTTTGGA	37193	GTACG
			TTCAAAGCT CATGAT		
			AGGTTTCGG GTACTA		

GAM122	LOC203536	3'	ATGCATCATTTGTGCAGTTTGA	43055	G C A
	A		TTCAA CTGTACG ATGAT CAT		
			AAGTTT GACGTGT TACTA GTA		
			_ T C		
GAM123	NFATC1	3'	AACCGGCATCCGTTTTGGA	12813	A__
			TCTAAAACGGAT GGTT		
			AGGTTTTGCCTA CCAA		
			CGG		
GAM123	NID	3'	AAAACCTACCCTGTCCTAGA	8338	AA A_
			TCTA ACGG TAGGTTTT		
			AGAT TGTC ATCCAAAA		
			CC CC		
GAM123	SLC19A3	3'	AAAACCTCAGTTTTAGA	24924	GGAT
			TCTAAAAC AGGTTTT		
			AGATTTTG TCCAAAA		
			AC__		
GAM124	GNPI	3'	AGCCATGGTTCACACATATGAC	11965	AG AGGA_
	A		TGTTATATGTGT G GCT		
			ACAGTATACACA T CGA		
			CT GGTAC		
GAM124	GPR65	5'	AGCTCCTCAGTCAACAAACA	30050	ATA GTAG_
			TGTT TGT GAGGAGCT		

ACAA ACA CTCCTCGA
 ____ ACTGA
 GAM124 MBL2 3' CTCCTCCTAGTACTAAC 5761 TAT _
 GTTA GTG TAGGAGGAG
 |||| ||| |||||
 CAAT CAT ATCCTCCTC
 ____ G
 GAM124 PLAG1 3' CTCTATACTACACATATTACA 8521 T GA_
 TGT ATATGTGTAG GGAG
 ||| ||||| |||
 ACA TATACACATC TCTC
 T ATA
 GAM124 SCN3A 3' AGCTATTACAAATATAACA 13796 G GGAGG
 TGTTATAT TGTA AGCT
 ||||| ||| |||
 ACAATATA ACAT TCGA
 A TA____
 GAM124 TEM7 3' CCCCTGCATATGACA 21672 GT A
 TGTTATATGT AGG GG
 ||||| ||| ||
 ACAGTATACG TCC CC
 ____ -
 GAM124 TPS1 3' AGCCCCTCCTGTTCAAACA 30336 ATA TG A
 TGTT TG TAGGAGG GCT
 ||| || ||||| |||
 ACAA AC GTCCTCC CGA
 A__ TT C
 GAM124 CSR1 3' AGCCCCTCCTCACACATA 18355 _ A
 TATGTGT AGGAGG GCT
 ||||| ||||| |||
 ATACACA TCCTCC CGA
 C C
 GAM124 DKFZP564F013 3' GCTATACACATAAAACA 45202 A GGAGG
 TGTT TATGTGTA AGC
 ||| ||||| |||
 ACAA ATACACAT TCG
 A A____
 GAM124 FLJ13072 5' CTGATCTTACACATATAA 43235 GG
 TTATATGTGTAGGA AG
 ||||| ||| ||
 AATATACACATTCT TC
 AG
 GAM124 KIAA1238 3' AGCCCCCAAAGTGCATATAATA 35213 _ A_ A A
 TGTTATATGT GT GG GG GCT
 ||||| || ||| |||
 ATAATATACG CA CC CC CGA
 T AA _ _
 GAM124 NYD-SP11 5' CTCCTCCTAAATGACA 25690 ATGTG
 TGTTAT TAGGAGGAG
 ||||| |||||

ACAGTA ATCCTCCTC
 A____
 GAM124 RP4-622L5 3' AGCTCCTCCCACCCCAACA 21199 ATAT TA
 TGTT GTG GGAGGAGCT
 ||| ||| |||||
 ACAA CAC CCTCCTCGA
 CCC_ _
 GAM124 SLC11A2 3' AGCCCCTCAAGTAATATAGCA 6221 GTGTAG A
 TGTTATAT GAGG GCT
 ||||| ||| |||
 ACGATATA CTCC CGA
 ATGAA_ C
 GAM124 UQCR 3' AGCTCCTCCCACCTCAGCA 13709 ATAT TA
 TGTT GTG GGAGGAGCT
 ||| ||| |||||
 ACGA CAC CCTCCTCGA
 CTC_ _
 GAM124 LOC146958 5' GCTCCTTAACACCAACA 40772 ATAT AG
 TGTT GTGT GAGGAGC
 ||| ||| |||||
 ACAA CACA TTCCTCG
 C_ _ A_
 GAM124 LOC147004 3' AGCTCCTCCTGCAGCTCAACA 40780 ATATG
 TGTT TGTAGGAGGAGCT
 ||| |||||
 ACAA ACGTCCTCCTCGA
 CTCG_
 GAM124 LOC153592 3' CTCCCCTTCATATATACA 41648 T T A
 TGT ATATGTG AGG GGAG
 ||| ||||| ||| |||
 ACA TATATAC TCC CCTC
 _ T _
 GAM124 LOC220776 3' AGCTCCTCCTCATGTTTCAACA 33929 AT_ T
 TGTT ATGTG AGGAGGAGCT
 ||| ||||| |||||
 ACAA TGTAC TCCTCCTCGA
 CTT _
 GAM124 LOC220827 3' CTCCCCTTACATACATACA 43845 T A A
 TGT AT TGTGTAGG GGAG
 ||| ||| ||||| |||
 ACA TA ATACATTC CCTC
 _ C C
 GAM124 LOC221814 5' TAGCCCCTCCCCCACATACACA 45096 TA_ TA A |||
 CA TGT TATGTG GGAGG GCT A
 ||| ||||| ||||| ||| |
 ACA ATACAC CCTCC CGA T
 CAC CC C |||
 GAM125 EBAF 3' GGACAGGGAATTGGGATACCT 32608 TT CCC
 AGGTATT G TCCCTGTCC
 ||||| | |||||

			TCCATAG T AGGGACAGG		
			GG TA_		
GAM125	GPC1	3'	GGACAGGGAGGGCCGGCGGCTC 7874	AG	ATTTT
	TG		CA GT GCCCTCCCTGTCC		
			GT CG CGGGAGGGACAGG		
			CT GCGGC		
GAM125	GRIN2A	3'	ACAGAGAGGGGAATACTT 6488	TG	C
			AGGTATTT CCCTC CTGT		
			TTCATAAG GGGAG GACA		
			__ A		
GAM125	HNRPK	3'	GGACATAGGCAAAATAACTTG 7915	G	CTCCC
			CAAG TATTTTGCC TGTCC		
			GTTC ATAAAACGG ACAGG		
			A AT__		
GAM125	HNRPK	3'	GGACATAGGCAAAATAACTTG 25279	G	CTCCC
			CAAG TATTTTGCC TGTCC		
			GTTC ATAAAACGG ACAGG		
			A AT__		
GAM125	MAGEA10	5'	GGACAGGGAGAGCAAGAGGTC 22035	TA	C
			GG TTTTGC CTCCCTGTCC		
			CT AGAACG GAGGGACAGG		
			GG A		
GAM125	MNT	3'	GACAGGGAGGGGGACCT 21564	ATTT	G
			AGGT T CCCTCCCTGTC		
			TCCA G GGGAGGGACAG		
			__ G		
GAM125	PDGFRB	3'	GGACAAAGAGGGCAAATGAGAT 32815	AT__	CC
	C		GGT TTTGCCCTC TGTCC		
			CTA AAACGGGAG ACAGG		
			GAGT AA		
GAM125	PIGK	3'	GACAGAGATCAGAATACATTG 33135	G	CCC C
			CAA GTATTTTG TC CTGTC		
			GTT CATAAGAC AG GACAG		
			A T__ A		
GAM125	PTGFRN	3'	GGACAAGGAAAGGATCAGATAC 33365	TG_ C_	C
	CT		AGGTATTT CC TCC TGTCC		
			TCCATAGA GG AGG ACAGG		
			CTA AA A		
GAM125	TR2	3'	GACTGAGCAAAATATCTCA 35795	A	CC CCT
			C AGGTATTTTGC TC GTC		

			A TCTATAAAACG AG CAG		
			C _ T_		
GAM125	BAG5	3'	GGACCAGCAATAATACCTTG 11307	_ CC_	
			CAAGGTATT TTGC TCC		
			GTTCCATAA AACG AGG		
			T ACC		
GAM125	BM-002	3'	AGGGAAAACAAAATACTT 18724	CCC	
			AGGTATTTTG TCCCT		
			TTCATAAAAC AGGGA		
			AAA		
GAM125	C8orf4	3'	GGACAGGGAGAGAAAATACC 21325	GCC	
			GGTATTTT CTCCCTGTCC		
			CCATAAAA GAGGGACAGG		
			GA_		
GAM125	CDW92	3'	ACAGGGATTTAATACCTT 27866	TTGCCC	
			AAGGTATT TCCCTGT		
			TTCCATAA AGGGACA		
			TTT_		
GAM125	DKFZP564I1171	3'	GACAGGGAGGGCCCATCACC 35445	ATTTT	
			GGT GCCCTCCCTGTC		
			CCA CGGGAGGGACAG		
			CTACC		
GAM125	DKFZp761J1523	3'	GACAGAGAGGGCAGCC 26061	ATTT C	
			GGT TGCCCTC CTGTC		
			CCG ACGGGAG GACAG		
			_ A		
GAM125	FLJ11155	3'	AGTGAGGCAGAAATACCTTG 20347	GC C	
			CAAGGTATTTT CCTC CT		
			GTTCCATAAAG GGAG GA		
			AC T		
GAM125	KIAA1237	3'	GGATCAGGGCAAACAACCTT 39220	GTA CCCT	
			AAG TTTTGCCCT GTCC		
			TTC AAAACGGGA TAGG		
			AAC C_		
GAM125	KIAA1376	3'	ACAGAGAAGTATCTTG 31821	TTGCCC C	
			CAAGGTATT TC CTGT		
			GTTCTATGA AG GACA		
			_ A		
GAM125	KIAA1416	5'	GGCTTTGAGGGCAAACACCTCA 41810	A AT CCT	
			C AGGT TTTGCCCTC GTC		

A TCCA AACCGGGAG CGG
 C C_ TTT
 GAM125 KIAA1913 5' ACAGGGAGAGGCGACCC 36576 TATT _
 GG TTGCC CTCCCTGT
 || |||| |||||
 CC AGCGG GAGGGACA
 C_ A
 GAM125 MGC19556 3' GGACAAAAAATGTAAAATACT 27317 CCTCCC_
 T AGGTATTTTGC TGTCC
 ||||| ||||
 TTCATAAAATG ACAGG
 TAAAAA
 GAM125 MGC8407 3' ACAGGGAGGGCTGATACCTCC 23479 A TT
 C AGGTATT GCCCTCCCTGT
 | |||| |||||
 C TCCATAG CGGGAGGGACA
 C T_
 GAM125 MORF4 5' GGACAAAAAGTGAAATACTTT 43643 TG CCTCCC
 AAGGTATTT C TGTCC
 ||||| | ||||
 TTTCATAAA G ACAGG
 GT AAAA_
 GAM125 PPM1A 3' ACAGGGAGAGCAGCAGCC 21997 ATT C
 GGT TTGC CTCCCTGT
 || |||| |||||
 CCG GACG GAGGGACA
 AC_ A
 GAM125 PRO1430 5' GGACAGGGAGAGAAAATACC 20675 GCC
 GGTATTTT CTCCCTGTCC
 ||||| |||||
 CCATAAAA GAGGGACAGG
 GA_
 GAM125 LOC119369 3' GACAGGGAGGGTCACCT 37207 ATTTT
 AGGT GCCCTCCCTGTC
 ||| |||||
 TCCA TGGGAGGGACAG
 C_
 GAM125 LOC126302 3' GGACAGGGCTCACACACCTCA 36824 A ATTT CCCT
 C AGGT TG CCCTGTCC
 | ||| || |||||
 A TCCA AC GGGACAGG
 C C_ ACTC
 GAM125 LOC129676 5' GGACAGGGAGGGAGCATCCCCC 37284 TATTTTG_
 T AGG CCCTCCCTGTCC
 ||| |||||
 TCC GGGAGGGACAGG
 CCCTACGA
 GAM125 LOC144667 3' ACAGAGAGGAAATCCT 40450 T TGC C
 AGG ATTT CCTC CTGT
 ||| ||| ||| |||

		TCC TAAA GGAG GACA		
		— — A		
GAM125	LOC146756 3'	GGACAGGGAAAGGGCCACC 40739	ATTTT	—
		GGT GCCC TCCCTGTCC		
		CCA CGGG AGGGACAGG		
		C— AA		
GAM125	LOC152275 3'	GGCAAAGGCAAAATACC 41458	CTCCC	
		GGTATTTTGCC TGTC		
		CCATAAACGG ACGG		
		AA—		
GAM125	LOC162083 5'	GGACAAGGAGGGCAGCGAC 40047	ATT	C
		GT TTGCCCTCC TGTCC		
		CA GACGGGAGG ACAGG		
		GC_ A		
GAM125	LOC200982 3'	GACAGGGAGAGGCCACTCCT 43375	TATTTT	_
		AGG GCC CTCCCTGTC		
		TCC CGG GAGGGACAG		
		TCAC_ A		
GAM125	LOC245728 5'	ACAGGAAGCAAATGCCTCA 43800	A	T CCTC
		C AGGTATTT GC CCTGT		
		A TCCGTAAA CG GGACA		
		C _ AA—		
GAM125	LOC254015 3'	GGACAGGGAAAGGGCCACC 46246	ATTTT	—
		GGT GCCC TCCCTGTCC		
		CCA CGGG AGGGACAGG		
		C— AA		
GAM125	LOC257106 3'	GACAGGGAGGACAGGGCC 45678	AT	C
		GGT TTTG CCTCCCTGTC		
		CCG GGAC GGAGGGACAG		
		_ A		
GAM125	LOC57109 3'	GGACAGAAAAGGGGCAGACACA 21656	AT_	CC_
	CC	GGT TTTGCCCT CTGTCC		
		CCA AGACGGGG GACAGG		
		CAC AAAA		
GAM126	B3GALT5 3'	TCGACTTGAACCACTCC 12701		
		GGAGTGGTTCAAG GG		
		CCTCACCAAGTTC CT		
		AG		
GAM126	B3GALT5 3'	TCGACTTGAACCACTCC 27029		
		GGAGTGGTTCAAG GG		

			CCTCACCAAGTTC	CT		
			AGIII			
GAM126	B3GALT5	3'	TCGACTTGAACCACTCC	27034	_____	
			GGAGTGGTTCAAG	GG		
			CCTCACCAAGTTC	CT		
			AGIII			
GAM126	B3GALT5	3'	TCGACTTGAACCACTCC	27039	_____	
			GGAGTGGTTCAAG	GG		
			CCTCACCAAGTTC	CT		
			AGIII			
GAM126	B3GALT5	3'	TCGACTTGAACCACTCC	27024	_____	
			GGAGTGGTTCAAG	GG		
			CCTCACCAAGTTC	CT		
			AGIII			
GAM126	CARD15	3'	GACCCCTTACCACTGCT	22717	G TC A	
			AG AGTGGT AAGGG TC			
			TC TCACCA TTCCC AG			
			G _ C			
GAM126	GATA2	3'	AAGCCGACACCACTCCTG	7800	TCAA GATC	
			CAGGAGTGGT	GG CTT		
			GTCCTCACCA	CC GAA		
			CAG_ _ _			
GAM126	HAP1	3'	AAGGATCTATACCCTCCTG	10072	T TCAAG	
			CAGGAG GGT	GGATCCTT		
			GTCCTC CCA	TCTAGGAA		
			_ TA_ _			
GAM126	KCNA7	3'	AAAGATCCCTTGACCCTG	25626	A TGGT C	
			CAGG G	TCAAGGGATC TT		
			GTCC C	AGTTCCCTAG AA		
			_ _ _ A			
GAM126	MYO1D	3'	AAGAATCCCGCTGGCATCCTG	35547	G GT A_ C	
			CAGGA TG	TCA GGGAT CTT		
			GTCCT AC	GGT CCCTA GAA		
			_ _ CG A			
GAM126	ERG-1	5'	GAAGGATCCTTCACCAGCCCC	22555	A_ TCA	
			GG G TGGT	AGGGATCCTTC		
			CC C ACCA	TTCCTAGGAAG		
			C G C_			
GAM126	FLJ10748	3'	AAGAATCCCTTCCTCTTG	20084	T TTCA C	
			CAGGAG GG	AGGGAT CTT		

GTTCTC CT TCCCTA GAA
 _ _ _ _ A
 GAM126 KIAA0319 3' AAGGACCCCTTGAATCCA 16757 _ A
 TGG TTCAAGGG TCCTT
 ||| ||||| |||||
 ACC AAGTTCCC AGGAA
 T C
 GAM126 MGC2306 3' AAGGCCGACACCACTCCTG 26349 TCAA GAT
 CAGGAGTGGT GG CCTT
 ||||| || |||||
 GTCCTCACCA CC GGAA
 CAG_ _ _
 GAM126 MGC2705 3' GACCCCTGAGCCACCCC 26416 A A A
 GG GTGGTTCA GGG TC
 || ||||| ||| ||
 CC CACCGAGT CCC AG
 C C _
 GAM126 X123 3' GAAGGATCCCTCTCCTCTCT 34650 T TTCA
 GGAG GG AGGGATCCTTC
 ||| || |||||
 TCTC CC TCCCTAGGAAG
 T TC_ _
 GAM126 LOC144453 3' AAAGATCCCCTCCTTCCT 37744 T TTCAA C
 AGGAG GG GGGATC TT
 |||| || ||||| ||
 TCCTT CC CCCTAG AA
 _ TC_ _ A
 GAM126 LOC149670 5' GAAGCCACTCAAACCATTC 38804 CA _ ATC
 GGAGTGGTT AG GG CTTC
 ||||| || || |||||
 CCTTACCAA TC CC GAAG
 AC A _ _
 GAM126 LOC157247 5' GAAAGACCTTTTGGACCACCCC 39575 A A C
 T AGG GTGGTTCAAGGG TC TTC
 ||| ||||| || |||||
 TCC CACCAGGTTTTTC AG AAG
 C C A
 GAM126 LOC203197 3' AAGGATCCCCAGCCCC 43007 AGT CAA
 GG GGTT GGGATCCTT
 || |||| |||||
 CC CCGA CCCTAGGAA
 C_ C_
 GAM126 LOC254559 5' GATCCCTTCTGAGCTCAC 46198 _ _
 GTG GTTCA AGGGATC
 ||| |||| |||||
 CAC CGAGT TCCCTAG
 T CT
 GAM126 LOC92661 3' GAAGGATCAGACCACCACCCCT 34721 A TCAAGG
 AGG GTGGT GATCCTTC
 ||| |||| |||||

			TCC CACCA CTAGGAAG		
			C CCAGA_		
GAM127	MEN1	5'	GTGTCTCAAAACAAACAAA 28299	—	
			TTTGTTTGTTTT GACAC		
			AAACAAACAAAA CTGTG		
			CT		
GAM127	MEN1	5'	GTGTCTCAAAACAAACAAA 28303	—	
			TTTGTTTGTTTT GACAC		
			AAACAAACAAAA CTGTG		
			CT		
GAM127	NR4A2	3'	CAGTTCAGACAAATGTAA 12854	TT	
			TTACATTTGTTTG TTG		
			AATGTAAACAGAC GAC		
			TT		
GAM127	SMP1	3'	GTGTCAAATGTTAATGAAATA 15611	A	TTTGT
			TATT CATTTG TTTGACAC		
			ATAA GTAAAT AAACTGTG		
			A TGT_		
GAM127	XYLB	3'	CAAAACAAACAAAGCAATA 11583	ACA	
			TATT TTTGTTTGTTTTG		
			ATAA AAACAAACAAAAC		
			CG_		
GAM127	HNRPC	3'	CAGTTCAACACAAATGTAA 25350	_	TT
			TTACATTTGT TTG TTG		
			AATGTAAACA AAC GAC		
			C TT		
GAM127	KIAA1364	3'	GTGTCAAAACACATTTAT 31815	TT	T
			AT GT TGTTTTGACAC		
			TA TA ACAAACACTGTG		
			TT C		
GAM127	KR18	3'	TGAAACGAAACAAATGTAATA 27122	_	
			TATTACATTTGTTT GTTTTG		
			ATAATGTAAACAAA CAAAGT		
			G		
GAM127	LOC221103	5'	AAACAATCAAATGTAATA 44777	T	
			TATTACATTTG TTGTTT		
			ATAATGTAAAC AACAAA		
			T		
GAM127	LOC90333	3'	TGTCATCTACAAACAAAT 31228	TT_	
			ATTTGTTTGT TGACA		

			TAAACAAACA ACTGT		
			TCT		
GAM128	CCND2	3'	TGACATCCTGCTTCTTCTTC 7520	CGAAAAA	
			GAAGAAGA GATGTCA		
			CTTCTTCT CTACAGT		
			TCGTC__		
GAM128	CDR2	5'	ACTCTTTCCCCGCCTTCTTTGT 37427	A AA_ T	
			ACGAAGAAG CG AAAGA GT		
			TGTTTCTTC GC TTTCT CA		
			C CCC _		
GAM128	MXI1	3'	TGACATCTTTTTAAAGCTT 12586	ACG_	
			AAG AAAAAGATGTCA		
			TTC TTTTCTACAGT		
			GAAA		
GAM128	MXI1	3'	TGACATCTTTTTAAAGCTT 28196	ACG_	
			AAG AAAAAGATGTCA		
			TTC TTTTCTACAGT		
			GAAA		
GAM128	NOTCH3	3'	GTCTTTTTCATCCTCTTC 6018	A C	
			GAAGA GA GAAAAAGAT		
			CTTCT CT CTTTTTCTG		
			C A		
GAM128	STAU2	3'	GCATTTTTCATATTCTTC 15721	GAC AA	
			GAAGAA GAAA GATGT		
			CTTCTT CTTT TTACG		
			ATA _		
GAM128	ALDH9	5'	GCTCTCCCCGCTTCTTCG 6361	A AAAA T	
			CGAAGAAG CG AGA GT		
			GCTTCTTC GC TCT CG		
			_ CCC_ _		
GAM128	FKSG44	3'	TGACCGTCTCGTCTTCCTC 25649	A AAAA _	
			GA GAAGACGA GATG TCA		
			CT CTTCTGCT CTGC AGT		
			C _ C		
GAM128	FLJ20232	3'	TGACATCTCTTTCGTCTCCT 21086	A A	
			AG AGACGAAA AGATGTCA		
			TC TCTGCTTT TCTACAGT		
			C C		
GAM128	GAPCENA	3'	GACACCTTTTGTTCCTTCTT 14492	A _ A	
			AAGAAG CGA AAAAG TGTC		

TTCTTC GTT TTTTC ACAG
 C G C
 GAM128 KIAA1040 3' ACATCTTTCTTGTTTCTT 35737 A A
 AAGA GACGA AAAGATGT
 |||| |||| ||||
 TTCT TTGTT TTTCTACA
 _ C
 GAM128 KIAA1165 3' ACATCTTTTAACTTCTCAGT 33473 GA ACGA
 AC AGAAG AAAAGATGT
 || |||| ||||
 TG TCTTC TTTTCTACA
 AC AA_
 GAM128 KIAA1913 5' GACCCTGCCGCCTTCTTCGT 36577 A AAAA AT
 ACGAAGAAG CG AG GTC
 |||| || || ||
 TGCTTCTTC GC TC CAG
 C CG_ C_
 GAM128 MRPL35 3' TGATGGATTTTCATTTCTTCG 18738 AC AGA
 CGAAGAAG GAAAA TGTCA
 |||| |||| ||||
 GCTTCTTT CTTT GTAGT
 A_ AG_
 GAM128 OSBPL7 5' TGACATCTCCTTCCTTC 19318 AC AA
 GAAG GAA AGATGTCA
 ||| || ||||
 CTTC CTT TCTACAGT
 _ CC
 GAM128 SEPT3 3' TGACCACACCTCCGTTTCTCC 21185 A AAAAAGAT
 GT ACG AGAAGACG GTCA
 || |||| ||||
 TGC TCTTTTGC CAGT
 C CTCCACAC
 GAM128 SLC12A8 5' CGTCTTCGTCTTCCTC 23894 A AAA
 GA GAAGACGA AGATG
 || |||| ||||
 CTCTTCTGCT TCTGC
 C _
 GAM128 LOC115123 3' GTCTTTTTCATCTCTTTCG 36248 GA C
 CGAA AGA GAAAAAGAT
 ||| || ||||
 GCTT TCT CTTTTTCTG
 TC A
 GAM128 LOC116028 3' TGACATCCTGGCTCCTCATCTT 36493 C AAAA_
 CTTC GAAGAAGA GA GATGTCA
 |||| || ||||
 CTTCTTCT CT CTACAGT
 A CCTCGGTC
 GAM128 LOC122553 3' ACATCTTTATTCCCTTCTT 36685 AC _
 AAGAAG GAA AAAGATGT
 |||| || ||||

			TTCTTC CTT TTTCTACA		
			C_ A		
GAM128	LOC145082 5'	TGACATCCCCCTGCCTCTATCT 40494	C_ AAAA_____		
		TCTTC	GAAGAAGA GA GATGTCA		
			CTTCTTCT CT CTACAGT		
			AT CCGTCCCC		
GAM128	LOC145773 3'	TGAAAGGCTTTTATCTTCTTC 37985	CGA ATG_		
		GAAGAAGA AAAAG TCA			
			CTTCTTCT TTTTC AGT		
			A_ GGAA		
GAM128	LOC146237 3'	TGACATGTGTCGTCTTCTC 40672	A AAAAG		
		GA GAAGACGA ATGTCA			
			CT CTTCTGCT TACAGT		
			_ GTG_		
GAM128	LOC150319 3'	GACACCCCTTTCTTCTTC 38894	CGAAA A_		
		GAAGAAGA AAG TGTC			
			CTTCTTCT TTC ACAG		
			_____ CCC		
GAM128	LOC152348 5'	TGACATCTTTTTTCCCCTT 41488	AC_		
		AAG GAAAAAGATGTCA			
			TTC TTTTTTCTACAGT		
			CCC		
GAM128	LOC201283 3'	ATGTCTTTTCTCACCTTCTC 30303	A AC A		
		GA GAAG GA AAAGATGT			
			CT CTTC CT TTTCTGTA		
			_ CA C		
GAM128	LOC91397 5'	TGACATTTTCTCCCCTTCCTC 32784	A AC AA		
		GA GAAG GA AAGATGTCA			
			CT CTTC CT TTTTACAGT		
			C CC C_		
GAM129	DIAPH2 3'	CTATTTTGTGAGAAAACCCTCAC 13560	C AC		
	A	TGT AGGGTTTTTC CAGAAATAG			
			ACA TCCCAAAG GTTTTTATC		
			C A_		
GAM129	RAB36 3'	CTATCTCTGGCACCTCTGA 11349	_ TTTCA A		
		TCAG GGT CCAGA ATAG			
			AGTC CCA GGTCT TATC		
			T C_____ C		
GAM129	SPAG8 3'	ATTTCTGGTGTGTGCAGACA 14815	AGG TTT		
		TGTC GT CACCAGAAAT			

ACAG CG GTGGTCTTTA
 A__ TGT
 GAM129 ZER6 3' ATTCCTGGTGTCTGATA 31740 GTTTT A
 TGTCAGG CACCAG AAT
 ||||| ||||| ||
 ATAGTCT GTGGTC TTA
 _____ C
 GAM129 LOC205795 5' ATTCCTGGGGCCCTGGCA 43610 TTCA A
 TGTCAGGGTT CCAG AAT
 ||||| ||||| ||
 ACGGTCCCGG GGTC TTA
 _____ C
 GAM130 FGFR1 3' TCACTCCCAGACATTCA 23364 T _ CTC
 TGA ATGTCTGG AG TGA
 || ||||| || ||
 ACT TACAGACC TC ACT
 _ C _
 GAM130 FGFR1 3' TCACTCCCAGACATTCA 23368 T _ CTC
 TGA ATGTCTGG AG TGA
 || ||||| || ||
 ACT TACAGACC TC ACT
 _ C _
 GAM130 NEUROD1 3' TTCATCAATTTTTATACATATC 8323 C CTC
 A TGATATGT TGGAG TGATGAA
 ||||| ||||| |||||
 ACTATACA ATTTT ACTACTT
 T TA_
 GAM130 AOP2 3' CATCAGAGAATGACTATCA 11340 T TGGAG
 TGATA GTC CTCTGATG
 ||||| || |||||
 ACTAT CAG GAGACTAC
 _ TAA_
 GAM130 C20orf110 3' CACCAGAGCTCTTGGATA 38832 _ A
 TGTCTG GAGCTCTG TG
 ||||| ||||| ||
 ATAGGT CTCGAGAC AC
 T C
 GAM130 SERP1 3' TTCACCAGAACTATTTTAATAT 15798 CTGG__ C A
 ATCA TGATATGT AG TCTG TGAA
 ||||| || ||||| ||
 ACTATATA TC AGAC ACTT
 ATTTTA A C
 GAM130 ZNF337 3' CATCAGAGGACACACTCA 33771 TA_ TGGAG
 TGA TGTC CTCTGATG
 || ||||| |||||
 ACT ACAG GAGACTAC
 CAC _____
 GAM130 LOC147077 3' TCACACTGGCTCCAGACA 38294 C_ A
 TGTCTGGAGCT TG TGA
 ||||| || ||||| ||

ACAGACCTCGG AC ACT
 TC _
 GAM130 LOC200197 3' TTCATCAGAGCTCGGC 42733 TG
 GTC GAGCTCTGATGAA
 ||| |||||
 CGG CTCGAGACTACTT

 —
 GAM130 LOC253747 5' TCATCAGAGCCTGGAATTCA 46552 TATG TG A
 TGA TC G GCTCTGATGA
 ||| || | |||||
 ACT AG C CGAGACTACT
 TA__ GT_
 GAM130 LOC86651 3' TCAGACCCCTCCAGACAT 34100 C__
 ATGTCTGGAG TCTGA
 ||||| ||||
 TACAGACCTC AGACT
 CCC
 GAM131 ADAMTS13 5' AGCTTCCAAGAGTAAACACTG 29124 CCA GTAA
 CAGTG AT TGGAAGCT
 |||| || |||||
 GTCAC TG ACCTTCGA
 AAA AGA_
 GAM131 ADAMTS13 5' AGCTTCCAAGAGTAAACACTG 29126 CCA GTAA
 CAGTG AT TGGAAGCT
 |||| || |||||
 GTCAC TG ACCTTCGA
 AAA AGA_
 GAM131 ADAMTS13 5' AGCTTCCAAGAGTAAACACTG 29128 CCA GTAA
 CAGTG AT TGGAAGCT
 |||| || |||||
 GTCAC TG ACCTTCGA
 AAA AGA_
 GAM131 GPRC5B 3' AGCCCCCATGTTCTCTGCACTG 18350 CAATGTA AA
 TT AACAGTGC ATGG GCT
 ||||| ||| |||
 TTGTCACG TACC CGA
 TCTCTTG CC
 GAM131 HD 3' AGCTTGGTGTCTTGGAAGTGT 7891 TG ATGG
 AACAGTGCCAA TA AAGCT
 ||||| || ||||
 TTGTCACGGTT GT TTCGA
 CT GG_
 GAM131 LMO7 3' AGCCTCCATACGAAAGCACTGT 11826 CAA A A
 T AACAGTGC TGTA TGGA GCT
 ||||| ||| ||| |||
 TTGTCACG GCAT ACCT CGA
 AAA _ C
 GAM131 M11S1 3' GCTTTGACACAGCACTGTT 12517 CAA AATG
 AACAGTGC TGT GAAGC
 ||||| || ||||

			TTGTCACG ACA TTTCG		
			AC_ G__		
GAM131	PDE1A	5'	AGCTTTGTACATCAGCACTGTT 11457	CA	ATG
			AACAGTGC ATGTA GAAGCT		
			TTGTCACG TACAT TTTCGA		
			AC G__		
GAM131	PTTG1IP	3'	GCTCTCCAGTGGCACTG 10535	ATGTAA	_
			CAGTGCCA TGGA AGC		
			GTCACGGT ACCT TCG		
			G_____ C		
GAM131	RAB36	3'	AGCCCTTGAACATGGCACTG 11348	A	AAT_ AA
			CAGTGCCA TGT GG GCT		
			GTCACGGT ACA CC CGA		
			_ AGTT _		
GAM131	TGFBR2	3'	CTAAGTACAGTGGCACTGTT 9238	A	A_
			AACAGTGCCA TGTA TGG		
			TTGTCACGGT ACAT ATC		
			G GA		
GAM131	7h3	3'	AGCTTTGAGCACTGCACTGTT 26915	CAA	AATG
			AACAGTGC TGT GAAGCT		
			TTGTCACG ACG TTTCGA		
			TC_ AG__		
GAM131	DKFZp547C176	3'	GTTACACCCTGGCACTGTT 33381	A__	
			AACAGTGCCA TGTAAT		
			TTGTCACGGT ACATTG		
			CCC		
GAM131	DKFZp586I021	3'	AGCCTCCCTCTACTCGGCACTG 26019	AAT	AT_ A
	T		ACAGTGCC GTA GGA GCT		
			TGTCACGG CAT CCT CGA		
			CT_ CTC C		
GAM131	EPB41L1	3'	AGCTCCCATCACAAGCTTGGCA 34936	___	A A
	TTG		CAGTGCCAA TGT ATGG AGCT		
			GTTACGGTT ACA TACC TCGA		
			CGA C C		
GAM131	FLJ10540	3'	CTTGAATTACATTAGCAC 19927	C	GG
			GTGC AATGTAAT AAG		
			CACG TTACATTA TTC		
			A AG		
GAM131	H11	3'	AGTTTCCACATTAGCACT 15691	C	AAT
			AGTGC AATGT GGAAGCT		

			TCACG TTACA CCTTTGA	
			A _	
GAM131	HYA22	3'	CTTTCATATTGGCAC 12387	GTA
			GTGCCAAT ATGGAAG	
			CACGGTTA TACTTTC	
			—	
GAM131	KIAA0553	3'	CCACACATTTGGCACTGTT 34634	_ AA
			AACAGTGCCAA TGT TGG	
			TTGTCACGGTT ACA ACC	
			T C_	
GAM131	KIAA0828	3'	AGCCCCTCCAGATTGGCACT 39510	GTAA A_
			AGTGCCAAT TGGA GCT	
			TCACGGTTA ACCT CGA	
			G_ CCC	
GAM131	KIAA1522	3'	GGCACCTCACTGGCACTG 32418	A TAAT AA
			CAGTGCCA TG GG GCT	
			GTCACGGT AC CC CGG	
			C T_ A_	
GAM131	KIAA1560	3'	AGCTTCCAGATAGCACCGTT 32100	A CAATGTAA
			AAC GTGC TGGAAGCT	
			TTG CACG ACCTTCGA	
			C ATAG_	
GAM131	MGC13105	3'	AGCTTCCACTTTGGGAACATGT 35406	_ G_ TGTA
			ACA GT CCAA TGGAAGCT	
			TGT CA GGTT ACCTTCGA	
			A AG TC_	
GAM131	MGC32043	3'	GCTTCCAGGCAGCCTGTT 29392	T CAA AA
			AACAG GC TGT TGGAAGC	
			TTGTC CG ACG ACCTTCG	
			_ _ G_	
GAM131	NPTXR	3'	TCATCATACTGGCACTGTT 27736	A A
			AACAGTGCCA TGT ATGG	
			TTGTCACGGT ATA TACT	
			C C	
GAM131	NPTXR	3'	TCATCATACTGGCACTGTT 15588	A A
			AACAGTGCCA TGT ATGG	
			TTGTCACGGT ATA TACT	
			C C	
GAM131	LOC145758	5'	GTTCACACTAGCACTGTT 40587	CAATG A GA
			AACAGTGC TA TG AGC	

		TTGTCACG	AT AC TTG		
		_____ C AC			
GAM131	LOC149837 3'	AGCCTTCAACAATGGCAC	41097	A AA A	
		GTGCCA TGT TGGA GCT			
		CACGGT ACA ACTT CGA			
		A _ C			
GAM131	LOC150605 5'	GCTCCCCATGGCACTGTT	41231	A TAAT A	
		AACAGTGCCA TG GG AGC			
		TTGTCACGGT AC CC TCG			
		- _ _ C			
GAM131	LOC155064 3'	GTTTCCATCAACACCGCT	39531	CCAA A_	
		AGTG TGT ATGGAAGC			
		TCGC ACA TACCTTTG			
		C _ AC			
GAM131	LOC160156 5'	AGCCTCCTCTCCTATCGGCACT	39990	A TAAT_ A	
	GTT	AACAGTGCC ATG GGA GCT			
		TTGTCACGG TAT CCT CGA			
		C CCTCT C			
GAM131	LOC197201 3'	GCTTCCTACCTGACATGTT	42463	G C AT AT	
		AACA TG CA GTA GGAAGC			
		TTGT AC GT CAT CCTTCG			
		- A C _ _			
GAM131	LOC91960 3'	AGCTTCTTGATTGGCAGTG	33608	G TAAT	
		CA TGCCAATG GGAAGCT			
		GT ACGGTTAT TCTTCGA			
		G GT _			
GAM132	GPR81 3'	ATTCCTATCCTCTGA	26280	GAAA T	
		TCAGAGGAT GGGA AT			
		AGTCTCCTA TCCT TA			
		_ T			
GAM132	HLA-DQA1 3'	CATATCCCTTTTCTCCTC	46724	T	
		GAGGA GAAAGGGATATG			
		CTCCT TTTTCCCTATAC			
		C			
GAM132	MAP3K7IP1 3'	GTGCCCCATCCTCTG	12762	AAA A	
		CAGAGGATG GGG TAT			
		GTCTCCTAC CCC GTG			
		_ _			
GAM132	NFRKB 5'	ATTCCTTCATCCTCTGA	12819	A	
		TCAGAGGATGAA GGGAT			

AGTCTCCTACTT CCTTA

GAM132 PCK3 3' ATCTTTTTCCCCTCTGA 36123 AT
TCAGAGG GAAAGGGAT
||||| |||||||
AGTCTCC CTTTTTCTA
C_

GAM132 PXN 3' CATATCCCTTCCCCAGATCTG 8755 GGA A__
CAGA TG AAGGGATATG
||| || |||||||
GTCT AC TTCCCTATAC
AG_ CCC

GAM132 RAD50 3' CATATCCCTTCCAGATGG 12294 GA_ TGAA
TCA GGA AGGGATATG
||| ||| |||||||
GGT CCT TCCCTATAC
AGA ____

GAM132 RAD50 3' CATATCCCTTCCAGATGG 28551 GA_ TGAA
TCA GGA AGGGATATG
||| ||| |||||||
GGT CCT TCCCTATAC
AGA ____

GAM132 AMOTL1 3' TGTACCCCCATTCTCTGA 36469 AAA _
TCAGAGGATG GGG ATA
||||||| ||| |||
AGTCTCTTAC CCC TGT
C_ A

GAM132 CXYorf1 5' CATTTCCCCATGCCTCTGA 39904 _ AAA T
TCAGAGG ATG GGGA ATG
||||||| ||| ||| |||
AGTCTCC TAC CCCT TAC
G _ T

GAM132 FLJ00060 3' CATACCCCCTGCCCTCCTCTGA 30628 TGAA A_
TCAGAGGA AGGG TATG
||||||| ||| ||| |||
AGTCTCCT TCCC ATAC
CCCG CC

GAM132 FLJ10244 5' ATCGTCTTTCCGTCCTCTGA 19779 _ _
TCAGAGGATG AAAGG GAT
||||||| ||| ||| |||
AGTCTCCTGC TTTCT CTA
C G

GAM132 FLJ20257 5' ATATCTTTGATCCCCTGA 21220 A G AG
TCAG GGAT AA GGATAT
||| ||| ||| ||| |||
AGTC CCTA TT TCTATA
C G _

GAM132 FLJ31951 3' CCTGCTTTCATCCCCTGA 29550 A _
TCAG GGATGAAAG GG
||| ||||||| ||

			AGTC CCTACTTTC CC	
			C GT	
GAM132	KIAA1001	3'	CATATCCCTTCTGTATCCT 17325	A__
			AGGATG AAGGGATATG	
			TCCTAT TTCCCTATAC	
			GTC	
GAM132	KIAA1321	3'	CATATCCCTCAGGCCTC 31192	A_ AA
			GAGG TGA GGGATATG	
			CTCC ACT CCCTATAC	
			GG _	
GAM132	PRO2435	5'	ATATATTTTCATCTCTGA 20600	G GG
			TCAGAG ATGAAAG ATAT	
			AGTCTC TACTTTT TATA	
			_ A_	
GAM132	PROL2	3'	CATATCCCTGGACTCTTGA 13684	_ GATGAA
			TCA GAG AGGGATATG	
			AGT CTC TCCCTATAC	
			T AGG__	
GAM132	TGOLN2	3'	ATCCGTTCCCTCCTCTGA 32022	T AG
			TCAGAGGA GAA GGAT	
			AGTCTCCT CTT CCTA	
			C G_	
GAM132	LOC126917	3'	ATTCTCCTCTCCTCTGA 36867	T AA
			TCAGAGGA GA GGGAT	
			AGTCTCCT CT TCTTA	
			_ CC	
GAM132	LOC144866	5'	TATCCTCTCCTCTGA 40479	T AAG
			TCAGAGGA GA GGATA	
			AGTCTCCT CT CCTAT	
			_ _	
GAM132	LOC145739	3'	GTTCCATCATCCTCTGA 37962	AA
			TCAGAGGATGA GGGAT	
			AGTCTCCTACT CCTTG	
			A_	
GAM132	LOC146287	5'	TGTCTCTCTCCTCTGA 40691	T AA
			TCAGAGGA GA GGGATA	
			AGTCTCCT CT CTCTGT	
			_ _	
GAM132	LOC149842	3'	CATATCCCACATTCTC 41090	AAA
			GAGGATG GGGATATG	

		CTCTTAC CCCTATAC	
		A__	
GAM132	LOC150951 5'	CATGGGCTATTCATCCTC 41277	A GA
		GAGGATGAA GG TATG	
		CTCCTACTT TC GTAC	
		A GG	
GAM132	LOC153277 3'	CATACCCCTTCTCCCTG 41604	A T A A
		CAG GGA GAA GGG TATG	
		GTC CCT CTT CCC ATAC	
		- - C -	
GAM132	LOC153727 5'	CATATCCCTCCTGTGCTC 41680	G AA
		GAG ATG AGGGATATG	
		CTC TGT TCCCTATAC	
		G CC	
GAM132	LOC220883 3'	CATGTCCTCTCACCCCATGA 43849	GA A AA
		TCA GG TGA GGGATATG	
		AGT CC ACT TCCTGTAC	
		AC C C_	
GAM132	LOC221662 3'	ATGCTTCCTCCTCTGA 44387	TGAAA _
		TCAGAGGA GGA TAT	
		AGTCTCCT CCTT GTA	
		_____ C	
GAM132	LOC257484 5'	CATGTCTCCCAGCCCCTGA 42813	A A AAA
		TCAG GG TG GGGATATG	
		AGTC CC AC CTCTGTAC	
		C G C_	
GAM132	LOC92539 5'	ATATTGCTTCCTCTGA 34499	TGAA G
		TCAGAGGA AG GATAT	
		AGTCTCCT TC TTATA	
		_____ G	
GAM132	LOC92719 3'	CGTGGCGCCCATCCTCTGA 34848	AAA GA_
		TCAGAGGATG GG TATG	
		AGTCTCCTAC CC GTGC	
		_____ GCG	
GAM133	DVL3 3'	CAATCTTGCCTGCCTTCTGG 10690	AA ACTT
		CCAGAA CA CAAGATTG	
		GGTCTT GT GTTCTAAC	
		CC CC_	
GAM133	NKTR 3'	ATTTTGAAGTTATTTTTT 11862	C
		AGAAAA AACTTCAAGAT	

			TTTTTT TTGAAGTTT		
			A		
GAM133	PTGER2	3'	ATTTTGAAATTGTTCCCTGG	6659	AA C
			CCAG AACAA TTCAAGAT		
			GGTC TTGTT AAGTTT		
			CC A		
GAM133	API5	3'	CAATCTTGACTTGT	13361	CA_ CT
	TA		TAC GAAAACAA TCAAGATTG		
			ATG TTTTGT AGTTCTAAC		
			ACG C_		
GAM133	FLJ12800	3'	CAATCTTGAGGACTCCCGGTG	23189	A_ AAACAA
			TACC GA CTTCAAGATTG		
			GTGG CT GGAGTTCTAAC		
			CC CA_		
GAM133	FLJ14600	3'	CAATCTTGAGGTGCCTTCTG	26574	AACA
			CAGAA ACTTCAAGATTG		
			GTCTT TGGAGTTCTAAC		
			CCG_		
GAM133	HHLA2	3'	GAGTTGTAACCATTTCTGGTA	13937	_____
			TACCAGAAA ACAACTT		
			ATGGTCTTT TGTTGAG		
			TACCAA		
GAM133	LOC146227	3'	CAATCTTGAATTTTATTTTCTG	38082	CAAC_
			CAGAAAA TTCAAGATTG		
			GTCTTTT AAGTTCTAAC		
			ATTTT		
GAM133	LOC170063	3'	CAATTTTAACCTTTTCTGGTA	42186	CAACTTC
			TACCAGAAAA AAGATTG		
			ATGGTCTTTT TTTAAC		
			TCCAA_		
GAM134	IL10RA	3'	GCAAATATCTCCCTCT	29998	T CTCA
			AGA GG AGATATTG		
			TCT CC TCTATAAACG		
			C _		
GAM134	IMPA1	3'	ATGTACTTAAAACATCTGAT	12056	GCTC _
			ATCAGATG AAG ATAT		
			TAGTCTAC TTC TGTA		
			AAAA A		
GAM134	RPL17	5'	GCAGCTGTTTGAATCATCTGAT	6696	GC AA T
			ATCAGATG TC GATA TTGC		

TAGTCTAC AG TTGT GACG
 TA C_ C
 GAM134 SCAP2 3' CAAATATCCTGGTGCGAT 10028 G _ A
 AT GC TCA GATATTTG
 || ||| |||||
 TA CG GGT CTATAAAC
 G T C
 GAM134 C15orf5 3' GCAGACTTTAACCATCTGAT 25213 CTC ATA
 ATCAGATGG AAG TTTGC
 ||||| || |||||
 TAGTCTACC TTC AGACG
 AAT _
 GAM134 FLJ13105 3' CAAATATCCTGTCAGCCAAATG 24571 GA _ A
 CA TGGCT CA GATATTTG
 || |||| || |||||
 GT ACCGA GT CTATAAAC
 AA CT C
 GAM134 KIAA1198 3' GCAAATATCCTTGTCTGAT 31710 TGGCT _
 ATCAGA CAAG ATATTTGC
 |||| ||| |||||
 TAGTCT GTTC TATAAACG
 TT_ C
 GAM134 KIAA1795 3' GCAAATTGGAAAGCCATCTTAT 35701 C CAAGAT
 AT AGATGGCT ATTTGC
 || ||||| |||||
 TA TCTACCGA TAAACG
 T AAGGT_
 GAM134 KIAA1915 3' CAAATATCTCAGTGCTACT 36269 A TCA_
 AG TGGC AGATATTTG
 || |||| |||||
 TC ATCG TCTATAAAC
 _ TGAC
 GAM134 LOC158798 5' CAAACATTCCATCTGG 39892 CTCAA A
 TCAGATGG GAT TTTG
 ||||| ||| |||||
 GGTCTACC TTA AAAC
 _ C
 GAM134 LOC221486 3' GCAAAAGACTTGAGCCATC 43744 ATA
 GATGGCTCAAG TTTGC
 ||||| |||||
 CTACCGAGTTC AAACG
 AGA
 GAM134 LOC51605 3' GCAAATATCTTGAGAACTTC 18061 TGG_
 GA CTCAAGATATTTGC
 || ||||| |||||
 CT GAGTTCTATAAACG
 TCAA
 GAM135 AK3 3' ATGAAGAGAATCTTATTA 15073 G CA
 TAATAAGATT TC CAT
 ||||| || |||

		ATTATTCTAA AG GTA	
		G AA	
GAM135	FLJ11210 3'	GTCGATGTGCATGCTTTTA 29975 TAAGA GT CACATCGAC ATTTT TA GTGTAGCTG CG C	TT C
GAM135	KIAA1145 3'	TGTAACGTGGAAATCTTAT 32682 ATAAGATT TCCAC ACA TATTCTAA AGGTG TGT _ CAA_	G ATCG
GAM135	MGC13105 3'	TGTCGATGCTTACATCTTA 35408 TAAGAT GT CATCGACA ATTCTA CA GTAGCTGT _ TTC	T CCA
GAM135	LOC200014 3'	CGGCTGGCCAATCTTAT 42690 ATAAGATTG CCA TCG TATTCTAAC GGT GGC C C_	T CA
GAM135	LOC202934 3'	TTGTCTTTTGACAATTTTA 43467 TAAGATTGTC GACAA ATTTTAACAG CTGTT TTTT_	CACATC
GAM135	LOC255465 3'	TTGTCTTTTGACAATTTTA 46459 TAAGATTGTC GACAA ATTTTAACAG CTGTT TTTT_	CACATC
GAM135	LOC257319 3'	TTGAATGATGGAAATCTTATTA 45835 TAATAAGATT TCCA CAT CGA ATTATTCTAA AGGT GTA GTT _ A A	G _ _
GAM136	JAG2 3'	TGCCCAGAACGCCCGCTCCAG 8006 CTGGA CGTT CTGGGCA GACCT GCAA GACCCGT CGCCC _	ACAGA T
GAM136	SYBL1 3'	TTGGAAAATACATCTGTTCCAG 12166 CTGGAACAGA GT TTC G GACCTTGTCT CA AAG T A TAA GT	C ____ TG
GAM136	FLJ10900 5'	CAGGAAAAATCTGTTCCA 32669 TGGAACAGA TTTCTG 	CG_

			ACCTTGTCT AAGGAC		
			AAA		
GAM136	FLJ20294	3'	GCCCAGAGGATGATCCAG 19347	A	GACGT
			CTGGA CA TTCTGGGC		
			GACCT GT GAGACCCG		
			A AG__		
GAM136	FLJ20297	5'	CAGAAACTCTGCTCCAG 19647	A	C
			CTGGA CAGA GTTTCTG		
			GACCT GTCT CAAAGAC		
			C _		
GAM136	FLJ22690	3'	ATGCCCAGATCACATTCCAG 24037	CAGACGTT	
			CTGGAA TCTGGGCAT		
			GACCTT AGACCCGTA		
			ACACT__		
GAM136	JM11	3'	ATGCCCAACCAGGTTCCA 27327	AGAC	TTC
			TGGAAC GT TGGGCAT		
			ACCTTG CA ACCCGTA		
			GAC_ _		
GAM136	KCNB2	5'	TGGAAATGCCTGCCCCAG 45964	AA	A
			CTGG CAG CGTTTCTG		
			GACC GTC GTAAAGGT		
			CC C		
GAM136	KIAA0064	5'	ATGCCCAGGCGATTGCGTCCCA 16459	AACA	T__
	G		CTGG GACGT TCTGGGCAT		
			GACC CTGCG GGACCCGTA		
			__ TTAGC		
GAM136	KIAA0202	3'	ATGTTGTAAACAGCTGTTCCA 32179	AC	CTG
			TGGAACAG GTTT GGCAT		
			ACCTTGTC CAAA TTGTA		
			GA TG_		
GAM136	KIAA0237	3'	ATGCCCAGATGCTGCCTCAG 16438	AA	ACGTT
			CTGG CAG TCTGGGCAT		
			GA CT GTC AGACCCGTA		
			CC GT__		
GAM136	KIAA0682	3'	ATGCCCAGCCTGTTCC 16900	ACGTTT	
			GGAACAG CTGGGCAT		
			CCTTGTC GACCCGTA		
			C__		
GAM136	KIAA1297	5'	ATGCCCAGAAGGCCACCCCCCA 35708	AACAGACG	
	G		CTGG TTTCTGGGCAT		

			GACC	GAAGACCCGTA		
			CCCCACCG			
GAM136	PB1	3'	CTCAAAACACCTATTCCAG	20307	C AC C	
			CTGGAA AG GTTT TGGG			
			GACCTT TC CAAA ACTC			
			A CA _			
GAM136	POLD3	3'	TATGCCCAATATGCTGCCTCA	44055	AA A TTC	
			TGG CAG CGT TGGGCATA			
			ACT GTC GTA ACCCGTAT			
			CC _ TA_			
GAM136	ZER6	3'	CTTAGAAAACATCTGCTCCA	31742	A CG_	
			TGGA CAGA TTTCTGGG			
			ACCT GTCT AAAGATTC			
			C ACA			
GAM136	LOC146485	5'	TATGCTGGAAACATTATCCCA	30071	AACA C TG G	
			TGG GA GTTTC G CATA			
			ACC TT CAAAG C GTAT			
			CTA_ A GT _			
GAM136	LOC153443	3'	ATGCCCAGCTTTCTCACCCCAG	39372	AAC_ CGTTT	
			CTGG AGA CTGGGCAT			
			GACC TCT GACCCGTA			
			CCAC TTC__			
GAM136	LOC153910	3'	CCCAGAAGAATGGTGTCCCA	39439	A GA _	
			TGG ACA CGTT TCTGGG			
			ACC TGT GTAA AGACCC			
			C G_ GA			
GAM136	LOC221421	3'	ATGCGCACCTGTTCAG	44320	ACGTTTC G	
			CTGGAACAG TG GCAT			
			GACCTTGTC AC CGTA			
			CC_____ G			
GAM136	LOC253805	3'	ATGCCCAGGTCTGCCTACTCC	46131	AC A TT	
			GGA AG CG TCTGGGCAT			
			CCT TC GT GGACCCGTA			
			CA C CT			
GAM136	LOC90190	3'	ATGCCCTGACTGTTCCA	30946	ACGTT T	
			TGGAACAG TC GGGCAT			
			ACCTTGTC AG CCCGTA			
			_____ T			
GAM136	LOC91115	3'	TATGCCCAATTTCTGCTTCCA	32399	_ C TTC	
			TGGAA CAGA GT TGGGCATA			

			ACCTT GTCT TA ACCCGTAT		
			C T _		
GAM137	BTN2A1	3'	CACACAATCCCCAGGGTTCCTG 27801	AT_ A_ A C	
	AG		TTCA GC TGGG AT GTGTG		
			GAGT TG ACCC TA CACAC		
			CCT GG C A		
GAM137	CECR6	3'	CATTGTCCCATGCCTTGAA 25636	T ATC	
			TTCAA GCATGGGA GTG		
			AAGTT CGTACCCT TAC		
			C GT_		
GAM137	ENAH	3'	CAAGATCACCACGCATTGAA 20125	A GA G	
			TTCAATGC TGG ATC TG		
			AAGTTACG ACC TAG AC		
			C AC A		
GAM137	FLJ11110	3'	CACACTTCTGCCCCCACTGCAT 20320	_ AATC_	
	TGAA		TTCAATGCA TGGG GTGTG		
			AAGTTACGT ACCC CACAC		
			C CCGTCTT		
GAM137	KIAA0884	5'	CAGACCTCCCTTGCATTGAA 34775	T ATC G	
			TTCAATGCA GGA GT TG		
			AAGTTACGT CCCT CA AC		
			T C_ G		
GAM137	LOC163682	3'	CACGCAGCCCATGCAGTGAA 42085	A AAT	
			TTCA TGCATGGG CGTG		
			AAGT ACGTACCC GCAC		
			G GAC		
GAM138	PLDN	5'	CTTCTGACGAGCCACACGTTTG 14744	A G_ A	
	C		GCAAACGT TGGC GT TAGAAG		
			CGTTTGCA ACCG CA GTCTTC		
			C AG _		
GAM138	MGC3101	3'	CTTCCACAGAGCTCGTTTGCA 23477	TAT GGTATA	
			TGCAAACG GGC GAAG		
			ACGTTTGC TCG CTTC		
			_ AGACAC		
GAM139	NR4A2	3'	CCCAAGCACTTCAAAGGAACTG 12855	A _ ACC_	
	G		CCA TTCCTTTGA GT GGG		
			GGT AAGGAAACT CA CCC		
			C T CGAA		
GAM139	TGFBR3	3'	CCCAGACTCAAGGAGTTGGT 9248	T ACC	
			ACCAATTCCTT GAGT GGG		

TGGTTGAGGAA CTCA CCC
 _ GA_
 GAM139 FLJ10560 3' CCCAAATGAAAAAGTTGGTGA 19936 CC GA ACC
 TCACCAATT TTT GT GGG
 ||||| ||| || |||
 AGTGGTTGA AAA TA CCC
 _ AG AA_
 GAM139 FLJ20727 3' CGTAAGGAATTGTGA 19638 C TTGAG C
 TCAC AATTCCT TAC G
 ||| ||||| |||
 AGTG TTAAGGA ATG C
 _ A
 GAM139 KIAA1775 3' CCCGGCAAGGGCAGGAATTGGG 26943 A TTGAGTA
 A TC CCAATTCCT CCGGG
 || ||||| ||||
 AG GGTTAAGGA GGCCC
 _ CGGGAAC
 GAM139 SYNPO2 3' CCCAGTTACTTAAGGA ACTAAG 35591 CAA_ T _C
 TGA TCAC TTCCTT GAGTA C GGG
 ||| ||||| ||||| |||
 AGTG AAGGAA TTCAT G CCC
 AATC _ T A
 GAM139 TXI1 5' CCCAGTACTTGGAGGAACTGG 20492 A TG C
 CCA TTCCTT AGTAC GGG
 ||| ||||| ||||| |||
 GGT AAGGAG TCATG CCC
 C GT A
 GAM140 CUL4B 3' CTGATGGTCTGTGAGAT 9640 A A A
 ATCTCATA AC CG CAG
 ||||| || |||
 TAGAGTGT TG GT GTC
 C _ A
 GAM140 F2R 3' CTGATCATGTTTATGAGA 7720 C _
 TCTCATAAACA GA CAG
 ||||| || |||
 AGAGTATTTGT CT GTC
 A A
 GAM140 PTPRO 3' CATCTGCATGGGTTGTGAGA 25028 A_ CGA
 TCTCATAA CA CAGATG
 ||||| || |||||
 AGAGTGTT GT GTCTAC
 GG AC_
 GAM140 SIRT3 3' CATCTGTTGGTTACAAGAT 14545 CATA A
 ATCT AAC CGACAGATG
 ||| ||| |||||
 TAGA TTG GTTGTCTAC
 ACA_ _
 GAM140 SLC16A1 3' TTTGAGTGTTTATAGAT 9014 C GA
 ATCT ATAAACAC CAGA
 ||| ||||| |||

				TAGA TATTTGTG GTTT	
				— A—	
GAM140	ABT1	3'	CATCTGTCAATGTGATGAT	15029	— AACAC
			ATC TCATA GACAGATG		
			TAG AGTGT CTGTCTAC		
			T AA—		
GAM140	CNIL	3'	CATCTGTCATGTGCGATGA	12353	AA C
			TCAT ACA GACAGATG		
			AGTA TGT CTGTCTAC		
			GC A		
GAM140	FLJ10876	3'	CATCTGTCAGTAATGAGA	20220	AA AC
			TCTCAT AC GACAGATG		
			AGAGTA TG CTGTCTAC		
			A_ A_		
GAM140	FLJ14957	3'	CATCTGTCTGCCACTGAGA	26679	TAAA C
			TCTCA CA GACAGATG		
			AGAGT GT CTGTCTAC		
			CACC —		
GAM140	FLJ20174	3'	CATCTGTCACTTTATGTAGAT	19267	— CAC
			ATCT CATAAA GACAGATG		
			TAGA GTATTT CTGTCTAC		
			T CA_		
GAM140	FLJ20847	5'	CATGTGCGCATTATGAG	45457	CA A G
			CTCATAAA CG CA ATG		
			GAGTATTT GC GT TAC		
			AC _ G		
GAM140	GBA2	5'	CATCTGTCTGGCTCATGAG	35178	AAA_ C
			CTCAT CA GACAGATG		
			GAGTA GT CTGTCTAC		
			CTCG —		
GAM140	KIAA0923	3'	CATTAAGAGTGTCTTATGAGA	15241	— GACA
			TCTCATAA ACAC GATG		
			AGAGTATT TGTG TTAC		
			C AGAA		
GAM140	KIAA0937	3'	CATCTTGTTGTGTCCCAAGA	44013	CATAA _
			TCT ACACGACA GATG		
			AGA TGTGTTGT CTAC		
			ACCC_ T		
GAM140	KIAA1203	3'	CATCTTATGTTTGTATGAGA	35468	AAC AC
			TCTCATA ACG AGATG		

			AGAGTAT TGT TCTAC		
			GTT AT		
GAM140	KIAA1796	3'	CATCTGTCAGTTATAGA 43964	C	ACAC
			TCTATAA GACAGATG		
			AGA TATT CTGTCTAC		
			_ GA_		
GAM140	TOB2	3'	CATTGGTGTGTTTAGAGAT 45765	A	ACA
			ATCTC TAAACACG GATG		
			TAGAG ATTTGTGT TTAC		
			_ GG_		
GAM140	TP53TG3	3'	CATCTATTCAATTTATGAGA 17669		CAC C
			TCTCATAAA GA AGATG		
			AGAGTATTT TT TCTAC		
			AC_ A		
GAM140	LOC147671	3'	CATTGGTGTGTTTAGAGAT 38377	A	ACA
			ATCTC TAAACACG GATG		
			TAGAG ATTTGTGT TTAC		
			_ GG_		
GAM140	LOC253805	3'	CATCTGTCATATGAGG 46134		AACAC
			TCTCATA GACAGATG		
			GGAGTAT CTGTCTAC		
			A_		
GAM141	TACC1	3'	GAGTCCTGACTCAGAACACCAA 12966	C	ACA AC
	CT		AGTTGGTGT CT TCA GCTC		
			TCAACCACA GA AGT TGAG		
			A CTC CC		
GAM141	TMEPAI	3'	AGCAGTTGAGCAAACACCAAC 21402		CCTACA _
			GTTGGTGT TCAAC GCT		
			CAACCACA AGTTG CGA		
			AACG_ A		
GAM141	FLJ00026	3'	AGCACTGATGTAGGAGATACAC 32424	TG G	AC
			GT GT TCCTACATCA GCT		
			CA TA AGGATGTAGT CGA		
			CA G CA		
GAM141	FLJ11320	3'	TGATGGTAAGACACCAAC 20428	C	_
			GTTGGTGTC TAC ATCA		
			CAACCACAG ATG TAGT		
			A G		
GAM141	FLJ14917	3'	AGCGCTGTAAAGCACCAAC 26665	CC	TCAA
			GTTGGTGT TACA CGCT		

			CAACCACG ATGT GCGA		
			AA C__		
GAM141	FLJ22794	5'	AGATGGGACGCAGGACACCAGC 44024	ACA AACG	
		T	AGTTGGTGTCTCCT TC CT		
			TCGACCACAGGA AG GA		
			CGC GGTA		
GAM142	D10S170	3'	TCCGATTTTTGCCTTCGAA 11919 TA TT		
			TT AAGGCAAA TTGGA		
			AA TTCCGTTT AGCCT		
			GC TT		
GAM142	HLF	3'	GATTTTCTAGTTTCCTGCCTTC 7905 A AATT_		
		AGA	TTT AAGGCA TTGGAAAATC		
			AGA TTCCGT GATCTTTTAG		
			C CCTTT		
GAM142	IL12B	3'	TTTCTATCTGATTTGCTTT 7944 T__		
			AAGGCAAATT TGGAAA		
			TTTCGTTTAG ATCTTT		
			TCT		
GAM142	IL1RAP	3'	TTTAAATATGCCTTTAAA 7941 AAT		
			TTTAAAGGCA TTTGGA		
			AAATTTCCGT AAATTT		
			AT_		
GAM142	SCNN1G	3'	TTTTTATTTTGGCTTTTAAA 6706 TTT		
			TTTAAAGGCAAA TGGAAA		
			AAATTTTCGTTT ATTTT		
			TT_		
GAM142	SLC24A1	3'	TTTATAATTTGCCCTTGAA 11103 A T		
			TTTAA GGCAAATT TGGA		
			AAGTT CCGTTTAA ATTT		
			C T		
GAM142	SMARCC1	3'	CCTCAGGTTTGCCTCTAA 9040 A T_		
			TTA AGGCAAATTT GG		
			AAT TCCGTTTGGA CC		
			C CT		
GAM142	ZNF192	3'	TTTCCAAAATTAACCTTTAAA 12993 CA		
			TTTAAAGG AATTTTGGA		
			AAATTTCC TTAAAACCTTT		
			AA		
GAM142	C21orf108	3'	TTTCCGTCTGTTTCCTTTAAA 42774 C ATTT		
			TTTAAAGG AA TGGAAA		

			AAATTTCC TT GCCTTT		
			_ GTCT		
GAM142	C8orf7	3'	TTTCTTATTTGCCTCTTAAA 39650	_	TTT
			TTTAA AGGCAAAT GGAAA		
			AAATT TCCGTTTA TCTTT		
			C T__		
GAM142	CHERP	3'	TTTCATTGTTTTGCCTTCAAA 13092	A	TTT_
			TTT AAGGCAAA TGGAA		
			AAA TTCCGTTT ACTTT		
			C TGTT		
GAM142	FLJ12121	5'	CCTTAGGTTTGCCCCTGAA 24538	AA	T_
			TTTA GGCAAATTT GG		
			AAGT CCGTTTGGA CC		
			CC TT		
GAM142	KIAA0475	3'	TTTCCACCTCTGCCTTTAAG 16952		AATTT
			TTTAAAGGCA TGGAAA		
			GAATTTCCGT ACCTTT		
			CTCC_		
GAM142	KIAA1317	5'	TCCATTGGATTGCACCTTTAAA 41630	CA_	_
			TTTAAAGG AATTT TGGA		
			AAATTTCC TTAGG ACCT		
			ACG TT		
GAM142	KIAA1434	3'	GATTTTCCAAAATTTTGGTGTG 34488	AAGGC	
	AA		TTTA AAATTTTGAAAAATC		
			AAGT TTAAAAACCTTTTAG		
			GTGGT		
GAM142	KIAA1462	3'	TTGAAAATTTGACCTTTAAA 43923	_	G
			TTTAAAGG CAAATTTT GA		
			AAATTTCC GTTTAAAA TT		
			A G		
GAM142	KIAA1829	3'	TCACCATTTGCCTGTAAA 31034	A	TT
			TTTA AGGCAAAT TGG		
			AAAT TCCGTTTA ACT		
			G CC		
GAM142	PTPRR	5'	TTTCTGTTTTGCTTTTAAA 28382		TTTT
			TTTAAAGGCAAA GGAAA		
			AAATTTTCGTTT TCTTT		
			TG_		
GAM142	TCFL5	3'	ATTTTCCAGATACTTGCTTT 13381	AT_	
			AAGGCAA TTTGAAAAAT		

			TTTCGTT AGACCTTTTA		
			CAT		
GAM142	LOC146243	3'	CTTTAGTTTGCCTTTAAA 40677	TT	
			TTTAAAGGCAAATT GG		
			AAATTTCCGTTTGA TC		
			TT		
GAM142	LOC153129	5'	GATTTTCCTTGTCACCTTTAAG 39360	CAA TTT	
			TTTAAAGG AT GGAAAATC		
			GAATTTCC TG CCTTTTAG		
			AC_ TT_		
GAM142	LOC202451	5'	TTTCCAACCTTCTACCTTTAAG 43441	CAAATT	
			TTTAAAGG TTGGAAA		
			GAATTTCC AACCTTT		
			ATCTTC		
GAM143	CUL3	3'	AACTTTTGGTAGGAAGGAAAAC 9643	A TCT	
	A		TGTT TCCTTCCTACT GAGTT		
			ACAA AGGAAGGATGG TTCAA		
			A TT_		
GAM143	BLOV1	3'	AACTCTTCTAAGGAAGGACACA 37519	TA ACTTCT	
			TGT TCCTTCCT GAGTT		
			ACA AGGAAGGA CTCAA		
			C_ ATCTT_		
GAM143	FLJ10849	3'	TGGAAATAGGAAGGACCACA 20206	TA C	
			TGT TCCTTCCTA TTCTG		
			ACA AGGAAGGAT AAGGT		
			CC A		
GAM143	MRPL35	3'	AGGAGAAAGGATAACA 18731	CCTA	
			TGTTATCCTT CTTCT		
			ACAATAGGAA GAGGA		
			A_		
GAM144	ATSV	3'	CATCCCCTCCCTCATCCTC 10520	AGA A	
			GAGGATGA AG GGATG		
			CTCCTACT TC CCTAC		
			CCC C		
GAM144	FANCA	3'	CATCCTCACTGCCGTCCTCAGG 5628	A_ AA	
	TG		CACCTGAGGATG AG GAGGATG		
			GTGGACTCCTGC TC CTCCTAC		
			CG A_		
GAM144	HNRPDL	3'	CCTCTTCTCCAATTTGTAGGT 11952	AG GA_	
			ACCTG GAT AGAAGAGG		

			TGGAT TTA TCTTCTCC		
			GT ACC		
GAM144	IL13RA1	3'	CATCCTCTTCTTTTAGCAG 7282	AGGAT	
			CTG GAAGAAGAGGATG		
			GAC TTTCTTCTCCTAC		
			GAT__		
GAM144	IL1RAP	3'	CCTTGTCTCATCTCAGGT 7940	G A A	
			ACCTGAG ATGA GA GAGG		
			TGGA CTC TACT CT TTCC		
			_ C G		
GAM144	KLHL3	3'	TCTCTTCATCACCAGGT 42271	AG A	
			ACCTG GATGAAGA GA		
			TGGAC CTACTTCT CT		
			CA _		
GAM144	MAT1A	3'	CATGCTCCTCTTCCCCAG 43666	A AT A G	
			CTG GG GAAGA GAG ATG		
			GAC CC CTTCT CTC TAC		
			_ _ C G		
GAM144	NDRG1	3'	CATCCTCTTCCATTAACCAG 29965	AG_ AA	
			CTG GATG GAAGAGGATG		
			GAC TTAC CTTCTCCTAC		
			CAA _		
GAM144	SLC7A6	3'	CATCCTCTTCTGTCCCTGG 10126	TGA GA	
			CC GGAT AGAAGAGGATG		
			GG CCTG TCTTCTCCTAC		
			TC_ _		
GAM144	TAGLN2	3'	CATCCTCTCCCCCATGCTTA 9620	G AAGA	
			TGAG ATG AGAGGATG		
			ATTC TAC TCTCCTAC		
			G CCCC		
GAM144	TCF3	3'	ATCCTCTCCCCTCAGG 35005	ATGAA A	
			CCTGAGG GA GAGGAT		
			GGACTCC CT CTCCTA		
			C_ _ _		
GAM144	20D7-FC4	3'	CATCCTCTCCCTCACCCCA 30538	A A AGA	
			TG GG TGA AGAGGATG		
			AC CC ACT TCTCCTAC		
			_ C CCC		
GAM144	ACAS2	3'	CATCCTCTTTGCCCCCTCAGG 20751	ATGAA	
			CCTGAGG GAAGAGGATG		

			GGACTCC	TTTCTCCTAC		
			CCCG_			
GAM144	ACAS2	3'	CATCCTCTTTGCCCCCTCAGG	29264	ATGAA	
			CCTGAGG	GAAGAGGATG		
			GGACTCC	TTTCTCCTAC		
			CCCG_			
GAM144	ATP10B	3'	CATAAGGGCTTCATCTCAAGTG	31734	C G	AAGAGG
			CAC TGAG	ATGAAG	ATG	
			GTG ACTC	TACTTC	TAC	
			A _	GGGAA_		
GAM144	CLSTN3	5'	CCTCCTCTTCACCCCCAGG	16273	A A	A
			CCTG GG	TGAAGA	GAGG	
			GGAC CC	ACTTCT	CTCC	
			C C	C		
GAM144	CNOT8	3'	CTTCCTTCCCCTCAGGT	11180	AT	AA
			ACCTGAGG	GAAG	GAGG	
			TGGACTCC	CTTC	CTTC	
			C_ _			
GAM144	FBP17	3'	ATCCTCTCCTTTCCAGG	36047	A TGA	A
			CCTG GGA	AG	AGAGGAT	
			GGAC CTT	TC	TCTCCTA	
			_ _	C		
GAM144	FLJ12671	3'	CATCCTCTTCCACGCTCAG	25242	GA	AA
			CTGAG TG	GAAGAGGATG		
			GACTC AC	CTTCTCCTAC		
			GC _			
GAM144	FLJ20294	3'	CCTCCTCCTCTTCCTCAG	19345	T A	A
			CTGAGGA	GA	GA	GAGG
			GACTCCT	CT	CT	CTCC
			T C	C		
GAM144	FLJ23510	5'	CATCCTGTCTTCATCCTCAAGT	24051	C	AG
	G		CAC TGAGGATGAAGA	AGGATG		
			GTG ACTCCTACTTCT	TCCTAC		
			A	G_		
GAM144	GABBR1	3'	CCTCTTCTAGTTACCACGG	22420	_ AG	GA
			CC TG	GAT	AGAAGAGG	
			GG AC	TTG	TCTTCTCC	
			C CA	A_		
GAM144	GABBR1	3'	CCTCTTCTAGTTACCACGG	7204	_ AG	GA
			CC TG	GAT	AGAAGAGG	

GG AC TTG TCTTCTCC
C CA A_
GAM144 GGA2 3' ATCCTCTTCCTTCACAG 28917 AGGA _
CTG TGAAG AAGAGGAT
||| ||||| |||||
GAC ACTTC TTCTCCTA
____ C
GAM144 GGA2 3' ATCCTCTTCCTTCACAG 17397 AGGA _
CTG TGAAG AAGAGGAT
||| ||||| |||||
GAC ACTTC TTCTCCTA
____ C
GAM144 KIAA0227 3' CATCCTCTCCTCTAGCAGGT 30450 AGGAT A A
ACCTG GA GA GAGGATG
||||| || || |||||
TGGAC CT CT CTCCTAC
GAT__ C _
GAM144 KIAA0514 3' CTTTTCCCCATCCTCAAGG 16207 _ AA
CCT GAGGATG GAAGAG
||| ||||| |||||
GGA CTCCTAC CTTTTC
A CC
GAM144 KIAA0703 5' CTTAACTTCATCCTCAAGG 16929 _ AA
CCT GAGGATGAAG GAG
||| ||||| ||||| |||
GGA CTCCTACTTC TTC
A AA
GAM144 KIAA1872 5' ATCCTCTTCCTCCTAGG 31517 G TGAA
CCT AGGA GAAGAGGAT
||| ||||| |||||
GGA TCCT CTTCTCCTA
_ C__
GAM144 LSFR2 3' GTTAGTCTTCATCCCCACGTG 30378 C A AGAG
CAC TG GGATGAAGA GAT
||| || ||||| ||||| |||
GTG AC CCTACTTCT TTG
C C GA_
GAM144 MGC10818 3' CATCCCTCCTTCATCCTT 24939 A A
GAGGATGAAG AG GGATG
||||||| || |||||
TTCCTACTTC TC CCTAC
C C
GAM144 RIP60 3' CATCCTCTTCCTTCCCA 15059 A TGAA
TG GGA GAAGAGGATG
|| ||| |||||
AC CCT CTTCTCCTAC
_ TC__
GAM144 LOC122786 3' CATATCTTCTTCACCCT 36699 A GG
AGG TGAAGAAGA ATG
||| ||||| |||

TCC ACTTCTTCT TAC
 C A_
 GAM144 LOC147136 5' CATCCTCCTCTTCCTCAGATG 38299 C TGA A
 CA CTGAGGA AGA GAGGATG
 || ||||| || |||||
 GT GACTCCT TCT CTCCTAC
 A ____ C
 GAM144 LOC158267 3' CATCCCTGGTGGTCATCTCAGG 39792 G AGA__ A
 TG CACCTGAG ATGA AG GGATG
 ||||| || || ||||
 GTGGACTC TACT TC CCTAC
 _ GGTGG _
 GAM144 LOC164714 5' ATCCAGCATCCTCAAGTG 42174 C AAGAAGA
 CAC TGAGGATG GGAT
 || ||||| ||
 GTG ACTCCTAC CCTA
 A GA____
 GAM144 LOC199796 5' CATCCTCTTCCAGGAGTTCCGG 36808 A GAA__
 CTG GGAT GAAGAGGATG
 || ||| |||||
 GGC CTTG CTTCTCCTAC
 _ AGGAC
 GAM144 LOC220522 3' CATCCTCAACATCCTCAAAGG 30353 __ AAGAA
 CCT GAGGATG GAGGATG
 || ||||| |||||
 GGA CTCCTAC CTCCTAC
 AA AA____
 GAM144 LOC222031 3' GTCCCCAGCCTCAGGTG 45134 A AAGAAGA
 CACCTGAGG TG GGAT
 ||||| || ||
 GTGGACTCC AC CCTG
 G C____
 GAM144 LOC253573 3' ATCGTCCATCCTACAGGT 46365 _ AAGAA G
 ACCTG AGGATG GA GAT
 |||| |||| || ||
 TGGAC TCCTAC CT CTA
 A ____ G
 GAM144 LOC91380 3' ATCCTCTTGCCCTCAGCTG 32755 C ATGAAG
 CA CTGAGG AAGAGGAT
 || |||| |||||
 GT GACTCC TTCTCCTA
 C G____
 GAM145 CASP8 3' AATAACACTGTCTCCT 6896 A TTTAT
 AGGA ACA GTGTTATT
 ||| || |||||
 TCCT TGT CACAATAA
 C ____
 GAM145 CASP8 3' AATAACACTGTCTCCT 27201 A TTTAT
 AGGA ACA GTGTTATT
 ||| || |||||

			TCCT TGT CACAATAA		
			C _____		
GAM145	CASP8	3'	AATAACACTGTCTCCT 27203	A	TTTAT
			AGGA ACA GTGTTATT		
			TCCT TGT CACAATAA		
			C _____		
GAM145	CASP8	3'	AATAACACTGTCTCCT 27204	A	TTTAT
			AGGA ACA GTGTTATT		
			TCCT TGT CACAATAA		
			C _____		
GAM145	GYP A	3'	TAACCAAGTAAATGTTTTCTAT 42263		GT_
			ATAGGAAACATTTAT GTTA		
			TATCTTTTGTAATG CAAT		
			AAC		
GAM145	ARNTL2	3'	AATAACCAAAGCAAATGTTTCC 21411	T	A___ T
	TTC		A AGGAAACATTT TG GTTATT		
			C TCCTTTGTAAA AC CAATAA		
			T CGAA _		
GAM145	SEC24B	3'	TAACAAGGAATGTTTCTTAT 13016		ATG
			ATAGGAAACATTT TGTTA		
			TATTCTTTGTAAG ACAAT		
			GA_		
GAM145	LOC138639	5'	TAATGTATAAATGTTCCCT 37139	A	TG
			AGG AACATTTATG TTA		
			TCC TTGTAAATAT AAT		
			C GT		
GAM146	BAZ2B	5'	TTTCCAACTTGACCTCA 15126	T	C
			TGA GTCAAGTT GGAGG		
			ACT CAGTTCAA CCTTT		
			C A		
GAM146	TRPV1	5'	GTCCACCCTCCCAGGCCGACGT 28012	AA	C_
	CA		TGATGTC GTT GGAGGGTGGAC		
			ACTGCAG CGG CCTCCACCTG		
			C_ AC		
GAM146	BNIP-S	5'	GCTCCCAAACCTTAACAGCA 28692	A C	C A
			TG TGT AAGTT GG GGGT		
			AC ACA TTCAA CC CTCG		
			G A A _		
GAM146	FLJ10661	3'	CCTCCAACCTTGACATCA 19996		C
			TGATGTCAAGTT GGAGG		

ACTACAGTTCAA CCTCC

GAM146 GW112 5' ACTGTCCGAATTGACATCA 13128 G G
TGATGTCAA TTCGGA GGT
||||||| ||||| |||
ACTACAGTT AAGCCT TCA

GAM146 MGC10812 3' CCCCAAATTTGACACCA 25409 A C A
TG TGTCAAGTT GG GG
|| ||||| || ||
AC ACAGTTTAA CC CC

GAM146 MGC16279 3' CCTCCAACCTTGACATCA 26731 C
TGATGTCAAGTT GGAGG
||||||| |||||
ACTACAGTTCAA CCTCC

GAM146 PME-1 3' GTCCACCCCTCCTCAACATCG 18233 CAAGTTC _
TGATGT GGAGGG TGGAC
||||| ||||| |||||
GCTACA CCTCCC ACCTG
ACT_ C

GAM146 SLC39A3 3' GTCCACCCCAACTCCTGACAGC 29360 A _ CGGA
A TG TGTCA AGTT GGGTGGAC
|| |||| ||| |||||
AC ACAGT TCAA CCCACCTG
G CC C_

GAM146 LOC158490 3' CCTCCAACCTTGACATCA 39850 C
TGATGTCAAGTT GGAGG
||||||| |||||
ACTACAGTTCAA CCTCC

GAM146 LOC220073 5' CCTCCAACCTTGACATCA 44876 C
TGATGTCAAGTT GGAGG
||||||| |||||
ACTACAGTTCAA CCTCC

GAM146 LOC90630 5' GTCCACCCCTCACCGACA 31826 AA TC GA
TGTC GT G GGGTGGAC
||| || | |||||
ACAG CA C CCCACCTG
C_ TC

GAM146 LOC91069 3' CCTCCAACCTTGACATCA 32348 C
TGATGTCAAGTT GGAGG
||||||| |||||
ACTACAGTTCAA CCTCC

GAM146 LOC92095 5' TCCACCCTGCCTCTGACAGCA 33774 A A TTC _
TG TGTCA G GG AGGGTGGGA
|| |||| | || |||||

AC ACAGT C CC TCCCACCT
 G _ T_ G
 GAM146 LOC92096 5' TCCACCCTGCCTCTGACAGCA 33778 A A TTC _
 TG TGTCA G GG AGGGTGGGA
 || |||| | || |||||
 AC ACAGT C CC TCCCACCT
 G _ T_ G
 GAM147 LOXL2 3' GCCACGTGCCCTCACCCAGCCC 8133 A AGATA CCT
 GG CT AGG CATGTGGC
 || || || |||||
 CC GA TCC GTGCACCG
 C CCCAC C_
 GAM147 LRP4 3' CCACTGATGAGGCCCTCCTAGC 32197 A ATAA _
 C GG CTAG GGCCTCAT GTGG
 || || ||||| |||
 CC GATC CCGGAGTA CACC
 _ CTC_ GT
 GAM147 SLC22A5 3' GCAAGGCCTTACCAGCC 9026 A AGA CA
 GG CT TAAGGCCT TGT
 || || ||||| |||
 CC GA ATTCCGGA ACG
 _ CC_ _
 GAM147 KIAA1872 3' GTGAGGCCCTACCTGACCC 31520 AC A A
 GG TAG TA GGCCTCAT
 || || || |||||
 CC GTC AT CCGGAGTG
 CA C C
 GAM147 MGC3248 3' GCCACATGATTAATCCAGTCT 26238 A A GCC
 GGACT GAT AG TCATGTGGC
 |||| || || |||||
 TCTGA CTA TT AGTACACCG
 C A _
 GAM147 PEPP3 3' GCCTTGGGGCCTTACCTACC 17235 AC A TGT
 GG TAG TAAGGCCTCA GGC
 || || ||||| |||
 CC ATC ATTCCGGGGT CCG
 _ C T_
 GAM147 LOC157349 3' GCCCATGGAGGCCTTTTCTAAT 39597 C T _ T
 CC GGA TAGA AAGGCCTC ATG GGC
 || || ||||| || |||
 CCT ATCT TTCCGGAG TAC CCG
 A T G _
 GAM147 LOC163231 5' CCACATGAGAACCAGTTC 40099 AGATAA C_
 GGACT GG CTCATGTGG
 |||| || |||||
 CTTGA CC GAGTACACC
 _ _ AA
 GAM147 LOC255527 5' GTCTCTGAGGCCTCATCCAGTT 46294 A A TGT
 C GGACT GAT AGGCCTCA GGC
 |||| || ||||| |||

CTTGA CTA TCCGGAGT CTG
 C C CT_
 GAM148 CASP2 3' TCCCCATCATCCACGCCA 6891 A AT
 TGGC TGGATGATG GA
 |||| ||||| ||
 ACCG ACCTACTAC CT
 C CC
 GAM148 CASP2 3' TCCCCATCATCCACGCCA 26854 A AT
 TGGC TGGATGATG GA
 |||| ||||| ||
 ACCG ACCTACTAC CT
 C CC
 GAM148 CASP2 3' TCCCCATCATCCACGCCA 26859 A AT
 TGGC TGGATGATG GA
 |||| ||||| ||
 ACCG ACCTACTAC CT
 C CC
 GAM148 CASP2 3' TCCCCATCATCCACGCCA 26864 A AT
 TGGC TGGATGATG GA
 |||| ||||| ||
 ACCG ACCTACTAC CT
 C CC
 GAM148 SFTP2 3' TCACACCACCCCCCATGCCA 13808 ATGA A A
 TGGCATGG TG TG TGA
 ||||| || || ||
 ACCGTACC AC AC ACT
 CCCC C _
 GAM148 AMOT 5' CATCATCACCATCACCA 28410 A A
 TGG TGATG TGATGATG
 || |||| |||||
 ACC ACTAC ACTACTAC
 _ C
 GAM148 AMOT 5' TCATCACCATCACCACCA 28418 CA A A
 TGG TGG TGATG TGATGA
 || || |||| |||||
 ACC ACC ACTAC ACTACT
 _ _ C
 GAM148 C5orf4 3' TCATCATCACCACCATCTCCCA 26183 CAT A A
 TGG GGATG TG TGATGATGA
 || |||| || |||||
 ACC TCTAC AC ACTACTACT
 C_ C C
 GAM148 C5orf4 5' TCATCATCACCACCATCTCCCA 18475 CAT A A
 TGG GGATG TG TGATGATGA
 || |||| || |||||
 ACC TCTAC AC ACTACTACT
 C_ C C
 GAM148 CAPN6 3' TCACCACCATCATCACCTCCG 15570 CAT A A A
 TGG GG TGATGATG TG TGA
 || || ||||| || |||

GCC CC ACTACTAC AC ACT
 T__ _ C C
 GAM148 DKFZp434J1015 3' TCATCATCATCATCTTCC 44507 CAT
 GG GGATGATGATGATGATGA
 || |||||
 CC TCTACTACTACTACT
 T__
 GAM148 FLJ12985 3' TCACCATCAAGCAATCCATGTC 24464 GA__ A
 A TGGCATGGAT TGATG TGA
 ||||| |||||
 ACTGTACCTA ACTAC ACT
 ACGA C
 GAM148 GGA2 3' TCATCATCATCATCTCTGCTA 28926 T
 TGGCA GGATGATGATGATGA
 ||||| |||||
 ATCGT TCTACTACTACTACT
 C
 GAM148 GGA2 3' TCATCATCATCATCTCTGCTA 17404 T
 TGGCA GGATGATGATGATGA
 ||||| |||||
 ATCGT TCTACTACTACTACT
 C
 GAM148 KIAA0125 5' CACCATCATCATCTTCCTCC 16690 CAT T A
 GG GGA GATGATGATG TG
 || ||| ||||| ||
 CC CCT CTACTACTAC AC
 T__ T C
 GAM148 KIAA0125 5' CATCATCATCACCACCA 16691 CA A
 TGG TGG TGATGATGATG
 ||| ||| |||||
 ACC ACC ACTACTACTAC
 _ _
 GAM148 KIAA0125 5' CATCATCATCATCCTCCTGTGC 30345 _ T
 GCAT GGA GATGATGATGATG
 ||||| ||| |||||
 CGTG CCT CTACTACTACTAC
 T C
 GAM148 KIAA0339 3' CACGACACCATCATCGATGCCA 35403 G A A A
 TGGCAT GATGATG TG TG TG
 ||||| ||||| || |||
 ACCGTA CTACTAC AC GC AC
 G C A _
 GAM148 KIAA1202 3' TCAAGTACTCATACCCACCCA 35640 CA A TG GA
 TGG TGG TGATGA AT TGA
 ||| ||| ||||| || |||
 ACC ACC ACTACT TG ACT
 C_ C CA A_
 GAM148 PEG10 3' TTACCATCATCATGCCA 17434 G A
 TGGCATG ATGATG TGA
 ||||| ||||| |||

ACCGTAC TACTAC ATT

— C

GAM148 PRPF8 3' CAGGATGTCACCAACCATGCCA 30677 A A G GA
TGGCATGG TG TGAT AT TG
||||||| || ||||| || ||
ACCGTACC AC ACTG TA AC
C C _ GG

GAM148 PRTD-NY3 5' CACCACCACCATCATCCTGGC 25193 G T A A A
G CA GGATGATG TG TG TG
| || ||||| || || ||
C GT CCTACTAC AC AC AC
G _ C C C

GAM148 RAI 3' CACCATCATCACATCCCCCA 13468 CAT A A
TGG GGATG TGATGATG TG
||| ||||| ||||| ||
ACC CCTAC ACTACTAC AC
C _ _ C

GAM148 SEZ6 5' CACCACCATCATCACCACCACC 36771 CA_ A A A
A TGG TGG TGATGATG TG TG
||| ||| ||||| || ||
ACC ACC ACTACTAC AC AC
ACC _ C C

GAM148 SEZ6 5' CATCATCACCACCACCATCACC 36772 C_ A A A
A TGG ATGG TG TG TGATGATG
||| ||||| || || |||||
ACC TACC AC AC ACTACTAC
AC _ C C

GAM148 LOC146227 5' CACCACCATCATCACCA 38083 A A A
TGG TGATGATG TG TG
||| ||||| || ||
ACC ACTACTAC AC AC
_ C C

GAM148 LOC146227 5' CACCACCATCATCACCACC 38084 CA A A A
GG TGG TGATGATG TG TG
|| ||| ||||| || ||
CC ACC ACTACTAC AC AC
_ _ C C

GAM148 LOC146227 5' CACCACCATCATCACCACCGCC 38085 A_ A A A
GGC TGG TGATGATG TG TG
||| ||| ||||| || ||
CCG ACC ACTACTAC AC AC
CC _ C C

GAM148 LOC146227 5' CACCATCATCACCACCGCCG 38086 A_ A A
TGGC TGG TGATGATG TG
||||| ||| ||||| ||
GCCG ACC ACTACTAC AC
CC _ C

GAM148 LOC146958 5' TCACCACCACACCATGCCA 40774 A A A A
TGGCATGG TG TG TG TGA
||||||| || || || |||

ACCGTACC AC AC AC ACT
 _ _ C C
 GAM148 LOC149464 3' TCATCATCATCATCATCCTCAT 40994 CAT_
 CC GG GGATGATGATGATGATGA
 || |||||
 CC CCTACTACTACTACT
 TACT
 GAM148 LOC150333 5' CATCATCACCATCACCAT 41197 A A
 ATGG TGATG TGATGATG
 ||| |||||
 TACC ACTAC ACTACTAC
 _ C
 GAM148 LOC150333 5' TCATCACCATCACCGTCACCGT 41199 ATG A A
 CA TGGC GATG TGATG TGATGA
 ||| ||| |||||
 ACTG CTGC ACTAC ACTACT
 CCA C C
 GAM148 LOC152315 5' TCAGCTGCCGTCATCCACACCA 39258 CA AT A_
 TGG TGGATGATG G TGA
 ||| ||||| | |||
 ACC ACCTACTGC T ACT
 AC CG CG
 GAM148 LOC153688 3' CATCATCATGTACCAAGCCA 41656 A ATG
 TGGC TGG ATGATGATG
 ||| ||| |||||
 ACCG ACC TACTACTAC
 A ATG
 GAM148 LOC157653 5' CAGGCTCATCATCCATCCA 39632 C TGA
 TGG ATGGATGATGA TG
 ||| ||||| ||
 ACC TACCTACTACT AC
 CGG
 GAM148 LOC219404 3' TCAGATCATCACCATGCCA 44910 A GA
 TGGCATGG TGATGAT TGA
 ||||| ||||| |||
 ACCGTACC ACTACTA ACT
 _ G_
 GAM148 LOC221468 3' TCACCACCATCATCATCGGCTG 29827 TG_ A A
 CT GGCA GATGATGATG TG TGA
 ||| ||||| || |||
 TCGT CTACTACTAC AC ACT
 CGG C C
 GAM148 LOC255624 3' TCACCATCAAGCAATCCATGTC 45352 GA_ A
 A TGGCATGGAT TGATG TGA
 ||||| ||||| |||
 ACTGTACCTA ACTAC ACT
 ACGA C
 GAM149 DYRK1A 3' ACAACCTTTCATGTAGCCCC 28159 A TTT
 GG GCTGC AAAGGTTGT
 || ||||| |||||

CC CGATG TTTCCAACA
 C TAC
 GAM149 GCNT1 5' CAACCTTCAAGGCCACGA 7237 GAGCT A
 TCGTG GCTTT AAGGTTG
 |||| |||| ||||
 AGCAC CGGAA TTCCAAC
 _____ C
 GAM149 C22orf19 3' ACAACCTTTAAAATGTTC 9772 TGC
 GAGC TTAAAGGTTGT
 |||| |||| ||||
 CTTG AAATTTCCAACA
 TA_
 GAM149 FLJ32332 3' ACAACCCCCAAAGTCCACG 29466 AGCT AAA
 CGTGG GCTTT GGTTGT
 |||| |||| ||||
 GCACC TGAAA CCAACA
 _____ CCC
 GAM149 FUSIP1 3' CAACCTTTAAAACATC 27622 GC C
 GA TG TTAAAGGTTG
 || || |||| ||||
 CT AC AAATTTCCAAC
 _ A
 GAM149 ORMDL2 3' ACAACCTTTCCCAGACTCC 15465 _ CTTT
 GGAG CTG AAAGGTTGT
 |||| || |||| ||||
 CCTC GAC TTTCCAACA
 A CC_
 GAM149 RAI 3' ACAACCTTCGGCCGCCCCAC 13466 A T TTA
 GTGG GC GCT AAGGTTGT
 |||| || || |||| ||||
 CACC CG CGG TTCCAACA
 C C C_
 GAM150 PRO1489 3' TTTCACATCCAAGTGCAC 20661 C
 GTGCGCTTGGA GTGAAA
 |||| |||| |||| ||||
 CACGTGAACCT CACTTT
 A
 GAM151 PACE 3' CGGCTGGTTTTGTGAAGA 8424 C TAT
 TCTTACAAAAC T G CCG
 |||| |||| || ||||
 AGAATGTTTTGG C GGC
 T ____
 GAM151 FLJ13241 3' CTCAGGAAGCTTTGTGAAGA 24707 ACTC A _
 TCTTACAAA GT TCC GAG
 |||| || || || ||||
 AGAATGTTT CG AGG CTC
 _____ A A
 GAM151 KIAA0546 3' GGGTAATTTTTGTGAAGA 35331 CTCG
 TCTTACAAAA TATCC
 |||| || || || ||||

AGAATGTTTT ATGGG
TA__

GAM151 KIAA1449 3' CTCAGATGTGTTCTTGTAGGA 21898 AACT C
TCTTACAA CGTATC GAG
||||| |||||
AGGATGTT GTGTAG CTC
CTT_ A

GAM151 LOC113523 3' CTCAAAATATGAGTTTTGTA 36151 CC_
TACAAAACGTCGTAT GAG
||||||| |||
ATGTTTTGAGTATA CTC
AAA

GAM151 LOC133584 5' CTCGGGCAGAGCTTTGTGAGA 37045 A GTA
TCTTACAAA CTC TCCGAG
||||| ||| |||||
AGAGTGTTT GAG GGGCTC
C AC_

GAM152 APXL 3' CCTGACTTCCCCTTATTC 7354 A GTA
GAATAAGG GAAG CAGG
||||| ||| |||
CTTATTCC CTTC GTCC
C A__

GAM152 ATP1B2 3' GTCTTCTCCTCCTCTCCA 7392 A ATA
TG AGA AGGAGAAGGT
|| ||| |||||
AC TCT TCCTCTTCTG
C CC_

GAM152 CBFA2T2 3' CTTGTGTCCCCTCCTCCCCCTC 11548 A AATA AA GT
CA TG AG AGGAG G ACAGG
|| || |||| | ||||
AC TC TCCTC C TGTC
C CCCC CC TG

GAM152 CRTAP 3' CTTTCTCTTTACTCTCCA 13061 A A
TG AGA TAAGGAGAAGG
|| ||| |||||
AC TCT ATTTCTCTTCC
C C

GAM152 EIF2C1 3' ACCTTACCCTTATTCCTC 14499 A AG
GA GAATAAGG AAGGT
|| ||||| ||||
CT CTTATTCC TTCCA
C CA

GAM152 GNB3 5' CCTGTACCCTCCCATCTC 7853 A A A A
GA TA GG GA GGTACAGG
|| || || |||||
CT AT CC CT CCATGTCC
C A _ C

GAM152 HTR1D 3' CCTGTACCCTTCCTTCTTC 6529 ATA AA
GAAGA AGGAG GGTACAGG
|||| |||| |||||

			CTTCT TCCTT CCATGTCC			
			___ C_			
GAM152	IGF1R	3'	CCTGTACCTCAGTGGATCTTCA 6556	A_	AG	GAA
			TGAAGA TA GA GGTACAGG			
			ACTTCT GT CT CCATGTCC			
			AG GA ___			
GAM152	KCNN4	5'	CCTAGCCCCTCCTTATTCTCA 8036	A	AA	AC
			TGA GAATAAGGAG GGT AGG			
			ACTCTTATTCCTC CCG TCC			
			___ C_ A_			
GAM152	MAPK14	3'	CCCATACCTTCTGGTTGCTTCA 29106	AA	GG	CA
			TGAAG TAA AGAAGGTA GG			
			ACTTC GTT TCTTCCAT CC			
			___ GG AC			
GAM152	MAPK14	3'	CCCATACCTTCTGGTTGCTTCA 29113	AA	GG	CA
			TGAAG TAA AGAAGGTA GG			
			ACTTC GTT TCTTCCAT CC			
			___ GG AC			
GAM152	MAPK14	3'	CCCATACCTTCTGGTTGCTTCA 7002	AA	GG	CA
			TGAAG TAA AGAAGGTA GG			
			ACTTC GTT TCTTCCAT CC			
			___ GG AC			
GAM152	NCSTN	3'	CCTGTACCTCTCTCTGCTCCTC 36508	A A	AG	A
	A		TGA GA TA GAGA GGTACAGG			
			ACT CT GT CTCT CCATGTCC			
			C C CT _			
GAM152	P23	3'	CCTAAGTCTCCTTTTCTTCA 13380	T	___	
			TGAAGAA AAGGAGA AGG			
			ACTTCTT TTCCTCT TCC			
			___ GAA			
GAM152	PRDM2	5'	CTGCACCGTCTACCCTTC 14534	AATAA	_	A A
			GAAG GG AGA GGT CAG			
			CTTC CC TCT CCA GTC			
			___ A G C			
GAM152	PRDM2	5'	CTGCACCGTCTACCCTTC 18001	AATAA	_	A A
			GAAG GG AGA GGT CAG			
			CTTC CC TCT CCA GTC			
			___ A G C			
GAM152	PTEN	5'	TCTCCTCCTTTTCTTCA 5859	T	A	
			TGAAGAA AAGGAG AGG			

ACTTCTT TTCCTC TCT
 T C
 GAM152 SHMT2 3' CCTGAGCCTCCTTATTC 11879 GAA A
 GAATAAGGA GGT CAGG
 ||||| ||| |||
 CTTATTCCT CCG GTCC
 _ A
 GAM152 SLC35A1 3' CCCCTCCTTATTCTCCA 13126 A AA
 TG AGAATAAGGAG GG
 || ||||| ||
 AC TCTTATTCCTC CC
 C C_
 GAM152 SMARCD1 3' CCTGTACCCTCCCCTGGTCTAC 29145 A ATA A A
 A TG AGA AGG GA GGTACAGG
 || ||| ||| || |||||
 AC TCT TCC CT CCATGTCC
 A GG_ C C
 GAM152 SMARCD1 3' CCTGTACCCTCCCCTGGTCTAC 9047 A ATA A A
 A TG AGA AGG GA GGTACAGG
 || ||| ||| || |||||
 AC TCT TCC CT CCATGTCC
 A GG_ C C
 GAM152 ATP9A 3' CCTGTCTGAACCCCTCGTTCTT 31080 TA AGAA_ T
 CA TGAAGAA AGG GG ACAGG
 ||||| ||| || |||||
 ACTTCTT TCC TC TGTCC
 GC CCAAG _
 GAM152 DKFZP434J193 3' ATCTGCTCCTTATCTCCA 35162 A A A
 TG AGA TAAGGAG AGGT
 || ||| ||||| |||||
 AC TCT ATTCCTC TCTA
 C _ G
 GAM152 DKFZP564M182 3' TCTTCCTCCTTATTCCTCA 38220 A _
 TGA GAATAAGGAG AAGG
 ||| ||||| |||||
 ACT CTTATTCCTC TTCT
 C C
 GAM152 FLJ10290 3' CTTTCCTCTCCTTTTCCTCA 19797 A T A TAC
 TGA GAA AAGGAGA GG AG
 ||| ||| ||||| || ||
 ACT CTT TTCCTCT CC TC
 C _ _ TT_
 GAM152 FLJ13194 3' CCCGTTCCCTTTTCTTCA 24787 T AA
 TGAAGAA AAGGAG GG
 ||||| ||||| ||
 ACTTCTT TTCCTT CC
 T GC
 GAM152 FLJ21870 3' CCTGTACCTCTTCTCTGCCCTC 23279 ATAA _
 GA GGAGA AGGTACAGG
 || |||| ||||| |||||

		CT TCTCT TCCATGTCC			
		CCCG TC			
GAM152	H_GS165L15.1 3'	CCTGGAAGACTCCTCAGTTCTT 11338	A_	AAGGTA	
	CA	TGAAGAAT AGGAG CAGG			
		ACTTCTTG TCCTC GTCC			
		AC AGAAG_			
GAM152	KIAA0295 3'	CCTGCTGCTTCTTATTCCTCA 33780	AA	A GTA	
		TG GAATAAGGAG AG CAGG			
		AC CTTATTCTTC TC GTCC			
		CC G _			
GAM152	KIAA0356 3'	TCTGTGTCCTCTTTACTCCCCA 32893	AA A	AA GT	
		TG GA TAAGGAG G ACAGG			
		AC CT ATTTCTC C TGTCT			
		CC C _ TG			
GAM152	KIAA0853 5'	TGCCTCTCCTTATCCTTCA 17440	A	A	
		TGAAG ATAAGGAGA GGTA			
		ACTTC TATTCCTCT CCGT			
		C _			
GAM152	KIAA1102 3'	CCTACTCTCCTCCATTCTCCA 34212	A	A_ _	
		TG AGAAT AGGAGA AGG			
		AC TCTTA TCCTCT TCC			
		C CC CA			
GAM152	KIAA1223 3'	CCTTAGTCTCCTTACTCTT 35245	A	_	
		AAGA TAAGGAGA AGG			
		TTCT ATTCCTCT TCC			
		C GAT			
GAM152	KIAA1467 3'	CCTGTACCTTGGCTACTTC 35453	AATAA	AG	
		GAAG GG AAGGTACAGG			
		CTTC TC TTCCATGTCC			
		A_ GG			
GAM152	MGC12966 3'	CCTGTACCCTAAAATTTTCA 26419	AAGG	AA	
		TGAAGAAT AG GGTACAGG			
		ACTTTTTA TC CCATGTCC			
		AAA_ _			
GAM152	MGC2306 3'	CTGCACCCTCTTCTCTTC 26353	ATAA	A A	
		GAAGA GGAGA GGT CAG			
		CTTCT CTTCT CCA GTC			
		_ C C			
GAM152	ORMDL2 3'	CCTTCTCTTATTCTCCA 15467	A	G	
		TG AGAATAAG AGAAGG			

AC TCTTATTC TCTTCC
 C _
 GAM152 P66 3' CCTTTCTTCTCCCCATTTTCA 21844 ATAA TAC
 TGAAGA GGAGAAGG AGG
 ||||| ||||| ||
 ACTTTT CCTCTTCT TCC
 ACC_ T_
 GAM152 PRO0159 5' CCTGCATCCTTCTCCCATTCCC 15372 AA AA TA_
 CA TG GAAT GGAGAAGG CAGG
 || ||| ||||| |||
 AC CTTA CCTCTTCC GTCC
 CC C_ TAC
 GAM152 LOC144740 5' CCAGGTGCTTTTCTCATTACTCT 37786 A G A_
 TCA TGAAGA TAA GAGAAGGTAC GG
 ||||| ||| ||||| ||
 ACTTCT ATT CTCTTTCGTG CC
 C A GA
 GAM152 LOC145820 3' TTTGAAC TTTCTCCCCACTCCT 37994 A ATAA A
 CA TGA GA GGAGAAGGT CAGG
 ||| || ||||| |||
 ACT CT CCTCTTTCA GTTT
 C CACC A
 GAM152 LOC148195 5' CCTCCTCCTCTTTCTTCA 40873 TA A
 TGAAGAA AGGAG AGG
 ||||| ||||| |||
 ACTTCT TCCTC TCC
 TC C
 GAM152 LOC148811 3' CCTGCATCTCTCCCCTTACTCT 38598 A A _ A
 TCA TGAAGA TAAGG GA AGGT CAGG
 ||||| ||||| || ||| |||||
 ACTTCT ATTCC CT TCTA GTCC
 C C C C
 GAM152 LOC148930 3' CCTTCTCCTTTCTTCA 38619 AAT
 TGAAG AAGGAGAAGG
 ||||| ||||| |||||
 ACTTC TTCCTCTTCC
 CT_
 GAM152 LOC149706 5' CCCATACCTCCTCCTCCCTTC 41059 AATA A CA
 GAAG AGGAG AGGTA GG
 |||| ||||| ||||| ||
 CTTC TCCTC TCCAT CC
 CC_ C AC
 GAM152 LOC152765 3' GTCTCCTCCTTGTTCTCCA 39319 A A
 TG AGAATAAGGAG AGGT
 || ||||| ||||| |||||
 AC TCTTGTTCTCCTC TCTG
 C C
 GAM152 LOC157247 5' CCTTCATCTCCTTACTCTCG 39574 A A _
 TGA GA TAAGGAGA AGG
 ||| || ||||| |||

			GCT CT ATTCCTCT TCC			
			_ C ACT			
GAM152	LOC201164 3'	TACAGTCTCCTTGTCCCTCA	42532	AGA	AG	
		TGA ATAAGGAGA GTA				
		ACT TGTTCTCT CAT				
		CCC GA				
GAM152	LOC221738 3'	CTTTCCTCTCCTCTTTCTTCA	45029	TA	A TAC	
		TGAAGAA AGGAGA GG AG				
		ACTTCTT TCCTCT CC TC				
		TC _ TT_				
GAM152	LOC221935 3'	CCTAACTCCTTATCTTCA	44499	A	A_	
		TGAAGA TAAGGAG AGG				
		ACTTCT ATTCCTC TCC				
		_ AA				
GAM152	LOC222128 5'	TATCTTCTTCTTATTCTTCA	44541			
		TGAAGAATAAGGAGAAGGTA				
		ACTTCTTATTCTTCTTCTAT				
GAM152	LOC253639 3'	ACCCTACTTATTCTTCA	45854	G AA		
		TGAAGAATAAG AG GGT				
		ACTTCTTATTC TC CCA				
		A _				
GAM152	LOC91807 5'	CTGTGCCTCTCCTCATTC	33385	A	A	
		GAAT AGGAGA GGTACAG				
		CTTA TCCTCT CCGTGTC				
		C _				
GAM153	AKAP13 3'	CAGTCTAAACTATCCAGTCA	43178	TAC	CC	
		TGACTGGAT TTAG CTG				
		ACTGACCTA AATC GAC				
		TCA T_				
GAM153	FLJ12700 3'	ACACAGGGTTAATAACCAATCA	24412	C A C	C	
		TGA TGG TTA TTAGCCCTG GT				
		ACT ACC AAT AATTGGGAC CA				
		A _ _ A				
GAM153	HPCAL4 3'	ACACAGGGCTAAGACTTGAACC	18385	A _	C	
	A	TGG TTA CTTAGCCCTG GT				
		ACC AGT GAATCGGGAC CA				
		A TCA A				
GAM153	LOC146243 3'	ACACAGGCCCCAGATCCAGTCA	40673	ACTTA	C C	
		TGACTGGATT GCC TG GT				

			ACTGACCTAG CGG AC CA	
			ACCC_ _ A	
GAM154	MDM1	3'	TGGATTGACTGTTGTTCTTC 21322	A_ CA
			GGAGGAACAACA CGA CCA	
			CTTCCTTGTTGT GTT GGT	
			CA A_	
GAM154	TNFRSF8	3'	GTGCCTGTGGTTGTTTCTCC 6911	A A_
			GGAGGAACAAC ACG CAC	
			CCTCTTTGTTG TGT GTG	
			G CC	
GAM154	FLJ13114	3'	GTTGGCTTGTGGTTCCTCC 23751	A CGACA
			GGAGGAAC ACAA CCAAC	
			CCTCCTTG TGTT GGTTG	
			G C_	
GAM154	HCA4	3'	GTCCCATTGTGTTCTCC 38025	A C_
			GGAGGAACA CAA GAC	
			CCTCCTTGT GTT CTG	
			_ ACC	
GAM154	IGF2AS	3'	GGGCCGTTGTTGCCTCTCC 18542	AA ACA
			GGAGG CAACAACG CC	
			CCTCT GTTGTTC GG	
			CC CG_	
GAM154	KIAA0476	3'	AGTTGGTACAGCTCTGTTCTTC 16904	ACAACGAC
	C		GGAGGAACA ACCAACT	
			CCTTCTTGT TGGTTGA	
			CTCGACA_	
GAM154	KIAA0652	3'	GGTGTGTCCTGTTCTCC 16410	ACAAC
			GGAGGAACA GACACC	
			CCTCCTTGT CTGTGG	
			CCTA_	
GAM154	KIAA0937	3'	GTTGGTGTCTGCCCTCC 44018	AA ACAAC
			GGAGG CA GACACCAAC	
			CCTCC GT CTGTGGTTG	
			C_ C_	
GAM154	STAT2	3'	TGGCTGTACCTGTTCTCC 11892	ACAACG _
			GGAGGAACA ACA CCA	
			CCTCCTTGT TGT GGT	
			CCA_ C	
GAM154	LOC145123	5'	TCTTTGCATTGTTCTCC 33533	_ C
			GGAGGAACAA CAA GA	

			CCTCCTTGTT GTT CT		
			AC T		
GAM154	LOC151512 5'	GTTGGTGAGCTGTTCTTCC	41363	ACAACGA	
		GGAGGAACA CACCAAC			
		CCTTCTTGT GTGGTTG			
		CGA____			
GAM154	LOC220549 5'	AGTTGGTGCCGTTGGTGCCGCC	44649	A AACAA A	
		GG GG CAACG CACCAACT			
		CC CC GTTGC GTGGTTGA			
		G GTG__ C			
GAM154	LOC220827 3'	TGGTGTCATCAGCTGTTTCTCC	43846	ACAAC_	
		GGAGGAACA GACACCA			
		CCTCTTTGT CTGTGGT			
		CGACTA			
GAM155	UBE2V1 3'	TAGATTGTAACCCCTCCA	9374	AA	
		TGGA GGGTTACAATTTA			
		ACCT CCCAATGTTAGAT			
		C_			
GAM155	UBE2V1 3'	TAGATTGTAACCCCTCCA	22526	AA	
		TGGA GGGTTACAATTTA			
		ACCT CCCAATGTTAGAT			
		C_			
GAM155	UBE2V1 3'	TAGATTGTAACCCCTCCA	22773	AA	
		TGGA GGGTTACAATTTA			
		ACCT CCCAATGTTAGAT			
		C_			
GAM155	VDAC3 3'	CAAAGAATTGTAATCCTCCCCA	12202	AA A	
		TGG AGGGTTACAATTT TTG			
		ACC TCCTAATGTTAAG AAC			
		CC A			
GAM155	LOC157349 5'	ACAATGGGAGCAACCCTTTGCA	39586	G ACAA	
		TG AAAGGGTT TTTATTGT			
		AC TTTCCCAA GGGTAACA			
		G CGA_			
GAM155	LOC170409 3'	TACAATAATCAGGGATTTTTC	40315	GTTACA	
	C	GGAAAGG ATTTATTGTA			
		CCTTTT TAAATAACAT			
		AGGGAC			
GAM156	ATP11A 3'	ATGTGGATGCCACATGCTGCTG	37802	T GCA AA_	
		CAGC GCA TGG TACGT			

GTCG CGT ACC GTGTA
 T AC_ GTAG
 GAM156 D12S2489E 5' CTATCCAACAGTTGTT 14292 CAGCA C
 AACAGCTG TGAATA G
 ||||| |||||
 TTGTTGAC ACCTTAT C
 A_ A
 GAM156 DKFZP434N1511 5' ACGTACGGGCCGCTGCAGCT 43933 AT AA_
 AGCTGCAGC GG TACGT
 ||||| || ||||
 TCGACGTCG CC ATGCA
 _ GGGC
 GAM156 LOC56906 3' ACGTATTCCCATTGCAGGTGTT 21342 G CAT
 AACA CTGCAG GGAATACGT
 ||| ||||| |||||
 TTGT GACGTT CCTTATGCA
 G AC_
 GAM157 ADCY2 3' CATTCTTCACGGATGCCGTA 32433 A
 TACGGCATCTGTGAA AATG
 ||||| |||||
 ATGCCGTAGGCACTT TTAC
 C
 GAM157 COL4A4 3' CACATTAAGCAAATGCTG 5552 C GAAA
 CGGCAT TGT AATGTG
 ||||| ||| |||||
 GTCGTA ACG TTACAC
 A AA_
 GAM157 FRK 3' TGCACATTTTTTCTATGC 7787 CTGT
 GCAT GAAAAATGTGCA
 ||| |||||
 CGTA TTTTACACGT
 TCT_
 GAM157 ZNF2 5' CACATTTTCGGACGTC 22067 A TGA
 GGC TCTG AAAATGTG
 ||| ||| |||||
 CTG AGGC TTTTACAC
 C _
 GAM157 DKFZP727G051 5' CACTCCCTGGCACAATGCCGTA 34428 C AAAAAT_
 TACGGCAT TGTG GTG
 ||||| ||| |||
 ATGCCGTA ACAC CAC
 _ GGTCCCT
 GAM157 ENAH 3' GCACATTTTCCACAATACATTG 20127 TC_ A
 C GCA TGTG AAAATGTG
 ||| ||| |||||
 CGT ACAC TTTTACACG
 TACATA C
 GAM157 KIAA1237 3' CACGTGCACAGATGCC 39218 AAAA
 GGCATCTGTG ATGTG
 ||||| |||||

CCGTAGACAC TGCAC
G____
GAM157 LRMP 5' CACACCTCTGCTGGATGCC 12807 _ _ AAAA
GGCATCT GT GA TGTG
||||| ||| |||
CCGTAGG CG CT ACAC
T T CC__
GAM157 MOST2 5' TGCACATTTCCCAGGACTGCC 21556 _ G AA
GGCA TCT TG AAATGTGCA
||| ||| || |||||
CCGT AGG AC TTTACACGT
C _ CC
GAM157 PALM 3' TGCACATTCTCACAGACACCGT 8441 CA AA
ACGG TCTGTGA AATGTGCA
||| ||||| |||||
TGCC AGACACT TTACACGT
AC C_
GAM157 LOC197285 3' CACATCCCCCACAGGTGCTG 42415 AAAA
CGGCATCTGTG ATGTG
||||||| |||
GTCGTGGACAC TACAC
CCCC
GAM157 LOC92283 3' CACTCACTTTCCACAGATGC 34093 _ AAT_
GCATCTGTG AAA GTG
||||||| ||| |||
CGTAGACAC TTT CAC
C CACT
GAM158 HHLA1 5' CAATATCACCCCTTACCAC 12265 ATGA A_
GTG TGAGG TGATATTG
||| |||| |||||
CAC ATTCC ACTATAAC
C__ CC
GAM158 FLJ13657 3' TTATCCCCCATCACTAA 24221 ATGA
TTAGTGATG GGATGA
||||||| |||||
AATCACTAC CCTATT
CCC_
GAM158 LOC158629 5' CAATACATACCAATCATCAC 42019 GA _ A
GTGATGAT GG ATG TATTG
|||||| || ||| |||||
CACTACTA CC TAC ATAAC
A_ A _
GAM158 LOC169436 5' CAACATCATCCTCATCAGCAGT 40276 G A A
GA TTA TG TGATGAGGATGAT TTG
||| || ||||| ||||| |||
AGT AC ACTACTCCTACTA AAC
G G C
GAM158 LOC255098 5' CAATACAGGTTTACCATCATT 45688 A GA A
A TTAGTGATG TGAG TG TATTG
||||||| ||| || |||||

			AATTACTAC ACTT AC ATAAC	
			C GG _	
GAM158	LOC96597	5'	CAACATCATCATTACTAA 33229	GGA
			TTAGTGATGATGA TG	
			AATCATTACTACT AC	
			ACA	
GAM159	CCNT2	3'	ACTACCAGATGTGTGCAGTGCA 27768	_ GTA_
			TGCACTGCAC TA GTAGT	
			ACGTGACGTG GT CATCA	
			T AGAC	
GAM159	DISC1	3'	ACTCAGTAACACAGTGCAGT 20732	C__ _
			ACTGCACTG ACT AGT	
			TGACGTGAC TGA TCA	
			ACAA C	
GAM159	DISC1	3'	ACTCAGTAACACAGTGCAGT 20733	C__ _
			ACTGCACTG ACT AGT	
			TGACGTGAC TGA TCA	
			ACAA C	
GAM159	ZNF268	3'	ACTACATGAATGCAGTGA 31497	CTG CTA
			TCACTGCA CA GTAGT	
			AGTGACGT GT CATCA	
			AA_ A__	
GAM159	GRP3	3'	ACTACTATCCATAAATGCAATG 17673	C CTGCACTA
	A		TCA TGCA GTAGTAGT	
			AGT ACGT TATCATCA	
			A AAATACC_	
GAM159	KIAA0205	3'	ACTACTACTGGTAAAATGCAG 17001	CTGC
			CTGCA ACTAGTAGTAGT	
			GACGT TGGTCATCATCA	
			AAAA	
GAM159	KIAA1237	3'	ACCACTAGACTTCAGTGCAGGG 39215	A CA__ A
	A		TC CTGCACTG CTAGT GT	
			AG GACGTGAC GATCA CA	
			G TTCA C	
GAM159	KIAA1789	5'	ACTACTACTAATTGCTCTGTG 33306	TGCACT C__
	A		TCAC GCA TAGTAGTAGT	
			AGTG CGT ATCATCATCA	
			TCT__ TCA	
GAM159	PA26	3'	ACCACTGCTGGCACAAGCAGTG 15806	AC CA A
	A		TCACTGC TG CTAGTAGT GT	

AGTGACG AC GGTCTGCA CA
 A_ AC C
 GAM159 PHF5A 3' ACTACTACCAGCAGAAAGGGA 26501 A GCA ACTA
 TC CT CTGC GTAGTAGT
 || ||| |||||
 AG GG GACG CATCATCA
 _ AAA AC_
 GAM159 LOC126603 5' ACTACTACTGCACAGCTGA 37151 _ CAC C
 TCA CTG TGCA TAGTAGT
 ||| ||| ||| |||||
 AGT GAC ACGT ATCATCA
 C _ C
 GAM160 COL4A6 3' AGCTATCAAAGGAAATG 27356 GTG GA
 CA TC TTTTGATAGCT
 || || |||||
 GT AG GAAACTATCGA
 AA_ _
 GAM160 FLJ14566 5' AGCCAGCCCCAGCACTGAGGA 26563 C CGATT ATA
 TCC CAGTGT TTG GCT
 ||| ||||| ||| |||
 AGG GTCACG GAC CGA
 A ACCCC _
 GAM160 LOC143153 3' AGCTACCTCCTCTCCACACTGG 37578 C TTTTGA_
 GGA TCCCCAGTGT GA TAGCT
 ||||| || |||
 AGGGGTCACA CT ATCGA
 C CTCCTCC
 GAM160 LOC143154 3' AGCTACCTCCTCTCCACACTGG 37585 C TTTTGA_
 GGA TCCCCAGTGT GA TAGCT
 ||||| || |||
 AGGGGTCACA CT ATCGA
 C CTCCTCC
 GAM161 FLJ10579 3' AGGGCTGGACCACTTGATAACT 19945 G AA_ TG TA
 TC GAAGTTAT CAAGT T G CT
 ||||| |||| | | ||
 CTTCAATA GTTCA G C GA
 _ CCA GT GG
 GAM162 KMO 3' CATTTTATTTTCCACCTTCAA 9779 A T TACT
 A TTT AAG TGGGAAAAT GTG
 ||| ||| ||||| |||
 AAA TTC ACCCTTTTA TAC
 C C TTT_
 GAM162 TACC1 3' CACAGTAATTTCCCTTTTAA 12962 TT A
 TAAAG GGGAAA TTACTGTG
 |||| ||||| |||||
 ATTTT CCCTTT AATGACAC
 T_ _
 GAM162 FENS-1 3' CACAATAATTCCCAACT 21890 AA C
 AGTTGGGA ATTA TGTG
 ||||| ||| |||

TCAACCCT TAAT ACAC
 _ A
 GAM162 FLJ10506 3' CACAGTAACCTCATTTTTGAA 19888 T AAAA
 TTAAAG TGGG TTACTGTG
 ||||| ||| |||||
 AAGTTTT ACTC AATGACAC
 T C__
 GAM162 KIAA1954 3' AATTTTCCCAGCCCTAAA 38091 AA
 TTTA GTTGGGAAAATT
 ||| |||||
 AAAT CGACCCTTTTAA
 CC
 GAM162 MGC32104 3' ACACTACCCAACCTTTAAA 29502 AAAAT C
 TTAAAGTTGGG TA TGT
 ||||| || |||
 AAATTTCAACCC AT ACA
 _ C
 GAM162 R3HDM 3' CACAATGTGACCCAACCTT 17660 AAAA _
 AAGTTGGG TTAC TGTG
 ||||| ||| |||
 TTCAACCC AGTG ACAC
 _ TA
 GAM162 LOC122509 5' CACAGTAACCTTTATCCAA 29760 A _
 TTGGG AAA TTACTGTG
 ||||| ||| |||||
 AACCT TTT AATGACAC
 A CC
 GAM162 LOC146138 3' TGGGACTTGCCCAACCTTTAAA 40658 AAAATTA
 TTAAAGTTGGG CTG
 ||||| ||| |||
 AAATTTCAACCC GGT
 GTTCAG_
 GAM162 LOC199958 3' ACAGCCCGCAACTTTTAAA 43265 _ AAAATTA
 TTAAAGTTG GG CTGT
 ||||| || |||
 AAATTTCAAC CC GACA
 G C_____
 GAM163 ARF1 3' GCCTAGCATAGATTTGC 34992 T TAAA
 GCGAATCTATG CTG GC
 ||||| ||| |||
 CGTTTAGATAC GAT CG
 _ C_____
 GAM163 LOC155438 3' TGCTTCACAGATGTGCCAGC 41767 GAATC A
 GC TATGTCTGT AAGCA
 || ||||| |||||
 CG GTGTAGACA TTCGT
 ACC_ C
 GAM163 LOC56891 5' TTACAGACACAGACCTGC 21323 AA A
 GCG TCT TGTCTGTAA
 ||| ||| |||||

CGT AGA ACAGACATT
 CC C
 GAM163 LOC89919 5' TGCTTTACAGATGATTGC 30467 G TAT
 GC AATC GTCTGTAAAGCA
 || ||| |||||
 CG TTAG TAGACATTTTCGT

 — —
 GAM164 CCND2 3' TGGAGAGCACAGCATGCCTTA 7521 A A GT
 TAAGGTAT CTGT TTT CA
 ||||| ||| || ||
 ATTCCGTA GACA GAG GT
 C C AG
 GAM164 EPHA3 3' ATTGACAACACAGCCT 11740 TATA AT
 AGG CTGT TTGTCAAT
 || ||| |||||
 TCC GACA AACAGTTA
 — C—
 GAM164 UBE2G2 3' GCAGTTTACAGTATTCCT 32377 T T—
 AGG ATACTGTA TTGT
 || ||||| |||
 TCC TATGACAT GACG
 T TTT
 GAM164 DKFZP547E1010 3' ATTGACAGCACATATACC 17879 C AT
 GGTATA TGT TTGTCAAT
 |||| ||| |||||
 CCATAT ACA GACAGTTA
 — C—
 GAM164 DKFZP547E1010 3' ATTGACAGCACATATACC 33243 C AT
 GGTATA TGT TTGTCAAT
 |||| ||| |||||
 CCATAT ACA GACAGTTA
 — C—
 GAM164 KIAA1789 5' ACTGTATACAGTATACTTTA 33307 TT—
 TAAGGTATACTGTAT GT
 ||||| ||| ||
 ATTTTCATATGACATA CA
 TGT
 GAM165 CDC25B 3' AACCAAGGACTGAGCACCCCTC 22411 A T A—
 GA GGTGCTCG GT TGGTT
 || ||||| || |||
 CT CCACGAGT CA ACCAA
 C — GGA
 GAM165 CDC25B 3' AACCAAGGACTGAGCACCCCTC 22415 A T A—
 GA GGTGCTCG GT TGGTT
 || ||||| || |||
 CT CCACGAGT CA ACCAA
 C — GGA
 GAM165 CLN5 5' GCCAGACCAAAGCACCTTC 13228 CGTGTA —
 GAAGGTGCT TGGT TGGC
 ||||| ||| |||

CTTCCACGA ACCA ACCG
 A_____ G
 GAM165 G6PC 3' GCCAACCAAGAGCACATTC 5655 G GTGTA
 GAA GTGCTC TGGTTGGC
 ||| ||||| |||||
 CTT CACGAG ACCAACCG
 A A____
 GAM165 MGAT1 3' AGCCAGGGCACGAGCCCT 8225 T A_
 AGG GCTCGTGT TGGTT
 ||| ||||| |||||
 TCC CGAGCACG ACCGA
 _ GG
 GAM165 KIAA0182 3' CAGTCAACAAGCACCTTC 35643 CG A GT
 GAAGGTGCT TGT TG TG
 ||||| ||| ||
 CTTCCACGA ACA AC AC
 _ _ TG
 GAM165 KIAA1061 3' GACCAGAACACGAGCCCCT 35267 T A_
 AGG GCTCGTGT TGGTT
 ||| ||||| |||||
 TCC CGAGCACA ACCAG
 C AG
 GAM165 PHYHIP 3' GGCCAACCACAGAATGCC 16511 GC G AT
 GGT TC TGT GGTGCGC
 ||| ||| |||||
 CCG AG ACA CCAACCGG
 TA _ _
 GAM165 STRAIT11499 5' GACCCACAGAGCACCTC 22211 A _ TAT
 GA GGTGCTC GTG GGT
 || ||||| ||| |||||
 CT CCACGAG CAC CCAG
 C A ____
 GAM165 LOC157753 3' GGCCAAGCAACGAGCACTT 39662 GTA G
 AGGTGCTCGT TG TTGGC
 ||||| ||| |||||
 TTCACGAGCA AC AACCGG
 _ G
 GAM165 LOC253070 3' GGCCAATCAGGCGGAGCACCT 46355 A
 AGGTGCTCGTGT TGGTTGGC
 ||||| |||||
 TCCACGAGCGG ACTAACCGG
 G
 GAM165 LOC257479 5' CCAACTCCGGCACCTTC 46050 T TGTAT
 GAAGGTGC CG GGTG
 ||||| || |||||
 CTTCCACG GC TCAACC
 _ C____
 GAM166 CHRNA2 3' CAGAGATGGCAGAGCCATCC 6401 TC TA
 GGA TG TCTGCCATCTCTG
 ||| || |||||

			CCT AC AGACGGTAGAGAC		
			___ CG		
GAM166	TCF8	3'	AGATCATCTACAGATTCTA 25037	TC CC	
			TAGGATCTGTA TG ATCT		
			ATCTTAGACAT AC TAGA		
			CT ___		
GAM166	C20orf97	3'	CAGAGATGACAACTGGCATCC 22138	_ _ ATC C	
	T		AGGAT CT GT TG CATCTCTG		
			TCCTA GG CA AC GTAGAGAC		
			C T A__ A		
GAM166	DKFZp762E1511	3'	GGAGACAACCACAGATCCTA 29936	ATC CCA	
			TAGGATCTGT TG TCTCT		
			ATCCTAGACA AC AGAGG		
			CCA ___		
GAM166	FLJ11618	5'	AGAAGGGGACACAGATCC 22791	A G A	
			GGATCTGT TCT CC TCT		
			CCTAGACA AGG GG AGA		
			C _ A		
GAM166	FLJ14326	3'	AGAGATGACACAGACCC 25903	A ATCT C	
			GG TCTGT G CATCTCT		
			CC AGACA C GTAGAGA		
			C ___ A		
GAM166	KIAA0863	3'	CAGAGACGTGGGTACAAACCCT 45633	ATC TG CA	
	G		TAGG TGTATC C TCTCTG		
			GTCC ACATGG G AGAGAC		
			CAA GT C_		
GAM166	KIAA0863	3'	CAGAGACGTGGGTACAAACCCT 17153	ATC TG CA	
	G		TAGG TGTATC C TCTCTG		
			GTCC ACATGG G AGAGAC		
			CAA GT C_		
GAM166	KIAA0914	3'	AGACGGTACATAATCCTA 17033	CTG C A	
			TAGGAT TAT TGCC TCT		
			ATCCTA ATA ATGG AGA		
			___ C C		
GAM166	KIAA1655	5'	CAGAGCCAGGAGACAGATCC 33082	A GCCAT	
			GGATCTGT TCT CTCTG		
			CCTAGACA AGG GAGAC		
			G ACC__		
GAM166	OR7C1	5'	CAGAGATGACATGGAGATCC 18960	G TC C	
			GGATCT TA TG CATCTCTG		

			CCTAGA GT AC GTAGAGAC		
			G _ A		
GAM166	SEC22C	3'	CAGAAATGGCAGAATAAATCT 10404	C A	C
			GGAT TGT TCTGCCAT TCTG		
			TCTA ATA AGACGGTA AGAC		
			A _ A		
GAM166	ZFP106	3'	TGAAGATACAGATCCTA 22835	GC	
			TAGGATCTGTATCT CA		
			ATCCTAGACATAGA GT		
			A _		
GAM166	LOC147043	5'	AGAAATGGGCAGATCC 42144	ATCTG	C
			GGATCTGT CCAT TCT		
			CCTAGACG GGTA AGA		
			_ A		
GAM166	LOC147229	3'	TAGAAAATACAGATCCTA 38321	_	
			TAGGATCTGTA TCTG		
			ATCCTAGACAT AGAT		
			AAA		
GAM167	CD3Z	3'	GGAAAAACCCGTCAATGTACT 6392	A	AA C
			GG TATATTGAC GTT TTCC		
			TC ATGTAAGT CAA AAGG		
			_ CC A		
GAM167	IL22RA2	3'	GAAGAACTTATCTTTATTCTCA 27522	T	TT C
			TGGGA ATA GA AAGTTCTTC		
			ACTCT TAT CT TTCAAGAAG		
			_ TT A		
GAM167	KCNJ10	3'	GGAATCTGATATCAACATATCC 8027	A	_ AG
	TA		TGGGATAT TTGA CA TTCT		
			ATCCTATA AACT GT AAGG		
			C ATA CT		
GAM167	C20orf12	3'	GAAATCATCAATATTCCCA 19959	T	CAAG
			TGGGA ATATTGA TTC		
			ACCCT TATAACT AAG		
			_ ACTA		
GAM167	KIAA0528	5'	GGAAGAACCCATCAAAGCCC 35841	ATATA	CAA
			GGG TTGA GTTCTTCC		
			CCC AACT CAAGAAGG		
			GA _ ACC		
GAM167	KIAA1493	3'	GAAAAATGAGACAATATATCC 32089	ACAA	C
			GGATATATTG GTT TTC		

CCTATATAAC TAA AAG
 AGAG A
 GAM167 LOC51145 3' GGATTTCACCTGTCAACTTACC 18248 A TA TCT_
 CCA TGGG TA TTGACAAGT TCC
 |||| || ||||| ||
 ACCC AT AACTGTTCA AGG
 C TC CTTT
 GAM167 LOC92218 3' AAGAACTTGTCAATCGCCT 33985 ATAT
 GGG ATTGACAAGTTCTT
 || |||||
 TCC TAACTGTTCAAGAA
 GC_
 GAM168 RASD1 3' CCAAGACTGGGACTATTCCCCA 18167 TA TATAA
 TGGG AATAGTCCC TTGG
 |||| ||||| ||||
 ACCC TTATCAGGG AACC
 C_ TCAG_
 GAM168 SRR 3' CCAAGATGAAACATTTACCCA 22474 A CCCTATAA
 TGGGTAAAT GT TTGG
 ||||| || ||||
 ACCCATTTA CA AACC
 _ AAGTAG_
 GAM168 DKFZp762E1511 3' CGAGAGGGACTATTACCCA 29933 A ATAA
 TGGGTAA TAGTCCCT TTG
 ||||| ||||| ||
 ACCCATT ATCAGGGA AGC
 _ G_
 GAM168 SDS3 3' CAATTCACCTATTTGCCCA 34318 CCCTAT
 TGGGTAAATAGT AATTG
 ||||| ||||
 ACCCGTTTATCA TTAAC
 C_
 GAM168 LOC151248 5' CCAATTATAAACTCATTACTCC 39086 _ AT CCC
 A TGG GTAA AGT TATAATTGG
 || |||| || |||||
 ACC CATT TCA ATATTAACC
 T AC A_
 GAM168 LOC153810 3' TATAATTGGCAACAGGAACATT 39412 AG _____ TAAT
 TACCCA TAAAT TCC CTA TG
 |||| || || ||
 ATTTA AGG GGT AT
 CA ACAAC||| TAAT
 GAM168 LOC170425 5' TATAGAGACTATTTAACCA 37551 G C
 TGG TAAATAGTC CTATA
 || ||||| ||||
 ACC ATTTATCAG GATAT
 A A
 GAM169 ASTN 3' ACAAGATGCCATCTGTCAA 34361 AT AA
 TTGACAGGT CAT TTGT
 ||||| || ||||

			AACTGTCTA GTA AACA		
			CC G_		
GAM169	CAPN2	3'	AATAATGATACTGTCAA 7485	G	A
			TTGACAG TATCAT ATT		
			AACTGTC ATAGTA TAA		
			_ A		
GAM169	FANCF	3'	GACAATTCCTCCTGTCAG 22922		TATCAT
			TTGACAGG AATTGTC		
			GACTGTCC TTAACAG		
			TCC__		
GAM169	C20orf108	3'	GGACAATTTCTCCACCTGCAA 28087	A	ATCAT
			TTG CAGGT AATTGTCC		
			AAC GTCCA TTAACAGG		
			_ CCTCT		
GAM169	CCNG2	3'	GAAGGTGCTGATACCTTCAA 10560	C	TA TG
			TTGA AGGTATCA AT TC		
			AACT TCCATAGT TG AG		
			_ CG GA		
GAM169	CDC42BPB	3'	ACAATTTACCTGTCAA 12657		TCAT
			TTGACAGGTA AATTGT		
			AACTGTCCAT TTAACA		

GAM169	KIAA0210	3'	GCTGTATATACCTGTCAA 16425	C	ATT
			TTGACAGGTAT ATA GT		
			AACTGTCCATA TAT CG		
			_ GT_		
GAM169	KIAA1486	3'	AACTGATGATACCTCCAA 33460	AC	AAT
			TTG AGGTATCAT TGT		
			AAC TCCATAGTA ACA		
			C_ GTC		
GAM169	LOC146823	3'	GACAATTCTGCCTTCAA 40748	C	TCAT
			TTGA AGGTA AATTGTC		
			AACT TCCGT TTAACAG		
			_ C__		
GAM170	ING1	3'	TGTATATTTTAAAGAATG 12062		TTA
			CATTCTTTAAAAAT ACA		
			GTAAGAAATTTTTA TGT		
			TA_		
GAM170	FLJ12476	3'	TTATTGTTTTAAAGAATGA 23069		ATT
			TCATTCTTTAAAA TAA		

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AGTAAGAAATTTT ATT
GTT
GAM170 KIAA1715 3' AATTGTGTTTGTTTTAAGGAAT 33787 ATTTA
GA TCATTCTTTAAAA ACAATT
||||||| ||||
AGTAAGGAATTTT TGTAA
GTTTG
GAM171 ACTR1B 3' GCTGTGGCCAGGGCCCCA 35053 AC ATTA C
TGGG GCT TG CCACAGC
||| || || |||||
ACCC CGG AC GGTGTCG
_ G_ C
GAM171 CBFA2T2 3' TGCTGTGGAACACATAAGCCCC 11555 AC AT C_
A TGGG GCT TATG CCACAGCA
||| ||| ||| |||||
ACCC CGA ATAC GGTGTCGT
_ _ ACAA
GAM171 CBFA2T2 3' GCTGTGGGCATCTTCTGCCCA 11550 A CTATT
TGGG CG ATGCCACAGC
||| || |||||
ACCC GT TACGGGTGTCG
_ CTTC_
GAM171 GPR30 3' CTGTGGGTGAAGCGCCTCA 7251 A ATTA
TGGG CGCT TGCCACAG
||| ||| |||||
ACTC GCGA GTGGGTGTC
C A_
GAM171 POU2AF1 3' TGCTGTGGAGGCCAAGACCCC 12895 ACG ATTAT _
GGG CT GCC CACAGCA
||| || ||| |||||
CCC GA CGG GTGTCGT
CA_ AC_ AG
GAM171 KIAA1950 5' TGCTGTGGGCCCCAGAAGCGCCC 44492 A A AT
A TGGG CGCT TT GCCCAGCA
||| ||| || |||||
ACCC GCGA GA CGGGGTGTCGT
_ A CC
GAM171 MGC2647 3' GCTGCGGGAGGGGACGGCACCC 36485 AC TA ATG_ A
CA TGGG GC TT CCC CAGC
||| || || ||| |||
ACCC CG AG GGG GTCG
CA GC GGGA C
GAM171 RTCD1 5' GCTGCGGGGCTGGGCCCCA 9822 AC ATTAT A
TGGG GCT GCCC CAGC
||| || ||| |||
ACCC CGG CGGG GTCG
_ GT_ C
GAM171 SCM1 3' TGCTGTGGCACCCCATCGCCCC 14540 A CTATTA C
A TGGG CG TGCC ACAGCA
||| || ||| |||||

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			ACCC GC	ACGG TGTCGT		
			C TACCCC	_		
GAM171	TRIM22	3'	CTGTGGGCTGGAAATCCCA	12718	CG_	TTAT
			TGGGA CTA	GCCCACAG		
			ACCCT GGT	CGGGTGTC		
			AAA	_____		
GAM172	A1BG	3'	GATGAAATGTCTGTTT	28277	CC	
			AAGCAGACA	TTTCGTC		
			TTTGTCTGT	AAAGTAG		

GAM172	ACO1	3'	TGGGAGGGGTGCTGC	7955	A	TCG
			GCAG CACCTT	TCCCA		
			CGTC GTGGGG	AGGGT		

GAM172	AKAP2	3'	TTTAGGATCGTGTCTGCTT	14065	CTTTC	C
			AAGCAGACAC	GTCC AAA		
			TTCGTCTGTG	TAGG TTT		
			C_____	A		
GAM172	CKN1	3'	TTTTGGGGCTCAATGTCTCCT	5534	C	CCTTTC
			AG AGACA	GTCCCAAAA		
			TC TCTGT	CGGGGTTTT		
			C	AACT_____		
GAM172	FACL2	3'	TTGGGGTTTTGAATGTTTGCTT	22097	CCT	_____
			AAGCAGACA	TTCG TCCCAA		
			TTCGTTTGT	AAGT GGGGTT		
			_____	TTT		
GAM172	FHL2	5'	TTTGGGACGGAGTCTCGCTT	7182	_	ACCT
			AAGC AGAC	TTCGTCCCAAA		
			TTCG TCTG	AGGCAGGGTTT		
			C	_____		
GAM172	HPS1	3'	TGGGACTGGGAGTGTCTGCT	5696	C TT	_
			AGCAGACAC	T C GTCCCA		
			TCGTCTGTG	A G CAGGGT		
			_____	GG T		
GAM172	MAN1A1	3'	GGAGATGATGTCTGCTT	44135	CCTT	_
			AAGCAGACA	TCGTC CC		
			TTCGTCTGT	AGTAG GG		
			_____	A		
GAM172	PSEN1	5'	TTGGGCTGGGTCTGCTT	14236	A	TTTCGT
			AAGCAGAC	CC CCCAA		

			TTCGTCTG GG GGGTT	
			_ TC__	
GAM172	SLC25A15	3'	GATGTAGGGTCTGCTT 15527	A TT
			AAGCAGAC CCT CGTC	
			TTCGTCTG GGA GTAG	
			_ T_	
GAM172	SNTB2	3'	TTTGAAAGGCTGAAGATGTCTG 28380	C C C__
	CT		AGCAGACA CTTT GTC CAAA	
			TCGTCTGT GAAG CGG GTTT	
			A T AAA	
GAM172	TAL1	3'	TTTGCTGTAAGATGTCTGTTT 9176	C T TCC
			AAGCAGACA CTT CG CAAA	
			TTTGTCTGT GAA GT GTTT	
			A T C__	
GAM172	TCFL4	3'	TTGGGATGGGCGTCTGCT 31772	A TTT
			AGCAGAC CC CGTCCCAA	
			TCGTCTG GG GTAGGGTT	
			C __	
GAM172	TRPS1	3'	GGCAGCAAAGATGTCTGTT 15356	C C C_
			AGCAGACA CTTT GT CC	
			TTGTCTGT GAAA CG GG	
			A _ AC	
GAM172	ZNF202	3'	TGGGTGAAATGTCTGC 9512	CC T
			GCAGACA TTTCG CCCA	
			CGTCTGT AAAGT GGGT	
			__ _	
GAM172	ARAP3	5'	TGGGATGGCTCTGCTT 22856	CACCTT
			AAGCAGA TCGTCCCA	
			TTCGTCT GGTAGGGT	
			C__	
GAM172	BRD4	3'	TGGGTGGGTGGCATCTCCT 15596	C CA T T
			AG AGA CC TTCG CCCA	
			TC TCT GG GGGT GGGT	
			C AC T _	
GAM172	C8orf2	3'	TTTTGGGAGCATTGAGCCTGC 14026	ACAC TC__
			GCAG CTT G TCCCAAAA	
			CGTC GAG C AGGGTTTT	
			C__ TTA G	
GAM172	FBP17	3'	TTTTGAGACGGGAGTCTCGCT 36051	_ ACC TT C
			AGC AGAC T CGTC CAAAA	

TCG TCTG A GCAG GTTTT
C ___GG A

GAM172 FLJ00007 3' TTTTGGGATCAGGTGCCTG 35316 A TTC
CAG CACCT GTCCCAAAA
||| |||| |||||||
GTC GTGGA TAGGGTTTT
C C__

GAM172 FLJ14957 3' TTTGGGAGTGTGTGTCTGTTT 26686 CTTTCG
AAGCAGACAC TCCCAAA
||||||| |||||
TTTGTCTGTG AGGGTTT
TGTG__

GAM172 FLJ31101 3' TTTTGGGAAAGGGAAAAATGTC 19689 _____ CG
TGTT GCAGACA CCTTT TCCCAAAA
||||| |||| |||||||
TGTCTGT GGGAA AGGGTTTT
AAAAA __

GAM172 GGA2 3' TTTTGGGACAATGCCTCTGTCC 17406 A CACCT C
A GCAGA TT GTCCCAAAA
| |||| | |||||||
C TGTCT AA CAGGGTTTT
C CCGT__

GAM172 GGA2 3' TTTTGGGACAATGCCTCTGTCC 28928 A CACCT C
A GCAGA TT GTCCCAAAA
| |||| | |||||||
C TGTCT AA CAGGGTTTT
C CCGT__

GAM172 GT650 3' TTTTGAAAATGACGGTGTCTGA 27434 _ TT CC_
CT AG CAGACACC TCGT CAAAA
|| ||||||| ||| |||||
TC GTCTGTGG AGTA GTTTT
A C_ AAA

GAM172 GTPBP1 3' TGGGATTTGGTGTCTGCT 10499 TTTC
AGCAGACACC GTCCCA
||||||| |||||
TCGTCTGTGG TAGGGT
TT__

GAM172 KIAA0711 3' GGGACGTGTCTGCTT 16959 CTTTC
AAGCAGACAC GTCCC
||||||| |||||
TTCGTCTGTG CAGGG

GAM172 KIAA0775 3' TTTGGGGTCCCAGAGCCTGCT 16323 ACAC CG_
AGCAG CTTT TCCCAAA
|||| | |||||
TCGTC GAGA GGGGTTT
C__ CCCT

GAM172 KIAA1538 3' TTTTGGGGCCAAGATGGCTGC 35438 A C TC
GCAG CA CTT GTCCCAAAA
||| || ||| |||||||

CGTC GT GAA CGGGGTTTT
G A C_
GAM172 KIAA1559 3' TTTTGAGACAGGGTGTC 36167 TC C
GACACCTT GTC CAAAA
||||||| ||| |||||
CTGTGGGA CAG GTTTT
— A
GAM172 KIAA1822 3' TTTTGGGATGAAATGTC 33557 CC
GACA TTTCGTCCCAAAA
||| |||||||||
CTGT AAAGTAGGGTTTT
—
GAM172 MGC21688 3' TTTGGAATGATGAAAGCATGT 29455 C_ —
ACA CTTTCGTC CAAA
||| ||||||| |||||
TGT GAAAGTAG GGTTT
AC TAA
GAM172 MGC3101 3' CGAGACCGGCCTTGTCTGCT 23476 — —
AGCAGACA CC TTTCG
||||||| || |||||
TCGTCTGT GG AGAGC
TCC CC
GAM172 RAI16 3' TGGGATGGGGCTTCTGCT 22972 CA TT
AGCAGA CCT CGTCCCA
||||| ||| |||||||
TCGTCT GGG GTAGGGT
TC —
GAM172 RDC1 3' TGGGACGGGTTTACTT 35849 C ACCTT
AAG AGAC TCGTCCCA
||| ||| |||||||
TTC TTTG GGCAGGGT
A —
GAM172 RYBP 5' TTTTGGGATTGTAGCGTCTGC 29909 AC TTC
GCAGAC CT GTCCCAAAA
||||| || |||||||
CGTCTG GA TAGGGTTTT
C_ TGT
GAM172 SEMA4F 3' TTGGGGTGGTTCTGCTT 10462 C TTTCG
AAGCAGA ACC TCCCAA
||||||| ||| |||||
TTCGTCT TGG GGGGTT
— T—
GAM172 SPEC1 3' GGCTGAAGAGTCTGCTT 21513 AC C
AAGCAGAC CTTT GTC
||||||| ||||| |||
TTCGTCTG GAAG CGG
A_ T
GAM172 TRIM5 5' TTTGGGACAAAACGT 26937 ACACC C
GCAG TTT GTCCCAAA
||| ||| |||||||

			TGTC	AAA CAGGGTTT		
			_____	A		
GAM172	TRIM5	5'	TTTGGGACAAA	ACTGT	26927	ACACC C
			GCAG	TTT GTCCCCAAA		
			TGTC	AAA CAGGGTTT		
			_____	A		
GAM172	TRIM5	5'	TTTGGGACAAA	ACTGT	26936	ACACC C
			GCAG	TTT GTCCCCAAA		
			TGTC	AAA CAGGGTTT		
			_____	A		
GAM172	WWP1	5'	TTTTGGGACATGGCC	ACTGCTT	39192	ACA TTTC
			AAGCAG	CC GTCCCCAAA		
			TTCGTC	GG CAGGGTTTT		
			ACC	TA__		
GAM172	LOC115110	5'	GGGTGAGGTGTCTGCT		35511	TCGT
			AGCAGACACCTT	CCC		
			TCGTCTGTGGAG	GGG		
			T__			
GAM172	LOC127428	5'	TGGGAGGAAGCGTCTGTTT		36901	AC G
			AAGCAGAC	CTTTC TCCCA		
			TTTGTCTG	GAAGG AGGGT		
			C_ _			
GAM172	LOC145662	3'	TTTTGGGAAGCGAGGTGTC		37919	TCG
			GACACCTT	TCCCCAAA		
			CTGTGGAG	AGGGTTTT		
			CGA			
GAM172	LOC146443	5'	TTTTGGGACAGAGTCTC		38150	CAC C
			GA	CTTT GTCCCCAAA		
			CT	GAGA CAGGGTTTT		
			CT_ _			
GAM172	LOC149372	3'	GGTTCGGAAGGTGACTGCTT		38731	A _TC
			AAGCAG	CACCTTTC G CC		
			TTCGTC	GTGGAAGG C GG		
			A	G TT		
GAM172	LOC151438	5'	GAAGGCAGGGTCTGCTT		41348	A T G
			AAGCAGAC	CCT TC TC		
			TTCGTCTG	GGA GG AG		
			_ C A			
GAM172	LOC151657	5'	TTTGGGACCCCGTGCCTCCT		41383	C A CTTTC
			AG AG CAC	GTCCCCAAA		

			TC TC GTG CAGGGTTT		
			C C CCC__		
GAM172	LOC151877	3'	TTGTGGAAAAATGTCTGTT 41399	CCT CG _	
			AGCAGACA TT TCC CAA		
			TTGTCTGT AA AGG GTT		
			__ AA T		
GAM172	LOC157931	3'	TGGGAAGGATGTGTCTGC 41906	CT G	
			GCAGACAC TTC TCCCA		
			CGTCTGTG AGG AGGGT		
			T_ A		
GAM172	LOC205251	5'	GACACTGGGCTGTCTGCTT 43589	_ TTC	
			AAGCAGACA CCT GTC		
			TTCGTCTGT GGG CAG		
			C TCA		
GAM172	LOC255177	3'	TTGGGTGAAATGTCTG 46205	CC T	
			CAGACA TTTCG CCCAA		
			GTCTGT AAAGT GGGTT		
			__ _		
GAM172	LOC256021	3'	TTTTAGGAATGAAGGTGTCT 46168	CG C	
			AGACACCTTT TCC AAAA		
			TCTGTGGAAG AGG TTTT		
			TA A		
GAM172	LOC51301	5'	TTTGGGGCAGCATTTCG 18675	CAC TTC	
			GCAGA CT GTCCCAAA		
			CGTTT GA CGGGGTTT		
			AC_ __		
GAM173	BACE	3'	CCTGAAAAATGACTGTCCCA 14418	A _ T	
			TGG ACAGTCATT TC GG		
			ACC TGTCAGTAA AG CC		
			C AA T		
GAM173	BACE	3'	CCTGAAAAATGACTGTCCCA 29086	A _ T	
			TGG ACAGTCATT TC GG		
			ACC TGTCAGTAA AG CC		
			C AA T		
GAM173	KIT	3'	CTTTCCAAGGCTTCTCCA 5731	AC ATTTC	
			TGGA AGTC TGGAAAG		
			ACCT TCGG ACCTTTC		
			CT A__		
GAM173	LIMK1	3'	CCTTTCCACACGCCGCTGCCCC 8124	AA CATTTC	
	AG		CTGG CAGT TGGAAAGG		

			GACC GTCG ACCTTTCC		
			CC CCGCAC		
GAM173	LIMK1	3'	CCTTTCCACACGCCGCTGCCCC	18799	AA CATTTC
	AG		CTGG CAGT TGGAAAGG		
			GACC GTCG ACCTTTCC		
			CC CCGCAC		
GAM173	LPIN1	3'	CTTTCCGGCCTGCTCCAG	33468	A TCATT
			CTGGA CAG CTGGAAG		
			GACCT GTC GGCCTTTC		
			C C_____		
GAM173	LRP4	3'	CCTCCCACCCCATAACTGTTCC	32198	C TTC_ AA
			GGAACAGT AT TGG AGG		
			CCTTGTCA TA ACC TCC		
			A CCCC C_		
GAM173	PDGFB	5'	CCTTTCCAGAAAATGTTGCA	8469	G GTCA
			TG AACA TTTCTGGAAAGG		
			AC TTGT AAAGACCTTTC		
			G A_____		
GAM173	SMCX	3'	CTTCCCCTGACTGTTCCA	10395	TTTCT A
			TGGAACAGTCA GG AAG		
			ACCTTGTCAGT CC TTC		
			C_____ C		
GAM173	TRPM6	3'	CCTTTCTTATTATAAGCTGTTTC	19198	CATTCT_
	CAG		CTGGAACAGT GGAAAGG		
			GACCTTGTCG TCTTTC		
			AATATTAT		
GAM173	ZNF42	5'	CCCTTCCAAAAACGATTTTTTC	9467	C_ A C A
	CA		TGGAA AGTC TTT TGGAA GG		
			ACCTT TTAG AAA ACCTT CC		
			TT C A C		
GAM173	ZNF74	3'	CCTCCCAGAAAGGGCCACACTC	9472	ACA_ A AA
	CAG		CTGGA GTC TTTCTGG AGG		
			GACCT CGG GAAGACC TCC		
			CACAC _ CC		
GAM173	COAS3	3'	TCCCTAACAACCTGTTTCAG	29122	CA TCT
			CTGGAACAGT TT GGA		
			GACTTTGTCA AA CCT		
			AC TC_		
GAM173	FLJ10408	5'	CTTCCAGAAGCAACCCAG	19850	AACA CA A
			CTGG GT TTTCTGGAA G		

GACC CA GAAGACCTT C
 ____ AC C
 GAM173 FLJ12707 3' AGAAAAGTGACTGCTCCAG 22609 A ____
 CTGGA CAGTCAT TTCT
 ||||| ||||| ||||
 GACCT GTCAGTG AAGA
 C AA
 GAM173 FLJ13204 3' CCTTTCCAATTTTTCTATTCCA 24115 C TCATTTC
 G CTGGAA AG TGGAAAGG
 ||||| || |||||
 GACCTT TC ACCTTTCC
 A TTTTTA_
 GAM173 IL18BP 3' CCTTCACTCTAATGGACTGTTC 12251 ATTTC ____
 CAG CTGGAACAGTC TGG AAGG
 ||||| ||||| ||||
 GACCTTGTGAG ATCT TTCC
 GTA__ CAC
 GAM173 KIAA0089 3' CCTAGGAAATGACTGTCCCA 34664 A ____
 TGG ACAGTCATTCT GG
 ||| ||||| ||||| ||
 ACC TGTCAGTAAAGG CC
 C AT
 GAM173 KIAA0410 3' CCTCTCATTGGATGACTATTC 16618 C CTG A
 GAA AGTCATTT GA AGG
 ||| ||||| || ||||
 CTT TCAGTAGG CT TCC
 A TTA C
 GAM173 KIAA0459 3' CCTCCCCAGTGCCTCTTCCAG 30573 C T TTT AA
 CTGGAA AG CA CTGG AGG
 ||||| || ||||| ||||
 GACCTT TC GT GACC TCC
 C C ____ CC
 GAM173 KIAA0534 3' CCTTCCTGCCAACTGTTCCA 35383 CATTTCT A
 TGGAACAGT GGAA GG
 ||||| ||||| ||||
 ACCTTGTC A CCTT CC
 ACCGT__ _
 GAM173 KIAA1755 3' CCCCTCCAGAGGTCTCGCTCGC 30749 _ ACAGTC AA
 AG CTG GA ATTTCTGGA GG
 ||| || ||||| ||||
 GAC CT TGGAGACCT CC
 G CGCTC_ CC
 GAM173 MGC9753 3' CCTTCCCAGAGGGTCTTACTGT 27241 CA__ A
 TCCAG CTGGAACAGT TTTCTGG AAGG
 ||||| ||||| ||||
 GACCTTGTC A GGAGACC TTCC
 TTCTG C
 GAM173 MPPE1 5' TTCAGCGGTGACTGCCCAG 23332 AA TT
 CTGG CAGTCAT CTGGA
 ||| ||||| ||||

			GACC GTCAGTG GACTT			
			C_ GC			
GAM173	PLSCR3	3'	CCCTTCCAGGGCCTCTGCTCCA 21632	A	TCAT	A
			TGGA CAG TTCTGGAA GG			
			ACCT GTC GGGACCTT CC			
			C TCC_ C			
GAM173	PLSCR3	3'	CCCTTCCAGGGCCTCTGCTCCA 43637	A	TCAT	A
			TGGA CAG TTCTGGAA GG			
			ACCT GTC GGGACCTT CC			
			C TCC_ C			
GAM173	PNMA5	3'	CTTTCCAGAGTACCCAG 36441	AACA	CAT	
			CTGG GT TTCTGGAAAG			
			GACC CA GAGACCTTTC			
			C_ T_			
GAM173	RPS6KA4	3'	CCCCTCCAGGGGGACTGCTCCA 10054	A	A TT	AA
			TGGA CAGTC T CTGGA GG			
			ACCT GTCAG G GACCT CC			
			C _GG CC			
GAM173	SETBP1	3'	CCTTGGCATGCTGTTCCA 17825	T	T T_	
			TGGAACAG CAT TC GG			
			ACCTTGTC GTA GG CC			
			_ C TT			
GAM173	LOC113523	3'	TTTAAAAATACTGTCCCAG 36157	A	C C	
			CTGG ACAGT ATTT TGGA			
			GACC TGTCA TAAA ATTT			
			C _ A			
GAM173	LOC124987	5'	TCTGATGAATGACTGTCCC 37265	A	CT_	
			GG ACAGTCATTT GGA			
			CC TGTCAAG TCT			
			C TAG			
GAM173	LOC127281	3'	CCTCCAGCCAGAGATATTCCA 36888	CAGTC	AA_	
			TGGA ATTCTGG AGG			
			ACCTT TAGAGACC TCC			
			A_ GACC			
GAM173	LOC143425	3'	CCTTTGAGCTAATGACTGTCTC 42353	_	T_ G A	
	CAG		CTGGA ACAGTCATT CT GAA GG			
			GACCT TGTCAAGTA GA TTT CC			
			C TC G _			
GAM173	LOC145195	3'	CCTTCCCATGCAGGATGACTGC 40514	A	C_ A	
	TC		GA CAGTCATTT TGG AAGG			

		CT GTCAGTAGG ACC TTCC		
		C ACGT C		
GAM173	LOC145719 5'	CCTTTCCAGCCCCTCTTTTCCA 40574	C TCATT	
	G	CTGGAA AG CTGGAAAGG		
		GACCTT TC GACCTTTCC		
		T TCCCC_		
GAM173	LOC145720 5'	CCCTTCCAGCCCCTCTTTTCCA 40563	C TCATT	A
	G	CTGGAA AG CTGGAA GG		
		GACCTT TC GACCTT CC		
		T TCCCC_ C		
GAM173	LOC148029 5'	CCTCCCAGAAATATGAGCTCAG 38444	AACA C	AA
		CTGG GT ATTTCTGG AGG		
		GACT TA TAAAGACC TCC		
		CGAG _ C_		
GAM173	LOC150290 3'	CCTCCCCAAAAACAGATTGACC 38932	AA A_ C	AA
	CAG	CTGG CAGTC TTT TGG AGG		
		GACC GTTAG AAA ACC TCC		
		CA AC A CC		
GAM173	LOC152698 5'	CTTCCAGAAGCAACCCAG 30312	AACA CA	A
		CTGG GT TTTCTGGAA G		
		GACC CA GAAGACCTT C		
		_ AC C		
GAM173	LOC153894 5'	CTTTCCAGAGCTACCCAG 39427	AAC CATT	
		CTGG AGT TCTGGAAAG		
		GACC TCG AGACCTTTC		
		CA_ _		
GAM173	LOC157280 5'	CTTCCAGAAGCAACCCAG 36593	AACA CA	A
		CTGG GT TTTCTGGAA G		
		GACC CA GAAGACCTT C		
		_ AC C		
GAM173	LOC158062 3'	CCCCTCCAAGTGTCTGTTCCAG 41914	T TC	AA
		CTGGAACAG CATT TGGA GG		
		GACCTTGTC GTGA ACCT CC		
		T _ CC		
GAM173	LOC197114 5'	CCCTTCCAGCCCCTCTTTTCCA 43187	C TCATT	A
	G	CTGGAA AG CTGGAA GG		
		GACCTT TC GACCTT CC		
		T TCCCC_ C		
GAM173	LOC200933 5'	TTCAGCACTAATGACTGCTCCA 43365	A T_	
	G	CTGGA CAGTCATT CTGGA		

GACCT GTCAGTAA GACTT
 C TCAC
 GAM173 LOC255448 5' CTTCCAGAAGCAACCCAG 45403 AACCA CA A
 CTGG GT TTTCTGGAA G
 ||| || |||||
 GACC CA GAAGACCTT C
 ____ AC C
 GAM173 LOC91050 3' CCTCCCAGATTGCATCTCCAG 32335 ACAT TT AA
 CTGGA G CA TCTGG AGG
 |||| | || |||| ||
 GACCT C GT AGACC TCC
 CTA _ T _ C _
 GAM174 D8S2298E 3' AACTTGGAAGAAGCTTC 12229 T CGG
 GAA CTTCTTTT GAGTT
 || ||||| ||||
 CTT GAAGAAGG TTCAA
 C ____
 GAM174 HGF 3' GAACTCCTAGAAATTTT 45224 TC TTTC
 GAA TTCT GGGAGTTC
 || ||| |||||
 CTT AAGA TCCTCAAG
 TA ____
 GAM174 KIAA1755 3' AACTCCTGGAAGACCCGA 30745 AA TTTT
 TCG TCTTC CGGGAGTT
 || |||| |||||
 AGC AGAAG GTCCTCAA
 CC ____
 GAM174 LOC145474 3' AGAACATGGAAAGAAAATTT 37867 C GGA
 GAAT TTCTTTTCG GTTCT
 ||| ||||| ||||
 TTTA AAGAAAGGT CAAGA
 A A _
 GAM174 LOC256283 5' GAATAAAAAGAAGATTC 46362 CGGGA
 GAATCTTCTTTT GTTC
 ||||| |||
 CTTAGAAGAAAA TAAG
 A ____
 GAM174 LOC90593 3' AACCTTGAAAAAGATTAGA 31763 G C A
 TC AATCTT TTTTCGGG GTT
 || |||| ||||| ||
 AG TTAGAA AAAAGTTC CAA
 A _ _
 GAM175 AOC3 3' CCAGCCCCTGGTACTCCCCC 9823 A TTT _
 GG GGGA GT TTAGGGGCTGG
 || ||| || |||||
 CC CCCT CA GGTCCCCGACC
 _ _ T
 GAM175 BBS4 3' TCCAGAACAAGTCCCTCC 26921 A
 GGAGGGATTGTGTT GGG
 ||||| |||

CCTCCCTGAACAAG CCT

A

GAM175 CXorf6 3' TCCAGCCCCCAGTGTCCCATCC 11994 _ TTGTTTA
GGA GGGAT GGGGCTGGA
||| ||||| |||||
CCT CCCTG CCCCACCT
A TGAC__

GAM175 DMPK 5' CCAGCCCTCACCCCC 10663 A ATT TTTA
GG GGG TG GGGGCTGG
|| ||| || |||||
CC CCC AC TCCCGACC

GAM175 MFGE8 3' CCAGCCCCTAAGCCCCGTCC 12558 _ ATTT
GGA GGG GTTTAGGGGCTGG
||| ||| |||||
CCT CCC CGAATCCCCGACC
G _

GAM175 MLLT7 3' CCAGCCCCCAAAGCAGCCCTTC 12575 AT A_
GGAGGG TTGTTT GGGGCTGG
||||| ||||| |||||
CTTCCC GACGAA CCCCACCC
_ AC

GAM175 PRKACA 3' TCCAGCCCCCACCACACCCCC 8598 A ATT TTTA
GG GGG TG GGGGCTGGA
|| ||| || |||||
CC CCC AC CCCCACCT
_ AC_ CCAC

GAM175 TEM6 3' CCAGCCCGAAATTCCTCC 22961 TTT AG
GGAGGGA GTTT GGGCTGG
||||| ||| |||||
CCTCCCT TAAA CCCCACCC
_ G_

GAM175 TFAP4 3' CCAGCCCCCACCTCTGCCTCC 9224 GATTT TTA
GGAGG GT GGGGCTGG
||||| || |||||
CCTCC CA CCCCACCC
GTCTC C_

GAM175 TNF 3' TCCAACCTTCCCAAACGCCTCC 43771 GA TTT GC
GGAGG TTTG AGGG TGGA
||||| ||| ||| |||
CCTCC AAAC TTCC ACCT
GC CC_ A_

GAM175 C20orf130 3' CCAACCCCTAGATCCCACC 30936 A TGTT C
GG GGGATT TAGGGG TGG
|| ||||| ||||| |||
CC CCCTAG ATCCCC ACC
A _ A

GAM175 DKFZP434K1772 3' CCAGCCCCTAGCCCCACTCC 33630 _ ATTT T
GGAG GG GTT AGGGGCTGG
||||| || |||||

CCTC CC CGA TCCCCGACC
 A C__ _
 GAM175 DKFZP564F0522 3' TCCAAAACAAATTCCTCC 34041 A
 GGAGGGATTTGTTT GGG
 |||||
 CCTCCTTAAACAAA CCT
 A
 GAM175 FLJ10661 3' CCCAAAAACAACCCCTCC 19995 AT AG
 GGAGGG TTGTTT GGG
 ||||| ||||| |||
 CCTCCC AACAAA CCC
 C_ AA
 GAM175 FLJ14950 5' TCCAGCCCCCTGTGTCACCCCGC 26676 A ATT TTT_
 C GG GGG TG AGGGGCTGGA
 || ||| || |||||
 CC CCC AC TCCCCGACCT
 G C_ TGTC
 GAM175 FLJ20847 5' TCCAGCCCCCTCCATCTCCC 45458 TT TTTA
 GGGA TG GGGGCTGGA
 ||| || |||||
 CCCT AC CCCCCGACCT
 CT CTC_
 GAM175 KIAA1100 5' CCAGCCCCCTCCACCCCCC 17084 A ATTT TT
 GG GGG GT AGGGGCTGG
 || ||| || |||||
 CC CCC CA TCCCCGACC
 _ _ _ CC
 GAM175 MRPL20 3' CCAGCCCCCTTGCCAACCCTCC 19696 A T TT
 GGAGGG TT GT AGGGGCTGG
 ||||| ||| |||||
 CCTCCC AA CG TCCCCGACC
 _ C T_
 GAM175 PP1628 5' CCAGCCCCCAGGAGGCCCTGC 24856 G AT G TA
 G AGGG TT TT GGGGCTGG
 | ||| ||| |||||
 C TCCC GA GA CCCCCGACC
 G CG G C_
 GAM175 PRKRI 5' CCAGCCCCTAGCTACATCTCTC 12943 T T
 C GGAGGGAT TG TTAGGGGCTGG
 ||||| || |||||
 CCTCTCTA AT GATCCCCGACC
 C C
 GAM175 SEMA6A 5' CCAGCCCCCACCCTGCCCCC 21880 A ATTT TTA
 GG GGG GT GGGGCTGG
 || ||| || |||||
 CC CCC CA CCCCCGACC
 C GCCC C_
 GAM175 SP2 3' CCAGCCCCGCCACAACCTCTCC 9080 AT TTA
 GGAGGG TTGT GGGGCTGG
 ||||| ||| |||||

CCTCTC AACA CCCCAGACC
 C_ CCG
 GAM175 TIAF1 3' CCAGCCCCCACCACC 27797 A ATTT TTA
 GG GGG GT GGGGCTGG
 || ||| || |||||
 CC CCC CA CCCCAGACC
 A _ C_
 GAM175 LOC124930 3' CCAGCCCCCACCACCGTCC 36766 _ ATT TTA
 GGA GGG TGT GGGGCTGG
 ||| ||| ||| |||||
 CCT CCC ACA CCCCAGACC
 G _ C_
 GAM175 LOC145719 5' CCTCTAAACACATCCCTCC 40573 T
 GGAGGGAT TGTTTAGGGG
 ||||| |||||
 CCTCCCTA ACAAATCTCC
 C
 GAM175 LOC145720 5' CCTCTAAACACATCCCTCC 40564 T
 GGAGGGAT TGTTTAGGGG
 ||||| |||||
 CCTCCCTA ACAAATCTCC
 C
 GAM175 LOC145725 3' CCAGCTCCACACACCCCCC 37947 A ATT TTA
 GG GGG TGT GGGGCTGG
 || ||| ||| |||||
 CC CCC ACA CCTCGACC
 _ C_ CA_
 GAM175 LOC145732 3' CCAGCTCCACACACCCCCC 37956 A ATT TTA
 GG GGG TGT GGGGCTGG
 || ||| ||| |||||
 CC CCC ACA CCTCGACC
 _ C_ CA_
 GAM175 LOC146562 3' CCAGCCCCCAGGCCCTCT 29178 A TTTA
 GGAGGG TTTG GGGGCTGG
 ||||| ||||| |||||
 TCTCCC GGAC CCCCAGACC
 _ _
 GAM175 LOC151878 5' TCCAGCCCCTCCACCCCTCC 39172 ATTT TT
 GGAGGG GT AGGGGCTGGA
 ||||| || |||||
 CCTCCC CA TCCCCGACCT
 _ CC
 GAM175 LOC197419 5' CCAGCCCCCAGTCCCCTCT 43209 AT TTTA
 GGAGGG TTG GGGGCTGG
 ||||| ||| |||||
 TCTCCC GAC CCCCAGACC
 CT _
 GAM175 LOC257551 3' TCCAACCTTCCCAAACGCCTCC 46645 GA TTT GC
 GGAGG TTTG AGGG TGGA
 ||||| ||||| ||||| |||||

			CCTCC AAC TTCC ACCT		
			GC CC_ A_		
GAM175	LOC257601	3'	TCCAACCTTCCCAAACGCCTCC 46696	GA	TTT GC
			GGAGG TTTG AGGG TGGA		
			CCTCC AAC TTCC ACCT		
			GC CC_ A_		
GAM175	LOC91300	5'	CCAGCCCCTGCTCAGCCCCTCC 45386	AT	TT
			GGAGGG TTG TAGGGGCTGG		
			CCTCCC GAC GTCCCCGACC		
			C_ TC		
GAM175	LOC91300	5'	CCAGCCCCTGCTCAGCCCCTCC 29005	AT	TT
			GGAGGG TTG TAGGGGCTGG		
			CCTCCC GAC GTCCCCGACC		
			C_ TC		
GAM176	CHD1	5'	TGTTGAAGAAAATTCATCT 6933	G	C C
			AGA GAA TT CTTCAGCA		
			TCT CTT AA GAAGTTGT		
			A A A		
GAM176	MAD2L1	3'	ATATTGCTGTATAGCTCCTTT 8170	A	TCCTT
			AGAGGA CT CAGCAATAT		
			TTTCCT GA GTCGTTATA		
			C TAT__		
GAM176	MSR1	3'	ATTGCTGATTTTCTCT 28960	CTTCCT	
			AGAGGAA TCAGCAAT		
			TCTCTTT AGTCGTTA		
			T_____		
GAM176	MSR1	3'	ATTGCTGATTTTCTCT 28962	CTTCCT	
			AGAGGAA TCAGCAAT		
			TCTCTTT AGTCGTTA		
			T_____		
GAM176	SED1	5'	ATATTGCCAGATGTCCTCT 15904	ACT	CTTCA
			AGAGGA TC GCAATAT		
			TCTCCT AG CGTTATA		
			GT_ AC__		
GAM176	TRIM39	5'	GTTGAAGGAAGCTTCTCT 22225	A	
			AGAGGA CTTCTTCAGC		
			TCTCTT GAAGGAAGTTG		
			C		
GAM176	COPS7B	3'	ATTGTGAAGGAGGCCCTC 22930	AA	G
			GAGG CTTCTTCA CAAT		

CTCC GGAGGAAGT GTTA
 CC _
 GAM176 KIAA1229 3' ATTGCTGAAAAATGAGTTT 31095 CC__
 GAACTT TTCAGCAAT
 ||||| |||||
 TTTGAG AAGTCGTTA
 TAAA
 GAM176 NRF 3' ATATTGCTGTGTCCCTC 18983 A TTCCTT
 GAGG AC CAGCAATAT
 ||| || |||||
 CTCC TG GTCGTTATA
 C T____
 GAM176 UBXD2 3' GATGTTTGA AACAGTTCCTCT 33914 TCC GC
 AGAGGAACT TTCA AATATC
 ||||| ||| |||||
 TCTCCTTGA AAGT TTGTAG
 CAA _
 GAM176 LOC115219 5' GATATTGCTGCTTGGTCTCTCT 36279 GA TCCTT
 AGAG ACT CAGCAATATC
 ||| ||| |||||
 TCTC TGG GTCGTTATAG
 TC TTC__
 GAM176 LOC158187 3' ATATTGCTGTCAGTTCCTC 41921 TCCTT
 GAGGAACT CAGCAATAT
 ||||| |||||
 CTCCTTGA GTCGTTATA
 CT____
 GAM177 COX7A1 5' AATCCGAGGAGCAGGACTC 7602 A AAC
 GA TCTTGT CCTCGGATT
 || ||||| |||||
 CT AGGACG GGAGCCTAA
 C A__
 GAM177 DNMT2 3' AATCATATTACAAGATTTTA 10669 CCCTCG
 TAGAATCTTGTA GATT
 ||||| ||||| |||
 ATTTTAGAACATT CTAA
 ATA____
 GAM177 C1QR1 3' TCTGGAATTACAAGATTTCTA 14338 _ CC T
 TAGAA TCTTGTA C CGGA
 ||||| ||||| | |||
 ATCTT AGAACATT G GTCT
 T AA _
 GAM177 FLJ23511 5' CCTAGGTTACAAGATCCTA 25965 A CTC
 TAG ATCTTGTAACC GG
 ||| ||||| ||| ||
 ATC TAGAACATTGG CC
 C AT_
 GAM177 KIAA0447 3' AATCCGAGAGTCCCAATTC 35491 CT TA C
 GAAT TG AC CTCGGATT
 ||| || || |||||

CTTA AC TG GAGCCTAA
 ___ CC A

GAM177 MSTP032 3' CCAAGGGGTAGGCAATTCTA 24906 CT AA___ C
 TAGAAT TGT CCCT GG
 ||||| ||| ||| ||
 ATCTTA ACG GGG A CC
 ___ GATG A

GAM178 BCL7A 3' CACCCTACTCACCGCTCTCCT 21990 A _ T
 AG AGGGCGGTG GTGG GGTG
 || ||||| ||| |||
 TC TCTCGCCAC CATC CCAC
 C T _

GAM178 CACNB1 3' CACCACTGCCCTCCCTTC 6384 C T TG
 GAAGGG GG GG GTGGTG
 ||||| || || |||||
 CTTCCC TC CC CACCAC
 _ _ GT

GAM178 DYRK1A 3' CACCACCACCACCACCATC 28161 A GC
 GA GG GGTGGTGGTGGTG
 || || ||||| |||||
 CT CC CCACCACCACCAC
 A A_

GAM178 ELK1 3' CACCACCACCACCACCCCTTCT 11729 C_
 AGAAGGG GGTGGTGGTGGTG
 ||||| ||||| |||||
 TCTTCCC CCACCACCACCAC
 CA

GAM178 FACL4 5' CACCACCGCGCGCCCCCGCTC 10762 A_ C _
 GA GGG GGTG GTGGTGGTG
 || ||| ||| ||||| |||||
 CT CCC CCGC CGCCACCAC
 CG _ G

GAM178 FACL4 5' CACCACCGCGCGCCCCCGCTC 23252 A_ C _
 GA GGG GGTG GTGGTGGTG
 || ||| ||| ||||| |||||
 CT CCC CCGC CGCCACCAC
 CG _ G

GAM178 FKBP1A 3' CACCATTCCCACCCACCCT 6471 C_ TG
 AGGG GGTGG GTGGTG
 ||| ||| |||||
 TCCC CCACC TACCAC
 AC CT

GAM178 H1F0 3' CACCACCACCTTTTGCCCCCTT 11794 C ____
 CT AGAAGGG GGT GGTGGTGGTG
 ||||| ||| ||||| |||||
 TCTTCCC CCG CCACCACCAC
 _ TTTT

GAM178 HOXB9 3' CACCTAGAACCTCCCTCCTTT 23445 A C GGT_
 AAAG AGGG GGT GGTG
 ||| ||| ||| |||

			TTTC TCCC CCA CCAC		
			C T AGAT		
GAM178	IL11	3'	CAAAGCCACCACCGTCCTTC 6278	GG	
			GAAGGGCGGTGGTGGT TG		
			CTTCCTGCCACCACCG AC		
			AA		
GAM178	KLHL3	3'	CACCATTACCCACCCCGTTC 42266 _ C _		
			GAA GGG GGTGG TGGTGGTG		
			CTT CCC CCACC ATTACCAC		
			G _ C		
GAM178	MADH3	3'	CACCACCGGCACCCTCCC 12522 C_ G		
			GGG GGTG TGGTGGTG		
			CCC CCAC GCCACCAC		
			TC G		
GAM178	MAPRE2	3'	CACCACTGCCACCACCCCTCTT 15545 A C TG		
	TT		AAAAGA GGG GGTGG GTGGTG		
			TTTTCT CCC CCACC CACCAC		
			C A GT		
GAM178	MAPT	5'	CACCACAGCCACCTTCT 12538 GC G		
			AGAAGG GGT GTGGTG		
			TCTTCC CCG CACCAC		
			A_ A		
GAM178	MAPT	5'	CACCACAGCCACCTTCT 18826 GC G		
			AGAAGG GGT GTGGTG		
			TCTTCC CCG CACCAC		
			A_ A		
GAM178	MAPT	5'	CACCACAGCCACCTTCT 18832 GC G		
			AGAAGG GGT GTGGTG		
			TCTTCC CCG CACCAC		
			A_ A		
GAM178	MAPT	5'	CACCACAGCCACCTTCT 18838 GC G		
			AGAAGG GGT GTGGTG		
			TCTTCC CCG CACCAC		
			A_ A		
GAM178	MFGE8	3'	CACCACCACACAGTCACCCCTC 12557 A C _ _		
			GA GGG GG TG GTGGTGGTG		
			CT CCC CT AC CACCACCAC		
			C A G A		
GAM178	MPP3	5'	CACCTCCACCCCTTCTTCC 7641 A C T		
			A AAGAAGGG GGTGG GGTG		

			C TTCTTCCC CCACC CCAC			
			C _ T			
GAM178	MSI1	3'	CATCCCCACCCGCCCTCT 8283	A _ T		
			AGA GGGCGG TGG GGTG			
			TCT CCCGCC ACC CTAC			
			C C C			
GAM178	MYH11	3'	GCACCACCACCACCACCCTAC 8301	A C_		
	T		AG AGGG GGTGGTGGTGGTG C			
			TC TCCC CCACCACCACCAC G			
			A CA			
GAM178	MYH11	3'	GCACCACCACCACCACCCTAC 23143	A C_		
	T		AG AGGG GGTGGTGGTGGTG C			
			TC TCCC CCACCACCACCAC G			
			A CA			
GAM178	NLGN2	3'	CACCACCACCACGCGCCTGCCT 42549	AA _		
			AG GGGCG GTGGTGGTGGTG			
			TC TCCGC CACCACCACCAC			
			CG G			
GAM178	NRXN2	3'	CACTGTCCCCACCCTCCTTC 28981	C T TG		
			GAAGGG GGTGG GG GTG			
			CTTCCT CCACC CT CAC			
			C C GT			
GAM178	NRXN2	3'	CACTGTCCCCACCCTCCTTC 28987	C T TG		
			GAAGGG GGTGG GG GTG			
			CTTCCT CCACC CT CAC			
			C C GT			
GAM178	NRXN2	3'	CACTGTCCCCACCCTCCTTC 17465	C T TG		
			GAAGGG GGTGG GG GTG			
			CTTCCT CCACC CT CAC			
			C C GT			
GAM178	PYCR1	3'	CACCATCCTGCCACCACCTTCT 34729	GC _		
			AGAAGG GGTGGT GGTGGTG			
			TCTTCC CCACCG CTACCAC			
			A_ TC			
GAM178	RAD23B	5'	CACCCCCACCGCCTTCCT 8784	A T		
			AG AGGGCGGTGG GGTG			
			TC TTCCGCCACC CCAC			
			C C			
GAM178	RAD50	3'	CAGTACCCACCACCTTCTTCT 12293	C _ G		
			AGAAGGG GGTGGTGG TG TG			

			TCTTCTT CCACCACC AT AC		
			— C G		
GAM178	RAD50	3'	CAGTACCCACCACCTTCTTCT 28550	C	— G
			AGAAGGG GGTGGTGG TG TG		
			TCTTCTT CCACCACC AT AC		
			— C G		
GAM178	RNMT	3'	CACCACCCTACACCCCCTC 9880	A C	GT_
			GA GGG GGTG GGTGGTG		
			CT CCC CCAC CCACCAC		
			C _ ATC		
GAM178	RORB	5'	ACCACCAACTCCTCCTCCT 13785	A C	TGG
			AG AGGG GG TGGTGGT		
			TC TCCT CC ACCACCA		
			C _ TCA		
GAM178	SMOH	3'	CACCTCTAACCCCCTCCCCTC 12161	A C T	_ T
			GA GGG GG GGT GG GGTG		
			CT CCC CC CCA TC CCAC		
			C T C A T		
GAM178	ST7	3'	CACCACCAAACTGCTCCTCCT 22428	A A	_ GG
	CC		A AG AGG GCGGT TGGTGGTG		
			C TC TCC CGTCA ACCACCAC		
			C C T AA		
GAM178	SYNGR1	3'	CACCACCATCCCCCATC 11061	A C T	
			GA GGG GG GGTGGTGGTG		
			CT CCC CC CTACCACCAC		
			A _ _		
GAM178	TCF2	5'	CACCCCCTCACCCCCTTCTTTT 13199	C	T T
			AAAAGAAGGG GGTGG GG GGTG		
			TTTTCTTCCC CCACT CC CCAC		
			— C _		
GAM178	TCF2	5'	CACCCCCTCACCCCCTTCTTTT 6073	C	T T
			AAAAGAAGGG GGTGG GG GGTG		
			TTTTCTTCCC CCACT CC CCAC		
			— C _		
GAM178	TEM7	3'	CACCGCATCACCACCCCTTC 21670	C_	G
			GAAGGG GGTGGTG TGGTG		
			CTTCCC CCACTAC GCCAC		
			CA _		
GAM178	TGFB1	5'	CACCACTGCGCCCTTCT 6318	G TG	
			AGAAGGGC G GTGGTG		

TCTTCCCG C CACCAC
 _ GT
 GAM178 VANGL2 3' ACCAGCCACCCCTGTCCT 35475 T _
 AGGGCGG GGTGG TGGT
 ||||| |||| ||||
 TCCTGTC CCACC ACCA
 C G
 GAM178 WNT2 3' CACCATCCACCTTCCCTTC 9427 C_ _
 GAAGGG GGTGG TGGTG
 ||||| |||| ||||
 CTTCCC CCACC ACCAC
 TT T
 GAM178 BIKE 3' CACCACCACCACCACCTACTTC 19038 _ C
 GAAG GG GGTGGTGGTGGTG
 ||| || |||||
 CTTC CC CCACCACCACCAC
 AT A
 GAM178 BIRC4 3' CCACCACCCTTCCCTCT 6834 A C T
 AGA GGG GG GGTGGTGG
 ||| ||| || |||||
 TCT CCC TC CCACCACC
 _ T _
 GAM178 C20orf12 3' CACAGCCACCACCTCTCTCCT 19957 A C G
 AG AGGG GGTGGTGGT GTG
 || ||||| ||||| |||
 TC TCTC CCACCACCG CAC
 C T A
 GAM178 CAPN6 3' CACCACCACCACCACCACTC 15566 AG C
 GA GG GGTGGTGGTGGTG
 || || |||||
 CT CC CCACCACCACCAC
 CA A
 GAM178 DIO2 5' TTATCACCACCCCCCTTTT 15175 C
 AGAAGGG GGTGGTGGTGG
 ||||| |||||
 TTTTCCC CCACCACTATT
 C
 GAM178 DKFZP434H132 5' CACCACCCACCACCCCACTT 36444 C_ _
 AGGG GGTGGTGG TGGTG
 ||| ||||| ||||
 TCCC CCACCACC ACCAC
 ACC C
 GAM178 DKFZP434L0718 3' CACCACCATCTCTCTCCTCTT 25819 A C T
 AAGA GGG GG GGTGGTGGTG
 ||| ||| || |||||
 TTCT CCT TC CTACCACCAC
 _ C T
 GAM178 DKFZp547O146 5' TTAGAACCACCGCCCCTCT 21486 A GG
 AGA GGGCGGTGGT TGG
 ||| ||||| |||

			TCT CCCGCCACCA ATT		
			C AG		
GAM178	EFNA5	5'	CATCCCACGCTTCTTTT 7684	G T	
			AAAAGAAGG CGGTGG GGTG		
			TTTTCTTCC GCCACC CTAC		
			— —		
GAM178	FLJ00001	3'	CCACCGCCTCCCCTTTC 39774	C T	
			GAAGGG GG GGTGGTGG		
			CTTTCC CC CCGCCACC		
			— T		
GAM178	FLJ12076	3'	CACCACCACCCATGCCCTCT 24823	A GT	
			AGA GGGCG GGTGGTGGT		
			TCT CCCGT CCACCACCAC		
			C AC		
GAM178	FLJ12363	3'	CACCACGCCAGCCTTCCCTT 25865	C_ _ TG	
			AAGGG GG TGG GTGGTG		
			TTCCC CC ACC CACCAC		
			TT G CG		
GAM178	FLJ13441	3'	CACCACCTGGGAAGCCCTTCT 23391	GGT_	
			AGAAGGGC GGTGGTG		
			TCTTCCCG CCACCAC		
			AAGGGT		
GAM178	FLJ14594	3'	CACCACCTGCCCTCCTTCT 26565	C _	
			AGAAGGG GGT GGTGGTG		
			TCTTCCT CCG CCACCAC		
			C T		
GAM178	FLJ20898	3'	CACCACCAAGTCACTTCCC 23850	C _	
			GGG GGTGG TGGTGGTG		
			CCC TCACT ACCACCAC		
			T GA		
GAM178	FLJ21603	3'	ACCACCACTCCTACCTTTT 24118	CG TG	
			GAAGGG G GTGGTGGT		
			TTTTCC C CACCACCA		
			AT CT		
GAM178	FLJ22938	3'	ACCACCGCTCCCCCTCCT 23985	A C T	
			AG AGGG GG GGTGGTGGT		
			TC TCCC CC TCGCCACCA		
			C _ _		
GAM178	GW112	3'	CACCCCCACCAACCCCTTCT 13130	C _ T_	
			AGAAGGG GGT GGTGG GGTG		

			TCTTCCC CCA CCACC CCAC		
			_ A CC		
GAM178	HRH3	3'	CACCTGCACACCGTCCCTCT	14107	A _ _
			AGA GGGCGGTG GT GGTG		
			TCT CCTGCCAC CG CCAC		
			C A T		
GAM178	KIAA0446	3'	CACCACCACCACTGCCCATCTT	34146	A
			AAGA GGGCGGTGGTGGTGGTG		
			TTCT CCCGTCACCACCACCAC		
			A		
GAM178	KIAA0563	5'	CACCACACCCGGCCCCCCTTC	16840	C _ TG
			GAAGGG GGT GG GTGGTG		
			CTTCCC CCG CC CACCAC		
			C G CA		
GAM178	KIAA0630	3'	ACCACCTCTACCCCTTTC	43059	C T
			GAAGGG GGTGG GGTGGT		
			CTTTCC CCATC CCACCA		
			_ T		
GAM178	KIAA0773	3'	CACCACACACCTTCCTTCT	16193	C _
			AGAAGGG GGTG GTGGTG		
			TCTTCCT CCAC CACCAC		
			T A		
GAM178	KIAA0903	3'	TTACCACCACCACCTTTT	35371	C
			AGAAGGG GGTGGTGGTGG		
			TTTTCCC CCACCACCATT		
			A		
GAM178	KIAA1016	5'	CACCACCACCACCACATC	44084	A GC
			GA GG GGTGGTGGTGGTG		
			CT CC CCACCACCACCAC		
			A A_		
GAM178	KIAA1554	3'	CACTGCCACCCCTCTTTT	45609	C _ TG
			AGAAGGG GGTG G GTG		
			TTTTCTC CCAC C CAC		
			C C GT		
GAM178	KIAA1582	5'	CACCACCACCACCACCACT	32584	_ C
			AG GG GGTGGTGGTGGTG		
			TC CC CCACCACCACCAC		
			A A		
GAM178	KIAA1817	3'	CACCACCGCTGCCAACCCT	33861	C_ TG
			AGGG GG GTGGTGGTG		

			TCCC CC CGCCACCAC		
			AA GT		
GAM178	KIAA1853	3'	CACCACCACGACAGCCCTTC 34383	G G	
			GAAGGGC GT GTGGTGGTG		
			CTTCCCG CA CACCACCAC		
			A G		
GAM178	KIAA1940	5'	CACCACCACCATCACCACTGCT 39004	AAG C	
			AG GG GGTGGTGGTGGTG		
			TC CC CTACCACCACCAC		
			GCA A		
GAM178	MARCKS	5'	CACCACCCCCACCCCCCTC 8166	A C T	
			GA GGG GGTGG GGTGGTG		
			CT CCC CCACC CCACCAC		
			C _ C		
GAM178	MGC15619	5'	CACCATGCCCGGCCTTCT 26158	G TG	
			AGAAGG CGG GTGGTG		
			TCTTC GCC TACCAC		
			G CG		
GAM178	MGC20460	5'	CACCACCACGCTCTCTACCCT 27586	C_____	
	TC		GAAGGG GGTGGTGGTGGTG		
			CTTCCC CCGCCACCACCAC		
			ATCCT		
GAM178	MGC2744	5'	CACCACCACCGTGGTCT 30325	AGG	
			AGA GCGGTGGTGGTG		
			TCT TGCCACCACCAC		
			GG_		
GAM178	MGC3248	3'	CATCTACCACCCTCTCCT 26237	A C _	
			AG AGGG GGTGGTGG TG		
			TC TCCT CCACCATC AC		
			C C T		
GAM178	NIR3	3'	CACCACCTGCCTTCTCTT 32926	_ _	
			AAGA AGGGC GGTGGTG		
			TTCT TTCCG CCACCAC		
			C T		
GAM178	P2RX1	5'	CACCTGCACCGCCCTGCTCTT 33352	_	GT
			AAGA AGGGCGGTG GGTG		
			TTCT TCCCGCCAC CCAC		
			CG GT		
GAM178	PEG10	3'	CACCACCGCCGCGCCTCCATC 17424	A__	
	TT		AAGA GGGCGGTGGTGGTGGTG		

TTCT TCCGCCGCCGCCACCAC
 ACC
 GAM178 PTPNS1 3' CACCACCACCACCACCT 28050 _ C
 AG GG GGTGGTGGTGGTG
 || || |||||
 TC CC CCACCACCACCAC
 A A
 GAM178 RPS6KA4 3' CACCACTGTGACCCCTTC 10052 C G TG
 GAAGGG GGT G GTGGTG
 ||||| ||| | |||||
 CTTCCC CCA T CACCAC
 _ G GT
 GAM178 SCAMP-4 3' CACCGCCCACCACCTCCT 27819 C _
 GGG GGTGGTGG TGGTG
 ||| ||||| |||||
 TCC CCACCACC GCCAC
 T C
 GAM178 SCLY 3' CACCGCCCACCACCCCTCCTGC 18589 A _ C _
 T AG AGG G GGTGGTGG TGGTG
 || ||| | ||||| |||||
 TC TCC C CCACCACC GCCAC
 G T C C
 GAM178 SEPT3 3' CACCACCACAGCCCCTCT 21178 A G
 AGA GGGC GTGGTGGTG
 ||| ||| |||||
 TCT CCG CACCACCAC
 C A
 GAM178 SEPT3 3' CACCACCAACCACCTTCTTC 21177 C _
 GAAGGG GGTGGT GGTGGTG
 ||||| ||||| |||||
 CTTCTT CCACCA CCACCAC
 _ A
 GAM178 SIRPB1 3' CACCTCCACCACCCCTCCCT 12706 C__ T
 AGGG GGTGGTGG GGTG
 ||| ||||| |||||
 TCCC CCACCACC CCAC
 TCC T
 GAM178 SLC12A8 3' CACCACCACCACCCAGCTATTT 23893 G _
 TTT AAAGAA GGC GGTGGTGGTGGTG
 ||||| ||| |||||
 TTTTTT TCG CCACCACCACCAC
 A AC
 GAM178 SRPK1 3' CACTGACCCTCCGCCCTTC 9109 T_ _
 GAAGGGCGG GGT GGTG
 ||||| ||| |||||
 CTTCCCGCC CCA TCAC
 TC G
 GAM178 UST 3' CACCTCCCACTGCCCCTC 12270 A T_
 GA GGGCGGTGG GGTG
 || ||||| |||||

		CT CCCGTCACC CCAC		
		C CT		
GAM178	VELI1	5' CACCACCACCACCTTCCTTC	11037	C
		GAAGGG GGTGGTGGTGGTG		
		CTTCCT CCACCACCACCAC		
		T		
GAM178	LOC126823	5' ACCCCACCGCCCTCCCTCT	36863	___ T
		AGA AGGGCGGTGG GGT		
		TCT TCCCGCCACC CCA		
		CCC		
GAM178	LOC129303	5' CACCACCACCACCTGGGCTCCC	36969	AA ___
	CT	AG GGGC GGTGGTGGTGGTG		
		TC CTCG CCACCACCACCAC		
		CC GTC		
GAM178	LOC146108	3' CACCATGCCCAGCCTCCTTCT	38061	C _ TG
		AGAAGGG GG TGG GTGGTG		
		TCTTCCT CC ACC TACCAC		
		_ G CG		
GAM178	LOC146237	3' CACCACCACCACCACCTTC	40665	GC
		GAAGG GGTGGTGGTGGTG		
		CTTCC CCACCACCACCAC		
		A_		
GAM178	LOC146745	5' CTGCCACCACCCTCTCTCT	38231	_ C TG
		AGA AGGG GGTGGTGG G		
		TCT TCTC CCACCACC C		
		C _ GT		
GAM178	LOC147071	5' CACCACACCCGGCCCCCCTTC	36134	C _ TG
		GAAGGG GGT GG GTGGTG		
		CTTCCC CCG CC CACCAC		
		C G CA		
GAM178	LOC147669	5' CACCACCACCATCCCCCTCT	40853	A C
		AGA GGG GGTGGTGGTGGTG		
		TCT CCC CTACCACCACCAC		
		C _		
GAM178	LOC148255	5' CACCACCACCACCAGCACC	38498	_ _
		GG GC GGTGGTGGTGGTG		
		CC CG CCACCACCACCAC		
		A A		
GAM178	LOC148255	5' CACCACCACCACCAGCACC	38499	_ _
		GG GC GGTGGTGGTGGTG		

		CC CG CCACCACCACCAC			
		A A			
GAM178	LOC148709 5'	CACCACAGCGTCCTCCT	38578	A	G G
		AG AGGGCG TG TGGTG			
		TC TCCTGC AC ACCAC			
		C G _			
GAM178	LOC148946 5'	CACCACCGCCTCCGCTCT	40936		T
		AGGGCGG GGTGGTGGTG			
		TCTCGCC CCGCCACCAC			
		T			
GAM178	LOC149296 5'	CACCACCACCCAGGCCTCCT	38693	C	___
		GGG GGT GGTGGTGGTG			
		TCC CCG CCACCACCAC			
		T GAC			
GAM178	LOC151174 5'	CGCAGCCCCACCGCCCT	41310		T G
		AGGGCGGTGG GGT GTG			
		TCCCGCCACC CCG CGC			
		_ A			
GAM178	LOC162333 5'	CACCCCATCACCAACCCT	42126	C_	T
		AGGG GGTGGTGG GGTG			
		TCCC CCACTACC CCAC			
		AA _			
GAM178	LOC163412 5'	CACCACCACCGCCTCCTC	39951	A_	
		GA GGGCGGTGGTGGTG			
		CT TCCGCCACCACCAC			
		CC			
GAM178	LOC196027 3'	CACCACCACCTTTTTCTTTT	42304		C
		AAAAGAAGGG GGTGGTGGTG			
		TTTTCTTTT CCACCACCAC			
		T			
GAM178	LOC196955 5'	ACCACCATCACCTCCTCC	37926	A C	
		A GGG GGTGGTGGTGGT			
		C TCC CCACTACCACCA			
		C T			
GAM178	LOC197408 5'	ACCACCACCATCCACTCT	43206	C _	
		AGGG GG TGGTGGTGGT			
		TCTC CC ACCACCACCA			
		A T			
GAM178	LOC200251 5'	CACGCCACCCCTCCTTCT	42754	C	TG
		AGAAGGG GGTGG GTG			

			TCTTCCT CCACC CAC		
			C CG		
GAM178	LOC201173 5'	CACCACACCCGGCCCCCCTTC 42213		C _	TG
		GAAGGG GGT GG GTGGTG			
		CTTCCC CCG CC CACCAC			
		C G CA			
GAM178	LOC201220 5'	CACCACACCCGGCCCCCCTTC 42220		C _	TG
		GAAGGG GGT GG GTGGTG			
		CTTCCC CCG CC CACCAC			
		C G CA			
GAM178	LOC201243 5'	CTGCCACCACCCTCTCTCT 42553	_	C	TG
		AGA AGGG GGTGGTGG G			
		TCT TCTC CCACCACC C			
		C _ GT			
GAM178	LOC220739 3'	CACCACCACCCACTGCCC 44655		_	
		GGGCGGTGG TGGTGGTG			
		CCCGTCACC ACCACCAC			
		C			
GAM178	LOC253715 5'	CACCACTACCCATTCTTT 46310	_	C _	
		AAAGAA GGG G GTGGTG			
		TTTCTT CCC C CACCAC			
		A A T			
GAM178	LOC255565 5'	CACTCACCAGCCTCCTTCT 45590	C _	_	
		AGAAGGG GG TGGTG GTG			
		TCTTCCT CC ACCAC CAC			
		_ G T			
GAM178	LOC256273 3'	ACCACCACCTGCTTGCTC 46124	_	_	
		GGGCG GT GGTGGTGGT			
		CTCGT CG CCACCACCA			
		T T			
GAM178	LOC90525 3'	CACCACCACCACCCTCT 31638	C		
		AGGG GGTGGTGGTGGTG			
		TCTC CCACCACCACCAC			
		-			
GAM179	ACP1 5'	CCTTCCTCCTCCAGGTAC 10509	A	A	AAA
		GTAC CTGGAG AGGA AGG			
		CATG GACCTC TCCT TCC			
		- C -			
GAM179	ACP1 5'	CCTTCCTCCTCCAGGTAC 13959	A	A	AAA
		GTAC CTGGAG AGGA AGG			

			CATG GACCTC TCCT TCC		
			— C —		
GAM179	ADAM19	3'	CCCCTTTTCTTTCCAGTGCCCA 27094	TA	AA A
			TG CACTGGAG GGAAAA GGG		
			AC GTGACCTT TCTTTT CCC		
			CC — C		
GAM179	ADRB3	5'	CCCTCCTTCCTTCTTTCCCTAC 5459	CACT	AA
			GTA GGAGAAGGAA AGGG		
			CAT TTTCTTCCTT TCCC		
			CCC_ CC		
GAM179	ATP2A2	3'	CCAGATCCCTCTCCAGTGACA 7401	A	A AAAA
			TGT CACTGGAGA GGA GG		
			ACA GTGACCTCT CCT CC		
			— C AGA_		
GAM179	BHMT2	3'	CCCTTCCCTTCCAGCCCACA 19116	ACA	GA AAA
			TGT CTGGA AGG AAGGG		
			ACA GACCT TCC TTCCC		
			CCC — C_		
GAM179	BRCA1	3'	CCCTAGCCCCCCCCAGTGTGCA 14162		AGAA AAAA
			TGTACACTGG GG AGGG		
			ACGTGTGACC CC TCCC		
			CCC_ GA_		
GAM179	BRCA1	3'	CCCTAGCCCCCCCCAGTGTGCA 14168		AGAA AAAA
			TGTACACTGG GG AGGG		
			ACGTGTGACC CC TCCC		
			CCC_ GA_		
GAM179	BRCA1	3'	CCCTAGCCCCCCCCAGTGTGCA 14174		AGAA AAAA
			TGTACACTGG GG AGGG		
			ACGTGTGACC CC TCCC		
			CCC_ GA_		
GAM179	BRCA1	3'	CCCTAGCCCCCCCCAGTGTGCA 14180		AGAA AAAA
			TGTACACTGG GG AGGG		
			ACGTGTGACC CC TCCC		
			CCC_ GA_		
GAM179	BRCA1	3'	CCCTAGCCCCCCCCAGTGTGCA 14187		AGAA AAAA
			TGTACACTGG GG AGGG		
			ACGTGTGACC CC TCCC		
			CCC_ GA_		
GAM179	BRCA1	3'	CCCTAGCCCCCCCCAGTGTGCA 14193		AGAA AAAA
			TGTACACTGG GG AGGG		

			ACGTGTGACC CC TCCC		
			CCC_ GA__		
GAM179	BRCA1	3'	CCCTAGCCCCCCCAGTGTGCA 14199	AGAA	AAAA
			TGTACACTGG GG AGGG		
			ACGTGTGACC CC TCCC		
			CCC_ GA__		
GAM179	BRCA1	3'	CCCTAGCCCCCCCAGTGTGCA 14207	AGAA	AAAA
			TGTACACTGG GG AGGG		
			ACGTGTGACC CC TCCC		
			CCC_ GA__		
GAM179	BRCA1	3'	CCCTAGCCCCCCCAGTGTGCA 14213	AGAA	AAAA
			TGTACACTGG GG AGGG		
			ACGTGTGACC CC TCCC		
			CCC_ GA__		
GAM179	BRCA1	3'	CCCTAGCCCCCCCAGTGTGCA 14219	AGAA	AAAA
			TGTACACTGG GG AGGG		
			ACGTGTGACC CC TCCC		
			CCC_ GA__		
GAM179	DDX6	3'	CCTTTTAACCCAGTGTAC 10644	AGAAGGA	
			GTACACTGG AAAAGG		
			CATGTGACC TTTTCC		
			CAA_____		
GAM179	GALGT	3'	CCCTCCTTTTTCCAGTGCCCA 7209	TA	AAAA
			TG CACTGGAGAAGG AGGG		
			AC GTGACCTTTTTC TCCC		
			CC C__		
GAM179	HLF	3'	CCCTTTTTCCTAGTGGTGTCA 7902	T	GAGA
			TG ACACTG AGGAAAAAGGG		
			AC TGTGGT TCCTTTTCCC		
			_ GA__		
GAM179	MN1	3'	CCCTCTGATTCTGCAGTGTACA 8272	G	GGAAAA
			TGTACACTG AGAA AGGG		
			ACATGTGAC TCTT TCCC		
			G AGTC__		
GAM179	RARB	5'	CTTCCTCCCCCTCGAGTGTACA 18238	G	AA AA
			TGTACACT GAG GGA AAG		
			ACATGTGA CTC CCT TTC		
			G CC CC		
GAM179	RELN	3'	CCTTCTCAAGACCGAGTGTACA 45281	_	_____
			TGTACACT GG AGAAGG		

ACATGTGA CC TCTTCC
 G AGAAC
 GAM179 SCA7 3' CCCTCCTTCCTTTTACTA 5883 _ AA
 TGG AGAAGGAA AGGG
 ||| ||||| |||
 ATC TTTTCCTT TCCC
 A CC
 GAM179 SH3BP4 3' CCCTCTTCCTTCCTGGGTGTAC 15852 TG A AA
 GTACAC G GAAGGAA AGGG
 ||||| | ||||| |||
 CATGTG C CTTTCCTT TCCC
 GT _ C_
 GAM179 TMEM1 3' CCTGGGAGCCTTCCCCAGTGTA 9290 A AAAA_
 TACACTGG GAAGG AGG
 ||||| ||||| |||
 ATGTGACC CTTCC TCC
 C GAGGG
 GAM179 BNIP-S 3' CCTTTTTCCTTCTAAGTCA 28689 C GG
 A ACT AGAAGGAAAAAGG
 | ||| ||||| |||||
 A TGA TCTTCCTTTTCC
 C A_
 GAM179 C1QTNF6 3' CCCTTCCCCCTTCTTCTTGCT 25655 TA CT AAA_
 CA TG CA GGAGAAGG AAGGG
 || || ||||| |||||
 AC GT TCTCTTCT TTCCC
 TC _ CCCCC
 GAM179 C20orf110 3' CCCTCCCCTTCTCCTCCAGTA 38836 ACT_ AAAA
 TAC GGAGAAGG AGGG
 ||| ||||| |||
 ATG CCTCTTCC TCCC
 ACCT CC_
 GAM179 CHK 3' CCCTTCCTCCTGATGGAGTGTG 6944 GGAGA AA
 CA TGTACACT AGGA AAGGG
 ||||| ||| |||||
 ACGTGTGA TCCT TTCCC
 GGTA G CC
 GAM179 CITED2 3' CCCTCACTTTCTCCAGTGCTCA 12726 TA AAAA
 TG CACTGGAGAAGG AGGG
 || ||||| ||||| |||
 AC GTGACCTCTTTC TCCC
 TC AC_
 GAM179 CTPS2 3' CCCTCTGTTCTCCAGCAAACA 21261 ACA _ AAAA
 TGT CTGGAGAA GGA GGG
 ||| ||||| ||| |||
 ACA GACCTCTT TCT CCC
 AAC G ____
 GAM179 FLJ13782 3' CCCTCTCCTTCTCCATGGGCA 24436 TA C AAA
 TG CA TGGAGAAGGA AGGG
 || || ||||| ||||| |||

AC GT ACCTCTTCCT TCCC
 GG _ C_
 GAM179 JIK 3' CCCTTCCTCCCCCGTGTCA 18405 T T AGAA AA
 TG ACAC GG GGA AAGGG
 || ||| || ||| ||||
 AC TGTG CC CCT TTCCC
 _ C C_ CC
 GAM179 KCND1 5' CCTTTTCCTCCCTGTAG 11422 G A_
 CTG AG AGGAAAAAGG
 ||| || |||||
 GAT TC TCCTTTTCC
 G CC
 GAM179 KIAA0240 3' CCCTTTTCCTGTATTGTA 44406 CTGGAGA
 TACA AGGAAAAAGGG
 ||| |||||
 ATGT TCCTTTTCCC
 TATG_
 GAM179 KIAA0417 3' CTCTCTCCTTCCCCAGTGTACA 35288 A AAA
 TGTACACTGG GAAGGA AGGG
 ||||| |||| |||
 ACATGTGACC CTTCT TCTC
 C C_
 GAM179 KIAA1509 3' CCCCTCCAGGCCAGTGTGCA 30875 AGAA AAAA
 TGTACACTGG GGA GGG
 ||||| ||| |||
 ACGTGTGACC CCT CCC
 GGA_ C_
 GAM179 MGC1127 3' CCCTTCCCTTTTCCAG 27308 AAA
 CTGGAGAAGG AAGGG
 ||||| ||||
 GACCTTTTCC TTCCC
 C_
 GAM179 SP192 5' CCCTTCCCCCCTTTTAAATG 22295 CTG AAA_
 TA TACA GAGAAGG AAGGG
 ||| ||||| ||||
 ATGT TTTTCC TTCCC
 AAA CCCC
 GAM179 TESK2 3' CCAGACCCTCTCCAGTGTAC 31651 A AAAAA
 GTACACTGGAGA GG GG
 ||||| || |||
 CATGTGACCTCT CC CC
 C AGA_
 GAM179 LOC122830 3' CCCTTTTTCCTTACAGTAACA 36705 AC GAG
 TGT ACTG AAGGAAAAAGGG
 || ||| |||||
 ACA TGAC TTCCTTTTCCC
 A_ A_
 GAM179 LOC220846 5' CCCTCCTTCCTTCTTCCCTAC 43661 CACT AA
 GTA GGAGAAGGAA AGGG
 || ||||| |||

			CAT TTTCTTCCTT TCCC		
			CCC_ CC		
GAM179	LOC55580	5'	CCCTTCCTCCTCCTCCAG 18995	A	AA
			CTGGAG AGGA AAGGG		
			GACCTC TCCT TTCCC		
			C CC		
GAM179	LOC91948	3'	CCTTCCCCTCCAGTGCGCA 33573	TA	AA AAA
			TG CACTGGAG GGA AGG		
			AC GTGACCTC CCT TCC		
			GC C_ ____		
GAM180	PDE4D	3'	TACTGAACACAATAATGCTG 36434	____	A
			CAGCATTA TGT TAGTA		
			GTCGTAAT ACA GTCAT		
			AAC A		
GAM180	RPA1	3'	CTTTTCACTTCAATTAATGCTG 8854	TGTAT	A
			CAGCATTA AGT AAAAG		
			GTCGTAAT TCA TTTTC		
			TAACT C		
GAM180	SOS2	3'	CTTTTACAAATAATGCT 34000	GTATA	
			AGCATTAT GTAAAAAG		
			TCGTAATA CATTTTTC		
			AA____		
GAM180	TRAM	3'	TGCTTTCTACTATATCTTTCAG 15593	ATTAT_	A
	C		GC GTATAGTA AAAGCA		
			CG TATATCAT TTTCGT		
			ACTTTC C		
GAM180	TRIM14	3'	CTTTTACTTCTCAGTGC 16668	TA TAT	
			GCAT TG AGTAAAAAG		
			CGTG AC TCATTTTTC		
			__ TCT		
GAM180	TRIM37	3'	TGCCTCTTACTATACGACTGTA 17618	____	AAA
	GTG		CATTAT GTATAGTAA GCA		
			GTGATG CATATCATT CGT		
			TCAG CTC		
GAM180	YWHAG	3'	GCTTTTTAGAATAATGC 14857	GTATAG	
			GCATTAT TAAAAAGC		
			CGTAATA ATTTTTCG		
			AG____		
GAM180	BLZF1	3'	CTTCCTATTTACATAATGT 9751	T	AA
			GCATTATGTA AGTA AAG		

			TGTAATACAT TTAT TTC		
			_ CC		
GAM180	DKFZP564D172	3'	CTTTTAAACACATAATGT 25752	ATAG	
			GCATTATGT TAAAAAG		
			TGTAATACA ATTTTTC		
			CAA_		
GAM180	FLJ10154	3'	TGCTACATCATAATGCTG 19746	TA_	
			CAGCATTATG TAGTA		
			GTCGTAATAC ATCGT		
			TAC		
GAM180	FLJ11996	5'	TGCCTTTTATGGATACATAATG 24533	A_ A	
	CT		AGCATTATGTAT GTAAAA GCA		
			TCGTAATACATA TATTTT CGT		
			GG C		
GAM180	KIAA1432	3'	TGCTTTTAAAAAATAAATGCT 33157	A ATAG	
			AGCATT TGT TAAAAAGCA		
			TCGTAA ATA ATTTTTCGT		
			_ AAAA		
GAM180	KIAA1946	3'	TGCCCTTTTATAATACATAAT 40121	A A_	
			ATTATGTAT GTAAAA GCA		
			TAATACATA TATTTT CGT		
			A CC		
GAM180	Spir-1	3'	TGCTTTTAAAAATAATGACT 32308 _	GTATAG	
			AG CATTAT TAAAAAGCA		
			TC GTAATA ATTTTTCGT		
			A AA__		
GAM180	TNRC6	3'	GCTCTCTACTATGCCTTGATG 34900	T_ AAA	
			CATTA GTATAGTA AGC		
			GTAGT CGTATCAT TCG		
			TC CTC		
GAM180	LOC143098	5'	TGCTCTCTGTACATGATACTG 37576	C TAAAA	
			CAG ATTATGTATAG AGCA		
			GTC TAGTACATGTC TCGT		
			A TC__		
GAM180	LOC220883	3'	CTTTTACGTTTGCAGATGC 43850	A TA_	
			GCATT TGTA GTAAAAAG		
			CGTAG ACGT CATTTTTC		
			_ TTG		
GAM180	LOC253981	3'	GCTTTTACTGGTTTATACTG 45867	T TA_	
			CA TATG TAGTAAAAAGC		

		GT ATAT GTCATTTTTCG		
		C TTG		
GAM180	LOC257464 3'	TACTTGAATACATAAGCTG 43168	A	___
		CAGC TTATGTAT AGTA		
		GTCG AATACATA TCAT		
		_ AGT		
GAM180	LOC55885 3'	TGCTTTTCTTTTACATAAT 20712	T_ T	
		ATTATGTA AG AAAAAGCA		
		TAATACAT TC TTTTTCGT		
		TT _		
GAM181	PIGC 5'	TCAACACAGCATGGAATTTCCA 8502	G CT AC A	
		TGGAAATT CC TG GT TTGA		
		ACCTTTAA GG AC CA AACT		
		_ T_ GA C		
GAM181	FLJ10408 5'	TGTCAAGGAGAATCTCCA 19851	A GC	
		TGGA ATT CCTTGACG		
		ACCT TAA GGA ACTGT		
		C GA		
GAM181	KIAA0350 3'	CAAGAAAAGGGCAGTCCCCA 30660	AA	GACGTA
		TGG ATTGCCCTT TTG		
		ACC TGACGGGAA AAC		
		CC AAG___		
GAM181	KIAA0892 3'	TGCTCAAGGCAATTTCCA 35174	C C	
		TGGAAATTGCC TTGA GTA		
		ACCTTTAACGG AACT CGT		
		- -		
GAM181	TRAF3 3'	ACTGCAAGGGCATTTTCCA 30039	T	AC
		TGGAAA TGCCCTTG GT		
		ACCTTT ACGGGAAC CA		
		T GT		
GAM181	LOC150245 3'	ACATCAGGAAGGGCAATTCCC 41159	A	___ C
		GG AATTGCCCT TGA GT		
		CC TTAACGGGA ACT CA		
		C AGG A		
GAM182	CACNA1C 5'	TTGATCAATATTTTCCAGTA 6383	AA	
		TACTGG AGGGTATTGATCAA		
		ATGACC TTTTATAACTAGTT		
		C_		
GAM182	FLJ11101 3'	TTAATGCTGCTTTTCCAGTA 20316		___
		TACTGGAAAGG GTATTGA		

			ATGACCTTTTC CGTAATT		
			GT		
GAM182	FYCO1	3'	TGACCAGCTCCTCCAGTCA 23715	T	AAG TA A
			A ACTGGA GG TTG TCA		
			A TGACCT CC GAC AGT		
			C ____ TC C		
GAM182	MKRN1	3'	GATCTAGCCTTTCCAGTA 15113		G TT
			TACTGGAAAGG TA GATC		
			ATGACCTTTCC AT CTAG		
			G ____		
GAM182	MKRN4	3'	GATCTAGCCTTTCCAGTATA 25042		G TT
			TATACTGGAAAGG TA GATC		
			ATATGACCTTTCC AT CTAG		
			G ____		
GAM182	MT01	3'	TTGATCAATACAACAGTATA 28603		GAAAGG
			TATACTG GTATTGATCAA		
			ATATGAC CATAACTAGTT		
			AA____		
GAM182	PPP1R10	3'	CAAACCCCTTTCCAGTAT 8574		TA
			ATACTGGAAAGGG TTG		
			TATGACCTTTCCC AAC		
			CA		
GAM182	STRIN	3'	TTGACCATAGTGTTTCCAGT 18398		G TAT A
			ACTGGAAAG G TG TCAA		
			TGACCTTTT T AC AGTT		
			G GAT C		
GAM182	TESK2	3'	CAGACCCTCTCCAGTGTA 31650		A A
			TATACTGGA AGGGT TTG		
			ATGTGACCT TCCCA GAC		
			C _		
GAM182	LOC150481	3'	TTGATCAATACCCGAGAAGTA 38983		GGAAA
			TACT GGGTATTGATCAA		
			ATGA CCCATAACTAGTT		
			AGAG_		
GAM182	LOC158191	3'	TTGATCAATACCGGAGAAGTA 39759		GGAAAG
			TACT GGTATTGATCAA		
			ATGA CCATAACTAGTT		
			AGAGG_		
GAM183	B4GALT6	3'	AGAAACGGGAAGCCACTA 30091	A	GT
			TAGT GCTTCC CGTTTTT		

ATCA CGAAGG GCAAAGA
 C ____
 GAM183 OTP 3' TGTAAGCAAGCCAC 25803 A CCGTC
 GT GCTT GTTTTTACA
 || ||| |||||
 CA CGAA CGAAAATGT
 C AA____
 GAM183 FLJ20160 3' GAGCAACAGAAGCTATTA 19257 C C
 TAGTAGCTTC GT GTTT
 ||||| || |||
 ATTATCGAAG CA CGAG
 A A
 GAM183 HMG17L1 3' TAAAAATGCAGAAGCTAT 22015 C T
 GTAGCTTC G CGTTTTTA
 ||||| | |||||
 TATCGAAG C GTAAAAAT
 A _
 GAM183 LOC123283 3' AAAAGCAGCAGCTACTA 37423 TCC C
 TAGTAGCT GT GTTTTT
 ||||| || |||||
 ATCATCGA CG CGAAAA
 ____ A
 GAM183 LOC143524 3' TAAAAACAGGTAAGCTGCTA 37629 _ GTC
 TAGTAGCTT CC GTTTTTA
 ||||| || |||||
 ATCGTCGAA GG CAAAAAT
 T A____
 GAM184 D10S170 3' AAATACCATTAGAAAATACT 11917 GTAC C
 AGTA TTC AATGGTATTT
 ||| ||| |||||
 TCAT AAG TTACCATAAA
 AA__ A
 GAM184 DPYD 3' AATACCATTCACTACTCA 30315 ACTTCC
 TGAGTAGT AATGGTATT
 ||||| |||||
 ACTCATCA TTACCATAA
 C_____
 GAM184 MYBL1 3' AATACCAAAATACTACT 32040 C CCAA
 AGTAGTA TT TGGTATT
 ||||| || |||||
 TCATCAT AA ACCATAA
 A _____
 GAM184 OTC 5' AAATAAATGGAAATAGTACTAC 6132 ____ ATGG
 TCA TGAGTAGTACT TCCA TATTT
 ||||| ||| |||
 ACTCATCATGA AGGT ATAAA
 TAA AA____
 GAM184 CASPR3 3' GCCTGGAAACACTACCA 27387 A AC AT
 TG GTAGT TTCCA GGT
 || |||| |||| |||

		AC CATCA AAGGT CCG	
		— CA —	
GAM184	KIAA1046	3' ATTGGAAGGAAATACTACTCA 17218	_____
		TGAGTAGTA CTTCCAAT	
		ACTCATCAT GAAGGTTA	
		AAAG	
GAM184	VDAC3	3' AAATACCACTGAAGAGGACAC 12201	A A _ A
		GT GT CTTC CA TGGTATTT	
		CA CA GGAG GT ACCATAAA	
		_ _ AA C	
GAM184	LOC143888	3' AATATTTTTTTAAAGCACTACTC 37664	A CC TG
	A	TGAGTAGT CTT AA GTATT	
		ACTCATCA GAA TT TATAA	
		C AT TT	
GAM184	LOC149271	5' AAATACCATTACCTCTATTCA 38672	TACTTCC
		TGAGTAG AATGGTATTT	
		ACTTATC TTACCATAAA	
		TCCA__	
GAM184	LOC149910	3' AAATACTGTAAAATCCTACTCA 38825	TACTTCCA
		TGAGTAG ATGGTATTT	
		ACTCATC TGTCATAAA	
		CTAAAA__	
GAM185	PLA2G2D	3' CTGCACAGTCTGGCCATGTGAC 14770	TA A__ AC
		GTCACA TGGC ACT GCAG	
		CAGTGT ACCG TGA CGTC	
		_ GTC CA	
GAM185	DKFZp761D221	3' TCTGGCCCTGCCATATGAACA 26059	CA ACTACG
		TGT CATATGGCA CAGA	
		ACA GTATACCGT GTCT	
		A_ CCCG__	
GAM185	KIAA0632	3' CTGCACACTCACATATGTGGCA 17807	GCAACTAC
		TGTCACATATG GCAG	
		ACGGTGTATAC CGTC	
		ACTCACA_	
GAM185	NDRG4	3' TCTGTCTCATAGCACATGTGAC 21700	ATG AACTAC
	A	TGTCACAT GC GCAGA	
		ACAGTGTA CG TGTCT	
		CA_ ATACTC	
GAM185	NDRG4	3' TCTGTCTCATAGCACATGTGAC 23215	ATG AACTAC
	A	TGTCACAT GC GCAGA	

			ACAGTGTA CG TGTCT	
			CA_ ATACTC	
GAM186	C1orf1	3'	TCTCTATTTTCAAAAAATACAA 6875	GTAT__
			TTGTATTTT ATAGAGA	
			AACATAAAA TATCTCT	
			AACTTT	
GAM186	CHST5	3'	TCTCTACTAAAAATGCAA 14441	GTATA
			TTGTATTTT TAGAGA	
			AACGTAAAA ATCTCT	
			ATC__	
GAM186	CYP4F3	3'	TCTCTACTAAAGTACAA 6593	TATA
			TTGTATTTTG TAGAGA	
			AACATGAAAT ATCTCT	
			C__	
GAM186	GGCX	3'	TTCTCTACTAAAAATACAA 6483	GTATA
			TTGTATTTT TAGAGAA	
			AACATAAAA ATCTCTT	
			ATC__	
GAM186	NR3C2	3'	CTTTTCTCTTGCCCCAAATCAC 6596	AT TATAT
	AA		TTGT TTTG AGAGAAAAG	
			AACA AAAC TCTCTTTTC	
			CT CCCGT	
GAM186	CCR6	3'	TCTCTACTAAAAATACAA 10578	GTATA
			TTGTATTTT TAGAGA	
			AACATAAAA ATCTCT	
			ATC__	
GAM186	CCR6	3'	TCTCTACTAAAAATACAA 25372	GTATA
			TTGTATTTT TAGAGA	
			AACATAAAA ATCTCT	
			ATC__	
GAM186	DKFZp761J139	5'	TTCTCTACTAAAATACAA 26038	TATA
			TTGTATTTTG TAGAGAA	
			AACATAAAAT ATCTCTT	
			C__	
GAM186	FLJ10656	3'	CTTTTCTCCACATACAGTGCAG 19989	TT ATA
			TTGTAT TGTAT GAGAAAAG	
			GACGTG ACATA CTCTTTTC	
			_ CAC	
GAM186	FLJ10751	3'	TTCTCTGATGTGCACAAACACA 20097	A _ _
	A		TTGT TTT TGTATAT AGAGAA	

		AACA AAA ACGTGTA TCTCTT	
		C C G	
GAM186	FLJ10751 3'	TTCTCTGATGTGCACAAACACA 20196	A _ _
	A	TTGT TTT TGTATAT AGAGAA	
		AACA AAA ACGTGTA TCTCTT	
		C C G	
GAM186	FLJ11710 5'	TCTCTACAAAAAATACAA 24277	GTATA
		TTGTATTTT TAGAGA	
		AACATAAAA ATCTCT	
		AAC__	
GAM186	FLJ12363 3'	TTCTCTACGTATAAAAAAATAC 25871	__ TA
	AA	TTGTATTT TGTA TAGAGAA	
		AACATAAA ATAT ATCTCTT	
		AAA GC	
GAM186	FLJ22054 3'	TTCTCTACTGAAAATACAA 45319	GTATA
		TTGTATTTT TAGAGAA	
		AACATAAAA ATCTCTT	
		GTC__	
GAM186	FLJ22167 3'	TCTCTACTAAAAATGCAA 23743	GTATA
		TTGTATTTT TAGAGA	
		AACGTAAAA ATCTCT	
		ATC__	
GAM186	FLJ31455 3'	TTCTCTACTGAAAATACAA 29580	GTATA
		TTGTATTTT TAGAGAA	
		AACATAAAA ATCTCTT	
		GTC__	
GAM186	HSA249128 3'	CTTTTCTCTACTTCCAAATCAC 19026	AT TATA
	AA	TTGT TTTG TAGAGAAAAG	
		AACA AAAC ATCTCTTTTC	
		CT CTTC	
GAM186	KIAA0408 3'	TCTCTGCTAAAAATACAA 16235	GTATA
		TTGTATTTT TAGAGA	
		AACATAAAA GTCTCT	
		ATC__	
GAM186	KIAA0798 3'	TCTCTGCTAAAAATACAA 16071	GTATA
		TTGTATTTT TAGAGA	
		AACATAAAA GTCTCT	
		ATC__	
GAM186	KIAA1950 3'	TTCTAAGAAAAACAAAATACAA 44494	ATATAG_
		TTGTATTTTGT AGAA	

			AACATAAAACA	TCTT		
			AAAAGAA			
GAM186	MGC11352	3'	TTCTCTACTAAAAATACAA	32357	GTATA	
			TTGTATTTT	TAGAGAA		
			AACATAAAA	ATCTCTT		
			ATC__			
GAM186	MRPL56	3'	TCTCTACTAAAAATGCAA	26659	GTATA	
			TTGTATTTT	TAGAGA		
			AACGTAAAA	ATCTCT		
			ATC__			
GAM186	NTN4	3'	TTGTCTATGTACAAAACACAA	31516	A	G
			TTGT TTTTGTATATAGA	AA		
			AACA AAAACATGTATCT	TT		
			C	G		
GAM186	RNF11	3'	TTCTACATACAAAACACAG	15707	A	A
			TTGT TTTTGTAT	TAGAG		
			GACA AAAACATA	ATCTT		
			C	C		
GAM186	LOC116071	3'	TCCTGGATACAGAACACAA	28816	A	A A
			TTGT TTTTGTAT	TAG GA		
			AACA AAGACATA	GTC CT		
			C	G	_	
GAM186	LOC159036	3'	TTCTCTACTAAAAATACAA	42055	GTATA	
			TTGTATTTT	TAGAGAA		
			AACATAAAA	ATCTCTT		
			ATC__			
GAM186	LOC196540	3'	TTCTCTACTAAAAATACAA	43152	GTATA	
			TTGTATTTT	TAGAGAA		
			AACATAAAA	ATCTCTT		
			ATC__			
GAM186	LOC220662	3'	TCTCTACTAAAAATACAA	43826	GTATA	
			TTGTATTTT	TAGAGA		
			AACATAAAA	ATCTCT		
			ATC__			
GAM186	LOC221178	3'	CTTTTCTACTAACAAAATACAA	44929	ATA	A
			TTGTATTTTGT	TAG GAAAAG		
			AACATAAAACA	ATC TTTTTC		
			__	A		
GAM186	LOC221490	5'	CTTTTCTCTACATACAGTGC	44986	TT	A
			GTAT TGTAT	TAGAGAAAAG		

			CGTG ACATA ATCTCTTTTC	
			— C	
GAM186	LOC254100	3'	TTCTCTACTAAAAATACAA 46130	GTATA
			TTGTATTTT TAGAGAA	
			AACATAAAA ATCTCTT	
			ATC—	
GAM186	LOC255328	3'	TTCTCTACTAAAAATGCAA 46181	GTATA
			TTGTATTTT TAGAGAA	
			AACGTAAAA ATCTCTT	
			ATC—	
GAM186	LOC90072	3'	TCTCTACTAAAAATACAA 30730	GTATA
			TTGTATTTT TAGAGA	
			AACATAAAA ATCTCT	
			ATC—	
GAM186	LOC92267	3'	TTCTCTACTAAAAAATACAA 34060	GTATA
			TTGTATTTT TAGAGAA	
			AACATAAAA ATCTCTT	
			AAATC	
GAM187	ANK1	3'	AATGCTGCAGTCTGCAC 5475	TACA
			GTGTA ACTGCAGCATT	
			CACGT TGACGTCGTAA	
			C—	
GAM187	ANK1	3'	AATGCTGCAGTCTGCAC 21728	TACA
			GTGTA ACTGCAGCATT	
			CACGT TGACGTCGTAA	
			C—	
GAM187	ANK1	3'	AATGCTGCAGTCTGCAC 30278	TACA
			GTGTA ACTGCAGCATT	
			CACGT TGACGTCGTAA	
			C—	
GAM187	FGFRL1	3'	AATGCTGCCTTGACACAC 22448	ATA CT
			GTGT CAA GCAGCATT	
			CACA GTT CGTCGTAA	
			CA_ C_	
GAM187	GALNT2	3'	GCAGCTGTACACGCTA 10800	AT A
			TAGCGTGT ACA CTGC	
			ATCGCACA TGT GACG	
			C_ C	
GAM187	UBE3A	3'	CTGTTAGGGTACATACGCTA 28361	A AACT
			TAGCGTGT TAC GCAG	

			ATCGCATA ATG TGTC		
			C GGAT		
GAM187	UBE3A	3'	CTGTTAGGGTACATACGCTA 28365	A	AACT
			TAGCGTGT TAC GCAG		
			ATCGCATA ATG TGTC		
			C GGAT		
GAM187	UBE3A	3'	CTGTTAGGGTACATACGCTA 6080	A	AACT
			TAGCGTGT TAC GCAG		
			ATCGCATA ATG TGTC		
			C GGAT		
GAM187	C12orf22	3'	GCTACAGTTGTGACTCACACT 25128	C	TA_ C
			AG GTG TACAAC TG AGC		
			TC CAC GTGTTGAC TCG		
			A TCA A		
GAM187	PNMA1	3'	CTGCAGTTACGGAGCTG 12645	G_	TACA
			TAGC TGTA ACTGCAG		
			GTCG GCAT TGACGTC		
			AG _		
GAM187	RNF8	3'	ATGCTGCAGTTAACAC 10093	ATAC	
			GTGT AACTGCAGCAT		
			CACA TTGACGTCGTA		
			A_		
GAM187	LOC256642	3'	AATGCTGCAACTTTTTTACACC 46079	C	TACAAC_
	TA		TAG GTGTA TGCAGCATT		
			ATC CACAT ACGTCGTAA		
			_ TTTTCA		
GAM188	AKT1	5'	GCACAGGGCCATCTGTCA 11652	AA	AT
			TGACAGAT CCCT TGT		
			ACTGTCTA GGGA ACG		
			CC C_		
GAM188	RAG1	3'	TCTACAAGTTTTCTGCCAA 6042	A	T CCTA
			TTG CAGA AAC TTGTAGA		
			AAC GTCT TTG AACATCT		
			C T _		
GAM188	FLJ10856	3'	CAGTACAGTTATTTGTCAA 20218	CC	
			TTGACAGATAAC TATTG		
			AACTGTTTATTG ATGAC		
			AC		
GAM188	KIAA0157	3'	ATCTACAATGTATATCTGACAA 25897	A	ACCC
			TTG CAGATA TATTGTAGAT		

			AAC GTCTAT GTAACATCTA		
			A AT__		
GAM189	C14orf1	3'	TCCAAGGGACAGGCAGTTCTTC 14030	CA_ A TT A	
		T	AGAAGAAT CT T CTT GA		
			TCTTCTTG GA A GAA CT		
			ACG C GG C		
GAM189	EGR3	3'	TCTAAGAAATCTATGTTCTCTGA 29959	AA CACT	
			TCAG GAAT ATTTCTTAGA		
			AGTC CTTG TAAAGAATCT		
			__ TATC		
GAM189	HYAL4	5'	CTGGGTTTCAGGTGATTCTCCTG 14593	A ATTT	
		A	TCAG AGAATCACT CTTAG		
			AGTC TCTTAGTGG GGGTC		
			C ACTT		
GAM189	PKIA	5'	AAGAAGTGACTTTTCTGA 13695	A ATT	
			TCAGAAGA TCACT TCTT		
			AGTCTTTT AGTGA AGAA		
			C __		
GAM189	POU2AF1	3'	AAGTTCAAGTGATTCTCCTG 12889	A ATTT	
			CAG AGAATCACT CTT		
			GTC TCTTAGTGA GAA		
			C ACTT		
GAM189	TERF1	3'	AGGTCAAGTGATTCTCCTG 18952	A ATT	
			CAG AGAATCACT TCT		
			GTC TCTTAGTGA GGA		
			C ACT		
GAM189	TIRAP	3'	CTAAAGAAGTGACTCACCTGA 27476	AA A ATT _	
			TCAG GA TCACT TCTT AG		
			AGTC CT AGTGA AGAA TC		
			CA C __ A		
GAM189	BIRC3	5'	TCTAAGAAATAAAAGTGCTTCT 33370	AAT __	
			AGAAG CACT ATTTCTTAGA		
			TCTTC GTGA TAAAGAATCT		
			__ AAA		
GAM189	DNAL4	3'	AAGAAGGAGATGATTCTTT 12304	_ A	
			GAAGAATCA CT TTTCTT		
			TTTCTTAGT GA GAAGAA		
			A G		
GAM189	FLJ10656	3'	AAATAGTGACTCCCTTGA 19987	AA A	
			TCAG GA TCACTATTT		

AGTT CT AGTGATAAA
 CC C
 GAM189 FLJ21240 3' TCTAAGCTGACCTAGTGATTCT 24280 A __ T_
 GCTGA TCAG AGAATCACTA TT CTTAGA
 |||| ||||| || |||||
 AGTC TCTTAGTGAT AG GAATCT
 G CC TC
 GAM189 FLJ21302 3' CTGGGTTCAAGCAATTCTTCTG 23184 CA ATTT
 A TCAGAAGAAT CT CTTAG
 ||||| || |||||
 AGTCTTCTTA GA GGGTC
 AC ACTT
 GAM189 KIAA0931 3' GAACAGTGTA CTCTTCTGA 33484 AT_ A
 TCAGAAGA CACT TTT
 ||||| ||| |||
 AGTCTTCT GTGA AAG
 CAT C
 GAM189 KIAA1348 3' CTAAGAAATTATCTTTTGA 34028 ATCACT
 TCAGAAGA ATTTCTTAG
 ||||| |||||
 AGTTTTCT TAAAGAATC
 AT____
 GAM189 NXN 3' AAGGTTCAAGTGATTCTCCTG 22804 A ATT_
 CAG AGAATCACT TCTT
 || ||||| |||
 GTC TCTTAGTGA GGAA
 C ACTT
 GAM189 LOC147299 5' TCTAAGAAATATTTTCTT 38334 TCAC
 AAGAA TATTTCTTAGA
 |||| |||||
 TTCTT ATAAAGAATCT
 TT__
 GAM189 LOC152627 5' AGATAGTGATTCCTCTGA 39293 A
 TCAGA GAATCACTATTT
 |||| |||||
 AGTCT CTTAGTGATAGA
 C
 GAM189 LOC221395 3' GAAATATGATCCTCCTGA 44183 A A C
 TCAG AG ATCA TATTC
 ||| || ||| |||||
 AGTC TC TAGT ATAAAG
 C C _
 GAM189 LOC222001 3' TCTAAACAGGCTTAATGATTCT 44640 C TT ____
 TC GAAGAATCA TA TCT TAGA
 ||||| || ||| |||||
 CTTCTTAGT AT GGA ATCT
 A TC CAA
 GAM189 LOC222070 5' AAGAACTGATGAATTTTCTGA 45174 A C _
 TCAGAAGA TCA TA TTTCTT
 ||||| ||| || |||||

			AGTCTTTT AGT GT AAAGAA		
			A A C		
GAM189	LOC255326	3'	CTATGATAATGATTCTTCTGG 46105	C	TCT
			TCAGAAGAATCA TATT TAG		
			GGTCTTCTTAGT ATAG ATC		
			A T__		
GAM190	BCL11A	3'	ATTGCATTTTACGCAAACCTTTG 23152	T C	ATTGT
	A		TCAA GT TG AATGCAAT		
			AGTTT CA AC TTACGTTA		
			_ A GCATT		
GAM190	CDT6	3'	TGCATCTGGCGATCAGACTCTG 22120	AAT	A__
	A		TCA GTCTGATTGT ATGCA		
			AGT CAGACTAGCG TACGT		
			CT_ GTC		
GAM190	GFR	3'	ATTGCATGCTGCTCAGAC 14634	TT_	A
			GTCTGA GTA TGCAAT		
			CAGACT CGT ACGTTA		
			CGT _		
GAM190	HEMGN	5'	GCACCATCAGACACCTGA 20499	AA	T AAT
			TCA TGTCTGAT GT GC		
			AGT ACAGACTA CA CG		
			CC C ____		
GAM190	KIAA0155	3'	ATTGCACCAAAGTACATTTGA 16001	_ GA	TAA
			TCAAATGT CT TTG TGCAAT		
			AGTTTACA GA AAC ACGTTA		
			T _ C__		
GAM190	USP25	3'	GCATGGCGCTCAGACATTT 15048	T	A
			AAATGTCTGA TGT ATGC		
			TTTACAGACT GCG TACG		
			C G		
GAM190	LOC200269	3'	TTAAAATCAGACATTTGA 42762		G
			TCAAATGTCTGATT TAA		
			AGTTTACAGACTAA ATT		
			A		
GAM191	CHS1	3'	ATGTTGTAGCAAACATTTCT 5525	_	TA
			AGAAATGTTT CTAT GACAT		
			TCTTTACAAA GATG TTGTA		
			C _		
GAM191	EP300	3'	TATGGAAGAGTTAAACATTTTC 7153	CT	AGA_
	T		AGAAATGTTT ATT CATA		

			TCTTTACAAA TGA GTAT	
			AT GAAG	
GAM191	GABPB1	3'	ATGTCTAATGTAACCTTCT 11760	AT TC
			AGAA GTT TATTAGACAT	
			TCTT CAA GTAATCTGTA	
			__ T_	
GAM191	LRP8	3'	ATGTGGGGGAAACATTTT 11004	ATTAG
			GAAATGTTTCT ACAT	
			TTTTACAAAGG TGTA	
			GG__	
GAM191	LRP8	3'	ATGTGGGGGAAACATTTT 27128	ATTAG
			GAAATGTTTCT ACAT	
			TTTTACAAAGG TGTA	
			GG__	
GAM191	MLLT2	3'	GTCTAGAAACATTTCT 12571	ATT
			AGAAATGTTTCT AGAC	
			TCTTTACAAAGA TCTG	

GAM191	NRXN1	3'	TATGTTGCTGGAACATTTCT 11223	TATTA
			AGAAATGTTTC GACATA	
			TCTTTACAAGG TTGTAT	
			TCG__	
GAM191	NRXN1	3'	TATGTTGCTGGAACATTTCT 28997	TATTA
			AGAAATGTTTC GACATA	
			TCTTTACAAGG TTGTAT	
			TCG__	
GAM191	PRDX3	3'	ATGTCTCAATGGAAACACTCT 36304	AA _
			AGA TGTTTCTATT AGACAT	
			TCT ACAAAGGTAA TCTGTA	
			C_ C	
GAM191	PSCD3	3'	ATGTCCAGAAGCATTTC 10423	ATTA
			GAAATGTTTCT GACAT	
			CTTTACGAAGA CTGTA	
			C__	
GAM191	RAG1	3'	ATGTCTTACTGAAACATTTT 6037	TATT
			GAAATGTTTC AGACAT	
			TTTTACAAAG TCTGTA	
			TCAT	
GAM191	RPS6KA5	3'	TATGTGATGAAAACATTTT 11144	C AG
			GAAATGTTT TATT ACATA	

			CTTTACAAA GTAG TGTAT		
			A _		
GAM191	SFRS7	3'	TATGAGAAATAGAAACATTTCT 29899	AGA	
			AGAAATGTTTCTATT CATA		
			TCTTTACAAAGATAA GTAT		
			AGA		
GAM191	SMARCA2	3'	TATGTCTACTGTAAACATTGCT 9034	A	C T
			AG AATGTTT TA TAGACATA		
			TC TTACAAA GT ATCTGTAT		
			G T C		
GAM191	SNX9	3'	ATGTCCTCAGCGACATTTCT 18328	T	ATTA
			AGAAATGTT CT GACAT		
			TCTTTACAG GA CTGTA		
			C CTC_		
GAM191	TAF1C	3'	ATGCCTAAGGGAGACATTT 12235	A	A
			AAATGTTTCT TTAG CAT		
			TTTACAGAGG AATC GTA		
			G C		
GAM191	C1QR1	3'	ATGTTCGGACTGGAAACATTTT 14331		_ TA
	T		AGAAATGTTTCTA T GACAT		
			TCTTTACAAAGGT G TTGTA		
			CA GC		
GAM191	FLJ22174	3'	ATGTCTAGCGGCGAACACTTC 22466	A	_ TA
			GAA TGTTT C TTAGACAT		
			CTT ACAAG G GATCTGTA		
			C C GC		
GAM191	KIAA0446	5'	TATGTCTAATAAATGATGTCCT 34154	A_	TC_
	CT		AGA ATGTT TATTAGACATA		
			TCT TGTA ATAATCTGTAT		
			CC TAA		
GAM191	KIAA1211	3'	ATGTCCAGTAGCATTCT 34160	TTT	A
			AGAAATG CTATT GACAT		
			TCTTTAC GATGA CTGTA		
			_ C		
GAM191	KLHL8	3'	ATGTCTAATGGAGTTCT 31475	ATGT	
			AGAA TTCTATTAGACAT		
			TCTT GAGGTAATCTGTA		
			_		
GAM191	POU4F2	3'	ATGTGATAGAGACATCTCT 10919	A	AG
			AGA ATGTTTCTATT ACAT		

		TCT TACAGAGATAG TGTA	
		C —	
GAM191	LOC152756 3'	TATGTCTAATGTTAGACATTTT 41551	C_
		GAAATGTTT TATTAGACATA	
		TTTTACAGA GTAATCTGTAT	
		TT	
GAM191	LOC196528 3'	ATGTCTAATAACCAGACTTC 42404	AT C_
		GAA GTTT TATTAGACAT	
		CTT CAGA ATAATCTGTA	
		— CCA	
GAM191	LOC219529 3'	TATGTGGAGAAACATTTT 44673	ATTAG
		GAAATGTTTCT ACATA	
		TTTTACAAAGA TGTAT	
		GG_	
GAM191	LOC221751 3'	ATGTCTAGCGCGAACACTTC 44188	A _TA
		GAA TGTTT C TTAGACAT	
		CTT ACAAG G GATCTGTA	
		C C GC	
GAM192	CLECSF5 3'	GTTGAGATCTTCATCCAA 14922	A GT
		TTGGATGAAGAT CT AC	
		AACCTACTTCTA GA TG	
		_ GT	
GAM192	NUMA1 5'	AGGACTGCAGCATCTTCATC 44880	A CA
		GATGAAGAT CTGTA TCCT	
		CTACTTCTA GACGT AGGA	
		C C_	
GAM192	ZNF146 5'	GATGTGGAAATATCTTCAGCCA 13994	A CTG_
	A	TTGG TGAAGATA TACATC	
		AACC ACTTCTAT GTGTAG	
		G AAAG	
GAM192	VI 3'	GGATGTATCCTCCAGCCAA 15108	A A ATACT
		TTGG TG AG GTACATCC	
		AACC AC TC TATGTAGG	
		G C C_	
GAM192	LOC152263 3'	AGGATGCACACATACTCATTCA 41482	AG AC A
	A	TTGGATGA AT TGT CATCCT	
		AACTTACT TA ACA GTAGGA	
		CA C_ C	
GAM192	LOC169966 3'	GATGTACAGTGAAGTATC 40165	AAGA
		GATG TACTGTACATC	

			CTAT GTGACATGTAG	
			GAA_	
GAM193	CDK10	3'	TGTGCAACCACTGCTTCTT 9768	A_ C
			AAGAAGCAG GT GTATG	
			TTCTTCGTC CA CGTGT	
			AC A	
GAM193	CDK10	3'	TGTGCAACCACTGCTTCTT 27557	A_ C
			AAGAAGCAG GT GTATG	
			TTCTTCGTC CA CGTGT	
			AC A	
GAM193	CHRNA3	3'	ATGACATACCTTGCTTCTT 6395	AGTC AC
			AAGAAGCAG GTATG CAT	
			TTCTTCGTT CATACT GTA	
			C_ A_	
GAM193	ELOVL4	3'	AATGGTCAAATCTCTCCACCTC 22927	AGCA TC A
	T		AGA GAG GT TGACCATT	
			TCT CTC TA ACTGGTAA	
			CCAC TC A	
GAM193	EML1	3'	AATGGTCACAGAATGCCTTTT 30036	A GAG GTA
			AAGA GCA TC TGACCATT	
			TTTT CGT AG ACTGGTAA	
			C A_ AC_	
GAM193	F2RL3	3'	GGATCAAACCTCTGCTTC 10083	CGTA _
			GAAGCAGAGT TGA CC	
			CTTCGTCTCA ACT GG	
			A_ A	
GAM193	IL1RN	3'	TGGTCACAGGACTCTGCCTC 6180	A GTA
			GA GCAGAGTC TGACCA	
			CT CGTCTCAG ACTGGT	
			C GAC	
GAM193	PXF	3'	ATGGTTACCCTGCTTCTT 8751	A CGTAT
			AAGAAGCAG GT GACCAT	
			TTCTTCGTC CA TTGGTA	
			C _	
GAM193	DCOHN	3'	ATGGTCATATATACTTGTT 25843	G C_
			AGCA AGT GTATGACCAT	
			TTGT TCA TATACTGGTA	
			_ TA	
GAM193	FLJ32334	3'	AATGGTCATAACAGTGCCTGTT 29363	A CG_
			AGCAG GT TATGACCAT	

			TTGTC CG	ATACTGGTAA		
			_ TGACA			
GAM193	KIAA1391	3'	AATGGTCATATCAAATGTTCTT	33402	G	GAGTC
			AAGAA CA	GTATGACCATT		
			TTCTT GT	TATACTGGTAA		
			_ AAC_			
GAM193	NY-REN-60	3'	AATGGTCACATGCCATCTCTTC	33316	C	GT_ A
			GAAG AGA	CGT TGACCATT		
			CTTC TCT	GTA ACTGGTAA		
			_ ACC C			
GAM193	SP329	5'	TCACACAACACTGCTTCT	25099	A	C A
			AGAAGCAG	GT GT TGA		
			TCTTCGTC	CA CA ACT		
			A A C			
GAM193	TESK2	3'	ATGGTCATGGCTGTTTC	31649	AGTCG	
			GAAGCAG	TATGACCAT		
			CTTTGTC	GTA CTGGTA		
			G_			
GAM193	LOC147622	5'	AATGGTATCTAACTCTGTTCT	40849	A	CGTATG
		T	AAG AGCAGAGT	ACCATT		
			TTC TTGTCTCA	TGGTAA		
			C	ATCTA_		
GAM193	LOC155435	3'	CAGCAGATTCTGCTTCTT	39569	GTA	
			AAGAAGCAGAGTC	TG		
			TTCTTCGTCTTAG	AC		
			ACG			
GAM194	AKAP13	3'	ACCAGAAGGGGAGGCCCTGGAA	14055	A	TA TG
			TTC CAG	TT TCCCTTCTGGT		
			AAG GTC	GG AGGGAAGACCA		
			_ CC _			
GAM194	CLC	3'	ACCAGAAGAGAAAATACTG	14907	G	C
			CAGTATTT	TC CTTCTGGT		
			GTCATAAA	AG GAAGACCA		
			_ A			
GAM194	FUT6	5'	ACCAGAAGAGAGCATCTG	5648	TATT	_ C
			CAG	TG TC CTTCTGGT		
			GTC	AC AG GAAGACCA		
			T_ G A			
GAM194	C20orf19	5'	ACCAGTTTCAGAATACTGTGAA	20541	GTCCCTT	
			TTCACAGTATTT	CTGGT		

AAGTGTCAATAAG GACCA
 ACTTT__
 GAM194 DKFZp434O0320 3' ACCAGAAAGGAACCGCCCTGT 40702 TA T C
 ACAG TT GT CCTTCTGGT
 ||| ||| |||||
 TGTC GA CA GGAAGACCA
 CC C A
 GAM194 FLJ12934 3' ACCAGCACTTACAAGCACTGTG 23173 A CCCTT
 AA TTCACAGT TTTGT CTGGT
 ||||| ||| |||
 AAGTGTCA GAACA GACCA
 C TTCAC
 GAM194 FLJ13441 5' ACCAGACAGACAGATACTGTGA 23389 CCT
 A TTCACAGTATTTGTC TCTGGT
 ||||| ||||| |||
 AAGTGTCA TAGACAG AGACCA
 AC_
 GAM194 FLJ20079 3' GGGGAGAAATACTATGAA 19175 C G
 TTCA AGTATTT TCCCT
 ||| ||||| |||
 AAGT TCATAAA AGGGG
 A G
 GAM194 KIAA0426 3' ACCAGAAATACATATTATGAA 16305 C T CCC
 TTCA AGTAT TGT TTCTGGT
 ||| ||||| ||| |||||
 AAGT TTATA ATA AAGACCA
 A C ____
 GAM194 KIAA1143 3' CTCTGGTACAGACAAATGCCAT 34074 CA _____ TTCT
 GAA CA GTATTTGTC CC G
 || ||||| || |
 GT CGTAAACAG GG C
 AC ACAIIT TCTT
 GAM194 SYNJ2 3' ACCAGAAAGAGACATCTATT 30941 TT C
 AGTA TGTC CTTCTGGT
 ||| ||| |||||
 TTAT ACAG GAAGACCA
 CT A
 GAM194 LOC220776 3' ACCAGAAAGGAACCTTCATCCTG 33928 T TT_ C
 CAG AT GT CCTTCTGGT
 ||| || |||||
 GTC TA CA GGAAGACCA
 C CTT A
 GAM194 LOC257239 5' ACCAGAAAGGAAGAACTCTGAA 46372 C A GTC
 TTCA AGT TTT CCTTCTGGT
 ||| ||| ||| |||||
 AAGT TCA AAG GGAAGACCA
 C _ AA_
 GAM194 LOC90594 3' ACCAGAAAGGAAACCCTATGAA 31773 C TA GTC
 TTCA AG TTT CCTTCTGGT
 ||| || ||| |||||

			AAGT TC AAA GGAAGACCA		
			A CC ____		
GAM195	COL10A1	3'	ATATTTCTGATGGTGCCTA 6105	AG C	
			TAGTGACCA GG AATAT		
			ATCACGTGGT TC TTATA		
			AG T		
GAM195	COX15	3'	AAGATATTGATGGCCCTA 10598	TA AGGG	
			TAGTG CCA CAATATCTT		
			ATCAC GGT GTTATAGAA		
			C_ A__		
GAM195	C20orf110	3'	AAGACTTCTTGGTACCTA 38830	T CAATA	
			TAG GTACCAAGGG TCTT		
			ATC CATGGTTCTT AGAA		
			_ C__		
GAM195	CGI-142	3'	GAAGTTGCCCTTAACCTA 18147	TACC A	
			TAGTG AAGGGCAAT TC		
			ATCAC TTCCCGTTG AG		
			CAA_ A		
GAM195	DIS3	3'	TAAGATATAAAATGGTACAC 17302	AGGGCA	
			GTGTACCA ATATCTTA		
			CACATGGT TATAGAAT		
			AAAA__		
GAM195	LOC153338	3'	AAGATATTTATTGTACAC 41607	C GGGC	
			GTGTAC AA AATATCTT		
			CACATG TT TTATAGAA		
			_ AT__		
GAM195	LOC202781	3'	ATTACTCTGCGGTACCTA 43444	A_ C	
			TAGTGACC AGGG AAT		
			ATCACATGG TCTC TTA		
			CG A		
GAM196	ATP8B2	5'	TTCTGCAGTTGATCC 32520	ACA	
			GGATCA ACTGTAGAA		
			CCTAGT TGACGTCTT		

GAM196	OCRL	3'	CTGTAATTGCCAAGTCCTCTAA 5819	CAA_ C	
			TTAGAGGAT CAA TGTA		
			AATCTCCTG GTT ATGTC		
			AACC A		
GAM196	OCRL	3'	CTGTAATTGCCAAGTCCTCTAA 7306	CAA_ C	
			TTAGAGGAT CAA TGTA		

			AATCTCCTG GTT ATGTC	
			AACC A	
GAM196	RAI3	3'	TCTAGGGGCCTGCTCCTCTAA 10114	T ACAA G
			TTAGAGGA CA CT TAGA	
			AATCTCCT GT GG ATCT	
			C CCG_ G	
GAM196	TDG	3'	CTGTGTGTTAATCCTCTAG 9206	C ACTG
			TTAGAGGAT AACA TAG	
			GATCTCCTA TTGT GTC	
			A GT__	
GAM196	BICD2	3'	TTCTACAGTCGTCGATTTTT 34854	A A
			GAGGATC AC ACTGTAGAA	
			TTTTTAG TG TGACATCTT	
			C C	
GAM196	C8orf13	3'	GCTGTTGCTGTCCTCTAA 39654	T A T
			TTAGAGGA CA CAAC GT	
			AATCTCCT GT GTTG CG	
			_ C T	
GAM196	DKFZp434D177	3'	TTCCAGTGATCATCCTCTAA 26011	CAACA TA
			TTAGAGGAT ACTG GAA	
			AATCTCCTA TGAC CTT	
			CTAG_ _	
GAM196	DKFZp761P1010	3'	GTTCTTGGAATCAATTCCTCTA 20479	TCAACAA T
	A		TTAGAGGA CTG AGAAC	
			AATCTCCT GGT TCTTG	
			TAACATA _	
GAM196	FLJ10535	3'	TCTTCAGAGCTAATCCTCTAA 19922	CAACAA T
			TTAGAGGAT CTG AGA	
			AATCTCCTA GAC TCT	
			ATCGA_ T	
GAM196	FLJ23186	3'	TTCTACAGTCTGGCTCTAA 30297	GA ACA
			TTAGAG TCA ACTGTAGAA	
			AATCTC GGT TGACATCTT	
			_ C_	
GAM196	KIAA0495	5'	TCCCCACTGTTGATCCTCTGA 31362	AC TA
			TTAGAGGATCAACA TG GA	
			AGTCTCCTAGTTGT AC CT	
			C_ CC	
GAM196	KIAA1126	3'	TCTATGCAACTTGATCCTCTAG 35611	CAACT
			TTAGAGGATCAA GTAGA	

			GATCTCCTAGTT TATCT		
			CAACG		
GAM196	MKP-7	3'	GGATTGTCAATCCTTTAA 33009	CA	_
			TTAGAGGAT ACAA CT		
			AATTCCTA TGTT GG		
			AC A		
GAM196	SCDGF-B	3'	TCTATTGTTCAATTCTCTAA 26984	CAAC	T
			TTAGAGGAT AAC GTAGA		
			AATCTCTTA TTG TATCT		
			AC__ T		
GAM196	SCDGF-B	3'	TCTATTGTTCAATTCTCTAA 24882	CAAC	T
			TTAGAGGAT AAC GTAGA		
			AATCTCTTA TTG TATCT		
			AC__ T		
GAM196	LOC145624	5'	TCTGCACTGATCCTCTA 40548	ACAAC	
			TAGAGGATCA TG TAGA		
			ATCTCCTAGT ACGTCT		
			C__		
GAM196	LOC199725	3'	TTTGCCTGTTGATCTCTAA 43244	G	ACT
			TTAGAG ATCAACA GTAGA		
			AATCTC TAGTTGT CGTTT		
			_ C__		
GAM196	LOC202459	3'	GTTTAAAGGCTGTCCAATCCTC 29816	CA_	A GTA
	TAA		TTAGAGGAT ACA CT GAAC		
			AATCTCCTA TGT GG TTTG		
			ACC C AAA		
GAM196	LOC257048	3'	CAGATGTTGAATCCTCTAA 46028	_	A
			TTAGAGGAT CAACA CTG		
			AATCTCCTA GTTGT GAC		
			A A		
GAM197	DIAPH2	3'	ATCTTAAATGTGTAAAGTCA 13559	GC	TA
			TGAC ACACATTTA AT		
			ACTG TGTGTAAAT TA		
			AA TC		
GAM197	FBXW1B	3'	TGGGTATTATGCAGTGC 27368	ACATT	
			GCAC TATAATACCCA		
			CGTG GTATTATGGGT		
			AC__		
GAM197	FBXW1B	3'	TGGGTATTATGCAGTGC 14666	ACATT	
			GCAC TATAATACCCA		

CGTG GTATTATGGGT
 AC____
 GAM197 FBXW1B 3' TGGGTATTATGCAGTGC 27378 ACATT
 GCAC TATAATACCCA
 ||| |||||
 CGTG GTATTATGGGT
 AC____
 GAM197 VHL 3' TGGGTATTTCTTGGCATGCATC 6164 C CA_ TTTAT
 GA GCA CA AATACCCA
 || ||| || |||||
 CT CGT GT TTATGGGT
 A ACG TCT____
 GAM197 ACTR1A 3' TGGATATGAGTGTGTGTGCA 31536 A ATAC
 TG CGCACACATTTATA CCA
 || ||||| |||
 AC GTGTGTGTGAGTAT GGT
 _ A____
 GAM197 CED-6 3' GGTATTATTCATGTGTCA 18432 C TT
 G ACACAT ATAATACC
 | |||| |||||
 A TGTGTA TATTATGG
 C CT
 GAM197 GABARAPL1 3' GGGGGAAATGTGTGTGTCA 25391 ATAATA
 TGACGCACACATTT CCC
 ||||| |||
 ACTGTGTGTGTAAA GGG
 GG____
 GAM197 MGC15396 3' TGAGTATTATGACAGTGTGCAT 27438 C AT C
 CA TGA GCACAC TTATAATAC CA
 ||| |||| ||||| ||
 ACT CGTGTG AGTATTATG GT
 A AC A
 GAM197 PELI1 5' GGTCTAAATGTGTATGTCA 21817 C TAAT
 TGACG ACACATTTA ACC
 |||| ||||| |||
 ACTGT TGTGTAAAT TGG
 A C____
 GAM197 LOC203411 3' ATTGTAACATGTGCTTCA 43565 C CA
 TGA GCACA TTTATAAT
 ||| |||| |||||
 ACT CGTGT AAATGTTA
 T AC
 GAM198 FLJ23516 3' GGA CTTAATTGATTGGTATATT 23747 A TA A
 GATA ACT AATCAATTAA TCC
 ||| ||| ||||| |||
 TTAT TGG TTAGTTAATT AGG
 A _ C
 GAM198 LOC148189 5' ATTTAATTGATTTC CAAGTT 38483 _
 AACTT AAATCAATTAAAT
 |||| |||||

TTGAA TTTAGTTAATTTA
 CC
 GAM199 CAT 3' TAACCCGCTCATCACTGGATGA 7487 _ G GC A
 A TTCA CC AGTGGTG CG GTTA
 |||| || ||||| || ||||
 AAGT GG TCACTAC GC CAAT
 A _ TC C
 GAM199 FLJ11101 3' ATTTTGCCACTACTCAGT 20313 C C
 AC GAGTGGTGGC GAGT
 || ||||| ||||
 TG CTCATCACCG TTTA
 A T
 GAM200 B4GALT4 3' TGCCCAGGTATGCCTTCCAG 9861 AC T
 CTGGA AGGCGT TCTGGGCA
 |||| |||| |||||
 GACCT TCCGTA GGACCCGT
 _ T
 GAM200 C14orf1 3' CCCAGAGGGCCTCCCCCAG 14028 AAC G
 CTGG AGGC TTTCTGGG
 |||| |||| |||||
 GACC TCCG GGAGACCC
 CCC _
 GAM200 EGF 5' TGCCCGGGCCATGCTCCAG 7689 A _ GTTT
 CTGGA CA GGC CTGGGCA
 |||| || |||| |||||
 GACCT GT CCG GGCCCGT
 C A _
 GAM200 FSTL3 3' TGCCCAGAAAAGTGCCCCTAG 12473 AACA _
 CTGG GGCG TTTCTGGGCA
 |||| |||| |||||
 GATC CCGT AAAGACCCGT
 C _ GA
 GAM200 IL1RN 3' TGCCCAGGCCTGCCTGTTCC 6179 TT
 GGAACAGGCG TCTGGGCA
 ||||| |||||
 CCTTGTCCGT GGACCCGT
 CC
 GAM200 INSR 3' CCCAGCCCTGTTCCAG 35154 C TTT
 CTGGAACAGG G CTGGG
 ||||| |||||
 GACCTTGTCC C GACCC
 _ _
 GAM200 ITGAL 3' TGCCCAGAACTGGACTCAG 7973 _ AA GCGT
 CTG G CAG TTCTGGGCA
 ||| |||| |||||
 GAC C GTC AAGACCCGT
 T AG _
 GAM200 JAG2 3' TGCCCAGAACGCCCGCTCCAG 8006 ACA T
 CTGGA GGCGTT CTGGGCA
 |||| |||| |||||

GACCT CCGCAA GACCCGT
 CGC _
 GAM200 JAM3 3' CCCAGAAGCCCTCAG 26553 GAAC C
 CTG AGG GTTTCTGGG
 ||| ||| |||||
 GAC TCC CGAAGACCC

 GAM200 LEF1 3' TGCCCAAACTGTCATCC 18392 ACA _ C
 GGA GGC GTTT TGGGCA
 ||| ||| ||| |||||
 CCT CTG CAAA ACCCGT
 A_ T _
 GAM200 MYO1E 5' GCCCAGAAGACTGCGTTCCAG 11442 A_ CG
 CTGGAAC GG TTTCTGGGC
 ||||| || |||||
 GACCTTG TC GAAGACCCG
 CG A_
 GAM200 NTSR1 3' TGCCCAAGGGCCACCAACCCCA 8372 AAC A C_ TC
 G CTGG GG GTT TGGGCA
 |||| || ||| |||||
 GACC CC CGG ACCCGT
 CCAA AC GA
 GAM200 PFAH1B1 3' TGCCCAGAGCACTACTCTCA 6013 T AC _ GTT
 C GGA AG GC TCTGGGCA
 | ||| || ||| |||||
 A TCT TC CG AGACCCGT
 C CA A _
 GAM200 PDK4 5' TGCCCAGACTCTTCACTCC 8477 AC_ C TT
 GGA AGG G TCTGGGCA
 ||| ||| | |||||
 CCT TTC C AGACCCGT
 CAC T_
 GAM200 PIK4CB 3' TGCCCAGCTCTACCCCTCCCAG 8513 AAC C TT_
 CTGG AGG GT CTGGGCA
 |||| ||| || |||||
 GACC TCC CA GACCCGT
 C_ C TCTC
 GAM200 PLEK 3' GCCCAGAGGAGCCCTATTCCA 8533 CA_ G
 TGGAA GGC TTTCTGGGC
 |||| ||| |||||
 ACCTT CCG GGAGACCCG
 ATC A
 GAM200 PTMS 5' GCCTCTGCCGCTCTTCCAG 8696 C TTTCT
 CTGGAA AGGCG GGGC
 ||||| |||| |||
 GACCTT TCCGC TCCG
 C CGTC_
 GAM200 RASGRP1 3' TGCCTGGGCACCTATTCACA 12303 _ C C TT TG
 TG GAA AGG GT C GGCA
 || ||| ||| || | |||

			AC CTT TCC CG G CCGT		
			A A A _ GT		
GAM200	REGL	3'	GCCCAGAAGGCACCAG 13257	AACAG G	
			CTGG GC TTTCTGGGC		
			GACC CG GAAGACCCG		
			A _ _ _		
GAM200	SELPLG	3'	TGCCCAGACCCCATTCCA 30020	CA C TT	
			TGGAA GG G TCTGGGCA		
			ACCTT CC C AGACCCGT		
			AC _ _ _		
GAM200	SLC12A7	3'	TGCCCAGAGCGTGTCCCAG 13375	A G GTT	
			CTGG ACA GC TCTGGGCA		
			GACC TGT CG AGACCCGT		
			C G _ _		
GAM200	SLC38A2	5'	GCCTTAGAACGCCTTTCCAG 21049	C CT	
			CTGGAA AGGCGTTT GGGC		
			GACCTT TCCGCAAG TCCG		
			_ AT		
GAM200	SYNGR1	3'	CACAGACGCTTGTTCCAG 11060	C	
			CTGGAACAGGCGTTT TG		
			GACCTTGTTGCGAGA AC		
			C		
GAM200	SYNGR1	3'	TGCCCAGGCTGCCCTGCCAG 11068	AA C T _	
			CTGG CAGG GT TCTGGGCA		
			GACC GTCC CG GGACCCGT		
			C _ _ TC		
GAM200	SYT4	5'	TGCCTCCTCCCTGTTCCAG 31293	CGTTTCT	
			CTGGAACAGG GGGCA		
			GACCTTGTCC TCCGT		
			CTCC _ _		
GAM200	TRIM9	3'	TGCCCACATGACCTGTTCC 27551	_ TTC	
			GGAACAGG CGT TGGGCA		
			CCTTGTCC GTA ACCCGT		
			A C _ _		
GAM200	TRPC1	3'	CCCAAACGGATCCTTCCCCAG 9305	AAC _ _ TC	
			CTGG AGG CGTT TGGG		
			GACC TCC GCAA ACCC		
			CCT TAG _ _		
GAM200	TRPV1	5'	TGCCGCTCACCTATTCCAG 28014	C C TTCTG	
			CTGGAA AGG GT GGCA		

			GACCTT TCC CA CCGT		
			A _ CTCG_		
GAM200	WHSC1	3'	TGCCCCGTTGCCTATCACAG 28453	_ AC	TTTCT
			CTG GA AGGCG GGGCA		
			GAC CT TCCGT CCCGT		
			A A_ TGC_		
GAM200	WHSC1	3'	TGCCCCGTTGCCTATCACAG 28470	_ AC	TTTCT
			CTG GA AGGCG GGGCA		
			GAC CT TCCGT CCCGT		
			A A_ TGC_		
GAM200	WHSC1	3'	TGCCCCGTTGCCTATCACAG 17189	_ AC	TTTCT
			CTG GA AGGCG GGGCA		
			GAC CT TCCGT CCCGT		
			A A_ TGC_		
GAM200	BCL2L1	3'	CCCCACACTTGTTCCAG 28892	C	TTCT
			CTGGAACAGG GT GGG		
			GACCTTGTTT CA CCC		
			A C_		
GAM200	BHMT	3'	CCCAGAGTCCTGCTCTCAG 7443	_ A	CGT
			CTG GA CAGG TTCTGGG		
			GAC CT GTCC GAGACCC		
			T C T_		
GAM200	C1orf16	3'	TGCCCATCTGCTGTCCCAG 16858	A G	TTTC
			CTGG ACAG CG TGGGCA		
			GACC TGTC GT ACCCGT		
			C _ CT_		
GAM200	C1QR1	3'	TGCCCAGGTGACCTGTTC 14340	CGTT	
			GAACAGG TCTGGGCA		
			CTTGTCC GGACCCGT		
			AGT_		
GAM200	C20orf28	3'	GCCTGGAGCACCTGCTCCAG 17720	A C T	TG
			CTGGA CAGG GTT C GGC		
			GACCT GTCC CGA G CCG		
			C A _ GT		
GAM200	CDC14B	3'	TGCCCAGGGTGCCCTGCCTCAG 27175	AA C _	
			CTGG CAGG GT TTCTGGGCA		
			GACT GTCC CG GGGACCCGT		
			CC _ T		
GAM200	CLSTN1	5'	GCTCGGAACCCACCCCAG 17257	AACA C T	
			CTGG GG GTT CTGGGC		

GACC CC CAA GGCTCG
 CCA_ _ _
 GAM200 CXYorf1 5' TGCCAAGTACCCTGCTCCAG 39914 A C TT G
 CTGGA CAGG GT CT GGCA
 |||| ||| || ||||
 GACCT GTCC CA GA CCGT
 C _ T_ A
 GAM200 DKFZp434G179 3' TGCCCAGGCTCCCAACCCAG 39043 AAC A C TT
 CTGG GG GT CTGGGCA
 ||| || |||||
 GACC CC CG GACCCGT
 CAAC T _
 GAM200 DKFZp566D133 3' CCCAGAGATTCTACCCAG 35544 AAC C
 CTGG AGG GTTTCTGGG
 ||| || |||||
 GACC TCT TAGAGACCC
 CA_ _
 GAM200 DKFZP586F1524 3' TGCCTACACCATGTTCCAG 17854 _ C TTCT
 CTGGAACA GG GT GGGCA
 ||||| || || ||||
 GACCTTGT CC CA TCCGT
 A A _
 GAM200 EPB41L1 3' TGCCCAGAAATTACCCCA 34946 AAC A C_
 TGG GG GTTTCTGGGCA
 ||| || |||||
 ACC CC TAAAGACCCGT
 _ AT
 GAM200 FLJ12229 5' CGGGAGGCCCGTCCCAG 24310 A A G
 CTGG AC GGC TTTCTG
 |||| || || ||||
 GACC TG CCG GAGGGC
 C C _
 GAM200 FLJ12529 3' TGCCCAGGGTCCTGCCCTCAG 24192 _ AA CGT
 CTG G CAGG TTCTGGGCA
 ||| || || |||||
 GAC C GTCC GGGACCCGT
 T CC T_
 GAM200 FLJ12688 3' CCCAGAGCCGTGCCCAG 36222 A_ A GTT
 CTGG AC GGC TCTGGG
 |||| || || ||||
 GACC TG CCG AGACCC
 CG _ _
 GAM200 FLJ14708 3' TGCCCAGGCCACTGGCCCCAG 26601 AA_ GCGTT
 CTGG CAG TCTGGGCA
 |||| || |||||
 GACC GTC GGACCCGT
 CCG ACC_
 GAM200 FLJ14855 3' CCCAGAAATTGAGCTTCAG 27059 AAC A _
 CTGG GGC GTTTCTGGG
 |||| || |||||

			GACT TCG TAAAGACCC		
			____ AGT		
GAM200	FLJ20069	3'	TGCCCAGATGTATACCCAG 19158	AACAG	TT
			CTGG GCG TCTGGGCA		
			GACC TGT AGACCCGT		
			CATA_ _		
GAM200	FLJ20232	3'	TGCCCGTTTGCCTGTTCC 21087	TTTC	
			GGAACAGGCG TGGGCA		
			CCTTGTCCGT GCCCGT		
			TT_		
GAM200	FLJ20294	3'	GCCCAGAGGATGATCCAG 19348	A	GGCGT
			CTGGA CA TTCTGGGC		
			GACCT GT GAGACCCG		
			A AG_		
GAM200	FLJ20507	3'	GCCCCCAGGCCACCTGCTCCGG 19514	A	C_ CT
			CTGGA CAGG GTTT GGGC		
			GGCCT GTCC CGGA CCCG		
			C AC CC		
GAM200	FLJ20507	3'	GCCCCCAGGCCACCTGCTCCGG 30222	A	C_ CT
			CTGGA CAGG GTTT GGGC		
			GGCCT GTCC CGGA CCCG		
			C AC CC		
GAM200	FTHFD	5'	TGCCCGGGACGCCCGCACCA 14479	AACA	T
			TGG GCGGTT CTGGGCA		
			ACC CCGCAG GGCCCGT		
			ACGC _		
GAM200	FYCO1	3'	CCCAGAACCACTCCTCCAG 23707	ACA	C _
			CTGGA GG GT TTCTGGG		
			GACCT CC CA AAGACCC		
			_ T CC		
GAM200	GDF10	5'	GCCCGGGTGCCTGCTCC 11410	A	TT
			GGA CAGGCG TCTGGGC		
			CCT GTCCGT GGGCCCG		
			C _		
GAM200	GMPPB	3'	TGCCCAGGGCTCCCCACCCAG 45820	AACA_	C T
			CTGG GG GTT CTGGGCA		
			GACC CC CGG GACCCGT		
			CACCC T _		
GAM200	HCCA2	5'	GCAGACACCTGTTCCA 33204	C	CTGG
			TGGAACAGG GTTT GC		

ACCTTGTCC CAGA CG
A ____

GAM200 IL14 5' TGCCTAGGGACACCTTTTCCAG 45706 C C TT
CTGGAA AGG GT CTGGGCA
||||| ||| || |||||
GACCTT TCC CA GATCCGT
T A GG

GAM200 ISL2 3' TGCTCAGGCCATTCCAG 35082 CA GTTT
CTGGAA GGC CTGGGCA
||||| ||| |||||
GACCTT CCG GACTCGT
A_ ____

GAM200 KCNB2 5' TGGAAATGCCTGCCCCAG 45965 AA
CTGG CAGGCGTTTCTG
||| |||||
GACC GTCCGTAAAGGT
CC

GAM200 KIAA0040 3' CCCAGAACTCACTTCTCAG 16095 _ CA C
CTG GAA GG GTTTCTGGG
||| ||| || |||||
GAC CTT CT CAAAGACCC
T CA _

GAM200 KIAA0237 3' TGCCCAGATGCTGCCTCAG 16457 GAAC _ T
CTG AGGC GT TCTGGGCA
||| ||| || |||||
GAC TCCG CG AGACCCGT
____ T T

GAM200 KIAA0415 3' TGCCCAGGTGTCCCCCCCAG 44478 AACA TT
CTGG GGCG TCTGGGCA
|||| ||| |||||
GACC CTGT GGACCCGT
CCCC _

GAM200 KIAA0469 3' TGGGGACACCTGTTCCAG 16898 C TT
CTGGAACAGG GT CTG
||||||| || |||
GACCTTGTCC CA GGT
A GG

GAM200 KIAA0495 5' GCCCCTCGGAGACCACTCCAG 31359 ACA GC ____
CTGGA G GTTTCT GGGC
||||| | ||||| |||
GACCT C CAGAGG CCCG
____ AC CTC

GAM200 KIAA0574 3' TGCCCAGAGCCTTCCTCCAG 34349 AC_ GTT
CTGGA AGGC TCTGGGCA
|||| ||| |||||
GACCT TCCG AGACCCGT
CCT ____

GAM200 KIAA0763 3' TGCCCCCGGCGCCTGCCAG 16972 AA TCT
CTGG CAGGCGTT GGGCA
||| ||||| |||

			GACC GTCCGCGG CCCGT		
			C_ CCC		
GAM200	KIAA0773	3'	TGCCCAGGTAGCCCCTCCCCAG 16195	AACA_ GTT	
			CTGG GGC TCTGGGCA		
			GACC CCG GGACCCGT		
			CCTCC AT_		
GAM200	KIAA0930	3'	CCCACGCCCAGTTCCAG 34914	A_ TTCT	
			CTGGAAC GCGT GGG		
			GACCTTG CCGCA CCC		
			AC _		
GAM200	KIAA0939	3'	CCCAGCCCTGTCCCAG 31059	A C TTT	
			CTGG ACAGG G CTGGG		
			GACC TGTCC C GACCC		
			C _		
GAM200	KIAA1014	3'	TGTCTTAACCCTGTTCCA 32571	C TCT	
			TGGAACAGG GTT GGGCA		
			ACCTTGTCC CAA TCTGT		
			_ T_		
GAM200	KIAA1297	5'	TGCCCAGAAGGCCACCCCCCAG 35722	AACA_ G	
			CTGG GGC TTTCTGGGCA		
			GACC CCG GAAGACCCGT		
			CCCCA _		
GAM200	KIAA1297	5'	TGCCCAGGAGCTGACTCCAG 35723	ACA GT	
			CTGGA GGC TTCTGGGCA		
			GACCT TCG AGGACCCGT		
			CAG _		
GAM200	KIAA1354	3'	TGCCCTGGTGCTGTTCCAG 30543	G TT T	
			CTGGAACAG CG TC GGGCA		
			GACCTTGTG GT GG CCCGT		
			_ _ T		
GAM200	KIAA1649	5'	GCCCAGAGGAAGTTCTCCAG 26107	ACA GT_	
			CTGGA GGC TTCTGGGC		
			GACCT TTG GAGACCCG		
			C_ AAG		
GAM200	KIAA1649	3'	CCCAGAGGAAGTTCTCCAG 33256	ACA GT_	
			CTGGA GGC TTCTGGG		
			GACCT TTG GAGACCC		
			C_ AAG		
GAM200	KIAA1656	3'	TGTTTCAGCGCCTGCTCCAG 32738	A TCT	
			CTGGA CAGGCGTT GGGCA		

GACCT GTCCGCGA TTTGT
 C C__
 GAM200 KIAA1870 5' CCCAGAAAACAGCTCCA 26708 ACAG _ _
 TGGA GC GTTT CTGGG
 |||| || |||| ||||
 ACCT CG CAAA GACCC
 ____ A A
 GAM200 KIAA1884 3' CCCAGCGGATGCCTATTCC 36294 C _
 GGAA AGGCGTTT CTGGG
 |||| |||| |||| ||||
 CCTT TCCGTAGG GACCC
 A C
 GAM200 KIAA1944 5' CCCAATGTCTGCTCCA 37227 A TTC
 TGGA CAGGCGT TGGG
 |||| |||| ||||
 ACCT GTCTGTA ACCC
 C ____
 GAM200 MAN1C1 5' TGCCCAGGGACCCCCATCCCGG 21646 AACAA C TT
 CTGG GG GT CTGGGCA
 |||| || || |||| ||||
 GGCC CC CA GACCCGT
 CTAC C GG
 GAM200 MGC19556 5' TGCCCAGTCTGGTGCCTGCCCC 27318 AA TTT__
 A TGG CAGGCG CTGGGCA
 || |||| || |||| ||||
 ACC GTCCGT GACCCGT
 CC GGTCT
 GAM200 MGC20460 5' CAGAAGCCTGTTCCAG 27587 GT
 CTGGAACAGGC TTCTG
 |||| |||| |||| ||||
 GACCTTGTCCG AAGAC

 GAM200 MICAL 5' TGCCCAGCTGCTGCCCTCCCCA 23011 AACAA _ TT
 G CTGG GGC GT CTGGGCA
 |||| || || |||| ||||
 GACC CCG CG GACCCGT
 CCTC T TC
 GAM200 My015 3' TGCCCAGATTTTGGTTTCCA 33108 CA G TT_
 TGGAA G CG TCTGGGCA
 |||| || || |||| ||||
 ACCTT T GT AGACCCGT
 __ G TTT
 GAM200 MYT1 3' CCCAGAAGTGTCCCAG 10875 AACAA
 CTGG GGCGTTTCTGGG
 |||| |||| |||| ||||
 GACC CTGTGAAGACCC

 GAM200 PCYT2 3' CCCAGCGCCTGGCTCCAG 8762 A_ TTT
 CTGGA CAGGCG CTGGG
 |||| |||| |||| ||||

			GACCT GTCCGC GACCC			
			CG ____			
GAM200	PIP5K2B	5'	CAGCGACGCCTGCCAG	28929	AA	T
			CTGG CAGGCGTT CTG			
			GACC GTCCGCAG GAC			
			C_ C			
GAM200	PIP5K2B	5'	CAGCGACGCCTGCCAG	9607	AA	T
			CTGG CAGGCGTT CTG			
			GACC GTCCGCAG GAC			
			C_ C			
GAM200	PISD	3'	CGGCTACCACCTGTTCCAG	15656	C_ TT	
			CTGGAACAGG GT CTG			
			GACCTTGTCC CA GGC			
			AC TC			
GAM200	PISD	3'	TGCCTGGAACCTGTCCCAG	15658	A CG TG	
			CTGG ACAGG TTTC GGCA			
			GACC TGTCC AAAG CCGT			
			C A_ GT			
GAM200	PME-1	3'	TGCCCAGGCACGCCATTTCCA	18234	CA T	
			TGGAA GCGT TCTGGGCA			
			ACCTT CCGCA GGACCCGT			
			TA C			
GAM200	PRAM-1	3'	TGCCCAGAACAGCGCTCC	34380	ACAG ____	
			GGA GCGT TTCTGGGCA			
			CCT CGCG AAGACCCGT			
			____ AC			
GAM200	PRO1163	5'	TGCCTGGGCGCCTACTCCA	20655	AC TT TG	
			TGGA AGGCGT C GGCA			
			ACCT TCCGCG G CCGT			
			CA _ GT			
GAM200	SLC39A3	3'	TGCCAGGACGGCCCCGTCCCA	29362	A A_ GT	
	G		CTGG AC GGC TTCTGGGCA			
			GACC TG CCG AGGACCCGT			
			C CC GC			
GAM200	TED	3'	GCCCAGAGCTCTCCAG	17918	ACA GTT	
			CTGGA GGC TCTGGGC			
			GACCT TCG AGACCCG			
			C_ ____			
GAM200	TSGA14	3'	TGCCCGTGTGCCTGTCCC	20796	A TTTC	
			GG ACAGGCG TGGGCA			

			CC TGTCCGT GCCCGT		
			C GT__		
GAM200	ZDHC2	5'	GCCCAGGAGCCCGTCCAG 18489	A A C	
			CTGGA C GG GTTTCTGGGC		
			GACCT G CC CGAGGACCCG		
			__ _		
GAM200	LOC115073	5'	TGCCCAAGGCAGAGCTGTTCCA 36243	GC__ C	
			G CTGGAACAG GTTT TGGGCA		
			GACCTTGTC CGGA ACCCGT		
			GAGA _		
GAM200	LOC115073	5'	TGCCCAGGGTGCCCTGCCCG 36244	AA C _	
			TGG CAGG GT TTCTGGGCA		
			GCC GTCC CG GGGACCCGT		
			C_ _ T		
GAM200	LOC123242	3'	GCCCAGAGTCCGTCCAG 37243	ACA GTT	
			CTGGA GGC TCTGGGC		
			GACCT CTG AGACCCG		
			GC_ _		
GAM200	LOC129138	3'	TGCCCATGTCTAATCCCAG 29020	AAC_ _ TTTC	
			CTGG AGG CG TGGGCA		
			GACC TCC GT ACCCGT		
			CTAA T _		
GAM200	LOC132235	5'	TGCCCAGAGTCATTCCCAG 37484	AACA GTT	
			CTGG GGC TCTGGGCA		
			GACC CTG AGACCCGT		
			CTTA _		
GAM200	LOC143310	3'	GCCCAGAAGTGGCCCG 37608	AA GGCG	
			CTGG CA TTTCTGGGC		
			GACC GT GAAGACCCG		
			CG _		
GAM200	LOC144317	5'	GCCCAGACGCTTGTC 37719	A TT	
			GG ACAGGCG TCTGGGC		
			CC TGTTGCG AGACCCG		
			C _		
GAM200	LOC144699	3'	TGCCCAGGGCTTGCTCCGG 37770	A C T	
			CTGGA CAGG GTT CTGGGCA		
			GGCCT GTCT CGG GACCCGT		
			C T _		
GAM200	LOC145717	5'	CCCAGTGGCCTCGTCCCAG 33191	A _ GTTT	
			CTGG AC AGGC CTGGG		

GACC TG TCCG GACCC
 C C GT__
 GAM200 LOC146520 5' TGCCCGTTTGCCCGTGCCAG 38189 A A TTTC
 CTGG AC GGCG TGGGCA
 ||| ||| |||||
 GACC TG CCGT GCCCGT
 G C TT__
 GAM200 LOC147664 3' TGCCCAGACCAGTTCC 38353 A CGTT
 GGAAC GG TCTGGGCA
 ||||| || |||||
 CCTTG CC AGACCCGT
 A ____
 GAM200 LOC148029 5' TGCCCAGAGCCTCTTGCCCCAG 38448 AA CGT
 CTGG CAGG TTCTGGGCA
 ||| ||| |||||
 GACC GTTC GAGACCCGT
 CC TCC
 GAM200 LOC149950 5' TGCCCAGAACATGATCTCAG 38841 _ A GGCGT
 CTG GA CA TTCTGGGCA
 ||| ||| |||||
 GAC CT GT AAGACCCGT
 T A AC__
 GAM200 LOC150245 3' TGCCCAGGCCACTCTCCAG 41165 ACA_ GTTT
 CTGGA GGC CTGGGCA
 |||| ||| |||||
 GACCT CCG GACCCGT
 CTCA ____
 GAM200 LOC152992 3' TGTCCGACGCCTGCCCA 39351 AA TCT
 TGG CAGGCGTT GGGCA
 || ||||| |||||
 ACC GTCCGCAG CCTGT
 CC ____
 GAM200 LOC154092 3' TGCCCAGAAGTCAAAGTCCAG 41682 ACA_ GT
 CTGGA GGC TTCTGGGCA
 |||| ||| |||||
 GACCT CTG AAGACCCGT
 GAAA ____
 GAM200 LOC158428 3' TGCCCAGAGAGCTGCCC 34923 AACA G
 GG GGC TTTCTGGGCA
 || ||| |||||
 CC TCG AGAGACCCGT
 CG__ _
 GAM200 LOC158434 5' TGCCTGGGCCTCCTGCTCCAG 41987 A CGTT TG
 CTGGA CAGG TC GGCA
 |||| ||| |||
 GACCT GTCC GG CCGT
 C TCC_ GT
 GAM200 LOC158515 5' TGCCCAGAGCCTATGTCC 40162 AC_ GTT
 GGA AGGC TCTGGGCA
 ||| ||| |||||

		CCT TCCG AGACCCGT		
		GTA ____		
GAM200	LOC161635 5'	TGCCCAGAACAGGTGGCCCAG	46186	AA GGC T
		CTGG CA GTT CTGGGCA		
		GACC GT CAA GACCCGT		
		CG GGA _		
GAM200	LOC195977 3'	CCCAGAGAACTGTTCC	42301	GCG
		GGAACAG TTTCTGGG		
		CCTTGTC AGAGACCC		
		A__		
GAM200	LOC199786 3'	TGCCACCGCCTTCTCCAG	42622	AC TTTC
		CTGGA AGGCG TGGGCA		
		GACCT TCCGC ACCCGT		
		CT C__		
GAM200	LOC200093 5'	TGCCAAGTACCCTGCTCCAG	31606	A C TT G
		CTGGA CAGG GT CT GGCA		
		GACCT GTCC CA GA CCGT		
		C _ T_ A		
GAM200	LOC200138 3'	TGCCTGGGCCCCATTCCAG	43280	CA C TT TG
		CTGGAA GG GT C GGCA		
		GACCTT CC CG G CCGT		
		AC _ _ GT		
GAM200	LOC200918 3'	TCCATGCCTGTCCCAG	42870	A TTTC
		CTGG ACAGGCG TGGG		
		GACC TGTCCGT ACCT		
		C ____		
GAM200	LOC205418 5'	GCCCAGATCAGCTGTCCAG	43598	A G GTT
		CTGGA CAG C TCTGGGC		
		GACCT GTC G AGACCCG		
		_ _ ACT		
GAM200	LOC220980 5'	TGGGAACGCCGCTCCAG	44741	ACA
		CTGGA GGCGTTTCTG		
		GACCT CCGCAAGGGT		
		CG_		
GAM200	LOC221751 5'	CCCAGGAGCCCCCAG	44189	AACA C
		CTGG GG GTTTCTGGG		
		GACC CC CGAGGACCC		
		C__ _		
GAM200	LOC245727 5'	CCCAGTGGCCTCGTCCCAG	43796	A _ GTTT
		CTGG AC AGGC CTGGG		

		GACC TG TCCG GACCC	
		C C GT__	
GAM200	LOC253001 3'	CCCCAGAGTCCGTCCAG 46059	ACA GTT
		CTGGA GGC TCTGGGC	
		GACCT CTG AGACCCG	
		GC_ _	
GAM200	LOC253070 5'	CCCAGCCCCACTCCTGTTCCA 46353	C TT_
		TGGAACAGG GT CTGGG	
		ACCTTGTCC CA GACCC	
		T CCC	
GAM200	LOC253805 3'	TGCCCAGGTCTGCCTACTCC 46138	AC TT
		GGA AGGCG TCTGGGCA	
		CCT TCCGT GGACCCGT	
		CA CT	
GAM200	LOC253959 3'	CCCAGAGATTCTACCCAG 45510	AAC C
		CTGG AGG GTTTCTGGG	
		GACC TCT TAGAGACCC	
		CA_ _	
GAM200	LOC254387 3'	TGCCCAGATGGGCTCTCCA 45489	ACA GTT
		TGGA GGC TCTGGGCA	
		ACCT TCG AGACCCGT	
		C_ GGT	
GAM200	LOC254532 5'	CCCAGAGCTTGGCGTTTCAG 46208	_ GTT
		CTGGAAC AGGC TCTGGG	
		GACTTTG TTCG AGACCC	
		CGG _	
GAM200	LOC255650 3'	CCCAGGAGCCCGCCAG 46248	AACA C
		CTGG GG GTTTCTGGG	
		GACC CC CGAGGACCC	
		CG_ _	
GAM200	LOC256158 5'	TGCCCAGGGCACCCCCAG 46633	AACA C T
		CTGG GG GTT CTGGGCA	
		GACC CC CGG GACCCGT	
		CC_ A _	
GAM200	LOC256248 5'	TGCCCAGAACTTAGGCCTCCA 46075	ACA GT_
		TGGA GGC TTCTGGGCA	
		ACCT CCG AAGACCCGT	
		_ GATTC	
GAM200	LOC256790 5'	CCCCAGAAGAGACCTCAG 45461	GAAC CG_
		CTG AGG TTTCTGGGC	

			GAC TCC GAAGACCCG	
			____ AGA	
GAM200	LOC89958	3'	CCCAGAAATGTCTCAG 30544	GAAC
			CTG AGGCGTTTCTGGG	
			GAC TCTGTAAAGACCC	

GAM200	LOC90362	5'	GCCCAGAAAAGCATCCA 31296	ACAG G
			TGGA GC TTTCTGGGC	
			ACCT CG AAAGACCCG	
			A__ A	
GAM200	LOC90678	3'	TGCCCAGGAGCCCCCATCC 28748	ACA C
			GGA GG GTTTCTGGGCA	
			CCT CC CGAGGACCCGT	
			ACC _	
GAM200	LOC90841	5'	TGCCCAGAAGGGCCCCA 32114	AACA G
			TGG GGC TTTCTGGGCA	
			ACC CCG GAAGACCCGT	
			____ G	
GAM200	LOC90925	3'	TGCCAGACACACCCTCCCCAG 32187	AACA C T G
			CTGG GG GT TCTGG CA	
			GACC CC CA AGACC GT	
			CCTC A C _	
GAM200	LOC91040	5'	TGCCAAGTACCCTGCTCCAG 32323	A C TT G
			CTGGA CAGG GT CT GGCA	
			GACCT GTCC CA GA CCGT	
			C _ T_ A	
GAM200	LOC91409	3'	TGCCCAGAGCACCCCTGCTC 32807	A C _
			GA CAGG GT TTCTGGGCA	
			CT GTCC CA GAGACCCGT	
			C _ C	
GAM200	LOC91663	5'	TGCTCTTACAGCCTGTTCCA 28754	GTTTCT
			TGGAACAGGC GGGCA	
			ACCTTGTCCG CTCGT	
			ACATT_	
GAM201	FCRH1	3'	AAACCATCCATGACCCCA 27496	AGA C
			TGG TTA GGATGGTTT	
			ACC AGT CCTACCAA	
			CC_ A	
GAM201	TRPM8	3'	AAACCACATCTCTACT 23512	TACGGA
			AGTGGAGAT TGGTTT	

		TCATCTCTA	ACCAAA		
		C_____			
GAM201	LOC154222 3'	AAACCATCCATTCACTG	41688	GATTAC	
		CAGTGGA	GGATGGTTT		
		GTCACCTT	CCTACCAAA		
		A_____			
GAM201	LOC221814 3'	ACCTGCTCCACAATCTCCAT	45089	AC T__	
		GTGGAGATT	GGA GGT		
		TACCTCTAA	CCT CCA		
		CA CGT			
GAM201	LOC91397 5'	AAAACCATCCTTAACCCCAT	32778	AGA C	
		GTGG	TTA GGATGGTTTT		
		TACC	AAT CCTACCAAAA		
		CC_ T			
GAM202	ARHGAP5 3'	ATTGTGAATAAAATTTTCT	37815	CGT	
		AGAGG	ATTTTATTCACAAT		
		TCTTT	TAAAATAAGTGTTA		
		T__			
GAM202	PRPF8 3'	ATTGTGAATAAGTGAATACAG	30675	GC _____	
		CTCTCA	GAGAG GTATTT TATTCACAAT		
		CTCTC	CATAAG ATAAGTGTTA		
		GA GTGA			
GAM203	CACNA2D2 3'	ACTGAAGGACCTGAGCTGGCCA	12646	A AAT C	
		TG CCAGCTTAG	TTCT CAGT		
		AC GGTCGAGTC	AGGA GTCA		
		C C_ A			
GAM203	FDX1 3'	CTGGAGAAATTATGACT	30259	C G	
		AG TTA	AATTTCTCCAG		
		TC AGT	TTAAAGAGGTC		
		_ A			
GAM203	BAG3 5'	AGAAGTTTCTAGCCGGCCA	10493	A A TA	
		TG CC GCT	GAATTTCT		
		AC GG CGA	TTTGAAGA		
		C C TC			
GAM203	FLJ21369 3'	ACTGGAGGACCAAGCTGGT	24183	AGAAT	
		ACCAGCTT	TTCTCCAGT		
		TGGTCGAA	AGGAGGTCA		
		CC_			
GAM203	MGC19556 3'	ACTGGAGAGGAAACTTGTCA	27311	C CTTAGAA	
		TGAC AG	TTTCTCCAGT		

ACTG TC GGAGAGGTCA
 T AAAA____
 GAM203 LOC90632 3' ACTGGAGAAATCAAAGTGATCA 31828 CCA A A
 TGA GCTT GA TTTCTCCAGT
 ||| ||| || |||||
 ACT TGAA CT AAAGAGGTCA
 AG_ A _
 GAM204 IL1RAPL1 5' GATTTTTCTGAATACGCA 15554 T C
 TG CGTAT CAGAAAAATT
 || ||| |||||
 AC GCATA GTCTTTTATAG
 _ A
 GAM204 LOC197322 5' TGATTGGAGTTCCGGATATGAC 43204 A AAA TG
 A TGTCGTATCC GAA T ATCA
 ||||| ||| | |||
 ACAGTATAGG CTT G TAGT
 C GA_ GT
 GAM204 LOC51313 3' TGATCAATTTTCCTCATGAC 18722 ATCC A
 GTCGT AG AAAATTGATCA
 ||| || |||||
 CAGTA TC TTTTAACTAGT
 C_ C
 GAM205 LARGE 3' CCAAAGTCACTCCTGTTTTG 11128 TTAATT A
 CAAA GGAGT ACTTTGG
 ||| ||| |||||
 GTTT CCTCA TGAAACC
 TGT_ C
 GAM205 LARGE 3' CCAAAGTCACTCCTGTTTTG 28600 TTAATT A
 CAAA GGAGT ACTTTGG
 ||| ||| |||||
 GTTT CCTCA TGAAACC
 TGT_ C
 GAM205 DKFZp434D177 3' CCAAAGTTATTTTAATCTAT 26008 TA
 AT ATTGGAGTAACTTTGG
 || |||||
 TA TAATTTTATTGAAACC
 TC
 GAM205 KIAA0895 3' CCAAAGTTATTTTATTTGA 44545 TAATT A
 TCAAAT GG GTAACCTTTGG
 ||| || |||||
 AGTTTA TT TATTGAAACC
 TT_ A
 GAM205 MGC13102 3' CCAACAGGGACTCCAATCAATC 26133 AA A AA _
 GGA TC ATT ATTGGAGT CT TTGG
 || ||| ||||| |||
 AG TAA TAACCTCA GA AACC
 GC C GG C
 GAM205 SCDGF-B 3' CCAAACCTACACCAATTAATTT 26981 A AC
 AAATTAATTGG GTA TTTGG
 ||||| ||| |||

			TTTAATTAACC CAT AAACC		
			A C_		
GAM205	SCDGF-B	3'	CCAAACTACACCAATTAATTT 24879	A	AC
			AAATTAATTGG GTA TTTGG		
			TTTAATTAACC CAT AAACC		
			A C_		
GAM205	LOC149010	3'	CCAAAGTTATTTTAATCTAT 38627	TA	
			AT ATTGGAGTAACTTTGG		
			TA TAATTTTATTGAAACC		
			TC		
GAM206	ACPT	3'	TCCCGAGGCTGCTCCAG 28044	A	ATT T
			CTGGA CAGTC TC GGA		
			GACCT GTCGG AG CCT		
			C _ C		
GAM206	ACPT	3'	TCCCGAGGCTGCTCCAG 28047	A	ATT T
			CTGGA CAGTC TC GGA		
			GACCT GTCGG AG CCT		
			C _ C		
GAM206	ADCY3	3'	TTCCAGAGCCCTCGTTCCA 10255	_	TCAT
			TGGAAC AG TTCTGGAA		
			ACCTTG TC GAGACCTT		
			C CC_		
GAM206	AKT1	3'	TTCTTGGTGACTGTCCCA 11655	A	TCT
			TGG ACAGTCATT GGA		
			ACC TGTCAGTGG CTT		
			C TT_		
GAM206	B3GNT3	3'	CCACCTGGTACTGTTCCAG 15532	C	TC_
			CTGGAACAGT ATT TGG		
			GACCTTGTC A TGG ACC		
			_ TCC		
GAM206	BACE	3'	TCCTGAAAAATGACTGTCCCA 29088	A	_ T
			TGG ACAGTCATT TC GGA		
			ACC TGTCAGTAA AG CCT		
			C AA T		
GAM206	BACE	3'	TCCTGAAAAATGACTGTCCCA 14420	A	_ T
			TGG ACAGTCATT TC GGA		
			ACC TGTCAGTAA AG CCT		
			C AA T		
GAM206	CCR2	3'	TCCAGAAAGCTCATCTCAG 6313	_	AC CA
			CTG GA AGT TTTCTGGA		

			GAC CT TCG AAAGACCT		
			T AC _		
GAM206	CD34	3'	TCCAGAAACGGCCATTTCAG 7536	ACA	A
			CTGGA GTC TTTCTGGA		
			GACTT CGG AAAGACCT		
			AC_ C		
GAM206	CD53	3'	TTCCAGAAAAAACTATCCAG 6170	AC	CA_
			CTGGA AGT TTTCTGGAA		
			GACCT TCA AAAGACCTT		
			A_ AAA		
GAM206	CENPB	3'	TCCAGAAGAAGGTCCAG 34464	A AG	AT
			CTGGA C TC TTCTGGA		
			GACCT G AG AAGACCT		
			_ GA _		
GAM206	DAZ	3'	TCAAGATGACTGCTTCA 10284	A	C
			TGGA CAGTCATTT TGG		
			ACTT GTCAGTAGA ACT		
			C _		
GAM206	DAZL	5'	CCAGAAGTGGTGCGCCA 33800	AA	G
			TGG CA TCATTTCTGG		
			ACC GT GGTGAAGACC		
			GC _		
GAM206	DGAT2	3'	TTCCAGCTTGCCCTGTTCTAG 26294	T_	TTT
			CTGGAACAG CA CTGGAA		
			GATCTTGTC GT GACCTT		
			CC TC_		
GAM206	DLG4	5'	TTCCAGAGACTATGTGCCCAG 7047	A_	GTCA
			CTGG ACA TTTCTGGAA		
			GACC TGT AGAGACCTT		
			CG ATC_		
GAM206	EGLN3	3'	TCCAGAAATTCCTGCAG 22619	GAA	TC
			CTG CAG ATTTCTGGA		
			GAC GTC TAAAGACCT		
			_ CT		
GAM206	EGLN3	3'	TCCAGAAATTCCTGCAG 27198	GAA	TC
			CTG CAG ATTTCTGGA		
			GAC GTC TAAAGACCT		
			_ CT		
GAM206	FUT1	3'	TTCCAGATGGCTGCCCCCAG 5646	AA_	TT
			CTGG CAGTCA TCTGGAA		

			GACC GTCGGT AGACCTT		
			CCC _		
GAM206	FUT9	3'	CCAGAAAAATGATTGTTTCA 33700		_
			TGGAACAGTCATT TCTGG		
			ACTTTGTTAGTAA AGACC		
			AA		
GAM206	GALNT2	3'	CCAAGATGACTGCTTCAG 10798	A	C
			CTGGA CAGTCATTT TGG		
			GACTT GTCAGTAGA ACC		
			C _		
GAM206	GPR63	5'	TTCCAGAATGTATTTCCA 25079	CAGT	T
			TGGAA CATT CTGGAA		
			ACCTT GTAA GACCTT		
			TAT_ _		
GAM206	GRM6	3'	TTCCAGAATTATTTATTCCA 6512	C	TCAT
			TGGAA AG TTCTGGAA		
			ACCTT TT AAGACCTT		
			A TATT		
GAM206	GUCY1A3	5'	TTCCAGAAGCAGGTTTCAG 31780	AGTCA	
			CTGGAAC TTTCTGGAA		
			GACTTTG GAAGACCTT		
			GAC_		
GAM206	GYPA	3'	TTCCAGAGGTGACATTC 42264	CA	
			GAA GTCATTTCTGGAA		
			CTT CAGTGGAGACCTT		
			A_		
GAM206	HOXA7	3'	TTCCAGAAAGTGATCACAG 13772	GAACA	_
			CTG GTCATTT CTGGAA		
			GAC TAGTGAA GACCTT		
			AC_ A		
GAM206	HOXC4	5'	TCCAGAAATGACGTCAG 15975	AACA	
			CTGG GTCATTTCTGGA		
			GACT CAGTAAAGACCT		
			G_		
GAM206	HPCAL1	5'	TCTGGGTTGGCTGTTCCAG 28639	TT	TG
			CTGGAACAGTCA TC GA		
			GACCTTGTCGGT GG CT		
			T_ GT		
GAM206	IRTA2	3'	TCCAAGTCTGTTTCAG 25298	T	TTTC
			CTGGAACAG CA TGGAA		

			GACTTTGTC GT ACCT		
			_ CA_		
GAM206	ITCH	3'	TTCCAGAAATCAGGTCTG 25564	_ _	
			CAG TC ATTTCTGGAA		
			GTC GG TAAAGACCTT		
			T AC		
GAM206	ITGA11	3'	TCCAGGCCTCTAGTTCCAG 14514	_ TCATT	
			CTGGAAC AG TCTGGA		
			GACCTTG TC GGACCT		
			A TCC_		
GAM206	KIP2	3'	TCCAGAAATGCTCCCCA 13089	AAC T	
			TGG AG CATTTCTGGA		
			ACC TC GTAAAGACCT		
			CC_ _		
GAM206	KRT16	5'	TCCAGAGGGTGTTCAG 45630	G ATT	
			CTGGAACA TC TCTGGA		
			GACCTTGT GG AGACCT		
			G _		
GAM206	LDOC1	3'	TTCCAGGAATAGCGCTCCAG 14693	ACA TC	
			CTGGA G ATTTCTGGAA		
			GACCT C TAAGGACCTT		
			CG_ GA		
GAM206	LZTR1	3'	TCCAGGCTGGCCTTCCAG 13640	CA TT	
			CTGGAA GTCA TCTGGA		
			GACCTT CGGT GGACCT		
			C_ C_		
GAM206	NYX	3'	TCCAGAGATGGCCCCAG 22889	AACA	
			CTGG GTCATTTCTGGA		
			GACC CGGTAGAGACCT		
			C_		
GAM206	OPA1	3'	TTCCAGAAATACAATGCTAG 28340	AACA C	
			CTGG GT ATTTCTGGAA		
			GATC CA TAAAGACCTT		
			GTAA _		
GAM206	OPA1	3'	TTCCAGAAATACAATGCTAG 28324	AACA C	
			CTGG GT ATTTCTGGAA		
			GATC CA TAAAGACCTT		
			GTAA _		
GAM206	OPA1	3'	TTCCAGAAATACAATGCTAG 28356	AACA C	
			CTGG GT ATTTCTGGAA		

			GATC CA TAAAGACCTT		
			GTAA _		
GAM206	OPA1	3'	TTCCAGAAATACAATGCTAG 28348	AACA C	
			CTGG GT ATTTCTGGAA		
			GATC CA TAAAGACCTT		
			GTAA _		
GAM206	OPA1	3'	TTCCAGAAATACAATGCTAG 28332	AACA C	
			CTGG GT ATTTCTGGAA		
			GATC CA TAAAGACCTT		
			GTAA _		
GAM206	PDGFB	5'	TTCCAGAAAATGTTGCA 8473	G GTCA	
			TG AACA TTTCTGGAA		
			AC TTGT AAAGACCTT		
			G A_		
GAM206	PRDM2	3'	TCAGGAAAACGTGTTCCA 14537	CA	
			TGGAACAGT TTTCTGG		
			ACCTTGTC AAGGACT		
			A_		
GAM206	PTGES	3'	CCAGAAATTCTGGCCCAG 11312	AA TC	
			CTGG CAG ATTTCTGG		
			GACC GTC TAAAGACC		
			CG T_		
GAM206	PTGIS	3'	CCAGAAGGCTGGGTCCAG 6668	A_ AT	
			CTGGA CAGTC TTCTGG		
			GACCT GTCGG AAGACC		
			GG _		
GAM206	PXMP3	5'	TTCCAGAGAATGTTTCAG 5860	GTCA	
			CTGGAACA TTTCTGGAA		
			GACTTTGT AGAGACCTT		
			A_		
GAM206	RIG	3'	CCAGATGGCTGCCCCAG 13105	AA TT	
			CTGG CAGTCA TCTGG		
			GACC GTCGGT AGACC		
			CC _		
GAM206	RNMT	3'	TCCAGGGTGACTCTCCA 9891	AC T	
			TGGA AGTCATT CTGGA		
			ACCT TCAGTGG GACCT		
			C_ _		
GAM206	SHC1	3'	TTCCAGAAGATGCCCTCCA 8972	ACA_ AT	
			TGGA GTC TTCTGGAA		

			ACCT TAG AAGACCTT		
			CCCG _		
GAM206	SLC1A1	3'	TCCAGGAGGACTGTTCTA 10380	A	
			TGGAACAGTC TTTCTGGA		
			ATCTTGTCAG GAGGACCT		
			-		
GAM206	SLC2A5	3'	TTCCAGAAATACCTGTCTAG 9001	A TC	
			CTGGA CAG ATTTCTGGAA		
			GATCT GTC TAAAGACCTT		
			- CA		
GAM206	SLC9A1	5'	CCAGAAAATTGCTTCCA 34856	- CA	
			TGGAA CAGT TTTCTGG		
			ACCTT GTTA AAAGACC		
			C _		
GAM206	SMARCC1	3'	TCCAGAAAGACCCAG 9042	AACA A	
			CTGG GTC TTTCTGGA		
			GACC CAG AAAGACCT		
			C _ _		
GAM206	STAR	3'	TTCCAGAAATATAGTCCA 5905	ACA C	
			TGGA GT ATTTCTGGAA		
			ACCT TA TAAAGACCTT		
			GA _ _		
GAM206	TAP2	3'	TTCAGAGCACACACTGTTCCAG 6143	CAT _	
			CTGGAACAGT TTCTGGA		
			GACCTTGTCAGAGACTT		
			CACAC		
GAM206	TJP1	3'	TTCCAAAGTACACTGTTTCA 9267	C _ C	
			TGGAACAGT ATTT TGGAA		
			ACTTTGTCA TGAA ACCTT		
			CA _		
GAM206	UBL1	3'	TTCATAATGACTTTCCA 9380	C TC	
			TGGAA AGTCATT TGGAA		
			ACCTT TCAGTAA ACTT		
			- T _		
GAM206	UNG	3'	TTCCAGAATCTGGCCCAG 9390	AA TCAT	
			CTGG CAG TTCTGGAA		
			GACC GTC AAGACCTT		
			CG T _		
GAM206	UNG	3'	TTCCAGAATCTGGCCCAG 28128	AA TCAT	
			CTGG CAG TTCTGGAA		

			GACC GTC AAGACCTT		
			CG T__		
GAM206	VDR	3'	CCAGGTGGCTGACCCAG	5945	AA TT
			CTGG CAGTCAT CTGG		
			GACC GTCGGTG GACC		
			CA _		
GAM206	ZNF74	3'	CCAGAAGGGCCACACTCCAG	9471	ACA__ A
			CTGGA GTC TTTCTGG		
			GACCT CGG GAAGACC		
			CACAC _		
GAM206	ABCC13	3'	TTCCAGAAACAGCCTCACAG	28974	_ ACA CA
			CTG GA GT TTTCTGGAA		
			GAC CT CG AAAGACCTT		
			A C__ AC		
GAM206	ALS2CR3	5'	TCCAGTCATGACTGTCCA	17414	A TT
			TGGA CAGTCAT CTGGA		
			ACCT GTCAGTA GACCT		
			_ CT		
GAM206	AP1GBP1	3'	TTCCAGAGACCACCTTCCCAG	27882	AACA CA
			CTGG GT TTTCTGGAA		
			GACC CA AGAGACCTT		
			CTTC CC		
GAM206	AP1GBP1	3'	TTCCAGAGACCACCTTCCCAG	27874	AACA CA
			CTGG GT TTTCTGGAA		
			GACC CA AGAGACCTT		
			CTTC CC		
GAM206	AP1GBP1	3'	TTCAGAGACCGTTCCA	14118	A ATT
			TGGAAC GTC TCTGGA		
			ACCTTG CAG AGACTT		
			C _		
GAM206	AP1GBP1	3'	TTCAGAGACCGTTCCA	27873	A ATT
			TGGAAC GTC TCTGGA		
			ACCTTG CAG AGACTT		
			C _		
GAM206	AP1GBP1	3'	TTCCAGAGACCACCTTCCCAG	14119	AACA CA
			CTGG GT TTTCTGGAA		
			GACC CA AGAGACCTT		
			CTTC CC		
GAM206	APPD	3'	TCCAGAAGCTGCCCAG	23604	AA CAT
			CTGG CAGT TTCTGGA		

			GACC GTCG AAGACCT		
			C_ _		
GAM206	C20orf164	5'	TTCCAGAATAGGCCACCCAG	38802	AACA AT
			CTGG GTC TTCTGGAA		
			GACC CGG AAGACCTT		
			CAC_ AT		
GAM206	C20orf177	3'	TCCAGAGAGGCACCCAG	31129	AACA A
			CTGG GTC TTTCTGGA		
			GACC CGG AGAGACCT		
			CCA_ _		
GAM206	COAS3	3'	TCCCTAACAACTGTTTCAG	29123	CA TCT
			CTGGAACAGT TT GGA		
			GACTTTGTCA AA CCT		
			AC TC_		
GAM206	COPS7B	3'	CCTGTTGGTACTGTTCCAG	22932	C TCT_
			CTGGAACAGT ATT GG		
			GACCTTGTCA TGG CC		
			_ TTGT		
GAM206	CSL4	3'	TTCCAGAAAAATCTTCCAG	18126	AC TCA
			CTGGA AG TTTCTGGAA		
			GACCT TC AAAGACCTT		
			_ TAA		
GAM206	DCAMKL1	3'	CCAGAAATGCTGCTTCCA	11113	_ T
			TGGAA CAG CATTTCTGG		
			ACCTT GTC GTAAAGACC		
			C _		
GAM206	DDX34	5'	CCAGAGATCACTGCAG	16159	GAA C
			CTG CAGT ATTTCTGG		
			GAC GTCA TAGAGACC		
			_ C		
GAM206	DKFZp434C0328	5'	TTCCAGAAAATGTTCC	19016	GTCA
			GGAACA TTTCTGGAA		
			CCTTGT AAAGACCTT		
			A_		
GAM206	DKFZP434H132	5'	TTCCAGAGGGCATGCCAG	36451	AACA AT
			CTGG GTC TTCTGGAA		
			GACC CGG GAGACCTT		
			GTA_ _		
GAM206	DKFZP434L1435	5'	TCCAGGGCCACGTTCCAG	46703	A CAT
			CTGGAAC GT TTCTGGA		

			GACCTTG CA GGGACCT		
			_ CC_		
GAM206	DKFZP434L1435	5'	TCCAGGGCCACGTTCCAG	44269	A CAT
			CTGGAAC GT TTCTGGA		
			GACCTTG CA GGGACCT		
			_ CC_		
GAM206	DKFZP434L1435	5'	TCCAGGGCCACGTTCCAG	46665	A CAT
			CTGGAAC GT TTCTGGA		
			GACCTTG CA GGGACCT		
			_ CC_		
GAM206	DKFZP564B147	5'	TTCCAGGAATAGCGCTCCAG	39937	ACA TC
			CTGGA G ATTTCTGGAA		
			GACCT C TAAGGACCTT		
			CG_ GA		
GAM206	DKFZP564I052	3'	CCAGAAATGACACTCACAG	33137	_ ACA
			CTG GA GTCATTTCTGG		
			GAC CT CAGTAAAGACC		
			A CA_		
GAM206	DNAJA2	3'	TTCATTTTGACTGTTCCA	30069	TTTC
			TGGAACAGTCA TGGA		
			ACCTTGTCAGT ACTT		
			TTT_		
GAM206	DOK4	3'	CCGGGGAATGACCACCCAG	19881	AACA _
			CTGG GTCATTTCT GG		
			GACC CAGTAAGGG CC		
			CAC_ G		
GAM206	DSCR1L1	3'	TTCCAGAATGCAGGTTCTA	12432	AGT T
			TGGAAC CATT CTGGAA		
			ATCTTG GTAA GACCTT		
			GAC _		
GAM206	EIF5	5'	TCCAGAGGTCGCCCAG	7699	AACA C
			CTGG GT ATTTCTGGA		
			GACC CG TGGAGACCT		
			_ C		
GAM206	FLJ10477	3'	TTAGAATAACTGTTCCA	19875	CAT
			TGGAACAGT TTCTGG		
			ACCTTGTC AAGATT		
			AT_		
GAM206	FLJ10781	3'	TTCTGCCGTGACTGTTT	20140	TTC
			GAACAGTCAT TGGA		

			CTTGTCA GTCTT		
			CC_		
GAM206	FLJ10898	5'	TTCCAGGACCTGGCCCAG	29895	AA TCAT
			CTGG CAG TTCTGGAA		
			GACC GTC AGGACCTT		
			CG C__		
GAM206	FLJ12221	3'	TTCCAGAAATCGACCCTCTA	31348	ACA _
			TGGA GTC ATTTCTGGAA		
			ATCT CAG TAAAGACCTT		
			CC_ C		
GAM206	FLJ12221	3'	TCCAAAGTGGCTGCCAG	31347	AA C
			CTGG CAGTCATTT TGGA		
			GACC GTCGGTGAA ACCT		
			C_ _		
GAM206	FLJ12294	5'	TTCCAAAAATACCCCAGTGT	24748	_____ C C
			CAG CTGGAACA GT ATTT TGGA		
			GACTTTGT CA TAAA ACCTT		
			GACCC _ A		
GAM206	FLJ12484	3'	TCCAGAACTTTGTTCTAG	23021	TCAT
			CTGGAACAG TTCTGGA		
			GATCTTGTT AAGACCT		
			TC_		
GAM206	FLJ12484	3'	TCCAGAACTTTGTTCTAG	34519	TCAT
			CTGGAACAG TTCTGGA		
			GATCTTGTT AAGACCT		
			TC_		
GAM206	FLJ12484	3'	TCCGGCTTGGCTGTTCCAG	23022	TTT
			CTGGAACAGTCA CTGGA		
			GACCTTGTCGGT GGCCT		
			TC_		
GAM206	FLJ12484	3'	TCCGGCTTGGCTGTTCCAG	34520	TTT
			CTGGAACAGTCA CTGGA		
			GACCTTGTCGGT GGCCT		
			TC_		
GAM206	FLJ12517	3'	CCAAGGATGCTGTTCTCAG	23267	_ T TC
			CTG GAACAG CATT TGG		
			GAC CTTGTC GTAG ACC		
			T _ GA		
GAM206	FLJ12707	3'	AGAAAAGTGACTGCTCCAG	22609	A _
			CTGGA CAGTCAT TTCT		

			GACCT GTCAGTG AAGA		
			C AA		
GAM206	FLJ13096	3'	TTAGAATACTGTTCCA 24569	CAT	
			TGGAACAGT TTCTGG		
			ACCTTGTCA AAGATT		
			T__		
GAM206	FLJ13984	3'	TTCCAGAAACCATTGCACCAG 24131	AA CA	
			CTGG CAGT TTTCTGGAA		
			GACC GTTA AAAGACCTT		
			AC CC		
GAM206	FLJ14457	5'	TCCAGAGAGATTCCCAG 26543	AAC A	
			CTGG AGTC TTTCTGGA		
			GACC TTAG AGAGACCT		
			C__ _		
GAM206	FLJ20051	3'	TCCAGAAGATAGACTTCAG 21164	AAC A__	
			CTGG AGTC TTTCTGGA		
			GA CT TCAG GAAGACCT		
			__ ATA		
GAM206	FLJ20508	3'	TTCCAGAACCTGCCACCAG 19521	AA_ TCAT	
			CTGG CAG TTCTGGAA		
			GACC GTC AAGACCTT		
			ACC C__		
GAM206	FLJ20984	3'	TTCTTTTGGTGACCCTCCAG 23896	ACA TCT	
			CTGGA GTCATT GGAA		
			GACCT CAGTGG TCTT		
			CC_ TTT		
GAM206	FLJ21302	3'	TTCCAGAGAGACATTCACA 23187	_ CA A	
			TG GAA GTC TTTCTGGAA		
			AC CTT CAG AGAGACCTT		
			A A_ _		
GAM206	FLJ22283	5'	TTCCGCCTGCGACAGTTCCAG 25948	A ATTTC	
			CTGGAAC GTC TGGAA		
			GACCTTG CAG GCCTT		
			A CGTCC		
GAM206	FLJ31951	3'	TTCCAAGGATCTAATCCAG 29553	AC TC TC	
			CTGGA AG ATT TGGAA		
			GACCT TC TAG ACCTT		
			AA __ GA		
GAM206	GOLGA1	3'	TTCCAGAGGCCGCTTCTCCAG 7866	AC CA	
			CTGGA AGT TTTCTGGAA		

			GACCT TCG GGAGACCTT		
			CT CC		
GAM206	HTGN29	5'	TTCCAGAGCACGTCTCCAG 21434	ACA CAT	
			CTGGA GT TTCTGGAA		
			GACCT CA GAGACCTT		
			CTG C__		
GAM206	IL14	5'	TCCAGGTCCCTTGTTCAG 45703	TCATT	
			CTGGAACAG TCTGGA		
			GACCTTGTT GGACCT		
			CCCT_		
GAM206	KBRAS2	3'	TCCAGAAAAAGGGTGTCCAG 19048	A G A_	
			CTGGA CA TC TTTCTGGA		
			GACCT GT GG AAAGACCT		
			_ G AA		
GAM206	KCNB2	5'	TGGAAATGCCTGCCCCAG 45965	AA T	
			CTGG CAG CATTTCTG		
			GACC GTC GTAAAGGT		
			CC C		
GAM206	KIAA0227	3'	TCCAGAAAGTTTGTACCA 30457	A TCA	
			TGG ACAG TTTCTGGA		
			ACC TGTT AAAGACCT		
			A TG_		
GAM206	KIAA0332	3'	CTAAGATGACTATCCA 31419	AC C	
			TGGA AGTCATTT TGG		
			ACCT TCAGTAGA ATC		
			A_ _		
GAM206	KIAA0416	5'	TTCCAGAGGGATATCC 17839	ACA A	
			GGA GTC TTTCTGGAA		
			CCT TAG GGAGACCTT		
			A_ _		
GAM206	KIAA0469	3'	TCCAGAGGCTGCACCCAG 16896	AA_ ATT	
			CTGG CAGTC TCTGGA		
			GACC GTCGG AGACCT		
			CAC _		
GAM206	KIAA0620	3'	CTGGAAATGACTGTTCCAG 31121	TG	
			CTGGAACAGTCATTTTC G		
			GACCTTGTCAGTAAAG C		
			GT		
GAM206	KIAA0748	3'	TTCCAGAAAATCTTCCA 16705	AC TCA	
			TGGA AG TTTCTGGAA		

			ACCT TC AAAGACCTT		
			___ TA_		
GAM206	KIAA0763	3'	TCCAGAAAAGATTTCAG 16971	AACA	A
			CTGG GTC TTTCTGGA		
			GACT TAG AAAGACCT		
			___ A		
GAM206	KIAA0836	5'	TTGTGGAATAAGTGTTCAG 32251	GTCAT	G
			CTGGAACA TTCTG AA		
			GACCTTGT AAGGT TT		
			GAAT_ G		
GAM206	KIAA0930	3'	TTCCAGAAAGGCCTCCAG 34919	ACA	A
			CTGGA GTC TTTCTGGAA		
			GACCT CGG AAAGACCTT		
			C_ _		
GAM206	KIAA1026	3'	TTCCAGAAATAACCACCAG 35279	AACA	C
			CTGG GT ATTTCTGGAA		
			GACC CA TAAAGACCTT		
			AC_ A		
GAM206	KIAA1056	3'	TTCCAGATGTCTGCTCCAG 17051	A T	TT
			CTGGA CAG CA TCTGGAA		
			GACCT GTC GT AGACCTT		
			C T _		
GAM206	KIAA1078	3'	TTAGAATGACTGTTACAG 32475	G	T
			CTG AACAGTCATT CTGG		
			GAC TTGTCAGTAA GATT		
			A _		
GAM206	KIAA1171	3'	TTCCAGGGGTCTGCCCAG 42484	AA	TC TT
			CTGG CAG AT CTGGAA		
			GACC GTC TG GACCTT		
			C_ _ GG		
GAM206	KIAA1171	3'	TTCCAGAGGGAGCCCTCCAG 42483	ACA	CA
			CTGGA GT TTTCTGGAA		
			GACCT CG GGAGACCTT		
			CC_ AG		
GAM206	KIAA1272	3'	TTCCAGAAATACAGGGTCC 34762	ACA_	C
			GGA GT ATTTCTGGAA		
			CCT CA TAAAGACCTT		
			GGA _		
GAM206	KIAA1297	3'	TCCAGAGGTACCCCAG 35719	AACA	C
			CTGG GT ATTTCTGGA		

			GACC CA TGGAGACCT		
			C _ _		
GAM206	KIAA1354	3'	CCCTGGTGCTGTTCCAG 30542	T TCT	
			CTGGAACAG CATT GG		
			GACCTTGTC GTGG CC		
			_ TC _		
GAM206	KIAA1391	3'	TTCCAGACGTTGTTCCA 33403	TCATT	
			TGGAACAG TCTGGAA		
			ACCTTGTT AGACCTT		
			GC _		
GAM206	KIAA1571	3'	TTCCAGAAAATGAGATTCCA 30568	CAG _	
			TGGAA TCATTT CTGGAA		
			ACCTT AGTAAA GACCTT		
			AG _ A		
GAM206	KIAA1753	3'	TCCAGAAACAACACTGCGG 32382	GAA CA	
			CTG CAGT TTTCTGGA		
			GGC GTCA AAAGACCT		
			_ AC		
GAM206	KIAA1855	3'	TTCCAGAAGTGGAGGCTCCAG 44362	ACAG	
			CTGGA TCATTTCTGGAA		
			GACCT GGTGAAGACCTT		
			CGGA		
GAM206	KIAA1872	3'	TTCCAGAAAAGGGCCCAG 31523	AACA A _	
			CTGG GTC TTTCTGGAA		
			GACC CGG AAAGACCTT		
			_ GA		
GAM206	L3MBTL2	5'	TCCAGGAGCTACTCCTCCA 42794	AC CA	
			TGGA AGT TTTCTGGA		
			ACCT TCA GAGGACCT		
			CC TC		
GAM206	LEC3	3'	TCCAGAAACCACGTCCA 17573	A A CA	
			TGGA C GT TTTCTGGA		
			ACCT G CA AAAGACCT		
			_ _ CC		
GAM206	LIN-7-C	3'	TCAGATGATTATTCCAG 20370	C TT	
			CTGGAA AGTCA TCTGG		
			GACCTT TTAGT AGACT		
			A _		
GAM206	LIPI	3'	TCAGTATAATTGTTCCAG 38844	C TT	
			CTGGAACAGT AT CTGG		

			GACCTTGTTA TA GACT		
			A T_		
GAM206	MGC10715	3'	TTCCAGAGATGCACTCC 23618	ACA _	
			GGA GT CATTTCTGGAA		
			CCT CA GTAGAGACCTT		
			_ C		
GAM206	MGC20576	5'	TCCAGGTGGGGACTGTTCC 29511	ATT_	
			GGAACAGTC TCTGGA		
			CCTTGTCAG GGACCT		
			GGGT		
GAM206	MGC3123	3'	CCAGGGTCAGCTGTTCCAG 23552	CAT	
			CTGGAACAGT TTCTGG		
			GACCTTGTCTG GGGACC		
			ACT		
GAM206	MGC5302	5'	TCCCAAATGATGCTCCAG 23531	ACA CT	
			CTGGA GTCATTT GGA		
			GACCT TAGTAAA CCT		
			CG_ C_		
GAM206	MGC9753	3'	TCCAGAAACTTTCCA 27245	C CAT	
			TGGAA AGT TTCTGGA		
			ACCTT TCA AAGACCT		
			- -		
GAM206	MGC9753	3'	CCAGAGGGTCTTACTGTTCCAG 27239	CA__	
			CTGGAACAGT TTTCTGG		
			GACCTTGTCA GGAGACC		
			TTCTG		
GAM206	MO25	3'	TCCCAATTGCTGTTTCAG 18417	C TCT	
			CTGGAACAGT ATT GGA		
			GACTTTGTCTG TAA CCT		
			T C_		
GAM206	MPPE1	5'	TTCAGCGGTGACTGCCCAG 23333	AA TT	
			CTGG CAGTCAT CTGGA		
			GACC GTCAGTG GACTT		
			C_ GC		
GAM206	PAK7	3'	TCCCAAATAGAAATGTTTCAG 34511	G _ CT	
			CTGGAACA TC ATTT GGA		
			GACTTTGT AG TAAA CCT		
			A A AC		
GAM206	PLSCR3	3'	TTCCAGGGCCTCTGCTCCA 43638	A TCAT	
			TGGA CAG TTCTGGAA		

			ACCT GTC GGGACCTT		
			C TCC_		
GAM206	PLSCR3	3'	TTCCAGGGCCTCTGCTCCA	21633	A TCAT
			TGGA CAG TTCTGGAA		
			ACCT GTC GGGACCTT		
			C TCC_		
GAM206	PPIL2	3'	TTCCAGGACCTGGCCCAG	15650	AA TCAT
			CTGG CAG TTCTGGAA		
			GACC GTC AGGACCTT		
			CG C__		
GAM206	PRO1430	5'	TCCAGAAATGTATACTTCCA	20676	CAGT_
			TGGAA CATTTCTGGA		
			ACCTT GTAAAGACCT		
			CATAT		
GAM206	RAB3D	3'	CCAGAAGTGCCTTCCA	10494	AC T
			TGGA AG CATTTCTGG		
			ACCT TC GTGAAGACC		
			_ C		
GAM206	RABEX5	3'	CCAGGGCACCGTTCTAG	15838	A CAT
			CTGGAAC GT TTCTGG		
			GATCTTG CA GGGACC		
			C C__		
GAM206	RGS11	3'	TTCCAGAATTTGTCCA	9926	A TCAT
			TGGA CAG TTCTGGAA		
			ACCT GTT AAGACCTT		
			_ T__		
GAM206	RNAHP	3'	TCCTGGTAACTGTTCCAG	14301	CATT T
			CTGGAACAGT TC GGA		
			GACCTTGTCA GG CCT		
			AT__ T		
GAM206	RoXaN	3'	TTCCAGAAACTGTGCATCTA	24606	__ CAT
			TGGA ACAGT TTCTGGAA		
			ATCT TGTCA AAGACCTT		
			ACG __		
GAM206	RPS6KA4	3'	TCCAGGGGGACTGCTCCA	10057	A A TT
			TGGA CAGTC T CTGGA		
			ACCT GTCAG G GACCT		
			C _ GG		
GAM206	SDCBP	3'	TTAGGATGACTGTTACAG	12137	G T
			CTG AACAGTCATT CTGG		

GAC TTGTCAGTAG GATT
 A _
 GAM206 SEC24D 3' TTCAGAATAACTTTCCAG 16801 C CAT
 CTGGAA AGT TTCTGGA
 ||||| ||| |||||
 GACCTT TCA AAGACTT
 _ AT_
 GAM206 SEPT3 3' TTCCAGAAATGACTTTAG 21186 AAC
 CTGG AGTCATTTCTGGAA
 ||| |||||
 GATT TCAGTAAAGACCTT

 GAM206 SHC3 5' TCCAGAAGGCTGTCCCGG 18843 A AT
 CTGG ACAGTC TTCTGGA
 ||| ||||| |||||
 GGCC TGTCGG AAGACCT
 C _
 GAM206 SLC37A1 3' CCAGAGGCTTTTCCAG 21035 C ATT
 CTGGAA AGTC TCTGG
 ||||| ||| |||||
 GACCTT TCGG AGACC
 T _
 GAM206 SMARCF1 3' TCCAGAAAAACGGATCACAG 20523 _ ACA CA
 CTG GA GT TTTCTGGA
 ||| || |||||
 GAC CT CA AAAGACCT
 A AGG A_
 GAM206 SR-BP1 3' TTCCAGAAAGACCCCA 12487 AACA A
 TGG GTC TTTCTGGAA
 ||| ||| |||||
 ACC CAG AAAGACCTT
 CC _ _
 GAM206 ST7L 3' TCCAGAAACAGCCTCCAG 29204 ACA CA
 CTGGA GT TTTCTGGA
 ||||| || |||||
 GACCT CG AAAGACCT
 C _ AC
 GAM206 ST7L 3' TCCAGAAACAGCCTCCAG 29209 ACA CA
 CTGGA GT TTTCTGGA
 ||||| || |||||
 GACCT CG AAAGACCT
 C _ AC
 GAM206 TCL6 3' TTCCAGAAGCTGCCCTCAG 15772 _ AA CAT
 CTG G CAGT TTCTGGAA
 ||| ||| |||||
 GAC C GTCG AAGACCTT
 T CC _
 GAM206 TCL6 3' TTCCAGAAGCTGCCCTCAG 14848 _ AA CAT
 CTG G CAGT TTCTGGAA
 ||| ||| |||||

GAC C GTCG AAGACCTT
 T CC ____
 GAM206 TSGA14 3' TTCCAGAACTTCTGCAG 20797 GAA TCA
 CTG CAG TTTCTGGAA
 ||| ||| |||||
 GAC GTC AAAGACCTT
 ____ TTC
 GAM206 TTYH2 3' TTCCAGAATCAATGCTGCAG 26380 GAA T ____
 CTG CAG CATT TCTGGAA
 ||| ||| ||| |||||
 GAC GTC GTAA AGACCTT
 ____ _ CTA
 GAM206 TUSP 3' TCCAGAAAGAATTCAG 21534 ACAG A
 CTGGA TC TTTCTGGA
 |||| | |||||
 GACTT AG AAAGACCT
 A ____ _
 GAM206 LOC123242 5' TTCCTAGTGACCATCCAG 37248 ACA TCT
 CTGGA GTCATT GGAA
 |||| ||||| |||
 GACCT CAGTGA CCTT
 AC_ T_
 GAM206 LOC134637 3' TTCCAGAAGCTGATTCC 37080 _ CAT
 GGAA CAGT TTCTGGAA
 ||| ||| |||||
 CCTT GTCG AAGACCTT
 A ____
 GAM206 LOC135398 3' TTCCAGAAGCCACTCCAG 37389 ACA CA
 CTGGA GT TTTCTGGAA
 |||| | |||||
 GACCT CA GAAGACCTT
 ____ CC
 GAM206 LOC143308 5' TTCCAGAATATATGCATCCAG 40350 A_ GTCAT
 CTGGA CA TTCTGGAA
 |||| | |||||
 GACCT GT AAGACCTT
 AC ATAT_
 GAM206 LOC144742 5' TTCCAGAGGCTCCCCCAG 37780 AAC_ ATT
 CTGG AGTC TCTGGAA
 ||| ||| |||||
 GACC TCGG AGACCTT
 CCCC ____
 GAM206 LOC145945 5' TTCCAGAAGCTTGTTT 40640 TCA
 GAACAG TTTCTGGAA
 |||| |||||
 CTTGTT GAAGACCTT
 C_
 GAM206 LOC147632 5' TTCCAGATGTTATTGTTCCAG 28829 C T
 CTGGAACAGT AT TCTGGAA
 ||||| || |||||

		GACCTTGTTA TG AGACCTT		
		T T		
GAM206	LOC147669 5'	TCCAGAAGCTGGACTGCAG 40855	GAA	AT__
		CTG CAGTC TTCTGGA		
		GAC GTCAG AAGACCT		
		__ GTCG		
GAM206	LOC149157 5'	CCAGCGGCAATGTTCCAG 38658	__	ATTT
		CTGGAACA GTC CTGG		
		GACCTTGT CGG GACC		
		AA C__		
GAM206	LOC149373 3'	TTCCAGAGTGAGCCGTTT 38721	A_	T
		GAAC G TCATT CTGGAA		
		CTTG C AGTGA GACCTT		
		C G _		
GAM206	LOC149935 3'	TCCAGAAGGTGTTGCCAG 30248	_	GTCA
		CTGG AACA TTTCTGGA		
		GACC TTGT GAAGACCT		
		G G__		
GAM206	LOC150157 5'	TCCAGAAAATGAAATTCC 41145	CAG	_
		GGAA TCATTT CTGGA		
		CCTT AGTAAA GACCT		
		AA_ A		
GAM206	LOC150271 3'	TCCAGAGGAGACAGTCCCAG 41174	A A A	
		CTGG AC GTC TTTCTGGA		
		GACC TG CAG GGAGACCT		
		C A A		
GAM206	LOC150279 3'	TTCCAGAAAGTTGTTCTA 38902	GTCA	
		TGGAACA TTTCTGGAA		
		ATCTTGT AAAGACCTT		
		TG__		
GAM206	LOC150407 3'	TTCCAGGAAGTAGCCCAG 38955	AAC	CAT
		CTGG AGT TTCTGGAA		
		GACC TCA AGGACCTT		
		CGA __		
GAM206	LOC152447 5'	TCGTGGAATAACTGTTCC 39274	C	_
		GGAACAGT ATTTT TGG		
		CCTTGTCA TAAGG GCT		
		A T		
GAM206	LOC153163 3'	CCAGAATGGCTCTCCA 39361	AC	T
		TGGA AGTCATT CTGG		

		ACCT TCGGTAA GACC		
		C_ _		
GAM206	LOC158062 3'	TCCAAGTGTCTGTTCCAG	41915	T TC
		CTGGAACAG CATT TGGA		
		GACCTTGTC GTGA ACCT		
		T _		
GAM206	LOC158292 5'	CCAGAAATGCTGTGATCAG	41933	A_ T
		CTGG ACAG CATTCTGG		
		GA CT TGTC GTAAAGACC		
		AG _		
GAM206	LOC196283 3'	TTCAGAGTGACTGCTCCA	42343	A T
		TGGA CAGTCATT CTGGA		
		ACCT GTCAGTGA GACTT		
		C _		
GAM206	LOC196812 3'	TTCCAGACTCTGTTACAG	43141	G TCATT
		CTG AACAG TCTGGAA		
		GAC TTGTC AGACCTT		
		A TC_		
GAM206	LOC196890 5'	TCCAGAAAATGAAATTCC	43156	CAG _
		GGAA TCATTT CTGGA		
		CCTT AGTAAA GACCT		
		AA_ A		
GAM206	LOC200035 3'	TTCCAGAAACAGACCCAG	36264	AACA A_
		CTGG GTC TTTCTGGAA		
		GACC CAG AAAGACCTT		
		C_ AC		
GAM206	LOC201229 5'	TTCCAGAAAGAAGACGCCAG	42546	AACAG A
		CTGG TC TTTCTGGAA		
		GACC AG AAAGACCTT		
		GCAGA _		
GAM206	LOC201252 3'	TCCAGAAATCTGCACAG	42557	GAA TC
		CTG CAG ATTTCTGGA		
		GAC GTC TAAAGACCT		
		AC_ _		
GAM206	LOC204285 5'	TTCCAGAATATACAGTTCCAG	43091	A CAT
		CTGGAAC GT TTCTGGAA		
		GACCTTG CA AAGACCTT		
		A TAT		
GAM206	LOC204970 3'	TCCAGAGAAGACATCCCAG	43074	AACA A
		CTGG GTC TTTCTGGAA		

			GACC CAG AGAGACCT		
			CTA_ A		
GAM206	LOC219654 3'	CCAGCGTGTCTGTTCCAG	43873	T TT	
		CTGGAACAG CAT CTGG			
		GACCTTGTC GTG GACC			
		T C_			
GAM206	LOC220064 3'	TTCCAGAAAAGCATGTCCG	44871	A GTCA	
		TGGA CA TTTCTGGAA			
		GCCT GT AAAGACCTT			
		_ ACG_			
GAM206	LOC221025 3'	TTCCAGAAACGGTGCTCC	44747	A G A	
		GGA CA TC TTTCTGGAA			
		CCT GT GG AAAGACCTT			
		C _ C			
GAM206	LOC221794 5'	CCAAGTGTTGTGACTGTGCCA	45072	A TT__ _	
		TGG ACAGTCAT CT GG			
		ACC TGTCAGTG GA CC			
		G TTGT A			
GAM206	LOC222256 3'	TTCCAGAAATGAGGGTGGCA	45251	GA AG	
		TG AC TCATTTCTGGAA			
		AC TG AGTAAAGACCTT			
		GG GG			
GAM206	LOC222614 5'	TTCCATGAAAATGCTCCAG	45307	A GTCA _	
		CTGGA CA TTTC TGGAA			
		GACCT GT AAAG ACCTT			
		C A__ T			
GAM206	LOC222962 3'	TTCCAGAGACGGTGTTTCCAG	44632	_ G A	
		CTGGAA CA TC TTTCTGGAA			
		GACCTT GT GG AGAGACCTT			
		T _ C			
GAM206	LOC253001 5'	TTCCTAGTGACCATCCAG	46062	ACA TCT	
		CTGGA GTCATT GGAA			
		GACCT CAGTGA CCTT			
		AC_ T__			
GAM206	LOC253639 3'	TTCCAGAGACCTATCTCAG	45857	_ ACA ATT	
		CTG GA GTC TCTGGAA			
		GAC CT CAG AGACCTT			
		T ATC ____			
GAM206	LOC254381 5'	TTCCAGAATCTGATCGCCAG	46545	AACA T_	
		CTGG GTCA TTCTGGAA			

			GACC TAGT AAGACCTT		
			GC__ CT		
GAM206	LOC254423	5'	TTCCAGTGCCTGATCCAG 46532	A T TTT	
			CTGGA CAG CA CTGGAA		
			GACCT GTC GT GACCTT		
			A C ____		
GAM206	LOC255452	3'	TTCCAGAAACACTGCCCC 46578	AA CA	
			GG CAGT TTTCTGGAA		
			CC GTCA AAAGACCTT		
			CC C_		
GAM206	LOC256520	3'	TCCAGAAATGCTGTCCA 45929	A T	
			TGGA CAG CATTTCTGGA		
			ACCT GTC GTAAAGACCT		
			- -		
GAM206	LOC257104	5'	CCAGCATCCCTGTTCCAG 46564	TC TT	
			CTGGAACAG AT CTGG		
			GACCTTGTC TA GACC		
			CC C_		
GAM206	LOC257282	5'	TCCAGTGGGTGACTGGCCCAG 46122	AA _	
			CTGG CAGTCATTT CTGGA		
			GACC GTCAGTGGG GACCT		
			CG T		
GAM206	LOC91409	3'	TCCAGGGGCCTGTCTCCAG 32806	_ TCA TT	
			CTGGA ACAG T CTGGA		
			GACCT TGTC G GACCT		
			C C_ GG		
GAM206	LOC91828	5'	TTCCAGAAGCACTTGCTTCAG 33410	A TCA	
			CTGGA CAG TTTCTGGAA		
			GACTT GTT GAAGACCTT		
			C CAC		
GAM207	OPA3	3'	TTGGACATGGCCTATGTACCTA 24776	A _ C A	
	A		TTA GTACATAG CCAT GT CGA		
			AAT CATGTATC GGTA CA GTT		
			C C _ G		
GAM207	LOC159184	5'	TTCAGGCTGGCTATGAACT 30162	A TC AC	
			AGT CATAGCCA GT GAA		
			TCA GTATCGGT CG CTT		
			A _ GA		
GAM208	ACVR1B	3'	CAGAAGTGCAGCCCCTCTCACA 10511	A AGA GGAA	
			TGT AGA GTTGC TTCTG		

ACA TCT CGACG AAGAC
 C CCC TG__
 GAM208 KIF3C 3' CAGGAAATGAACCTTCTTACA 8056 A G GAA
 TGTAAGAAG GTT CG TTCTG
 ||||| ||| || ||||
 ACATTCTTC CAA GT AGGAC
 C _ AA_
 GAM208 AP3S2 3' CAGAATTATGACTCTTC 12438 GCGG
 GAAGAGTT AATTCTG
 ||||| |||||
 CTTCTCAG TTAAGAC
 TA__
 GAM208 DRIL2 3' CAGAATTTACCTCATCTCACA 13183 A A TTGCG
 TGT AGA GAG GAATTCTG
 ||| ||| ||| |||||
 ACA TCT CTC TTTAAGAC
 C A CA__
 GAM208 FLJ23311 5' CAGAATTCTGCACCCTTC 23992 A T
 GAAG GT GCGGAATTCTG
 ||| ||| |||||
 CTTC CA CGTCTTAAGAC
 C _
 GAM208 KIAA0193 3' CAGGAGGCAGCTCTCCCCACA 16539 AAGA GGAA
 TGT AGAGTTGC TTCTG
 ||| ||||| |||||
 ACA TCTCGACG AGGAC
 CCCC G__
 GAM208 MGC4172 3' TCCCCATCTTCTTGCA 23601 GT C
 TGTAAGAAGA TG GGA
 ||||| ||| |||
 ACGTTCTTCT AC CCT
 _ C
 GAM208 LOC112609 3' GGAATTCTGCAAGACAACCTCTT 36058 G_____ AATT
 CTTCCA AGAAGAGTT CGG CT
 ||||| ||| ||
 TCTTCTCAA GTC GG
 CAGAACIII TTAA
 GAM208 LOC196484 5' CAGAATTCCACCCATCTTTCA 31485 A GTTGC
 A GAAGA GGAATTCTG
 ||||| |||||
 A TTTCT CCTTAAGAC
 C ACCCA
 GAM208 LOC220073 5' CAGAATTCCACCCATCTTTCA 44873 A GTTGC
 A GAAGA GGAATTCTG
 ||||| |||||
 A TTTCT CCTTAAGAC
 C ACCCA
 GAM208 LOC91069 3' CAGAATTCCACCCATCTTTCA 32345 A GTTGC
 A GAAGA GGAATTCTG
 ||||| |||||

			A TTTCT CCTTAAGAC		
			C ACCCA		
GAM209	IGF2R	3'	TTGGAATAAGGCATGGCTCA 6560	— —	
			TGA CTA CCTTATTCCAA		
			ACT GGT GGAATAAGGTT		
			C AC		
GAM209	NEDD4	3'	GTCAGATTGTGTCAAGTCA 34692	T CTTAT CA	
			TGACTTGAC AC TC AC		
			ACTGAACTG TG AG TG		
			— TT— AC		
GAM209	RAD17	5'	TGTGAATAACTCAAGTCA 28481	CTACC —	
			TGACTTGA TTATTCA		
			ACTGAACT AATAAG GT		
			C— T		
GAM209	BC022889	3'	GGACAAGATAATTCAAGTCA 40685	C_ C AT	
			TGACTTGA TA CTT TCC		
			ACTGAACT AT GAA AGG		
			TA A C_		
GAM210	CDH3	3'	TCTTCAAACGTTAGAGA 7545	ACCA CCA	
			TCTCTAAC GT TGAAGA		
			AGAGATTG CA ACTTCT		
			— AA_		
GAM210	DYRK1A	3'	ATCTTCATGGATAGCTCAGAGG 7092	AACACCA	
			TCTCT GTCCATGAAGAT		
			GGAGA TAGGTACTTCTA		
			CTCGA_		
GAM210	DYRK1A	3'	ATCTTCATGGATAGCTCAGAGG 28160	AACACCA	
			TCTCT GTCCATGAAGAT		
			GGAGA TAGGTACTTCTA		
			CTCGA_		
GAM210	DYRK1A	3'	ATCTTCATGGATAGCTCAGAGG 28185	AACACCA	
			TCTCT GTCCATGAAGAT		
			GGAGA TAGGTACTTCTA		
			CTCGA_		
GAM210	FLT1	3'	ATCCTCATGTTACTCAGTGTTA 7765	C_ C_ A	
			GAGA TCTCTAACAC AGT CATGA GAT		
			AGAGATTGTG TCA GTACT CTA		
			AC TT C		
GAM210	IL22RA2	3'	ATCTTCTTCATGGTGTTAGGGA 27521	GTCCAT	
			TCTCTAACACCA GAAGAT		

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AGGGATTGTGGT CTTCTA
      ACTT__
GAM210 JRK 3' ATCTCCATGACGATGGTGTAA 41834 TC GTC_ A
      GGA TC TAACACCA CATG AGAT
      || ||||| ||| |||
      AG ATTGTGGT GTAC TCTA
      GA AGCA C
GAM210 PDK4 3' TGGAAAACTAGTGTTAGGGA 46444 C ____
      TCTCTAACAC AG TCCA
      ||||| || |||
      AGGGATTGTG TC AGGT
      A AAAA
GAM210 PPP1R8 3' TCTGTGACTGGTGCCATAGA 28858 A__ _ T
      TCTA CACCAGTC CA GA
      ||| ||||| |||
      AGAT GTGGTCAG GT CT
      ACC T _
GAM210 PPP1R8 3' TCTGTGACTGGTGCCATAGA 15342 A__ _ T
      TCTA CACCAGTC CA GA
      ||| ||||| |||
      AGAT GTGGTCAG GT CT
      ACC T _
GAM210 PPP1R8 3' TCTGTGACTGGTGCCATAGA 8572 A__ _ T
      TCTA CACCAGTC CA GA
      ||| ||||| |||
      AGAT GTGGTCAG GT CT
      ACC T _
GAM210 RNASE1 5' CTTCAGACTGGTGTCTGA 8836 TA CA
      TC ACACCAGTC TGAAG
      || ||||| |||
      AG TGTGGTCAG ACTTC
      TC _
GAM210 SMARCD1 3' TCTAGATAGTGTTAGAGA 9049 CA CAT
      TCTCTAACAC GTC GA
      ||||| ||| ||
      AGAGATTGTG TAG CT
      A_ AT_
GAM210 SMARCD1 3' TCTAGATAGTGTTAGAGA 29147 CA CAT
      TCTCTAACAC GTC GA
      ||||| ||| ||
      AGAGATTGTG TAG CT
      A_ AT_
GAM210 TACSTD2 5' TCAGGACTGGTGTAGG 8161 A
      TCTAACACCAGTCC TGA
      ||||| |||
      GGATTGTGGTCAGG ACT
      _
GAM210 TGFB2 3' CTTATCTGGTGTAAAGA 9241 C TCCATG
      TCT TAACACCAG AAG
      ||| ||||| |||

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AGA ATTGTGGTC TTC
 _ TA____
 GAM210 TK2 3' ATCTTCATGTGGACATTGAGA 10958 TAACA GTC
 TCTC CCA CATGAAGAT
 ||| ||| |||||
 AGAG GGT GTACTTCTA
 TTACA ____
 GAM210 WASF1 5' ATCCCCAGCTAGACTAGTGTTG 10031 C CA__ AA
 GAGA TCTCTAACAC AGTC TG GAT
 ||||| ||| || |||
 AGAGGTTGTG TCAG AC CTA
 A ATCG CC
 GAM210 DKFZp434N074 5' ATCCTCATGGACCCAATGGAGA 31389 ACACCA A
 TCTCTA GTCCATGA GAT
 ||||| ||||| |||
 AGAGGT CAGGTACT CTA
 AACC__ C
 GAM210 FLJ21477 3' ATCTTTGTCTGGTGCCAGA 24789 AA TCC TG
 TCT CACCAG A AAGAT
 ||| ||||| | |||||
 AGA GTGGTC T TTCTA
 CC __ GT
 GAM210 HSPC054 3' ATCTCCATGAATCCTAGTTAGG 15433 ACCA C A
 GA TCTCTAAC GT CATG AGAT
 ||||| || ||| |||||
 AGGGATTG TA GTAC TCTA
 ATCC A C
 GAM210 P37NB 3' ATTTTCTATACTGGTGTTAGA 12434 CCAT
 TCTAACACCAGT GAAGAT
 ||||| |||||
 AGATTGTGGTCA CTTTTA
 TAT_
 GAM210 LOC114971 3' CTCCATGGATTTCAGGGA 36209 AACACC A
 TCTCT AGTCCATG AG
 ||||| ||||| ||
 AGGGA TTAGGTAC TC
 C__ C
 GAM210 LOC133686 3' TCTTCACCTGTGTTAGG 37056 C TCCA
 TCTAACAC AG TGAAGA
 ||||| || |||||
 GGATTGTG TC ACTTCT
 _ C__
 GAM210 LOC146226 5' ATCTTCATGTGGACATTGAGA 40662 TAACA GTC
 TCTC CCA CATGAAGAT
 ||| ||| |||||
 AGAG GGT GTACTTCTA
 TTACA ____
 GAM210 LOC253263 3' GTGGATTGGTGCCAGAGA 46361 AA
 TCTCT CACCAGTCCAT
 ||||| ||||| |||||


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AGAGA GTGGTTAGGTG
CC
GAM210 LOC90362 5' ATCTTTATGCTGCATTAGAGA 31295 CAC TC
TCTCTAA CAG CATGAAGAT
||||| ||| |||||||
AGAGATT GTC GTATTTCTA
AC_ _
GAM210 LOC91263 3' TCCAGCGTGATGGTGTAGG 32596 GTC AA_
TCTAACACCA CATG GA
||||||| ||| ||
GGATTGTGGT GTGC CT
A_ GAC
GAM211 ADAMTS3 3' GAGATGCATGCTTTGTTCTGTG 15509 _
C GTAT GCAAAGCATGCATCTC
||| |||||||||
CGTG TGTTTCGTACGTAGAG
TCT
GAM211 ARF4L 3' GAGATGGGATGTCTTTGCATAT 34604 AG _ G_
CTCT AGA TATGCAAAG CAT CATCTC
||| ||||||| ||| |||||
TCT ATACGTTTC GTA GTAGAG
CT T GG
GAM211 ELAVL2 5' GAGATGCAGCAGCTTACTCCT 10717 A T AAA A
AG AGTA GC GC TGCATCTC
|| ||| || || |||||||
TC TCAT CG CG ACGTAGAG
C T A_ _
GAM211 FRK 5' GGGACTTTGCATACTCT 7785 A CATGCA
AGA GTATGCAAAG TCTC
||| ||||||| |||
TCT CATACGTTTC AGGG
_ _
GAM211 SPON1 3' GAGACATCCTTTCTGAATACTT 31302 GC_ C CA
CT AGAAGTAT AAAG ATG TCTC
||||||| ||||| ||| |||
TCTTCATA TTTC TAC AGAG
AGTC C _
GAM211 TCEA1 3' CATGCTTTGCACTCTCCT 39202 A TA
AG AG TGCAAAGCATG
|| || |||||||||
TC TC ACGTTTCGTAC
C TC
GAM211 C5orf4 5' GAGATGCATTGGTAGCAACT 18474 A AAAGC
AGT TGC ATGCATCTC
||| ||| |||||||
TCA ACG TACGTAGAG
_ ATGGT
GAM211 C5orf4 3' GAGATGCATTGGTAGCAACT 26180 A AAAGC
AGT TGC ATGCATCTC
||| ||| |||||||

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		TCA ACG TACGTAGAG	
		_ ATGGT	
GAM211	FLJ10292 3'	ATGCATGCCCATTGCCTTC 19800	TAT A__
		GAAG GCAA GCATGCAT	
		CTTC CGTT CGTACGTA	
		__ ACC	
GAM211	FLJ11175 3'	ATGCATGCCCTGTGGCACCCCTC 20360	A TA AAA__
	T	AGA G TGC GCATGCAT	
		TCT C ACG CGTACGTA	
		_ CC GTGTCC	
GAM211	FLJ14054 3'	GAGTAGGCCTCCATACTTC 23785	CAAA A A
		GAAGTATG GC TGC TC	
		CTTCATAC CG ATG AG	
		CTC_ G _	
GAM211	HPCAL4 3'	CATGCTCCTGCATACTCCT 18387	A A_
		AG AGTATGCA AGCATG	
		TC TCATACGT TCGTAC	
		C CC	
GAM211	KIAA0931 3'	ATGCAGTTTCTTCATACTTCT 33483	CA_ A
		AGAAGTATG AAGC TGCAT	
		TCTTCATAC TTTG ACGTA	
		TTC _	
GAM211	KIAA0931 3'	GAGATTCTGGCCTCTGCATATT 33485	G AA_ ATGC
	CT	AGAA TATGCA GC ATCTC	
		TCTT ATACGT CG TAGAG	
		_ CTC GTCT	
GAM211	KIAA1001 3'	GAGTTAGCCTTGCATATCCCT 17327	AA A AT A
		AG GTATGCAA GC GC TC	
		TC TATACGTT CG TG AG	
		CC C AT _	
GAM211	KIAA1198 3'	GAGATGCACACCTTCGCTTCT 31709	ATGCA CA_
		AGAAGT AAG TGCATCTC	
		TCTTCG TTC ACGTAGAG	
		C__ CAC	
GAM211	PXR2b 3'	AGATGCATGCCTCTTTGGCTCT 18633	A ATGCAAA
		AGA GT GCATGCATCT	
		TCT CG CGTACGTAGA	
		_ GTTTCTC	
GAM211	LOC120856 3'	ATGCATAAGCTATATACTTC 36632	CAA _
		GAAGTATG AGC ATGCAT	

CTTCATAT TCG TACGTA
A__ AA
GAM211 LOC200853 5' ATGCATGCGAGGTGCTTC 42866 GCAAA
GAAGTAT GCATGCAT
||||| |||||
CTTCGTG CGTACGTA
GAG__

GAM211 LOC203084 3' CATGCTTTGCACTCTCCT 42280 A TA
AG AG TGCAAAGCATG
|| || |||||
TC TC ACGTTTCGTAC
C TC

GAM212 ACP2 3' TGGGCCCTCGCTCCTGAC 7319 CTTT ACA
GTCAG GC AGGGCCCA
|||| || |||||
CAGTC CG TCCCGGGT
CT__ C__

GAM212 ANGPT2 5' GCTCTGTAAAAGCTGACA 6818 GC A
TGTCAGCTTT ACA GGGC
||||||| ||| |||
ACAGTCGAAA TGT CTCG
A__ _

GAM212 COL5A3 3' TTGAACCCCCATGCAATGAGCT 17934 __ CAA CC
AGCTT TGCA GGG CAA
|||| ||| ||| |||
TCGAG ACGT CCC GTT
TA ACC AA

GAM212 DLEU2 3' TGGACCCTTGTGTTTTGA 12639 CTTT C
TCAG GCACAAGGG CCA
|||| ||||| |||
AGTT TGTGTTCCC GGT
T__ A

GAM212 JAM3 3' TGGGCCCTGTGAAGCCAGCA 26556 CA TG CAA
TGT GCTT CA GGGCCCA
||| ||| || |||||
ACG CGAA GT CCCGGGT
AC GT __

GAM212 MYCL2 3' TTGGGCCCTCGCACCAGCCTGC 11859 CA T_ ACA
A TGT GCT TGC AGGGCCCAA
||| ||| ||| |||||
ACG CGA ACG TCCCGGGTT
TC CC C__

GAM212 NGFR 3' TTGGGCCCTCCTGAAACTTACA 8337 C C G CA
TGT AG TTT CA AGGGCCCAA
||| ||| ||| |||||
ACA TC AAA GT TCCCGGGTT
T _ _ CC

GAM212 POU3F1 3' GGGCCCCCGCCGGCGCGCTGCA 29832 T TT ACAA__
TG CAGC TGC GGGCCC
|| ||| ||| |||||

AC GTCG GCG CCCGGG
 _ C_ GCCGCC
 GAM212 SEPN1 3' GGCCCTTGTGGGGTGA 32990 G TTG
 TCA CT CACAAGGGCC
 ||| || |||||
 AGT GG GTGTTCCCGG
 G _
 GAM212 VAT1 3' TGGGCCCTGCCAAGGCGACA 13068 A CACA
 TGTC GCTTTG AGGGCCCA
 ||| ||||| |||||
 ACAG CGGAAC TCCCGGGT
 _ CG_
 GAM212 BRPF3 3' TCTTGTGCCAAACTGACA 44345 C T
 TGTCAG TT GCACAAGG
 ||||| || |||||
 ACAGTC AA CGTGTCT
 A C
 GAM212 DKFZP434P0721 3' TGAGCACAGCAAGCTGACA 31871 T ACAAGG C
 TGTCAGCTT GC GC CA
 ||||| || || ||
 ACAGTCGAA CG CG GT
 _ ACA_ A
 GAM212 FAM3D 5' GCCCTCGGGTGGAAGCTGAC 29029 G A_
 GTCAGCTTT CAC AGGGC
 ||||| || ||||
 CAGTCGAAG GTG TCCCG
 _ GGC
 GAM212 FHX 3' TTGGGTGATGTGTGCAAACTG 20464 T C AGG_
 CA TG CAG TTTGCACA GCCCAA
 || ||| ||||| |||||
 AC GTC AAACGTGT TGGGTT
 _ A GTAG
 GAM212 FLJ12800 3' TGGGCCCCACAAGCTGCCA 23195 T _ CACAA
 TG CAGCTT TG GGGCCCA
 || ||||| || |||||
 AC GTCGAA AC CCCGGGT
 C C _
 GAM212 FLJ13955 3' GCCCCTGCACAAGGCTGACA 24110 CA A
 TGTCAGCTTTG CA GGGC
 ||||| || ||||
 ACAGTCGGAAC GT CCCG
 AC C
 GAM212 FLJ20666 3' TTTTGACAAAGCTGACA 19587 CA
 TGTCAGCTTTG CAAGG
 ||||| || ||||
 ACAGTCGAAAC GTTTT
 A_
 GAM212 FLJ20958 3' GGGCCCTTACCCAGACAGACA 22647 AGC CAC
 TGTC TTTG AAGGGCCC
 ||| ||| |||||

ACAG AGAC TTCCCGGG
 AC_ CCA
 GAM212 GIT2 3' GCATGTTCAAAGCTGACA 29214 C AGG
 TGTCAGCTTTG ACA GC
 ||||| ||
 ACAGTCGAAAC TGT CG
 T A__
 GAM212 HPIP 3' GGCCCTTGAGAAGCTGATA 21739 GCA
 TGTCAGCTTT CAAGGGCC
 ||||| |||||
 ATAGTCGAAG GTTCCCGG
 A__
 GAM212 KIAA0544 3' GGGCCCTTGGTGTGCTCACA 35114 C TT A
 TGT AGC TGC CAAGGGCCC
 ||| ||| |||||
 ACA TCG GTG GTTCCCGGG
 C T_ _
 GAM212 KIAA1198 3' GGCCCCCTAGTAGCTGGCA 31711 TT ACAA
 TGTCAGCT GC GGGCC
 ||||| || |||||
 ACGGTCGA TG CCCGG
 _ ATCC
 GAM212 MGC12538 3' TGGATGATGTTCCACAACAAAGC 26483 CACAA ____
 TGACA GTCAGCTTTG GGGC CCA
 ||||| ||| |||
 CAGTCGAAAC CTTG GGT
 AACA_ TAGTA
 GAM212 MGC15854 5' GGGCCCCTGCGCCCGGGCTGGC 29645 T_ A A
 A TGTCAGCTT GC CA GGGCCC
 ||||| || |||||
 ACGGTCGGG CG GT CCCGGG
 CC C C
 GAM212 MGC2541 3' TGGGCCCTGGCTTAAGCCGACA 27966 A T_ A A
 TGTC GCTT GC CA GGGCCCA
 ||| ||| || |||||
 ACAG CGAA CG GT CCCGGGT
 C TT _ _
 GAM212 MGC4707 3' GGCCCCAAGCTGACA 23563 T CACAA
 TGTCAGCTT G GGGCC
 ||||| | |||||
 ACAGTCGAA C CCCGG
 _ _ _
 GAM212 POLM 3' TTGAGCCCCTGCTGGTGTGCTG 43786 T TTT AA____ C
 CA G CAGC GCAC GGGC CAA
 | ||| ||| ||| |||
 C GTCG TGTG CCCG GTT
 _ _ GTCGTC A
 GAM212 SRCRB4D 3' TGGGCCCTCAGGGGCTGCA 28031 T GCACA
 TG CAGCTTT AGGGCCCA
 || ||||| |||||

		AC GTCGGGG	TCCCGGGT		
		— AC—			
GAM212	LOC126669 3'	TTGAGGTTGTGACACAAGCTGA	37160	— —	AGG —
	CA	TGTCAGCTT TG CACA	GCC CAA		
		ACAGTCGAA AC GTGT	TGG GTT		
		C A — A			
GAM212	LOC131000 3'	CCAAACAGTGTGCAAAACTCAC	37349	C C	AG—
	A	TGT AG TTTGCACA	GG		
		ACA TC AAACGTGT	CC		
		C A GACAAA			
GAM212	LOC147639 5'	GGCCTGATCTGCAAAGCTGCA	38346	T	CAA_
		TG CAGCTTTGCA	GGGCC		
		AC GTCGAAACGT	TCCGG		
		— CTAG			
GAM212	LOC148189 5'	TTGGACCCCCGGGCTGGCTGCA	38487	T TT	ACAA C
		TG CAGCT GC	GGG CCAA		
		AC GTCGG CG	CCC GGTT		
		— T_ GGCC A			
GAM212	LOC151124 5'	CCAGTGGCCAAAGCTGACA	41301	CA	AG
		TGTCAGCTTTG CA	GG		
		ACAGTCGAAAC GT	CC		
		CG GA			
GAM212	LOC157381 3'	CCAAAGTGCAAAGTGACA	41789	G	AAG
		TGTCA CTTTGAC	GG		
		ACAGT GAAACGTG	CC		
		— AAA			
GAM212	LOC158450 5'	GGTTATCAAAGCTGACA	39842		CACAAG
		TGTCAGCTTTG	GGCC		
		ACAGTCGAAAC	TTGG		
		TA—			
GAM212	LOC158504 5'	GGTTATCAAAGCTGACA	39853		CACAAG
		TGTCAGCTTTG	GGCC		
		ACAGTCGAAAC	TTGG		
		TA—			
GAM212	LOC199923 3'	CCCCTGTGCAGATGACA	42668	GC	A
		TGTCA TTTGCACA	GGG		
		ACAGT AGACGTGT	CCC		
		— C			
GAM212	LOC90246 5'	TGGGCTCACAAAAGTGA	31004	C	CACAA
		TCAG TTTG	GGGCCA		

			AGTC AAAC CTCGGGT		
			A A_		
GAM212	LOC91450	5'	CTCTGTGCAAAGCTGCCA 32855	T	A
			TG CAGCTTTGCACA GGG		
			AC GTCGAAACGTGT CTC		
			C _		
GAM213	KIAA1229	3'	CTTAGGAATTTCATATGCACCTT 31098	AA	AA
	A		TAAGGT ATAT AATTTTAAAG		
			ATTCCA TATA TTAAGGATTC		
			CG C_		
GAM214	ROBO1	3'	CCAAACAAAACCTGAACCACAAA 28583	GC	GAATCG
			TTTG GGT TTTGTTTG		
			AAAC CCA AAACAAACC		
			A_ AGTCA_		
GAM214	ROBO1	3'	CCAAACAAAACCTGAACCACAAA 8848	GC	GAATCG
			TTTG GGT TTTGTTTG		
			AAAC CCA AAACAAACC		
			A_ AGTCA_		
GAM214	LOC149422	3'	CCAAACAAAACAAAACAAA 38743	GCG	GAATC
			TTTG GT GTTTGTTTG		
			AAAC CA CAAACAAACC		
			AAA AAA_		
GAM214	LOC92568	3'	CCAAACAAACAAACAAA 34576	GCG	GAATC
			TTTG GT GTTTGTTTG		
			AAAC CA CAAACAAACC		
			AAA AA_		
GAM215	BAT1	5'	TACGCGCTCTCCCTGTTTAG 27907	G	ATT A
			TTAAA AG GA AGCGCGTA		
			GATTT TC CT TCGCGCAT		
			G C_ C		
GAM215	BAT1	5'	TACGCGCTCTCCCTGTTTAG 11014	G	ATT A
			TTAAA AG GA AGCGCGTA		
			GATTT TC CT TCGCGCAT		
			G C_ C		
GAM215	NCOA3	3'	CGCTCTTTTCAATCTCTT 13284	_	C
			AAGAGATTGAAA G GCG		
			TTCTCTAACTTT C CGC		
			T T		
GAM215	UBE2L3	3'	ACTGCTTCAATCTACTT 9355	_	A C
			AAG AGATTGAA GCG GT		

TTC TCTAACTT CGT CA
 A _ _
 GAM215 KIAA0391 5' GCCGACCCCAATCTCTTTAA 16139 AAAG_ C
 TTAAAGAGATTG CG GT
 ||||| ||
 AATTTCTCTAAC GC CG
 CCCC_ _
 GAM215 RAB20 5' ACGCGCTTCCTCTCTT 19463 TT A
 AAGAGA GAA GCGCGT
 |||| ||
 TTCTCT CTT CGCGCA
 C_ _
 GAM215 SLC12A5 3' GACGCGCTTTGTCCTT 21855 A TG A
 AAG GAT AAAGCGCGT C
 ||| |||||
 TTC CTG TTTCGCGCA G
 _ _ C
 GAM216 EGLN1 5' CTGCGCCTCGGCGTCCCGAGG 22584 C _ ATTA _
 A TCC CGGG AC TC AGGCGCAG
 ||| ||| |||||
 AGG GCCC TG GG TCCGCGTC
 A C C_ _ C
 GAM216 RPS6KA2 5' GCGCCTGGGATGCCGGGGA 22105 GA A
 TCCCCGG CATT TCAGGCGC
 ||||| ||| |||||
 AGGGGCC GTAG GGTCCGCG
 _ _
 GAM216 GMEB2 3' CTGCACCCAGCCAGGTCCCTGG 14740 _ ATTATCA C
 GGA TCCCC GGGAC GG GCAG
 |||| ||| ||||
 AGGGG CCCTG CC CGTC
 T GACCGAC A
 GAM216 HS6ST 3' CTGCCCCCAATGCCCCGAGG 31072 C A ATCA C
 CC CGGG CATT GG GCAG
 || ||| ||| ||||
 GG GCCC GTAA CC CGTC
 A C CC_ _
 GAM216 HS6ST1 3' CTGCCCCCAATGCCCCGAGG 11230 C A ATCA C
 CC CGGG CATT GG GCAG
 || ||| ||| ||||
 GG GCCC GTAA CC CGTC
 A C CC_ _
 GAM216 KIAA0339 3' CTGCACCCCAAGTCCTGGGGA 35404 ATTATCA C
 TCCCCGGGAC GG GCAG
 ||||| ||||
 AGGGGTCCTG CC CGTC
 ACCC_ _ A
 GAM216 LOC115051 3' CTGCCCCCAATGCCCCGAGG 30160 C A ATCA C
 CC CGGG CATT GG GCAG
 || ||| ||| ||||

		GG GCCC GTAA CC CGTC	
		A C CC__ _	
GAM216	LOC123096 3'	CTGCACCAGGCGTCCTGGGGA 36721	ATTA A C
		TCCCCGGGAC TC GG GCAG	
		AGGGGTCCTG GG CC CGTC	
		C__ A A	
GAM216	LOC220549 5'	TGCGCCCGGCTCCCGGGGG 44652	CATTA A
		TCCCCGGGA TC GGCGCA	
		GGGGGCCCT GG CCGCGT	
		C__ C	
GAM216	LOC253100 5'	GCGCCTGAGCCCCCGGGGG 46600	ACATTA
		TCCCCGGG TCAGGCGC	
		GGGGGCCC AGTCCGCG	
		CCG__	
GAM216	LOC51054 5'	CTGATAATCCCCGGGGA 18042	AC
		TCCCCGGG ATTATCAG	
		AGGGGCCC TAATAGTC	
		C_	
GAM216	LOC84661 5'	GCGCCAGACTGGTATCCGGGG 26303	_ ATTATCA
	A	TCCCCGGG AC GGCGC	
		AGGGGCCT TG CCGCG	
		A GTCAGAC	
GAM217	ACVR1 3'	CAAGGCAGACGTCGTACCCAGC 6761	TAGC C TG
		GCT AC AC CTGCCTTG	
		CGA TG TG GACGGAAC	
		CCCA C CA	
GAM217	DPYSL2 3'	CAGTTCAGAAGTGCTAAGCT 7062	CA _
		AGCTTAGCAC CTG CTG	
		TCGAATCGTG GAC GAC	
		AA TT	
GAM217	FOXF2 3'	AAGGCAGTGCTAAGC 7186	ACCACT
		GCTTAGC GCTGCCTT	
		CGAATCG TGACGGAA	

GAM217	MADH4 3'	AAGGTGGCAATGCTTAAACT 11829	C _ CCAC TG
		AG TTA GCA TGC COTT	
		TC AAT CGT ACG GGAA	
		A T A__ GT	
GAM217	MAPK1 3'	AAGGTTGCAGTGCTGAGCTG 8615	CAC T
		CAGCTTAGCAC TGC GCCTT	

			GTCGAGTCGTG ACG TGGAA		
			____ T		
GAM217	NT5M	3'	AGGCAGCAGGCACCAAGCTG 21436	AGCACCA	
			CAGCTT CTGCTGCCT		
			GTCGAA GACGACGGA		
			CCACG__		
GAM217	PTP4A2	3'	CAAAACAGCATACCTGCTAAGC 9550	CCAC	CC
	T		AGCTTAGCA TGCTG TTG		
			TCGAATCGT ACGAC AAC		
			CCAT AA		
GAM217	PTPRD	5'	GGAGGCAGTGATTCCAAGCTG 28178	AGCAC	G
			CAGCTT CACTGCT CC		
			GTCGAA GTGACGG GG		
			CCTTA A		
GAM217	PTPRD	5'	GGAGGCAGTGATTCCAAGCTG 28179	AGCAC	G
			CAGCTT CACTGCT CC		
			GTCGAA GTGACGG GG		
			CCTTA A		
GAM217	PTPRD	5'	GGAGGCAGTGATTCCAAGCTG 28180	AGCAC	G
			CAGCTT CACTGCT CC		
			GTCGAA GTGACGG GG		
			CCTTA A		
GAM217	PTPRD	5'	GGAGGCAGTGATTCCAAGCTG 8722	AGCAC	G
			CAGCTT CACTGCT CC		
			GTCGAA GTGACGG GG		
			CCTTA A		
GAM217	RAB6A	3'	CAAAGCAGCAGTTCTACCAAGC 8775	AGCACC	C
			GCTT ACTGCTGC TTG		
			CGAA TGACGACG AAC		
			CCATCT A		
GAM217	RFC1	3'	GGAGCAGTAGTACTAAGGC 8820	_ C C	G
			GC TTAG AC ACTGCT CC		
			CG AATC TG TGACGA GG		
			G A A _		
GAM217	DKFZP434P211	3'	CAAGTCCTGCGATGCTAAGT 15864	CCAC	TGC_
			GCTTAGCA TGC CTTG		
			TGAATCGT GCG GAAC		
			A__ TCCT		
GAM217	KIAA0354	3'	GTCAGTGGTGCTATGCTG 16998	T _	
			CAGC TAGCACCCTG C		

			GTCG ATCGTGGTGAC G		
			T T		
GAM217	KIAA0748	3'	CAAGGGGAGATGGTGCTAA 16701	_ G G	
			TTAGCACCA CT CT CCTTG		
			AATCGTGGT GA GG GGAAC		
			A _ _		
GAM217	KIAA1056	3'	AAGGTAGCGGCCTAAGCT 17043	CACCA	
			AGCTTAG CTGCTGCCTT		
			TCGAATC GGCGATGGAA		
			C _ _		
GAM217	KIAA1505	5'	CAAGGCAGCTCTGCTCAGC 45192	T CCACT	
			GCT AGCA GCTGCCTTG		
			CGA TCGT CGACGGAAC		
			C CT _		
GAM217	PTDSS2	3'	AGGCAGCGATGCTGAGC 25074	CCAC	
			GCTTAGCA TGCTGCCT		
			CGAGTCGT GCGACGGA		
			A _		
GAM217	RAB6C	3'	CAAAGCAGCAGTCCGACCAAGC 25833	AGCACC C	
			GCTT ACTGCTGC TTG		
			CGAA TGACGACG AAC		
			CCAGCC A		
GAM217	RASSF2	3'	CAAGGGAGCGATACTAAGGC 16392	_ CACCAC G	
			GC TTAG TGCT CCTTG		
			CG AATC GCGA GGAAC		
			G ATA _ G		
GAM217	SNPH	3'	CAAGGCAGGAGGTACACCAGCT 16290	TAGCACCA G	
	G		CAGCT CT CTGCCTTG		
			GTCGA GA GACGGAAC		
			CCACATG _ G		
GAM217	TNKS2	3'	CAAAGCAGCAGTGGCCTCTA 24911	CA _ C	
			TAG CCACTGCTGC TTG		
			ATC GGTGACGACG AAC		
			TCC A		
GAM217	WIT-1	5'	CAAGAAGAAAGTGCTAAGCTG 17987	CACTG GC	
			CAGCTTAGCAC CT CTTG		
			GTCGAATCGTG GA GAAC		
			AAA _ A _		
GAM217	YKT6	3'	AAGGGTTTGGTCTAAGCTG 13317	C CT TG	
			CAGCTTAG ACCA GC CCTT		

		GTCGAATC TGGT TG GGAA	
		_ T_ _	
GAM217	LOC150174 3'	CAAGTCCTGCGATGCTAAGT 38871	CCAC TGC_
		GCTTAGCA TGC CTTG	
		TGAATCGT GCG GAAC	
		A_ TCCT	
GAM217	LOC150213 3'	CAAGTCCTGCGATGCTAAGT 36955	CCAC TGC_
		GCTTAGCA TGC CTTG	
		TGAATCGT GCG GAAC	
		A_ TCCT	
GAM217	LOC150236 3'	CAAGTCCTGCGATGCTAAGT 38904	CCAC TGC_
		GCTTAGCA TGC CTTG	
		TGAATCGT GCG GAAC	
		A_ TCCT	
GAM217	LOC158450 3'	CAAGGCAGCATTCACTAAGC 39841	CACCAC
		GCTTAG TGCTGCCTTG	
		CGAATC ACGACGGAAC	
		ACTT_	
GAM217	LOC158504 3'	CAAGGCAGCATTCACTAAGC 39852	CACCAC
		GCTTAG TGCTGCCTTG	
		CGAATC ACGACGGAAC	
		ACTT_	
GAM217	LOC158677 5'	AGGCAGCAAAGCTG 42022	CACCAC
		CAGCTTAG TGCTGCCT	
		GTCGAATC ACGACGGA	
		AA_	
GAM217	LOC219347 3'	AAGGCAGCAAGCAAGGC 44676	A ACCAC
		GCTT GC TGCTGCCTT	
		CGGA CG ACGACGGAA	
		A A_	
GAM217	LOC222962 3'	CAGCAGTGATGCCAGCTG 44626	TA C
		CAGCT GCA CACTGCTG	
		GTCGA CGT GTGACGAC	
		C_ A	
GAM217	LOC245811 5'	GGCAGCGGCGCTAAGC 45071	A ACT
		GCTTAGC CC GCTGCC	
		CGAATCG GG CGACGG	
		C _	
GAM217	LOC254826 3'	CAAGACAACAACAGTGGTGGGC 46433	TAG C C_
		GCT CACCACTG TG CTTG	

			CGG GTGGTGAC AC GAAC	
			____ A AACA	
GAM218	DMD	5'	GCTGCATAATAAATGACTGA 5571	T ____
			TCAGTCATTT TTAT AGC	
			AGTCAGTAAA AATA TCG	
			T CG	
GAM218	LASS2	3'	ATCGTAAGAATGACTGA 33622	TATAGC
			TCAGTCATTTTT CGAT	
			AGTCAGTAAGAA GCTA	
			T_____	
GAM219	FLJ14525	3'	CAAGAAATCAGCAACCAGC 26547	GAC GG _
			GCT GG GC GATTTCTTG	
			CGA CC CG CTAAAGAAC	
			____ AA A	
GAM219	KIAA1280	5'	CAAGAAATCTTAGAACCAGC 34547	ACGGG C
			GCTG GG GATTTCTTG	
			CGAC TT CTAAAGAAC	
			CAAGA _	
GAM219	VIAAT	3'	CAAGGGCGAGCCCCGCCGCG 27883	T A GAT
			CGC G CGGGGGC TTCTTG	
			GCG C GCCCCCG GGGAAC	
			_C AGC	
GAM219	LOC197201	3'	CAAGAAATCTTGTGTCA 42461	G GC
			TGACG GG GATTTCTTG	
			ACTGT TT CTAAAGAAC	
			G _	
GAM219	LOC221895	3'	CAAGAAATCCTCACCAGCAGT 44444	AC _ C
			GCTG GG GGG GATTTCTTG	
			TGAC CC CTC CTAAAGAAC	
			GA A _	
GAM220	BCL7A	5'	CAAGAGACCCGCAAGAACTTG 21989	AC_ C AT
	CA		TGCAA TCTT GC GTTTCTTG	
			ACGTT AGAA CG CAGAGAAC	
			CAA _ CC	
GAM220	CCND1	3'	AAGAAGAAAAAGGTTTGCA 27598	T CGCATG
			TGCAAAC CTT TTTCTT	
			ACGTTTG GAA GAAGAA	
			_ AAA_	
GAM220	CHS1	3'	AGTATGCAAGAAGTTTGCA 5524	_ C
			TGCAAAC CTT GCATGTT	

ACGTTTGA GAA CGTATGA
 A _
 GAM220 EIF2B1 3' CAAGAAACACTTGCTGAATCTG 30004 AACTC _ _
 CA TGCA TTC GCA TGTTTCTTG
 |||| ||| ||| |||||
 ACGT AAG CGT ACAAAGAAC
 CT__ T TC
 GAM220 MOCS2 5' AAGAAATAAAAGCGTTGCA 10873 ACTCTT A__
 TGCAA CGC TGTTTCTT
 |||| ||| |||||
 ACGTT GCG ATAAAGAA
 _____ AAA
 GAM220 MTCP1 5' AAGAAACAGAAGTTTGTAGCA 15483 AACT GCA
 TGC CTTC TGTTTCTT
 || ||| |||||
 ACG GAAG ACAAAGAA
 ATTT_ _
 GAM220 N4BP2 5' CAAGAAGAGGTGTAGAGTTTGC 20003 T ATG
 A TGCAAACCTCT CGC TTTCTTG
 ||||| ||| |||||
 ACGTTTGAGA GTG GAAGAAC
 T GA_
 GAM220 RALGPS1A 3' CAAGAAACATGCATTTTGGCA 16016 AACTCTTC
 TGC GCATGTTTCTTG
 || |||||
 ACG CGTACAAAGAAC
 GTTTTA__
 GAM220 LOC144348 5' AAACGCAAAGGTTTGCA 37720 T C AT
 TGCAAAC CTT GC GTTT
 ||||| ||| |||
 ACGTTTG GAA CG CAAA
 _ A _
 GAM220 LOC196418 5' AAACGCAAAGGTTTGCA 42368 T C AT
 TGCAAAC CTT GC GTTT
 ||||| ||| |||
 ACGTTTG GAA CG CAAA
 _ A _
 GAM221 BCAS1 3' CATGTATATATTCTTCTGA 9730 CCATCAC
 TCAGAGGAG ATACATG
 ||||| |||||
 AGTCTTCTT TATGTAC
 ATA__
 GAM221 CKTSF1B1 3' TCATGGAAGAGGCTCCTCTGA 15026 A ACATA
 TCAGAGGAGCC TC CATGA
 ||||| ||| |||||
 AGTCTCCTCGG AG GTACT
 _ AAG_
 GAM221 CTPS 3' CGTGTAAGGCTCCTCTG 42714 TCACA
 CAGAGGAGCCA TACATG
 ||||| |||||

GTCTCCTCGGT ATGTGC
 C____
 GAM221 ECT2 3' CATGTATGTGCCACTTCTGA 19871 AGCCAT
 TCAGAGG CACATACATG
 ||||| |||||
 AGTCTTC GTGTATGTAC
 ACC____
 GAM221 HEM1 5' TCATGTATATGAACTTCTC 11808 CCA C
 GAGGAG TCA ATACATGA
 ||||| || |||||
 CTCTTC AGT TATGTACT
 A__ A
 GAM221 TGFBR2 3' TCACACATGCAGTGGTTCTCTG 9244 G CA ACA
 A TCAGAG AGCCAT CAT TGA
 ||||| ||||| || |||
 AGTCTC TTGGTG GTA ACT
 _ AC CAC
 GAM221 DKFZP564D0478 3' TCATGCTGGTGATGGCTCCCCT 25809 A ATA
 GG TCAG GGAGCCATCAC CATGA
 ||| ||||| ||||| |||||
 GGTC CCTCGGTAGTG GTACT
 C GTC
 GAM221 FLJ22169 3' ATGGGACGGCTCCTCTGA 23519 A A
 TCAGAGGAGCC TC CAT
 ||||| || |||||
 AGTCTCCTCGG AG GTA
 C G
 GAM221 KIAA0205 5' CATGCATTCTTCCGGCTCCTCT 17005 ATCACATA_
 GA TCAGAGGAGCC CATG
 ||||| |||||
 AGTCTCCTCGG GTAC
 CCTTCTTAC
 GAM221 KIAA0685 5' CATGTGTGTGCGGCC 16149 A AT
 GG GCC CACATACATG
 || ||| |||||
 CC CGG GTGTGTGTAC
 _ C_
 GAM221 LOC196283 3' CATGTATCAGTCCTCTGA 42339 GCCATCAC
 TCAGAGGA ATACATG
 ||||| |||||
 AGTCTCCT TATGTAC
 GAC____
 GAM221 LOC203248 3' CACATGTGTGACCTCTCTGA 43017 G CCA CA
 TCAGAG AG TCACATA TG
 ||||| || ||||| ||
 AGTCTC TC AGTGTGT AC
 _ C__ AC
 GAM221 LOC219731 5' ATGTCTGGTCCTCTGA 44717 G TCACAT
 TCAGAGGA CCA ACAT
 ||||| || |||||

AGTCTCCT GGT TGTA
 _ C____
 GAM222 SAR1 3' ACATTTAGATACTTCATA 21350 TACA
 TATGA TATCTAAATGT
 |||| |||||
 ATACT ATAGATTTACA
 TC__
 GAM222 SLC4A4 3' ACATTTAGATATATTTGTGT 9835 ____
 ATACA TATCTAAATGT
 |||| |||||
 TGTGT ATAGATTTACA
 TTAT
 GAM222 TFDP2 3' ACATTTAGATAATTTATAGTA 12972 TACA
 TACTATGA TATCTAAATGT
 ||||| |||||
 ATGATATT ATAGATTTACA
 TA__
 GAM222 KIAA0923 3' ACATTAGTGATATACTCATAG 15238 TAC ____
 TA TACTATGA ATATCTA AATGT
 ||||| ||||| |||||
 ATGATACT TATAGGT TTACA
 CA_ GA
 GAM222 ZNF238 3' ACATCTAGCTTTGACAATCATA 13042 A__ TAT A
 GTA TACTATGAT CA CTA ATGT
 ||||| || |||||
 ATGATACTA GT GAT TACA
 ACA TTC C
 GAM223 DUSP4 5' GGGCAGCGCTGGCGCCAGC 7090 A ACAA
 GTTGGC CCA CGTTGCCC
 ||||| || |||||
 CGACCG GGT GCGACGGG
 C C____
 GAM223 NPC1 3' TGAACACCGGATGGTGCCAAC 5815 ACAA T CC
 GTTGGCACCA CG TG CA
 ||||| || |||||
 CAACCGTGGT GC AC GT
 AG__ C AA
 GAM223 TCFL4 3' GGGCAACATTTGGCCCAA 31770 CA CAAAC
 TTGG CCAA GTTGCCC
 ||| ||| |||||
 AACC GGTT CAACGGG
 C_ TA__
 GAM223 ZNF277 5' TAGCGTTTCTACTGGTGCCA 22535 AC__
 TGGCACCA AAACGTTG
 ||||| |||||
 ACCGTGGT TTTGCGAT
 CATC
 GAM223 C11orf9 3' GGTATTTGTGTCATGTGCCAAC 14946 CA_ CGT
 GTTGGCAC ACAA TGCC
 ||||| ||||| |||

			CAACCGTG TGT TT ATGG		
			TAC ____		
GAM223	DKFZP564I0422	3'	GGGCATT TACTGTGTGCCAAC	25435	CA AACGT
			GTTGGCAC ACA TGCCC		
			CAACCGTG TGT ACGGG		
			__ CATT		
GAM223	FLJ12076	3'	GGCCTGCTGGTGCCAGC	24825	A AACGTT
			GTTGGCACCA CA GCC		
			CGACCGTGGT GT CGG		
			C C ____		
GAM223	FLJ22596	5'	GGA CTTGCCCGTTGGTGCCAGC	24705	AAA TTG
			GTTGGCACCAAC CG CC		
			CGACCGTGGTTG GT GG		
			CCC TCA		
GAM223	HA-1	3'	GGCCTTGTTGGTGCCAC	32654 T	ACGTT
			GT GGCACCAACAA GCC		
			CA CCGTGGTTGTT CGG		
			C C ____		
GAM223	KIAA1056	3'	GGCCTGTGCCACTGGTGCCAGC	17048	ACAA_ TT
			GTTGGCACCA ACG GCC		
			CGACCGTGGT TGT CGG		
			CACCG C_		
GAM223	KIAA1193	3'	TGGGCAGCTGCTACTCAGTGCC	33607	CAACAAAC_
	AAC		GTTGGCAC GTTGCCCA		
			CAACCGTG CGACGGGT		
			ACTCATCGT		
GAM223	KIAA1753	3'	GGGCAGTGCTGCCGTGCCAAC	32380	CAA AA
			GTTGGCAC CA CGTTGCC		
			CAACCGTG GT GTGACGGG		
			CC_ C_		
GAM223	PCDH10	5'	ATGTTTAACGGTGCCAAC	21882	AAC
			GTTGGCACC AAACGT		
			CAACCGTGG TTTGTA		
			CAA		
GAM223	PCDH10	5'	ATGTTTAACGGTGCCAAC	26767	AAC
			GTTGGCACC AAACGT		
			CAACCGTGG TTTGTA		
			CAA		
GAM223	LOC151162	5'	GGGACTGCTGGTTGCCAAC	41308	_ A AACGTTG
			GTTGGCA CCA CA CCC		

			CAACCGT GGT GT	GGG	
			T C CA_____		
GAM223	LOC203377	5'	GGGACTGCTGGTTGCCAAC	43543	_ A AACGTTG
			GTTGGCA CCA CA	CCC	
			CAACCGT GGT GT	GGG	
			T C CA_____		
GAM223	LOC219654	3'	TGGGCGGCGTGCCTGTGCCAAC	43879	CAACAA
			GTTGGCAC	ACGTTGCCCA	
			CAACCGTG	TGCGGCGGGT	
			TCCG__		
GAM223	LOC220070	3'	AACGTTTGTGCCAAC	29819	CAAC
			GTTGGCAC	AAACGTT	
			CAACCGTG	TTGCAA	

GAM223	LOC56959	5'	CAATTTTGTGCGTGCCAAT	39839	A C
			GTTGGCACC ACAA	GTTG	
			TAACCGTGG TGTTT	TAAC	
			C _		
GAM224	ANK1	3'	GTCGATATTGATTACTTTA	30287	A
			TAAAGTAATCAATA	CGGT	
			ATTCATTAGTTAT	GCTG	
			A		
GAM224	FER	5'	ATCCTACTGTTACTGATCAC	11755	A A A
			GT ATCA TAACGGTA	GAT	
			CA TAGT ATTGTCAT	CTA	
			C C C		
GAM224	BIRC3	5'	ATCTTACCATTATTTTAC	33367	TC C
			GTAA AATAA GGTAAGAT		
			CATT TTATT CCATTCTA		
			_ A		
GAM224	LOC196382	5'	TCTTAGCGGATTACTT	43148	AATAA G
			AAGTAATC	CG TAAGA	
			TTCATTAG	GC ATTCT	
			_____ G		
GAM224	LOC93097	5'	ATCTCACCGGGGAAATTATTTT	35354	CAATAA A
	A		TAAAGTAAT	CGGT AGAT	
			ATTTTATTA	GCCA TCTA	
			AAGGG_ C		
GAM225	GPX3	3'	AATTGTTCTGCTCTAACTGA	7878	A
			TTAGTTA AGCAGAACGATT		

AGTCAAT TCGTCTTGTTAA
 C
 GAM226 MGC1136 5' CCGAGTCCCTTTATGTCA 23453 TATTA C
 TGGCATA GAGGGAC CGG
 ||||| ||||| ||
 ACTGTAT TTCCCTG GCC
 _____ A
 GAM226 MGC4796 3' ACCGGGTCCCTCCAGGCTGCTG 30826 TATA_ A
 CC GGCA TT GAGGGACCCGGT
 ||| || |||||
 CCGT GA CTCCCTGGGCCA
 CGTCG C
 GAM226 LOC92539 5' ACCAGGAAAATAATATGTACCA 34497 C GAGGGA C
 TGG ATATATTA CC GGT
 || ||||| || |||
 ACC TGTATAAT GG CCA
 A AAAA_ A
 GAM227 TRIM 3' TATTTCAAAAATTGTCAAA 18532 CGCTA
 TTTGACA TTTGAAATA
 ||||| |||||
 AACTGT AACTTTAT
 TAA_
 GAM227 FLJ22060 3' TATTTTCATCGTGTTTCAAA 23867 C TATT
 TTTGA ACGC TGAAATA
 |||| ||| |||||
 AACT TGTG ACTTTAT
 T CT_
 GAM227 HBP1 3' TATTATTTCAAATAAATGGAAA 14563 GA CGC
 A TTT CA TATTTGAAATAATA
 ||| || |||||
 AAA GT ATAACTTTATTAT
 AG AA_
 GAM227 LOC148823 3' TATTTCAAGTCAGTGCTCAAA 29795 _ GCT
 TTTGA CAC ATTTGAAATA
 |||| ||| |||||
 AACT GTG TGAACTTTAT
 C AC_
 GAM228 FOXO1A 3' TTTTGTATATAAGCAGTAGA 7760 TC C
 TCTACTG TA ATACAGAA
 ||||| || |||||
 AGATGAC AT TATGTTTT
 GA A
 GAM228 HUS1 3' CCCTTCTATTTAGAGTAGA 43789 TG C AC
 TCTAC TCTA AT AGAAGGG
 |||| ||| || |||||
 AGATG AGAT TA TCTTCCC
 _ T _
 GAM228 BIVM 3' CTGTATAAAGACAGTAGA 19253 AC
 TCTACTGTCT ATACAG
 ||||| |||||

			AGATGACAGA TATGTC		
			AA		
GAM228	C6orf37	3'	TGTATATATACACAGTAGA 33516	C C__	
			TCTACTGT TA ATACA		
			AGATGACA AT TATGT		
			C ATA		
GAM228	KIAA1615	3'	TTCTGTATGTAGACGTAGA 34089	T	
			TCTAC GTCTACATACAGAA		
			AGATG CAGATGTATGTCTT		
			—		
GAM228	PAK7	3'	ACCAGGACTATGTAGAAGTAGA 34508	G	CAGAAG
			TCTACT TCTACATA GGT		
			AGATGA AGATGTAT CCA		
			— CAGGA_		
GAM228	SMOC2	3'	CCTTCCACATGTTAACAGTAGA 35833	CT	ACA
			TCTACTGT ACAT GAAGG		
			AGATGACA TGTA CTTCC		
			AT CAC		
GAM228	LOC150372	3'	CCCCTCTGGTGGACAGAGA 38937	A	ATA A
			TCT CTGTCTAC CAGA GGG		
			AGA GACAGGTG GTCT CCC		
			— — C		
GAM228	LOC151760	5'	ACCCCTTTCTGCAGAAAGTA 41388	G	ACATA _
			TACT TCT CAGAA GGGT		
			ATGA AGA GTCTT CCCA		
			A C__ T		
GAM228	LOC221300	3'	CCTATATATAGACAGTAG 44146	C	CAGA
			CTACTGTCTA ATA AGG		
			GATGACAGAT TAT TCC		
			A A__		
GAM228	LOC221489	5'	CCCACATGTTGACAGTAGA 44982	T	ACAGAA
			TCTACTGTC ACAT GGG		
			AGATGACAG TGTA CCC		
			T CA__		
GAM229	ABCD2	3'	AGGAAGTATATGATCTGACTT 11657	C AAA	_
			AAG CA ATCAT TACTTCCT		
			TTC GT TAGTA ATGAAGGA		
			A C__ T		
GAM229	EGFR	3'	AGAAAGTATTTGATTTTGTCT 11721	C	T_ C
			AG CAAAAATCA TACTT CT		

			TC GTTTTTAGT ATGAA GA		
			T TT A		
GAM229	GALNT7	3'	GAGGAAGTTTGT TTTT 18878	T TT	
			AAAA CA ACTTCCTC		
			TTTTT GT TGAAGGAG		
			T T_		
GAM229	HIF1A	3'	GAAGAAATTTTTTTTGGC 7266	TC A	
			GCCAAAAA ATT CTTC		
			CGGTTTTT TAA GAAG		
			TT A		
GAM229	MEN1	5'	GAGGAAGTGT CATCTCTGGCT 44844	AAAATCAT	
	T		AAGCCA TACTTCCTC		
			TTCGGT GTGAAGGAG		
			CTCCTACT		
GAM229	MYO1B	3'	GAGAAAGTAATGATTCCTAAAG 14523	CAAA_ C	
	C		GC AATCATTACTT CTC		
			CG TTAGTAATGAA GAG		
			AAATCC A		
GAM229	TBL2	3'	GAGAATGTGATTTTTGGC 14821	TAC	
			GCCAAAAATCAT TTC		
			CGGTTTTTAGTG GAG		
			TAA		
GAM229	TBL2	3'	GAGAATGTGATTTTTGGC 26867	TAC	
			GCCAAAAATCAT TTC		
			CGGTTTTTAGTG GAG		
			TAA		
GAM229	APOL2	3'	GAAGAAGTAGTTTACTTTGGAC 25162	_ AATC C	
	T		AG CCAA ATTACTTC TC		
			TC GGTTT TGATGAAG AG		
			A CATT A		
GAM229	AUTL1	3'	AAGAGTGATTTTTGAGCT 26645	_ A	
			AGC CAAAAATCATT CTT		
			TCG GTTTTTAGTGA GAA		
			A _		
GAM229	B1	3'	AGGAAGTAGTTGCCTTTGGTCA 15800	A AATC	
			A GCCAAA ATTACTTCCT		
			A TGGTTT TGATGAAGGA		
			C CCGT		
GAM229	BAG5	3'	GAGAAAGGGGAAATTTTTGGTT 11305	CA TA C	
			AGCCAAAAAT T CTT CTC		

			TTGGTTTTTA G GAA GAG		
			AA GG A		
GAM229	CDK5RAP3	5'	GAAGAATATTTTTGGC 24851	C A	
			GCCAAAAAT ATT CTTC		
			CGGTTTTTA TAA GAAG		
			— —		
GAM229	DDX28	5'	GAGAGTGAACCTTGGCTTA 20410	AAA A	
			TAAGCCAA TCATT CTT		
			ATTCGGTT AGTGA GAG		
			CCA —		
GAM229	DKFZP434L187	5'	AGGAAACTTGGTTTTTTGGC 34117	— TTAC	
			GCCAAAAA TCA TTCCT		
			CGGTTTTT GGT AAGGA		
			T TCA_		
GAM229	FLJ13322	5'	GAAGTGAATCCTTGGCTTA 24059	AA CA	
			TAAGCCAA AT TTA CTTC		
			ATTCGGTT TA AGTGAAG		
			CC —		
GAM229	FLJ14564	3'	AAGTGGTGATTTTTGGTT 37593		
			AGCCAAAAATCATTACTT		
			TTGGTTTTTAGTGGTGAA		
GAM229	FLJ20086	3'	AAGTGATGTTTCTGGCTTA 19188	A T	
			TAAGCCA AAA CATTACTT		
			ATTCGGT TTT GTAGTGAA		
			C —		
GAM229	FLJ20445	3'	GAGGTCATTGTTTTTGGCTTA 19480	C T	
			TAAGCCAAAAAT AT ACTTC		
			ATTCGGTTTTTG TA TGGAG		
			T C		
GAM229	GIT2	3'	AAGTAATGATCTTCTGGT 29212	— A	
			GCCA AA ATCATTACTT		
			TGGT TT TAGTAATGAA		
			C C		
GAM229	H2AFJ	3'	AAGTAATGATTAAAGCTTG 20236	CAAA	
			TAAGC AATCATTACTT		
			GTT CG TTAGTAATGAA		
			AAA_		
GAM229	NPD009	5'	GAGGTCTGACTTTTGGCT 45562	A TT	
			AGCCAAAA TCA ACTTC		

			TCGGTTTT AGT TGGAG	
			C C_	
GAM229	OSBPL2	3'	AGGAAGTAATGGGAAGGGGTT 29317	AAAAA
			AGCC TCATTACTTCCT	
			TTGG GGTAATGAAGGA	
			GGAAG	
GAM229	OSBPL2	3'	AGGAAGTAATGGGAAGGGGTT 16849	AAAAA
			AGCC TCATTACTTCCT	
			TTGG GGTAATGAAGGA	
			GGAAG	
GAM229	P15-2	3'	GAAGAAGTGGAGTTTTTTGGTT 20784	TCA C
			AGCCAAAAA TTA CTTC TC	
			TTGGTTTTT GGTGAAG AG	
			TGA A	
GAM229	UBE2G1	3'	GAAGTAGTCTTTGGCTTA 9348	AATC
			TAAGCCAAA ATTACTTC	
			ATTCGGTTT TGATGAAG	
			C_	
GAM229	LOC133418	3'	AAGTTGACTTTTGGCTT 37037	A TT
			AAGCCAAAA TCA ACTT	
			TCGGTTTT AGT TGAA	
			C _	
GAM229	LOC143098	5'	GAGGAAATAATACAGATTTTGG 37575	A _ C
	CT		AGCCAAAA TC ATTA TTCCTC	
			TCGGTTTT AG TAAT AAGGAG	
			_ ACA A	
GAM229	LOC145622	3'	GAGGAAGAGTACTCTTTGGCTT 37910	AATC A
	G		TAAGCCAAA ATT CTTCCTC	
			GTTTCGGTTT TGA GAAGGAG	
			CTCA _	
GAM229	LOC148195	3'	AGGAAATAATGATTGGC 40872	AAA C
			GCCA ATCATT TTCCT	
			CGGT TAGTAAT AAGGA	
			_ A	
GAM229	LOC221510	3'	GAAGTTCATTTTGGTTTA 43769	ATCATT
			TAAGCCAAAA ACTTC	
			ATTTGGTTTT TGAAG	
			ACT_	
GAM230	CNTFR	3'	CATCCGATTTCTCCTCCTGCC 7577	A T_ A_
			GG CAGGAGG ATC ATG	

			CC GTCCTCC TAG TAC		
			— TCTT CC		
GAM230	DSC3	3'	TGCCATTCTCCTGCCT 7654 A TATCA A		
			AGG CAGGAGG ATG CA		
			TCC GTCCTCT TAC GT		
			— C		
GAM230	DSC3	3'	TGCCATTCTCCTGCCT 23665 A TATCA A		
			AGG CAGGAGG ATG CA		
			TCC GTCCTCT TAC GT		
			— C		
GAM230	NEBL	3'	ATGTCATTGATATAATTTCCCT 13098 AC GAG		
	A		TAGG AG GTATCAATGACAT		
			ATCC TT TATAGTTACTGTA		
			CT AA_		
GAM230	PCDHA9	3'	ATGTCATTGTCTCCCGCCCTA 15209 ACA GT TC		
			TAGG GGAG A AATGACAT		
			ATCC CCTC T TTA CTGTA		
			CGC TG_		
GAM230	RPP30	3'	TGCCATTCTCCTGCCT 13124 A TATCA A		
			AGG CAGGAGG ATG CA		
			TCC GTCCTCT TAC GT		
			— C		
GAM230	AFAP	3'	ATGTCATTTTATTCCCCTCC 22291 CA GTATC		
			GGA GGAG AATGACAT		
			CCT CCTT TTA CTGTA		
			CC ATT_		
GAM230	FLJ10583	3'	TGCTATTCCTCCTGTCC 19950 TATC A		
			GGACAGGAGG AATG CA		
			CCTGTCCTCC TTAT GT		
			— C		
GAM230	FLJ20208	3'	ATGCCACTTTTGCCCTCCTGCCC 19292 A TCAA A		
	TG		TAGG CAGGAGGTA TG CAT		
			GTCC GTCCTCCGT AC GTA		
			C TTTC C		
GAM230	FLJ23519	3'	TGCCATTCTCCTGTCT 25977 TATCA A		
			GGACAGGAGG ATG CA		
			TCTGTCCTCT TAC GT		
			— C		
GAM230	TADA3L	3'	TGCCATTCTCCTGCCT 28548 A TATCA A		
			AGG CAGGAGG ATG CA		

TCC GTCCTCT TAC GT
 — C
 GAM230 USP24 3' CGTGAATACTTCCTGTCCTA 43817 CA
 TAGGACAGGAGGTAT ATG
 |||||
 ATCCTGTCCTTCATA TGC
 AG
 GAM230 LOC118987 3' ATGTCACTTCAGAACTTCCTG 36607 A A AA__
 CCCTA TAGG CAGGAGGT TC TGACAT
 ||| ||||| || |||||
 ATCC GTCCTTCA AG ACTGTA
 C A ACTTC
 GAM230 LOC138046 3' ATGTCATTTACCTCCTGTTCC 37115 _ ATC
 TA TAGGA CAGGAGGT AATGACAT
 ||||| ||||| |||||
 ATCCT GTCCTCCA TTA CTGTA
 T CT_
 GAM230 LOC147178 3' CATTGAGTACCTCCTGCCC 30742 A _
 GG CAGGAGGTA TCAATG
 || ||||| |||||
 CC GTCCTCCAT AGTTAC
 C G
 GAM230 LOC147991 3' GTTGGCGATACCTCACATCCTA 38436 CAG AA
 TAGGA GAGGTATC TGAC
 ||||| ||||| |||||
 ATCCT CTCCATAG GTTG
 ACA CG
 GAM230 LOC155434 3' CACTGGTAGCTCCTGTCC 41771 G A
 GGACAGGAG TATCA TG
 ||||| ||||| |||||
 CCTGTCCTC ATGGT AC
 G C
 GAM230 LOC199699 3' TGCCATTCTCCTGTCT 42597 TATCA A
 GGACAGGAGG ATG CA
 ||||| ||||| |||||
 TCTGTCCTCT TAC GT
 — C
 GAM230 LOC93048 5' ATGTCACTTCAGAACTTCCTG 35295 A A AA__
 CCCTA TAGG CAGGAGGT TC TGACAT
 ||| ||||| || |||||
 ATCC GTCCTTCA AG ACTGTA
 C A ACTTC
 GAM231 APLP2 3' ACTGTCTGTTGTTTACCTA 43699 CCC T
 TAGGTGAACA AC GACAGT
 ||||| || |||||
 ATCCATTTGT TG CTGTCA
 — T
 GAM231 APXL 3' ACTGTCAGTGGGAAACC 7351 GAACA
 GGT CCCACTGACAGT
 || ||||| |||||

			CCA GGGTGA	CTGTCA		
			AA__			
GAM231	COL1A2	3'	ATTGTTAGGTGCTGACCTA	5542	GAA CAC	
			TAGGT CACC TGACAGT			
			ATCCA GTGG ATTGTTA			
			GTC ____			
GAM231	FUT6	3'	CTGCCTGGGGATTACCTA	5651	CA CTGA	
			TAGGTGAA CCCA CAG			
			ATCCA	CTT GGGT GTC		
			AG CC__			
GAM231	JJAZ1	3'	ACCATCAGATGCAGTTCCTA	17654	T ACC _ CA	
			TAGG GAAC CA CTGA GT			
			ATCC CTTG GT GACT CA			
			_ AC_ A AC			
GAM231	PTPRZ1	3'	ACTGCAGTATTCACCTA	8745	CACCC A	
			TAGGTGAA ACTG CAGT			
			ATCCA	CTT TGAC GTCA		
			A____ _			
GAM231	ARHGEF15	3'	ACTGTCAGTGGAGATACT	17316	AACAC	
			GGTG CCACTGACAGT			
			TCAT GGTGA	CTGTCA		
			AGA__			
GAM231	DATF1	3'	ACTGGTGAACGTTACCT	22651	ACC TGA	
			AGGTGAAC CAC CAGT			
			TCCA	CTTG GTG GTCA		
			CAA ____			
GAM231	DATF1	3'	ACTGGTGAACGTTACCT	28062	ACC TGA	
			AGGTGAAC CAC CAGT			
			TCCA	CTTG GTG GTCA		
			CAA ____			
GAM231	DKFZP434J046	5'	TTACCAGCATGAAGTTCACCTA	35152	ACC C ACA	
			TAGGTGAAC CA TG GTAA			
			ATCCA	CTTG GT AC CATT		
			AA_ _ GAC			
GAM231	DKFZp761B0514	3'	TCAGAGGAAGTAAATGTTCACT	26051	C_____ A	
	TA		TAGGTGAACA CC CTGA			
			ATTCA	CTTGT GG GACT		
			AAATGAA A			
GAM231	FAM3C	3'	TACCTTCAGATGTTCACT	17039	CCCA CA	
			GGTGAACA CTGA GTA			

TCACTTGT GACT CAT
 A___ TC
 GAM231 FLJ20337 3' TTACTGTCACCTTCACT 19394 CACCCAC
 GGTGAA TGACAGTAA
 ||||| |||||
 TCACTT ACTGTCATT
 CC____
 GAM231 FUT10 3' TTACTGCCTTTTGTGGAAATTC 26393 CAC TGA____
 ACCTA TAGGTGAA CCAC CAGTAA
 ||||| ||| |||||
 ATCCACTT GGTG GTCATT
 AAA TTTTCC
 GAM231 HEF1 3' TTGCAAGTGTTCACCT 13112 CCAC A
 AGGTGAACAC TG CAG
 ||||| || |||
 TCCACTTGTG AC GTT
 A___ _
 GAM231 KIAA0903 5' ACTGAAACAGCTTCACCTA 35367 CACCCA A____
 TAGGTGAA CTG CAGT
 ||||| ||| |||||
 ATCCACTT GAC GTCA
 C____ AAA
 GAM231 MBLL39 3' TTACTGTCATGTCATTTACC 29577 CACC C
 GGTGAA CA TGACAGTAA
 ||||| || |||||
 CCATTT GT ACTGTCATT
 ACT_ _
 GAM231 MBLL39 3' TTACTGTCATGTCATTTACC 12320 CACC C
 GGTGAA CA TGACAGTAA
 ||||| || |||||
 CCATTT GT ACTGTCATT
 ACT_ _
 GAM231 LOC127703 3' CTGCACTGTGGGTGTCCACC 36906 A ___ A
 GGTG ACACCCAC TG CAG
 ||| ||||| || |||
 CCAC TGTGGGTG AC GTC
 C TC _
 GAM231 LOC145241 5' TACTGTCAGGCTGGGCCCTCCC 31483 T ACA ____
 GG GA CCA CTGACAGTA
 || || ||| |||||
 CC CT GGGT GACTGTCAT
 _ CCC CG
 GAM231 LOC157503 3' ACTGTCAGCAGGCAGTGACC 41811 GA A_ CA
 GGT AC CC CTGACAGT
 ||| || || |||||
 CCA TG GG GACTGTCA
 G_ AC AC
 GAM231 LOC163231 5' ACTGTCAGCCAGTCATTCACC 40094 C_ CCA
 GGTGAA AC CTGACAGT
 ||||| || |||||

			CCACTT TG GACTGTCA	
			AC ACC	
GAM232	ARSD	3'	GCTTCTGGGAGACCTCGGGGA 14317	AACC_ A
			TCCCCGA CCCA GGGGC	
			AGGGGCT GGGT CTTCG	
			CCAGA _	
GAM232	BRF1	3'	GCTTCTCGAGGGCTTGGGGGA 7258	G A CCA
			TCCCC AA CCC AGGGGC	
			AGGGG TT GGG TCTTCG	
			G C AGC	
GAM232	DDX3	5'	GCCGCCCTCTCAGTTTCGGG 23433	CCCCAA
			CCCGAAAC GGGGCGGC	
			GGGCTTTG TCCCGCCG	
			ACTC__	
GAM232	DDX3	5'	GCCGCCCTCTCAGTTTCGGG 7037	CCCCAA
			CCCGAAAC GGGGCGGC	
			GGGCTTTG TCCCGCCG	
			ACTC__	
GAM232	DVL1	3'	GCCACAGGGAGGGAGGTCTTGG 29842	A _ AAGG__
			GGA TCCCCGA ACC CCC GGC	
			AGGGGTT TGG GGG CCG	
			C A AGGGACA	
GAM232	EN2	3'	GCCACCTCAAGGCCTTGGGGGA 7145	AA CCAA C
			TCCCCGA CC GGGG GGC	
			AGGGGTT GG CTCC CCG	
			CC AA__ A	
GAM232	GAS7	5'	GCCGCCCGGGCAGGTCCCG 9716	AA __ AA
			CG ACC CCC GGGGCGGC	
			GC TGG GGG CCCC GCCG	
			CC AC _	
GAM232	GPX3	3'	GCCACCCCTGCTCCTTCGGAGG 7879	_ ACCCCCA C
			A TCC CCGAA AGGGG GGC	
			AGG GGCTT TCCCC CCG	
			A CCTCG__ A	
GAM232	KLHL1	5'	GCCGCCTCCGGAGCTTCGG 21919	ACC CAA
			CCGAA CC GGGGCGGC	
			GGCTT GG CTCCGCCG	
			CGA C__	
GAM232	MLC1	3'	GCCAGGGGGTTTGAGGA 17525	C G AAGG
			TCC C AAACCCCC GGC	

			AGG G TTTGGGGG CCG		
			A _ A _		
GAM232	MLC1	3'	GCCAGGGGGTTTGAGGA 29219	C G	AAGG
			TCC C AAACCCCC GGC		
			AGG G TTTGGGGG CCG		
			A _ A _		
GAM232	NEURL	3'	CCCTGAAGGTTTGGGGA 10411	G	CC
			TCCCC AAACC CAAGGG		
			AGGGG TTTGG GTTCCC		
			_ AA		
GAM232	NF1	5'	GCCGCCCCCGCGCGGGGA 5813	AAACCC	AA
			TCCCCG CC GGGGCGGC		
			AGGGGC GG CCCC GCCG		
			GCC_ CC		
GAM232	NTSR1	5'	GTCCTCGGGGGCCTGGGGA 8370	AAA	AA
			TCCCCG CCCCC GGGGC		
			AGGGGT GGGGG TCCTG		
			CC_ C_		
GAM232	PRKCL1	5'	GCCGCCCCTCCCTCCGCGCGG 31329	AAACCCCCA	
	GA		TCCCCG AGGGGCGGC		
			AGGGGC TCCCCGCCG		
			GCGCCTCCC		
GAM232	RAD52	3'	GCCCTCAGGAGTTTGGG 28645	C	CAA
			CCCGAAAC CC GGGGC		
			GGGTTTTG GG TCCCG		
			A AC_		
GAM232	ROR2	3'	TTTTTTGGGAATTCAAGGGA 10899	C_	ACC
			TCCC GAA CCCAAGGGG		
			AGGG CTT GGGTTTTT		
			AA AA_		
GAM232	SERPINE2	5'	GCCGCCCCCTGGGGATCCAGCG 36988	AAAC_	A
			CG CCCCCA GGGGCGGC		
			GC GGGGT CCCC GCCG		
			GACCTA C		
GAM232	SLC20A2	5'	GCTCGGAGTTTCGGGGA 13603	C	CAAG
			TCCCCGAAAC CC GGGC		
			AGGGGCTTTG GG CTCG		
			A _		
GAM232	SLC30A3	5'	GCCGCCCTGCGGGGATCCCGGG 9527	AAAC	AA
	GG		TCCCCG CCCC GGGGCGGC		

			GGGGGC GGGG TCCGCCG		
			CCTA CG		
GAM232	SPON1	3'	CTTTTGGGGGTTTCAGAGGA 31301	CCGA	
			TCC AACCCCAAGGG		
			AGG TTGGGGGTTTTC		
			AGAC		
GAM232	VEGF	3'	GCCTCCCTCAGGGTTTCGGG 9408	CCA C	
			CCCGAAACCC AGGGG GGC		
			GGGCTTTGGG TCCCT CCG		
			AC_ _		
GAM232	VEGF	3'	GCTCTGACCAGGAGTTTGGGGA 9409	AC CCAA_	
			TCCCCGAA CC GGGGC		
			AGGGGTTT GG TCTCG		
			GA ACCAG		
GAM232	C20orf50	5'	GCCGCCTCAGGGACTTGAGGA 34718	_ AA CCAA	
			TCC CCGA CCC GGGGCGGC		
			AGG GGTT GGG CTCCGCCG		
			A CA A__		
GAM232	CACNG4	3'	GCGTTGGGGGTCCCGGGGG 15745	AA GGG	
			TCCCCG ACCCCAA GC		
			GGGGGC TGGGGGTT CG		
			CC G__		
GAM232	CAMKK1	3'	CCTGGGGGTTCGGGGA 26069	A A	
			TCCCCGAA CCCCCA GG		
			AGGGGCTT GGGGGT CC		
			- -		
GAM232	CAMP-GEFII	3'	GCCTGGGGTTTCGGG 13882	CAAG	
			CCCGAAACCCC GGGC		
			GGGCTTTGGGG TCCG		

GAM232	CLDN7	5'	CCGCCTGGCCTTCGGGGA 6989	AC CCAAG	
			TCCCCGAA CC GGGCGG		
			AGGGGCTT GG TCCGCC		
			CC _____		
GAM232	CLDN7	5'	CCGCCTGGCCTTCGGGGA 45384	AC CCAAG	
			TCCCCGAA CC GGGCGG		
			AGGGGCTT GG TCCGCC		
			CC _____		
GAM232	DKFZP434N1511	5'	GCCGGGGGTTTGAGGA 43936	C G AAGG	
			TCC C AAACCCCC GGC		

		AGG G TTTGGGGG CCG			
		A _ _ _ _			
GAM232	EPB41L1	3'	GCCACCAGGGTTTGGGGA	34941	G CCAA _
			TCCCC AAACCC GG GGC		
			AGGGG TTTGGG CC CCG		
			_ A _ _ A		
GAM232	FLJ20886	5'	GCCCCTTGGGGGTTTCAGGGA	45595	C A
			TCCC GAA CCCCCAAGGGGC		
			AGGG CTT GGGGGTTCCCCG		
			A _		
GAM232	FLJ23024	3'	GCCTCTCTGGAGACTTGGGGA	24473	AACCC _
			TCCCCGA CCA AGGGGC		
			AGGGGTT GGT TCTCCG		
			CAGA_ C		
GAM232	FLJ31709	5'	GCCGCTTCTGCAAGGTCTCAGG	29457	C A CCCA
	GA		TCCC GA ACC AGGGGCGGC		
			AGGG CT TGG TCTTCGCCG		
			A C AACG		
GAM232	GPCR150	5'	GCCGCCCCCTGCAGTCCGGAGA	15708	C AA CCC A
			TC CCG AC CA GGGGCGGC		
			AG GGC TG GT CCCC GCCG		
			A C_ AC_ C		
GAM232	HELO1	5'	GCCGCCCCCTTGGGCTAAAAGG	22384	GAAACC
			CC CCCAAGGGGCGGC		
			GG GGGTTCCCCGCCG		
			AAAATC		
GAM232	IDI2	3'	GCTGATCCTGAAAGTCTTGGGG	27092	A CCCCCA GG
	A		TCCCCGA AC AGG CGGC		
			AGGGGTT TG TCC GTCG		
			C AAAG_ TA		
GAM232	KIAA0515	5'	GCCGGGAGGGTTTGGGGA	31926	G _ AAGG
			TCCCC AAACCC CC GGC		
			AGGGG TTTGGG GG CCG		
			_ A G _ _		
GAM232	KIAA0561	3'	GCCGCCCCCTGAAGGCGG	32765	AAA CC A
			CCG CC CA GGGGCGGC		
			GGC GG GT CCCC GCCG		
			_ AA C		
GAM232	KIAA1052	3'	GCCTTCGGAGGCTCAGGGA	17314	C AA C AA
			TCCC GA CC CC GGGGC		

AGGG CT GG GG TTCCG
 A C_ A C_
 GAM232 KIAA1509 3' CCAGGGGGTTTGGGGA 30874 G AA
 TCCCC AAACCCCC GG
 |||| ||||| ||
 AGGGG TTTGGGGG CC
 _ A_
 GAM232 KIAA1855 3' GCCCTTCGGAGATTCGGGGA 44360 ACCC A
 TCCCCGAA CC AGGGGC
 ||||| || |||||
 AGGGGCTT GG TTCCCG
 AGA_ C
 GAM232 LASP1 3' GCGATTTGGGGGCTCGGGGA 12800 AA GG
 TCCCCGA CCCCCAAG GC
 ||||| ||||| ||
 AGGGGCT GGGGGTTT CG
 C_ AG
 GAM232 MGC13057 5' GCTCCGGGAGCTTCGGAGA 26126 C ACC AA
 TC CCGAA CCC GGGGC
 || |||| || |||||
 AG GGCTT GGG CCTCG
 A CGA _
 GAM232 NTN4 5' GCCGCCCCCAGGTGCCCGGG 31514 AA_ CCCAA
 CCG ACC GGGGCGGC
 ||| || |||||
 GGGC TGG CCCC GCCG
 CCG ACC_
 GAM232 PPI5PIV 3' GCCGCCTTTCGGGGATCCGAGG 21276 _ AAAC A
 GA TCCC CG CCCC AGGGGCGGC
 ||| || ||| |||||
 AGGG GC GGGG TTTCCGCCG
 A CTA_ C
 GAM232 SKIP 3' CCCTCTAGGGGCTTTGGGGA 18598 A CA_
 TCCCCGAA CCCC AGGG
 ||||| ||| |||
 AGGGGTTT GGGG TCCC
 C ATC
 GAM232 SKIP 3' CCCTCTAGGGGCTTTGGGGA 28261 A CA_
 TCCCCGAA CCCC AGGG
 ||||| ||| |||
 AGGGGTTT GGGG TCCC
 C ATC
 GAM232 WDR13 5' GCCGCTCCGGGGGGCCTC 19553 AA AA
 GA CCCCC GGGGCGGC
 || |||| |||||
 CT GGGGG CCTCGCCG
 CC G_
 GAM232 ZNF340 5' CCGCCTGGCTTTGGGGGTCCCG 41033 _ AA _
 GAGG CC CCG ACCCCAAGG GGCGG
 || ||| ||||| |||||

		GG GGC TGGGGGTTTC CCGCC	
		A CC GGT	
GAM232	LOC113763 3'	CCAGTCTTTTGGGGGTTTC 28802	_ _
		GAAACCCCAAGG GGC GG	
		CTTTGGGGGTTTT CTG CC	
		T A	
GAM232	LOC145482 3'	GCAGGATTGGGGGTTTCGG 37877	GGG_
		CCGAAACCCCAA GC	
		GGCTTTGGGGGTT CG	
		AGGA	
GAM232	LOC145694 5'	GCTGTCCCGGGACCCCGAGGA 40557	C AAAC CAA
		TCC CG CCC GGGGCGGC	
		AGG GC GGG CCCTGTCG	
		A CCCA _	
GAM232	LOC149171 5'	GCTCCTGGAGGCCCTGGGGA 38667	AAA C A
		TCCCCG CC CCA GGGGC	
		AGGGGT GG GGT CCTCG	
		CCC A _	
GAM232	LOC149706 5'	CCAAGGGATGGGGGTTTGGGGA 41058	G AG_
		TCCCC AAACCCCA GG	
		AGGGG TTTGGGGT CC	
		_ AGGGAA	
GAM232	LOC164382 3'	CCAAGGAGGGATTTGGGGA 42164	A _ AAG
		TCCCCGAA CCC CC GG	
		AGGGGTTT GGG GG CC	
		A A AA_	
GAM232	LOC166042 5'	CTTTTGGGATTCCGGGGA 40200	A CC
		TCCCCG AA CCCAAGGG	
		AGGGGC TT GGGTTTTC	
		C A_	
GAM232	LOC204161 5'	CCTTGGGGATTTCGGAGGA 43580	_ AC
		TCC CCGAA CCCAAGG	
		AGG GGCTT GGGGTTCC	
		A A_	
GAM232	LOC204161 5'	GCCCTGGAGGCCTTGGGGA 43581	AA C AG
		TCCCCGA CC CCA GGGC	
		AGGGGT GG GGT CCCG	
		CC A _	
GAM232	LOC253955 5'	GCTCTTTTGGAGGCCACAGGGA 45328	CGAAA _ C
		TCCC CC CC AAGGGGC	

			AGGG GG GG TTTCTCG		
			ACACC A T		
GAM233	BMP6	3'	CGGGGCGCCCTTGTCT 7454	T T A	
			AGACAAGG GT TCC CG		
			TCTGTTCC CG GGG GC		
			_ C _		
GAM233	CACNB1	3'	CTGGAGCTTGTCTTG 6386	GTGT C	
			TAAGACAAG TTCCA G		
			GTTCTGTTC GAGGT C		
			_____ A		
GAM233	DISC1	3'	CCGTGGAACCTGTTT 20735	A GTT	
			AGACA GGT TCCACGG		
			TTTGT CCA AGGTGCC		
			- -		
GAM233	ENC1	3'	CCGTGGAGATCGCTTTTCT 9698	C _	
			AGA AAGGTG TTTCCACGG		
			TCT TTTCCG AGAGGTGCC		
			_ T		
GAM233	FBXW1B	3'	CCGTGGAAGCACACTCT 14662	CAAG	
			AGA GTGTTTCCACGG		
			TCT CACGAAGGTGCC		
			CA__		
GAM233	FBXW1B	3'	CCGTGGAAGCACACTCT 27364	CAAG	
			AGA GTGTTTCCACGG		
			TCT CACGAAGGTGCC		
			CA__		
GAM233	FBXW1B	3'	CCGTGGAAGCACACTCT 27374	CAAG	
			AGA GTGTTTCCACGG		
			TCT CACGAAGGTGCC		
			CA__		
GAM233	PBX3	3'	CTGTAAAACCTTGTCTTA 12867	GTTTCC	
			TAAGACAAGGT ACGG		
			ATTCTGTTCCA TGTC		
			AAA__		
GAM233	PCDHGA11	5'	CCGCGGAATATCGGCTTA 20983	ACAA T A	
			TAAG GGTGTT CC CGG		
			ATTC CTATAA GG GCC		
			GG__ _ C		
GAM233	PCDHGA11	5'	CCGCGGAATATCGGCTTA 25788	ACAA T A	
			TAAG GGTGTT CC CGG		

ATTC CTATAA GG GCC
 GG__ _ C
 GAM233 PCDHGA11 5' CCGCGGAATATCGGCTTA 25789 ACAA T A
 TAAG GGTGTT CC CGG
 ||| ||||| || |||
 ATTC CTATAA GG GCC
 GG__ _ C
 GAM233 PLAG1 3' TGTTAACACCTTATTTTA 8527 C TC
 TAAGA AAGGTGTT CA
 ||||| ||||| ||
 ATTTT TTCCACAA GT
 A TT
 GAM233 TRPS1 3' CCGTGGAATAATGTTT 15349 AGG
 AGACA TGTTTCCACGG
 ||||| ||||| |||||
 TTTGT ATAAAGGTGCC
 A__
 GAM233 AKAP9 5' CCGTGAGCTTGCCGTC 12313 AA T_
 GAC GGTG TTCCACGG
 ||| ||| |||||
 CTG CCGT GAGGTGCC
 __ TC
 GAM233 ARHGDIG 3' CCGCATGGGCCTTGTCTT 6851 GTTT __
 AAGACAAGGT CCA CGG
 ||||| ||| |||
 TTCTGTTCCG GGT GCC
 ____ AC
 GAM233 FLJ00001 3' CCGTGGAAGCCTCTGCCTC 39776 CA_ T
 GA AGG GTTTCCACGG
 || ||| ||||| |||||
 CT TCT CGAAGGTGCC
 CCG C
 GAM233 FLJ13842 3' CGTGGAAGAATTGCTTA 23928 A GGTG
 TAAG CAA TTTCCACG
 ||||| ||| |||||
 ATTC GTT AGAGGTGC
 _ A__
 GAM233 GNG4 3' CCGTGGAATGGTTTTCTTA 10808 C G T
 TAAGA AAG TGTT CCACGG
 ||||| ||| ||| |||||
 ATTCT TTT GTAA GGTGCC
 _ G _
 GAM233 KCNS1 5' CCGATAACACCTTGCATC 8042 __ CCA
 GA CAAGGTGTTT CGG
 || ||||| |||
 CT GTTCCACAAA GCC
 AC TA_
 GAM233 KIAA0513 3' CCGTGGAAGCCCTGCCTCT 16352 CA_ T
 AGA AGG GTTTCCACGG
 ||| ||| ||||| |||||

TCT TCC CGAGGGTGCC
 CCG _
 GAM233 KIAA0555 3' CCATGGAAACACTAGTC 16683 AA C
 GAC GGTGTTTCCA GG
 ||| ||||| ||
 CTG TCACAAAGGT CC
 A_ A
 GAM233 KIAA1497 3' CCGTAGAAAGTACTTTGTC 33526 _ C
 GACAAGGTG TTTC ACGG
 ||||| ||| |||
 CTGTTTCAT AAAG TGCC
 G A
 GAM233 MAN1C1 3' CCGCAGGGATGCCTTGCCTT 21644 A TT CA
 AAG CAAGGTGT C CGG
 ||| ||||| | |||
 TTC GTTCCGTA G GCC
 C GG AC
 GAM233 LOC124402 3' CCGTGGAGGACCACCCTG 29766 A _
 CA GGTG TTTCCACGG
 || ||| |||||
 GT CCAC GGAGGTGCC
 C CA
 GAM233 LOC142955 5' CCGTGTGCAGCACCTTCCTC 37573 C_ TC_
 GA AAGGTGTT CACGG
 || ||||| |||
 CT TTCCACGA GTGCC
 CC CGT
 GAM233 LOC147054 5' CCGTGGAAGAGTTGTCTT 40790 GGTG
 AAGACAA TTTCCACGG
 ||||| |||||
 TTCTGTT GAAGGTGCC
 GA_
 GAM233 LOC150538 5' CCGTGGAATCTTGTT 38991 GTT
 GACAAGGT TCCACGG
 ||||| |||||
 TTGTTCTA AGGTGCC
 _
 GAM233 LOC153454 5' CCATGAAGGAGCACCTTATC 39374 C _ C
 GA AAGGTGTTTC CA GG
 || ||||| |||
 CT TTCCACGAGG GT CC
 A AA A
 GAM233 LOC196411 3' CCATGGAACCCTTGTTT 42363 T T C
 AGACAAGG GTT CCA GG
 ||||| ||| ||| ||
 TTTGTTCC CAA GGT CC
 _ _ A
 GAM233 LOC200317 3' CCGTGGAGGCAGCTAGCTC 42802 CA_ G
 GA AG TGTTTCCACGG
 || || |||||

			CT TC ACGGAGGTGCC		
			CGA G		
GAM233	LOC200609 5'	CCGTGGACATGTTGTTCA	43327	A G TT	
		A GACAA GTG TCCACGG			
		A TTGTT TAC AGGTGCC			
		C G _			
GAM233	LOC203595 5'	CCATGGGAACAACCCCGTC	43605	AA _ C	
		GAC GGT GTTTCCA GG			
		CTG CCA CAAGGGT CC			
		CC A A			
GAM233	LOC254196 5'	CCGCAGACGCCTTGTCT	46476	CCA	
		AGACAAGGTGTTT CGG			
		TCTGTTCCGCAGA GCC			
		C _			
GAM233	LOC255040 3'	CCGCAGGGTAACCTTGTCT	46108	GTT A _	
		AGACAAGGT TCC CGG			
		TCTGTTCCA GGG GCC			
		AT _ AC			
GAM233	LOC255041 3'	CCGCAGGGTAACCTTGTCT	46111	GTT A _	
		AGACAAGGT TCC CGG			
		TCTGTTCCA GGG GCC			
		AT _ AC			
GAM233	LOC91907 3'	CCGTAGAAAGTACTTTGTC	33520	_ C	
		GACAAGGTG TTTC ACGG			
		CTGTTTCAT AAAG TGCC			
		G A			
GAM234	ADORA1 3'	GTTGGAAATTGGGTGTGCCCTG	6329	CA CA _	
		CAG CACACCCAA CAAT			
		GTC GTGTGGGTT GTTG			
		CC AAAG			
GAM234	CREBL2 3'	TGTAATTGTATGTCTGTGTGT	6997	CC AC	
		GCACACA CA ACAATTACA			
		TGTGTGT GT TGTTAATGT			
		CT A _			
GAM234	EGR2 3'	TGCAATTGTGTTGGAAGTGTCC	5972	C AC A	
	T	AG ACAC CCAACACAATT CA			
		TC TGTG GGTTGTGTAA GT			
		C AA C			
GAM234	FLT1 3'	TGTAAGTGTGTGTGTGTGTG	7767	C _ A	
	T	GCACACAC CA ACACA TTACA			

			TGTGTGTG GT TGTGT AATGT		
			T G C		
GAM234	GATA3	3'	TGTAATTGTTGTTTGTATGT 7808	C CC CA	
			GCA ACA CAACA ATTACA		
			TGT TGT GTTGT TAATGT		
			A TT _		
GAM234	LAPTM5	3'	TGTAATTGCTTTGTGTGC 13619	CCCAACA	
			GCACACA CAATTACA		
			CGTGTGT GTTAATGT		
			TTC _		
GAM234	PDGFB	3'	TGTAAGTTGTGCAGGGTGTGT 8472	C AA _	
	ACTG		CAG ACACACCC CACAAT TACA		
			GTC TGTGTGGG GTGTTG ATGT		
			A AC GA		
GAM234	SLC6A6	3'	TGTAATTGTGGGTATGTGTGC 9008	_ AAC	
			GCACAC ACCC ACAATTACA		
			CGTGTG TGGG TGTTAATGT		
			TA _		
GAM234	TNFSF6	3'	TGCAATTGTAGGGTGTGTGT 6275	AAC A	
			GCACACACCC ACAATT CA		
			TGTGTGTGGG TGTTAA GT		
			GA_ C		
GAM234	C8orf13	3'	TGTAAATTCTGGCGTGTGCTG 39659	A CAACACAA	
			CAGCACAC CC TTACA		
			GTCGTGTG GG AATGT		
			C TCTTA _		
GAM234	DKFZP434E2135	3'	TGTAATTGTGGGCATGT 25120	CA AAC	
			ACA CCC ACAATTACA		
			TGT GGG TGTTAATGT		
			AC _		
GAM234	DKFZp762L0311	3'	TGCAATTGTGTGGCAGCTTGCT 20800	CACAC A A	
			AGCA CCA CACAATT CA		
			TCGT GGT GTGTTAA GT		
			TCGAC _ C		
GAM234	ESM1	3'	TGTAGATTTGTAAATGTGTGT 13914	CCC CAA	
			GCACACA AACA TTACA		
			TGTGTGT TTGT GATGT		
			AAA TTA		
GAM234	FLJ13798	3'	TGTAATTGTGTCTCGTTTGTGT 42112	C CCA	
			GCACA AC ACACAATTACA		

			TGTGT TG TGTGTTAATGT		
			T CTC		
GAM234	FLJ20047	5'	TGTAATTGTGACTCATGTGTCA 19145	C	CCCAA
			G ACACA CACAATTACA		
			A TGTGT GTGTTAATGT		
			C ACTCA		
GAM234	G2	3'	TGATGTCCAGTGTGTGCTG 33114	CCA	_
			CAGCACACAC ACA CA		
			GTCGTGTGTG TGT GT		
			ACC A		
GAM234	KIAA0016	3'	GTAAATATGTGAGGTGTGCTG 16532	ACCCA	CAA
			CAGCACAC ACA TTAC		
			GTCGTGTG TGT AATG		
			GAG_ ATA		
GAM234	KIAA1822	3'	GGGGGTGCGGGTGTGTGCTG 33555	AA	AA
			CAGCACACACCC CAC TT		
			GTCGTGTGTGGG GTG GG		
			C_ GG		
GAM234	KOC1	3'	AATTGTGTTGGGTGTGGGT 43777	A	
			GC CACACCCAACACAATT		
			TG GTGTGGGTTGTGTAA		
			G		
GAM234	MEF-2	3'	TGCAATTGTGTCTGGTATGCT 32182	CAC CA	A
			AGCA ACC ACACAATT CA		
			TCGT TGG TGTGTAA GT		
			A_ TC C		
GAM234	MGC20496	3'	TGTAATTGTGATTTACCTGTGC 27426	CACCCAA	
			GCACA CACAATTACA		
			CGTGT GTGTTAATGT		
			CCATTTA		
GAM234	N4BP3	3'	TGTAAGTGGCAGGTGTGTGT 32942	CAA	AA
			GCACACACC CAC TTACA		
			TGTGTGTGG GTG AATGT		
			ACG _		
GAM234	PTK6	5'	TGTGGGTGCTGGGTGTGGCTG 12602	A	A AA
			CAGC CACACCCA CAC TTACA		
			GTCG GTGTGGGT GTG GGTGT		
			_ C _		
GAM234	LOC145622	3'	AATTGCCTCTGGGTGTGTGT 37903	ACA_	
			GCACACACCCA CAATT		

			TGTGTGTGGGT GTTAA		
			CTCC		
GAM234	LOC154092 3'	TGTGCCAGGGGTGTGCTG	41683	A AA_	
		CAGCACAC CCC CACA			
		GTCGTGTG GGG GTGT			
		_ ACC			
GAM234	LOC170063 3'	AATTTGTTGGGTATACACTG	42185	CACAC C	
		CAG ACCCAACA AATT			
		GTC TGGGTTGT TTAA			
		ACATA _			
GAM234	LOC205327 3'	TAATTGTGTTTGTGACT	43106	_ CACCC	
		AG CACA AACACAATTA			
		TC GTGT TTGTGTTAAT			
		A _			
GAM234	LOC221463 3'	TGTAGGGCAGGTAGGGTGTGTG	44206	A ACAA_	
	CTG	CAGCACACACCC AC TTACA			
		GTCGTGTGTGGG TG GATGT			
		A GACGG			
GAM234	LOC221466 5'	TGTAAATGTCTAGGCATGTGCT	44997	CA CAAC A	
	G	CAGCACA CC ACA TTACA			
		GTCGTGT GG TGT AATGT			
		AC ATC_ A			
GAM234	LOC51031 3'	TAAGTGTGTTGGATGAGTG	18154	A C A	
		CAC CA CCAACACA TTA			
		GTG GT GGTGTGT AAT			
		A A C			
GAM235	APOL1 3'	CCGGTAAGTAAACAGTCA	9732	G CG GA	
		TGACTGTT TACT C TGG			
		ACTGACAA ATGA G GCC			
		_ AT _			
GAM235	DHCR24 3'	TGCCATCGCCTCCATCAGCCA	16528	A T TACTC	
		TG CTG TG GCGATGGCA			
		AC GAC AC CGCTACCGT			
		C T CTC_			
GAM235	GGT2 5'	CCATCTACAACAGCA	36488	A CTCGC	
		TG CTGTTGTA GATGG			
		AC GACAACAT CTACC			
		_ _			
GAM235	XK 3'	GCCATCAGCAACATCA	22059	C ACTCGC	
		TGA TGTTGT GATGGC			

ACT ACAACG CTACCG
 _ A_
 GAM235 DKFZp434C0328 3' TCACTTAGAATACCAACAGTCA 19015 _ C GCGA
 TGACTGTTG TA TC TGG
 ||||| || ||
 ACTGACAAC AT AG ACT
 C A ATTC
 GAM235 FLJ21195 3' CCACCGCCACCCAGCAGTCA 22825 TACTC A
 TGACTGTTG GCG TGG
 ||||| || ||
 ACTGACGAC CGC ACC
 CCAC_ C
 GAM235 MEGF11 3' CCATCAAATTACAACAGCCA 26205 A CTCGC
 TG CTGTTGTA GATGG
 || ||||| ||||
 AC GACAACAT CTACC
 C TAAA_
 GAM235 LOC153937 5' TTGCCATCACCGGTGAACAGCT 39449 _ G T C_
 CA TGA CTGTT TAC CG GATGGCAA
 || |||| || || |||||
 ACT GACAA GTG GC CTACCGTT
 C _ _ CA
 GAM235 LOC85414 3' TTGCCATCACAGAGACACAG 26954 T A GC_
 CTGT GT CTC GATGGCAA
 ||| || || |||||
 GACA CA GAG CTACCGTT
 _ _ ACA
 GAM236 ABL1 3' ATGCACACGGCTGGTCA 11636 ATTCA
 TGACCAGCCGT TGCAT
 ||||| ||||
 ACTGGTCGGCA ACGTA
 C_
 GAM236 ABL1 3' ATGCACACGGCTGGTCA 14225 ATTCA
 TGACCAGCCGT TGCAT
 ||||| ||||
 ACTGGTCGGCA ACGTA
 C_
 GAM236 FLT1 3' AAGATGCACTGAAACTTAGC 7761 C_ A _
 GC GT TTCA TGCATCTT
 || || |||| |||||
 CG CA AAGT ACGTAGAA
 ATT A C
 GAM236 SCN1A 3' AAGATGCACAATGGCTAGTCA 42828 C ATTCA
 TGAC AGCCGT TGCATCTT
 ||| |||| |||||
 ACTG TCGGTA ACGTAGAA
 A AC_
 GAM236 WHSC1 3' AAGATGCAGTCTCTGCTGATCA 17174 C CGTATTCA
 TGA CAGC TGCATCTT
 || || |||||

			ACT GTCG	ACGTAGAA		
			A	TCTCTG__		
GAM236	WHSC1	3'	AAGATGCAGTCTCTGCTGATCA	28438	C	CGTATTCA
			TGA CAGC	TGCATCTT		
			ACT GTCG	ACGTAGAA		
			A	TCTCTG__		
GAM236	WHSC1	3'	AAGATGCAGTCTCTGCTGATCA	28455	C	CGTATTCA
			TGA CAGC	TGCATCTT		
			ACT GTCG	ACGTAGAA		
			A	TCTCTG__		
GAM236	FLJ10408	5'	CATGAGTGTGTGGTCA	19849	GC	
			TGACCA	CGTATTCATG		
			ACTGGT	GTGTGAGTAC		
			—			
GAM236	SYNJ2	3'	AAGATGCATAGTTGACCAGTCA	30940	CAGCCGT	C
			TGAC	ATT ATGCATCTT		
			ACTG	TGA TACGTAGAA		
			ACCAGT_ _			
GAM236	SYT13	3'	AAGATGCATGAGACATTGTAGT	44884	_ CC	A
	CA		TGAC	CAG GT TTCATGCATCTT		
			ACTG	GTT CA GAGTACGTAGAA		
			AT	A_ _		
GAM236	LOC152698	5'	CATGAGGGTGTGGTCA	30311	_ GTA	
			TGACCA	GCC TTCATG		
			ACTGGT	TGG GAGTAC		
			G	—		
GAM236	LOC157280	5'	CATGAGGGTGTGGTCA	36590	_ GTA	
			TGACCA	GCC TTCATG		
			ACTGGT	TGG GAGTAC		
			G	—		
GAM236	LOC255448	5'	CATGAGGGTGTGGTCA	45400	_ GTA	
			TGACCA	GCC TTCATG		
			ACTGGT	TGG GAGTAC		
			G	—		
GAM237	CMKLR1	5'	CAGCCACAGCCAGAGGAGCC	10276	GGA	C
			GGC	TTCTCTGGCTG GGCTG		
			CCG	AGGAGACCGAC CCGAC		
			—	A		
GAM237	FGF23	3'	CAGCCACAGCCAGAGGGCCC	21790	AT	C
			GG	TCTCTGGCTG GGCTG		

CC GGAGACCGAC CCGAC
 CG A
 GAM237 PIM1 5' AGCCGCAACGCCACCCGC 43755 ATTCTC ____
 GCGG TGGC TGC GGCT
 ||| ||| |||||
 CGCC ACCG ACGCCGA
 C_____ CA
 GAM237 THBD 5' GCGGCCAGAGAACCCAGC 5921 _ A
 GC GG TTCTCTGGCTGC
 || || |||||
 CG CC AAGAGACCGGCG
 A C
 GAM237 KIAA1056 5' AGCCGCAGCCAAATAGC 17044 GG CTC
 GC ATT TGGCTGCGGCT
 || ||| |||||
 CG TAA ACCGACGCCGA
 A_ ____
 GAM237 LOC118786 5' CAGCCGCTAGTCAGAACCACCA 37198 C ATTC _
 TGG GG TCTGGCT GCGGCTG
 ||| || ||||| |||||
 ACC CC AGACTGA CGCCGAC
 A A_____ T
 GAM238 KIAA0441 3' AATTCACAAAACCTTCCAA 16706 AC
 TTG AGTTTTGTGAATT
 ||| |||||
 AAC TCAAAACACTTAA
 CT
 GAM238 KIAA0481 5' AGAAAATCCAGCAGCTGTCAG 35566 _ T A_
 TTGACAGTT TTG GA TTCT
 ||||| ||| || |||
 GACTGTCGA GAC CT AAGA
 C _ AA
 GAM238 KIAA0721 3' AGAAAACAAAACCTGGCAA 45923 A GAA
 TTG CAGTTTTGT TTCT
 ||| ||||| |||
 AAC GTCAAAACA AAGA
 G A_
 GAM238 KIAA0721 3' AGAAAACAAAACCTGGCAA 22316 A GAA
 TTG CAGTTTTGT TTCT
 ||| ||||| |||
 AAC GTCAAAACA AAGA
 G A_
 GAM238 KIAA1854 3' GAGAGTCGCAAAACCTGCCAA 35531 A A
 TTG CAGTTTTGTGA TTCTC
 ||| ||||| |||||
 AAC GTCAAAACGCT GAGAG
 C _
 GAM238 LOC131870 3' AGAGGCAAAACCTGTC 37014 GAA
 GACAGTTTTGT TTCT
 ||||| |||

CTGTCAAAACG GAGA

GAM238 LOC202018 3' AATTCAAAACTGTCAA 42957 TG
TTGACAGTTT TGAATT
||||||| |||||
AACTGTCAAA ACTTAA

GAM239 NCALD 3' AACATGTATGACAGGGGACCA 25741 C AA C
TGG TC CCTGTCATACA GTT
||| || ||||| |||
ACC AG GGACAGTATGT CAA

_ G_ A
GAM239 C20orf20 3' AACGTGTGTGTCAGTTGGACCA 20243 CT C T
TGG CAAC TG CATAACGTT
||| ||| || |||||
ACC GTTG AC GTGTGTGCAA
AG _ T

GAM239 DKFZP434I0714 5' AACGTGTGGTCGGGCCGAGC 41527 AA TCA
GCTC CCTG TACACGTT
|||| ||| |||||
CGAG GGGC GTGTGCAA
CC TG_

GAM239 DKFZP564L0862 5' ACGTGTGCAGCTCAGCCA 23530 CAAC CAT
TGGCT CTGT ACACGT
|||| ||| |||||
ACCGA GACG TGTGCA
CTC_ _

GAM239 KIAA1649 3' AGCGGATGAAGGTTGAGCCA 26101 G ACA
TGGCTCAACCT TCAT CGTT
||||||| ||| |||
ACCGAGTTGGA AGTA GCGA
_ G_

GAM239 PRDM15 3' AACGTGTATTCTCTTTGAACTA 30915 C CCTGTC
TGG TCAA ATACACGTT
||| ||| |||||
ATC AGTT TATGTGCAA
A TCTCT_

GAM240 CMAR 5' TGCAGCAACAAGGAAATGACGC 11698 G A A
A TCGCT ATTCCTTG TGTTG CA
|||| ||||| |||| ||
ACGCA TAAAGGAAC ACGAC GT
G A _

GAM240 DMD 5' CAACAGGGGAAATCAGCA 10167 G A
TGC TGATTCCTTG TG
||| ||||| ||| ||
ACG ACTAAAGGGAC AC

_ A
GAM240 DMD 5' CAACAGGGGAAATCAGCA 10173 G A
TGC TGATTCCTTG TG
||| ||||| ||| ||

ACG ACTAAAGGGAC AC
 _ A
 GAM240 C11orf25 3' CAAAACAAGGAAATCACACA 25398 C ATG
 TG GTGATTTCTTG TTG
 || ||||| ||
 AC CACTAAAGGAAC AAC
 A AA_
 GAM240 MGC22014 3' TCAACGTTCTGAAACCAC 32223 A CTT
 GTG TTTC GATGTTGA
 ||| ||| |||||
 CAC AAAG TTGCAACT
 C TC_
 GAM240 SGKL 3' TGTCTTGAGAAAGAAATCAC 14929 ____ TG TGTT
 GTGATTTCT CT A GACA
 ||||| || | |||
 CACTAAAG GA T CTGT
 AAA GT ____
 GAM241 CTNS 3' AAACCTCCTTCCCTCTGCCCA 11381 T CTTTA
 TG GGCAGAGGGGA GTTT
 || ||||| |||
 AC CCGTCTCCCTT CAAA
 _ CCTC_
 GAM241 RASGRP1 3' AAATAAGCCAATAGCACCA 12300 TG AGAGG A
 TG GC GG CTTTAGTTT
 || || || |||||
 AC CG CC GAAATCAAA
 CA ATAA_ _
 GAM241 XRCC2 3' AAATAAGAGCTGCACA 11899 G AGGGGA
 TGTG CAG CTTTAGTTT
 ||| ||| |||||
 ACAC GTC GAAATCAAA
 _ GA____
 GAM241 DKFZP434O047 5' AAACCAAAGCCCCCTTTCT 17858 C A A
 GG AGAGGGG CTTT GTTT
 || ||||| ||| |||
 TC TTTCCCC GAAA CAAA
 _ C C
 GAM241 FBXO9 3' GGAGTCCCCCCTGCCCA 27259 T A
 TG GGCAG GGGGACTTT
 || ||| |||||
 AC CCGTC CCCCTGAGG
 _ C
 GAM241 FLJ21940 3' AAATAAGCCTGCAAGCGCCA 23106 AGAG__ A
 C GTGGC GGG CTTTAGTTT
 |||| | |||||
 CACCG TCC GAAATCAAA
 CGAACG _
 GAM241 FLJ22031 3' AAATAAGTGCTCTGCCCA 24675 T GGG T
 TG GGCAGAG ACTT AGTTT
 || ||||| ||| |||||

			AC CCGTCTC TGAA TCAAA		
			— G — —		
GAM241	IRF7	5'	CTGTAGCCCCCTCTGCCA 10250	A T	
			TGGCAGAGGGG CT TAG		
			ACCGTCTCCCC GA GTC		
			C T		
GAM241	IRF7	5'	CTGTAGCCCCCTCTGCCA 7302	A T	
			TGGCAGAGGGG CT TAG		
			ACCGTCTCCCC GA GTC		
			C T		
GAM241	IRF7	5'	CTGTAGCCCCCTCTGCCA 10252	A T	
			TGGCAGAGGGG CT TAG		
			ACCGTCTCCCC GA GTC		
			C T		
GAM241	IRF7	5'	CTGTAGCCCCCTCTGCCA 10248	A T	
			TGGCAGAGGGG CT TAG		
			ACCGTCTCCCC GA GTC		
			C T		
GAM241	KIAA1229	3'	TAAACTAAAGAGCTTCTGCACA 31101	G GGA	
			TGTG CAGAGG CTTTAGTTTA		
			ACAC GTCTTC GAAATCAAAT		
			— GA_		
GAM241	KIAA1431	3'	AAACTAAAGCCCATGGACCA 31550	CAGAG A	
			TGG GGG CTTTAGTTT		
			ACC CCC GAAATCAAA		
			AGGTA —		
GAM241	PP1628	3'	AAACTGGGCCCCCATGCCACA 24854	GA A T	
			TGTGGCA GGGG CTT AGTTT		
			ACACCGT CCCC GGG TCAAA		
			AC — —		
GAM241	QKI	3'	AACTCGTCCCCTCTTCCACA 32615	C TTT	
			TGTGG AGAGGGGAC AGTT		
			ACACC TCTCCCCTG TCAA		
			T C_		
GAM241	SDCCAG33	5'	AAACTGGTCCCCTCCACCA 12369	CA TT	
			TGG GAGGGGACT AGTTT		
			ACC CTCCCCTGG TCAAA		
			AC —		
GAM241	SNPH	3'	GGAGCCCCCTCTGCCACA 16300	A	
			TGTGGCAGAGGGG CTTT		

ACACCGTCTCCCC GAGG

C

GAM241 LOC145644 5' AAATAAAGAAGGCCACAC 32288 CAGA GA__

GTGG GGG CTTTAGTTT

|||| ||| |||||

CACC CCC GAAATCAAA

A__ GGAA

GAM242 ADCY6 3' CCTCCAGACCCTGCTAACC 17587 T GAA

GGTT GGT GGTCTGGAGG

|||| ||| |||||

CCAA TCG CCAGACCTCC

_ TC_

GAM242 ADCY6 3' CCTCCAGACCCTGCTAACC 21975 T GAA

GGTT GGT GGTCTGGAGG

|||| ||| |||||

CCAA TCG CCAGACCTCC

_ TC_

GAM242 DTR 3' CCCCTCCACCAAACCCCA 7659 A A TCT

TG GGTTTGGTG AGG GG

|| ||||| ||| ||

AC CCAAACAC TCC CC

C C _

GAM242 FZD10 3' CAGAAACCTCCATCAAACCTCA 14051 A _

TGAGGTTTGGTG AGG TCTG

||||||| ||| |||

ACTCCAAACTAC TCC AGAC

C AA

GAM242 HOXC4 5' CCCCAGACCTCCAGAAATGACG 15973 G TGG__ A A

TCA

TGA GTT TG AGGTCTGG GG

||| ||| || ||||| ||

ACT CAG AC TCCAGACC CC

G TAAAG C _

GAM242 DNAJB5 3' CCCCAAACCTCCAAATCCCA 14588 A TGA C A

TG GGTTTGG AGGT TGG GG

|| ||||| ||| ||| ||

AC CTAAACC TTCA ACC CC

C _ A _

GAM242 DRIL2 3' CCGCCCCCGCCAAACCTCA 13185 AA CT

TGAGGTTTGGTG GGT GG

||||||| ||| ||

ACTCCAAACCGC CCG CC

CC _

GAM242 KIAA0418 3' CCTACCCCACCACACCCCA 15996 A T AA CT

TG GGT TGGTG GGT GG

|| ||| |||| ||| ||

AC CCA ACCAC CCA CC

C C C_ T_

GAM242 PIP5K2B 3' CCTCCAAACCTGGCCAAGCCCA 9608 A GA C

TG GGTTTGGT AGGT TGGAGG

|| ||||| ||| |||||

AC CCGAACCG TCCA ACCTCC
 _ G_ A
 GAM242 PIP5K2B 3' CCTCCAAACCTGGCCAAGCCCA 9609 A GA C
 TG GGT TTGGT AGGT TGGAGG
 || ||||| ||| |||||
 AC CCGAACCG TCCA ACCTCC
 _ G_ A
 GAM242 PRO2900 3' CCTCCAGGCTCCACTCACCAGA 20708 A____
 CCTCA TGAGGTTTGGTGA GGTCTGGAGG
 ||||| |||||
 ACTCCAGACCACT TCGGACCTCC
 CACC
 GAM242 RAI15 3' CCCCCAACCCCAACCAGACCTCA 33118 AA C A
 TGAGGTTTGGTG GGT TGG GG
 ||||| ||| |||
 ACTCCAGACCAC CCA ACC CC
 CC _ _
 GAM242 SEC14L2 5' CTCCCGCCCCCAAACCCCA 14805 A TGAA CT
 TG GGT TTGG GGT GGAG
 || ||||| ||| |||
 AC CCAAACC CCG CCTC
 C C_ C_
 GAM242 LOC127534 3' CCCCCTGGCACCAAATCCCA 37167 A AA CT A
 TG GGT TTGGTG GGT GG GG
 || ||||| ||| |||
 AC CTAAACCAC TCA CC CC
 C GG _ _
 GAM242 LOC143916 3' CCTCCAAACCTTCAGACCTC 37650 TGG C
 GAGGTT TGAAGGT TGGAGG
 ||||| ||||| |||||
 CTCCAG ACTTCCA ACCTCC
 _ A
 GAM242 LOC253917 5' CCTCCAGACCCTATCAACAGCC 46065 _ AA
 TCA TGAGGT TTGGTG GGTCTGGAGG
 ||||| ||||| |||||
 ACTCCG AACTAT CCAGACCTCC
 AC C_
 GAM242 LOC92568 3' CCTCCTTGACCAAACCTCA 34577 G TCT
 TGAGGTTTGGT AAGG GG
 ||||| ||||| ||| |||
 ACTCCAAACCA TTCC CC
 G T_
 GAM242 LOC93589 3' CTCCCCCGACCAAACCCCA 35978 A GAA TCT
 TG GGT TTGGT GG GGAG
 || ||||| ||| |||
 AC CCAAACCA CC CCTC
 C G_ C_
 GAM243 KIF3C 3' TACCCAAATCAGCCCC 8060 T TATT
 GG GGCTGATTT GGTA
 || ||||| |||

CC CCGACTAAA CCAT
 — C___
 GAM243 KIAA1828 5' ACTTCCAAAACCAGCCACCGCT 36524 A A ATT
 AG GGTGGCTG TTTT GGT
 || ||||| ||| ||
 TC CCACCGAC AAAA TCA
 G C CCT
 GAM243 Kv6.3 3' CAGGCAAATCACGCCACCTC 28564 _ TA
 GAGGTGGC TGATTT TTG
 ||||| ||||| |||
 CTCCACCG ACTAAA GAC
 C CG
 GAM243 MATR3 3' ATACCAATAAAAAGAAAACCCT 20819 A GG_ GA
 AG GGT CT TTTTATTGGTAT
 || || |||||
 TC CCA GA AAAATAACCATA
 _ AAA _
 GAM243 RRN3 3' ATACCAATAAAAGGTACCTC 20486 G GAT
 GAGGTG CT TTTATTGGTAT
 ||||| || |||||
 CTCCAT GA AAATAACCATA
 G _
 GAM243 LOC253039 3' ATAAAATCAGCCACTCT 45993 G
 AGAG TGGCTGATTTTAT
 ||| |||||
 TCTC ACCGACTAAAATA
 _
 GAM243 LOC51634 3' ATTTTAAATCAGCCAGCTC 18100 G TT
 GAG TGGCTGATTTTA GGT
 ||| ||||| |||
 CTC ACCGACTAAAAT TTA
 G TT
 GAM244 SIRT1 3' CTAGAGATCAACTTTCTC 14541 AATCAA C
 GGGAAAGT GATC CTAG
 ||||| ||| |||
 CTCTTTCA CTAG GATC
 A_ A
 GAM244 ZNF10 3' ACCAGAGATCTTGATCTCTCTC 17692 A TA C A
 GGGA AG ATCAAGATC CT GT
 ||| || ||||| || ||
 CTCT TC TAGTTCTAG GA CA
 C _ A C
 GAM244 ARHGEF11 5' CTAGAAAATTACTTTCCC 16639 CAAGATCC
 GGGAAAGTAAT CTAG
 ||||| |||
 CCCTTTCATTA GATC
 AAA_
 GAM244 LRP1B 5' ACCAGCTTCGAGTTACTTTCCC 20637 CAA TCC A
 GGGAAAGTAAT GA CT GT
 ||||| || ||

			CCCTTTCATTG CT GA CA		
			AG_ TC_ C		
GAM244	RAI15	3'	CAGGGGGATTACTTCCC 33117	A	AAGA A
			GGGAA GTAATC TCCCT G		
			CCCTT CATTAG GGGGA C		
			_ _ _ _ C		
GAM244	SDF1	3'	ACTAGGGATCCCTCATCTGTCC 43687	A	TAATCAA
	C		GGGA AG GATCCCTAGT		
			CCCT TC CTAGGGATCA		
			G TACTCC_		
GAM244	LOC149373	3'	ACTAGGGATCCCACTTCTC 38717	A	AATCAA
			GGGAA GT GATCCCTAGT		
			CTCTT CA CTAGGGATCA		
			_ CC_		
GAM244	LOC257464	5'	ACTCTGGTCCCACTACTTTCC 43160	ATCAA	CCT
			GGAAAGTA GATC AGT		
			CCTTTCAT CTGG TCA		
			CAACC TC_		
GAM245	ARF3	3'	ACTTTGCCTCTTCTCCTGCCTC 7377	TT	TC
			GAGGTAGGAGA GA CAAAGT		
			CTCCGTCCTCT CT GTTTCA		
			T_ CC		
GAM245	FE65L2	3'	TGGACAGTTGGCTCTACCTC 28396	_ A_	A
			GAGGTAG G GATTG TCCA		
			CTCCATC C TTGAC AGGT		
			T GG _		
GAM245	FE65L2	3'	TGGACAGTTGGCTCTACCTC 28397	_ A_	A
			GAGGTAG G GATTG TCCA		
			CTCCATC C TTGAC AGGT		
			T GG _		
GAM245	RARA	3'	TCAACCTCCCCCCTGCCTCG 6690	_ _	A
			CGAGGTA GGAG TTGA		
			GCTCCGT CCTC AACT		
			CCCC C		
GAM245	SED1	3'	ACTTCAAGCAATTCTCCTGCCT 15902	_	ATCCA
	C		GAGGTAGGAGA TTG AAGT		
			CTCCGTCCTCT AAC TTCA		
			T GAAC_		
GAM245	SEL1L	3'	ACCTTGGATCAGTGGTCACCTC 11500	A AG	A
			GAGGT GG ATTGATCCAA GT		

			CTCCA CT T	GACTAGGTT CA		
			_ GG	C		
GAM245	FLJ10853	3'	ACTTTAAACATTTTCCTAACTC	20209	G	TGATCC
			GAG TAGGAGAT	AAAGT		
			CTC ATCCTTTA	TTTCA		
			A	CAAA_		
GAM245	FLJ20511	3'	ACTCTGGACCTGCCTGCCTC	19526		AGATTGA A
			GAGGTAGG	TCCA AGT		
			CTCCGTCC	AGGT TCA		
			GTCC_	C		
GAM245	KIAA1026	3'	GGCGATCTGCCCCACCTC	35276	A _	AT
			GAGGT GG AGATTG	CC		
			CTCCA CC TCTAGC	GG		
			C G	_		
GAM245	KIAA1198	3'	ACCTTGATCCACCCACCTCG	31701	A AGATT	_ A
			CGAGGT GG	GATC CAA GT		
			GCTCCA CC	CTAG GTT CA		
			C AC_	T C		
GAM245	KIAA1536	3'	ACTTCATCCTCTCCTACCTGG	21921	G	TT CCA
			C AGGTAGGAGA	GAT AAGT		
			G TCCATCCTCT	CTA TTCA		
			G	C_ C_		
GAM245	KIAA1615	3'	ACCTTGATCCCCCTGCCTCG	34080		AGATT _ A
			CGAGGTAGG	GATC CAA GT		
			GCTCCGTCC	CTAG GTT CA		
			CC_	T C		
GAM245	LOC146227	3'	ACTCTGCCTCCCTCCACCTC	38080	A	ATT TC A
			GAGGT GGAG	GA CA AGT		
			CTCCA CCTC	CT GT TCA		
			C	C_ CC C		
GAM245	LOC148137	3'	CTTGGGCTCCTACCTC	29517		ATTGA A
			GAGGTAGGAG	TCCAA G		
			CTCCATCCTC	GGTT C		
			_	C		
GAM245	LOC92876	5'	GGTGATCCACCTACCTCG	35039	A_	GAT
			CGAGGTAGG	GATT CC		
			GCTCCATCC	CTAG GG		
			AC	T_		
GAM246	ACVRL1	5'	TCCCGGGAGGCTGCCGCGCCA	5453		AG
			TGGCGCGGTAGCCTT	TGGGA		

ACCGCGCCGTCGGAG GCCCT

G_

GAM246 E2F2 5' TCCCCCGGCCTCCGCGCCA 10293 TA TTAGT
TGGCGCGG GCC GGA
||||| ||| |||
ACCGCGCC CGG CCCT
TC CC__

GAM246 PDGFRA 3' CTCCCACTCCATACCCCGCCA 12882 C GCCTT
TGGCG GGTA AGTGGGAG
||||| ||| |||||
ACCGC CCAT TCACCCTC
C ACC__

GAM246 PLA2G2D 3' TCTCCACCAAGAGGCCACC 14773 A A__
GGT GCCTT GTGGGAGA
||| ||| |||||
CCA CGGAG CACCCTCT
C AAC

GAM246 CPLX1 3' CTCCGGGCAGAGACCACGCGC 13451 AGC A G_
C GGC GCGT CTT GT GGAG
||||| ||| |||
CCGCGCCA GAG CG CCTC
CCA A GG

GAM246 DKFZP566K1924 5' CCCCCGAGCCGCGCGCCA 36519 TA C AGT
TGGCGCGG GC TT GGG
||||| ||| |||
ACCGCGCC CG AG CCC
GC _ GCC

GAM246 PAXIP1L 3' CTCCCACTAAAAAGCTAACTCC 34739 CGCGG C_
A TGG TAGC TTAGTGGGAG
||| ||| |||||
ACC ATCG AATCACCCTC
TCA__ AAA

GAM246 LOC147791 3' CTCCCACCCCTCCTCCCCGCGC 40858 T_ CCTTA
CA TGGCGCGG AG GTGGGAG
||||| ||| |||||
ACCGCGCC TC CACCCTC
CC CTCCC

GAM246 LOC149296 5' CTCCCACTAGTTACCCACCCCA 38695 CGC_ CT
TGG GGTAGC TAGTGGGAG
||| ||| |||||
ACC CCATTG ATCACCCTC
CCAC _

GAM247 APBA1 3' GGGCATCTGAAGCTTTACCA 34647 C T CCCC
TGG AAAGTTT CA GCCC
||| ||| ||| |||
ACC TTTCGAA GT CGGG
A _ CTA_

GAM247 BMP1 3' CGGGGTGAAACCTCCCA 12773 CAA T
TGG AG TTTCACCCCG
||| ||| |||||

			ACC TC AAAGTGGGGC		
			C__ C		
GAM247	CAPN10	3'	GGGCAGCAGGAAC TTTGCC 23354	CACCCC	
			GGCAAAGTTTT GCCC		
			CCGTTTCAAGG CGGG		
			ACGA__		
GAM247	CDKN2B	5'	GGCGGGGCAGTGAGGACTCCGC 27809	AA	__
			GC AGTTTTCA CCCC GCC		
			CG TCAGGAGT GGGGCGG		
			CC GAC		
GAM247	CDKN2D	5'	GGGCGGGGCGGGGGGCTTTGC 7554	TT A_	
			GCAAAGTT C CCCC GCC		
			CGTTTCGG G GGGGCGGG		
			GG GC		
GAM247	DAAM2	3'	GGGCAAGATGAAGGCTTCCA 44330	CA	CCCC
			TGG AAGTTTTCA GCCC		
			ACC TTCGGAAGT CGGG		
			__ AGAA		
GAM247	FLRT2	3'	GGCAAGGTGAAGGCATTGCCA 14882	A	CC
			TGGCAA GTTTTCACC GCC		
			ACCGTT CGGAAGTGG CGG		
			A AA		
GAM247	GPC6	5'	GGGCAAGGTGAAGAGCGCACC 12261	CAAA	_ CC
			GG GTTTT CACC GCCC		
			CC CGAGA GTGG CGGG		
			ACG_ A AA		
GAM247	LBR	3'	GGTGT TTGAAAATTTGCCA 29853	G	CCC
			TGGCAA TTTTCA CGCC		
			ACCGTTT AAAAGT GTGG		
			_ TT_		
GAM247	LFG	3'	GGGCGGGGTGGGATTTTGC 37696	T TT	
			GCAAAG T CACCCCGCCC		
			CGTTTT A GTGGGCGGG		
			T GG		
GAM247	LYN	5'	GGGCGGGGCGGCCGCGCCA 8154	AAA TT A	
			TGGC GT TC CCCC GCC		
			ACCG CG GG GGGGCGGG		
			_ CC C		
GAM247	MBD3	3'	GGACAGGGTGAGGCTCCCA 10022	CAA T CG_	
			TGG AGTTT CACCC CC		

			ACC TCGGA GTGGG GG		
			C__ _ ACA		
GAM247	MLC1	3'	GGGCGGCCTGCAGACCCTGCCA 29220	AA	T CC
			TGGCA GTTT CA CCGCCC		
			ACCGT CAGA GT GGCGGG		
			CC C CC		
GAM247	MLC1	3'	GGGCGGCCTGCAGACCCTGCCA 17526	AA	T CC
			TGGCA GTTT CA CCGCCC		
			ACCGT CAGA GT GGCGGG		
			CC C CC		
GAM247	MMP11	3'	GGGCAGGGAGGCTTTGGCA 12578	G	TCA C
			TG CAAAGTTT CCC GCCC		
			AC GTTTCGGA GGG CGGG		
			G _ _ A		
GAM247	NEU3	3'	GCAAAATGAAAATTTTGCC 13455		CCCC
			GGCAAAGTTTTC A GC		
			CCGTTTAAAAGT CG		
			AAAA		
GAM247	PODXL	3'	GGGCAGGGGTGAAACTCCAGC 11876	AA_	T _
			GC AGTTT CACCCC GCCC		
			CG TCAAA GTGGGG CGGG		
			ACC _ _ A		
GAM247	SLC2A3	3'	GGCACATGACAACTTTGCCA 13817		T CCCC
			TGGCAAAGTT TCA GCC		
			ACCGTTTCAA AGT CGG		
			C ACA_		
GAM247	TCEA1	3'	GGCAAAGATGAGAACTTCCCA 39203	CA	CCCC_
			TGG AAGTTTTC A GCC		
			ACC TTCAAGAGT CGG		
			C_ _ AGAAA		
GAM247	TIC	3'	GGGCGGGGTGGGGCCTCCA 14829	CAA	T TT
			TGG AG T CACCCCGCCC		
			ACC TC G GTGGGGCGGG		
			_ _ C GG		
GAM247	TSG	3'	GGACAGGGTGAAAATGCT 21812	AAG	CG_
			GGCA TTTTCACCC CC		
			TCGT AAAAGTGGG GG		
			_ _ ACA		
GAM247	TXNRD1	5'	CGGGGAGGCTTTTCCA 9336	C	TCA
			TGG AAAGTTT CCCC		

			ACC TTTCGGA GGGGC		
			T ____		
GAM247	A2BP1	5'	GGGCGGGGCTGACCTGCC 20807	AA	TTCA
			GGCA GTT CCCCCGCC		
			CCGT CAG GGGGCGGG		
			C_ TC__		
GAM247	A2BP1	5'	GGGCGGGGCGCTCTGCCA 20808	A	TTTCA
			TGGCA AGT CCCCCGCC		
			ACCGT TCG GGGGCGGG		
			C CG__		
GAM247	AP4B1	5'	GGGCGGGGCGAACCCTGCC 13359	AA TT	A
			GGCA G TTC CCCCCGCC		
			CCGT C AAG GGGGCGGG		
			__CC C		
GAM247	ARHU	3'	GGGCGGGGCGTGTAGCCAGCCA 22184	AAA	TTCA_
			TGGC GTT CCCCCGCC		
			ACCG CGA GGGGCGGG		
			AC_ TGTGC		
GAM247	DKFZp547I094	3'	GGCAGGGCAGGGGCTCCA 25857	CAA	CA C
			TGG AGTTTT CCC GCC		
			ACC TCGGGG GGG CGG		
			__ AC A		
GAM247	DOC2B	5'	GGGCGGGGCGGCGCTGCC 9638	AA TTT	A
			GGCA GT C CCCCCGCC		
			CCGT CG G GGGGCGGG		
			CG __C		
GAM247	FASTK	3'	GGGTGGGGGAGCCCTGGCCA 24730	AA TT	A
			TGGC AG TTC CCCCCGCC		
			ACCG TC GAG GGGGTGGG		
			G_ CC _		
GAM247	FLJ12975	3'	GGCGGGGTCTCTGTCA 34480	A	TTTTC
			TGGCA AG ACCCCGCC		
			ACTGT TC TGGGGCGG		
			C ____		
GAM247	FLJ14297	3'	GGCTCCCGTGAAAACCTCTATCA 24391	CAA	CCC_
			TGG AGTTTTTAC GCC		
			ACT TCAAAAGTG CGG		
			ATC CCCT		
GAM247	FLJ21687	3'	GGCGGGGTGGGGCTGCC 24290	AA T TT	
			GGCA G T CACCCCGCC		

			CCGT C G GTGGGGCGG		
			__ GG		
GAM247	FLJ22559	5'	GGGCGGGGTGTCGCCGCCA	24465	AAA TTTC
			TGGC GT ACCCGGCC		
			ACCG CG TGGGGCGGG		
			C__ CTGC		
GAM247	FLJ23071	3'	GCAGGGCCAGGCTTTGGCA	24847	G TCA C
			TG CAAAGTTT CCC GC		
			AC GTTTCGGA GGG CG		
			G CC_ A		
GAM247	FLJ23168	3'	GGGTTTAGAAATCTTTGCCA	24652	T ____
			TGGCAAAG TTTC ACCC		
			ACCGTTTC AAAG TGGG		
			T ATT		
GAM247	jdp2	3'	GGCGGGGTGCATTTCCA	28230	C GTTTT
			TGG AAA CACCCCGCC		
			ACC TTT GTGGGGCGG		
			_ AC__		
GAM247	KIAA0557	3'	GCGTGAAAACCTTGCC	38207	A CCC
			GGCAA GTTTTCAC GC		
			CCGTT CAAAAGTG CG		
			C ____		
GAM247	KIAA0599	5'	GCAGGTAGCCGACTTTGCCA	37857	TTC_ CC
			TGGCAAAGTT ACC GC		
			ACCGTTTCAG TGG CG		
			CCGA A_		
GAM247	KIAA0674	5'	GGCGGGTGAAGTTTGCCA	30400	GT C
			TGGCAA TTTCACCC GCC		
			ACCGTTT GAAGTGGG CGG		
			__ __		
GAM247	KIAA1340	3'	GGCTAAAAAACTTTGTCA	34296	CACCCC
			TGGCAAAGTTTT GCC		
			ACTGTTTCAAAA CGG		
			AAAT__		
GAM247	KIAA1465	3'	GGGCGGGGTCTTTTTTCCA	30505	C TTTTC
			TGG AAAG ACCCGCCC		
			ACC TTTT TGGGGCGGG		
			_ TTCT_		
GAM247	KIAA1649	3'	GGGCGGGGCAGGCGCTA	26109	AAA TCA
			TGGC GTTT CCGGCC		

			ATCG CGGA GGGGCGGG		
			___ C__		
GAM247	KIAA1918	3'	GGCAGGGGCTTTGTCA 36215	TTTCA	C
			TGGCAAAGT CCC GCC		
			ACTGTTTCG GGG CGG		
			_____ A		
GAM247	MGC11349	3'	GGGCAAGTTGATTTTGCCA 24760	TTC	CCC
			TGGCAAAGTT AC GCCC		
			ACCGTTTTAG TG CGGG		
			T__ AA__		
GAM247	MGC2821	5'	GCGGGGTGGGGGCTGCC 23489	AA	TT
			GGCA GTT CACCCCGC		
			CCGT CGG GTGGGGCG		
			___ GG		
GAM247	MGC35558	3'	GCAGGGAGGGAACCTTGCCA 29614	A	TT A C
			TGGCAA GTT C CCC GC		
			ACCGTT CAA G GGG CG		
			_ GG A A		
GAM247	MGC4368	5'	GGGCGGGGATGGCTCGGCCA 23700	AA	TTCA
			TGGC AGTT CCCC GCCC		
			ACCG TCGG GGGGCGGG		
			GC TA__		
GAM247	MGC7036	5'	GGGCGAGGTAGGACTCTGCC 29694	A	TC CC
			GGCA AGTTT ACC GCCC		
			CCGT TCAGG TGG CGGG		
			C GA A__		
GAM247	PCANAP7	5'	GGGCGGGGCAACGGCTCCCCA 44838	CAA	TTCA
			TGG AGTT CCCC GCCC		
			ACC TCGG GGGGCGGG		
			CC_ CAAC		
GAM247	PIP5K2B	5'	GGGCGGGGCGGCCGCTGCC 28930	AA	TT A
			GGCA GT TC CCCC GCCC		
			CCGT CG GG GGGGCGGG		
			___ CC C		
GAM247	PIP5K2B	5'	GGGCGGGGCGGCCGCTGCC 9614	AA	TT A
			GGCA GT TC CCCC GCCC		
			CCGT CG GG GGGGCGGG		
			___ CC C		
GAM247	SDF1	3'	GGGCAGGGCCCCAGGCATTGCC 43691	A	TCA_ C
	A		TGGCAA GTTT CCC GCCC		

			ACCGTT CGGA GGG CGGG		
			A CCCC A		
GAM247	SLK	5'	GCAGGGAAGAGAACTTTGCC 16281	CA__	C
			GGCAAAGTTTT CCC GC		
			CCGTTTCAAAG GGG CG		
			AGAA A		
GAM247	ZFP106	3'	GGGCAGGGGGACTTCACCA 22833	CA	TTCA _
			TGG AAGTT CCCC GCCC		
			ACC TTCAG GGGG CGGG		
			AC ____ A		
GAM247	LOC130617	5'	GGGCGGGGCAGGGAGCCCGCCA 29025	AAA	TT A_
			TGGC GTT C CCCC GCCC		
			ACCG CGA G GGGGCGGG		
			CC_ GG AC		
GAM247	LOC132332	3'	GCAGAGTGAAGGCATGTCA 37488	AA	CCC
			TGGCA GTTTTCAC GC		
			ACTGT CGGAAGTG CG		
			A_ AGA		
GAM247	LOC144195	3'	GGCACATGACAACTTTGCCA 30265	T	CCCC
			TGGCAAAGTT TCA GCC		
			ACCGTTTCAA AGT CGG		
			C ACA_		
GAM247	LOC144893	5'	GGGCAGGGGAGACTGCCGCCA 40461	AA_	TCA C
			TGGC AGTTT CCC GCCC		
			ACCG TCAGA GGG CGGG		
			CCG ____ A		
GAM247	LOC146375	5'	GGGCCGAGAACTTTGCCA 38141	AC	
			TGGCAAAGTTTTC CCC		
			ACCGTTTCAAGAG GGG		
			CC		
GAM247	LOC157543	5'	GGCTTTGAAGAACTTTGCCA 39611	_	CCCC
			TGGCAAAGTTTT CA GCC		
			ACCGTTTCAAGA GT CGG		
			A TT__		
GAM247	LOC201294	3'	GGACGGGGAGCTTGCCA 42568	A	TTCA _
			TGGCAA GTT CCCCC CC		
			ACCGTT CGA GGGGC GG		
			_ ____ A		
GAM247	LOC202181	5'	GGCGTCTGTGAAAACCCCA 42969	CAAA	CC_
			TGG GTTTTCAC CGCC		

			ACC CAAAAGTG GCGG		
			C___ TCT		
GAM247	LOC203084	3'	GGCAAAGATGAAAACCTCCCA	42281	CA CCCC_
			TGG AAGTTTTCA GCC		
			ACC TTCAAAGT CGG		
			C_ AGAAA		
GAM247	LOC203427	5'	GGGCGGGGCCTGGGGCCCGCCA	43045	AAA CA_
			TGGC GTTTT CCCC GCCC		
			ACCG CGGGG GGGGCGGG		
			CC_ TCC		
GAM247	LOC219855	3'	GGGCAAGACAATGGAACTTCC	43997	CA CCCC__
	A		TGG AAGTTTTCA GCCC		
			ACC TTCAAAGT CGGG		
			___ AACAGAA		
GAM247	LOC219994	5'	GGCAGGGTGAGGGGCGCCA	44835	AAAG C
			TGGC TTTTCACCC GCC		
			ACCG GGGAGTGGG CGG		
			CG_ A		
GAM247	LOC51103	5'	GGCGGAAGAATTTTGCCA	31446	CACC
			TGGCAAAGTTTT CCGCC		
			ACCGTTTAAAGA GGCGG		
			A___		
GAM248	BCLG	5'	TGACATGACAGCCATTCC	25053	AGAG CA
			GGAATGGCTGT CA TCA		
			CCTTACCGACA GT AGT		
			___ AC		
GAM248	BCLG	5'	TGACATGACAGCCATTCC	28967	AGAG CA
			GGAATGGCTGT CA TCA		
			CCTTACCGACA GT AGT		
			___ AC		
GAM248	MSN	3'	TGCTCCACAGCCATCCCA	30229	A A
			TGG ATGGCTGT GAGCA		
			ACC TACCGACA CTCGT		
			C C		
GAM248	ZNF42	5'	TGCCCTACAGCCCTTCCA	9468	T A
			TGGAA GGCTGTAG GCA		
			ACCTT CCGACATC CGT		
			C C		
GAM248	DKFZP434I0714	3'	TGTTTAGCCATTCTA	41531	GTA
			TGGAATGGCT GAGCA		

ATCTTACCGA TTTGT

GAM248 FLJ14082 3' GACATGCCCTGCAGCCCCA 24611 AAT A CA
TGG GGCTGTAG GCA TC
||| ||||| ||| ||
ACC CCGACGTC CGT AG

____ C AC
GAM248 KIAA0632 3' ATGTGCTCGGCCCCCA 17806 AAT GTA
TGG GGCT GAGCACAT
||| ||| |||||
ACC CCGG CTCGTGTA

C_____
GAM248 KIAA1010 3' ATGAGAGCTCCAGCCATTCCA 35669 TA ACA
TGGAATGGCTG GAGC TCAT
||||||| ||| |||
ACCTTACCGAC CTCG AGTA
____ AG_

GAM248 LOC148089 3' ATGACACACTCCTCGGTCATTC 38449 TA CACA
C GGAATGGCTG GAG TCAT
||||||| ||| |||
CCTTACTGGC CTC AGTA
TC ACAC

GAM248 LOC222031 3' ATGGCCCCACAGCCATTGCA 45130 G AGA A
TG AATGGCTGT GC CAT
|| ||||| || |||
AC TTACCGACA CG GTA
G CCC _

GAM248 LOC93589 3' TGT TTCAGCTCATTCCA 35980 _ TA
TGGAATG GCTG GAGCA
||||| ||| |||||
ACCTTAC CGAC TTTGT
T _

GAM249 UBE2G2 3' GCAGATGCTTTTCTTATAATCT 32376 C T TG
A TAGA TAT AGG GGGCATCTGC
||| ||| ||| |||||
ATCT ATA TTC TTCGTAGACG
A _ TT

GAM249 LOC147118 5' CAAATGCCCCACGGTAG 40807 AG C
CTATT GTGGGGCAT TG
|||| ||||| ||| ||
GATGG CACCCCGTA AC
____ A

GAM249 LOC148089 3' GCAGATGCCCCACACCACCACT 38452 ATTAG_
CT AGACT GTGGGGCATCTGC
|||| |||||
TCTGA CACCCCGTAGACG
CCACCA

GAM249 LOC220883 3' GCAGATGCCAAAATAATGTC 43851 T GGTGG
GAC ATTA GGCATCTGC
||| ||| |||||

CTG TAAT CCGTAGACG
 _ AAAA_
 GAM249 LOC51279 3' GCAGACACCCACCTGTGCCCC 18617 ACTAT CA
 TA TAG TAGGTGGGG TCTGC
 ||| ||||| |||||
 ATC GTCCACCCC AGACG
 CCGGT AC
 GAM250 OPA3 3' AACCAGGACGACCTGCAAGG 24774 A_ AATCC
 CCT CAGGTT TCCTGGTT
 ||| ||||| |||||
 GGA GTCCAG AGGACCAA
 AC C____
 GAM250 SFRP1 3' GAACCAAAGGGAGGCTCTCTG 8931 TTAAT ____
 TAGG CTACAGG CCTCCT GGTTTC
 ||||| ||||| |||||
 GATGTCT GGAGGG CCAAG
 CTC__ AAAA
 GAM250 STS 3' GAACCAGTTATTTAACCTGTA 5909 TCCTC
 TACAGGTAA CTGGTTC
 ||||| |||||
 ATGTCCAATT GACCAAG
 TATT_
 GAM250 TRAF1 3' GAACCAGGCTTGAACCGTAGG 12199 A TAA T_
 CCTAC GGT TCC CCTGGTTC
 ||||| ||| |||||
 GGATG CCA AGG GGACCAAG
 _ ____ TTC
 GAM250 KIAA1165 3' GACTTTAGGATTAACCTGTA 33477 CCT
 TACAGGTTAATCCT GGTT
 ||||| |||||
 ATGTTCAATTAGGA TCAG
 TT_
 GAM250 KIAA1822 3' GAACCAGGAGAAAGGGGTGAGG 33552 A GGTTAATC
 CCT CA CTCCTGGTTC
 ||| || |||||
 GGA GT GAGGACCAAG
 _ GGGGAAA_
 GAM250 PRIC285 3' GAACCAGGAAGGAAACCCTGTG 30804 TTAA _
 G CTACAGG TCCT CCTGGTTC
 ||||| ||| |||||
 GGTGTCC AGGA GGACCAAG
 CAA_ A
 GAM250 LOC146714 5' GAACCAGGAGGGTGGCC 40721 A
 GGTTA TCCTCCTGGTTC
 ||||| |||||
 CCGGT GGGAGGACCAAG
 _
 GAM250 LOC149832 5' GAACCAGGAGAAGATGGTTGTG 41081 GTTA _
 GG CCTACAG ATC CTCCTGGTTC
 ||||| ||| |||||

GGGTGTT TAG GAGGACCAAG
GG__ AA

GAM250 LOC159110 3' AACCAGGAAGGACGTAG 39942 AGGTTAA _
CTAC TCCT CCTGGTT
|||| ||| |||||
GATG AGGA GGACCAA
C_____ A

GAM250 LOC159116 3' AACCAGGAAGGACGTAG 39940 AGGTTAA _
CTAC TCCT CCTGGTT
|||| ||| |||||
GATG AGGA GGACCAA
C_____ A

GAM250 LOC199958 3' AACCAGGGTGAACCCTCAGG 43264 ACA TAA C
CCT GGT TC TCCTGGTT
||| ||| || |||||
GGA CCA AG GGGACCAA
CTC ____ T

GAM250 LOC205251 5' AACCAAAAGGATTGGGTTTG 43587 GG _ CC
CA TT AATCCT TGGTT
|| || ||||| |||||
GT GG TTAGGA ACCAA
TT G AA

GAM250 LOC220021 3' GAACCAGGAAGACTCATGTGTG 44852 G TAA C
GG CCTACA GT TC TCCTGGTTC
||||| || || |||||
GGGTGT TA AG AGGACCAAG
G CTC A

GAM250 LOC254100 3' GAACCAGGAGAATTGCTTG 46128 T C
CAGGT AAT CTCCTGGTTC
||||| ||| |||||
GTTTCG TTA GAGGACCAAG
_ A

GAM250 LOC56920 3' CGAACCAGAAGCACTGAGATTA 21382 _____ C |||
ACCT GTTAATC CT CTGGTTC G
||||| || ||||| |
CAATTAG GA GACCAAG C
AGTCAC A |||

GAM251 ALDH3B2 3' GGATTTATCACCAAGACA 6358 C _
TG CTTGGTG GAGTTC
|| ||||| |||||
AC GAACCAC TTTAGG
A TA

GAM251 EZH1 3' AGTAGTTAAACTGCTAAGC 7715 C GG C
GC TTGGT AGTT AACTACT
|| |||| ||| |||||
CG AATCG TCAA TTGATGA
_ _ A

GAM251 GATA2 3' TAGCCGAACCTCCAGGCTGGGC 7806 TGG_ AA
GCCT TGGAGTTC CTA
|||| ||||| |||

CGGG ACCTCAAG GAT
 TCGG CC
 GAM251 PPIF 3' AGCAGTTGAACCTGGG 12282 TGGT A A
 CCT GG GTTCAACT CT
 ||| || ||||| ||
 GGG TC CAAGTTGA GA
 ____ _ C
 GAM251 TGFBR3 3' TAGTGTACCAATTCCACCAAG 9251 C CA____
 ACA TG CTTGGTGGAGTT ACTA
 || ||||| |||
 AC GAACCACCTTAA TGAT
 A CCACTG
 GAM251 APOL2 3' AGCAGTGCAGCCACCAGGGCA 25160 AGTTCA A
 TGCCTTGGTGG ACT CT
 ||||| ||| ||
 ACGGGACCACC TGA GA
 GACG__ C
 GAM251 CALN1 3' AGTGGAGACCCCCCAAGGCA 25511 T A CAA
 TGCCTTGG GG GTT CTACT
 ||||| || ||| ||||
 ACGGAACC CC CAG GGTGA
 C C A__
 GAM251 DKFZP434E2135 3' AGTAGTTGAAGTCCAGGGCA 25111 TGG G
 TGCCT TGA TTCAACTACT
 |||| ||| |||||
 ACGGG ACCT AAGTTGATGA
 ____ G
 GAM251 DKFZP586F1524 3' AGTAAACCTCTCCACCAAGG 17852 TTCAAC
 CTTGGTGGAG TACT
 ||||| |||
 GGAACCACCTC ATGA
 TCCAA_
 GAM251 FLJ10853 3' TAGTTGAACTTGACAGCA 20216 CTTG G
 TGC GT GAGTTCAACTA
 ||| || |||||
 ACG CA TTCAAGTTGAT
 A__ G
 GAM251 FLJ23071 3' TTGTCACCCCACCAAGCCA 24848 C A T_
 TG CTTGGTGG GT CAA
 || ||||| || |||
 AC GAACCACC CA GTT
 C C CT
 GAM251 KIAA0261 3' TAGTCAAACCCAGGGTA 33835 TGGA CA
 TGCCTTGG GTT ACTA
 ||||| ||| |||
 ATGGGACC CAA TGAT
 ____ AC
 GAM251 MGC2306 3' TAGCCGAAGTCCAGGCTGGGC 26356 TGG_ AA
 GCCT TGGAGTTC CTA
 ||| ||||| |||

			CGGG ACCTCAAG GAT		
			TCGG CC		
GAM251	ZNFN1A2	3'	AGCAGTCCATTTCTACCAAGGC 18389	TTCA	A
	A		TGCCTTGGTGGAG ACT CT		
			ACGGAACCATCTT TGA GA		
			TACC C		
GAM251	LOC149603	3'	AGTAGTTGAATTTTGCAAAGC 34969	CTTG	TG
			GC G GAGTTCAACTACT		
			CG C TTAAAGTTGATGA		
			AAA_ GT		
GAM251	LOC221466	3'	AGTAGCCAGCTCACCAAGGC 44991	G	CAA
			GCCTTGGTG AGTT CTACT		
			CGGAACCAC TCGA GATGA		
			_ CC_		
GAM251	LOC91380	5'	AGCAGTTGGTTTACCAAGCA 32754	C	GT A
			TGC TTGGTGGA TCAACT CT		
			ACG AACCATT T GGTTGA GA		
			_ _ C		
GAM252	KNSL1	3'	AGAGTTCACAAAAAGCC 10861	GCGA	T
			GGTTTT GT GAACTCT		
			CCGAAA CA CTTGAGA		
			AA_ _		
GAM252	CDC14B	3'	CAAAATTGCAAAAGCCTTA 9758	_	G_
			TAAGGTTTT GCGA TTG		
			ATTCCGAAA CGTT AAC		
			A AA		
GAM252	CDC14B	3'	CAAAATTGCAAAAGCCTTA 27162	_	G_
			TAAGGTTTT GCGA TTG		
			ATTCCGAAA CGTT AAC		
			A AA		
GAM252	ELSPBP1	5'	CAGAGCTCTTGGGAGCAGAACC 22703	GAGTT_	A
	TTA		TAAGGTTTTGC GA CTCTG		
			ATTCCAAGACG CT GAGAC		
			AGGGTT C		
GAM252	FLJ11164	3'	CAGAAGATGCTACAAAACCT 20355	CG	TGAAC
			AGGTTTTG AGT TCTG		
			TCCAAAAC TCG AGAC		
			A_ TAGA_		
GAM252	RHOBTB2	3'	CAGAGCCCAACTCAAGGCTT 30559	GC	AA
			AGGTTTT GAGTTG CTCTG		

			TTCGGAA CTCAAC GAGAC		
			— CC		
GAM252	LOC150577	5'	CAGAACTAGAAGCAAAACC 41218	GAG AAC	
			GGTTTTGC TTG TCTG		
			CCAAAACG GAT AGAC		
			AA_ CA_		
GAM253	CALU	3'	GCAGCAAGCATTATACGGT 6885 A C		
			GCCG TGTGGTGCTTGC GC		
			TGGC ATATTACGAACG CG		
			— A		
GAM253	EGLN1	5'	GCAAGCACCATGTGTT 22585 CG		
			AGC ATGTGGTGCTTGC		
			TTG TACACCACGAACG		
			TG		
GAM253	FLJ11155	5'	GCAGCAAGCACCTGCCTCAGCT 20348 C T _ C		
			AGC GA GT GGTGCTTGC GC		
			TCG CT CG CCACGAACG CG		
			A C T A		
GAM253	FLJ12697	3'	CGGAGCACCAACCCCGGC 44473 AT TG		
			GCCG GTGGTGCT CCG		
			CGGC CACCACGA GGC		
			CC —		
GAM253	KIAA1023	3'	GCAGCAAAGCTGTATCTGCTA 19091 C TG GC C		
			TAGC GATG GT TTGC GC		
			ATCG CTAT CG AACG CG		
			T GT A_ A		
GAM253	KIAA1941	3'	TGGCAGCACATTGAGATCGGCT 36952 GTG___ T		
	A		TAGCCGAT GTGCT GCCG		
			ATCGGCTA CACGA CCGT		
			GAGTTA _		
GAM253	LOC149912	5'	GGCAGCAAGCACTAAGCTG 41087 CGATG C		
			TAGC TGGTGCTTGC GCC		
			GTCG ATCACGAACG CGG		
			A___ A		
GAM253	LOC155179	3'	GCAGCAAAGCTGTATCTGCTA 39558 C TG GC C		
			TAGC GATG GT TTGC GC		
			ATCG CTAT CG AACG CG		
			T GT A_ A		
GAM253	LOC199958	3'	GGAAAAGCACCATCAGC 43266 C GCCG		
			GC GATGTGGTGCTT CC		

			CG CTACACCACGAA GG		
			A AA_		
GAM253	LOC219731	5'	CGGCGGGTCACGACATCGGC 44718	G _	
			GCCGATGT GTG CTTGCCG		
			CGGCTACA CAC GGGCGGC		
			G T		
GAM253	LOC254735	5'	TGGCCCATCACCACCATCAACT 45838	CC _ CT CC	
	A		TAG GATG TGGTG TG GCCA		
			ATC CTAC ACCAC AC CGGT		
			AA C T_ C_		
GAM254	FBN2	3'	CCATATGTGCTACCCACA 7725 AT _		
			TGTG GTAGCAC GTGG		
			ACAC CATCGTG TACC		
			C_ TA		
GAM254	JPH3	3'	GCCTCAGTGCTACACCACA 21827 A GT_		
			TGTG TGTAGCAC GGC		
			ACAC ACATCGTG CCG		
			C ACT		
GAM254	LOC145371	3'	AGACCTATGCCACATCACA 37843 A CGT _		
			TGTGATGT GCA GG CT		
			ACACTACA CGT CC GA		
			C AT_ A		
GAM255	B4GALT6	3'	TAATGTCTTCTATATGTAATA 30095 TTGTA		
			TATTGCATATAGA GTTA		
			ATAATGTATATCT TAAT		
			TCTG_		
GAM255	CCR2	3'	TATATGTATATGCAATA 6312 G T		
			TATTGCATATA AT GTA		
			ATAACGTATAT TA TAT		
			G _		
GAM255	KLF5	3'	GCTACATATATGCAATA 7463 GAT		
			TATTGCATATA TGTAGT		
			ATAACGTATAT ACATCG		
			—		
GAM255	NAALAD2	3'	TAACTTTCAATAAATGCAATA 11963 ATAG T_		
			TATTGCAT ATTG AGTTA		
			ATAACGTA TAAC TCAAT		
			AA_ TT		
GAM255	PGRMC2	3'	TAACTGCCATATATGTAATA 13012 GATT		
			TATTGCATATA GTAGTTA		

			ATAATGTATAT CGTCAAT		
			AC__		
GAM255	LOC92270	5'	AACTACAATCTGAGCAA 34061	ATA	
			TTGC TAGATTGTAGTT		
			AACG GTCTAACATCAA		
			A__		
GAM256	CROT	3'	GTATACCCTCTATTACA 22125	A A	
			TGTAGTAGA GGTG TAC		
			ACATTATCT CCAT ATG		
			C _		
GAM256	D10S170	3'	TGTGGCGTACCTTCTCCACA 11920	AGT	ATA
			TGT AGAAGGTG CTACA		
			ACA TCTTCCAT GGTGT		
			CC_ GC_		
GAM256	MHC2TA	3'	AGTATTACTTCTGCTACA 5776	G	
			TGTAGTAGAAG TGATACT		
			ACATCGTCTTC ATTATGA		
			-		
GAM256	NLGN2	5'	GTGCAGCCTGCCCGCTACCACA 42551	A AA	ATA A
			TGT GTAG GGTG CT CAC		
			ACA CATC CCGT GA GTG		
			C GC CC_ C		
GAM256	SCAP2	3'	GTAACATATAGTCTACTATA 10030	AG__	A
			TGTAGTAGA GTG TAC		
			ATATCATCT TAC ATG		
			GATA A		
GAM256	DKFZP566M114	3'	TAGTGTTAATTCTACACA 25814	A	GG
			TGT GTAGAA TGATACTA		
			ACA CATCTT ATTGTGAT		
			_ A_		
GAM256	FLJ22833	3'	GTGTAGTTTTTATACTACA 23123	GAAGGT	T
			TGTAGTA GA ACTACAC		
			ACATCAT TT TGATGTG		
			AT__ T		
GAM256	LHX6	3'	GTAACATCCATCCTGCTACA 15698	AA__	A
			TGTAGTAG GGTG TAC		
			ACATCGTC CTAC ATG		
			CTAC A		
GAM256	PSKH1	3'	TGTGGTATCTCCCCCTACCACA 33869	A AA	T
			TGT GTAG GG GATACTACA		

ACA CATC CC CTATGGTGT
 C CC T
 GAM257 CASP4 5' CCTATGGCAGAAGGCAACCA 27142 _ A T
 TGGTTGCCT CT GT CATAGG
 ||||| || || |||||
 ACCAACGGA GA CG GTATCC
 A _ _
 GAM257 HLA-DQA1 3' TCCAGTAACACAGAAGCAACCA 46727 C A_ C A
 A TTGGTTGC TCT GTT AT GGA
 ||||| || || || |||||
 AACCAACG AGA CAA TG CCT
 A CA _ A
 GAM257 FLJ11210 3' CCTATGAACTAATGACAAC 29972 CCTC
 GTTG TAGTTCATAGG
 ||| |||||
 CAAC ATCAAGTATCC
 AGTA
 GAM257 FLJ14564 3' TCCCACAACAATGGCTAACCAA 37599 _ TCTA CATA
 T ATTGGTT GCC GTT GGA
 ||||| || || |||||
 TAACCAA CGG CAA CCT
 T TAA_ CAC_
 GAM257 KIAA1854 3' CCTACCAGAGGCAACCAA 35527 A TCAT
 TTGGTTGCCTCT GT AGG
 ||||| || || |||||
 AACCAACGGAGA CA TCC
 C _ _
 GAM257 PIP3-E 3' CCTTAGACCAAAGGCAACACAA 33178 _ CTA CAT
 TTG GTTGCCT GTT AGG
 || ||||| || |||||
 AAC CAACGGA CAG TCC
 A AAC AT_
 GAM257 LOC135932 3' TCCTATAAACAGAATGGGCGAC 37499 _ A C
 CAAT ATTGGTTGCC TCT GTT ATAGGA
 ||||| || || |||||
 TAACCAGCGG AGA CAA TATCCT
 GTA _ A
 GAM258 HSPA8 5' CAGAAAAGACAAACATTTCA 13369 A GATGC
 TGAAATGTTTG TCT CTG
 ||||| || || |||||
 ACTTTACAAAC AGA GAC
 _ AAA_
 GAM258 IL24 3' CAGATCCTCAATAAACATTTCA 13719 _
 TGAAATGTTT GATCTG
 ||||| || || |||||
 ACTTTACAAA CTAGAC
 TAACTC
 GAM258 LIG4 5' GCAGAAAAAATCAGACACTTCA 8108 A CTGATGC
 TGAA TGTTTGAT CTGC
 ||| ||||| |||||

			ACTT ACAGACTA	GACG		
			C	AAAAA__		
GAM258	C11orf23	3'	CAAGCATCACCAATGAACATTT	20300	GATC_	C
	CA		TGAAATGTTT	TGATGC TG		
			ACTTTACAAG	ACTACG AC		
			TAACC	A		
GAM258	DKFZP434F0318	3'	GCATTTTAGATCAAACAATTCA	25141	A	__
			TGAA TGTTTGATCT	GATGC		
			ACTT ACAAAC TAGA	TTACG		
			A	TT		
GAM258	GFR	3'	GCAATGACCAAATATTTCA	14638	A TGA	
			TGAAATGTTTG TC	TGC		
			ACTTTATAAAC AG	ACG		
			C TA_			
GAM258	KIAA1301	3'	CAGGCATTGCCCAAACATTTTC	32975	ATC	
			GAAATGTTTG	TGATGCCTG		
			CTTTACAAAC	GTTACGGAC		
			CC_			
GAM258	KIAA1922	3'	CAGGCATCAGATTGTTTTCGTC	36453	AATGTT	
	A		TGA	TGATCTGATGCCTG		
			ACT	GTTAGACTACGGAC		
			GCTTTT			
GAM258	PPP1R16B	3'	CAGGCATCAGCAGTCCCATTCA	30767	A TTT	__
			TGAA TG	GAT CTGATGCCTG		
			ACTT AC	CTG GACTACGGAC		
			_ C_	AC		
GAM258	PRO2958	3'	GCATTTTAAATCAAACATTTTC	20626	CT__	
			GAAATGTTTGAT	GATGC		
			CTTTACAAACTA	TTACG		
			AATT			
GAM258	LOC145725	5'	GCAGGCATCAAAC TTTACATCC	37950	AA	TTGATC
	CA		TG ATGT	TGATGCCTGC		
			AC TACA	ACTACGGACG		
			CC	TTTCAA		
GAM258	LOC145732	5'	GCAGGCATCAAAC TTTACATCC	37959	AA	TTGATC
	CA		TG ATGT	TGATGCCTGC		
			AC TACA	ACTACGGACG		
			CC	TTTCAA		
GAM258	LOC146540	3'	CAGACATCATTACATTTCA	38198	TTGATC	C
			TGAAATGT	TGATG CTG		

			ACTTTACA	ACTAC GAC		
			TT____	A		
GAM258	LOC196957 5'	GCAGGCATCAA	ACTTTACATCC	42431	AA	TTGATC
	CA	TG ATGT	TGATGCCTGC			
		AC TACA	ACTACGGACG			
		CC	TTTCAA			
GAM258	LOC196961 5'	GCAGGCATCAA	ACTTTACATCC	42440	AA	TTGATC
	CA	TG ATGT	TGATGCCTGC			
		AC TACA	ACTACGGACG			
		CC	TTTCAA			
GAM258	LOC197138 5'	GCAGGCATCAA	ACTTTACATCC	42458	AA	TTGATC
	CA	TG ATGT	TGATGCCTGC			
		AC TACA	ACTACGGACG			
		CC	TTTCAA			
GAM258	LOC199957 3'	CAAGCACCAGATCAGACA	42672		A	C
		TGTTTGATCTG	TGC TG			
		ACAGACTAGAC	ACG AC			
		C	A			
GAM258	LOC256940 5'	CAGAGCTAATTA	AACATTTCA	46154		CTGAT _
		TGAAATGTTTGAT	GC CTG			
		ACTTTACAAATTA	CG GAC			
		AT____	A			
GAM259	AES	3' ACAAGACACAGCGGAGCT	6803		CC	GG
		AGCTCCGC	TGTG TTGT			
		TCGAGGCG	ACAC AACA			
		__	AG			
GAM259	CNTN2	3' ACAACCCAGGTGACGATGC	11523		_ _	CTG
		GC TC	CGCC TGGGTTGT			
		CG AG	GTGG ACCCAACA			
		T CA	__			
GAM259	GABRE	5' TACAGAGTGCAGGGCAGAGCTT	22532		C	GG
		AAGCTC	GCCCTGTG TTGTA			
		TTCGAG	CGGGACGT GACAT			
		A	GA			
GAM259	LENG4	3' ACAATGTGGGGTCGGAGCTT	23578		_	TG GG
		AAGCTCCG	CCC T GTTGT			
		TTCGAGGC	GGG G TAACA			
		T	GT __			
GAM259	LZTR1	3' ACAACCCACCTGGA	ACTT 13635		C	CCCT
		AAG TCCG	GTGGGTTGT			

			TTC AGGT CACCCAACA		
			A C__		
GAM259	NLGN2	3'	ACAACCTGCACACGGAGCT 42548	CCC	TG
			AGCTCCG TG GGTGT		
			TCGAGGC AC CCAACA		
			AC_ GT		
GAM259	C21orf25	3'	CAGCCTGCACAGGGCAAGGC 31798	CC	__
			GCT GCCCTGTG GGTGT		
			CGG CGGGACAC CCGAC		
			AA GT		
GAM259	FLJ22814	3'	ACCCAGGGCAGGGGGAAGC 24440	_ G	__
			GCT CC CCCTGT GGGT		
			CGA GG GGGACG CCGA		
			A _ GGA		
GAM259	FLJ23519	3'	CACGAGGGCAGGACACAGCTT 25974	__ _	__
			AAGC TCC GCCCT GTG		
			TTCG AGG CGGGA CAC		
			ACAC A G		
GAM259	HSGP25L2G	3'	ACAAGCTGAAGGCAGCAGCTT 31133	CC_	CTG G
			AAGCT GCC TGG TTGT		
			TTCGA CGG GTC AACA		
			CGA AA_ G		
GAM259	KIAA1257	3'	TACAGTCCCAAGGAGGA 31437	GC G	_
			TCC CCT TGGG TTGTA		
			AGG GGA ACCC GACAT		
			A_ _ T		
GAM259	MGC11352	5'	ACAGAGGCACAGGGCAGGC 32353	CC	GG_
			GCT GCCCTGTG TTGT		
			CGG CGGGACAC GACA		
			A_ GGA		
GAM259	MGC2721	3'	ACAACCTGCAAAAACGGAGCT 26461	CCC_	TG
			AGCTCCG TG GGTGT		
			TCGAGGC AC CCAACA		
			AAAA GT		
GAM259	SSB-3	3'	ACACTCCAGGGCGGAGTT 28099	T T	
			AGCTCCGCCCTG GGGT GT		
			TTGAGGCGGGAC CTCA CA		
			__		
GAM259	TUSP	5'	GGGACACAGGGCCAAGCTT 21531	CC	GG
			AAGCT GCCCTGTG TT		

			TTCGA CGGGACAC GG		
			AC AG		
GAM259	LOC124987 5'	ACGGCAAACGCGGAGCT	37264	CCT	GG
		AGCTCCGC GT GTTGT			
		TCGAGGCG CA CGGCA			
		___ AA			
GAM259	LOC145725 5'	ACATCACAGGGCAAGC	37944	CC	GT
		GCT GCCCTGTGG TGT			
		CGA CGGGACACT ACA			
		A_ _			
GAM259	LOC145732 5'	ACATCACAGGGCAAGC	37953	CC	GT
		GCT GCCCTGTGG TGT			
		CGA CGGGACACT ACA			
		A_ _			
GAM259	LOC157918 5'	ACAACCCATCAAGCGGAG	41892	CCT	
		CTCCGC GTGGGTTGT			
		GAGGCG TACCCAACA			
		AAC			
GAM259	LOC196957 5'	ACATCACAGGGCAAGC	42426	CC	GT
		GCT GCCCTGTGG TGT			
		CGA CGGGACACT ACA			
		A_ _			
GAM259	LOC196961 5'	ACATCACAGGGCAAGC	42435	CC	GT
		GCT GCCCTGTGG TGT			
		CGA CGGGACACT ACA			
		A_ _			
GAM259	LOC197138 5'	ACATCACAGGGCAAGC	42453	CC	GT
		GCT GCCCTGTGG TGT			
		CGA CGGGACACT ACA			
		A_ _			
GAM259	LOC254439 3'	CAACTTCCAGGACGGAGCTT	45433	C	TG
		AAGTCCG CCTG GGTTG			
		TTCGAGGC GGAC TCAAC			
		A CT			
GAM259	LOC255196 3'	TACAACCTGGGCAACAGAGC	46414	C___	TGT
		GCTC GCCC GGGTTGTA			
		CGAG CGGG TCCAACAT			
		ACAA _			
GAM259	LOC257437 5'	ACAGAGGCACAGGGCAGGC	43854	CC	GG_
		GCT GCCCTGTG TTGT			

			CGG CGGGACAC GACA		
			A_ GGA		
GAM259	LOC90019	3'	ACAGCCCCAAGGCAGAGCT 28869	C	CTG
			AGCTC GCC TGGGTTGT		
			TCGAG CGG ACCCGACA		
			A A_		
GAM259	LOC91496	5'	TACAACTTAAAAGGAACTT 32920	C	GCCCTG
			AAG TCC TGGGTTGTA		
			TTC AGG ATTCAACAT		
			A AAA_		
GAM260	AGL	3'	TTCTATTGAGTATTATAAGATA 6295	CTG _	C
			TATCTTATGAT AC CAA AGAA		
			ATAGAATATTA TG GTT TCTT		
			_ A A		
GAM260	AGL	3'	TTCTATTGAGTATTATAAGATA 6300	CTG _	C
			TATCTTATGAT AC CAA AGAA		
			ATAGAATATTA TG GTT TCTT		
			_ A A		
GAM260	AGL	3'	TTCTATTGAGTATTATAAGATA 6308	CTG _	C
			TATCTTATGAT AC CAA AGAA		
			ATAGAATATTA TG GTT TCTT		
			_ A A		
GAM260	AGL	3'	TTCTATTGAGTATTATAAGATA 5468	CTG _	C
			TATCTTATGAT AC CAA AGAA		
			ATAGAATATTA TG GTT TCTT		
			_ A A		
GAM260	AGL	3'	TTCTATTGAGTATTATAAGATA 6285	CTG _	C
			TATCTTATGAT AC CAA AGAA		
			ATAGAATATTA TG GTT TCTT		
			_ A A		
GAM260	AGL	3'	TTCTATTGAGTATTATAAGATA 6290	CTG _	C
			TATCTTATGAT AC CAA AGAA		
			ATAGAATATTA TG GTT TCTT		
			_ A A		
GAM260	DACH	3'	CTGTTGGTCAGAAAGATG 28038	ATGA	
			TATCTT TCTGACCAACAG		
			GTAGAA AGACTGGTTGTC		
			_		
GAM260	DSG1	3'	CTGTTGGTTTCACAGATA 7655	TA	TCT
			TATCT TGA GACCAACAG		

			ATAGA ACT TTGGTTGTC		
			C_ _		
GAM260	NGFRAP1	5'	CTGCTGGTCAGAGCACCAAG 15716	A_ A	A
			CTT TG TCTGACCA CAG		
			GAA AC AGACTGGT GTC		
			CC G C		
GAM260	P4HA1	3'	TTCTGTTGGTATCACAGAAGA 6627	A	ATCTG
			TCTT TG ACCAACAGAA		
			AGAA AC TGGTTGTCTT		
			G ACTA_		
GAM260	ATP1B4	3'	TTCTATTGGTCAGACATTGATG 14329	TT A	C
			TATC ATG TCTGACCAA AGAA		
			GTAG TAC AGACTGGTT TCTT		
			T_ _ A		
GAM260	KIAA1209	3'	TTCTGTTGGCCAGGACACAGAT 30475	TA A	A
			ATCT TG TCTG CCAACAGAA		
			TAGA AC GGAC GGTTGTCTT		
			C_ A C		
GAM260	MGC15482	3'	CTGTTGAGGTGCCCATAAGA 26696	_	GAC
			TCTTATG ATCT CAACAG		
			AGAATAC TGGA GTTGTC		
			CCG _		
GAM260	LOC130733	3'	TGGAATCGAAATCATAAGATA 37004	C_ _	
			TATCTTATGAT TGA CCA		
			ATAGAATACTA GCT GGT		
			AA AA		
GAM260	LOC152059	3'	TTCTGCCTCAACCATGAGATA 39210	ATC	CCAA
			TATCTTATG TGA CAGAA		
			ATAGAGTAC ACT GTCTT		
			CA_ CC_		
GAM260	LOC154743	3'	TCTGTTGGTGATCTCATAA 39480	TCTG	
			TTATGA ACCAACAGA		
			AATACT TGGTTGTCT		
			CTAG		
GAM261	PDGFRB	3'	CCAGCTGCCCCATCCC 32813	CTCTCTT	A
			GGGATGGGGC AGT GG		
			CCCTACCCCG TCG CC		
			_ A		
GAM261	PML	3'	CCATACTGCAGCCCCATCCCA 27076	CTCTCT	_
			TGGGATGGGGC TAGTA GG		

			ACCCTACCCCG	GTCAT CC		
			AC_____A			
GAM261	PSD	5'	CCCACTCCCTGGCCCTCATCCC	8668	_	TCTCTT A
	A		TGGGATG GGGCC	AGT GG		
			ACCCTAC CCCGG	TCA CC		
			T TCCC_	C		
GAM261	SERPINB9	3'	CCTCTAAAAGGAAACCCCATCC	10364		CC C_ T
	CA		TGGGATGGGG	TCT TTAG AGG		
			ACCCTACCCC	AGG AATC TCC		
			AA AA	_		
GAM261	SLA2	3'	CCATTAACCAGGCCCAACCCA	25941	A	CTC A
			TGGG TGGGGCCT	TTAGT GG		
			ACCC ACCCCGGA	AATTA CC		
			_	CC_ _		
GAM261	APOL3	3'	CCTACCAAGAAAAACAGTCTCA	15674		GGGGCCTC A
			TGGGAT	TCTT GTAGG		
			ACTCTG	AGAA CATCC		
			ACAAAA_	C		
GAM261	ERAP140	3'	CTGGAAAAAGAAGCCCCAGCCC	37084	A	C C AG
	A		TGGG TGGGGC	TCT TT TAG		
			ACCC ACCCCG	AGA AA GTC		
			G	A A AG		
GAM261	IKKE	3'	AGGGCAAGATCCCATCCCA	15201	GC	_
			TGGGATGGG	CT CTCT		
			ACCCTACCC	GA GGGA		
			TA AC			
GAM261	LOC127534	3'	CCTTGAAGATGCCCCACCCCA	37168	A	CTC AGT
			TGGG TGGGGC	TCTT AGG		
			ACCC ACCCCG	AGAA TCC		
			C	T_ GT_		
GAM261	LOC145082	5'	CCCACCAAACCTCCGCCTCATCC	40492		CTCTCTTA A
	CA		TGGGATGGGGC	GT GG		
			ACCCTACTCCG	CA CC		
			CCTCAAAC	C		
GAM261	LOC170082	3'	CCCACTGGTGCTGAGACCCAC	40169	A	C TC_ A
	CC		GGG TGGGG	CTC TTAGT GG		
			CCC ACCCC	GAG GGTCA CC		
			_	A TCGT C		
GAM261	LOC220370	3'	CCATTGCAGAGAGACTCCATCC	44598	C	_ A
	CA		TGGGATGGGG	CTCTCT TAGT GG		

ACCCTACCTC GAGAGA GTTA CC
A C _
GAM261 LOC221540 3' AGGAGACCCCTCCCA 45043 T CC
TGGGA GGGG TCTCTT
||||| ||| |||||
ACCCT CCCC AGAGGA

— —
GAM261 LOC257545 3' AGGAGACCCCTCCCA 46691 T CC
TGGGA GGGG TCTCTT
||||| ||| |||||
ACCCT CCCC AGAGGA

— —
GAM261 LOC257598 3' AGGAGACCCCTCCCA 46748 T CC
TGGGA GGGG TCTCTT
||||| ||| |||||
ACCCT CCCC AGAGGA

— —
GAM262 FLJ21432 3' CACCAAAATAGTGCTCGAGT 23765 C TAT _
AC CGA GCG TATTTTGGTG
|| ||| ||| |||||
TG GCT CGT ATAAAACCAC
A _ G
GAM262 LOC204010 5' CACCAGTGGGCACATCG 43081 A G TT
CGAT TGC TAT TGGTG
||||| ||| ||| |||||
GCTA ACG GTG ACCAC
C G _
GAM263 HDAC5 3' AGGATCCACTACTGTCTTTAA 29221 CCATAACTT
TTAAAGACAG ATCCT
||||||| |||||
AATTTCTGTC TAGGA
ATCACC_

GAM263 IL1F5 3' AGAATAAATTTTCGGCTGTTTT 14595 AT C C
AAGACAGCC AA TTAT CT
||||||| || ||| ||
TTTTGTCGG TT AATA GA
CT A A

GAM263 SERPINB9 3' ATAAGTTATGGCCATCTT 10360 CA
AAGA GCCATAACTTAT
||||| |||||
TTCT CGGTATTGAATA
AC

GAM263 RI58 3' AGGATGCTGTGGCTGTTCT 14792 _ ACT
AGA CAGCCATA TATCCT
||| ||||| |||||
TCT GTCGGTGT GTAGGA
T C_

GAM264 ADAM17 3' CCAGAGTTTTTTATGTAGCAGGG 9156 C_ C
AA TTCCCTGCTACAT AC CTGG
||||||| || |||

			AAGGGACGATGTA	TG GACC	
			TTTT A		
GAM264	ADAM17	3'	CCAGAGTTTTTATGTAGCAGGG	22409	C___ C
	AA		TTCCCTGCTACAT	AC CTGG	
			AAGGGACGATGTA	TG GACC	
			TTTT A		
GAM264	HDAC4	3'	GTCCAGGGCAGATGGCAGAGGA	12668	_ TA A_
			TCC CTGC	CATC CCCTGGAC	
			AGG GACG	GTAG GGGACCTG	
			A _	AC	
GAM264	PPP2R5B	3'	TGTCCAGGGGGCCAGAGAG	12915	C CTACATCA
			TTC CTG	CCCTGGACA	
			GAG GAC	GGGACCTGT	
			A CCG	_____	
GAM264	RERE	3'	TCCAGGGTTTGCAGGGA	14410	TACATC
			TCCCTGC	ACCCTGGA	
			AGGGACG	TGGGACCT	
			TT	_____	
GAM264	SCN4A	3'	GGGGCGTGCAGCAGGGAA	5890	A CA
			TTCCCTGCT	CAT CCC	
			AAGGGACGA	GTG GGG	
			C CG		
GAM264	THBS1	3'	GTGCAGATGTAGCAGG	9256	ACCC G
			CCTGCTACATC	TG AC	
			GGACGATGTAG	AC TG	
			_____	G	
GAM264	C17orf31	3'	CCAGTGTAGCACGGAA	18998	C TCACC
			TTCC TGCTACA	CTGG	
			AAGG ACGATGT	GACC	
			C	_____	
GAM264	CGI-96	3'	TCCAGTTGGGCAGCAGGGAA	17926	ACA CC
			TTCCCTGCT	TCA CTGGA	
			AAGGGACGA	GGT GACCT	
			CG_	T_	
GAM264	DRIL2	3'	CCAGAGGATGCAGGGAA	13184	TAC ACC
			TTCCCTGC	ATC CTGG	
			AAGGGACG	TAG GACC	
			_____	GA_	
GAM264	FLJ14957	3'	CCAAAGTGGGAGGCAGGGAG	26680	ACA CC
			TTCCCTGCT	TCAC TGG	

			GAGGGACGG GGTG ACC		
			AG_ AA		
GAM264	KIAA1056	5'	TGCCCAGGGTGAATCAATGGAA 17050	CTGCTACA	A
			TTCC TCACCCTGG CA		
			AAGG AGTGGGACC GT		
			TAACTA_ C		
GAM264	KIAA1323	5'	GTCCAGGATGCCAAGGGA 31567	GCTA CAC	
			TCCCT CAT CCTGGAC		
			AGGGA GTA GGACCTG		
			ACC_ _		
GAM264	LANO	3'	TGTCCTGGATGTGGCAGGGAA 20130	ACCCT	
			TTCCCTGCTACATC GGACA		
			AAGGGACGGTGTAG CCTGT		
			GT_		
GAM264	MGC3101	3'	GTCCAGGAGCAGCAGAGGA 23478	_ ACATCAC	
			TCC CTGCT CCTGGAC		
			AGG GACGA GGACCTG		
			A CGA_		
GAM264	RNF24	3'	GTCCAGAGCCCCAGCAGGGAG 14088	ACATCACC	
			TTCCCTGCT CTGGAC		
			GAGGGACGA GACCTG		
			CCCCGA_		
GAM264	LOC123346	5'	TGCCCAGGCAAAAGCAGGGAA 37250	ACATCAC	A
			TTCCCTGCT CCTGG CA		
			AAGGGACGA GGACC GT		
			AAAC_ C		
GAM264	LOC148932	3'	TGTCCAGGGCCTCACAGGGAG 38626	CTACATCA	
			TTCCCTG CCCTGGACA		
			GAGGGAC GGGACCTGT		
			ACTCC_		
GAM264	LOC150139	3'	TCCAGGGTGAAAAGGGAG 38861	GCTACA	
			TTCCCT TCACCCTGGA		
			GAGGGA AGTGGGACCT		
			AA_		
GAM264	LOC150397	3'	CCGTTGTTGACGGAGCAGGGAA 38961	ACA _ CC	
			TTCCCTGCT TCA C TGG		
			AAGGGACGA AGT G GCC		
			GGC T TT		
GAM264	LOC152502	3'	CCAGGACGTGGCGGCAGGGGA 29835	A_ CAC	
			TTCCCTGCT CAT CCTGG		

			AGGGGACGG GTG GGACC		
			CG CA_		
GAM264	LOC51667	3'	TGTCCAGGGCAGGGTCCTGGGA 18200	TGCT	ATCA
	A		TTCCC AC CCCTGGACA		
			AAGGG TG GGGACCTGT		
			TCC_ GGAC		
GAM264	LOC91695	3'	TCCAGTTGGGCAGCAGGGAA 33253	ACA	CC
			TTCCCTGCT TCA CTGGA		
			AAGGGACGA GGT GACCT		
			CG_ T_		
GAM265	EVA1	3'	AAAAGGTTACATAGATATG 12378	AAG	
			CATATCTATGTAG TTT		
			GTATAGATACATT AAA		
			GGA		
GAM265	KIAA0630	3'	TTTCTACATAATATGGTA 43065	C	
			TACCATAT TATGTAGAAG		
			ATGGTATA ATACATCTTT		
			—		
GAM265	PRO1598	3'	CTGGCTACATAGATAAGTA 20569	CA	A_
			TAC TATCTATGTAG AG		
			ATG ATAGATACATC TC		
			A_ GG		
GAM265	SART3	3'	AAAAC TTCTTGCTGAATGGTA 16248	A	TATGT
			TACCAT TC AGAAGTTTT		
			ATGGTA AG TCTTCAAAA		
			_ TCGT_		
GAM265	LOC158450	5'	TTCTACATAGATGTGGTA 39846		
			TACCATATCTATGTAGAA		
			ATGGTGTAGATACATCTT		
GAM265	LOC158504	5'	TTCTACATAGATGTGGTA 39857		
			TACCATATCTATGTAGAA		
			ATGGTGTAGATACATCTT		
GAM265	LOC196812	3'	GAAGCTCATAGATAT 43136	TAGA	
			ATATCTATG AGTTTT		
			TATAGATAC TCGAAG		
			—		
GAM266	CALB1	3'	AATGTAAAATTCATAGCA 11367	C	G
			TGC ATGAA TTTACGTT		

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ACG TACTT AAATGTAA
  A  A
GAM266 HNRPD 3' AAACAGCGGGAACCTTCATTGCA 11947 C TA
TGC ATGAAGTT CGTTGTTT
||| ||||| |||||
ACG TACTTCAA GCGACAAA
  T  GG
GAM266 IL24 3' AACTGAACTTCAGAGCA 13718 CA C
TGC TGAAGTTTA GTT
||| ||||| |||
ACG ACTTCAAGT CAA
  AG  _
GAM266 SLC10A2 5' AACAAACCTTCATGGCA 6060 TTTACG
TGCCATGAAG TTGT
||||||| |||
ACGGTACTTC AACAA
CA_
GAM266 TCF7 3' AAACAACATGTGAGCATGGT 9191 GAA _
GCCAT GTTTAC GTTGTTT
|||| |||| |||||
TGGTA CGAGTG CAACAAA
_ TA
GAM266 DKFZP434P0111 3' CAGCAAAGCCTCATGGCA 33452 A AC
TGCCATGA GTTT GTTG
||||||| ||| |||
ACGGTACT CGAA CGAC
C A_
GAM266 KIAA0495 3' GACAAAACCTCATGGCA 31358 A ACGT
TGCCATGA GTTT GTT
||||||| ||| |||
ACGGTACT CAAA ACAG
C _
GAM266 LOC139221 5' AACAAACGTGTTCAAGCA 37330 CA GTT
TGC TGAA TACGTTGTT
||| ||| |||||
ACG ACTT GTGCAACAA
A_ _
GAM266 LOC257482 3' AAACAACCAACCCTTCATGGC 45232 TTTAC
GCCATGAAG GTTGTTT
||||||| |||||
CGGTACTTC CAACAAA
CCAAC
GAM266 LOC90346 5' AAACCTCAAAAACCTTCATGGCA 28746 ACGTT
TGCCATGAAGTTT GTT
||||||| |||
ACGGTACTTCAAA CAAA
AACTT
GAM267 ATP1B2 3' ACCCCCCGCCACACACACACAC 7388 _ CGA AC
GT TGTGTGTG CG GGGT
|| ||||| || |||

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			CA ACACACAC GC CCCA		
			C ACC CC		
GAM267	KIAA0711	5'	CCTTCACACACACAAC 16957	C	CGAC
			GTTGTGTGTG GA GGG		
			CAACACACAC CT TCC		
			A ____		
GAM267	RDC1	3'	CTGCAAATCTGCACACACAACG 35847	_	CGA_
	AA		TTCGTTGTGTGTGC GA CGG		
			AAGCAACACACACG CT GTC		
			T AAAC		
GAM267	VAV3	3'	ACCTCCCCCGCACACACAC 12756	T	ACGAC
			GT GTGTGTGCG GGGT		
			CA CACACACGC TCCA		
			_ CCCC_		
GAM267	LOC147837	3'	ACCTCTGTACACACACAA 38390	C	AC
			TTGTGTGTG GACG GGGT		
			AACACACAC CTGT TCCA		
			A C_		
GAM268	NRCAM	5'	CGTTTCACAAAATCTTTTGTGA 11449	T	CCG_ C
	A		TTCA CAAA TT GTGAAACG		
			AAGT GTTT AA CACTTTGC		
			_ TCTA A		
GAM268	DKFZP586P0123	5'	TCGCCGGTTTCATGAA 45466	C	TTC
			TTCAT AAACCG GTGAA		
			AAGTA TTTGGC CGCTT		
			C ____		
GAM268	MP1	5'	CAGAACGATTGATGAA 17359	AC	G
			TTCATCAA CGTTC TG		
			AAGTAGTT GCAAG AC		
			A_ _		
GAM268	PMAIP1	3'	CGTTTCATCAATTTGAAGAA 22100	A	ACC C
			TTC TCAA GTT GTGAAACG		
			AAG AGTT TAA TACTTTGC		
			A ____ C		
GAM268	Rpo1-2	3'	CACTGACAATTTGATGAG 21098	CC	C
			TTCATCAAA GTT GTG		
			GAGTAGTTT CAG CAC		
			AA T		
GAM268	LOC220002	3'	CTTTCACCTGGTTTATGAA 44048	C	TTC C
			TTCAT AAACCG GTGAAA G		

AAGTA TTTGGT CACTTT C
 _ _ _ A
 GAM269 FAM8A1 3' CAAACTAGTCCAGTTTA 18380 GTA
 TAAGC GACTAGTTTG
 |||| |||||
 ATTTG CTGATCAAAC
 AC_
 GAM269 IMP-2 5' GCTAGTCACACCTATTTGA 13305 AGC A
 TCAAATA GT GACTAGT
 ||||| || |||||
 AGTTTAT CA CTGATCG
 CCA _
 GAM270 FREB 3' GTTCTAGTTTGTATCCCCTCAA 26467 AT CAATTTT
 TTGA GGA GCTAGAAC
 ||| || |||||
 AACT CCT TGATCTTG
 CC ATGTT_
 GAM270 FLJ12610 3' TCTAGTGATCTGCCACCTCAA 24151 A_ A ATT TG
 TTGA TGG CA T CTAGA
 ||| ||| | ||||
 AACT ACC GT A GATCT
 CC C CT_ GT
 GAM270 RAB40A 5' TCTAGCAAAATCCATGTCC 39932 _
 GGACA ATTTTGCTAGA
 |||| |||||
 CCTGT TAAAACGATCT
 ACC
 GAM270 LOC131870 3' GCAAAACTGTCCATTGAA 37018 G A
 TT AATGGACA TTTTGC
 || ||||| |||||
 AA TTACCTGT AAAACG
 G C
 GAM270 LOC154222 3' TCTAAGAAAACCATCCATTCA 41693 CAA GC
 TGAATGGA TTTT TAGA
 ||||| ||| |||
 ACTTACCT AAAA ATCT
 ACC GA
 GAM270 LOC155064 3' CTTAAAAAACTGTCCATTAA 39529 A GCT
 TTGAATGGACA TTTT AG
 ||||| ||| ||
 AATTTACCTGT AAAA TC
 C AAT
 GAM270 LOC201194 3' CTAGTGGCTTTGCCATTCAA 43218 A TT TG
 TTGAATGG CAA T CTAG
 ||||| || | |||
 AACTTACC GTT G GATC
 _ TC GT
 GAM270 LOC91351 3' TTCCAGCAAAATTCCA 32700 CA A
 TGGA ATTTTGCT GAA
 ||| ||||| |||

			ACCT TAAAACGA CTT		
			— C		
GAM271	SLC25A12	3'	CATCTTTGTACAGAGACA 9805	GAC	TTT
			TGTCTC TGC AAGATG		
			ACAGAG ATG TTCTAC		
			AC_ T_		
GAM271	ATP9A	3'	CATCTTAAAGTTGGAGCA 31078	T	GA CT
			TG CTC GCTTTAAGATG		
			AC GAG TGAAATTCTAC		
			_ GT_		
GAM271	FBXO21	3'	CATCTTAGAGATGGAGACA 27321		GA CTG
			TGTCTC CTTTAAGATG		
			ACAGAG GAGATTCTAC		
			GTA_		
GAM271	FLJ22601	3'	CATCTTAAACATGTTGA 24211	_	C
			TCGAC TG TTTAAGATG		
			AGTTG AC AAATTCTAC		
			T A		
GAM271	IL10RB	3'	CTTAGAGGTCGAGGCA 6244		TG
			TGTCTCGAC CTTTAAG		
			ACGGAGCTG GAGATTC		
			—		
GAM271	MGC13102	3'	TTTGGGGCCCGAGACA 26134		ACT
			TGTCTCG GCTTTAAG		
			ACAGAGC CGGGGTTT		
			C_		
GAM271	SPEC1	3'	ATCTTAAGCCCGAGCA 21509	T	ACT T
			TG CTCG GCTT AAGAT		
			AC GAGC CGAA TTCTA		
			_ C_ _		
GAM271	LOC147645	3'	CATCTTAAAACAGATCAGA 38357	C _	C
			TCT GA CTG TTTAAGATG		
			AGA CT GAC AAATTCTAC		
			_ A A		
GAM271	LOC150378	3'	CATCCTTGAAGCCCAGACA 38921		CGACT _
			TGTCT GCTTTAAG ATG		
			ACAGA CGAAGTTC TAC		
			CC_ C		
GAM271	LOC152313	3'	CATCTTAAGTAGCCGAACA 41474	C A	T
			TGT TCG CTGCTT AAGATG		

			ACA AGC GATGAA TTCTAC		
			_ C _		
GAM271	LOC164397 5'	CATCCAGGCAGTCAAGCA	40150	T C	TAA
		TG CT GACTGCTT GATG			
		AC GA CTGACGGA CTAC			
		_ A C _			
GAM271	LOC220763 5'	CATCTTAAAGAAGATCAGACA	36301	C _ G	
		TGTCT GA CT CTTTAAGATG			
		ACAGA CT GA GAAATTCTAC			
		_ A A			
GAM271	LOC90317 5'	CATCTTAGACTTCATCAGACA	31206	C C C _	
		TGTCT GA TG TTTAAGATG			
		ACAGA CT AC AGATTCTAC			
		_ _ TTC			
GAM272	KLHL3 3'	GCTGAGCAAACATATTCCAG	42270	C CG A	
	TT	AATTG AG TGA TTTGCTCAGC			
		TTGAC TT ACT AAACGAGTCG			
		C AT C			
GAM272	SLC24A1 3'	CAAACACACGCTGCAATT	11100	AA	
		AATTGCAGCGTG TTTG			
		TTAACGTGCGCAC AAAC			
		AC			
GAM272	SUFU 3'	GCAGACTCAGCTGCAATT	18255	G A	
		AATTGCAGC TGA TTTGC			
		TTAACGTGCG ACT AGACG			
		_ C			
GAM272	ARFGAP1 3'	CTGGCGCTCACGCTGC	20110	ATT T	
		GCAGCGTGA TGC CAG			
		CGTCGCACT GCG GTC			
		C _ _			
GAM272	CCNE2 3'	CTAAGCAAACAAGTTGGAATT	27711	G G AA C	
		AATT CAGC TG TTTGCT AG			
		TTAA GTTG AC AAACGA TC			
		G A _ A			
GAM272	CCNE2 3'	CTAAGCAAACAAGTTGGAATT	11050	G G AA C	
		AATT CAGC TG TTTGCT AG			
		TTAA GTTG AC AAACGA TC			
		G A _ A			
GAM272	DKFZp762E1511 3'	CTGAGCAAAACTGCAG	29934	CGTGAA	
		TTGCAG TTTGCTCAG			

GACGTC AAACGAGTC
 A____
 GAM272 KIAA0553 3' CTGATATAACTCAGGCTGCAAT 34638 G A TGC
 T AATTGCAGC TGA TT TCAG
 ||||| ||| || ||||
 TTAACGTCG ACT AA AGTC
 G C TAT
 GAM272 KIAA1200 3' CTGTGTTCACTGAATT 31264 G C ATTT T
 AATT CAG GTGA GC CAG
 |||| ||| ||| || ||||
 TTAA GTC CACT TG GTC
 _ A _ T
 GAM272 MGC12760 5' GCTGAGCCGCGCCACGCTGCAA 26450 AATTT
 TTGCAGCGTG GCTCAGC
 ||||| ||| |||||
 AACGTCGCAC CGAGTCG
 CGCGC
 GAM272 LOC153505 3' GCTTCACGCTGCAGT 39383 TTT
 ATTGCAGCGTGAA GC
 ||||| ||| ||
 TGACGTCGCACTT CG

 GAM272 LOC157503 3' CAAATAGCACGCTGAATT 41812 G A_
 AATT CAGCGTG ATTTG
 |||| ||||| |||||
 TTAA GTCGCAC TAAAC
 _ GA
 GAM272 LOC162333 5' CTGAGCAAACCTCTGTA 42128 C GAAT
 TGCAG GT TTGCTCAG
 |||| || |||||
 ATGTC CA AACGAGTC
 T _
 GAM272 LOC253782 3' CTGAGCAGCATTACACTACAAT 45797 C C AT
 ATTG AG GTGA TTGCTCAG
 |||| || ||| |||||
 TAAC TC CATT GACGAGTC
 A A AC
 GAM273 FGF23 3' GCATTAAATGAAGCCTTACC 21794 AC _
 GGTAAGCTTCATT GTGC
 |||| ||||| |||
 CCATT CGAAGTAA TACG
 C_ AT
 GAM273 KCNJ16 3' TACAATGAAGATTTACC 20729 CG
 GGTAAGCTTCATTGTG
 |||| |||||
 CCATTT GAAGTAACAT
 A_
 GAM273 LDHB 5' GCAAAGCACAAAGAACATTTAT 8087 CGC A
 C GGTAAGCTTCATTGTG
 |||| ||| |||||

			CTATTT AAG AACACGAAACG			
			AC_ A			
GAM273	OPCML	3'	GCAAAGTGAAGAGTCCACC 8396	AA G	G	
			GGT AC CTTTCATT TGC			
			CCA TG GAAGTGA ACG			
			CC A A			
GAM273	PRKACA	3'	GCAAATGAACGAAGCGCCAACC 8597	AAA	ATT GC_	
			GGT CGCTTC GT TTTGC			
			CCA GCGAAG CA AAACG			
			ACC ____ AGT			
GAM273	ROCK2	3'	ACAAAAAAGCGTTTACC 32835	CA_		
			GGTAAACGCTT TTGT			
			CCATTTGCGAA AACA			
			AAA			
GAM273	CYYR1	3'	GCAAATTTTATGAAGTGCCTAC 27514	AA	TGTGC	
	C		GGTA CGCTTCAT TTTGC			
			CCAT GTGAAGTA AAACG			
			CC TTTT_			
GAM273	KIAA1036	3'	GCAAATGAAGCCCTTACC 17126	AC	G	
			GGTAA GCTTCATT TGC			
			CCATT CGAAGTAA ACG			
			CC A			
GAM273	SBBI31	3'	CAAGGAGTGAAGCGCCCACC 15266	AAA	GTG	
			GGT CGCTTCATT CTTTG			
			CCA GCGAAGTGA GGAAC			
			CCC ____			
GAM273	LOC124842	5'	GCAAAGCACTCAACAGCCACC 37261	AAAC	TCATT	
			GGT GCT GTGCTTTGC			
			CCA CGA CACGAAACG			
			C__ CAACT			
GAM273	LOC138399	5'	GCAGGTTTCCAATGAAGCCCCA 37131	AAAC	T__ T	
	CC		GGT GCTTCATTG GCTT GC			
			CCA CGAAGTAAC TGGA CG			
			CCC_ CTT _			
GAM273	LOC221814	5'	CAAAACACAATGACTTGGTTAC 45090	A CT	C	
	T		GGTAA CG TCATTGTG TTTG			
			TCATT GT AGTAACAC AAAC			
			G TC A			
GAM273	LOC90317	5'	GCAAAGCCTTTAAAGCGTCTTC 31207	TAA	CATTGT	
	C		GG ACGCTT GCTTTGC			

			CC TGC GAA CGAAACG		
			TTC ATTTC_		
GAM274	SURB7	3'	AATAATTTGTGTCAGCATTTTC	10463	TTG GTTG
	A		TGAAA GC ACAAATTATT		
			ACTTT CG TGTTTAATAA		
			TA_ ACTG		
GAM274	LOC221035	3'	TTTGTCAACACCAATTACA	44745	A C
			TG AATTGG GTTGACAAA		
			AC TTAACC CAACTGTTT		
			A A		
GAM274	LOC221405	5'	AATAACCTGTTTCATATGCCAAT	45065	A _ _ AA
	TCA		TGAA TTGGCGT TGA CA TTATT		
			ACTT AACCGTA ACT GT AATAA		
			_ T T CC		
GAM274	LOC51701	3'	AATAATTCATTTCTGGGCTAAT	18344	GTT CA_
	TTCA		TGAAATTGGC GA AATTATT		
			ACTTTAATCG CT TTAATAA		
			GGT TTAC		
GAM275	SLC9A5	3'	TGTCACCACCTGAACATTC	30066	C_
			GAATGTTTAGG GACG		
			CTTACAAGTCC CTGT		
			ACCA		
GAM276	FGF5	3'	CATCAGTATAGTGTTTTA	10773	G G_
			TAAAACAC TGTG GATG		
			ATTTTGTG ATAT CTAC		
			_ GA		
GAM276	FGF5	3'	CATCAGTATAGTGTTTTA	27000	G G_
			TAAAACAC TGTG GATG		
			ATTTTGTG ATAT CTAC		
			_ GA		
GAM276	NORE1	3'	CATCATCGTCATGTGTTT	25441	TGG
			AAACACGTG GATGATG		
			TTTGTGTAC CTACTAC		
			TG_		
GAM276	NRIP1	3'	CATCTGGAGCACTTGTTTTA	30118	C G_
			TAAAACA GTGT GGATG		
			ATTTTGT CACG TCTAC		
			T AGG		
GAM276	PKNOX1	3'	CATTTTACACAGTTTTA	10913	AC
			TAAAAC GTGTGGGATG		

ATTTTG CACATTTTAC
 A_
 GAM276 TIA1 3' CATCCACATTGTTT 22734 C G
 TAAAACA GTGTGG ATG
 ||||| ||||| ||
 ATTTTGT TACACC TAC
 - -
 GAM276 TIA1 3' CATCCACATTGTTT 22559 C G
 TAAAACA GTGTGG ATG
 ||||| ||||| ||
 ATTTTGT TACACC TAC
 - -
 GAM276 CPLX1 3' CATCAAGTCTCCACGTGTTT 13446 T _
 AAACACGTG GGA TGATG
 ||||| ||||| |||||
 TTTGTGCAC CTCT ACTAC
 - GA
 GAM276 DKFZp434A2417 3' CATCATATGTTTCACAGTGT 32862 G _
 A TAAAACAC TGTGGG ATGATG
 ||||| ||||| |||||
 ATTTTGTG AACTT TACTAC
 - GTA
 GAM276 DKFZp761B1514 3' CATCACCTTTGCCGTGTTT 26046 T _ A
 TAAAACACG GT GGG TGATG
 ||||| || |||||
 ATTTTGTGC CG TCC ACTAC
 C TT _
 GAM276 FLJ20136 3' CATCATCATTCATGTTTT 19228 C TGG
 AAA ACGTG GATGATG
 || ||||| |||||
 TTT TGTAC CTACTAC
 T TTA
 GAM276 KIAA0410 3' CATTCTACAGTGT 16617 G
 TAAAACAC TGTGGGATG
 ||||| |||||
 ATTTTGTG ACATCTTAC
 -
 GAM276 KIAA1908 5' CATCATCCGCTGGTGCTT 36329 A GT G
 TAAA CAC GTGG ATGATG
 |||| ||||| |||||
 ATTT GTG CGCC TACTAC
 C GT _
 GAM276 PEG10 3' CATCATCTTTCACATGTTCA 17427 A C TG
 A AACA GTG GGATGATG
 | |||| |||||
 A TTGT CAC TCTACTAC
 C A TT
 GAM276 PHF7 5' CACCGACACGTATTT 18580 C G A
 TAAAA ACGTGT GG TG
 |||| ||||| || ||

ATTTT TGCACA CC AC
 A G _
 GAM276 PRRG1 3' CACTTCACACTTGTTTTA 6651 C GA
 TAAAACA GTGTGG TG
 ||||| ||||| ||
 ATTTTGT CACACT AC
 T TC
 GAM276 LOC129198 3' CATCATCCTGAGGCTGTGTCA 37463 A _ G_
 A ACAC GT TGGGATGATG
 | ||| || |||||
 A TGTG CG GTCCTACTAC
 C T GA
 GAM276 LOC145719 5' CATCATCCTGGGCACGCCGT 40571 A_ _
 AC CGTGT GGGATGATG
 || |||| |||||
 TG GCACG TCCTACTAC
 CC GG
 GAM276 LOC145720 5' CATCATCCTGGGCACGCCGT 40561 A_ _
 AC CGTGT GGGATGATG
 || |||| |||||
 TG GCACG TCCTACTAC
 CC GG
 GAM276 LOC158295 5' CATCATCCTCTGATGTTT 41938 _ TGT
 AAACA CG GGGATGATG
 ||||| || |||||
 TTTGT GT TCCTACTAC
 A C_
 GAM276 LOC197114 5' CATCATCCTGGGCACGCCGT 43185 A_ _
 AC CGTGT GGGATGATG
 || |||| |||||
 TG GCACG TCCTACTAC
 CC GG
 GAM276 LOC197117 5' CATCATCCTGGACACGCCGT 43194 A_ _
 AC CGTGT GGGATGATG
 || |||| |||||
 TG GCACA TCCTACTAC
 CC GG
 GAM277 DNMT2 3' TTGAACAGATATTTGTACACCA 10673 T TG C
 TG TGTACAAAT CTG TCAA
 || ||||| || ||||
 AC ACATGTTTA GAC AGTT
 C TA A
 GAM277 ELL 3' TTGAGTCTATTTTGTACAA 13281 TTGCT
 TTGTACAAA GCTCAA
 ||||| |||||
 AACATGTTT TGAGTT
 TTATC
 GAM277 MAP3K7IP2 3' TTGAGCAGTGGGTGACACAACA 17489 ACAA TG
 TGTTGT T CTGCTCAA
 ||||| | |||||

ACAACA G GACGAGTT
CAGTG GT

GAM277 MRPL49 3' ATTTAAGCTATTAAATTTGTA 34477 GCT___ C
CAATA TGTGTACAAATT GCT AAAT
||||||| ||| |||
ATAACATGTTTAA CGA TTTA
AATTAT A

GAM277 WHSC1 3' ATTTGAGCACTTTTTATACACA 14248 T C TTGC
TGT GTA AAA TGCTCAAAT
||| ||| ||| |||||
ACA CAT TTT ACGAGTTTA
_ A TTC_

GAM277 CGI-203 5' TGAGCCCAGTACAACA 21676 AAAT CT
TGTTGTAC TG GCTCA
||||| || |||||
ACAACATG AC CGAGT
___ C_

GAM277 CNOT8 3' ATTTGAAATTTTTGTACAATA 11178 TTGCTGC
TGTTGTACAAA TCAAAT
||||||| |||||
ATAACATGTTT AGTTTA
TTAA___

GAM277 FLJ21709 3' TGAGCAGCAACAGCA 38173 ACAAAT
TGTTGT TGCTGCTCA
||||| |||||
ACGACA ACGACGAGT

GAM277 FLJ21939 3' ATTTGAACACACTGTACAATA 22802 AAT C C
TGTTGTACA TG TG TCAAAT
||||||| || || |||||
ATAACATGT AC AC AGTTTA
C_ _ A

GAM277 LOC152503 3' GCAGCAAACCTGTACAACA 41519 AA
TGTTGTACA TTGCTGC
||||||| |||||
ACAACATGT AACGACG
CA

GAM277 LOC152897 5' TGTACACAACCTGTACAAC 39328 AA C CT
GTTGTACA TTG TG CA
||||||| ||| || ||
CAACATGT AAC AC GT
CC _ AT

GAM278 PDE4D 3' ACCTCACTGTCTATCTGCCAGGA 36426 A A TTCGA_ C
TC CTGGCA ATG AG GT
|| ||||| ||| || ||
AG GACCGT TAC TC CA
_ C TGTCAC _

GAM278 TRPC6 5' TACGCTTCGCTACCACCAGCGG 10977 A CAAAT T_
TC CTGG GT CGAAGCGTA
|| ||| || |||||

			GG GACC CA GCTTCGCAT		
			C AC__ TC		
GAM279	DDX6	3'	GTTGCACTAACTGCTGGT 10647	A A C	
			ACCAGCAG TTA TGC AAC		
			TGGTCGTC AAT ACG TTG		
			_ C _		
GAM279	ELMO2	3'	TTGGCATTTCAGTATTGGTGG 28395	G _ _	
			CCA CAG ATT AATGCCAA		
			GGT GTT TGA TTACGGTT		
			G A C		
GAM279	HGF	3'	TGTCATTATTTGCTGGT 45230	T C	
			ACCAGCAGAT AATG CA		
			TGGTCGTTTA TTAC GT		
			_ T		
GAM279	ARHGAP5	5'	TGTTGGTCCTGCTGGT 37822	ATTAAT	
			ACCAGCAG GCCAACA		
			TGGTCGTC TGGTTGT		
			C_____		
GAM279	DKFZP434P0721	3'	TGTTGAGGAAACAATCTGTTG 31872	AATG _	
			CAGCAGATT CC AACA		
			GTTGTCTAA GG TTGT		
			CAAA AG		
GAM279	FLJ13189	3'	TGTTGGCATCATCTCT 24334	C TA	
			AG AGAT ATGCCAACA		
			TC TCTA TACGGTTGT		
			_ C_		
GAM279	FLJ20456	3'	CGTGTTGGCGGGCATCTGT 19494	TAA	
			GCAGAT TGCCAACACG		
			TGTCTA GCGGTTGTGC		
			CGG		
GAM279	FLJ20695	3'	CGTATCAACAGTGGATTTGCTG 19613	AA_ CCAAC	
			GT ACCAGCAGATT TG ACG		
			TGGTCGTTTAG AC TGC		
			GTG AACTA		
GAM279	KIAA1754	3'	TTGGGATCTGCTGGT 31682	AATG	
			ACCAGCAGATT CCAA		
			TGGTCGTCTAG GGTT		

GAM279	NAP1L2	3'	TGTAGCTATTAATCTGTGG 22497	G _ CA	
			CCA CAGATTAAT GC ACA		

		GGT GTCTAATTA CG TGT		
		— T A—		
GAM279	LOC150159 3'	GTATGTATTAGTCTGCTGG 29182	CA	
		CCAGCAGATTAATGC AC		
		GGTCGTCTGATTATG TG		
		TA		
GAM279	LOC164714 3'	CGTGTTGGCCTTTTCTGCTG 42180	TT T	
		CAGCAGA AA GCCAACACG		
		GTCGTCT TT CGGTTGTGC		
		T_ C		
GAM279	LOC196485 3'	TGTTGGCAGTAGTGCTGC 42383	_ A	
		GCAG ATTA TGCCAACA		
		CGTC TGAT ACGGTTGT		
		G G		
GAM279	LOC199858 5'	CGTGTTGGCTCCCTGACTGGT 42636	_ ATTAAT	
		ACCAG CAG GCCAACACG		
		TGGTC GTC CGGTTGTGC		
		A CCT__		
GAM279	LOC202986 3'	TGTTGGCAGTAATGCTGC 43474	_ A	
		GCAG ATTA TGCCAACA		
		CGTC TAAT ACGGTTGT		
		G G		
GAM279	LOC222060 5'	CGTGTTGGCGGGAGCCTGT 45159	AT AA	
		GCAG T TGCCAACACG		
		TGTC A GCGGTTGTGC		
		CG GG		
GAM279	LOC222160 5'	GTGTTGATTTTGTGCTGGT 45168	TTAATGC	
		ACCAGCAGA CAACAC		
		TGGTCGTTT GTTGTG		
		TTA__		
GAM280	DNMT3B 5'	TCCCGCCAGCCAGCCCGAC 13764	A CGA ACTA	
		GTCGG GC GC GCGGGA		
		CAGCC CG CG CGCCCT		
		C AC_ AC__		
GAM280	MAP3K8 5'	CCCGGCGTGCTCGGCTCCCACA 11705	C TAG	
		TGT GGAGCCGAGCAC CGGG		
		ACA CCTCGGCTCGTG GCCC		
		C CG_		
GAM280	PABPC1 5'	TCCCGCTGCCCGGACCCGACA 8420	AG A CTA	
		TGTCGG CCG GCA GCGGGA		

ACAGCC GGC CGT CGCCCT
CA C ____

GAM280 SLC8A2 3' TCCTGTTGTGCTCAGCCCCAAC 32970 C A C T
A TGT GG GC GAGCAC AGCGGGA
||| || ||||| |||||
ACA CC CG CTCGTG TTGTCCT
A C A _

GAM280 FLJ13855 5' CCCACGCTCAGCTCCGAC 23343 C ACTAGC
GTCGGAGC GAGC GGG
||||||| ||| |||
CAGCCTCG CTCG CCC
A CA ____

GAM280 FLJ14431 3' TCCCGCTAGGCCACCTCCAAC 26528 C CCGA A
A TGT GGAG GC CTAGCGGGA
||| ||| || |||||
ACA CCTC CG GATCGCCCT
A CACC _

GAM280 KIAA0373 5' CCCGCTAATGTTTCCATCA 16184 TC CCGA C
TG GGAG GCA TAGCGGG
|| ||| ||| |||||
AC CCTT TGT ATCGCCC
TA ____ A

GAM280 MGEA6 5' CCCGCAGCCGGCTCCGCA 12560 T A ACTA
TG CGGAGCCG GC GCGGG
|| ||||| || |||||
AC GCCTCGGC CG CGCCC
_ _ A ____

GAM280 LOC116349 3' CCCACTGCCACTCCGACA 36556 CCGA CTA C
TGTCGGAG GCA G GGG
||||||| ||| | |||
ACAGCCTC CGT C CCC
AC_ _ A

GAM281 CD28 3' TGTGTCTTTTGAAGAGAGCAT 12786 AGTTTA
ATGCTCTCTT ACACA
||||||| |||||
TACGAGAGAA TGTGT
GTTTTTC

GAM281 IRS1 3' GTTGGGTGGAGAGAGTATT 12069 AG
AATGCTCTCTT TTAAAC
||||||| |||||
TTATGAGAGAG GGGTTG
GT

GAM281 LEF1 3' TGTTAAATGAGCATTGA 18393 TCTTAG
TCAATGCTC TTTAACA
||||||| |||||
AGTTACGAG AAATTGT
TA ____

GAM281 MMP19 3' TG TTCATAAGAGAGGACTGA 23078 ATG GTTT
TCA CTCTCTTA AACA
||| ||||| |||||

			AGT GAGAGAAT TTGT		
			CAG AC__		
GAM281	MMP19	3'	TGTTTCATAAGAGAGGACTGA 8270	ATG	GTTT
			TCA CTCTCTTA AACAA		
			AGT GAGAGAAT TTGT		
			CAG AC__		
GAM281	STMN1	3'	GTGTTTCTAGAGAACAGTTGA 12092	GC_	T TTT
			TCAAT TCTCT AG AACAC		
			AGTTG AGAGA TC TTGTG		
			ACA _ T__		
GAM281	EML4	3'	GAAC TAAGAGAGCATTGG 21143		
			TCAATGCTCTCTTAGTTT		
			GGTTACGAGAGAATCAAG		
GAM281	FLJ22969	3'	GTGTTATTTAAGAGATCA 34066	C	TT
			TG TCTCTTAG TAACAC		
			AC AGAGAATT ATTGTG		
			T T_		
GAM281	FLJ23153	3'	AAACACTAGAAAAAGCATTGA 23906	C_	TA_
			TCAATGCT TCT GTTT		
			AGTTACGA AGA CAAA		
			AAA TCA		
GAM281	FLJ30567	3'	TGTCAACTAAAGCATTGG 29635	CTC	TA
			TCAATGCT TTAGTT ACA		
			GGTTACGA AATCAA TGT		
			_ C_		
GAM281	KIAA1946	3'	TGTGTTAAGTAAAGAACAT 40122	C C	T
			ATG TCT TTAGTT AACACA		
			TAC AGA AGTCAA TTGTGT		
			A A _		
GAM281	PDE11A	3'	TGTGTTATCCAAAGAACATTGG 18869	C	CTTAGTT
			TCAATG TCT TAACACA		
			GGTTAC AGA ATTGTGT		
			A AACCT__		
GAM281	TUCAN	3'	TGTATTTGCTGAAAGAGAGCA 17320	_	TTA_
			TGCTCTCT TAGT ACA		
			ACGAGAGA GTCG TGT		
			AA TTTA		
GAM281	LOC118851	5'	TGTCAAGAAGCATTGA 37205	C	AGTTTA
			TCAATGCT TCTT ACA		

AGTTACGA AGAA TGT
 _ C_
 GAM281 LOC144742 5' GAACTGAGAGCATGA 37778 A TT
 TCA TGCTCTC AGTTT
 ||| ||||| ||||
 AGT ACGAGAG TCAAG

_ _
 GAM281 LOC147353 3' TGTTAATAAGAGCATTG 40838 CTTAGT
 CAATGCTCT TTAACA
 ||||| ||||
 GTTACGAGA AATTGT
 AT_

GAM281 LOC221687 3' ACTATAGGGAGAGCATGGA 44301 A _
 TC ATGCTCTCT TAGT
 || ||||| ||||
 AG TACGAGAGG ATCA
 G GAT

GAM282 ALOX15 3' GACAGAGTCTCACTTTTGACA 6810 G AACCC G_
 TG CAAAGTGA GAC TGTT
 || ||||| ||| ||||
 AC GTTTCAC TCTG ACAG
 A _ AG

GAM282 DAZ 3' AACACAAGCATTTCAC TTTCTCC 10281 CA CCCGAC
 A
 TGG AAGTGAAA GTGTT
 ||| ||||| ||||
 ACC TTCAC TTT CACAA
 TC ACGAA_

GAM282 SLC6A5 5' ATAGCGGGTTTCACCCTCCA 10417 CAAA AC
 TGG GTGAAACCCG GT
 ||| ||||| ||| ||
 ACC CACTTTGGGC TA
 TCC_ GA

GAM282 WHSC1 3' TCGACTTCATTTTGCCA 28450 ACC
 TGGCAAAGTGAA CGA
 ||||| ||||| |||
 ACCGTTT TACTT GCT
 CA_

GAM282 WHSC1 3' TCGACTTCATTTTGCCA 28467 ACC
 TGGCAAAGTGAA CGA
 ||||| ||||| |||
 ACCGTTT TACTT GCT
 CA_

GAM282 WHSC1 3' TCGACTTCATTTTGCCA 17186 ACC
 TGGCAAAGTGAA CGA
 ||||| ||||| |||
 ACCGTTT TACTT GCT
 CA_

GAM282 MGC21738 3' GCTCTAAGTTTCACTTTTCCA 29677 C CC_ C
 TGG AAAGTGAAAC GA GT
 ||| ||||| ||| ||

ACC TTTCAC TTTG CT CG
 T AAT _
 GAM282 LOC150280 3' ACGCGAGTCCACTTTGCCA 38912 AA C A
 TGGCAAAGTG AC CG CGT
 ||||| || ||
 ACCGTTTCAC TG GC GCA
 C_ A _
 GAM283 DAPP1 3' CAACATCAGCCTGGCCAACATG 15731 T C
 ATGAA TCATCGTGT CGGGCT GA GTTG
 ||||| |||| || ||
 AGTAGTACA GTCCGA CT CAAC
 ACCG _ A
 GAM284 MGC12538 3' ACTGGATGATGTTCAACA 26479 CACGC G
 TGT ACATCATC CAGT
 || ||||| ||
 ACA TGTAGTAG GTCA
 AACT _
 GAM284 NUP160 3' ACTGTAAATGATGTGTACAACA 42327 CAC C_
 TGT GCACATCAT GCAGT
 || ||||| ||
 ACA TGTGTAGTA TGTCA
 ACA AA
 GAM285 NEBL 3' GCCAATAATACAAACCGTT 13100 C ACG
 AACG GTTTGTATTG GGT
 ||| ||||| ||
 TTGC CAAACATAAT CCG
 C AA_
 GAM285 FLJ12389 3' GTCACCCGTCAACCAGAGCGTG 30235 GTA
 CGCGTTT TTGACGGGTGAC
 ||||| |||||
 GTGCGAG AACTGCCCACTG
 ACC
 GAM285 FLJ20300 3' GTCACCTAGTTATACAAAC 19366 T _
 GTTTGTAT GAC GGGTGAC
 ||||| || |||||
 CAAACATA TTG TCCACTG
 _ A
 GAM285 LOC147054 5' GTCACCCGGCAGCAAACACG 40795 C AT A
 CG GTTTGT TG CGGGTGAC
 || |||| || |||||
 GC CAAACG AC GCCCACTG
 A _ G
 GAM286 CEACAM6 3' ACAAACTCAGAGAAATGTGTC 8308 GATACAA
 GACACATTT TTTTGT
 ||||| ||||
 CTGTGTAAA AAAACA
 GAGACTC
 GAM286 COCH 3' ACAAACTATTAAGTATGTC 10291 C CAA
 GACA ATTTGATA TTTTGT
 ||| ||||| ||||

			CTGT TGAATTAT AAAACA		
			A C__		
GAM286	JJAZ1	3'	ACAAATGTCATCAAATATGTTG 17653	C _ AT	
	A		TCGACA ATTTGAT ACA TTTGT		
			AGTTGT TAACTA TGT AAACA		
			A C __		
GAM286	KIAA1223	3'	ACAAAATTGCACCTTGTGTC 35243	TTTGATA	
			GACACA CAATTTTGT		
			CTGTGT GTTAAAACA		
			TCCAC__		
GAM286	MGC4655	3'	ACAAAATTGTCATCTATGTATC 27144	C TT _	
			GA ACAT GAT ACAATTTTGT		
			CT TGTA CTA TGTTAAAACA		
			A T_ C		
GAM286	R32184_3	3'	ACAAAATTGTGTTTGT 27247	TTT	
			ACA GATACAATTTTGT		
			TGT TTGTGTTAAAACA		

GAM287	AGL	3'	GTATATTTTATATGATTTACTT 5467	CT T A	
	A		TAAG AATCATATAAA TA AC		
			ATTC TTAGTATATTT AT TG		
			AT T A		
GAM287	AGL	3'	GTATATTTTATATGATTTACTT 6284	CT T A	
	A		TAAG AATCATATAAA TA AC		
			ATTC TTAGTATATTT AT TG		
			AT T A		
GAM287	AGL	3'	GTATATTTTATATGATTTACTT 6289	CT T A	
	A		TAAG AATCATATAAA TA AC		
			ATTC TTAGTATATTT AT TG		
			AT T A		
GAM287	AGL	3'	GTATATTTTATATGATTTACTT 6294	CT T A	
	A		TAAG AATCATATAAA TA AC		
			ATTC TTAGTATATTT AT TG		
			AT T A		
GAM287	AGL	3'	GTATATTTTATATGATTTACTT 6299	CT T A	
	A		TAAG AATCATATAAA TA AC		
			ATTC TTAGTATATTT AT TG		
			AT T A		
GAM287	AGL	3'	GTATATTTTATATGATTTACTT 6306	CT T A	
	A		TAAG AATCATATAAA TA AC		

ATTC TTAGTATATTT AT TG
 AT T A
 GAM287 RPS6KC1 3' GGTTTATATGATTAAATTA 14800 GC
 TAA TAATCATATAAATT
 ||| |||||
 ATT ATTAGTATATTTGG
 AA
 GAM288 ITK 3' GAGCTTCAAAGCAACTTT 12076 CC CCAT
 AAAGTTGT TGA GCTC
 ||||| || |||
 TTTCAACG ACT CGAG
 AA T____
 GAM288 MTNR1A 3' TGAGCAAATGGAACAATTTT 12582 _ TGACCA
 AAAGTTGT CC TGCTCA
 ||||| || |||||
 TTTTAACA GG ACGAGT
 A TAA____
 GAM288 OPHN1 5' GGCCCTGGTCAGGAAACT 8405 G T_
 AGTT TCCTGACCA GCT
 ||| ||||| |||
 TCAA AGGACTGGT CGG
 _ CC
 GAM288 RAG1 3' GTTACATCAGGACAACCTTT 6040 CCAT
 AAAGTTGTCCTGA GC
 ||||| |||
 TTTCAACAGGACT TG
 ACAT
 GAM288 SLC18A3 5' GTCTGCTCGGCCAGGACAGC 9019 A AT TC
 GTTGTCTG CC GC AC
 ||||| || |||
 CGACAGGAC GG CG TG
 C CT TC
 GAM288 AQP10 3' AGCTATGATTAGGACAAC 27840 C _
 GTTGTCTG CAT GCT
 ||||| ||| |||
 CAACAGGATT GTA CGA
 A T
 GAM288 BTBD3 3' TGAGTATTTCCAGGACAAC 17341 ACC
 GTTGTCTG ATGCTCA
 ||||| |||||
 CAACAGGAC TATGAGT
 CTT
 GAM288 DRCTNNB1A 3' GTGAACCTGGAAATACAACCTTT 26316 CCTGA TGC
 AAAGTTGT CCA TCAC
 ||||| ||| |||
 TTTCAACA GGT AGTG
 TAAA_ CCA
 GAM288 FLJ10700 3' TGAGCATGGTTCTAACACCT 20021 T CCT
 AG TGT GACCATGCTCA
 || ||| |||||

TC ACA TTGGTACGAGT
 C ATC
 GAM288 FLJ23053 3' GGCAGAGTCAAGACGAACT 23207 _ C CA
 AGTT GTC TGAC TGCT
 |||| ||| |||| ||||
 TCAA CAG ACTG ACGG
 G A AG
 GAM288 FLJ30663 3' GGTAATGTGTCAGGAACAACTT 38462 _ C GCTC
 T AAAGTTGT CCTGAC AT ACC
 ||||| ||||| || |||
 TTTCAACA GGA CTG TA TGG
 A _ AAA_
 GAM288 GP5 3' GTAAGCATGGTTCATCTT 10818 T TCCT C
 AAG TG GACCATGCT AC
 ||| || ||||| ||
 TTC AC TTGGTACGA TG
 T _ A
 GAM288 HEYL 3' GACAGGAACAAGGACA ACTCC 15931 A GA_ A C
 A AGTTGTCCT CC TG TC
 | ||||| || |||
 C TCAACAGGA GG AC AG
 C ACAA _ _
 GAM288 KIAA0254 3' TGAGCATAGGGGGACAGC 16507 GA _
 GTTGTCTCT CC ATGCTCA
 ||||| || |||||
 CGACAGGG GG TACGAGT
 _ A
 GAM288 KIAA0447 3' GGCCACAGTCAGGGCAACTTT 35495 CA CT
 AAAGTTGTCCTGAC TG C
 ||||| ||| |
 TTTCAACGGGACTG AC G
 AC CG
 GAM288 KIAA0547 3' GCACAGGACA ACTTT 16696 ACCA
 AAAGTTGTCCTG TGC
 ||||| |||
 TTTCAACAGGAC ACG
 _
 GAM288 KIAA0892 3' GTGAGCATGATCGCGACACT 35171 T C C
 AGT GTC TGA CATGCTCAC
 ||| ||| ||| |||||
 TCA CAG GCT GTACGAGTG
 _ C A
 GAM288 KIAA1223 3' TGAGCATGTGTCCACAGC 35249 CCT _
 GTTGT GAC CATGCTCA
 |||| ||| |||||
 CGACA CTG GTACGAGT
 CC_ T
 GAM288 KIAA1354 3' AGCATGTAAATCAGGAACAACT 30540 _ C_
 TT AAAGTTGT CCTGA CATGCT
 ||||| ||||| |||||

		TTTCAACA GGA	CT GTACGA	
		A	AAAT	
GAM288	MGC14859	3'	TGGGGGTCAGGACAATTTT	31006 ATG
			AAAGTTGTCCTGACC	CTCA
			TTTTAACAGGACTGG	GGGT

GAM288	P2RX1	3'	GTGTGCCAGGCCAGGACAGC	33358 A AT T
			GTTGTCCTG	CC GC CAC
			CGACAGGAC	GG CG GTG
			C	AC T
GAM288	SEPT3	3'	GGCAGGGAGTTCAGGACAAC	21184 ____ A
			GTTGTCCTGA	CC TGCT
			CAACAGGACT	GG ACGG
			TGA	G
GAM288	LOC150095	5'	GGTGAGCATGGCCAGAC	41131 C A
			GTC TG	CCATGCTCACC
			CAG AC	GGTACGAGTGG
			_	C
GAM288	LOC163915	5'	GGCGGTACCAGGACAGCTT	42100 ACCA
			AAGTTGTCCTG	TGCT
			TTCGACAGGAC	GCGG
			CATG	
GAM288	LOC165568	5'	CATGCTTGGGAAGCAACTTT	40138 ____ TG C
			AAAGTTGT	CC A CATG
			TTTCAACG	GG T GTAC
			AA	GT C
GAM288	LOC197285	3'	AGCCACTGGTCAGGACCAC	42413 T T__
			GT GTCCTGACCA	GCT
			CA CAGGACTGGT	CGA
			C	CAC
GAM288	LOC256997	5'	GGTGAGCACAGCCACAGAGAGC	45653 G C ACCA__
		T	AGTT TC TG	TGCTCACC
			TCGA AG AC	ACGAGTGG
			G _	ACCGAC
GAM289	CXorf6	3'	AAGTCACCTCCAAGTGTAGC	11989 TACAT
			GCTACATTTG	TGACTT
			CGATGTGAAC	ACTGAA
			CTCC_	
GAM289	HNRPD	3'	AAGTCATTACAAATGTG	11948 CAT
			TACATTTGTA	TGACTT

GTGTAAACAT ACTGAA
T__

GAM289 SLC9A3R1 3' TCAATGTACAAATCAGC 34864 AC
GCT ATTTGTACATTGA
||| |||||
CGA TAAACATGTAAC
C_

GAM289 ZFP36L1 3' AAGTCAATTTGTCAGTAGC 11361 ATT _ C
GCTAC TG TA ATTGACTT
|||| || || |||||
CGATG AC GT TAACTGAA
__ T T

GAM289 ARHGAP10 3' GATAGTTGTATACAAATGAGC 21888 A CAT T
GCT CATTTGTA TGA CT ATC
||| ||||| ||||| |||
CGA GTAAACAT GTTGA TAG
_ AT_ _

GAM289 GBTS1 3' AATGACCACAAATGTAGC 29724 A__
GCTACATTTGT CATT
||||||| |||
CGATGTAAACA GTAA
CCA

GAM289 KIAA0547 3' ATAGGGCTGTACAAATATAG 16694 C TTGA
CTA ATTTGTACA CTTAT
||| ||||| |||||
GAT TAAACATGT GGATA
A CG__

GAM289 MEGF10 3' AAGTCAATACACAAATGTGC 26207 T AC
GC ACATTTGT ATTGACTT
|| ||||| |||||
CG TGTAACA TAACTGAA
_ CA

GAM289 LOC146455 3' AAGTCAATTCTATGTAGT 38154 TTGTAC
GCTACAT ATTGACTT
||||| |||||
TGATGTA TAACTGAA
TCT__

GAM289 LOC204084 3' GAGCTGATGTACAAACACAGC 43085 ACA GA
GCT TTTGTACATT CTT
||| ||||| |||
CGA AAACATGTAG GAG
CAC TC

GAM290 RDX 3' TACTACCTCACTACTACA 8808 _
TG TAGTAGTGA TAGTA
||||||| |||||
ACATCATCACT ATCAT
CC

GAM290 XK 3' TAAAGCTACCATGTTAATAC 22062 G _
GTA TGATA GTAGCTTTA
||| ||||| |||||

			CAT ATTGT CATCGAAAT		
			A AC		
GAM291	ANGPT1	3'	GGTACAAAAAGCCTGTAA 29289	C	ATA
			TTACAGGC TTT TACC		
			AATGTCCG AAA ATGG		
			A AAC		
GAM291	SLC2A3	3'	ACATAGGTATATATATGCCATG 13815	_	CTT C
			CA GGC TATATACC ATGT		
			GT CCG ATATATGG TACA		
			A TAT A		
GAM291	FLJ13110	3'	ACATAAAATGTGAAAGCCTGTA 23219	C	ACCC
	A		TTACAGGC TTTATAT ATGT		
			AATGTCCG AAGTGTA TACA		
			A AAA_		
GAM292	ACRC	3'	ATCAAAAAATAAAAGTTTT 27517	AG	
			AAAGCTTTTATTT TGAT		
			TTTTGAAAATAAA ACTA		
			AA		
GAM292	ALDH3A2	3'	ATCACTGTGTGAAGCTTTCA 34340	A	TATT
			A AAAGCTTT TAGTGAT		
			A TTTCGAAG GTCACTA		
			C TGT_		
GAM292	FOXF1	3'	ATCGGTAAATAAAAGTTTTT 7183	G	
			AAAAGCTTTTATTTA TGAT		
			TTTTTGAAAATAAAT GCTA		
			G		
GAM292	GAS11	3'	ATCAGCAAATGAAAGCTTTT 7220	AG	
			AAAAGCTTTTATTT TGAT		
			TTTTCGAAAGTAAA ACTA		
			CG		
GAM292	NCSTN	3'	ATTACAAATAGAAGCTT 36507	A	
			AAGCTTTTATTT GTGAT		
			TTCGAAGATAAA CATTA		
			-		
GAM292	PTGS2	3'	ATCACCTGTAAAAGCTT 6683	TTA	
			AAGCTTTTAT GTGAT		
			TTCGAAAATG CACTA		
			TC_		
GAM292	RNGTT	3'	GTTATCACATGTGAAAGCTTTT 9896	TTA	
			AAAAGCTTTTAT GTGATAAC		

			TTTTCGAAAGTG CACTATTG		
			TA_		
GAM292	ATP9A	3'	GTCACATGATAAAAGTTT 31086	TA	
			AAGCTTTTATT GTGAT		
			TTTGAAAATAG CACTG		
			TA		
GAM292	BDG-29	3'	CACGGAAATGAAAGCCTTTT 35814	A	A_
			AAAA GCTTTTATTT GTG		
			TTTT CGAAAGTAAA CAC		
			C GG		
GAM292	CPR2	3'	GTCATGAGTAAAAGCTT 25177	G	
			AAGCTTTTATTTA TGAT		
			TTCGAAAATGAGT ACTG		
			—		
GAM292	DKFZp761D221	3'	GTTACCACTTTTAAAAAGCTT 26057	ATTT_	A
			TTT AAAAAGCTTTT AGTG TAAC		
			TTTTTCGAAAA TCAC ATTG		
			ATTT C		
GAM292	ERMAP	3'	CACCAACGTAGAAGCTTTT 20606	_	A
			AAAAAGCTTTTAT TT GTG		
			TTTTTCGAAGATG AA CAC		
			C C		
GAM292	FBXO5	3'	GTCACCTTTCTAAAGCTTTT 14466	TATTTA	
			AAAAAGCTTT GTGAT		
			TTTTTCGAAA CACTG		
			TCTTTC		
GAM292	FLJ10450	3'	GTTGATACAAATAAAAGTTTTT 19863	A	A
			AAAAGCTTTTATTT GTG TAAC		
			TTTTTGAAAATAAA CAT GTTG		
			_ A		
GAM292	FLJ22009	3'	GTCTTAAAATAAAAGCTTTT 30244	AGT	
			AAAAGCTTTTATTT GAT		
			TTTTCGAAAATAAA CTG		
			ATT		
GAM292	KIAA1204	3'	GTCACCATAGATAAAAGC 34316	—	
			GCTTTTATTTA GTGAT		
			CGAAAATAGAT CACTG		
			AC		
GAM292	KIAA1458	3'	GTCATCTAAAAGCTTTT 34206	TTTA	
			AAAAGCTTTTA GTGAT		

			TTTTCGAAAAT TACTG		
			C__		
GAM292	MGC24447	3'	ATTACCCCCGTGAAAGCTTTT 28702	TTA_	
			AAAAGCTTTTAT GTGAT		
			TTTTCGAAAGTG CATTA		
			CCCC		
GAM292	MST4	3'	TTATCAAGCTTCAAAAAGCTTT 18610	ATTTAG_	
	TT		AAAAAGCTTTT TGATAA		
			TTTTTCGAAAA ACTATT		
			ACTTCGA		
GAM292	STRIN	3'	GCTGAATAACAGCTCTTT 18396 A T		
			AAA AGCT TTATTTAGT		
			TTT TCGA AATAAGTCG		
			C C		
GAM292	LOC145622	3'	GTCATAAAAAAAAGCTTT 37912 A A		
			AAAGCTTTT TTT GTGAT		
			TTTCGAAAA AAA TACTG		
			A A		
GAM292	LOC219401	5'	TTATTAGTAATAGAAGCT 44596 T G		
			AGCTTTTATT A TGATAA		
			TCGAAGATAA T ATTATT		
			_G		
GAM292	LOC257443	3'	GTCATCTAAAAGCTTTT 45874 TTTA		
			AAAAGCTTTTA GTGAT		
			TTTTCGAAAAT TACTG		
			C__		
GAM293	HTRA3	3'	TTCACAAAAGCTTCCATG 42944 ACA A CG		
			CATG AAG GCG TTTGTGAA		
			GTAC TTC CGT AAACACTT		
			C__ _ CA		
GAM293	KAL1	3'	TTCACTGCAGCTCCTGTCA 5720 AA GC TT		
			TGACA GAGC GT GTGAA		
			ACTGT CTCG CG CACTT		
			C_ A_ T_		
GAM293	SLC6A12	3'	TCACAAACACTCGGCATG 9011 ACAA CGC		
			CATG GAG GTTTGTGA		
			GTAC CTC CAAACACT		
			GG__ A__		
GAM293	ZNF18	3'	TCACGTGTGTTCTTTGTCAT 38250 TT		
			ATGACAAAGAGCGCG TGTGA		

TACTGTTTCTTGTGT GCACT

GAM293 ABLIM 3' TCACTGCACTCCTTTGTCAT 8120 _ C TTT
ATGACAAAG AG GCG GTGA
||||||| || ||| ||||
TACTGTTTC TC CGT CACT

C A _

GAM293 ABLIM 3' TCACTGCACTCCTTTGTCAT 13553 _ C TTT
ATGACAAAG AG GCG GTGA
||||||| || ||| ||||
TACTGTTTC TC CGT CACT

C A _

GAM293 ARHGEF9 3' CACACATAGCCCTTTTCATG 17537 C A GC T
CATGA AAAG GC GT TGTG
||||| |||| || || ||||
GTACT TTTC CG TA ACAC

_ C A _ C

GAM293 ATPW 5' TCACGGAGGCTCTTTGTCA 17909 GCG
TGACAAAGAGC TTTGTGA
||||||| |||||
ACTGTTTCTCG AGGCACT

G _

GAM293 KIAA1371 3' CACATGTTATGCTCTTTTCA 42906 C CGTT_
TGA AAAGAGCG TGTG
||| ||||| ||||
ACT TTTCTCGT ACAC

_ ATTGT

GAM293 KIAA1462 3' TTCACAGAAACCCTCCCTCATG 43922 CAAA CGCG
CATGA GAG TTTGTGAA
||||| ||| |||||
GTACT CTC AGACACTT

CC _ CCAA

GAM293 KIAA1643 3' CACAGGCTCTTTGGCA 32238 A GCGT
TG CAAAGAGC TTGTG
|| ||||| |||||
AC GTTTCTCG GACAC

G _

GAM293 MGC13251 3' GCTGCGCGCTCCTCATG 26437 CAAA TT
CATGA GAGCGCGT GT
||||| ||||| ||
GTACT CTCGCGCG CG

C _ T _

GAM293 MGC15476 3' TTCACAAAGTGCCCCCTCCATG 29690 ACAAAGA G
CATG GCGC TTTGTGAA
||||| ||||| |||||
GTAC CGTG AAACACTT

CTCCCC _ _

GAM293 LOC114971 3' TCACCTCTGGCTCTTTGCCA 36210 A G TTT
TG CAAAGAGC CG GTGA
|| ||||| || ||||

			AC GTTTCTCG GT CACT		
			C _ CTC		
GAM293	LOC144848	3'	TTCACAAACAGCCTCTGTCA 36423	A A GC	
			TGACA AG GC GTTTGTGAA		
			ACTGT TC CG CAAACACTT		
			C _ A_		
GAM293	LOC201181	5'	CACTGTGCTCTCTGTCA 42534	A TTT	
			TGACA AGAGCGCG GTG		
			ACTGT TCTCGTGT CAC		
			C _		
GAM294	IL22RA2	3'	TACAGCAAAATAAAAATTTAAC 27523	C ACGAA	
	A		TGTTAA TTTT TTGCTGTA		
			ACAATT AAAA AACGACAT		
			T ATAA_		
GAM294	SLC1A3	3'	GCATAAAAGTTAACA 10384	CGAAT	
			TGTTAACTTTTA TGC		
			ACAATTGAAAAT ACG		
GAM294	UBE2A	3'	TACAGCAATTGTAGTAACTGAC 9342	ACTT G	
	A		TGTTA TTAC AATTGCTGTA		
			ACAGT GATG TTAACGACAT		
			CAAT _		
GAM294	KIAA0193	3'	TACAGCCTGGCAAAAGTTAA 16545	A_ AATT	
			TTAACTTTT CG GCTGTA		
			AATTGAAAA GT CGACAT		
			CG C_		
GAM294	KIAA0972	3'	TACAGTGGGGGTAAGTCACA 17227	TA GAA TG	
			TGT ACTTTTAC T CTGTA		
			ACA TGAAAATG G GACAT		
			C_ GG_ GT		
GAM294	LOC145231	3'	TACAGCAACCATAGGAAGCTAA 40520	A ACGAA	
	TA		TGTTA CTTTT TTGCTGTA		
			ATAAT GAAGG AACGACAT		
			C ATACC		
GAM295	ADCY7	3'	CAACAATGCTGGTAAGGG 6779	TA	
			CTCTTGTT CATTGTTG		
			GGAATGG GTAACAAC		
			TC		
GAM295	JPH2	3'	CAATGAAACAAGACAATGA 45332	CCAC A	
			TCA TCTTGTTT CATTG		

			AGT AGAACAAA GTAAC		
			AAC_ _		
GAM295	DKFZP564O0423	5'	AACAATGGCAACATGGT	44061	CTCT TA
			ACCA TGTT CATTGTT		
			TGGT ACAA GTAACAA		
			_____ CG		
GAM295	LOC124801	3'	CAACAAAAAAGAACAAGAG	36763	ACA_
			CTCTTGTTT TTGTTG		
			GAGAACAAG AACAAC		
			AAAA		
GAM295	LOC57086	3'	TGTCAAACAAGAGAGATGA	21618	CCA _
			TCA CTCTTGTTT ACA		
			AGT GAGAACAAA TGT		
			AGA C		
GAM296	CACNA1C	5'	AAAACAAACGTGTATCTAAATG	6378	TT__
	T		ACATTTA TGCGTTTGT		
			TGTAAAT GTGCAACAAAA		
			CTAT		
GAM296	USP6	3'	AAAACAAACAATTATAATGTTG	43806	TATTTGC
	T		ATAACATT GTTTGTTT		
			TGTTGTAA CAAACAAAA		
			TATTAA_		
GAM296	OLFM3	3'	AAAACAAATTGTTTAAATGTT	39957	TTT _
			AACATTTA GCG TTTGTTT		
			TTGTAAAT TGT AAACAAAA		
			TT_ T		
GAM296	LOC256714	3'	AAAACCAGGCGCAAACAAA	46081	A _
			TTT TTTGCGTTTG TTTT		
			AAA AAACGCGGAC AAAA		
			C C		
GAM297	ARHGEF7	5'	GCTCAGCGCTTGTGCTCTG	9984	TGA CACC
			CAGAGCACA GT GAGC		
			GTCTCGTGT CG CTCG		
			TCG A__		
GAM297	CSF1R	3'	TCGGCCCAGCTCTGAA	11710	ACA A TCA
			TTCAGAGC TG G CCGA		
			AAGTCTCG AC C GGCT		
			__ C __		
GAM297	RAB27A	3'	GCTATATTCCCATTGCTCTGAA	10929	C AGTCACCG
			TTCAGAGCA ATG AGC		

			AAGTCTCGT TAC TCG	
			_ CCTTATA_	
GAM297	TMEPAI	3'	GCTCGATGACTTGTCTCTG 21406	C TG C
			CAGAG ACA AGTCA CGAGC	
			GTCTC TGT TCAGT GCTCG	
			_ _ A	
GAM297	KIAA0367	3'	GCTCTCTAGCTCTTGCACTCTG 33424	CA T CACC
	AA		TTCAGAG CA GAGT GAGC	
			AAGTCTC GT CTCG CTCG	
			AC T ATCT	
GAM297	KIAA0543	3'	GCTCAGTGACAAGGGCTTTGAA 34177	ACATGA C
			TTCAGAGC GTCAC GAGC	
			AAGTTTCG CAGTG CTCG	
			GGAA_ A	
GAM297	KIAA0794	3'	CTCAGCTTTGTGCTCTGA 39179	T CACC
			TCAGAGCACA GAGT GAG	
			AGTCTCGTGT TTCG CTC	
			_ A_	
GAM297	KIAA1486	3'	GCTCATATGAACACTGCTCTGA 33462	CATGAG CC_
	A		TTCAGAGCA TCA GAGC	
			AAGTCTCGT AGT CTCG	
			CACA_ ATA	
GAM297	SERF2	5'	GCCCGCGGTTCCACCGCTCTGA 12342	ACAT GT AC A
	A		TTCAGAGC GA C CG GC	
			AAGTCTCG CT G GC CG	
			CCAC TG C_ C	
GAM297	LOC158987	3'	CTCGATGAGTGCTCTG 42047	ATGAG C
			CAGAGCAC TCA CGAG	
			GTCTCGTG AGT GCTC	
			_ A	
GAM297	LOC165352	5'	CTCAGATGTGGCCCTGAA 42157	A A GA ACC
			TTCAG GC CAT GTC GAG	
			AAGTC CG GTG TAG CTC	
			C _ _ A_	
GAM297	LOC219649	3'	GCTCGGTGACTCACGTCTG 44666	GCA A
			CAGA C TGAGTCACCGAGC	
			GTCT G ACTCAGTGGCTCG	
			_ C	
GAM297	LOC221692	3'	GCCCGCCTTCACGGCTCTGAA 44299	ACA TCAC A
			TTCAGAGC TGAG CG GC	

			AAGTCTCG ACTT GC CG		
			GC_ CC_ C		
GAM297	LOC90826	3'	ACTCAGTGACATCTGAA 32048	___	A
			TTCAGA GCAC TGAGT		
			AAGTCT TGTG ACTCA		
			ACA _		
GAM298	CD3Z	3'	AAACGCTCTCTGCTCTGCTTTT 6390	AATC	AAA
			AAAAGCA GCA AGCGTTT		
			TTTTCGT CGT TCGCAA		
			CT_ CTC		
GAM298	CLASP1	5'	TTTTTAGATTTGCTTTT 32544	GC	
			AAAAGCAAATC AAAAA		
			TTTTCGTTTAG TTTT		
			A_		
GAM298	DGAT2	5'	GCTTTTCACAGTTTGCTTTT 26291	CGCA	
			AAAAGCAAAT AAAAGC		
			TTTTCGTTTG TTTTCG		
			ACAC		
GAM298	DMXL1	3'	TTTTTTGCAACTGTGCTTTT 12025	AATC_	
			AAAAGCA GCAAAAAG		
			TTTTCGT CGTTTTT		
			GTCAA		
GAM298	SNX9	3'	AACACTTTTTGGACTTTGT 18327	_ G	C
			GCAA TC CAAAAAG GTT		
			TGTTT AG GTTTTTC CAA		
			C _ A		
GAM298	UNC5C	3'	AAACGCTTTTTTATTGCT 9818	ATCGC	
			AGCAA AAAAAGCGTTT		
			TCGTT TTTTTCGCAA		
			A_		
GAM298	UVRAG	3'	TGCTTTCAAGATTTGCTTTT 9396	GCAA	
			AAAAGCAAATC AAAGCG		
			TTTTCGTTTAG TTTCGT		
			AAC_		
GAM298	FLJ10097	3'	TTTTTGTGATTTACTTTT 33990	C	
			AAAAG AAATCGCAAAA		
			TTTTC TTTAGTGTTTTT		
			A		
GAM298	FLJ23416	3'	AAACGCTTCTGCAAACATTTGT 25959	C_	AA
			TTTT		
			AAAAGCAAAT GCA AAGCGTTT		

TTTTGTTTA CGT TTCGCAAA
 CAAA C_
 GAM298 KIAA1317 5' AACTTTTTTTCGACTTGTTTT 41620 A C
 AAAGCAA TCGCAAAAAG GTT
 ||||| ||||| ||
 TTTTGTT AGCGTTTTTT CAA
 C T
 GAM298 NYD-SP29 5' GCCCTTGCGATTTCTTTT 36861 C AAA
 AAAAG AAATCGCAA GC
 ||||| ||||| ||
 TTTTC TTTAGCGTT CG
 CC_
 GAM298 SSH2 3' AGAGGCTTGCAGATTTGCTTT 31175 _ AAA G
 AAAGCAAATC GCA AGC TTT
 ||||| || |||||
 TTTCGTTTAG CGT TCG AGA
 A _ G
 GAM299 APOL1 3' TGTCGCCAAGTTGGAGTG 9735 AG A
 CAC CCGAT TTGGCGACA
 || ||||| |||||
 GTG GGTTG AACCGCTGT
 A_ _
 GAM299 ATP5B 5' TGTCGCCAAAGCCCATGGTG 30007 CA_ CGATA
 CATCA GC TTGGCGACA
 ||||| || |||||
 GTGGT CG AACCGCTGT
 ACC A____
 GAM299 CXX1 5' TGCCGATCCGGCCTGCGA 10026 A _ AT
 TC CAG CCG ATTGGCG
 || ||||| |||||
 AG GTC GGC TAGCCGT
 C C C_
 GAM299 HTR4 3' GCGCCCTGGCTGTGCTG 6543 T ATATT A
 CA CACAGCCG GGCG C
 || ||||| |||||
 GT GTGTCGGT CCGC G
 C C_ C
 GAM299 PPP1R8 5' TGCCATCGGCTGTGA 28859 TAT
 TCACAGCCGA TGGCG
 ||||| |||||
 AGTGTGGCT ACCGT

 GAM299 TCF19 3' CCAGTGTGATGGCTGTGA 46657 _
 TCACAGCCG ATATTGG
 ||||| |||||
 AGTGTGGT TGTGACC
 AG
 GAM299 TCF19 3' CCAGTGTGATGGCTGTGA 46706 _
 TCACAGCCG ATATTGG
 ||||| |||||

			AGTGTCCGGT TGTGACC	
			AG	
GAM299	TEAD3	3'	GCGACATAAAATCCAGCTGTGA 9213	C_ AT_____ GCGA
	TG		ATCACAGC GAT TG C	
			TAGTGTCTG CTA AC G	
			AC AAATIII AGCG	
GAM299	TNFSF5	3'	TGTCACCTTGCAGGCTGTGGTG 5520	GATATT C
			CATCACAGCC GG GACA	
			GTGGTGTCTGG CC CTGT	
			ACGTT_ A	
GAM299	WBSCR1	3'	TGTTGGTATTTCAGCTGTGATG 22726	C_ TG
			CATCACAGC GATAT GCG	
			GTAGTGTCTG TTATG TGT	
			AC GT	
GAM299	WBSCR1	3'	TGTTGGTATTTCAGCTGTGATG 25709	C_ TG
			CATCACAGC GATAT GCG	
			GTAGTGTCTG TTATG TGT	
			AC GT	
GAM299	XRCC5	3'	TGCCATCGCTGTGATG 22115	C TAT
			CATCACAGC GA TGGCG	
			GTAGTGTCTG CT ACCGT	
			— —	
GAM299	C7orf13	3'	CGCCTTATGGCTGTGGTG 26341	G TT
			CATCACAGCC ATA GGCG	
			GTGGTGTCTGG TAT CCGC	
			— T_	
GAM299	CAMKK2	3'	GCGACACATCTGATCAGCTGTG 13313	C AT_____ GCGA
	GTG		TCACAGC GAT TG C	
			GGTGTCTG CTA AC G	
			A GTCTACIII AGCG	
GAM299	DKFZP434K1772	5'	TGTCTGAGCCCCGGCTGTGATG 33635	ATATT ____
			CATCACAGCCG GGC GACA	
			GTAGTGTCTGGC CCG CTGT	
			C_____ AGT	
GAM299	FLJ11850	3'	TGCCGTGACTGTGATG 22952	C ATAT
			CATCACAG CG TGGCG	
			GTAGTGTC GT GCCGT	
			A _____	
GAM299	FLJ12934	3'	TGCCAGTACCAACTGGGATG 23179	A CCGA
			CATC CAG TATTGGCG	

			GTAG GTC ATGACCGT		
			G AACC		
GAM299	FLJ22795	3'	TGCTAGCAGCTGTGATG 24691	CGATA	
			CATCACAGC TTGGCG		
			GTAGTGTCG GATCGT		
			AC__		
GAM299	IL14	5'	TGCCAACTCACTGTGATG 45705	CC TA	
			CATCACAG GA TTGGCG		
			GTAGTGTC CT AACCGT		
			A_ C_		
GAM299	KIAA0161	3'	TGCCACTAACACTGTGATG 16434	CCGA T	
			CATCACAG TA TTGGCG		
			GTAGTGTC AT ACCGT		
			ACA_ C		
GAM299	KIAA0240	3'	TGTCGCCAACATGGGGATG 44408	ACAG G A	
			CATC CC AT TTGGCGACA		
			GTAG GG TA AACCGCTGT		
			___ G C		
GAM299	KIAA1340	3'	TGCACATCAGCTGTGATG 34300	C ATTG	
			CATCACAGC GAT GCG		
			GTAGTGTCG CTA CGT		
			A CA__		
GAM299	KIAA1872	3'	TGGAGCCACCGGCTGTGA 31521	ATAT GA	
			TCACAGCCG TGGC CA		
			AGTGTCGGC ACCG GT		
			C__ AG		
GAM299	MGC4170	5'	GTCGCCGGAGCTGCAATG 23606	CA CGATA	
			CAT CAGC TTGGCGAC		
			GTA GTCG GGCCGCTG		
			AC A__		
GAM299	RNF40	3'	TGCTCCATCGGCTGTGA 16569	ATT	
			TCACAGCCGAT GGCG		
			AGTGTCGGCTA TCGT		
			CC_		
GAM299	SPTLC2	3'	TGTCATCAGCTGTGAT 11287	C TAT	
			ATCACAGC GA TTGGCG		
			TAGTGTCG CT ACTGT		
			A _		
GAM299	TP53INP1	3'	TGTTCTTCTACTGGCTGTGATG 36121	A TT C	
			CATCACAGCCG TA GG GACA		

		GTAGTGTCTGGT AT TC TTGT		
		C CT _		
GAM299	TP53INP1 3'	TGTTCTTCTACTGGCTGTGATG 27112		A TT C
		CATCACAGCCG TA GG GACA		
		GTAGTGTCTGGT AT TC TTGT		
		C CT _		
GAM299	LOC130074 3'	CATCATCTGGCTGTGATG 37470		_ AT
		CATCACAGCC GAT TG		
		GTAGTGTCTGG CTA AC		
		T CT		
GAM299	LOC145717 3'	CGCTAGCAGCTGTGATG 33193		CGATA
		CATCACAGC TTGGCG		
		GTAGTGTCTG GATCGC		
		AC__		
GAM299	LOC146488 3'	CCAATATCAATTGTGTG 35041	T	CC
		CA CACAG GATATTGG		
		GT GTGTT CTATAACC		
		_ AA		
GAM299	LOC148089 3'	GTCGCAGGATCCGGCTGTGG 38453		_ ATTG
		TCACAGCCG AT GCGAC		
		GGTGTCTGGC TA CGCTG		
		C GGA_		
GAM299	LOC200772 3'	TGTCACCAATGTCTGTGA 43347	GCC	C
		TCACA GATATTGG GACA		
		AGTGT CTGTAACC CTGT		
		_ A		
GAM299	LOC220537 3'	TGCTAGCAGCTGTGATG 43624		CGATA
		CATCACAGC TTGGCG		
		GTAGTGTCTG GATCGT		
		AC__		
GAM299	LOC221882 5'	TCCTCCGATGGCTGTGA 44435	GAT	C_
		TCACAGCC ATTGG GA		
		AGTGTCTGG TAGCC CT		
		_ TC		
GAM299	LOC253675 3'	TCACCAATATCATTGGA 46266	A CC	C
		TC CAG GATATTGG GA		
		AG GTT CTATAACC CT		
		_ A_ A		
GAM299	LOC54466 3'	TGTCAATTTCTGGCTGTGA 21076		T
		TCACAGCCGA ATTGGCG		

			AGTGTCCGGCT TAACTGT		
			T		
GAM300	ERCC5	5'	CTTAGGACGCAGCCGCCTC 5596	ACGC	GT A
			GAGGCGGCT GCG C AAG		
			CTCCGCCGA CGC G TTC		
			____ AG A		
GAM300	IL8RA	3'	TTGCCTAGGCATAGCCTGCCTC 6268	_ C GC_ T	
	A		TGAGGC GGCTA GC GG CAA		
			ACTCCG CCGAT CG CC GTT		
			T A GAT _		
GAM300	LAMA4	5'	TGGTTGCGCAGCCACCTC 8071	C AC GT	
			GAGG GGCT GCGCG CA		
			CTCC CCGA CGCGT GT		
			A _ TG		
GAM300	PTMA	5'	TTGCTCGCCGCAGCCGCCTC 8693	A C GT	
			GAGGCGGCT CG GCG CAA		
			CTCCGCCGA GC CGC GTT		
			C _ TC		
GAM300	PTPRO	5'	CTACGTTTCATAGCCGTCTCA 25011	C__ CG	
			TGAGGCGGCTA GCG G		
			ACTCTGCCGAT TGC C		
			ACT AT		
GAM300	PTPRO	5'	CTACGTTTCATAGCCGTCTCA 25020	C__ CG	
			TGAGGCGGCTA GCG G		
			ACTCTGCCGAT TGC C		
			ACT AT		
GAM300	PTPRO	5'	CTACGTTTCATAGCCGTCTCA 25030	C__ CG	
			TGAGGCGGCTA GCG G		
			ACTCTGCCGAT TGC C		
			ACT AT		
GAM300	PYGB	3'	TGACCACCACTGTGCCCTCA 8769	C T CGC__	
			TGAGG GGC ACG GGTCA		
			ACTCC CCG TGT CCAGT		
			_ _ CACCA		
GAM300	C1QTNF4	5'	TGTCCGCTGCCGCCTCA 25654	TACGC T	
			TGAGGCGGC GCGG CA		
			ACTCCGCCG CGCC GT		
			T__ T		
GAM300	CDCA4	3'	TGAGTGCTCACAGCCGCCTC 19663	ACGC G	
			GAGGCGGCT GCG TCA		

			CTCCGCCGA CGT AGT		
			CACT G		
GAM300	KIAA0876	5'	CCGCGCACGCCGCCTCA 32296	TAC	
			TGAGGCGGC GCGCGG		
			ACTCCGCCG CGCGCC		
			CA_		
GAM300	KIAA1257	3'	CTGCTGCGTGCCACCTCA 31433	C T _	
			TGAGG GGC ACGC GCGG		
			ACTCC CCG TGCG CGTC		
			A _ T		
GAM300	KLHL6	3'	GACCCTCAGCGTACCCGCCTCA 28210	C GC__	
			TGAGGCGG TACGC GGTC		
			ACTCCGCC ATGCG CCAG		
			C ACTC		
GAM300	MAD4	3'	TGGTCAGCATAGCCGCCCA 13172	A C GC GT	
			TG GCGGGCTA GC G CA		
			AC CCGCCGAT CG C GT		
			_ A A_ TG		
GAM300	MGC13007	5'	GCTACGCGCAGCCGCCTCA 26121	A CG	
			TGAGGCGGCT CGCG GT		
			ACTCCGCCGA GCGC CG		
			C AT		
GAM300	MGC13251	3'	CTTTGGCTCCCAGCCACCTCA 26435	C ACGCGC	
			TGAGG GGCT GGTCAAAG		
			ACTCC CCGA TCGGTTTC		
			A CCC__		
GAM300	MRPL20	3'	TGTCCACGTGCCGCCTCA 19700	TAC C T	
			TGAGGCGGC GCG GG CA		
			ACTCCGCCG TGC CC GT		
			_ A T		
GAM300	PHACS	5'	TGCGCGGTAGCCGCCCCA 26324	A _	
			TG GCGGGCTAC GCGCG		
			AC CCGCCGATG CGCGT		
			C G		
GAM300	PRKWNK2	5'	CTGCAAGACGCGCCGCCTCA 43521	TA C__	
			TGAGGCGGC CG GCGG		
			ACTCCGCCG GC CGTC		
			C_ AGAA		
GAM300	SEC14L1	3'	TGGCCCGCACGCCGCCTCA 8906	TAC C	
			TGAGGCGGC GCG GGTCA		

			ACTCCGCCG CGC CCGGT		
			CA_ _		
GAM300	SEC8	3'	CTTTGACCACACACAGTGATGC 22361	GC	GCGC_
	CT		AGGCG TAC GGTCAAAG		
			TCCGT GTG CCAGTTTC		
			A_ ACACACA		
GAM300	ZDHC2	5'	CCGACGCCGCCGCCTCA 18487	TAC	_
			TGAGGCGGC GCG CGG		
			ACTCCGCCG CGC GCC		
			C_ A		
GAM300	LOC145123	5'	TTGCTCGCCGCAGCCGCCTC 33534	A C	GT
			GAGGCGGCT CG GCG CAA		
			CTCCGCCGA GC CGC GTT		
			C _ TC		
GAM300	LOC147229	5'	CCGCCTGCATGCCGCCTCA 38316	TAC	_
			TGAGGCGGC GC GCGG		
			ACTCCGCCG CG CGCC		
			TA_ TC		
GAM300	LOC151009	5'	CCGCACGCATAGTGCCCCA 41291	A	_ C
			TG GGCGGCTA CG GCGG		
			AC CCGTCGAT GC CGCC		
			C AC A		
GAM300	LOC220058	5'	GCGGCGCGACCGCCTCA 44083	CTA	G
			TGAGGCGG CGCGC GT		
			ACTCCGCC GCGCG CG		
			A_ G		
GAM300	LOC254892	5'	CTTTGCCTTCGCAGCCGCCTC 45737	AC	C_ T
			GAGGCGGCT GCG GG CAAAG		
			CTCCGCCGA CGC CC GTTTC		
			_ TT _		
GAM301	FLJ14686	3'	AGTAATAACTAGTTGGCCAACT 26599	A	_ CGCG_
	GA		TCA TTGGCCAAC AG ACT		
			AGT AACCGGTTG TC TGA		
			C A AATAA		
GAM301	HTMP10	3'	GTGGTGTTGGCCCATTTGA 27050	T	G
			TCAAT GGCCAACA CGC		
			AGTTA CCGGTTGT GTG		
			C G		
GAM301	SEC14L1	3'	CAAGTCGCATTTGCCACTTGA 8900	T	CAACAGC
			TCAA TGGC GCGACTTG		

			AGTT ACCG CGCTGAAC		
			C TTTA__		
GAM301	LOC153688	3'	CAAGGCCTGGCCAATTGG 41654	ACA C GA	
			TCAATTGGCCA G GC CTTG		
			GGTTAACCGGT C CG GAAC		
GAM302	CHRM1	3'	TGTCCTGACTGTCCTACAATAT 45443	TAA ____ _	
	CA		TGATATTGT ACA AGG CA		
			ACTATAACA TGT TCC GT		
			TCC CAG T		
GAM302	DAAM1	3'	TGCTTGTTCTAACAATAT 17366	_ G	
			ATATTGTTA AACAAG CA		
			TATAACAAT TTGTTC GT		
			C _		
GAM302	ITPR2	3'	TGCTATTAACAGTATCA 7995	ACAA	
			TGATATTGTAA GGCA		
			ACTATGACAATT TCGT		
			A__		
GAM302	NCALD	3'	TTGCCAAACAATATCA 25748	AAACAA	
			TGATATTGTT GGCA		
			ACTATAACAA CCGTT		
			A_____		
GAM302	PPP2R5E	3'	TGTTGCCTTACTTTTTAATA 12924	TT AC	
			TATTG AA AAGGCAACA		
			ATAAT TT TTCCGTTGT		
			TT CA		
GAM302	RFP	3'	TGTTGCCTTGCCACGTCCTGTC 13263	TTGTTAAA	
	A		TGATA CAAGGCAACA		
			ACTGT GTTCCGTTGT		
			CCTGCACC		
GAM302	SLIT2	5'	TGCCTTGTTCCATATTA 11192	T TTA	
			TGATA TG AACAAGGCA		
			ATTAT AC TTGTTCCGT		
			_ C_		
GAM302	SOS2	3'	TTGCCTTGTCCTTGGATCCTCA 34001	TATTG _	
			TGA TTAA ACAAGGCAA		
			ACT GGTT TGTTCCGTT		
			CCTA_ C		
GAM302	ARHGEF9	3'	TGCCTTGTCATTATTA 17543	T TTAA	
			TGATA TG ACAAGGCA		

ATTAT AC TGTTC CGT
 T ____
 GAM302 CIP29 3' TGTCTTTTGACAATACCA 26150 A CA
 TG TATTGTTAAA AGGCA
 || ||||| ||||
 AC ATAACAGTTT TCTGT
 C ____
 GAM302 DKFZP434N093 3' TGCCTTGTTGAAAATTTCA 38993 T GTTA
 TGA ATT AACAAAGGCA
 ||| ||| |||||
 ACT TAA TTGTTCCGT
 T AAG_
 GAM302 KCNK13 3' TTGCCTTGTTTCATTAATC 22593 ATT T
 GAT GT AAACAAGGCAA
 ||| || |||||
 CTA TA TTTGTTCCGTT
 AT_ C
 GAM302 KIAA0227 3' TGTTCCTTCACTTAATAATATC 30458 AC_ C
 A TGATATTGTTAA AAGG AACA
 ||||| ||| |||
 ACTATAATAATT TTCC TTGT
 CAC _
 GAM302 SENP7 3' TGTTTTTTAACAATATTA 21824 CA
 TGATATTGTTAAA AGGCA
 ||||| ||||
 ATTATAACAATTT TTTGT

 GAM302 LOC151414 3' GTTTCCTAACAATATCA 39111 AAACA C
 TGATATTGTT AGG AAC
 ||||| ||| |||
 ACTATAACAA TCC TTG
 ____ T
 GAM302 LOC253926 5' TGTTACCTTCCAAGGACAATGT 45501 AAAC_ C
 CA TGATATTGTT AAGG AACA
 ||||| ||| |||
 ACTGTAACAG TTCC TTGT
 GAACC A
 GAM302 LOC90826 5' TGCTTTGCTTAACAACATC 32051 A A
 GAT TTGTAA CAAGGCA
 ||| ||||| |||||
 CTA AACAATT GTTTCGT
 C C
 GAM303 FLJ10579 3' AAAGCTATAGGAACAAAGCACA 19942 CGCGAAC_
 T ATGTGCTT TAGCTTT
 ||||| |||||
 TACACGAA ATCGAAA
 ACAAGGAT
 GAM304 BMP6 3' CCCCCAAAAACCCACCA 7452 A GTCGG
 TGGTG GTT TTGGGGG
 ||||| ||| |||||

			ACCAC CAA AACCCCC		
			C A_____		
GAM304	COL15A1	3'	TCCCCCAACCCCCACCCAC	7590	AGT TC
			GTG TG GGTTGGGGGA		
			CAC AC CCAACCCCCT		
			CCC CC		
GAM304	PAX7	5'	CCCCCAACCTCCACCCAC	15133	AGT TC
			GGTG TG GGTTGGGGG		
			CCAC AC CCAACCCCC		
			CCC CT		
GAM304	PAX7	5'	CCCCCAACCTCCACCCAC	8445	AGT TC
			GGTG TG GGTTGGGGG		
			CCAC AC CCAACCCCC		
			CCC CT		
GAM304	STX1A	3'	CCCCCAACCCCTTCACCA	10946	TTGTC
			TGGTGAG GGTTGGGGG		
			ACCACTT CCAACCCCC		
			CC_____		
GAM304	BCL2L1	3'	TCCCCCAACCCCCACCCAC	28895	AGT TC
			GTG TG GGTTGGGGGA		
			CAC AC CCAACCCCCT		
			CCC CC		
GAM304	C20orf98	3'	CCCCCAGCCCACCCACCA	35413	A TGTC
			TGGTG GT GGTTGGGGG		
			ACCAC CA CCGACCCCC		
			C C_____		
GAM304	DKFZp547O146	5'	CCCCCAACCTCTGGCTCCA	21484	T TC
			TGG GAGTTG GGTTGGGGG		
			ACC CTCGGT CCAACCCCC		
			_ CT		
GAM304	FLJ11539	5'	CCCCCAACTCCCTCCA	24085	T TTGTC
			TGG GAG GGTTGGGGG		
			ACC CTC TCAACCCCC		
			_ CC_____		
GAM304	ST7L	3'	CCCCCAACCACCCACCA	19334	A TGTC
			TGGTG GT GGTTGGGGG		
			ACCAC CA CCAACCCCC		
			C _____		
GAM304	ST7L	3'	CCCCCAACCACCCACCA	28976	A TGTC
			TGGTG GT GGTTGGGGG		

ACCAC CA CCAACCCCC
 C ____
 GAM304 ST7L 3' CCCCCAACCAACCCACCA 29206 A TGTC
 TGGTG GT GGTTGGGGG
 ||||| || |||||
 ACCAC CA CCAACCCCC
 C ____
 GAM304 TED 3' CCCCCAACCTACCCCCACC 17915 AGTT C
 GGTG GT GGTTGGGGG
 |||| || |||||
 CCAC CA CCAACCCCC
 CCC_ T
 GAM304 ZFP91 3' TCCCCCTCCCAACCCTCCATA 27578 TGA TC TT
 TATGG GTTG GG GGGGGA
 |||| |||| || |||||
 ATACC CAAC CC CCCCCT
 TCC _ T_
 GAM304 LOC150157 5' CCCCCAACCTTCCACCTCA 41142 T TC_
 TGAG TG GGTTGGGGG
 |||| || |||||
 ACTC AC CCAACCCCC
 C CTT
 GAM305 CD5 3' CCCCTCCCCAACCCCTCA 15476 G AGTTTTC
 TGAGGGGG TTG GGGG
 ||||| || ||||
 ACTCCCC AAC CCCC
 _ CCCT_
 GAM305 LOC148930 3' CCCCTGCCCATCAACCCCTCTC 38618 GTTTT
 A TGAGGGGGGTTGA CGGGGG
 ||||| |||| |||||
 ACTCTCCCCAACT GTCCCC
 ACCC_
 GAM305 LOC158310 5' CCAGAACCAAACCCCCCTCA 41944 GA C
 TGAGGGGGGTT GTTTT GG
 ||||| |||| ||||
 ACTCCCCCAA CAAGA CC
 AC _
 GAM305 LOC256950 3' CCCCCACCCCAACCCCCCT 45699 A_ TTTC
 AGGGGGGTTG GT GGGGG
 ||||| || ||||
 TCCCCCAAC CA CCCCC
 CC ____
 GAM306 CD28 3' TGGATATTTTCTACCTA 12785 C TAGC
 TAG GTAGAGAG ATCCA
 || ||||| ||||
 ATC CATCTTTT TAGGT
 _ TA_
 GAM306 MPP5 3' TTGTGGATCAGACTCTACAC 22840 AG AGC
 GT AGAGT ATCCACAA
 || |||| |||||

			CA TCTCA TAGGTGTT			
			CA GAC			
GAM306	PIK3C2B	3'	TGCAGATGCTACTGACTGC	8510	AG	CA
			GTAG AGTAGCATC CA			
			CGTC TCATCGTAG GT			
			AG AC			
GAM306	DKFZP727C091	5'	TGAATGCTACTTGGATGC	32908	AGA	C
			GCGT GAGTAGCAT CA			
			CGTA TTCATCGTA GT			
			GG_ A			
GAM306	DKK3	3'	TGCGAACACTGAACTCTACGC	14924	AG	CA_ _
			GCGTAGAG TAG TC CA			
			CGCATCTC GTC AG GT			
			AA ACA C			
GAM306	KIAA0323	3'	TGCAGAGCATTCTCTAC	31698	A A	CA
			GTAGAGAGT GC TC CA			
			CATCTCTTA CG AG GT			
			_ _ AC			
GAM306	KIAA1023	3'	TGTGGATGGGGCCTAGC	19099	G	AGA AG
			GC TAG GT CATCCACA			
			CG ATC CG GTAGGTGT			
			_ _ _ GG			
GAM306	KIAA1196	3'	TGCCCCACTCCCTACGCTG	30824	A	A_
			TAGCGTAG GAGT GCA			
			GTCGCATC CTCA CGT			
			C CC			
GAM306	LOC112817	3'	TGTGGATGCTTTTCCTACGC	28784	A	T
			GCGTAG GAG AGCATCCACA			
			CGCATC CTT TCGTAGGTGT			
			_ _			
GAM306	LOC253675	3'	TTGCAGATGCTACCCTCATAC	46269	_ A	CA
			GTA GAG GTAGCATC CAA			
			CAT CTC CATCGTAG GTT			
			A C AC			
GAM307	EIF1A	3'	AACTTAATCTCATCTAATGTAA	42717	G	AG T
	A		TTTACA TA TG GATTAAGTT			
			AAATGT AT AC CTAATTCAA			
			A CT T			
GAM307	DCLRE1A	3'	AATCATACCTACTGTAAA	34279	A	
			TTTACAGTA GTGTGATT			

AAATGTCAT CATACTAA
 C
 GAM307 FLJ31737 3' AACCTAATTTCAATCTTACTGT 29588 __ T A
 AAA TTTACAGTAAG TG GATTA GTT
 ||||| || ||||
 AAATGTCATTC AC TTAAT CAA
 TA T C
 GAM307 LOC145134 5' AACTCAGGACCTTACTGTGAA 40499 T GA A
 TTTACAGTAAG GT TT AGTT
 ||||| || ||||
 AAGTGTCAATTC CA GA TCAA
 _ G _ C
 GAM308 TCF12 3' CACCACTCTGAGGCTAATTA 9202 CG AACG _
 TAAT G TC GAGTGGTG
 ||| | |||||
 ATTA C AG CTCACCAC
 AT GG__ T
 GAM308 BTN2A1 3' CACCGCTCATCCCGAT 27802 AAC C
 ATCGG GT GAGTGGTG
 |||| |||||
 TAGCC TA CTCGCCAC
 C__ _
 GAM308 PP35 3' CACCCTCAGAGATTCTGATTA 13872 CG _ T
 TAATCGGAA TC GAG GGTG
 ||||| || ||||
 ATTAGTCTT AG CTC CCAC
 AG A _
 GAM308 LOC159121 3' CACCCTGACTCATTCCGATTA 42062 C__ G T
 TAATCGGAA GTC AG GGTG
 ||||| || ||||
 ATTAGCCTT CAG TC CCAC
 ACT _ _
 GAM309 FZD4 3' TCTCCAGAATGCCAGCCAG 14487 AC A
 CTGG CTGGCATTCT GAGA
 ||| ||||| |||
 GACC GACCGTAAGA CTCT
 _ C
 GAM309 NPY2R 3' CTCTAGACAAAATCCATCA 6610 C CC_ GCAT
 TGA TGA TG TCTAGAG
 ||| ||| || |||||
 ACT ACCT AC AGATCTC
 _ AAA _
 GAM309 OAS3 3' CTCTAGAGCAAGGCCCA 12860 A G AT
 TGG CCT GC TCTAGAG
 ||| ||| || |||||
 ACC GGA CG AGATCTC
 C A _
 GAM309 DKFZP564O1664 3' CTCTAGAATAGCCACCCA 25102 ACC _
 TGG TGGC ATTCTAGAG
 ||| ||| |||||

		ACC ACCG TAAGATCTC		
		C__ A		
GAM309	FLJ12800	3' TCTCTACTCCCAGGTCCAG	23194	CATTC
		CTGGACCTGG TAGAGA		
		GACCTGGACC ATCTCT		
		CTC__		
GAM309	FLJ21459	3' TCTCTAGAACAGGGATTCCA	23720	__ GCA
		TGGA CCTG TTCTAGAGA		
		ACCT GGAC AAGATCTCT		
		TAG __		
GAM309	KIAA0329	3' CTGGCCCAGGCCAGTC	16878	A CATT
		GA CTGG CCTGG CTAG		
		CTGACC GGACC GGTC		
		C C__		
GAM309	KIAA1416	3' CTCCAGAATCTCCAGTC	41806	CCTG C A
		GA CTGGA G ATTCT GAG		
		CTGACCT C TAAGA CTC		
		__ _ C		
GAM309	SDF1	3' CTGGGGGTGCCAGGACCAGTCA	43688	A AG
		TGACTGG CCTGGCATTCT AG		
		ACTGACC GGACCGTGGGG TC		
		A G_		
GAM309	LOC146667	5' TCTCTAGGAGAAATCCCGTCA	40711	T CCTGGCA
		TGAC GGA TTCTAGAGA		
		ACTG CCT AGGATCTCT		
		C AAAG__		
GAM309	LOC153937	3' CTCAGAACACAAGATCCAGTCA	39446	C GGCA A
		TGACTGGA CT TTCT GAG		
		ACTGACCT GA AAGA CTC		
		A ACAC _		
GAM309	LOC254057	3' CTCTAGAATACCAGGATCC	46346	_ C
		GGA CCTGG ATTCTAGAG		
		CCT GGACC TAAGATCTC		
		A A		
GAM309	LOC91050	3' CTGGCCACCAGGTCCAGT	32336	CATT
		ACTGGACCTGG CTAG		
		TGACCTGGACC GGTC		
		ACC_		
GAM310	ITPR3	3' CCCACTCTGCCAGACACCCTGA	7996	CTATAGC A
	CA	TGTCAGGG CA AGTGGG		

ACAGTCCC GT TCACCC
 ACAGACC C
 GAM310 MAPRE2 3' CCCACCCCGGCTGCTCTTGACA 15547 _ TAT AAA
 TGT CAGG GC AGCC GTGGG
 ||||| || ||| ||||
 ACAGTTC CG TCGG CACCC
 T _ CCC
 GAM310 RPL15 3' CCCACTTTGACTATGAGTATAC 8859 _ _ C
 C GG GCT ATAG CAAAGTGGG
 || ||| ||| |||||
 CC TGA TATC GTTTCACCC
 ATA G A
 GAM310 FLJ10737 3' CCAGGGCCTAGCCCTGACA 20065 TA AAAG
 TGT CAGGGCTA GCC TGG
 ||||| ||| |||
 ACAGTCCCGAT CGG ACC
 C_ G_
 GAM310 HABP2 3' CCCACTCTCCTTGGCACCCTGA 10343 CTATA _
 CA GTCAGGG GCCAA AGTGGG
 ||||| ||| |||||
 CAGTCCC CGGTT TCACCC
 A_ CCTC
 GAM310 KIAA0553 3' CCCACTTTGGCATTTCCTAAC 34637 C CT A
 GT AGGG AT GCCAAAGTGGG
 || ||| || |||||
 CA TCCT TA CGGTTTCACCC
 A TT _
 GAM310 LOC221839 5' TTGGCTACAACCCTGACA 44432 CTA
 TGT CAGGG TAGCCAA
 ||||| |||||
 ACAGTCCC ATCGGTT
 AAC
 GAM310 LOC92305 3' CCAGGGCACAGCCCTGACA 28758 ATA AAAG
 TGT CAGGGCT GCC TGG
 ||||| ||| |||
 ACAGTCCCGA CGG ACC
 CA_ G_
 GAM311 FLJ20276 3' TCCAACTATCAATAGTCAGGTT 19329 G C_ AA
 CAA TTGAAC TGAC TGATG TTGGA
 ||||| ||| ||| |||||
 AACTTG ACTG ACTAT AACCT
 G ATA C_
 GAM311 MIG 3' CCAATTCATCCTCACTCAG 8246 AC CCT
 TTGA GTGA GATGAATTGG
 ||| ||| |||||
 GACT CACT CTA CTTAACC
 _ C_
 GAM311 PLPL 3' CCAAAAGGTCACATT CAG 21398 C GATGAA
 TTGAA GTGACCT TTGG
 ||||| ||||| |||

			GA	CT	CA	CT	GA		AA	CC	
			A		A						
GAM311	SERF1B	3'	CCAAATAGGTCACATTCA	23257	C		ATGAA				
			TGAA GTGACCTG	TTGG							
			ACTT CACTGGAT	AA	CC						
			A		A						
GAM311	WNT2B	3'	TCCAATTCAAGCCTCTCAACTC	23695	ACG		CCTGA_				
	AA		TTGA TGA	TGAATTGGA							
			AACT ACT	ACTTAACCT							
			CA_ CTCCGA								
GAM311	WNT2B	3'	TCCAATTCAAGCCTCTCAACTC	10394	ACG		CCTGA_				
	AA		TTGA TGA	TGAATTGGA							
			AACT ACT	ACTTAACCT							
			CA_ CTCCGA								
GAM311	LOC149842	5'	TCCAACCCATAGGTCAC	41092	A		AA				
			GTGACCTG TG	TTGGA							
			CACTGGAT AC	AACCT							
			_ CC								
GAM311	LOC203292	3'	TCAATGCCAAGGCCACGTTCAA	43502	A		GATGA				
			TTGAACGTG CCT	ATTGG							
			AACTTGCAC GGA	TAACT							
			C ACCG_								
GAM311	LOC91813	5'	CCAATTCTGGTTTCACATTCAG	33397	C		CCTGAT				
			TTGAA GTGA	GAATTGG							
			GA	CTT CACT	CTTAACC						
			A	TTGGT_							
GAM312	D8S2298E	3'	TACCACACAATATTTTCATGATT	12230	C		GGA _				
	CAA		TTGAATCA GAAG	TG GTGGTA							
			AACTTAGT CTTT	AC CACCAT							
			A	ATA A							
GAM312	LOC149182	5'	ACCGCCCCCATGATTCAA	40968	CGAA		AT				
			TTGAATCA	GGG GGTGGT							
			AACTTAGT	CCC CCGCCA							
			A_ _								
GAM312	LOC51301	5'	TACCACCATTCTTCATAATTC	18673	CAC		G				
			GAAT	GAAGG ATGGTGGTA							
			CTTA	CTTCT TACCACCAT							
			ATA	_							
GAM313	PIAS3	3'	GACCCTGTGCCCTCCTTCCCA	12744	C		TTT T A				
			TGG AAGGAGG	GT CAG GTC							

ACC TTCCTCC CG GTC CAG
 C ____ T C
 GAM313 C20orf139 5' GACTCTGGGCACCCCTCTCACC 41106 CAA TT
 A TGG GGAGG TGTT CAGAGTC
 ||| |||| |||||
 ACC TCTCC ACGGGTCTCAG
 AC_ CC
 GAM313 FLJ13322 5' GACCCTGGAGGCCCCCTCACA 24060 GCA A TG A
 TG AGG GGTT TTCAG GTC
 || ||| |||| |||||
 AC TCC CCGG AGGTC CAG
 AC_ C ____ C
 GAM313 KIAA0293 3' GACCCCAGCTCCCCTTCTCGCC 30395 A TTT CAGA
 A TGGC AGGAGG GTT GTC
 |||| ||||| ||| |||
 ACCG TCTTCC CGA CAG
 C CCT CCC_
 GAM313 NETO1 5' GACCCTGTCCTCCCCCGCCA 29069 AA__ TTTGTT A
 TGGC GGAGG CAG GTC
 |||| |||| ||| |||
 ACCG CCTCC GTC CAG
 CCCC T____ C
 GAM313 LOC147229 3' ACCCTGCAGTCTCCTTGCCA 38315 GT TGTT A
 TGGCAAGGAG T CAG GT
 ||||| ||| ||| |||
 ACCGTTCTC A GTC CA
 TG C____ C
 GAM313 LOC149837 3' ACTCTCTGACCTCCTCACC 41096 CA TGTC
 GG AGGAGGTT AGAGT
 || ||||| |||||
 CC TCCTCCAG TCTCA
 AC TC____
 GAM313 LOC154214 3' ACTCTGCACCTCCTTCCA 39467 C TTGTT
 TGG AAGGAGGT CAGAGT
 ||| ||||| |||||
 ACC TTCCTCCA GTCTCA
 _ C____
 GAM314 MSL3L1 5' GGCAAGAAAAGCTGTAGCTCGC 13671 A ____ GTACC
 C GGC AGC AGT TTCTTGCC
 ||| ||| ||| |||||
 CCG TCG TCG AAGAACGG
 C ATG AA____
 GAM314 MTF1 3' GGCATGAGGTACAATGCCTGCC 12581 A G CT
 A TGGCA GCA TGTACCTT TGCC
 |||| ||| ||||| |||
 ACCGT CGT ACATGGAG ACGG
 C A T_
 GAM314 SCD 3' GCAAGAGGAACCTCTCGCCA 11490 A C T A T
 TGGC AG AG GT CCT CTTGC
 |||| || || ||| |||||

ACCG TC TC CA GGA GAACG
 C _ _ A _
 GAM314 SLC26A3 5' GGCAAGAAGAAGTGTTCACCA 5576 CA GTGTAC
 TGG AGCA CTTCTTGCC
 ||| |||| |||||
 ACC TTGT GAAGAACGG
 AC GAA__
 GAM314 STAU2 5' GGCAAGAAGAGGCTGCCTACCA 15722 CAA GTAC
 TGG GCAGT CTTCTTGCC
 ||| |||| |||||
 ACC CGTCG GAAGAACGG
 ATC GA__
 GAM314 TRPM6 3' GCAAGAAGATCCCAGTGCTTGC 19201 G TAC_
 C GGCAAGCA TG CTTCTTGC
 ||||| || |||||
 CCGTTCGT AC GAAGAACG
 G CCTA
 GAM314 DKFZP564O0423 3' CAAAAAGATACTGGTTGC 44064 G AC C
 GCAA CAGTGT CTT TTG
 ||| ||||| ||| |||
 CGTT GTCATA GAA AAC
 G _ _ A
 GAM314 FLJ10688 5' CAAGAAAGTAGTGAGAGTTTGC 20013 AGTG__ C
 CA TGGCAAGC TAC TTCTTG
 ||||| ||| |||||
 ACCGTTTG ATG AAGAAC
 AGAGTG A
 GAM314 FLJ12960 3' GCAAGAAGTCACTTATCACCA 23917 CAAGC TAC
 TGG AGTG CTTCTTGC
 ||| |||| |||||
 ACC TCAC GAAGAACG
 ACTAT T__
 GAM314 KIAA1668 3' GAATGCACTGCTTGCCA 33027 CC
 TGGCAAGCAGTGTA TTC
 ||||| ||||| |||
 ACCGTTTCGTACGT AAG
 _
 GAM314 MAD4 3' GCAAAAAAGTAAATGCTGC 13171 A GTG C C
 GCA GCA TAC TT TTGC
 ||| ||| ||| |||
 CGT CGT ATG AA AACG
 _ AAA A A
 GAM314 MGC4643 3' GGCAAGAAGGTATCCTCTTCCC 26440 C C TG
 A TGG AAG AG TACCTTCTTGCC
 ||| ||| ||| |||||
 ACC TTC TC ATGGAAGAACGG
 C _ CT
 GAM314 WIRE 3' GCAAGAAAGGAGTTTGCCA 38314 AGTGTA _
 TGGCAAGC CCTT CTTGC
 ||||| ||||| |||||

		ACCGTTTG	GGAA GAACG		
		A_____	A		
GAM314	LOC125988 5'	GGCAAGAAAGACTACACCTTCC	36803	C CA	CC__
	A	TGG AAG GTGTA TTCTTGCC			
		ACC TTC CACAT AAGAACGG			
		_ _ CAGA			
GAM314	LOC143451 3'	GCGTTAGCAACACTGCTCACCA	37621	CA	AC TCT
		TGG AGCAGTGT CT TGC			
		ACC TCGTCACA GA GCG			
		AC AC TT_			
GAM314	LOC145125 3'	GCCTTAGCAACACTGCTCACCA	37798	CA	AC TCTT
		TGG AGCAGTGT CT GC			
		ACC TCGTCACA GA CG			
		AC AC TTC_			
GAM314	LOC148109 5'	GGCAAGAAGGGCAGGCTCACCA	38463	CA AG	A
		TGG AGC TGT CCTTCTTGCC			
		ACC TCG ACG GGAAGAACGG			
		AC G_ _			
GAM314	LOC148696 5'	GCAAGAAGGTAGGGTTGC	40893	TG_	
		GCAG TACCTTCTTGC			
		CGTT ATGGAAGAACG			
		GGG			
GAM314	LOC149506 3'	GCAAGAAGAGCAGCGCCTGGCA	41009	G A AG	AC
		TG CA GC TGT CTTCTTGC			
		AC GT CG ACG GAAGAACG			
		G C CG A_			
GAM314	LOC254440 3'	GGCTTAGCAACACTGCTCACCA	46375	CA	AC TCTT
		TGG AGCAGTGT CT GCC			
		ACC TCGTCACA GA CGG			
		AC AC TT_			
GAM315	GPRC5B 3'	CCTCAATCCCCGCAAAC	18352	C ACA	AT
		TGG TTGC GG GATTGAGG			
		ATC AACG CC CTAAC			
		A _ C_			
GAM315	IL20RA 3'	GCCTTTTGTTCCTGTGCAAAC	15791	GC	TGATT
	A	TG TTGCACAGGA GAGGC			
		AC AACGTGTCCT TTCCG			
		A_ TTGTT			
GAM315	MAP1A 3'	CCTCGCCCCAAGCAAGCCA	8184	ACA	ATGAT
		TGGCTTGC GG TGAGG			

			ACCGAACG CC	GCTCC		
			AA_ CC__			
GAM315	VPS26	3'	CCTCAAATTGTGCAACCA	11326 C	GATGA	
			TGG TTGCACAG	TTGAGG		
			ACC AACGTGTT	AACTCC		
			_ A__			
GAM315	CDH22	5'	GCCCCAGCCCCGCGCAGGCCA	22215	ACA ATGA A	
			TGGCTTGC GG	TTG GGC		
			ACCGGACG CC	GAC CCG		
			CG_ CC_ C			
GAM315	LOC124930	3'	GCCCCCTGGCCTGTGCAAGCC	36769	ATGATTGA	
			GGCTTGCACAGG	GGC		
			CCGAACGTGTCC	CCG		
			GGTCCC__			
GAM315	LOC130074	3'	GCCCATGAGTCCCTGTGCAGAC	37474	CT _ GAT A	
			CA	TGG TGCACAGG AT	TG GGC	
			ACC ACGTGTCC TG	AC CCG		
			AG C AGT _			
GAM315	LOC133584	5'	GCCTCAATACGATCATAGAAGC	37046	GCACAG __	
			CA	TGGCTT GAT G	ATTGAGGC	
			ACCGAA CTA C	TA ACTCCG		
			GATA__ G A			
GAM315	LOC145216	3'	GCCCCAACTCTGCTCCCAGCAA	40506	ACA T__ _ A	
			GCCA	TGGCTTGC GGA	GA TTG GGC	
			ACCGAACG CCT	CT AAC CCG		
			AC_ CGT C C			
GAM315	LOC199232	3'	GCCCCGCGGGACCTGTGCAAGC	42880	ATGAT A	
			GCTTGCACAGG	TG GGC		
			CGAACGTGTCC	GC CCG		
			AGGGC C			
GAM315	LOC200933	3'	GCCTCAATATTTAACAACAAGC	43362	CACAGGATG	
			CA	TGGCTTG	ATTGAGGC	
			ACCGAAC	TA ACTCCG		
			AACAATTTA			
GAM315	LOC92249	3'	CCTCAATCACCTCATACCA	34022	CT CAC A	
			TGG TG	AGG TGATTGAGG		
			ACC AC	TCC ACTAACTCC		
			AT __ _			
GAM316	AP1G1	3'	CCTTTTTCCGCACTTCT	6800	CTA A	
			AGAAG	CGGAAAAA GG		

			TCTTC GCCTTTTT CC		
			AC_ _		
GAM316	CIAS1	5'	GAAACCTTTTTTCCATGGCTC 11321	A C	
			GA GCTA GGAAAAAAGGTTTC		
			CT CGGT CCTTTTTTCCAAAG		
			_ A		
GAM316	F2R	3'	GAAACCTTCCTGCTGAGCCTC 7721	A A AAAA	
			GA GCT CGG AAGGTTTC		
			CT CGA GTC TTCCAAAG		
			C _ GTCC		
GAM316	LIMK1	3'	AAACTGCCCCCGAGCTTCTT 18793	A AAAAAA	
			AAGAAGCT CGG GGTTT		
			TTCTTCGA GCC TCAA		
			_ CCGC_		
GAM316	MAP1B	3'	GCCTTTCACAGCTTCTT 12535	ACG AAA	
			AAGAAGCT GAA AGGT		
			TTCTTCGA CTT TCCG		
			CA_ _		
GAM316	MAP1B	3'	GCCTTTCACAGCTTCTT 25712	ACG AAA	
			AAGAAGCT GAA AGGT		
			TTCTTCGA CTT TCCG		
			CA_ _		
GAM316	MMP2	3'	AAACCAAGCCGTGGCTTC 10872	AAAAAA	
			GAAGCTACGG GGTTT		
			CTTCGGTGCC CCAA		
			GAA_		
GAM316	MMP25	3'	AACCTTTTCCGTTGCT 22819	T AA	
			AGC ACGGAAA AGGTT		
			TCG TGCCTTT TCAA		
			T _		
GAM316	MYO1A	5'	GCCTTTTCCCAGCTTC 11861	AC A	
			GAAGCT GG AAAAAGGT		
			CTTCGA CC TTTTCCG		
			_ C		
GAM316	OPA1	3'	TTTTTTCCGCAGACTTCTT 28326	_ A	
			AAGAAG CT CGGAAAAAA		
			TTCTTC GA GCCTTTTTT		
			A C		
GAM316	OPA1	3'	TTTTTTCCGCAGACTTCTT 28334	_ A	
			AAGAAG CT CGGAAAAAA		

			TTCTTC GA GCCTTTTTT		
			A C		
GAM316	OPA1	3'	TTTTTTCCGCAGACTTCTT 28342	_	A
			AAGAAG CT CGGAAAAAA		
			TTCTTC GA GCCTTTTTT		
			A C		
GAM316	OPA1	3'	TTTTTTCCGCAGACTTCTT 28350	_	A
			AAGAAG CT CGGAAAAAA		
			TTCTTC GA GCCTTTTTT		
			A C		
GAM316	OPA1	3'	TTTTTTCCGCAGACTTCTT 28358	_	A
			AAGAAG CT CGGAAAAAA		
			TTCTTC GA GCCTTTTTT		
			A C		
GAM316	POLR2A	5'	AAACCTTTTCCTTTTCCCTTCT 6641	CTAC	_____
	T		AAGAAG GGAAAA AAGGTTT		
			TTCTTC CCTTTT TTCCAAA		
			_____ CCTT		
GAM316	C21orf25	3'	AAGCTTCCTTCCGTAGCCTCTT 31795	A	AAA
			AAGA GCTACGGAA AGGTTT		
			TTCT CGATGCCTT TTCGAA		
			C CC_		
GAM316	CBLN1	3'	GAAATCTTTCTCCCTAGC 10556	C	AA
			GCTA GGA AAAGGTTTC		
			CGAT CCT TTTCTAAAG		
			C C_		
GAM316	CREG	3'	AAACCACTCTCCACAGCTTTTT 9945	AC	AAAAA
			AAGAAGCT GGA GGTTT		
			TTTTTCGA CCT CCAAA		
			CA CTCA_		
GAM316	FLJ10724	3'	CTTCTTCATAGCTTCT 20051	CG	A
			AGAAGCTA GAA AAAG		
			TCTTCGAT CTT TTTC		
			A_ C		
GAM316	FLJ14011	5'	AAACCTTTAGTCGAAGCTTCT 22648	A	AAA
			AGAAGCT CGG AAAGGTTT		
			TCTTCGA GCT TTTCCAAA		
			A GA_		
GAM316	FLJ23510	3'	TCTTTCTTTCTGTAACCTCTT 24055	A C	_
			AAG AG TACGAAA AAAGG		

			TTC TC ATGTCTTT TTTCT		
			C A C		
GAM316	IL1RAPL1	3'	AAACCCTTTTTTTTGCTTC 15550	TAC	A
			GAAGC GGAAAAA GGTTT		
			CTTCG TTTTTTT CCAA		
			____ C		
GAM316	KIAA0455	3'	GACACCCCGCAGCTTCT 35882	A	AAAAA T
			AGAAGCT CGG GGT TC		
			TCTTCGA GCC CCA AG		
			C _____ C		
GAM316	KIAA0945	3'	AGGCCCTTCTGTAGCCTC 17289	A	AAAA
			GA GCTACGGAA GGTTT		
			CT CGATGTCTT CCGGA		
			C C____		
GAM316	NECL1	3'	GCCCTTTCGTGGCTTCT 22167		AAA
			AGAAGCTACGGAAA GGT		
			TCTTCGGTGCCTTT CCG		
			C____		
GAM316	P311	3'	TCTTCCTTTCGTAGCCTC 11162	A	A_
			GA GCTACGGAAA AAGG		
			CT CGATGCCTTT TTCT		
			C CC		
GAM316	RAB10	5'	GAGCCTTTTTCCCACGCTTC 41280	TAC	A
			GAAGC GG AAAAAGGTTT		
			CTTCG CC TTTTCCGAG		
			CA_ C		
GAM316	SR-BP1	3'	GAGGCCTTTCATAGCT 12486	C	AAA
			AGCTA GGAA AGGTTTC		
			TCGAT CCTT TCCGGAG		
			A _____		
GAM316	TOB2	3'	AAACCTTTTCTCCCCTTTC 45759	CTAC	A
			GAAG GGA AAAAGGTTT		
			CTTT CCT TTTTCCAAA		
			CC__ C		
GAM316	ZDHC3	3'	GAAACCCCTTTTTTAGCTTTT 18687	CG	AAAA
			AGAAGCTA GAA GGTTTC		
			TTTTCGAT TTT CCAAAG		
			TT CCC_		
GAM316	LOC115265	3'	GAAACCCCAAATGTAGTCTCTT 36308	AG	GAAAAA
			AAGA CTACG GGTTTC		

		TTCT GATGT CCAAAG	
		CT AAACC__	
GAM316	LOC145719 3'	ACTTTTTTTTCCACAACCTTTT 40569	CTAC
		AAGAAG GGAAAAAAGGT	
		TTTTTC CCTTTTTTCA	
		AACA	
GAM316	LOC145720 3'	ACTTTTTTTTCCACAACCTTTT 40559	CTAC
		AAGAAG GGAAAAAAGGT	
		TTTTTC CCTTTTTTCA	
		AACA	
GAM316	LOC147671 3'	AAACCTTTTCTCCCCTTTC 38374	CTAC A
		GAAG GGA AAAAGGTTT	
		CTTT CCT TTTTCCAA	
		CC__ C	
GAM316	LOC148137 3'	GCCTCTCCCCAGCTTCTT 29518	AC AAAA
		AAGAAGCT GGA AGGT	
		TTCTTCGA CCT TCCG	
		CC C__	
GAM316	LOC150295 3'	GACCTCCCCCGTGGCTCCTT 41179	A AAAAA
		AAG AGCTACGG AGGT	
		TTC TCGGTGCC TCCAG	
		C CCC__	
GAM316	LOC197117 3'	ACTTTTTTTTCCACAACCTTTT 43192	CTAC
		AAGAAG GGAAAAAAGGT	
		TTTTTC CCTTTTTTCA	
		AACA	
GAM316	LOC221755 3'	GAAACCCCTTTTTTTTCTGTCCC 44385	CT ____
	TT	AAG ACGGAAAAAA GGTTTC	
		TTC TGTCTTTTTT CCAAAG	
		CC TCC	
GAM316	LOC254020 5'	GAAACCTTTTCTGTGCGGTC 45987	A T AA
		GA GC ACGGAAAA GGTTTC	
		CT CG TGTCTTTT CCAAAG	
		G C C_	
GAM316	LOC91250 5'	GAATAAGAGTTCCTGTAGCTCC 32547	A _ AAAAG
	T	AG AGCTAC GGAA GTTT	
		TC TCGATG CCTT TAAG	
		C T GAGAA	
GAM316	LOC92539 5'	AAACCTTTTTTCTTAACTTT 34494	C C
		GAAG TA GGAAAAAAGGTTT	

TTTC AT TCTTTTTTCCAAA
 A _
 GAM317 SOCS5 3' CACCTAAGTCTATATTCAGT 15224 CA T GAT
 TAG AATATAGA CT GGTG
 ||| ||||| || |||
 GTC TTATATCT GA CCAC
 AC _ AT_
 GAM317 DKFZp434F1719 3' CTAGTAGATCTGTACCTACTA 25989 CAAA A
 TAG TATAGATCTG TGG
 ||| ||||| |||
 ATC ATGTCTAGAT ATC
 ATCC G
 GAM317 KIAA0841 3' ACCACCATATCTGGCTA 35358 AAATA C A
 TAGC TAGAT TG TGGT
 ||| |||| || |||
 ATCG GTCTA AC ACCA
 _ T C
 GAM317 KIAA1317 3' CACTCAAATCTATATGTGCCAG 41625 A A C TG
 CT GCA ATATAGAT TGA GTG
 || ||| ||||| || |||
 GA CGT TATATCTA ACT CAC
 C G A _
 GAM317 KIAA1546 3' CAGATCTACAATTTGCTA 33713 A_
 TAGCAAAT TAGATCTG
 ||||| |||||
 ATCGTTTA ATCTAGAC
 AC
 GAM317 MESDC2 3' CAATAGATCTATCCTTGCCAG 35889 A AT A
 CT GCAA ATAGATCTG TG
 || ||| ||||| ||
 GA CGTT TATCTAGAT AC
 C CC A
 GAM317 LOC163479 5' CACCATCAGATCCATCAGCGCT 39956 AAATATA
 G TAGC GATCTGATGGTG
 ||| ||||| |||||
 GTCG CTAGACTACCAC
 CGACTAC
 GAM317 LOC51696 3' CACCAGAACTAATTTGCTA 18309 A A A
 TAGCAAAT TAG TCTG TG
 ||||| || ||| ||
 ATCGTTTA ATC AGAC AC
 _ A C
 GAM318 PIK3R3 3' TATGTTTCAGAAGCCAACAAA 30607 CAT G
 TTTGT GCTTCTGAA ATG
 |||| ||||| |||
 AAACA CGAAGACTT TAT
 AC_ G
 GAM318 FLJ11342 3' TTTCAGAAGCATAATAAA 20432 C
 TTTGT ATGCTTCTGAAG
 |||| ||||| |||||

		AAATA TACGAAGACTTT	
		A	
GAM318	KIAA0397 3'	CATTTGAGAAACATGACAAA 30893	C GA
		TTTGT CATG TTCT AGATG	
		AAACAGTAC AAGA TTTAC	
		A G_	
GAM318	LOC149146 5'	CTTCAGAAGAACGACAAA 38655	ATG
		TTTGTC CTTCTGAAG	
		AAACAG GAAGACTTC	
		CAA	
GAM318	LOC164684 3'	AACAAATAAAAGCATGATAAA 40158	C AAGA
		TTTGT CATGCTT TG TGTT	
		AAATAGTACGAA AT ACAA	
		A AA_	
GAM318	LOC200563 5'	TTTCAGAAACAGAACAAA 43320	CA C
		TTTGT TG TTCTGAAG	
		AAACA AC AAGACTTT	
		AG A	
GAM318	LOC253832 3'	TAACATCTTTAATAGCACAGCA 45498	CA TC
	AA	TTTGT TGCT TGAAGATGTTA	
		AAACG ACGA ATTTCTACAAT	
		AC TA	
GAM319	LEP 3'	ATGGGTCCAGGGTTGATCACA 5734	AAACA
		TGTGATCAACCC TCGT	
		ACACTAGTTGGG GGTA	
		ACCTG	
GAM319	FLJ20051 3'	ACAATGTTTTCTTGATTACA 21161	CCC C
		TGTGATCAA AAACAT GT	
		ACATTAGTT TTTGTA CA	
		CT_ A	
GAM319	ITGB5 3'	ACGGCTGCTCGGCTTGATCACA 29922	C AAA _
		TGTGATCAA CC CA TCGT	
		ACACTAGTT GG GT GGCA	
		C CTC C	
GAM319	KIAA1784 3'	ATGTTGCTCAGGCTGGTCACA 32483	A CA_
		TGTGATCA CC AACAT	
		ACACTGGT GG TTGTA	
		C ACTCG	
GAM319	MAIL 3'	ATACCCTTTGGATTGATCACA 25404	C CATC
		TGTGATCAA CCAA GTAT	

			ACACTAGTT GGT TT CATA		
			A CC__		
GAM319	SDS3	3'	TACGATGTGTGTGTCACA 34321	T	ACCCAA
			TGTGA CA ACATCGTA		
			ACACT GT TGTAGCAT		
			_ GTG__		
GAM320	GAB2	3'	ACTAAGGACACAAGAATCA 14646	TC	C
			TGATTCTT GTTCTT GT		
			ACTAAGAA CAGGAA CA		
			CA T		
GAM320	GAB2	3'	ACTAAGGACACAAGAATCA 27842	TC	C
			TGATTCTT GTTCTT GT		
			ACTAAGAA CAGGAA CA		
			CA T		
GAM320	PRG4	3'	CTGTAAAAGAAAAAGAATCA 12384	CG	CGT
			TGATTCTTT TTCTT CAG		
			ACTAAGAAA AAGAA GTC		
			A_ AAT		
GAM320	FLJ13612	3'	CTGTAAGAACGAAAGAAT 24863		CGT
			ATTCTTTCGTTCTT CAG		
			TAAGAAAGCAAGAA GTC		
			T__		
GAM321	DAAM2	3'	AGCACTTGAATGCTTAGCT 44328	A	TACA
			AGCTAAGCA TTA GCT		
			TCGATTTCGT AGT CGA		
			A TCA_		
GAM321	ESRRBL1	3'	CTGCCTTTGCCTCAGCTTTAT 19742	AA_	TTATA
			ATAAAGCT GCAA CAG		
			TATTTTCA CGTT GTC		
			CTC TCC__		
GAM321	BIRC2	5'	AGCTGTGTGAACCTTAGCTTT 33371	CAA	
			AAAGCTAAG TTATACAGCT		
			TTTCGATTC AGTGTGTCGA		
			A__		
GAM321	CBX3	3'	CTGTATATTGTTTACTTTAT 14140	C	T
			ATAAAG TAAGCAAT ATACAG		
			TATTTT ATTTGTTA TATGTC		
			- -		
GAM321	CBX3	3'	CTGTATATTGTTTACTTTAT 18660	C	T
			ATAAAG TAAGCAAT ATACAG		

TATTTT ATTTGTTA TATGTC

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GAM321 KCNV1 3' TATAATACTTAGCTTTA 15712 CA
      TAAAGCTAAG ATTATA
      ||||| ||||
      ATTTGATTTC TAATAT
      A_
GAM321 KIAA1715 3' AGCTACAGTGATCTTAGCTT 33789 CA AC_
      AAGCTAAG ATTAT AGCT
      ||||| |||| |||
      TTCGATTTC TAGTG TCGA
      _ ACA
GAM321 MFN1 3' CTGAGGATGATTGTAGCT 19602 G A__
      AGCTAA CAATTAT CAG
      ||||| ||||| |||
      TCGATT GTTAGTA GTC
      _ GGA
GAM321 Rab11-FIP2 3' AGCTATTGAGGCTTAGCTTTAT 17095 AA TAC
      ATAAAGCTAAGC TTA AGCT
      ||||| ||| |||
      TATTTGATTTCG AGT TCGA
      G_ TA_
GAM321 SNRK 3' GCTGTATTATAGCCTTAT 19310 A AGCAATT
      ATAA GCTA ATACAGC
      ||| ||| |||||
      TATT CGAT TATGTCG
      C AT_____
GAM321 LOC155434 3' AGCTGTATGCGTTCTAGCTGTA 41770 A _ AAT
      T ATA AGCTA AGC TATACAGCT
      ||| ||||| ||| |||||
      TAT TCGAT TTG GTATGTCGA
      G C C_
GAM321 LOC158563 3' AGCCATGCTTTCTTAGCTTTAT 39867 C T ACA
      ATAAAGCTAAG AA TAT GCT
      ||||| ||| ||| |||
      TATTTGATTTC TT GTA CGA
      T C C_
GAM321 LOC257358 3' AGCTGAACGCCTGCTTAGCTT 46387 ATTATA
      AAGCTAAGCA CAGCT
      ||||| |||
      TTCGATTTCG GTCGA
      CCGCAA
GAM321 LOC91660 5' AGCTGCACAGCGGCTAACTAGC 33206 _ AATTATA
      TTTAT ATAAAGCTA AGC CAGCT
      ||||| ||| |||
      TATTTGAT TCG GTCGA
      CAA GCGACAC
GAM322 LY95 5' ACGGTGTTTGTGTCCCTGGGTA 11241 TCA
      TACCCG ATACAAACACCGT
      ||||| |||||
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			ATGGGT TGTGTTTGTGGCA		
			CCC		
GAM322	RELN	3'	TTACAGTGGCAGTATTGAC 45283	AAA	C
			GTCAATAC CAC GTAA		
			CAGTTATG GTG CATT		
			ACG A		
GAM322	LHX6	3'	TACAGTGTTTGTGGGATG 15699	AA	C
			CGTC TACAAACAC GTA		
			GTAG GTGTTTGTG CAT		
			G_ A		
GAM322	RAB40A	5'	ACGTTTGTCTGTATTGATGAG 39925	C	_ C_
	TA		TAC CGTCAATACA AACA CGT		
			ATG GTAGTTATGT TTGT GCA		
			A C TT		
GAM322	LOC116113	3'	TTACAGTGTCTGTTGGTGG 44288	GT	CAA C
			CC CAATA ACAC GTAA		
			GG GTTGT TGTG CATT		
			TG C_ A		
GAM322	LOC200107	5'	TTACGGTGCGGTTGAGAAGTA 42708	CCG	ACAAA
			TAC TCAAT CACCGTAA		
			ATG AGTTG GTGGCATT		
			AAG GC__		
GAM322	LOC206426	3'	ACGGTGTTTGTGAAGGG 43114	GTCAA	
			CCC TACAAACACCGT		
			GGG GTGTTTGTGGCA		
			AA__		
GAM322	LOC257017	5'	TACAGTATTTGTGTTGGC 46497	C	C
			GTCAATACAAA AC GTA		
			CGGTTGTGTTT TG CAT		
			A A		
GAM323	ADAR	3'	TATGTGTCCCTTGATAACA 6776	AC	G
			TGTTATCAA GGGGCA ATA		
			ACAATAGTT CCCTGT TAT		
			_ G		
GAM323	ADAR	3'	TATGTGTCCCTTGATAACA 17962	AC	G
			TGTTATCAA GGGGCA ATA		
			ACAATAGTT CCCTGT TAT		
			_ G		
GAM323	ADAR	3'	TATGTGTCCCTTGATAACA 17969	AC	G
			TGTTATCAA GGGGCA ATA		

			ACAATAGTT CCCTGT TAT		
			— G		
GAM323	CRYZ	3'	TATCTGCATTTGTCTGGTAACA 7619	A	—
			TGTTATCA ACGGG GCAGATA		
			ACAATGGT TGTTT CGTCTAT		
			C A		
GAM323	NOS1	5'	ATCTTGGCCTGATAGCA 6229	AACG	G —
			TGTTATCA GG CA GAT		
			ACGATAGT CC GT CTA		
			— G T		
GAM323	PPP3R1	3'	TATCCATTTGTTTGATTACA 37531	T	GCA
			TGT ATCAAACGGG GATA		
			ACA TAGTTTGTTT CTAT		
			T AC—		
GAM323	SFRS1	3'	ATCTGTAAACTGATGACA 13800	AACGG	
			TGTTATCA GGCAGAT		
			ACAGTAGT TTGTCTA		
			CAAA—		
GAM323	AKAP6	3'	TATCTGCTTAGTATTAACA 10491	TCAA	GG
			TGTTA AC GGCAGATA		
			ACAAT TG TCGTCTAT		
			TA— AT		
GAM323	KIAA1843	3'	TATCTGCCCATGAAAACA 31163	A	AACG
			TGTT TCA GGGCAGATA		
			ACAA AGT CCCGTCTAT		
			A A—		
GAM323	P37NB	5'	TTGTTCCGTCTGTAACA 12437	T A	
			TGTTA CA ACGGGGCAG		
			ACAAT GT TGCCTTGTT		
			— C		
GAM323	SLC37A1	3'	TATCTGCCCTTTGAAATA 21036	A	AC
			TGTT TCAA GGGGCAGATA		
			ATAA AGTT TCCCGTCTAT		
			— —		
GAM323	LOC256502	3'	ATCTCCAACCCTTCTGATAACA 45366	AAC	GC—
			TGTTATCA GGG AGAT		
			ACAATAGT CCC TCTA		
			CTT AACC		
GAM324	COL4A3	3'	ACAAAACATTAACTAGTGTTA 5545	CCG	CC
			TAATACTAG TTAGTG TTGT		

			ATTGTGATC AATTAC AACA		
			A__ AA		
GAM324	COL4A3	3'	ACAAAACATTAACTAGTGTTA 25352	CCG	CC
			TAATACTAG TTAGTG TTGT		
			ATTGTGATC AATTAC AACA		
			A__ AA		
GAM324	COL4A3	3'	ACAAAACATTAACTAGTGTTA 25358	CCG	CC
			TAATACTAG TTAGTG TTGT		
			ATTGTGATC AATTAC AACA		
			A__ AA		
GAM324	KIAA1014	3'	CAAGACACTCTATGTATTA 32568	_ CCGTT	C
			TAATAC TAG AGTG CTTG		
			ATTATG ATC TCAC GAAC		
			T _____ A		
GAM324	PER3	3'	ACAAGTAATGTAAAAGCTAGTA 18820	CG _ GC	
	T		ATACTAGC TTA GT CTTGT		
			TATGATCG AAT TA GAACA		
			AA G AT		
GAM324	YAP1	3'	CATTAACGACTAGATTA 12752	A C	
			TAAT CTAG CGTTAGTG		
			ATTA GATC GCAATTAC		
			_ A		
GAM324	LOC201627	3'	AAGGCATCTAGTATTA 42894	CCGTTA	
			TAATACTAG GTGCCTT		
			ATTATGATC TACGGAA		

GAM325	ABLIM	3'	TGGTTAAACACCATGA 8122	C CC	
			TCA TGGTGTT AACTA		
			AGT ACCACAA TTGGT		
			_ AA		
GAM325	ABLIM	3'	TGGTTAAACACCATGA 13555	C CC	
			TCA TGGTGTT AACTA		
			AGT ACCACAA TTGGT		
			_ AA		
GAM325	KIAA1042	3'	GATAGGAAACCAAGTGA 17352	G AAC	
			TCACTGGT TTCC TATC		
			AGTGACCA AAGG ATAG		

GAM325	MGC13007	5'	TATGATGGTAACTCCAAGTGA 26123	T CCA	
			TCACTGG GTT ACTATCATA		

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AGTGACC CAA TGGTAGTAT
      T ____
GAM325 USP20 3' TGATTGGAACACCAGGA 13504 A ACT
      TC CTGGTGTTCCTCA ATCA
      || ||||| |||
      AG GACCACAAGGT TAGT

      - - -
GAM325 LOC144811 3' GGTAGAGGGAACACCATGA 40455 C AA
      TCA TGGTGTTCCT CTATC
      ||| ||||| |||
      AGT ACCACAAGG GATGG
      GA
GAM325 LOC92235 5' TGGAAGCTGAAACACCAG 34012 C A A
      CTGGTGTTCCTCA CT TCA
      ||||| || |||
      GACCACAA GT GA GGT
      A C A
GAM326 ACVR1 3' TGAATCCATCTGTCTCCCT 6764 C AA _
      AGG AGATA GTGGAT CCG
      ||| ||| ||||| |||
      TCC TCTGT TACCTA GGT
      C C_ A
GAM326 BTG2 3' GGTCCTGCCTTTT 13630 ATAAAGT
      AAAAAGGCAG GGATC
      ||||| |||
      TTTTCCGTC CCTGG

      - - -
GAM326 CLN2 3' GTTTACTTGTCTGCCTT 5968 A
      AAGGCAGATAA GTGGAT
      ||||| |||||
      TTCCGTCTGTT CATTTG

      - - -
GAM326 DIAPH2 3' TTGTTTTATCTCCCTTTCC 13563 A C TG
      A AAAGG AGATAAAG G
      | |||| ||||| |
      C TTTCC TCTATTTT T
      C C GT
GAM326 FOXD2 3' GGGTCTCCCTTTCTGCCTTTCC 10789 A TA T_
      A AAAGGCAGA AAG GGATCC
      | ||||| || |||||
      C TTTCCGTCT TTC TCTGGG
      C _ CC
GAM326 GLS 3' CATTTAGCTATCTGCCTCTTT 17106 A _
      AAA AGGCAGATA AAGTG
      ||| ||||| |||
      TTT TCCGTCTAT TTTAC
      C CGA
GAM326 GPM6A 3' TCCTATCCAGCCTTTT 11781 A_ AAGT
      AAAAAGGC GATA GGA
      ||||| ||| |||

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			TTTTTCCG CTAT CCT		
			AC _____		
GAM326	HTR6	5'	CGGGGCCCTCATCTGCTTT 6549	AA T AT	
			AAGGCAGAT AG GG CCG		
			TTTCGTCTA TC CC GGC		
			C_ _ GG		
GAM326	IL12RB2	3'	GATGCCTCATCTTGCCTTTCC 7280	A _ AAAGT _	
			A AAAGGCA GAT GG ATC		
			C TTTCCGT CTA CC TAG		
			C T CT_ G		
GAM326	LAIR1	3'	CGGACCCACTCTCTGCCTT 8068	TAA A	
			AAGGCAGA AGTGG TCCG		
			TTCCGTCT TCACC AGGC		
			C_ C		
GAM326	LAIR1	3'	CGGACCCACTCTCTGCCTT 22322	TAA A	
			AAGGCAGA AGTGG TCCG		
			TTCCGTCT TCACC AGGC		
			C_ C		
GAM326	MTCP1	5'	ATTCACCTGCCTTTCC 15484	A ATAAA	
			A AAAGGCAG GTGGAT		
			C TTTCCGTC CACTTA		
			C _____		
GAM326	PLA2R1	3'	GGAGTCTCATCTGTCTTTCC 14295	A AA TGGA	
			A AAAGGCAGAT AG TCC		
			C TTTCTGTCTA TC AGG		
			C C_ TG_		
GAM326	SOCS5	3'	CGAATCCACTCTCATGTCTTTT 15225	GATAA C	
			AAAAGGCA AGTGGAT CG		
			TTTTCTGT TCACCTA GC		
			ACTC_ A		
GAM326	TCFL4	3'	ATTCATTCTGCCTT 31769	TAA	
			AAGGCAGA AGTGGAT		
			TTCCGTCT TCACTTA		

GAM326	ADNP	3'	GGTTTATTTTATCTGCCTTTT 17647		
			AAAAGGCAGATAAAGTGGATC		
			TTTTCCGTCTATTTTATTTGG		
GAM326	ALTE	3'	GGAACCTACCTGCCTTTCA 11105	A ATAAA A	
			A AAAGGCAG GTGG TCC		

A TTTCCGTC CATC AGG
 C A
 GAM326 CENTA2 3' GTTTACTTGTCTGCCTCTTT 20444 A A
 AAA AGGCAGATAA GTGGAT
 ||| ||||| |||||
 TTT TCCGTCTGTT CATTTG
 C _
 GAM326 DKFZP434B172 3' GTCCCTTTCTGCCTT 34702 TA T
 AAGGCAGA AAG GGAT
 ||||| ||| |||
 TTCCGTCT TTC CCTG
 _ _
 GAM326 DKFZp586G0123 5' ATCCAGGAGTTTCTCCTTTTT 45693 C TAAAG_
 AAAAAGG AGA TGGAT
 ||||| ||| |||||
 TTTTTC TCT ACCTA
 _ TTGAGG
 GAM326 EVI5 3' GTCTTATCTGCCTTTTT 12213 AAGT
 AAAAAGGCAGATA GGAT
 ||||| ||||| |||
 TTTTCCGTCTAT TCTG
 _ _
 GAM326 FLJ14280 3' CGGACGCGCTGCTCACCTGTCT 24340 ATAA__ GA
 TTTT AAAAAGGCAG AGTG TCCG
 ||||| ||| |||||
 TTTTCTGTC TCGC AGGC
 CACTCG GC
 GAM326 FLJ22127 3' GAGGCCCTCTCTGCCTTTCC 23042 A TAA T A_
 A AAAGGCAGA AG GG TC
 | ||||| || || ||
 C TTTCCGTCT TC CC AG
 C C_ _ GG
 GAM326 FLJ30681 3' TGGCTCTTATCTACCTTT 44107 C T AT
 AAAGG AGATAAAG GG CCG
 ||||| ||||| || |||
 TTTCC TCTATTTC TC GGT
 A _ _
 GAM326 KIAA1831 3' CCCTTTGACCTGCCTTTTT 31902 A_ T
 AAAAAGGCAG TAAAG GG
 ||||| ||||| ||
 TTTTCCGTC GTTTC CC
 CA _
 GAM326 KIAA1854 3' GTCTACCTACCTGCCTT 35534 A AA
 AAGGCAG TA GTGGAT
 ||||| || |||||
 TTCCGTC AT CATCTG
 C C_
 GAM326 LBP-9 3' CAGTTTTATGCTGCCTTT 15875 _ _
 AAAGGCAG ATAAAG TG
 ||||| ||||| ||

			TTCCGTC TATTTT AC		
			G G		
GAM326	MACF1	3'	GATTTGTTTTATCCACTTTTTT 14380	CA	TG
			AAAAAGG GATAAG GATC		
			TTTTTTC CTATTTT TTAG		
			AC GT		
GAM326	PRDM15	3'	CGGGGCCGCATCTGCCT 30916	AAA	AT
			AGGCAGAT GTGG CCG		
			TCCGTCTA CGCC GGC		
			____ GG		
GAM326	PRO1386	5'	CACTTCACTCTGCCTTTT 25288	TA_	
			AAAAGGCAGA AAGTG		
			TTTTCCGTCT TTCAC		
			CAC		
GAM326	SCDGF-B	3'	GCCCTATCTGCACTTTTT 24880	_	AA
			AAAAAG GCAGATA GT		
			TTTTTC CGTCTAT CG		
			A CC		
GAM326	SCDGF-B	3'	GCCCTATCTGCACTTTTT 26982	_	AA
			AAAAAG GCAGATA GT		
			TTTTTC CGTCTAT CG		
			A CC		
GAM326	SH3BGRL2	3'	CCACCTTATTGCCTTTCC 25527	A	A A
			A AAAGGCAG TAA GTGG		
			C TTTCCGTT ATT CACC		
			C _ C		
GAM326	TUSP	3'	ATCCTTATTTGCCTTT 21522	AGT	
			AAAGGCAGATAA GGAT		
			TTTCCGTTTATT CCTA		

GAM326	LOC124222	3'	TTCCTTCCCTGCCTTTT 36742	ATA	T
			AAAAGGCAG AAG GGA		
			TTTTCCGTC TTC CTT		
			CC_ _		
GAM326	LOC139422	5'	GGGATCACCTGCCTTTT 37343	ATAAA	A
			AAAAAGGCAG GTGG TCC		
			TTTTTCCGTC CACT GGG		
			____ A		
GAM326	LOC145871	5'	CGGCATTTTCCCATCTGCCTTT 40621	____	GAT
	T		AAAAGGCAGAT AAAGTG CCG		

TTTTCCGTCTA TTTTAC GGC
 CCC ____
 GAM326 LOC148394 5' CGGATCCAAGGTCCTGCCT 40881 _ AAAG
 AGGCAG AT TGGATCCG
 ||||| || |||||
 TCCGTC TG ACCTAGGC
 C GA__
 GAM326 LOC148534 3' GATGTCTTTTCTGCCTTT 38548 T TGG
 AAAGGCAGA AAAG ATC
 ||||| ||| ||
 TTTCCGTCT TTTC TAG
 _ TG_
 GAM326 LOC148697 3' GGAGCCACCTGCCTTTCC 38574 A ATAAA A_
 A AAAGGCAG GTGG TCC
 | ||||| ||| ||
 C TTTCCGTC CACC AGG
 C ____ CG
 GAM326 LOC164714 3' CGGATCCAGATCTGCC 42179 AAAG
 GGCAGAT TGGATCCG
 ||||| |||||
 CCGTCTA ACCTAGGC
 G__
 GAM326 LOC199858 3' GGTATTCTTAACTGCCTTTTT 42640 A AGT _
 AAAAAGGCAG TAA GGAT CC
 ||||| ||| ||| ||
 TTTTCCGTC ATT CTTA GG
 A ____ T
 GAM326 LOC200982 3' GGCTGTCCCCTGCCTTTCC 43377 A ATAAAGT _
 A AAAGGCAG GGAT CC
 | ||||| ||| ||
 C TTTCCGTC CCTG GG
 C C_____ TC
 GAM326 LOC255714 5' GGCCCTCATCTGCCTTT 46141 AA T AT
 AAAGGCAGAT AG GG CC
 ||||| || || ||
 TTTCCGTCTA TC CC GG
 C_ _ _
 GAM326 LOC57228 5' CGGGGTGCTGATCTGCCT 21707 AA GA
 AGGCAGAT AGTG TCCG
 ||||| ||| |||
 TCCGTCTA TCGT GGGC
 G_ G_
 GAM326 LOC91531 5' CGGCTCCCTATCTGTC 32973 AA T T
 GGCAGAT AG GGA CCG
 ||||| || ||| ||
 CTGTCTA TC CCT GGC
 _ _ C
 GAM327 EBAF 3' TGTCTTAGAGAACTTGTCA 32609 C C
 TGGCAAGTTC CTAA ATA
 ||||| ||| |||

ACTGTTCAAG GATT TGT
 A C
 GAM327 NAPB 3' ACGTTATGAAACTAACCA 34766 CA CCCTAA
 TGG AGTT CATAACGT
 ||| ||| |||||
 ACC TCAA GTATTGCA
 AA AA____
 GAM327 PTPN1 3' ACATTATGTTAGAGAGGTAGC 8701 AAG C C
 GC TTC CTAACATAA GT
 || ||| ||||| ||
 CG GAG GATTGTATT CA
 ATG A A
 GAM327 KIAA0960 3' ACATTATGTCAGATTATGTACT 44514 TCC____ A C
 TGCTA TGGCAAGT CT ACATAA GT
 ||||| || ||||| ||
 ATCGTTCA GA TGTATT CA
 TGTATTA C A
 GAM327 LOC158187 3' ACGTACAGAAAATTTGCCA 41920 CC AACATA
 TGGCAAGTT CT ACGT
 ||||| || |||
 ACCGTTTAA GA TGCA
 AA CA____
 GAM327 LOC90620 5' TACGCTAAAAAAGGGAACTTCC 31805 C AACA A
 A TGG AAGTTCCCT TA CGTA
 ||| ||||| || |||
 ACC TTCAAGGGA AT GCAT
 _ AAAA C
 GAM328 CX3CR1 3' ACAAATGATGGACCCAATGCA 34973 ATATG CC
 C GTGCATTGG ATTAT TGT
 ||||| |||| |||
 CACGTAACC TAGTA ACA
 CAGG_ AA
 GAM328 ENG 5' ACAGGATAAGGCCCAGCGCAC 5589 A ATATGA
 GTGC TTGG TTATCCTGT
 ||| ||| |||||
 CACG GACC AATAGGACA
 C CGG____
 GAM328 MLLT3 3' ACAGGACGAATGCATATTCAAC 10866 CA _ A_
 AC GTG TTGGATATG ATT TCCTGT
 ||| ||||| ||| |||||
 CAC AACTTATAC TAA AGGACA
 _ G GC
 GAM328 TGFA 3' CAGGATAAACCCAATACAT 9230 C ATATGA
 GTG ATTGG TTATCCTG
 ||| ||| |||||
 TAC TAACC AATAGGAC
 A CA____
 GAM328 FLJ10388 3' ACAAGTGATACATCCAATGCA 19841 ATG CC
 TGCATTGGAT ATTAT TGT
 ||||| |||| |||

ACGTAACCTA TAGTG ACA
 CA_ A_
 GAM328 HT002 3' ACAGGATGCAACCACAACAC 15278 CAT ATA AT
 GTG TGG TG TATCCTGT
 ||| ||| || |||||
 CAC ACC AC GTAGGACA
 AAC A_ _
 GAM328 KIAA1831 3' CAGAGAATATCCAATGCA 31901 GATTA _
 TGCATTGGATAT TC CTG
 ||||| ||| |||
 ACGTAACCTATA AG GAC
 _ A
 GAM328 MGC3251 3' ACAGACGTTGCACCATATCCAT 25730 T ATTATC_
 GCAC GTGCAT GGATATG CTGT
 ||||| ||||| |||
 CACGTA CCTATAC GACA
 _ CACGTTGCA
 GAM328 LOC149134 5' ACAGAGGGGTCCACACCCAGTG 40956 ATAT_ ATC
 CAC GTGCATTGG GATT CTGT
 ||||| ||| |||
 CACGTGACC CTGG GACA
 CACAC GGA
 GAM328 LOC220074 3' CAGGATAAGCCACTGCAC 29824 T ATATGA
 GTGCA TGG TTATCCTG
 ||||| ||| |||||
 CACGT ACC AATAGGAC
 C G_
 GAM329 AP1G1 3' TTCTGGAGGCTACTTTGCACTC 6802 A T_ CAG
 TTCC A AAGAGTGCAA GCC CAGAA
 | ||||| ||| |||||
 C TTCTCACGTT CGG GTCTT
 C TCAT AG_
 GAM329 BCL11B 3' TTCTGTTCGATGCACTCTTT 23170 A CCC
 AAAGAGTGCA TG AGCAGAA
 ||||| || |||||
 TTTCTCACGT GC TTGTCTT
 A _
 GAM329 CACNA1C 3' TCCGCTGAGCGCTCTTTT 6382 AATGCC A
 AAAAGAGTGC CAGC GA
 ||||| ||| ||
 TTTTCTCGCG GTCG CT
 A_ C
 GAM329 CEP2 5' CTGCTGGGCGTGAACACCCT 14044 A CA_
 AG GTG ATGCCCAGCAG
 || ||| |||||
 TC CAC TCGGGTCGTC
 C AAG
 GAM329 CHD2 3' TTCTGCTGGTGATAAACTCTTT 6937 GCA GC
 AAAGAGT AT CCAGCAGAA
 ||||| || |||||

			TTTCTCA TA GGTCGTCTT		
			AA_ GT		
GAM329	DISC1	3'	CTGCTGGGCTGCTTCTTT 20737	T AT	
			AAAGAG GCA GCCCAGCAG		
			TTTCTT CGT CGGGTCGTC		
			— —		
GAM329	EIF2C1	3'	TCTGCACTGTCCTGCACTCTTT 14506	AT CCA	
			AAAGAGTGCA GC GCAGA		
			TTTCTCACGT TG CGTCT		
			CC TCA		
GAM329	FCN3	5'	TTCTACTGGAAGTTTGCACTTT 9745	TGC_ C	
			AGAGTGCAA CCAG AGAA		
			TTTCACGTT GGTC TCTT		
			TGAA A		
GAM329	FCN3	5'	TTCTACTGGAAGTTTGCACTTT 9746	TGC_ C	
			AGAGTGCAA CCAG AGAA		
			TTTCACGTT GGTC TCTT		
			TGAA A		
GAM329	HHIP	5'	CTGCTGGGCAGTGGCGTTC 22841	AA_	
			GAGTGC TGCCCAGCAG		
			CTTGCG ACGGGTCGTC		
			GTG		
GAM329	MMP14	3'	CTGCCCCGGCATTGCATCTTCC 11436	A G CA_	
			A AAGA TGCAATGCC GCAG		
			C TTCT ACGTTACGG CGTC		
			C _ CCC		
GAM329	MS4A4A	3'	TTCTACTGGGCATAATTATATC 23450	GTGCA_ C	
	TT		AAGA ATGCCCAG AGAA		
			TTCT TACGGGTC TCTT		
			ATATTAA A		
GAM329	NEO1	3'	TTCTGAGTCATTGCATCCTCT 8320	_ CCCAG	
			AGAG TGCAATG CAGAA		
			TCTC ACGTTAC GTCTT		
			CT TGA_		
GAM329	PML	3'	TTCTGTCACCCTTGCACTCT 27081	TGCCCA	
			AGAGTGCAA GCAGAA		
			TCTCACGTT TGTCTT		
			CCCAC_		
GAM329	PML	3'	TTCTGTCACCCTTGCACTCT 27085	TGCCCA	
			AGAGTGCAA GCAGAA		

			TCTCACGTT	TGTCTT		
			CCCAC_			
GAM329	SOX9	3'	CTGGGAAACATTTGCACTCTTT	5900	TG_____	
	T		AAAAGAGTGCAA	CCCAG		
			TTTTCTCACGTT	GGGTC		
			TACAAA			
GAM329	STAT3	3'	CTGGCATTGCACTTTTT	9122	C	
			AAAGAGTGCAATGCC	AG		
			TTTTTCACGTTACGG	TC		
			—			
GAM329	STAT3	3'	CTGGCATTGCACTTTTT	29269	C	
			AAAGAGTGCAATGCC	AG		
			TTTTTCACGTTACGG	TC		
			—			
GAM329	ZNF236	3'	TTCTGCTTTTAATGCACTTTTT	14276	A CCC	
			AAAGAGTGCA	TG AGCAGAA		
			TTTTTCACGT	AT TCGTCTT		
			A TT_			
GAM329	CTCFL	3'	TTCTGCTAAACTACTCTTTT	40139	CAATGCCC	
			AAAAGAGTG	AGCAGAA		
			TTTTCTCAT	TCGTCTT		
			CAAAA_			
GAM329	CYB5-M	3'	CTGCCAGTTGCATTCTTCC	45378	A GCCCA	
			A AAGAGTGCAAT	GCAG		
			C TTCTTACGTTG	CGTC		
			C AC_			
GAM329	CYB5-M	3'	CTGCCAGTTGCATTCTTCC	24952	A GCCCA	
			A AAGAGTGCAAT	GCAG		
			C TTCTTACGTTG	CGTC		
			C AC_			
GAM329	DRF1	3'	TCTCTGGGCACTGTACTCT	24749	A C	
			AGAGTGCA	TGCCAG AGA		
			TCTCATGT	ACGGGTC TCT		
			C _			
GAM329	DUSP14	3'	TCTACTGGATTAGCCCTACTCT	13884	CAAT ____ C	
	TT		AAAGAGTG	GC CCAG AGA		
			TTTCTCAT	CG GGTC TCT		
			CC_ ATTA	A		
GAM329	EREG	3'	TCTGTAATTGCACTTTTT	7157	GCCCA	
			AAAGAGTGCAAT	GCAGA		

TTTTTCACGTTA TGTCT
 A____
 GAM329 FLJ10276 3' TTCTGCTGAACACCCACTGTTC 19793 A G CAA CC
 C A AA AGTG TG CAGCAGAA
 || ||| || |||||
 C TT TCAC AC GTCGTCTT
 C G CC_ AA
 GAM329 FLJ10315 5' TTCTGCTAGCTCATAGCACTCT 19819 A A CCC_
 TCG A AAGAGTGC ATG AGCAGAA
 ||||| || |||||
 G TTCTCACG TAC TCGTCTT
 C A TCGA
 GAM329 FLJ10811 3' TCTGCTGAGCGCCTTCT 20166 T AAT C
 AGAG GC GC CAGCAGA
 ||| || |||||
 TCTT CG CG GTCGTCT
 C _ A
 GAM329 FLJ11336 5' TCTGCTGGGGAGCCTCTT 20431 T AATG
 AAGAG GC CCCAGCAGA
 ||| || |||||
 TTCTC CG GGGTCGTCT
 _ AG_
 GAM329 FLJ21865 3' TCTGCTGGGTGTAAGTGTCTCT 23002 CA_
 AGAGTG ATGCCCAGCAGA
 |||| |||||
 TCTCGT TGTGGGTCGTCT
 CAA
 GAM329 FLJ23360 3' CTGCTGGGCACCCTGGCTC 23335 G A_
 GAGT CA TGCCCAGCAG
 ||| || |||||
 CTCG GT ACGGGTCGTC
 _ CCC
 GAM329 HINT3 3' TTGAAGCATTGCATCTTTT 28879 G CCAG
 AAAAGA TGCAATGC CAG
 |||| ||||| ||
 TTTTCT ACGTTACG GTT
 _ AA_
 GAM329 KIAA0630 5' TTCTACTGCAGCAGCTGCTACT 43064 _ A_ C_ C
 CTTT AAAGAGT GCA TGC CAG AGAA
 ||||| || || |||||
 TTTCTCA CGT ACG GTC TCTT
 T CG AC A
 GAM329 KIAA0712 3' TCTGCTGGACAGTGGACTGTT 16267 G G A C
 AA AGT CA TG CCAGCAGA
 || ||| || |||||
 TT TCA GT AC GGTCGTCT
 G G G A
 GAM329 KIAA0855 3' CTGCAGCAGTTGCACTCTTTT 17373 _ CCA
 AAAAGAGTGCAA TGC GCAG
 ||||| || |||

			TTTTCTCACGTT ACG CGTC	
			G A__	
GAM329	KIAA1001	3'	TTCTGCTCACACAATTGCACTC 17329	GCCC__
			GAGTGCAAT AGCAGAA	
			CTCACGTTA TCGTCTT	
			ACACAC	
GAM329	KIAA1018	3'	CTGGAATTACACTTTTTT 17357	C GC
			AAAAGAGTG AAT CCAG	
			TTTTTTTAC TTA GGTC	
			A A__	
GAM329	KIAA1884	3'	TCTGCTGGGCATCACCT 36298	A CA
			AG GTG ATGCCCAGCAGA	
			TC CAC TACGGGTCGTCT	
			C __	
GAM329	MacGAP	3'	TTCTGTCTACTGTACTCTT 27292	A CCCA
			AAGAGTGCA TG GCAGAA	
			TTCTCATGT AT TGTCTT	
			C C__	
GAM329	PIP5K1C	3'	CTGCCCACTGCACTCTTT 35018	A CCCA
			AAAGAGTGCA TG GCAG	
			TTTCTCACGT AC CGTC	
			C C__	
GAM329	PRO1855	3'	TTCTGCTGGACACAACCTCTTT 20577	TGCAA C
	T		AAAAGAG TG CCAGCAGAA	
			TTTTCTC AC GGTCGTCTT	
			CAAC_ A	
GAM329	RPH3A	3'	TCTGTTTCATTGACTCTTTT 17309	G CCC
			AAAAGAGT CAATG AGCAGA	
			TTTTCTCA GTTAC TTGTCT	
			_ T__	
GAM329	TBX19	3'	TCTGAACATTCAATGCACTTT 11625	CCCAG_
			AGAGTGCAATG CAGA	
			TTTCACGTTAC GTCT	
			TTACAA	
GAM329	TRIM4	3'	TCTGCCTATGTTGCACTCT 26905	GCCCA
			AGAGTGCAAT GCAGA	
			TCTCACGTTG CGTCT	
			TATC_	
GAM329	LOC116228	3'	TTCTGCTGGGCACGGTGGCTC 36536	_ AA
			GAGT GC TGCCCAGCAGAA	

CTCG TG ACGGGTCGTCTT
G GC

GAM329 LOC134145 3' TCTGCTAGTCACTTTTTT 37061 CAAT CC
AAAAGAGTG GC AGCAGA
||||||| || |||||
TTTTTTCAC TG TCGTCT
____ A_

GAM329 LOC145980 5' CTAGGCTGCTGCTCTTT 40649 _ AT C
AAAGAGT GCA GCC AG
||||||| ||| ||| ||
TTTCTCG CGT CGG TC
T ____ A

GAM329 LOC145988 3' CTGCAGCAGTTGCACTCTTTT 38037 _ CCA
AAAAGAGTGCAA TGC GCAG
||||||| ||| ||| |||
TTTTCTCACGTT ACG CGTC
G A_

GAM329 LOC146901 3' CTGAAAGTACACTCTTTT 40763 CAA CCAG
AAAAGAGTG TGC CAG
||||||| ||| |||
TTTTCTCAC ATG GTC
____ AAA_

GAM329 LOC150166 5' CTGCTATTAGGTATTGCTCTCT 41147 A T C____
TCC A AAGAG GCAATGCC AGCAG
| ||||| ||||| |||||
C TTCTC CGTTATGG TCGTC
C T ATTA

GAM329 LOC151429 3' TCTGCTGGGCTCTGCCTC 41345 T AT
GAG GCA GCCCAGCAGA
||| ||| ||||| |||||
CTC CGT CGGGTCGTCT
_ CT

GAM329 LOC162333 5' TTCTGCTGGGCAAAGGTTGTC 42142 GT AA_
GA GC TGCCCAGCAGAA
|| || ||||| |||||
CT TG ACGGGTCGTCTT
GT GAA

GAM329 LOC199920 5' CTGGGACATCACACTTTTTT 42660 CA _
AAAAGAGTG ATG CCCAG
||||||| ||| |||||
TTTTTTCAC TAC GGGTC
AC A

GAM329 LOC200734 5' TCTGCTGCGGCGCCCTCTT 42843 T AAT _
AAGAG GC GCC CAGCAGA
||||| || ||| |||||
TTCTC CG CGG GTCGTCT
C ____ C

GAM329 LOC200734 3' TTCAACTGCATTGCATCCTCTT 42844 ____ CC CA
AAGAG TGCAATGC AG GAA
||||| ||||| || |||

TTCTC ACGTTACG TC CTT
 CT _ AA
 GAM329 LOC219899 3' CTCTCGGGCATTGCATTC 43991 _ C
 GAGTGCAATGCCC AG AG
 ||||| || ||
 CTTACGTTACGGG TC TC
 C _
 GAM329 LOC51337 3' CTGCTGGGCGTTCCCTT 18764 TGC
 GAG AATGCCCAGCAG
 || |||||
 TTC TTGCGGGTCGTC
 CC_
 GAM329 LOC83690 3' TCTGATATTGCACTTCTT 25486 _ CCCAG
 AAGA GTGCAATG CAGA
 ||| ||||| |||
 TTCT CACGTTAT GTCT
 T A_
 GAM329 LOC90917 5' TCTGCCGGGCATTGTTTGTTC 32171 AGT A
 AAG GCAATGCCC GCAGA
 || ||||| |||
 TTT TGTTACGGG CGTCT
 GTT C
 GAM329 LOC91149 3' TTCTGCTGACTAATGCACTC 32460 A CC
 GAGTGCA TG CAGCAGAA
 ||||| || |||||
 CTCACGT AT GTCGTCTT
 A CA
 GAM329 LOC92568 3' TCTGAGGAAAACATGGCACTCT 34581 A C_ AG
 T AAGAGTGC ATG CC CAGA
 ||||| || || |||
 TTCTCACG TAC GG GTCT
 G AAAA A_
 GAM330 CCND1 3' GCGGAGTCTGTCTGTGACG 27600 AAACAA AG
 CGTCACAG AGG TCGT
 ||||| || |||
 GCAGTGTC TCT GGCG
 CTG_ GA
 GAM330 CENPA 3' ATGACTTTCCTCTGTAAC 7559 C AACAAA
 GT ACAGA GGAGTCGT
 || |||| |||||
 CA TGTCT TTTCAGTA
 A CC_
 GAM330 DPYD 3' ATGGCTTATTTCTATGAC 30316 C CAAAG
 GTCA AGAAA GAGTCGT
 ||| |||| |||||
 CAGT TCTTT TTCGGTA
 A A_
 GAM330 EGFL4 5' GGCCCTGGCTTCTGCGACG 30968 A ACAA A
 CGTC CAGAA AGG GTC
 ||| |||| ||| |||

			GCAG GTCTT TCC CGG		
			C CGG_ _		
GAM330	HOXD4	3'	ACATCATTGTTTCTATGAC 15977	C	A GA
			GTCA AGAAACAA G GT		
			CAGT TCTTTGTT C CA		
			A A TA		
GAM330	WDR1	3'	ATTTCTCTATTTCTGTGACG 18954		CAA
			CGTCACAGAAA AGGAGT		
			GCAGTGTCTTT TCTTTA		
			ATC		
GAM330	AFAP	3'	ACCCCTTGCCTCTGTGGC 22290	AA	A A
			GTCACAGA CAA GG GT		
			CGGTGTCT GTT CC CA		
			CC C _		
GAM330	ARHGEF15	3'	ACCCTGCTTGTTTCTGCAGC 17315	CA	_ A
			GT CAGAAACAA AGG GT		
			CG GTCTTTGTT TCC CA		
			AC CG _		
GAM330	ATF3	3'	ACAGGCCGCTCTGTGGC 10241	AACAAA	A_ _
			GTCACAGA GG GTC GT		
			CGGTGTCT CC CGG CA		
			_ GC A		
GAM330	FLJ12409	3'	ACTTCGTGCTCTGTGAC 24752	A_	AAA
			GTCACAGA AC GGAGT		
			CAGTGTCT TG CTTCA		
			CG _		
GAM330	FLJ12783	3'	TATGGCTTTGTCCCTATGAC 25420	C AA	AAG
			GTCA AG ACA GAGTCGTA		
			CAGT TC TGT TTCGGTAT		
			A CC _		
GAM330	FLJ12910	5'	TACCGCCTCTGTTTCTGCGGCG 23800	A	A AGTC
			CGTC CAGAAACA AGG GTA		
			GCGG GTCTTTGT TCC CAT		
			C C GC_		
GAM330	FLJ14251	3'	GCTCTATTTCTGTGGC 24325	CAAA	
			GTCACAGAAA GGAGT		
			CGGTGTCTTT TCTCG		
			A_		
GAM330	FLJ20315	5'	TACGACTTGGCTTTCTGAAACG 19380	CA	CAAAG
			CGT CAGAAA GAGTCGTA		

			GCA GTCTTT TTCAGCAT		
			AA CGG__		
GAM330	FLJ21162	3'	TGAGGCTTGTCTTGCCAC 24307	CA	AA AG
			GT CAGAAACA GG TCG		
			CA GTCTTTGT TC AGT		
			CC __ GG		
GAM330	FLJ23342	3'	GAGACCTTTGTTTCTGTGATG 23898		AG
			CGTCACAGAAACAAAGG TC		
			GTAGTGTCTTTGTTTCC AG		
			AG		
GAM330	HH114	3'	TACGGCTTCCTGACTTCTGTGA 26251	ACAA	_
	C		GTCACAGAA AGGA GTCGTA		
			CAGTGTCTT TCCT CGGCAT		
			CAG_ T		
GAM330	KIAA0798	3'	TGATATCTATTCTGTGAC 16072	ACAA	A
			GTCACAGAA AGG GTCG		
			CAGTGTCTT TCT TAGT		
			A__ A		
GAM330	MANBAL	3'	TCCTTCTGCTTCTGTGACG 22621	A	_
			CGTCACAGAA CA AAGGA		
			GCAGTGTCTT GT TTCCT		
			C C		
GAM330	OPRL1	3'	GCTGCCTTCAGCCCTGTGACG 6616	AAACA	_
			CGTCACAG AAGG AGT		
			GCAGTGTC TTCC TCG		
			CCGAC G		
GAM330	SLC17A6	3'	ACACTTATTTCTGTGA 21595	CAAAG	C
			TCACAGAAA GAGT GT		
			AGTGTCTTT TTCA CA		
			A__ _		
GAM330	LOC139221	3'	ACTATTTTGTGTTTATGAC 37331	CA	G
			GTCA GAAACAAAG AGT		
			CAGT TTTTGTGTTT TCA		
			A_ A		
GAM330	LOC145844	3'	ACCTCTTCTTTCTGTGAC 37999	ACAA	TC
			GTCACAGAA AGGAG GT		
			CAGTGTCTT TCTTC CA		
			__ TC		
GAM330	LOC150290	5'	GCTATTCCTTTCTGCGACG 38933	A	ACAA C
			CGTC CAGAA AGGAGT GT		

			GCAG GTCTT TCCTTA CG		
			C _ _ T		
GAM330	LOC164382	3'	ACCCCTTATGCCTGTGACG 42161	AAA _ A	
			CGTCACAG CA AAGG GT		
			GCAGTGTC GT TTCC CA		
			C _ A C		
GAM330	LOC203350	3'	ACTTCCTGTCTCTGTGAC 43528	A AA	
			GTCACAGA ACA GGAGT		
			CAGTGTCT TGT CTTCA		
			C C _		
GAM330	LOC221362	3'	CTTCTTCATTTCTGTGAGG 45021	G CA	
			C TCACAGAAA AAGGAG		
			G AGTGTCTTT TTCTTC		
			G AC		
GAM330	LOC222060	5'	ACAACCTCCTTCATTCTTTGTGA 45157	_ CA C	
			TCACAGA AA AAGGAGT GT		
			AGTGTTT TT TTCCTCA CA		
			C AC A		
GAM330	LOC254413	5'	ACAACCTCCACTCTGTGAC 46396	AACAAA C	
			GTCACAGA GGAGT GT		
			CAGTGTCT CCTCA CA		
			CA _ _ A		
GAM330	LOC92573	5'	GGCCCTTTTCCTGTGACG 34601	AAAC A	
			CGTCACAG AAAGG GTC		
			GCAGTGTC TTTCC CGG		
			CT _ _		
GAM331	BACH2	3'	TGAGCCATCTCATGACCCCA 22381	CA C _ G	
			TGG TCATGAGA GC CG		
			ACC AGTACTCT CG GT		
			CC AC A		
GAM331	CASP2	3'	TCCTGACCTCATGATCCA 26855	C ACG C	
			TGG ATCATGAG CG GA		
			ACC TAGTACTC GT CT		
			_ CA _ C		
GAM331	CASP2	3'	TCCTGACCTCATGATCCA 26860	C ACG C	
			TGG ATCATGAG CG GA		
			ACC TAGTACTC GT CT		
			_ CA _ C		
GAM331	CASP2	3'	TCCTGACCTCATGATCCA 26865	C ACG C	
			TGG ATCATGAG CG GA		

			ACC TAGTACTC GT CT		
			— CA_ C		
GAM331	CASP2	3'	TCCTGACCTCATGATCCA 6892	C	ACG C
			TGG ATCATGAG CG GA		
			ACC TAGTACTC GT CT		
			— CA_ C		
GAM331	CAV1	3'	TTCTGCCTTCTCATGATCCA 7491	C	C_ C
			TGG ATCATGAGA GCG GAA		
			ACC TAGTACTCT CGT CTT		
			— TC —		
GAM331	H3F3B	3'	TTCTTGCTTCTCATGATGC 11797		C C
			GCATCATGAGA GCG GAA		
			CGTAGTACTCT CGT CTT		
			T T		
GAM331	IGF2R	3'	TTCAGGTTCTCATGATACCA 6559	C	C GC
			TGG ATCATGAGA GC GAA		
			ACC TAGTACTCT TG CTT		
			A _ GA		
GAM331	STAC	3'	TTTCCTCCCTCTCTGATGCCA 9121		T CGCGC
			TGGCATCA GAGA GAAA		
			ACCGTAGT CTCT CTTT		
			— CCCTC		
GAM331	ZNF264	3'	TCTTGACCTCATGATCCA 9462	C	ACG C
			TGG ATCATGAG CG GA		
			ACC TAGTACTC GT CT		
			— CA_ T		
GAM331	BTN3A1	3'	TCTTGACCTCATGATCCA 13922	C	ACG C
			TGG ATCATGAG CG GA		
			ACC TAGTACTC GT CT		
			— CA_ T		
GAM331	C13orf1	3'	TCCTGACCTCATGATCCA 21694	C	ACG C
			TGG ATCATGAG CG GA		
			ACC TAGTACTC GT CT		
			— CA_ C		
GAM331	CNNM1	3'	TTCTTTGGGTCCCCTGATGCCA 21613		TGA G C_
			TGGCATCA GAC CG GAA		
			ACCGTAGT CTG GT CTT		
			CCC G TT		
GAM331	FLJ12960	3'	TCCTGACCTCATGATCCA 23920	C	ACG C
			TGG ATCATGAG CG GA		

			ACC TAGTACTC	GT CT		
			— CA_ C			
GAM331	FLJ20813	3'	TCCTGACCTCATGATCCA	19679	C	ACG C
			TGG ATCATGAG	CG GA		
			ACC TAGTACTC	GT CT		
			— CA_ C			
GAM331	FLJ31101	3'	TCCTGACCTCATGATCCA	19686	C	ACG C
			TGG ATCATGAG	CG GA		
			ACC TAGTACTC	GT CT		
			— CA_ C			
GAM331	GTF2E1	3'	TCCTGACCTCATGATCCA	12037	C	ACG C
			TGG ATCATGAG	CG GA		
			ACC TAGTACTC	GT CT		
			— CA_ C			
GAM331	HSPC065	3'	TCCTGACCTCATGATCCA	15455	C	ACG C
			TGG ATCATGAG	CG GA		
			ACC TAGTACTC	GT CT		
			— CA_ C			
GAM331	KIAA0450	5'	TTCAGCAGCATGATGCCA	16037		AGAC GC
			TGGCATCATG	GC GAA		
			ACCGTAGTAC	CG CTT		
			GA__ A_			
GAM331	KIAA1143	3'	TCCTGACCTCATGATCCA	34077	C	ACG C
			TGG ATCATGAG	CG GA		
			ACC TAGTACTC	GT CT		
			— CA_ C			
GAM331	PRO0365	5'	TCCTGACCTCATGATCCA	15390	C	ACG C
			TGG ATCATGAG	CG GA		
			ACC TAGTACTC	GT CT		
			— CA_ C			
GAM331	RAB33B	3'	TCTTGACCTCATGATCCA	25332	C	ACG C
			TGG ATCATGAG	CG GA		
			ACC TAGTACTC	GT CT		
			— CA_ T			
GAM331	TUCAN	3'	TCCTGACCTCATGATCCA	17319	C	ACG C
			TGG ATCATGAG	CG GA		
			ACC TAGTACTC	GT CT		
			— CA_ C			
GAM331	LOC130535	3'	TTGTGCATCTCATGATAACA	37478	GC	CGC
			TG ATCATGAGA	GCGAA		

			AC TAGTACTCT TGTTT		
			AA AC_		
GAM331	LOC143879	5'	GCCGAGTCATATCATGATGCCA 37660		___ GC_
			TGGCATCATGA GAC GC		
			ACCGTAGTACT CTG CG		
			ATA AGC		
GAM331	LOC146854	5'	GCTTCTTTTTCATGATGCCA 38255		CGC_
			TGGCATCATGAGA GC		
			ACCGTAGTACTTT CG		
			TTCTT		
GAM331	LOC146909	3'	TCTGACCTCATGATCCA 38269	C	ACG C
			TGG ATCATGAG CG GA		
			ACC TAGTACTC GT CT		
			_ CA_ _		
GAM331	LOC169693	3'	TCCAGCACTCATGATGCCA 42208		AC GC
			TGGCATCATGAG GC GA		
			ACCGTAGTACTC CG CT		
			A_ AC		
GAM331	LOC200014	3'	TCCTGACCTCATGATCCA 42694	C	ACG C
			TGG ATCATGAG CG GA		
			ACC TAGTACTC GT CT		
			_ CA_ C		
GAM331	LOC55893	5'	GCAGGCGTTCCCATGATGCCA 20731		A_ _
			TGGCATCATG GACGC GC		
			ACCGTAGTAC TTGCG CG		
			CC GA		
GAM331	LOC89919	3'	TCCGGACCTCATGATCCA 30465	C	ACG C
			TGG ATCATGAG CG GA		
			ACC TAGTACTC GC CT		
			_ CAG _		
GAM332	LOC56926	5'	CGACAGGCAGCGCGGCTG 36041		T AAC A
			TAGCCGT CT GCCT TCG		
			GTCGGCG GA CGGA AGC		
			C _ C		
GAM333	GR6	3'	AACTTTCTAAGGCAGCTA 14278		ACCCT
			TAGCTGCCTTA GGAGTT		
			ATCGACGGAAT TTTCAA		
			C_		
GAM333	ILF3	3'	CCATGGACAAGGCAGCTA 10845		AA C
			TAGCTGCCTT CC TGG		

			ATCGACGGAA GG ACC		
			CA T		
GAM333	KIAA1841	3'	TAACCTCCTTAAAACAGTTA 39027	CC	CCCT
			TAGCTG TTAA GGAGTTA		
			ATTGAC AATT CCTCAAT		
			AA ____		
GAM333	pcnp	3'	ATAACTCCAGAGAAGCAGC 21625	C	AACC
			GCTGC TT CTGGAGTTAT		
			CGACG AA GACCTCAATA		
			_ GA_		
GAM333	WNT16	3'	AGCCTAAGAGCTAAGGCAGT 27673	ACCC_	A
			GCTGCCTTA TGG GTT		
			TGACGGAAT ATC CGA		
			CGAGA _		
GAM333	WNT16	3'	AGCCTAAGAGCTAAGGCAGT 18169	ACCC_	A
			GCTGCCTTA TGG GTT		
			TGACGGAAT ATC CGA		
			CGAGA _		
GAM333	LOC127294	3'	AACTCCAGGACAAGGCA 36893	AAC	
			TGCCTT CCTGGAGTT		
			ACGGAA GGACCTCAA		
			CA_		
GAM333	LOC139770	3'	GCTTCAAGGCAGCTG 37147	TAACCC	
			TAGCTGCCT TGGAGT		
			GTCGACGGA ACTTCG		

GAM334	ATP8B2	3'	TGCAAAAATTATATCA 32518	ACG	
			TGATGTAATTTTT GCA		
			ACTATATTAAAAA CGT		

GAM334	VLDLR	3'	AAGTGCTAAAAAATTAAACCA 34449	ATG	AC
			TG TAATTTTT GGCAGTT		
			AC ATTAAAAA TCGTGAA		
			CAA A_		
GAM334	KIAA1026	3'	AGTGTGTAAAAATCAATCA 35273	GTA	G
			TGAT ATTTTTACG CACT		
			ACTA TAAAAATGT GTGA		
			AC_ _		
GAM334	LOC135818	3'	GCCATAATAAAAATTACAT 37094	C_	
			ATGTAATTTTGA GGC		

			TACATTAAAAAT CCG		
			ATA		
GAM335	CYP1A1	3'	CTGGGAACATCACATTCCTCT 6114	TAAC T A	
			AGAGGAAT AT TTCT CAG		
			TCTCCTTA TA AAGG GTC		
			CAC_ C _		
GAM335	PPP2R5C	3'	TCTGTAGAAAAATACATACTTCC 8588	T AC_	
			GGAA TA ATTTTCTACAGA		
			CCTT AT TAAAAGATGTCT		
			C ACA		
GAM335	ALDH9	3'	GATAATGTTAATTCTCT 6360 G	T	
			AGAG AATTAACATT TC		
			TCTC TTAATTGTAA AG		
			_ T		
GAM335	BHLHB2	3'	CTGTAGGCTAATTCCTCT 9753	ACATTT	
			AGAGGAATTA TCTACAG		
			TCTCCTTAAT GGATGTC		
			C_____		
GAM335	C21orf41	3'	TCTGCAAAAAGTGAATTCTTC 28732	AA CTA	
			GAGGAATT CATTTT CAGA		
			CTTCTTAA GTGAAA GTCT		
			_ AAC		
GAM335	DKFZP564D206	3'	CTGTAGTTTTTAATTCCTC 44428	CATTTT	
			GAGGAATTAA CTACAG		
			CTCCTTAATT GATGTC		
			TT_____		
GAM335	DKFZP761D0211	3'	CTGTAGAGTCCATTCCCCT 25737	A TA ATTT	
			AG GGAAT AC TCTACAG		
			TC CCTTA TG AGATGTC		
			C CC _____		
GAM335	FLJ12649	3'	GTGGGGTATGTTTAATTCCTCT 23834	_ T	
			AGAGGAATTAA CAT TTCTAC		
			TCTCCTTAATT GTA GGGGTG		
			T T		
GAM335	FLJ13441	3'	TCTGTAGAAAACGTTAATTT 23399	A	
			GAATTAAC TTTTCTACAGA		
			TTTAATTG AAAAGATGTCT		
			C		
GAM335	MGC2306	3'	TCTGTAAAAAATGTATGCTATC 26357	ATTA_ C	
			CTCT AGAGGA ACATTTT TACAGA		

			TCTCCT	TGTA	AAAA	ATGTCT		
			ATCGTA	A				
GAM335	MGC26684	3'	CTGTATTTCCCTTAATTCCTC	29372		CATTTTC		
			GAGGAATTAA	TACAG				
			CTCCTTAATT	ATGTC				
			CCCTTT_					
GAM335	SCYA28	3'	CTACAGAGACAATTCCTC	21250		AACAT	AC	
			GAGGAATT	TTTCT	AG			
			CTCCTTAA	AGAGA	TC			
			C_	CA				
GAM335	LOC152627	5'	TCCATAGATAGTGATTCCTCT	39298		TAA	T	CA
			AGAGGAAT	CATT	TCTA	GA		
			TCTCCTTA	GTGA	AGAT	CT		
			_	T	AC			
GAM335	LOC153937	5'	TGAAGGAAACACTAATTCCTC	39448		ACA	A	
			GAGGAATTA	TTTTCT	CA			
			CTCCTTAAT	AAAGGA	GT			
			CAC	A				
GAM335	LOC200609	5'	TCCATAGAAATATTTCAATTCC	43335		AACAT_	CA	
			TCT	AGAGGAAT	TTTCTA	GA		
			TCTCCTTAA	AAAGAT	CT			
			CTTTAT	AC				
GAM335	LOC92249	3'	TCTGTAGAAGCCTCTATCTCCT	34025		AT	ACAT	
			CT	AGAGGA	TA	TTTCTACAGA		
			TCTCCT	AT	GAAGATGTCT			
			CT	CTCC				
GAM336	ABCA3	5'	GCTGAGCAACTGAACCT	6745		AAAAG	C	
			AGGT	CAG	TGCTCAGC			
			TCCA	GTC	ACGAGTCG			
			A_	A				
GAM336	BAALC	5'	AGCCGAGCAGCCGCTGGGCGCT	24193		_	AAA	A
			C	GAG	GT	AGC	GCTGCTC	GCT
			CTC	CG	TCG	CGACGAG	CGA	
			G	GG_	C	C		
GAM336	F7	3'	GCTGAGCCTCCTTACCTC	5609		AA	C	CT
			GAGGTA	AG	AG	GCTCAGC		
			CTCCAT	TC	TC	CGAGTCG		
			_	C	_			
GAM336	F7	3'	GCTGAGCCTCCTTACCTC	21238		AA	C	CT
			GAGGTA	AG	AG	GCTCAGC		

CTCCAT TC TC CGAGTCG
 _ C _
 GAM336 GFI1 3' CTGAACAGTTACTTCA 11770 AAAGCA C
 TGAGGTA GCTG TCAG
 ||||| ||| ||||
 ACTTCAT TGAC AGTC
 _ A _
 GAM336 LEF1 3' AGCTGAGCAGCTTTTCTCC 18390 TA GC
 GG AAA AGCTGCTCAGCT
 || ||| ||||| |||||
 CC TTT TCGACGAGTCGA
 TC _
 GAM336 NR1I2 5' AGCACTGCCTTTACTTCA 9971 A C
 TGAGGTAAA GCAG TGCT
 ||||| ||| ||||
 ACTTCATTT CGTC ACGA
 C _
 GAM336 SLC21A2 3' AGCTTCCCTCAGCTCTTACCTC 12156 AA C CTC_
 A TGAGGTA AG AGCTG AGCT
 ||||| || |||| ||||
 ACTCCAT TC TCGAC TCGA
 _ _ TCCCT
 GAM336 BCAA 3' TGAAGTCTTTTCTCA 18513 T CTGC
 TGAGG AAAAGCAG TCA
 |||| ||||| |||
 ACTCC TTTTCGTC AGT
 _ A _
 GAM336 C20orf139 3' AGCTAAGGTCAGCTGTTACCTC 41104 AAA _ C_
 A TGAGGTA GCAGCTG CT AGCT
 ||||| ||||| || ||||
 ACTCCAT TGTCGAC GG TCGA
 _ T AA
 GAM336 CHST3 3' TGGAAGCTGCTCTTTACCTCA 10486 _ GC
 TGAGGTAAA AGCAGCT TCA
 ||||| ||||| |||
 ACTCCATTT TCGTCGA GGT
 C A_
 GAM336 DKFZP434D146 3' GCTGAGCAGTTCACTTCA 17872 AAAAGC
 TGAGGT AGCTGCTCAGC
 ||||| ||||| |||||
 ACTTCA TTGACGAGTCG
 C _
 GAM336 DKFZP434H132 3' AGCTAAGCAGCTGCTGGGACTC 17761 GTAAA C
 A TGAG AGCAGCTGCT AGCT
 ||| ||||| |||||
 ACTC TCGTCGACGA TCGA
 AGGG_ A
 GAM336 FLJ13902 3' AGCCGAGACCAGCCTTTTACCT 23951 CA _ A
 C GAGGTAAAAG GCTG CTC GCT
 ||||| ||| ||| |||

CTCCATTTTC CGAC GAG CGA
 _ CA C
 GAM336 FLJ14936 3' AGCTGAGCAACTGGAGCCTCG 26042 AAAAG C
 TGAGGT CAG TGCTCAGCT
 ||||| || |||||
 GCTCCG GTC ACGAGTCGA
 AG_ A
 GAM336 FLJ20337 3' AGCTGAGCAGCTGGAGCC 19392 AAAAG
 GGT CAGCTGCTCAGCT
 || |||||
 CCG GTCGACGAGTCGA
 AG_
 GAM336 FLJ20689 3' AGCTGTATTGTATTTTACCTCA 19702 _ CTGCT
 TGAGGTAAAA GCAG CAGCT
 ||||| || ||||
 ACTCCATTTT TGTT GTCGA
 A AT_
 GAM336 FLJ20689 3' AGCTGTATTGTATTTTACCTCA 19598 _ CTGCT
 TGAGGTAAAA GCAG CAGCT
 ||||| || ||||
 ACTCCATTTT TGTT GTCGA
 A AT_
 GAM336 KIAA0009 3' GAAAGCTGCTTTCACGTCA 16023 G A GC
 TGA GT AAAGCAGCT TC
 || || ||||| ||
 ACT CA TTTCGTCGA AG
 G C A_
 GAM336 LBP-9 3' GCTGGTACCTTTACCTC 15877 AAGC C T
 GAGGTAA AG TGC CAGC
 ||||| || || ||||
 CTCCATT TC ATG GTCG
 _ C _
 GAM336 MGC26684 3' AGCCAAGCAGCTGCCTTCCTT 29371 TAAAA CA
 GAGG GCAGCTGCT GCT
 || ||||| ||
 TTCC CGTCGACGA CGA
 TTC_ AC
 GAM336 MGC26744 5' AGCGCGCTCTTACCTCA 29471 A A T
 TGAGGTAA AGC GC GCT
 ||||| || || ||||
 ACTCCATT TCG CG CGA
 C _ _
 GAM336 PRC1 3' AGCCACGCTGTTTACCTCA 10119 AA T_
 TGAGGTAA GCAGC GCT
 ||||| || || ||||
 ACTCCATT TGTCG CGA
 _ CAC
 GAM336 SLC11A2 3' AGCTGCTGCTTTTACTTCA 6222 T
 TGAGGTAAAAGCAGC GCT
 ||||| ||||| ||||

ACTTCATTTTCGTCTCG CGA
 T
 GAM336 VRP 5' GCTGAGCCATTCTCCTCA 13925 TAAA C CT
 TGAGG AG AG GCTCAGC
 |||| ||| |||||
 ACTCC TC TT CGAGTCG
 ____ _ AC
 GAM336 LOC112840 3' AGCTATCCTTTTGCCTTTACCT 27955 A CTGCTC
 CA TGAGGTAAA GCAG AGCT
 ||||| ||| |||
 ACTCCATTT CGTT TCGA
 C TTCCTA
 GAM336 LOC122970 5' AGCCTGGCTACTTTTGCCTCA 36713 C ____
 TGAGGTAAAAG AGCT GCT
 ||||| ||| |||
 ACTCCGTTTTTC TCGG CGA
 A TC
 GAM336 LOC145955 5' AGTGCTCTCTTACCTCA 40641 A C T
 TGAGGTAA AG AGC GCT
 ||||| || ||| |||
 ACTCCATT TC TCG TGA
 C _ _
 GAM336 LOC146481 3' AGCTGGGTGCACCCTGACCCCA 38174 A AAAAGCA T
 TG GGT GC GCTCAGCT
 || ||| || |||||
 AC CCA CG TGGGTCTGA
 C GTCCCA_ _
 GAM336 LOC146957 3' GCTGAGCTCTCACCTCA 38280 AAAAGC CT
 TGAGGT AG GCTCAGC
 |||| || |||||
 ACTCCA TC CGAGTCG
 C_ _ T_
 GAM336 LOC204084 5' AGCTGAGCAACCGCTCTGTCT 43083 GT AA AGC
 AG A AGC TGCTCAGCT
 || | ||| |||||
 TC T TCG ACGAGTCGA
 TG C_ CCA
 GAM336 LOC253841 5' AGCCCCAGCTGCTCCTCCTCA 46091 TAAA CTCA
 TGAGG AGCAGCTG GCT
 |||| ||||| |||
 ACTCC TCGTCGAC CGA
 TCC_ CC_
 GAM336 LOC254173 3' AGCTGGGTTACTTTGACCTCA 46287 A CAGCT
 TGAGGT AAAG GCTCAGCT
 |||| ||| |||||
 ACTCCA TTTC TGGGTCTGA
 G AT_
 GAM337 CPNE3 3' TCTCTGCAATGCCTCAAGG 9997 A CATAA
 CC TG GCATTGCAGAGA
 || || |||||

			GG AC CGTAACGTCTCT		
			A TC__		
GAM337	DYT1	3'	CAAGCACACATGCATGGCA 5577	AA__ A	
			TGCCATGCAT GC TTG		
			ACGGTACGTA CG AAC		
			CACA _		
GAM337	GALGT	3'	TCTCTGCAATGCTGTGGGCA 7214	ATG A	
			TGCC CATA GCATTGCAGAGA		
			ACGG GTGT CGTAACGTCTCT		
			__ _		
GAM337	RTN1	3'	TCTCTGCAATGCTTCTGTAGC 22110	CA T	
			GC TGCA AAGCATTGCAGAGA		
			CG ATGT TTCGTAACGTCTCT		
			_ C		
GAM337	SFRP1	3'	TCTCTGCAACACTTTGAGGACA 8934	_ ATG T CA	
			TG CC CA AAG TTGCAGAGA		
			AC GG GT TTC AACGTCTCT		
			A A__ _ AC		
GAM337	CALN1	3'	CTCTGCAAGTGCTACTGGCA 25514	TGCATA _	
			TGCCA AGCATT GCAGAG		
			ACGGT TCGTGA CGTCTC		
			CA__ _ A		
GAM337	DNAM-1	3'	TCTTATGTACTCATGCATGG 13341	A CAT _	
			CCATGCAT AG TGCA GAGA		
			GGTACGTA TC ATGT TTCT		
			C __ A		
GAM337	EZFIT	3'	TCCCTGCAGTGCACGCTGGCA 22198	T ATAA A	
			TGCCA GC GCATTGCAG GA		
			ACGGT CG CGTGACGTC CT		
			_ CA__ C		
GAM337	KIAA1500	3'	CTCTTCTGATGCATGGCA 32065	A CATTGC	
			TGCCATGCAT AG AGAG		
			ACGGTACGTA TC TCTC		
			G T__		
GAM337	SEF	3'	CTTCCAAGCACATGCATGGCA 34426	AA A CA	
			TGCCATGCAT GC TTG GAG		
			ACGGTACGTA CG AAC TTC		
			CA _ C_		
GAM337	SEZ6	5'	CTCCAGGGCCCAGCATGGCA 36773	ATAA A CA	
			TGCCATGC GC TTG GAG		

ACGGTACG CG GAC CTC
 ACC_ G _
 GAM337 LOC221477 3' TCTCTGTGGGTCTCATGAACAG 44260 CATG A CA TG
 CA TGC CAT AG T CAGAGA
 ||| ||| || | |||||
 ACG GTA TC G GTCTCT
 ACAA C TG GT
 GAM337 LOC50999 3' CTCTGCAACACTTGCAGAACA 18116 CCA TA CA
 TG TGCA AG TTGCAGAG
 || ||| || |||||
 AC ACGT TC AACGTCTC
 AAG _ AC
 GAM338 NFYC 3' ACAGCTGCTACCCCCAAGA 15492 TA AAC CT
 TCTT GG GTG CAGCTGT
 ||| || ||| |||||
 AGAA CC CAT GTCGACA
 CC _ C_
 GAM338 KIAA0042 3' TTGAGCAGTTCCTAAAGA 17014 G
 TCTTTAGGAAC TGCTCAG
 ||||| |||||
 AGAAATCCTTG ACGAGTT
 _
 GAM338 KIAA0322 3' AACAGCTGCAGGCTCCAAAGA 44559 A ACGT _
 TCTTT GGA GCT CAGCTGTT
 |||| || ||| |||||
 AGAAA CCT CGG GTCGACAA
 _ _ _ AC
 GAM338 LOC115400 5' TTGAGCACATCCCAAAAGA 36348 A AAC
 TCTTT GG GTGCTCAG
 |||| || |||||
 AGAAA CC CACGAGTT
 A CTA
 GAM338 LOC51701 3' TTGAGCCATTCCTAAAGA 18346 CGT
 TCTTTAGGAA GCTCAG
 ||||| |||||
 AGAAATCCTT CGAGTT
 AC_
 GAM339 KCNQ1 3' GCAAGCTTTTCCTAATA 5723 C
 TATTAGG AAAAGCTTGC
 ||||| |||||
 ATAATCC TTTTCGAACG
 _
 GAM339 PTGIS 3' CATTGAGCAGTCAGTCCCCCA 6667 A CAAAA_ T
 TA TATT GG GCT GCTGAATG
 ||| || ||| |||||
 ATAA CC TGA CGACTTAC
 C CCTGAC _
 GAM339 HSPC065 3' CATTGAGCAAAAGCCCTGA 15450 CAAAA _
 TTAGG GCT TGCTGAATG
 |||| ||| |||||

AGTCC CGA ACGACTTAC
 _____ AA
 GAM339 LOC148760 3' TCAGCAAGCCTTGTTG 40898 G AA
 TAG CAA GCTTGCTGA
 ||| ||| |||||
 GTT GTT CGAACGACT
 G C_

GAM339 LOC221773 3' ATTCAACAAGCACCTAGTA 43761 CAAAA C
 TATTAGG GCTTG TGAAT
 ||||| ||||| |||||
 ATGATCC CGAAC ACTTA
 A_____ A

GAM339 LOC51696 3' CATTCAGCAAGCTCCTGA 18310 CAAA
 TTAGG AGCTTGCTGAATG
 ||||| |||||
 AGTCC TCGAACGACTTAC

GAM340 AQP6 5' AAAAGCCAGGGTCAGCCA 27610 AA A
 TGGC GATCCTG CTTT
 ||| ||||| |||||
 ACCG CTGGGAC GAAAA
 A_ C

GAM340 MAPRE3 3' GTAAAGTACATGCCATG 14717 AGATCC _
 CATGGCA TG ACTTTTAC
 ||||| || |||||
 GTACCGT AC TGAAAATG
 _____ A

GAM340 RAB23 3' GGTAACCTTAAATCTTGCCA 18401 CCTGACT
 TGGCAAGAT TTTACC
 ||||| |||||
 ACCGTTCTA AAATGG
 AATTCCC

GAM340 APOL4 3' GTAAAAGTCTCGTTGCTCAT 24976 _ _ TCCT
 ATG GCAA GA GACTTTTAC
 ||| ||| || |||||
 TAC CGTT CT CTGAAAATG
 T G _____

GAM340 DKFZP564G092 5' GTAGAGACAGGATTTACCATG 17876 CA AC
 CATGG AGATCCTG TTTTAC
 ||||| ||||| |||||
 GTACC TTTAGGAC GAGATG
 AC A_

GAM340 FLJ00001 3' AGCAGGACCTTGTCATG 39771 A A
 CATGGCAAG TCCTG CT
 ||||| ||||| |||||
 GTACTGTTC AGGAC GA
 C _

GAM340 FLJ10846 3' GTAGAGACAGGGTCTCACCATG 20200 CA AC
 CATGG AGATCCTG TTTTAC
 ||||| ||||| |||||

			GTACC TCTGGGAC GAGATG		
			AC A_		
GAM340	FLJ11539	3'	GGCAAAAGCGTAGATCTTGTCA 24088	C_ A A	
			TGGCAAGATC TG CTTTT CC		
			ACTGTTCTAG GC GAAAA GG		
			AT _ C		
GAM340	GGA2	3'	GTAGAGACAGGATTTACCATG 28922	CA AC	
			CATGG AGATCCTG TTTTAC		
			GTACC TTTAGGAC GAGATG		
			AC A_		
GAM340	GGA2	3'	GTAGAGACAGGATTTACCATG 17401	CA AC	
			CATGG AGATCCTG TTTTAC		
			GTACC TTTAGGAC GAGATG		
			AC A_		
GAM340	KIAA0903	3'	AAAAGTCTGTCTTGCCA 35365	CCT	
			TGGCAAGAT GACTTTT		
			ACCGTTCTG CTGAAAA		
			T_		
GAM340	KIAA1546	3'	AGAGGTTATCTTACCAT 33712	C CCT	
			ATGG AAGAT GACTTTT		
			TACC TTCTA TTGGAGA		
			A _		
GAM340	LOXL4	3'	AGTCATCCCTGAATCTTGCCA 25928	_ C_	
			TGGCAAGAT C TGA		
			ACCGTTCTA G ACTGA		
			A TCCCT		
GAM340	STK17B	5'	GTAAAAGTGATCCTGCCA 10421	A TG	
			TGGCA GATCC ACTTTTAC		
			ACCGT CTAGG TGAAAATG		
			C _		
GAM340	TUSP	5'	AAAAGAAACAAAATCTTGCCA 21518	CC A_	
			TGGCAAGAT TG CTTTT		
			ACCGTTCTA AC GAAAA		
			AA AAA		
GAM340	LOC169611	3'	GTAGAGACAGGATTTACCATG 40285	CA AC	
			CATGG AGATCCTG TTTTAC		
			GTACC TTTAGGAC GAGATG		
			AC A_		
GAM341	GAB2	5'	CCTTTGGTATCATCATGAAA 14649	_ TT	
			TTTCATGATGA ATT GGG		

AAAGTACTACT TGG TCC
 A TT
 GAM341 GHR 3' CTTTTCCCAAATGTTGAAA 5674 TGATGA
 TTTCA ATTTTGGGAAAAG
 |||| ||||||||
 AAAGT TAAAACCCTTTTC
 TG____
 GAM341 GJA1 3' TTTTTTAAACTCATCACAGAA 5681 A_ A
 TTC TGATGA TTTTGGGAAA
 || |||| ||||||||
 AAG ACTACT AAAATTTTTT
 AC C
 GAM341 HCFC1 3' CCCAAATCGTCATGGAA 35156 AT
 TTTTCATGATGA TTTGGG
 |||||||| ||||
 AAGGTACTGCT AAACCC
 —
 GAM341 NTRK2 3' TTTTCCCATCACCAGAAA 12850 A A ATTT
 TTTC TG TGA TGGGAAAA
 ||| || |||||
 AAAG AC ACT ACCCTTTT
 _ C _
 GAM341 PSMD5 3' CTTTCCCCAAGAATTATCATGG 11480 A A
 AA TTTTCATGATGA TTTTGGG AAAG
 |||||||| ||||| |||
 AAGGTACTATT AGAACCC TTTC
 A C
 GAM341 RDS 3' CTTCCCCCAAGATACCCATCTT 5864 T A_ AA
 GAAA TTTCA GATG ATTTTGGG AAG
 |||| ||| |||||| |||
 AAAGT CTAC TAGAACCC TTC
 T CCA CC
 GAM341 TMEPAI 3' TTTCCCAAAAATGAAA 21408 GATGAA
 TTTTCAT TTTTGGGAAA
 |||| ||||||||
 AAAGTA AAAACCCTTT
 —
 GAM341 TRIM9 3' CCAAGAAATTCACCATGAAA 17513 A G_
 TTTTCATG TGAATTTT GG
 |||||| |||||| ||
 AAAGTAC ACTTAAAG CC
 C AA
 GAM341 BPESC1 3' CTTTTCCCTCCACCATGAAG 22375 A AATTTT
 TTTTCATG TG GGGAAAAG
 |||||| || ||||||
 GAAGTAC AC CCCTTTTC
 C CT____
 GAM341 C1orf22 3' CCCATGCCAAATTCATCATGAA 24836 _____
 G TTTTCATGATGAATTT TGGG
 |||||||||| |||

GAAGTACTACTTAAA ACCC
CCGT

GAM341 FLJ14075 3' CTTTCCCCACGGCTTTAATCAT 24375 _ _ TT A
GAAA TTTTCATGAT GAA T TGGG AAAG
||||||| ||| | ||| |||
AAAGTACTA TTT G ACCC TTTC
A C GC C

GAM341 KIAA0852 5' CTTTCCCCAAAATTTCCACAGA 17249 A AT_ A
AA TTTC TG GAATTTTGGG AAAG
|||| | ||||||| |||
AAAG AC TTAAAAACCC TTTC
_ ACC C

GAM341 KIAA1203 3' CTAAATAACTATCATGAAA 35469 A__
TTTCATGATG ATTTTGGG
||||||| |||||||
AAAGTACTAT TAAATTC
CAA

GAM341 MAP3K2 3' TCCCAAAATGTCAGAA 13387 A GA
TTC TGAT ATTTTGGGA
||| ||| |||||||
AAG ACTG TAAAACCT

GAM341 ROBO4 3' TCCCAACCTCACCATGGAA 21136 A ATT
TTTCATG TGA TTGGGA
||||||| ||| |||||||
AAGGTAC ACT AACCCT
C CC_

GAM341 SE70-2 5' TCCTACTCATCATGGAA 22665 ATTT
TTTCATGATGA TGGGA
||||||||| |||||
AAGGTACTACT ATCCT
C__

GAM341 TTY7 3' TTTCCCCCATCATGAAA 25674 AATTTT
TTTCATGATG GGGAAA
||||||||| |||||||
AAAGTACTAC CCCTTT
C_____

GAM341 LOC130074 3' CTAAAGCTCATCATGAAA 37472 A
TTTCATGATGA TTTTGGG
||||||||| |||||||
AAAGTACTACT GAAATTC
C

GAM341 LOC152457 3' CCCAGAGAAATTCACCATGA 39278 A ____
TCATG TGAAT TTTGGG
||||| ||||| |||||||
AGTAC ACTTA AGACCC
C AAG

GAM341 LOC170106 5' CTTTGGCTGGAATTGATCATG 40174 G TG G_
AAA TTTCATGAT AATTT G AAAAG
||||||||| ||||| | |||||

AAAGTACTA TTAAG C TTTTC
 G GT GG
 GAM341 LOC200860 3' TTCCCAGCCTCATGAAA 43358 TGAATT
 TTTCATGA TTGGGAA
 ||||| |||||
 AAAGTACT GACCCTT
 CC____
 GAM341 LOC221300 3' TTCCTTTTCTCATGAAA 44149 T TTTT
 TTTCATGA GAA GGGAA
 ||||| || |||||
 AAAGTACT CTT TCCTT
 _ T____
 GAM341 LOC90161 3' CTTCTCCCAAAGCGCCACTGAA 30903 _ A AA A
 A TTTCA TG TG TTTTGGGA AAG
 |||| || || ||||| |||||
 AAAGT AC GC GAAACCCT TTC
 C C _ C
 GAM342 MPP2 3' AAGTTTCTCCAGATTTCT 30078 A
 AGAGATCT GAGAACTT
 ||||| |||||
 TCTTTAGA CTCTTTGAA
 C
 GAM342 RPP30 5' AGTAAGTTTCTCCGAATCCCT 13121 A CTA G
 AG GAT GAGAACTTA CT
 || ||| ||||| ||||| ||
 TC CTA CTCTTTGAAT GA
 C AGC _
 GAM342 TACSTD2 3' AAGTCCCTCCAGATTTCT 8158 A AA
 AGAGATCT GAG ACTT
 ||||| || |||||
 TCTTTAGA CTC TGAA
 C CC
 GAM342 GRIN3A 3' AGCTCACTCTCTAGGTCTC 28529 AACTT
 GAGATCTAGAGA AGCT
 ||||| ||||| |||||
 CTCTGGATCTCT TCGA
 CAC____
 GAM342 P5-1 3' AGGTTCTCCAGATCTCT 13494 A A
 AGAGATCT GAGAA CTT
 ||||| ||||| |||||
 TCTCTAGA CTCTT GGA
 C _
 GAM342 POLD3 3' TAAGTTCATCTAGATCTC 44054 GA
 GAGATCTAGA AACTTA
 ||||| ||||| |||||
 CTCTAGATCT TTGAAT
 AC
 GAM342 LOC147639 3' GGCTTTCTCTAAATCCT 38347 A C ACTT
 AG GAT TAGAGAA AGCT
 || ||| ||||| |||||

			TC CTA ATCTCTT	TCGG		
			— A —			
GAM342	LOC154282	3'	AGACTACCTCTCTAGATTTCT	41696	AACT	—
			AGAGATCTAGAGA	TAG CT		
			TCTTTAGATCTCT	ATC GA		
			CC— A			
GAM343	IER5	3'	AGCTAGACCCGCTTCA	18611	AAT	TGCG
			TGAGGCG	GT CTAGCT		
			ACTTCGC	CA GATCGA		
			C—			
GAM343	LOC149535	3'	AAAGCTAGCACAAACGGAGCTCA	38770	G GAA	C
			TGAG C	TGTTG GCTAGCTTT		
			ACTC G	GCAAC CGATCGAAA		
			— AG— A			
GAM344	FLT1	3'	GCCCAGCAAATAGTGAT	7766	C	C
			ATCACTAT	TGCTG GGT		
			TAGTGATA	ACGAC CCG		
			A —			
GAM344	BLCAP	3'	ACCTGGGGCAGATAAAATGC	13518	CAC	G T
			GCAT	TATCTGCT CGG GT		
			CGTA	ATAGACGG GTC CA		
			AA— G —			
GAM344	KIAA0711	3'	ACACCACAGTTCTGAATAGTGA	16954	CT—	C
		T	ATCACTAT	GCTG GGTGT		
			TAGTGATA	TGAC CCACA		
			AGTCT	A		
GAM344	LOC135293	3'	ACCTTCACAGTAGTGAT	37491	T C C—	
			ATCACTA	CTG TG GGT		
			TAGTGAT	GAC AC CCA		
			— — TT			
GAM344	LOC222962	3'	ACCACAGCAGTGATGC	44625	ATCT	C
			GCATCACT	GCTG GGT		
			CGTAGTGA	CGAC CCA		
			— A			
GAM344	LOC92973	5'	ACACCGCAACAGAATGAT	35183	CTA	C
			ATCA	TCTG TGCGGTGT		
			TAGT	AGAC ACGCCACA		
			A— A			
GAM345	ARNT2	3'	ATAGCTGTGTTCTGATCCCA	16933	A	CTGTAG
			TGG ATCAGG	ACAGCTAT		

			ACC TAGTCC	TGTCGATA		
			C	TTG__		
GAM345	RALBP1	3'	ATAGCTGTGATTACCCACCC	13657	AATCA C TAG_	
	CA		TGG	GG TG ACAGCTAT		
			ACC	CC AC TGTCGATA		
			CCAC_	C TTAG		
GAM345	CSR1	3'	AGCTGTGGTCCTCTGATTCCA	18356	CTGTAG	
			TGGAATCAGG	ACAGCT		
			ACCTTAGTCT	TGTCGA		
			CCTGG_			
GAM345	KIAA0601	3'	ATAGCTGTGAATACCCGCTCCA	31326	ATCA C AG	
			TGGA	GG TGT ACAGCTAT		
			ACCT	CC ATA TGTCGATA		
			CG_	C AG		
GAM345	KIAA1505	5'	GTCTCAGCCTGATCCCA	45193	A	T
			TGG	ATCAGGCTG AGAC		
			ACC	TAGTCCGAC TCTG		
			C	_		
GAM345	MR	5'	GTCTACAGCCTGACCCA	25256	AA	
			TGG	TCAGGCTGTAGAC		
			ACC	AGTCCGACATCTG		
			C_			
GAM345	PTK6	5'	AGCTGTGCTGCCCTGATTCCA	12596	_ T A	
			TGGAATCAGG	C GT GACAGCT		
			ACCTTAGTCC	G CG CTGTCGA		
			C T	_		
GAM345	SPTLC2	3'	AGTTTAACACAGCCTGATTG	11272	AGAC	
			GAATCAGGCTGT	AGCT		
			CTTAGTCCGACA	TTGA		
			CAAT			
GAM345	UBXD2	3'	CTGCCACAGCCTGCCTCCA	33912	AT	AGA
			TGGA	CAGGCTGT CAG		
			ACCT	GTCCGACA GTC		
			CC	CC_		
GAM345	LOC112868	3'	AGCCTCCAGCCTGACCCCA	36075	AA	T ACA
			TGG	TCAGGCTG AG GCT		
			ACC	AGTCCGAC TC CGA		
			CC	C _		
GAM345	LOC256176	5'	ATAGCATAGGCAGCCTGACTCC	46169	A	AGACA
	A		TGGA	TCAGGCTGT GCTAT		

ACCT AGTCCGACG CGATA
 C GATA_
 GAM346 MYO1D 3' ACACTCATAGTTTTGCCA 35548 AG _
 TGGCAAGA GT AGTGT
 ||||| || ||||
 ACCGTTTT TA TCACA
 GA C
 GAM346 OGN 3' GTGCACACTACCTTCCCA 23655 CAA _
 TGG GAAGGTAGTGT CAC
 || ||||| ||||
 ACC CTTCCATCACA GTG
 C
 GAM346 OGN 3' GTGCACACTACCTTCCCA 26899 CAA _
 TGG GAAGGTAGTGT CAC
 || ||||| ||||
 ACC CTTCCATCACA GTG
 C
 GAM346 OGN 3' GTGCACACTACCTTCCCA 15275 CAA _
 TGG GAAGGTAGTGT CAC
 || ||||| ||||
 ACC CTTCCATCACA GTG
 C
 GAM346 FLJ20898 3' TGGCGCCTGCCTTCTGGCCA 23852 A _
 TGGC AGAAGGTAG TGTCA
 |||| ||||| ||||
 ACCG TCTTCCGTC GCGGT
 G C
 GAM346 FLJ30058 3' ATTGGTGTTTACACCCTCTTGT 29581 A A T_
 CA TGGCAAGA GGT GTG CACCAAT
 ||||| || || |||||
 ACTGTTCT CCA CAT GTGGTTA
 C _ TT
 GAM346 KIAA0903 3' TGATAAAAAGTCTGTCTTGCCA 35370 A TAG_
 TGGCAAGA GG TGTCA
 ||||| || ||||
 ACCGTTCT TC ATAGT
 G TGAAAA
 GAM346 MNAB 5' TGGTGACACTTGTAAGTGTCA 20822 AGAAGGT
 TGGCA AGTGTACCA
 |||| |||||
 ACTGT TCACAGTGGT
 CAAATGT
 GAM346 SCYD1 3' TGGTGACATGTCTTTTCTTGC 43714 TA_
 GCAAGAAGG GTGTCACCA
 ||||| |||||
 CGTTCTTTT TACAGTGGT
 CTG
 GAM346 LOC146445 3' TGGTGACACCAGGTCTGTCCA 40700 CA AGGTA
 TGG AGA GTGTCACCA
 || || |||||

ACC TCT CACAGTGGT
 TG GGAC_
 GAM346 LOC221103 5' TGGCAACCTGCCTTCTGGCCA 44780 A T CA
 TGGC AGAAGGTAG GT CCA
 |||| ||||| || |||
 ACCG TCTTCCGTC CA GGT
 G _ AC
 GAM347 PTPN2 3' CACAAGCCCAACATCTCA 8705 CGCCGAC T
 TGAGAT GG GTTTGTG
 ||||| || |||||
 ACTCTA CC CGAACAC
 CAA_____
 GAM347 C20orf108 3' CACAAACAGCTAAGACAATCTC 28081 CGCCGAC _
 A TGAGAT GG TGT TTGTG
 ||||| || |||||
 ACTCTA TC ACAAACAC
 ACAGAA_ G
 GAM347 KIAA0884 3' ACACCGTCAGCAATCCA 34773 A C C
 TG GAT GC GACGGTGT
 || ||| || |||||
 AC CTA CG CTGCCACA
 _ A A
 GAM347 PPP1R16B 3' CACAGGCATCAGCAGTCCCA 30765 A C CGAC
 TG GAT GC GGTGTTTGTG
 || ||| || |||||
 AC CTG CG CTACGGACAC
 C A A____
 GAM347 LOC144100 3' ACACCGTCAGCGCTCCCA 37676 A T C
 TG GA CGC GACGGTGT
 || ||| || |||||
 AC CT GCG CTGCCACA
 C C A
 GAM347 LOC145138 5' CACAGCCCCTCGGCGATCTCA 40503 C T T
 TGAGATCGCCGA GG GTT GTG
 ||||| || ||| |||
 ACTCTAGCGGCT CC CGA CAC
 C _ _
 GAM347 LOC151234 3' CACAAACACCTCCATCTCA 39079 CGCC C
 TGAGAT GA GGTGTTTGTG
 ||||| || |||||
 ACTCTA CT CCACAAACAC
 C_____
 GAM348 KIAA0828 3' TTCAGATCTTTGTACCTTA 39517
 TGAGGTACAAAGATCTGAA
 |||||
 ATTCCATGTTTCTAGACTT
 GAM348 LOC157909 5' CAATCCTTTTCTGTACCTCA 39678 AA TCT A
 TGAGGTACA GA GA GATTG
 ||||| || || |||

ACTCCATGT CT TT CTAAC
 _ TT_ C
 GAM349 IDH3A 3' TTCATTTTCACTGGATACAT 12053 C TGCC
 GTG ATCCAGTGA AATGAA
 ||| ||||| |||||
 TAC TAGGTCAC T TACTT
 A T_ _
 GAM349 LPIN1 3' TTCATTGTGTTGTACTGGATGC 33470 AT _
 A TGCATCCAGTG GC CAATGAA
 ||||| || |||||
 ACGTAGGTCAT TG GTTACTT
 GT T
 GAM349 LPP 5' TTTCATTGTTCCACTGGACGC 12108 A AT C
 GC TCCAGTG GC AATGAAA
 || ||||| || |||||
 CG AGGTCAC TG TTACTTT
 C CT _
 GAM349 RS1 3' TCATTGGCACTTAGAGCGC 5879 A CAG _
 GTGC TC TGA TGCCAATGA
 ||| || ||| |||||
 CGCG AG ATT ACGGTTACT
 _ _ C
 GAM349 RXRA 3' TCACTGGCCTTGCTGGAGGCAC 8873 A TG T A
 GTGC TCCAG A GCCA TGA
 ||| |||| | ||| |||
 CACG AGGTC T CGGT ACT
 G GT C C
 GAM349 C6orf32 5' CATTACATCTGGATGTAC 17994 GT CC
 GTGCATCCA GATG AATG
 ||||| ||| |||
 CATGTAGGT CTAC TTAC
 _ A_
 GAM349 FLJ12221 3' TCACCTGCTAGTCACTGGACGT 31346 A _ CAA
 AC GTGC TCCAGTGAT GC TGA
 ||| ||||| || |||
 CATG AGGTCAC TG CG ACT
 C AT TCC
 GAM349 FLJ20986 5' TTGGCATCACCGGTGCAC 23731 T A
 GTGCA CC GTGATGCCAA
 |||| || |||||
 CACGT GG CACTACGGTT
 _ C
 GAM349 HUMAGCGB 5' TTCATTGGTAACCTGGACCAC 14957 CA TGA
 GTG TCCAG TGCCAATGAA
 || |||| |||||
 CAC AGGTC ATGGTTACTT
 C_ CA_
 GAM349 KIAA0831 3' TTTCATTATTTTGCCTGGATC 17211 C ATGCC_
 CAC GTG ATCCAGTG AATGAAA
 ||| ||||| |||||

			CAC TAGGTCAC	TTACTTT	
			C	GTTTTA	
GAM349	LOC129607	3'	CATTGAACTGGATGCAT	36973	GATGC
			GTGCATCCAGT	CAATG	
			TACGTAGGTCA	GTTAC	
			A		
GAM349	LOC150819	5'	CATGGTCACAGGATGCAC	41246	A AT A
			GTGCATCC GTG	GCCA TG	
			CACGTAGG CAC	TGGT AC	
			A		
GAM349	LOC152905	3'	TTCTACATCACTGGACAC	30334	CA CCAAT
			GTG TCCAGTGATG	GAA	
			CAC AGGTCACTAC	CTT	
				AT	
GAM350	F2RL3	3'	AAACACAGAAGAAACGTGA	10078	CGAAAC
			TCAC	CTTCTGTGTTT	
			AGTG	GAAGACACAAA	
			CAAA		
GAM350	SNX6	5'	AAACTACAGAAGCTTGGTGA	22216	AAC
			TCACCGA	CTTCTGT GTTT	
			AGTGGTT	GAAGACA CAAA	
			C	T	
GAM350	TIAL1	3'	AAACACAGTGAGCCGGGA	22740	A AAAC
			TC CCG	CTT CTGTGTTT	
			AG GGC	GAG GACACAAA	
				C T	
GAM350	TNFSF15	5'	AAACACAGAAGAATAGGGGGA	11597	A_ GAAAC
			TC CC	CTTCTGTGTTT	
			AG GG	GAAGACACAAA	
			GG	ATAA	
GAM350	CALN1	3'	AAACACGTGAACTTTGGTGA	25509	ACC
			TCACCGAA	TTC TGTGTTT	
			AGTGGTTT	AAG GCACAAA	
			C	T	
GAM350	FLJ11053	3'	AACACAGAAGACTTCTGTGA	42775	C AC
			TCAC GAA	CTTCTGTGTT	
			AGTG CTT	GAAGACACAA	
			T	CA	
GAM350	FLJ11273	3'	AACATAATTTTGGTGA	20391	CCTTC
			TCACCGAAA	TGTGTT	

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AGTGGTTTT ATACAA
A____
GAM350 FLJ12700 3' AAACACAGAAGGGGCAGGGA 24411 A GAAA
TC CC CCTTCTGTGTTT
|| || |||||
AG GG GGAAGACACAAA
_ ACGG
GAM350 FLJ21736 3' AAACACAGAATATGGGA 24456 A AAACC
TC CCG TTCTGTGTTT
|| || |||||
AG GGT AAGACACAAA
_ AT__
GAM350 GOLGA3 3' ACCGGAAGGTCCAGGTGA 12513 GAA T
TCACC ACCTTCTG GT
|||| ||||| ||
AGTGG TGAAGGC CA
ACC _
GAM350 GPR64 3' AAATACAGAAACCTCAGTGA 12314 C AACC
TCAC GA TTCTGTGTTT
|||| || |||||
AGTG CT AAGACATAAA
A CCA_
GAM350 HEMGN 5' AAACACAGAATTGAAGGTGG 20498 GAAACC
TCACC TTCTGTGTTT
|||| |||||
GGTGG AAGACACAAA
AAGTT_
GAM350 KIAA1200 3' AAACACAGAAGACTATTTTC 31260 C__
GAAA CTTCTGTGTTT
|||| |||||
CTTT GAAGACACAAA
ATCA
GAM350 KIAA1456 3' AAACACAGGTCATCAGTGA 33260 C AACCT
TCAC GA TCTGTGTTT
|||| || |||||
AGTG CT GGACACAAA
A ACT_
GAM350 KIAA1494 3' ATATAAAGGTTTGGTGA 33960 G C
TCACC AAACCTT TGTGT
|||| ||||| ||||
AGTGG TTTGGAA ATATA
_ _
GAM350 KIAA1508 3' AAACACAGAATTCAGTGA 30992 C ACC
TCAC GAA TTCTGTGTTT
|||| || |||||
AGTG CTT AAGACACAAA
A _
GAM350 MGC5338 5' AAACACAGCTGATTTTCAGTGG 23497 C CCTT
TCAC GAAA CTGTGTTT
|||| || |||||

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			GGTG CTTT GACACAAA		
			A AGTC		
GAM350	NIFU	5'	AGGCGCAAAGCTTCGGTGA 33435	AC	C
			TCACCGAA CTT TGTGTTT		
			AGTGGCTT GAA ACGCGGA		
			C_ _		
GAM350	PB1	3'	AAACACTTGGGTTTGGTGA 19977	G	TCT
			TCACC AAACCT GTGTTT		
			AGTGG TTTGGG CACAAA		
			_ TT_		
GAM350	TA-PP2C	3'	AAACACAGAAGCATGAGTGG 29280	_	AAAC
			TCAC CG CTTCTGTGTTT		
			GGTG GT GAAGACACAAA		
			A AC_		
GAM350	LOC128989	3'	AAACTCTGAGGCTTTGGTGA 36937	A	CTGT
			TCACCGAA CCTT GTTT		
			AGTGGTTT GGAG CAAA		
			C TCT_		
GAM350	LOC150577	3'	AAACACAGAAGGCGGTG 41214	AAA	
			CACCG CCTTCTGTGTTT		
			GTGGC GGAAGACACAAA		

GAM350	LOC256950	3'	CGCCGAAGGCTTTGGTGA 45700	A	T
			TCACCGAA CCTTC GTG		
			AGTGGTTT GGAAG CGC		
			C C		
GAM350	LOC91263	5'	AACACAGAAGACTTCTGTGA 32593	C	AC
			TCAC GAA CTTCTGTGTT		
			AGTG CTT GAAGACACAA		
			T CA		
GAM350	LOC91628	3'	AAACACAGACCTTGGTGA 33161	AACCT	
			TCACCGA TCTGTGTTT		
			AGTGGTT AGACACAAA		
			CC_		
GAM351	NRAS	3'	AAACAGTGTCTTGAGCTCTAA 8359	A	TGCAAC
			TTA AGCTTA CACTGTTT		
			AAT TCGAGT GTGACAAA		
			C TCT_		
GAM351	LOC154739	5'	AGTATTGCATAACTTTAA 41714	C	CC
			TTAAAG TTATGCAA ACT		

			AAT TTC AATACGTT TGA		
			— A—		
GAM351	LOC203276	3'	AGTATTGCATAACTTTAA 43481	C	CC
			TTAAAG TTATGCAA ACT		
			AAT TTC AATACGTT TGA		
			— A—		
GAM351	LOC203305	3'	AGTATTGCATAACTTTAA 43505	C	CC
			TTAAAG TTATGCAA ACT		
			AAT TTC AATACGTT TGA		
			— A—		
GAM351	LOC254243	3'	AGTATTGCATAACTTTAA 46507	C	CC
			TTAAAG TTATGCAA ACT		
			AAT TTC AATACGTT TGA		
			— A—		
GAM351	LOC255870	3'	AAACAGTGATTGAGTTTGTT 45405	TT G C	
			AGC AT CAA CACTGTTT		
			TTG TG GTT GTGACAAA		
			TT A A		
GAM351	LOC90038	3'	AGTATTGCATAACTTTAA 30644	C	CC
			TTAAAG TTATGCAA ACT		
			AAT TTC AATACGTT TGA		
			— A—		
GAM352	AXL	3'	TAGCATCACCATCTGTAAA 7425	CCGA	
			TTTACAG TGATGTTG		
			AAATGTC ACTACGAT		
			TACC		
GAM352	AXL	3'	TAGCATCACCATCTGTAAA 22446	CCGA	
			TTTACAG TGATGTTG		
			AAATGTC ACTACGAT		
			TACC		
GAM352	EIF5	3'	TCCTCAACAGGATGTAAA 7700	G GATGA	
			TTTACA CC TGTGAGGA		
			AAATGT GG ACAACTCCT		
			A _____		
GAM352	FLJ20972	3'	TCCTGTGTCATCAATGTAAA 24627	GCC TG TG	
			TTTACA GATGA T AGGA		
			AAATGT CTACT G TCCT		
			AA_ GT__		
GAM352	LOC200399	5'	TCCTCAACAAAATACTGGC 42812	__ GA	
			GCCG AT TGTTGAGGA		

			CGGT TA ACAACTCCT			
			CA AA			
GAM352	LOC90786	5'	CCCATATCATCAGCTG	32013	C	T A
			CAGC GATGATGT G GG			
			GTCG CTACTATA C CC			
			A _ _			
GAM352	LOC92267	5'	GTCCTCAACAAGCACGAGCTG	34057	_ A A _	
			CAGC CG TG TGTTGAGGAC			
			GTCG GC AC ACAACTCCTG			
			A _ GA			
GAM353	GGA3	3'	ACAAATGTTACACTAGACA	15197	A	C
			TGTCTAGT TAATAT TGT			
			ACAGATCA ATTGTA ACA			
			C A			
GAM353	GGA3	3'	ACAAATGTTACACTAGACA	28900	A	C
			TGTCTAGT TAATAT TGT			
			ACAGATCA ATTGTA ACA			
			C A			
GAM353	RFC1	5'	CTACAGATACTTATGAAGACA	8818	AG	_
			TGTCT TATAA TATCTGTAG			
			ACAGA GTATT ATAGACATC			
			A_ C			
GAM353	C20orf106	3'	ATCCACAGATATTGGGACA	28091	AGTA	A
			TGTCT TAATATCTGT GAT			
			ACAGG GTTATAGACA CTA			
			_ _ C			
GAM353	EREG	3'	ATTGATATTATATTAAACA	7155	C	T
			TGT TAGTATAATATC GT			
			ACA ATTATATTATAG TA			
			A T			
GAM353	KIAA1046	5'	ATCTACTCTTATACTGACA	17217	T	TATCT
			TGTC AGTATAA GTAGAT			
			ACAG TCATATT CATCTA			
			_ CT _			
GAM353	MRPL20	3'	TATCTACAACCCAATAACAGAC	19698	AG	AATATC
	A		TGTCT TAT TG TAGATA			
			ACAGA ATA ACATCTAT			
			CA ACCCA _			
GAM353	NTT73	5'	CTACAGAATACTGGACA	19824	AATA	
			TGTCTAGTAT TCTGTAG			

ACAGGTCATA AGACATC

GAM353 POFUT1 3' ATCCACAGCCTTACACTAGGCA 34884 A TAT A
TGTCTAGT TAA CTGT GAT
||||||| ||| ||| |||
ACGGATCA ATT GACA CTA
C CC_ C

GAM353 LOC146237 3' ACAGATATTAACTGATCA 40664 TC A
TG TAGT TAATATCTGT
|| ||| |||||
AC GTCA ATTATAGACA
TA A

GAM353 LOC148562 3' TATTGGAGAAGATATTCCACTA 38566 AT GTA__
GACA TGTCTAGT AATATCT GATA
||||||| ||||| |||
ACAGATCA TTATAGA TTAT
CC AGAGG

GAM353 LOC200197 3' TGTCTACCAACTAGACA 42732 ATAATATCT
TGTCTAGT GTAGATA
||||||| |||||
ACAGATCA CATCTGT
AC_____

GAM354 MTMR2 3' ACATTATATTGGAATGAA 18242 CC T
TTCA CCA GTATGATGT
||| ||| |||||
AAGT GGT TATATTACA
AA _

GAM354 BIRC1 3' ACTTTCATACATGGATGAA 10880 CC T_
TTCA CCATGTATGA GT
||| ||||| ||| ||
AAGT GGTACATACT CA
A_ TT

GAM354 DAPK2 3' CATCATCACGGGGTGAA 15633 A T
TTCACCCC TG ATGATG
||||||| || |||||
AAGTGGGG AC TACTAC
C _

GAM354 FLJ20128 3' ACTCCAGCACGGGGTGAA 19221 A A AT
TTCACCCC TGT TG GT
||||||| ||| || ||
AAGTGGGG ACG AC CA
C _ CT

GAM354 OR2C3 3' AGTTTACATCGAGCAAAGTGA 37174 CCCA A
TCAC TGT TGATGTAACT
||| ||| |||||
AGTG ACG GCTACATTTGA
AA_ A

GAM354 RAP2B 3' AGTTTTAAATACATGGAAGGAA 45859 ACC GATGT
TTC CCATGTAT AACT
||| ||||| |||

			AAG GGTACATA TTTGA		
			GAA AAT__		
GAM354	RODH-4	3'	AGTCTACACCCTCCCACGGGGT 9806	A TATGA_	A
			GGA TTCACCCC TG TGTA ACT		
			AGGTGGGG AC ACAT TGA		
			C CCTCCC C		
GAM354	LOC151742	3'	CACATATATGAAGTGAA 29241	CC	A
			TTCAC CATGTATG TG		
			AAGTG GTATATAC AC		
			AA _		
GAM354	LOC219529	3'	TTTACATTGTCAGAGTGAA 44675	CCCA T TG	
			TTCAC TG A ATGTAAA		
			AAGTG AC T TACATTT		
			AG__ _GT		
GAM354	LOC90459	3'	TATATCATATAGGGTGAA 31491	CA	
			TTCACCC TGTATGATGTA		
			AAGTGGG ATATACTATAT		
			_		
GAM355	BCL7A	3'	ATTTTCAGAAAATAAAAAATTTCA 21987	ACCCCA	
			TGAAATTTTTG CTGAAAT		
			ACTTTAAAAAT GACTTTA		
			AAAA__		
GAM355	MSR1	3'	TTGGTGGATCAAAAATGCCA 28961	AA	CC TG
			TG ATTTTTGA CCAC A		
			AC TAAAACT GGTG T		
			CG A_ GT		
GAM355	MSR1	3'	TTGGTGGATCAAAAATGCCA 28963	AA	CC TG
			TG ATTTTTGA CCAC A		
			AC TAAAACT GGTG T		
			CG A_ GT		
GAM355	NUP62	3'	AGCGGGATCAAGAATTTCA 18626	C	A
			TGAAATTTTTGA CCC CT		
			ACTTTAAGAACT GGG GA		
			A C		
GAM355	VPS41	3'	ATTTTCAGTGAAGTCATTTTGCT 15736	ATTTT_	CC
			TCA TGAA TGAC CACTGAAAT		
			ACTT ACTG GTGACTTTA		
			CGTTTT AA		
GAM355	KIAA1538	3'	TTCAGAATAGGTCAAAATTC 35435	AT	CCA_
			GAA TTTTGACC CTGAA		

		CTT AAAACTGG GACTT		
		___ ATAA		
GAM355	KIAA1712 3'	ATTCATGCTTGGTCAAAAACA 33538	AA	C___ C
		TCA TGA TTTTGGACC CA TGAAAT		
		ACT AAAAAGTGG GT ACTTTA		
		AC TTC _		
GAM355	KIAA1906 3'	TGGTCTTAAGGCAAAAATTTCA 36232	A	_____
		TGAAATTTTGG CC CCA		
		ACTTTAAAAAC GG GGT		
		_ AATTCT		
GAM355	PEG10 3'	CAGTGGGAGAAAGTTCA 17426	A	GAC
		TGAA TTTT CCCACTG		
		ACTT AAAGA GGGTGAC		
		G _		
GAM355	SLC2A10 3'	TAGTGTAACAAAAATTTCA 25064		ACCC
		TGAAATTTTGG CACTG		
		ACTTTAAAAAC GTGAT		
		AAAT		
GAM355	LOC143153 3'	TCAGTGGGGTTCACCTTCA 37582		ATTTT
		TGAA GACCCCACTGA		
		ACTT TTGGGGTGACT		
		CCAC__		
GAM355	LOC143154 3'	TCAGTGGGGTTCACCTTCA 37588		ATTTT
		TGAA GACCCCACTGA		
		ACTT TTGGGGTGACT		
		CCAC__		
GAM355	LOC144289 5'	TTAGGGGCCAAGAAATTTCA 40398	GAC	A
		TGAAATTTT CCC CTGAA		
		ACTTTAAAGA GGG GATT		
		ACC _		
GAM355	LOC219294 3'	TCAGTGGGGTTCACCTTCA 44689		ATTTT
		TGAA GACCCCACTGA		
		ACTT TTGGGGTGACT		
		CCAC__		
GAM355	LOC219295 3'	TCAGTGGGGTTCACCTTCA 44683		ATTTT
		TGAA GACCCCACTGA		
		ACTT TTGGGGTGACT		
		CCAC__		
GAM355	LOC91170 3'	ATTCAGTGGAGTGAAGTTCA 32479	ATT	G C
		TGAA TTT AC CCACTGAAAT		

			ACTT GAA TG GGTGACTTTA		
			___ G A		
GAM356	CLK2	3'	ACAAGAGAACGAGCCAGAGTT 6971	ATAA	
			AACTCTGGCT CTTTGT		
			TTGAGACCGA GAGAACA		
			GCAA		
GAM356	EIF2C1	3'	ACAAAAGCTGGTTAGGTT 14498	T TAA	
			AAC CTGGCTA CTTTGT		
			TTG GATTGGT GAAAACA		
			_ C _		
GAM356	FLT1	3'	ACAAAAGCAGGCTAGAG 7762	ATAA	
			CTCTGGCT CTTTGT		
			GAGATCGG GAAAACA		
			AC _		
GAM356	HOXD4	3'	ACAAAAGTTAGCCTTAGAGTT 15976	_ TA	
			AACTCT GGCTA ACTTTTGT		
			TTGAGA CCGAT TGAAAACA		
			TT _		
GAM356	MOG	3'	ACAGAATACTAGCCAGAG 8277	TAAC	
			CTCTGGCTA TTTTGT		
			GAGACCGAT AAGACA		
			CAT _		
GAM356	SALL2	3'	ACAAAAGGACCTCCCAGAGTT 31934	CTATAA	
			AACTCTGG CTTTGT		
			TTGAGACC GAAAACA		
			CTCCAG		
GAM356	C20orf130	3'	ACAAAGACTCAGCCAAGAGTT 30933	_ ATAAC	
			AACTCT GGCT TTTTGT		
			TTGAGA CCGA GAAACA		
			A CTCA _		
GAM356	C8orf17	3'	ACAAAACAGAGCAAGAGTT 21505	G ATAAC	
			AACTCT GCT TTTTGT		
			TTGAGA CGA AAAACA		
			A GAC _		
GAM356	CAMKK2	5'	ACAAAAATTAGCCAAGT 13308	C TAAC	
			ACT TGGCTA TTTTGT		
			TGA ACCGAT AAAACA		
			_ TA _		
GAM356	DIM1	3'	ACAAAAGTCACAGTCTGAG 13524	T ATA	
			CTC GGCT ACTTTTGT		

			GAG CTGA TGAAAACA		
			T CAC		
GAM356	ELOVL2	3'	ACAAAAGTAGACCAAAGT 19386	C _	ATA
			ACT TGG CT ACTTTTGT		
			TGA ACC GA TGAAAACA		
			A A _		
GAM356	FLJ14440	3'	ACAAGAGTGCATACCAGA 26530	C A_	
			TCTGG TAT ACTTTTGT		
			AGACC ATA TGAGAACA		
			_ CG		
GAM356	FLJ21687	3'	ACAGAGCCCTACAGCCAGGG 24288	A AC_	
			CTCTGGCT TA TTTTGT		
			GGGACCGA AT GAGACA		
			C CCC		
GAM356	KIAA0798	3'	ACAAAAGTTTCCTGAGT 16065	T CTAT	
			ACTC GG AACTTTTGT		
			TGAG CC TTGAAAACA		
			T T_		
GAM356	KIAA1404	3'	ACAAAATTAGCTGGGCGTT 31047	_ TG	TAAC
			AAC TC GCTA TTTTGT		
			TTG GG CGAT AAAACA		
			C GT TA_		
GAM356	KIAA1456	3'	ACAAAAATTAGCCAGGTT 33261	T	TAAC
			AAC CTGGCTA TTTTGT		
			TTG GACCGAT AAAACA		
			_ TAA_		
GAM356	KIAA1580	5'	ACAGGATATAACCGGAGTT 34404	C AC	
			AACTCTGG TATA TTTTGT		
			TTGAGGCC ATAT AGGACA		
			A _		
GAM356	KIAA1950	3'	ACAAACAGGGCAGCCAGAG 44482	ATAA _	
			CTCTGGCT CT TTTGT		
			GAGACCGA GA AAACA		
			CGG_ C		
GAM356	MYLE	3'	ACAGGAACCCAGCCAGAGTT 15233	ATAAC	
			AACTCTGGCT TTTTGT		
			TTGAGACCGA AGGACA		
			CCCA_		
GAM356	PADI1	3'	ACAAAAGCTAGCCTGGA 31053	_ TAA	
			TCT GGCTA CTTTGT		

			AGG CCGAT GAAAACA		
			T C__		
GAM356	SLC17A6	3'	ACAAAAGTTAAGAAGCCA	21594	A__
			TGGCT TAAC TTTTGT		
			ACCGA ATTGAAAACA		
			AGA		
GAM356	LOC116411	5'	ACAAAAGTTATCAAAGAG	36564	GGCT
			CTCT ATAAC TTTTGT		
			GAGA TATTGAAAACA		
			AAC_		
GAM356	LOC143308	5'	ACAAATTAGAACCAGAGTT	40346	CTA CT
			AACTCTGG TAA TTTGT		
			TTGAGACC ATT AAACA		
			AAG _		
GAM356	LOC145384	3'	ACAAAGGGCTAATAGCCAGA	37860	AA__
			TCTGGCTAT CTTTTGT		
			AGACCGATA GGAAACA		
			ATCG		
GAM356	LOC85479	5'	ACAAAAGTAGGCTAGA	26956	ATA
			TCTGGCT ACTTTTGT		
			AGATCGG TGAAAACA		
			A__		
GAM357	AAT1	3'	AAAAGAAAACAGTAAATGAA	39226	AAAAG
			TTCATTTACTG TCTTTT		
			AAGTAAATGAC AGAAAA		
			AAA__		
GAM357	FACL5	3'	ACTTTTCCAGTAAATGAAG	32106	_
			CTTCATTTACTG AAAAGT		
			GAAGTAAATGAC TTTTCA		
			C		
GAM357	PTPRC	3'	AAGACATAAATGAGGA	28143	CTGAAAA
			TCTTCATTTA GTCTT		
			AGGAGTAAAT CAGAA		
			A_____		
GAM357	PTPRC	3'	AAGACATAAATGAGGA	8717	CTGAAAA
			TCTTCATTTA GTCTT		
			AGGAGTAAAT CAGAA		
			A_____		
GAM357	ZNF146	3'	AAAAGACTTCAAGTAAATATAA	13992	C_ GAA
	GA		TCTT ATTTACT AAGTCTTTT		

			AGAA TAAATGA TTCAGAAAA		
			TA AC_		
GAM357	BZW1	3'	AAAAGACTTTTTTTTAAA 16127 CT		
			TTTA GAAAAGTCTTTT		
			AAAT TTTTTCAGAAAA		
			TT		
GAM357	ENPP4	3'	AAAAGATATAGCAAATGAAGA 17238	A	AAAA
			TCTTCATTT CTG GTCTTTT		
			AGAAGTAAA GAT TAGAAAA		
			C A__		
GAM357	FLJ23056	3'	AAAAGCAGCAGCAAATGAAGA 23806	A	AAAA T
			TCTTCATTT CTG G CTTT		
			AGAAGTAAA GAC C GAAAA		
			C GA__		
GAM357	NUCKS	3'	AAAAGACTCCTTCTCCCAAAGA 22935	ATT	TACT A_
	AGA		TCTTC GAA AGTCTTTT		
			AGAAG CTT TCAGAAAA		
			AAACCCT CC		
GAM357	TSP-NY	3'	AAAAGACTTCTCTGTAAAGA 26302	A	T A
			TC TTTAC GA AAGTCTTTT		
			AG AAATG CT TTCAGAAAA		
			_ T C		
GAM357	LOC151098	5'	AAAACACTCCTCAGTAAATG 39048	AA	C
			CATTTACTGA AGT TTTT		
			GTAAATGACT TCA AAAA		
			CC C		
GAM357	LOC151579	3'	AAAAGACTTTTTTTTAAA 34421	CT	
			TTTA GAAAAGTCTTTT		
			AAAT TTTTTCAGAAAA		
			TT		
GAM357	LOC158476	3'	ACTTCCTCAGTAAAGGAAGA 41995	A	A_
			TCTTC TTTACTGA AAGT		
			AGAAG AAATGACT TTCA		
			G CC		
GAM357	LOC200982	3'	AAGGGGTTTCTAACAAATGAAG 43370	ACT_	AG
	A		TCTTCATTT GAAA TCTT		
			AGAAGTAAA CTTT GGAA		
			CAAT GG		
GAM357	LOC201516	5'	ACTACTCGAGTAAATGAA 42581	_	AA
			TTCATTTACT GA AGT		

AAGTAAATGA CT TCA
 G CA
 GAM357 LOC90593 3' AAAAGGTATCAGTAATTGAAGA 31762 T AAAG
 TCTTCA TTA CTGA TCTTTT
 ||||| ||||| |||||
 AGAAGT AATGACT GGAAAA
 T AT__
 GAM358 DKFZp547C176 3' TCATAATTCAGCATTA 33382 TATCAGT
 TTAATGCTG TTGTGA
 ||||| |||||
 AATTACGAC AATACT
 TT____
 GAM358 FLJ12806 3' CTCAGACTTAATACAGCA 23111 C_ TG
 TGCTGTAT AGTT TGAAG
 ||||| ||| |||||
 ACGACATA TCAG ACTTC
 AT _
 GAM358 LOC222160 5' CTCATTATTTTGATGACAGCA 45166 _ TTT_
 TTAA TTAATGCTGT ATCAG GTGAAG
 ||||| ||||| |||||
 AATTACGACA TAGTT TACTTC
 G TTAT
 GAM358 LOC51696 3' AAACAATACAGCATTA 18304 CA
 TTAATGCTGTAT GTTT
 ||||| |||||
 AATTACGACATA CAAA
 A_
 GAM359 ESRRG 3' ACAGGGTAGAATTAGAGACAAT 32994 AG__ C
 GTTGT GA TCTACCCTGT
 |||| || |||||
 TAACA TT AGATGGGACA
 GAGA A
 GAM359 C1QTNF2 3' ACAGAGCAAGACCCCACTG 25650 A AC ACC_
 TA TACAGTTGT GG TCT CTGT
 ||||| || ||| |||||
 ATGTCAACA CC AGA GACA
 _ CC ACGA
 GAM359 FLJ32865 3' ACAGGGTGTGGACTCAACT 29423 T GA C
 AGTTG AG CT TACCCTGT
 |||| || || |||||
 TCAAC TC GG GTGGGACA
 _ A_ T
 GAM359 JAM1 3' ACAGACCTCCCTACAGCTGTA 29324 ACTCTACC
 TACAGTTGTAGG CTGT
 ||||| |||||
 ATGTCGACATCC GACA
 CTCCA__
 GAM359 JAM1 3' ACAGACCTCCCTACAGCTGTA 29344 ACTCTACC
 TACAGTTGTAGG CTGT
 ||||| |||||

			ATGTCGACATCC	GACA	
			CTCCA__		
GAM359	JAM1	3'	ACAGACCTCCCTACAGCTGTA	29333	ACTCTACC
			TACAGTTGTAGG	CTGT	
			ATGTCGACATCC	GACA	
			CTCCA__		
GAM359	JAM1	3'	ACAGACCTCCCTACAGCTGTA	18857	ACTCTACC
			TACAGTTGTAGG	CTGT	
			ATGTCGACATCC	GACA	
			CTCCA__		
GAM359	LOC160646	3'	ACAGGGTAAAATCCTGCAGC	39999	CTC
			GTTGTAGGA TACCCTGT		
			CGACGTCCT ATGGGACA		
			AAA		
GAM359	LOC201627	3'	CAGGGTAGAAAGACTGTA	42896	GTAGGAC
			TACAGTT TCTACCCTG		
			ATGTCAG AGATGGGAC		
			AA__		
GAM360	NRCAM	3'	AAGACAGTTTATTAGAAATAGC	11447	A TTG
	A		TGCTAT TCTAATG TTGTCTT		
			ACGATA AGATTAT GACAGAA		
			A TT_		
GAM360	UPF3A	3'	GGGATAAACTAGATATAGCA	23276	ATGTTG
			TGCTATATCTA TTGTCTT		
			ACGATATAGAT AATAGGG		
			CA__		
GAM360	UPF3A	3'	GGGATAAACTAGATATAGCA	27987	ATGTTG
			TGCTATATCTA TTGTCTT		
			ACGATATAGAT AATAGGG		
			CA__		
GAM360	KIAA1679	3'	AACTTATCCATGTAGATATAGC	34748	_ TT__
	A		TGCTATATCTA ATG GTT		
			ACGATATAGAT TAC CAA		
			G CTATT		
GAM360	LOC163882	3'	AAGGACATCAGAAATAGCA	39969	A A G
			TGCTAT TCT ATGTT TT		
			ACGATA AGA TACAG AA		
			A C G		
GAM361	LOC149465	3'	CATAATATTATGCATAATA	38759	C C
			TATTATGCG AATAT TGTG		

			ATAATACGT TTATA ATAC		
			A _		
GAM361	LOC90591	3'	CACATGGTATTGCACATGA 31758	C _	
			TTATG GCAATATC TGTG		
			AGTAC CGTTATGG ACAC		
			A T		
GAM362	GNE	3'	ACTTCATCCTGAAGTTTGC 11976	AA C	
			GCAAAT TA GGATGAAGT		
			CGTTTG GT CCTACTTCA		
			AA _		
GAM362	MS4A1	3'	ACTGACATGATATTATTTGC 5631	_ GATGA	
			GCAAATAATA CG AGT		
			CGTTTATTAT GT TCA		
			A ACAG_		
GAM362	TIMP3	3'	TTACTTCACCCCAAGTCCTGCT 5935	_ AATAATAC A	
	GC		GC GCA GG TGAAGTAA		
			CG CGT CC ACTTCATT		
			T CCTGAAC_ C		
GAM362	TRPC5	3'	TTACTTTTCATTATTATTTGC 14851	CGG _	
			GCAAATAATA ATGAA GTAA		
			CGTTTATTAT TACTT CATT		
			_ T		
GAM362	FLJ10511	5'	TACCTCATCCGTAGGTGTG 19900	AATAA A	
			CGCA TACGGATGA GTA		
			GTGT ATGCCTACT CAT		
			GG_ C		
GAM362	IL-17RE	3'	TTACTTCAGTCGCCTCTGCGC 29465	AATAATA GA	
			GCGCA CG TGAAGTAA		
			CGCGT GC ACTTCATT		
			CTCC_ TG		
GAM362	LOC150848	3'	TCACCATATGTTATTTGC 41258	C_ A	
			GCAAATAATA GG TGA		
			CGTTTATTGT CC ACT		
			ATA _		
GAM362	LOC253868	3'	ACTTCATCCGCAGGATTCCAGC 45746	GCA AATA	
			GC AAT CGGATGAAGT		
			CG TTA GCCTACTTCA		
			ACC GGAC		
GAM362	LOC257465	3'	TCACTCCTCATTATTTGTGC 39667	AC _	
			GCGCAAATAAT GGA TGA		

CGTGTTTATTA CCT ACT
CT C

GAM362 LOC93206 3' TTA~~CTTC~~ACCATTTATTGTGC 35519 A TAC A
GCGCAA TAA GG TGAAGTAA
||||| ||| || |||||
CGTGTT ATT CC ACTTCATT
_ TA_ _

GAM363 EGFL5 5' ACACCACTGGGTTTTGGTGTGA 41874 A AGT_ AA
GA TCT CACA AACCCAGT TGT
||| ||| ||||| |||
AGA GTGT TTGGGTCA ACA
_ GGTT CC

GAM363 ODF2 5' ACGTTGAGATCACTGTGTAGA 8384 A AACCCAG
TCTACACA GT TAATGT
||||| || |||||
AGATGTGT CA GTTGCA
_ CTAGA_

GAM363 TES 3' ACTTTTTACTTGTATAGA 35631 C CCC
TCTA ACAAGTAA AGT
||| ||||| |||
AGAT TGTTTCATT TCA
A TT_

GAM363 TMOD3 3' ATAATGTACAGGTCATTTGTGT 15857 A _____ GTAA
AGA TACACAAGT ACC CA T
||||| ||| || |
ATGTGTTTA TGG GT A
C ACAIIT AATG

GAM363 CNIL 3' TGCTGAATTACTTGTGAAGA 12355 A CC
TCT CACAAGTAA CAGTA
||| ||||| |||||
AGA GTGTTTCATT GTCGT
A AA

GAM363 DKFZP564I0422 3' ACATTACTGAATTTGTGAAGA 25431 A AACC
TCT CACAAGT CAGTAATGT
||| ||||| |||||
AGA GTGTTTA GTCATTACA
A A_

GAM363 HT014 3' ACACCACTGGGAGGGTTGTGTA 21634 GTAA AA
GG TCTACACAA CCCAGT TGT
||||| ||||| |||
GGATGTGTT GGGTCA ACA
GGGA CC

GAM363 KIAA0193 3' CAGTAATGTACAGGATTCCTTG 16540 T _ _____ GTAA
TGTAGA CACAAG AA CC CA TG
||||| ||| || |||
GTGTTC TT GG GT AC
C A ACAIIT AATG

GAM363 KIAA0276 3' CTGAGTTATTTGTACAGA 35135 AC C
TCT ACAAGTAAC CAG
||| ||||| |||

			AGA TGTTTATTG GTC		
			CA A		
GAM363	LOC115073	3'	ACATTACTGTAATTTTGTGTA	36237	TAACC
			TACACAAG CAGTAATGT		
			ATGTGTTT GTCATTACA		
			TAAT_		
GAM364	PSR	3'	TATGTCATCATCAGCCCA	32503	A ATT
			TG GT GTGATGACATA		
			AC CG TACTACTGTAT		
			C AC_		
GAM364	RAI17	3'	CATCACAATCTCACCCA	43859	A T
			TG GTGAG ATTGTGATG		
			AC CACTC TAACACTAC		
			C _		
GAM364	SEC24A	3'	CATACTAATAGTCACTCA	40233	G TG
			TGAGTGA TATTG ATG		
			ACTCACT ATAAT TAC		
			G CA		
GAM364	LOC255565	5'	CACACTGATTACTCACTCA	45589	TT__ A
			TGAGTGAGTA GTG TG		
			ACTCACTCAT CAC AC		
			TAGT _		
GAM364	LOC256512	5'	ATGTCACCAATGTACTCGCCCA	46047	A TG A
			TG GTGAGTAT TG TGACAT		
			AC CGCTCATG AC ACTGTA		
			C TA C		
GAM364	LOC93166	5'	CACACACACTCACTCA	35459	AT A
			TGAGTGAGT TGTG TG		
			ACTCACTCA ACAC AC		
			C_ _		
GAM365	C20orf21	3'	TAACGACAACAAACCGGTCACA	19442	ACTCAGC A
			TGTGACCG TGTT GTTA		
			ACACTGGC ACAG CAAT		
			CAAACA_ _		
GAM365	GIT2	3'	AACTGTTGAGTTGATCACA	16595	C T
			TGTGA CGACTCAGC GTT		
			ACACT GTTGAGTTG CAA		
			A T		
GAM365	GIT2	3'	AACTGTTGAGTTGATCACA	27677	C T
			TGTGA CGACTCAGC GTT		

A C A C T G T T G A G T T G C A A
 A T
 GAM365 GIT2 3' A A C T G T T G A G T T G A T C A C A 27690 C T
 T G T G A C G A C T C A G C G T T
 |||| ||||| ||
 A C A C T G T T G A G T T G C A A
 A T
 GAM365 MGC10981 3' T A A A A T G C T G A G T C G A T C C C A 26388 T C T G_
 T G G A C G A C T C A G C T T A
 || || ||||| ||
 A C C T G C T G A G T C G A A T
 C A T A A
 GAM365 MO25 3' A A C T A A C A A C T G A C A A A T C A 18412 C C G A C C
 T G A T C A G T G T T A G T T
 || || ||||| ||
 A C T A G T C A C A A T C A A
 A A A C _ A
 GAM366 SCAMP1 3' T A T G T G C A T T T T G T A G T A 11291 C G C
 T A C C A A A A T G C A C T A
 || ||||| ||
 A T G G T T T A C G T G A T
 A T T
 GAM366 BLCAP 5' C C A T T A G G T C G G T T C C T G C 13521 A _ G C
 G C A A A T A C C T A A T G G
 || || ||||| ||
 C G T T T G T G G A T T A C C
 C C G C
 GAM366 C20orf108 3' C C A T T A G G T G A T G C T T T G G 28082 C A A A G
 C C G A T C A C C T A A T G G
 || || ||||| ||
 G G T T A G T G G A T T A C C
 T T C G _
 GAM366 FLJ32332 3' C C A C C A G G T C C T G C C T T T T G C G 29467 T _ A A
 G T G T A C C G C A A A A G C A C C T T G G
 ||||| || || ||
 G T G G C G T T T T C G T G G A A C C
 C T C C C C
 GAM366 KIAA0350 3' C C A C C A G G G G C A T T A G G T A 30662 G C A A A A A
 T A C C A A T G C C C T T G G
 || || || || ||
 A T G G T T A C G G G A A C C
 A _ G C C
 GAM366 KIAA0515 3' C C A C C A G T G G C C T T G C G G T A 31921 A A T A C A A
 T A C C G C A A G C C T T G G
 |||| || || ||
 A T G G C G T T C G G A A C C
 C _ G T C C
 GAM366 LOC221405 3' C C A T T A G G G A C C A T C T G T G 45067 A A C A_
 C G C A A T G C C T A A T G G
 || || ||||| ||

			GTGT TAC GGATTACC		
			C_ CAG		
GAM367	CCNF	3'	CCAGAGGCGTTCGTATGTG 7525	A	GTA
			TACATAC AACGC TGG		
			GTGTATG TTGCG ACC		
			C GAG		
GAM367	DIRC1	3'	CCTTTATTCGTTTGTACTCA 27508	TACA	C T_
			TGAGTACA AACG GTA GG		
			ACTCATGT TTGC TAT CC		
			_____ T TT		
GAM367	KIAA0022	3'	TCCAGTAACATTTTTATGTACT 17028	C	CGCGTA
	CA		TGAGTACATA AAA TGGA		
			ACTCATGTAT TTT ACCT		
			T ACAATG		
GAM367	KIAA0265	3'	CCATTACATGCACATGTACTCA 34625	ACAAAC	____
			TGAGTACAT GCGT ATGG		
			ACTCATGTA CGTA TACC		
			CA_____ CAT		
GAM367	KIAA0352	3'	CCATTTTCTTGGTATGTACTCA 16822	AAACGCGT	
			TGAGTACATAC ATGG		
			ACTCATGTATG TACC		
			GTTCTTT_		
GAM367	KIAA1040	3'	TCCTTAAATTTGTATGTATCA 35744	G	CGCG T
			TGA TACATACAAA TA GGA		
			ACT ATGTATGTTT AT CCT		
			_ AA_ T		
GAM367	KIAA1093	5'	TCCATTTCTACCTTGTATGCCT 33064	TA	ACGCGT_
	CA		TGAG CATACAA ATGGA		
			ACTC GTATGTT TACCT		
			C_ CCATCTT		
GAM367	PFTK1	3'	TGCGTCTATATGATACTCA 14754	_	CAA
			TGAGTA CATA ACGCG		
			ACTCAT GTAT TGCGT		
			A ATC		
GAM367	LOC150468	5'	TCCAGCCAAGTTTGTATACCTC 38975	TAC	GCGTA
	A		TGAG ATACAAAC TGGA		
			ACTC TATGTTTG ACCT		
			CA_ AACCG		
GAM367	LOC158314	3'	TCCACATTACTTATGTACTCA 41954	CAAACGC	A
			TGAGTACATA GT TGGA		

			ACTCATGTAT	TA ACCT	
			TCAT__	C	
GAM368	AHR	3'	TGATGACAATCAGTTA	7337	AGAT
			TAAGTGGT	TGTCATCA	
			ATTGACTA	ACAGTAGT	
GAM368	ASTN	3'	TGATTGGGAAATCTGCCAG	34363	G_ _
			CTGGTAGATT	TCA TCA	
			GACCGTCTAA	GGT AGT	
			AG	T	
GAM368	ESRRBL1	3'	ATGACAAATATGCCAGTT	19740	GA_
			AACTGGTA	TTGTCAT	
			TTGACCGT	AACAGTA	
			ATA		
GAM368	GUCY1A3	5'	ATGACATCCCAGTTA	31778	TA T
			TAAGTGG	GAT GTCAT	
			ATTGACC	CTA CAGTA	
GAM368	HADHSC	3'	GTGATTATTACACCAGTTA	11799	A_ T
			TAAGTGGT	GAT GTCAT	
			ATTGACCA	TTA TAGTG	
			CA	T	
GAM368	IL24	3'	GTGATGACATTCCCTGCTA	13720	AT__
			TGGTAG	TGTCATCAC	
			ATCGTC	ACAGTAGTG	
			CCTT		
GAM368	PTEN	3'	GTGTCAGATTACCAGTTA	5858	A T
			TAAGTGGTAG	TTG CAT	
			ATTGACCATT	GAC GTG	
			A	T	
GAM368	RARB	3'	ATGACATAACTACACAGTTA	18236	_ AT_
			TAAGTGGTAG	TGTCAT	
			ATTGAC	CATC ACAGTA	
			A	AAT	
GAM368	RARB	3'	ATGACATAACTACACAGTTA	6692	_ AT_
			TAAGTGGTAG	TGTCAT	
			ATTGAC	CATC ACAGTA	
			A	AAT	
GAM368	TIMP3	3'	TGATGACAATGAAATTAG	5934	AG_
			CTGGT	ATTGTCATCA	

			GATTA TAACAGTAGT		
			AAG		
GAM368	AKAP11	3'	ATGACAGACCAGTTA	18366	AGA
			TAAGTGGT TTGTCAT		
			ATTGACCA GACAGTA		
			—		
GAM368	BMF	3'	TGAGGAATCTACCAGTTG	27281	G A
			TAAGTGGTAGATT TC TCA		
			GTTGACCATCTAA GG AGT		
			— —		
GAM368	C1QTNF7	3'	GTGATAAAACCAGTTG	25667	AGA
			TAAGTGGT TTGTCAT		
			GTTGACCA AATAGTG		
			A_		
GAM368	C6orf37	3'	GTGATGACAATATGGGTT	33513	G GA
			AACT GTA TTGTCATCAC		
			TTGG TAT AACAGTAGTG		
			G _		
GAM368	CLDN1	3'	ATGATACTTAACCAGTTA	22082	A T
			TAAGTGGT GA TGTCAT		
			ATTGACCA TT ATAGTA		
			A C		
GAM368	DKFZP434K0427	5'	GTGATGACAATATGACTA	25840	AG_
			TGGT ATTGTCATCAC		
			ATCA TAACAGTAGTG		
			GTA		
GAM368	DKFZP586P0123	5'	GTGATGACAAACTGACCA	45465	_ A
			TGGT AG TTGTCATCAC		
			ACCA TC AACAGTAGTG		
			G A		
GAM368	FLJ10283	5'	ATGACGAAGCCATTACCAGT	19795	A_____
			ACTGGTAG TTGTCAT		
			TGACCATT AGCAGTA		
			ACCGA		
GAM368	FLJ10525	3'	GTGATAAATATACCAGTT	19914	GA_
			AACTGGTA TTGTCAT		
			TTGACCAT AATAGTG		
			ATA		
GAM368	KIAA0410	3'	ATGATTACCTAACCAGTTA	16615	_ ATT
			TAAGTGGT AG GTCAT		

			ATTGACCA TC TAGTA		
			A CAT		
GAM368	MGC16384	3'	GTGATGTTGGATGCCAGTTA	27595	GATTGT
			TA ACTGGTA CATCAC		
			ATTGACCGT GTAGTG		
			AGGTT_		
GAM368	SAE1	3'	ATGATCCTACCAGTTG	12003	ATT
			TA ACTGGTAG GTCAT		
			GTTGACCATC TAGTA		
			C_		
GAM368	SDS3	3'	GTGATGACAATTAAATCA	34320	A_
			TGGT GATTGTCATCAC		
			ACTA TTAACAGTAGTG		
			AA		
GAM368	SEMA4G	5'	TGATGACAAGGTGTACTA	45414	G _
			TGGTA AT TGTCATCA		
			ATCAT TG ACAGTAGT		
			G GA		
GAM368	LOC113115	5'	GTGATGAAGAAGCCAGTTA	28789	AGATTG
			TA ACTGGT TCATCAC		
			ATTGACCG AGTAGTG		
			AAGA_		
GAM368	LOC125228	3'	GCAGTTACCTACCAGTTA	36791	___
			TA ACTGGTAG ATTGT		
			ATTGACCATC TGACG		
			CAT		
GAM368	LOC144848	3'	TGAAGATTACCAGTTA	36422	GATT A
			TA ACTGGTA GTC TCA		
			ATTGACCAT TAG AGT		
			___ A		
GAM368	LOC145622	5'	GTGATGACCATATCCAGT	37913	TAG T
			ACTGG AT GTCATCAC		
			TGACC TA CAGTAGTG		
			TA_ C		
GAM368	LOC151996	5'	GTGATCTGGAAATCTACCA	41415	GT _
			TGGTAGATT CA TCAC		
			ACCATCTAA GT AGTG		
			AG CT		
GAM368	LOC157273	3'	ATGACCTTCTACCAGTTG	41780	TT
			TA ACTGGTAGA GTCAT		

		GTTGACCATCT CAGTA		
		TC		
GAM368	LOC160897 3'	GTGATGCATTTTACCAG 40010	T T	
		CTGGTAGA TG CATCAC		
		GACCATTT AC GTAGTG		
		T _		
GAM368	LOC200347 5'	GTGATGACAACCTTTGGT 42807	TG T A	
		AC G AG TTGTCATCAC		
		TG T TC AACAGTAGTG		
		GT _ _		
GAM368	LOC220729 3'	GTGATGACAGAATCAG 35448	AGA	
		CTGGT TTGTCATCAC		
		GACTA GACAGTAGTG		
		A _		
GAM368	LOC256337 3'	ATGAACAAAACCAGTTA 45419	AGA _	
		TAAGTGGT TTGT CAT		
		ATTGACCA AACA GTA		
		A _ A		
GAM368	LOC90342 5'	TGATGGGAACATCTACCA 31256	_ G	
		TGGTAGAT T TCATCA		
		ACCATCTA A GGTAGT		
		CA G		
GAM368	LOC96810 3'	GTGACTCCACCAGTTA 34926	A TT	
		TAAGTGGT GA GTCAT		
		ATTGACCA CT CAGTG		
		C _		
GAM369	CUL3 3'	CCAAGCATACAATTTGAGC 9645	CC_	
		GCTTA GTATGCTTGG		
		CGAGT CATACGAACC		
		TTAA		
GAM369	DPYSL3 3'	CCAAGCATAGAAATCCCTG 7071	A GC ACCG	
		CAG GA TT TATGCTTGG		
		GTC CT AG ATACGAACC		
		C AA _		
GAM369	NFE2L1 3'	CCAAACACACAAGCTCTC 9196	ACC A C	
		GAGAGCTT GT TG TTGG		
		CTCTCGAA CA AC AACC		
		_ C A		
GAM369	SIM2 3'	CCAAATACATTAACAAGCTCTT 11517	ACC_ GC	
		GAGAGCTT GTAT TTGG		

			TTCTCGAA CATA AACC		
			CAATTA _		
GAM369	SORCS1	3'	CCAAGCATGCCAGCTTCTG 27483	G	TACC
			CAGA AGCT GTATGCTTGG		
			GTCT TCGA CGTACGAACC		
			_ C _		
GAM369	TRAF1	3'	CCAAGCAGAGAAGCTCTC 12198	ACCGTA	
			GAGAGCTT TGCTTGG		
			CTCTCGAA ACGAACC		
			GAG _		
GAM369	VCL	3'	CCAACTACAACCAAGCTCTCTG 9402	ACC_	TGC
			CAGAGAGCTT GTA TTGG		
			GTCTCTCGAA CAT AACC		
			CCAA C _		
GAM369	VCL	3'	CCAACTACAACCAAGCTCTCTG 15191	ACC_	TGC
			CAGAGAGCTT GTA TTGG		
			GTCTCTCGAA CAT AACC		
			CCAA C _		
GAM369	EPHA7	3'	TCCAAACACCTTGAGCTCTCT 10725	CCGTA	C
			AGAGAGCTTA TG TTGGA		
			TCTCTCGAGT AC AACCT		
			TCC _ A		
GAM369	FLJ20273	3'	TCCAAACACTGGAAAGCTCTC 21115	A	TA C
			GAGAGCTT CCG TG TTGGA		
			CTCTCGAA GGT AC AACCT		
			A C _ A		
GAM369	FLJ21865	3'	TCCAAGCACCGGGAAGACCTC 23001	AG	A TA
			GAG CTT CCG TGCTTGGA		
			CTC GAA GGC ACGAACCT		
			CA G C _		
GAM369	GIT1	3'	TCCAAGTGGGGCAGCTCTC 15258	TA	GTA
			GAGAGCT CC TGCTTGGA		
			CTCTCGA GG GTGAACCT		
			CG _		
GAM369	KIAA0210	3'	CCACCATGCCAATAAGGCTCTC 16421	ACC_	CT
			GAGAGCTT GTATG TGG		
			CTCTCGGA CGTAC ACC		
			ATAAC C _		
GAM369	KIAA0336	3'	CACACAGTATGCTCTCTG 16011	T	C A
			CAGAGAGC TAC GT TG		

			GTCTCTCG ATG CA AC		
			T A C		
GAM369	KIAA1130	3'	TCCAAGCACCACGACTCCCTG 31287	A	CTTAC A_
			CAG GAG CGT TGCTTGGA		
			GTC CTC GCA ACGAACCT		
			C A__ CC		
GAM369	KIAA1831	5'	TCCAAGGCCCCCAGCAGGCTCT 31907		ACCGTAT _
		C	GAGAGCTT GC TTGGA		
			CTCTCGGA CG AACCT		
			CGACCCC G		
GAM369	MCJ	5'	CCAAGTATATAAAGCTCCCTG 14899	A	ACC
			CAG GAGCTT GTATGCTTGG		
			GTC CTCGAA TATATGAACC		
			C A_		
GAM369	Rabip4R	3'	TCCAACTATACGGTCAGCCCTC 19717	A T	C
			GAG GCT ACCGTATG TTGGA		
			CTC CGA TGGCATAT AACCT		
			C C C		
GAM369	SPIB	3'	TCCAAGCACAAAGGAACCTCCTG 9093	A C A	GTA
			CAG GAG TT CC TGCTTGGA		
			GTC CTC AA GG ACGAACCT		
			_ _ _ AAC		
GAM369	UBN1	3'	TCTGGCTGCAGTAAGCTCCCTG 18854	A	C T T
			CAG GAGCTTAC GTA GCT GG		
			GTC CTCGAATG CGT CGG CT		
			C A _ T		
GAM369	LOC145368	5'	TCCAAAACCCGGACAAGCTCTT 37830	A_	TATGC
			GAGAGCTT CCG TTGGA		
			TTCTCGAA GGC AACCT		
			CA CCAA_		
GAM369	LOC150423	5'	TCCAAAACCCGGACAAGCTCTT 38970	A_	TATGC
			GAGAGCTT CCG TTGGA		
			TTCTCGAA GGC AACCT		
			CA CCAA_		
GAM369	LOC153232	5'	CCAAGCACGTAGCCCTTT 41597	A	TAC AT
			AGAG GCT CGT GCTTGG		
			TTTC CGA GCA CGAACC		
			C T_ _		
GAM369	LOC221486	3'	TCCAAAGAAACACTAAGCTCTC 43746		CC ATG _
		TG	CAGAGAGCTTA GT CTT GGA		

GTCTCTCGAAT CA GAA CCT
 CA AA_ A
 GAM369 LOC256310 5' TCCATCACAGTGAGCTCCCTG 46096 A C ATGCT
 CAG GAGCTTAC GT TGGA
 ||| ||||| || ||||
 GTC CTCGAGTG CA ACCT
 C A CT____
 GAM370 NSF 3' AAGTAATTTACAAACCTCTCA 31586 AC _
 TGAGGG TTGTAGAT ACTT
 ||||| ||||| ||||
 ACTCTC AACATTTA TGAA
 CA A
 GAM370 MRPL20 3' TGAAGTATCCAGCGCTC 19699 AC TA
 GGG TTG GATACTTCA
 ||| ||| |||||
 CTC GAC CTATGAAGT
 GC _
 GAM370 NUCKS 3' GAAAACATCTACAAGCCCCCA 22936 A A AC_
 TG GGG CTTGTAGAT TTC
 || ||| ||||| |||
 AC CCC GAACATCTA AAG
 C C CAA
 GAM370 LOC146138 3' TTGAAATACTGTGCCTCA 40659 G TT GATAC
 TGAGG AC GTA TTCAA
 ||||| || ||| |||||
 ACTCC TG CAT AAGTT
 G T_ A____
 GAM370 LOC254250 5' ATTGAAGTAGGCTCAAACCCTC 46356 AC T A_
 A TGAGGG TTG AG TACTTCAAT
 ||||| ||| || |||||
 ACTCCC AAC TC ATGAAGTTA
 A_ _ GG
 GAM371 SRGAP2 3' AACTGGTACCCACACTTGCCCT 36877 A T C TA
 AG GC AAG GTGG TACTAGTT
 || ||| |||| |||||
 TC CG TTC CACC ATGGTCAA
 C _ A C_
 GAM371 ADAMTSL1 3' AGCCTACCAGCTTAGCTC 29253 G TA
 GAGCTAAGC TGGTA CT
 ||||| |||| |||
 CTCGATTCTG ACCAT GA
 _ CC
 GAM371 CHST3 3' AACCAGCAGGGGAGCACTTGGCT 10472 C GGTATA A
 C GAGCTAAG GT CT GTT
 ||||| || || |||
 CTCGGTTC CG GA CAA
 A AGGGAC C
 GAM371 KIAA1344 3' AACTAGCATAATTAAGTTAGTT 35868 CGTGG A
 CT AGAGCTAAG TAT CTAGTT
 ||||| ||| |||||

			TCTTGATTC	ATA GATCAA		
			AATTA	C		
GAM372	ANXA8	3'	CCATGCCCTCAGCACC	ACT 7339	AATATA	
			AGTGGTGCT	GCATGG		
			TCACCACGA	CGTACC		
			CTCC	_		
GAM372	INPP5B	3'	CCATTGGTTAGCAC	ACT 45734	G	ATAGC
			AGTG	TGCTAAT ATGG		
			TCAC	ACGATTG TACC		
			GT	_		
GAM372	NSF	3'	CCTCTCTACTAGCAC	CATCA 31588	A	ATA CAT
			A	GTGGTGCTA TAG GG		
			A	TACCACGAT ATC CC		
			C	C_ TCT		
GAM372	C13orf1	3'	CCATACTATATTAAC	CACATT 21690	_ GC	C
			AGTG	GT TAATATAG ATGG		
			TTAC	CA ATTATATC TACC		
			A	A_ A		
GAM372	MGC12972	3'	GCCACGTCCCAGCAC	CACTT 26405	AATATA	A
			AAGTGGTGCT	GC TGGC		
			TTCACCACGA	TG ACCG		
			CCC	_ C		
GAM372	PEG10	3'	CCATGCTACATTTTC	ATC 17429	CT A	
			GGTG	AAT TAGCATGG		
			CTAC	TTA ATCGTACC		
			TT	C		
GAM372	LOC142972	3'	CCATGCCCTCAGCACC	ACT 32476	AATATA	
			AGTGGTGCT	GCATGG		
			TCACCACGA	CGTACC		
			CTCC	_		
GAM372	LOC92140	3'	CCATAATTAACATCA	CTTA 33889	C	ATAGC
			TAAGTGGTG	TAAT ATGG		
			ATTC	ACTAC ATTA TACC		
			A	A_		
GAM373	KCNJ15	3'	CACAGGGGCGCCATC	CAGGTTT 8031	_	A AGCA
	AA		TTAAACCTGG	TGGC CT GTG		
			AATTTGGACC	ACCG GG CAC		
			T	C GGA_		
GAM373	CNNM1	3'	CACCTGAGGCCACC	AGG 21605	AC	CA
			CCTGGTGGC	TAG GTG		

GGACCACCG GTC CAC
GA _
GAM373 DKFZp761N1114 3' CACTGCTAGTAATCAAGG 38606 _ GGC
CCT GGT ACTAGCAGTG
||| ||| |||||
GGA CTA TGATCGTCAC
A A_
GAM373 KIAA0323 3' CACTTGACTGGCCACCAG 31688 AC _ _
CTGGTGGC TAG CA GTG
||||| ||| |||
GACCACCG GTC GT CAC
_ A T
GAM373 KIAA0848 3' CACTGCTAGTGTACAG 17213 GTG
CTG GCACTAGCAGTG
||| |||||
GAC TGTGATCGTCAC
A_
GAM373 KIAA1200 3' CACCACTAGTGCCTCTGGATTT 31262 C TG T CA
AG TTAAC C G GGCAC TAG GTG
||||| | ||||| |||
GATTT G C CCGTGATC CAC
A GT T AC
GAM373 MAPK11 3' CACTGCTGAGACCCACAGGTCT 8627 A G CA _
AA TTA ACCTG TGG CT AGCAGTG
||| ||||| ||| || |||||
AAT TGGAC ACC GA TCGTCAC
C _ CA G
GAM373 LOC133418 3' CACTGCTTTCCCCACCAGG 37041 CACT
CCTGGTGG AGCAGTG
||||| |||||
GGACCACC TCGTCAC
CCTT
GAM373 LOC153338 5' CACTGCTAACTATGCAGG 41609 _ CAC
CCTG GTGG TAGCAGTG
||||| |||||
GGAC TATC ATCGTCAC
G A_
GAM373 LOC255098 3' CACTGCTTTCCCCACCAGG 45689 CACT
CCTGGTGG AGCAGTG
||||| |||||
GGACCACC TCGTCAC
CCTT
GAM374 ACP1 3' TCAACATCTAAGCCTGTTG 10510 CTACC T
TAACAGGC ATGTT GA
||||| ||||| |||
GTTGTCCG TACAA CT
AATC_ _
GAM374 ACP1 3' TCAACATCTAAGCCTGTTG 13960 CTACC T
TAACAGGC ATGTT GA
||||| ||||| |||

			GTTGTCCG TACAA CT	
			AATC_ _	
GAM374	DBY	3'	TCAAACATGGTTATTTCTGT 11028	CCT_
			ACAGG ACCATGTTTGA	
			TGTCT TGGTACAACT	
			TTAT	
GAM374	HPSE	3'	TCAAATGTATGCCTGTTA 13480	C CAT
			TAACAGGC TAC GTTTGA	
			ATTGTCCG ATG TAAACT	
			T _	
GAM374	SELL	3'	TCAAACATGAAGTGTGTT 6316	G CTAC
			AACA GC CATGTTTGA	
			TTGT TG GTACAACT	
			G AA_	
GAM374	FLJ10287	3'	CAAATATATGGTAGGACTGTTA 21154	G _
			TAACAG CCTACCATGT TTG	
			ATTGTC GGATGGTATA AAC	
			A TA	
GAM374	FRAT1	3'	TCAAACATGCGGTGCCATG 11982	_ _ AC
			CA GGC CT CATGTTTGA	
			GT CCG GG GTACAACT	
			A T C_	
GAM374	KIAA1143	3'	CAAACTGGGGGCTTGTTA 34070	A T
			TAACAGGCCT CCA GTTTG	
			ATTGTTCGGG GGT CAAAC	
			_ _	
GAM374	KIAA1283	5'	CAAATCTGAGGCCTGT 35662	AC T
			ACAGGCCT CA GTTTG	
			TGTCCGGA GT TAAAC	
			_ C	
GAM374	KIAA1719	3'	CAAACATGGACCTGTTG 33816	CCTA
			TAACAGG CCATGTTTG	
			GTTGTCC GGTACAAAC	
			A_	
GAM374	LASP1	3'	TCAAACCTTTCTGGCCTGTTA 12802	TACCAT
			TAACAGGCC GTTTGA	
			ATTGTCCGG CAAACT	
			TCTTTC	
GAM374	MGC4707	3'	TCACGCCGTAGCCTGTTA 23564	C CAT T
			TAACAGGC TAC GT TGA	

			ATTGTCCG ATG CG ACT	
			_ C _ C	
GAM374	LOC150139	3'	TCAAACATGGGTTTTGTTG 38860	CCTA
			TAACAGG CCATGTTTGA	
			GTTGTTT GGTACAACT	
			TG _	
GAM375	NR5A2	3'	GCATCAGCTGTACCTACAATA 9916	AC T T
			TATTGTAG TATG G CTGATGC	
			ATAACATC ATGT C GACTACG	
			C _ _ _	
GAM375	CXYorf1	5'	GCATCAGACACAGGTACAGCA 39908	AG _ A
			TGT ACT TGTGTCTGATGC	
			ACG TGG ACACAGACTACG	
			ACA _	
GAM375	DKFZP434L0718	3'	GCATCAGACCTGTTCCACA 25820	A CT T
			TGT GA ATG GTCTGATGC	
			ACA CT TGT CAGACTACG	
			C _ _ C	
GAM375	FLJ21302	3'	CAGTTACATAGTCTACAATA 23183	T
			TATTGTAGACTATGTG CTG	
			ATAACATCTGATACAT GAC	
			T	
GAM375	LOC200093	5'	GCATCAGACACAGGTACAGCA 31600	AG _ A
			TGT ACT TGTGTCTGATGC	
			ACG TGG ACACAGACTACG	
			ACA _	
GAM375	LOC91040	5'	GCATCAGACACAGGTACAGCA 32317	AG _ A
			TGT ACT TGTGTCTGATGC	
			ACG TGG ACACAGACTACG	
			ACA _	
GAM376	GPR48	5'	GGGGGCGGCGGGGGACATCGG 20550	A C A
			TC ATG CCCCC CCGCCCC	
			GG TAC GGGGG GGCGGGGG	
			C A C	
GAM376	MTCP1	5'	GGGGGCGGCAGGGAGGCGGC 15487	AAT _ CA
			GTC GCC CCC CCGCCCC	
			CGG CGG GGG GGCGGGGG	
			_ _ A AC	
GAM376	NPAT	3'	GGAATGGGATATTGACA 33386	CCC CCG
			TGTCAATG CCCA CCC	

			ACAGTTAT GGGT GGG		
			A__ AA_		
GAM376	SLC12A7	3'	TGGAGGCGGCGGTGGCACTGA 13376	A	CC A C
			TCA TGCC CC CCGCC CCA		
			AGT ACGG GG GGCGG GGT		
			C T_ C A		
GAM376	WNT3A	3'	GGGAGGTTTGGGGGGCATCAAC 26975	CA	CC _
			GT ATGCCCCCA GCC CCC		
			CA TACGGGGGGT TGG GGG		
			AC T_ A		
GAM376	BLCAP	3'	CGGGAGGGGAGGCATTGACA 13522	_	A_
			TGTCAATGCC CCCC CCG		
			ACAGTTACGG GGGG GGC		
			A AG		
GAM376	CABP5	3'	CGGGAGGGAGGGCATTGGCA 21260	_	A_
			TGTCAATGCCC CCC CCG		
			ACGGTTACGGG GGG GGC		
			A AG		
GAM376	FLJ12425	3'	TGGTTGGGGGGCATCAGCA 41564	CA	_
			TGT ATGCCCCCA CCG		
			ACG TACGGGGGGT GGT		
			AC T		
GAM376	KIAA1981	3'	GGGGGCGGTGGCGGTGACA 42610	ATGC	C
			TGTCA CC CCACCGCCCCC		
			ACAGT GG GGTGGCGGGGG		
			____ C		
GAM376	PSR	3'	GGAGCGTTGGAGGCATTGGCA 32502	CC	C C
			TGTCAATGCC CCA CGC CC		
			ACGGTTACGG GGT GCG GG		
			A_ T A		
GAM376	SCYB11	3'	TGGTTACGGTGGAGACATTGAC 42260	CCCC	CCC
	A		TGTCAATG CCACCG CCA		
			ACAGTTAC GGTGGC GGT		
			AGA_ ATT		
GAM376	SMOC2	5'	GGGAGCGGTGGGGAGAGCAT 35836	C__	C
			ATGC CCCACCGC CCC		
			TACG GGGGTGGCG GGG		
			AGA A		
GAM376	STAT2	3'	TGGTGGGGAGCACAGACA 11893	AA	C
			TGTC TGC CCCCACCG		

			ACAG ACG GGGGTGGT		
			AC A		
GAM376	VI	3'	TGGGGGCGGTGGGGAGGT 15109 _		
			GCC CCCACCGCCCCCA		
			TGG GGGGTGGCGGGGGT		
			A		
GAM376	ZNF238	3'	TGGGGGGGTGTCAAAGAACTTG 13047	TGCCCCC_	G
	ACA		TGTCAA CACC CCCCCA		
			ACAGTT GTGG GGGGGT		
			CAAGAACT _		
GAM376	LOC125228	5'	GGGGGCGGCAGGGGGCTAGC 36793	CAAT	CA
			GT GCCCCC CCGCCCCC		
			CG CGGGGG GGCGGGGG		
			AT_ AC		
GAM376	LOC147671	3'	GGGAAGGGGGCATTGAC 38378	CACCG	
			GTCAATGCCCCC CCC		
			CAGTTACGGGGG GGG		
			AA_		
GAM376	LOC158563	3'	GCAATGGAATGGACATTGGCA 39869	_ CC_	CC
			TGTCAATG CC CCA GC		
			ACGGTTAC GG GGT CG		
			A TAA AA		
GAM376	LOC197285	3'	GGAGCTGGTCTGGGGAGCATTG 42416	_ C_	_ C
	AC		GTCAATGC CCCC ACC GC CC		
			CAGTTACG GGGG TGG CG GG		
			A TC T A		
GAM376	LOC221839	5'	GGCGGTGGCATCGACA 44431	A	CCCC
			TGTC ATGCC ACCGCC		
			ACAG TACGG TGGCGG		
			C _		
GAM376	LOC90092	3'	GGGGGTGGGGGGGCACCAAGCA 30790	CAA_	AC
			TGT TGCCCCCC CGCCCCC		
			ACG ACGGGGGG GTGGGGG		
			AACC _		
GAM376	LOC91252	3'	TGGGGGCGGTGAGGGCTCCAC 32555	CAAT	CC
			GT GCCC CACCGCCCCCA		
			CA CGGG GTGGCGGGGGT		
			CCT_ A_		
GAM376	LOC91960	5'	TGGGGGCGGCGGGGCTAGGAC 33615	AAT	CCA
			GTC GCCCC CCGCCCCCA		

			CAG CGGGG GGCGGGGGT		
			GAT C__		
GAM377	D12S2489E	3'	CAGTGAGAGTGCAACCCCA 14291	AATCA	CTT
			TGG TGT CTCTCACTG		
			ACC ACG GAGAGTGAC		
			CCA__ T__		
GAM377	PEX10	3'	CAGTGAGAACAGCAGCCCA 8480	AATCA	T TC
			TGG TG CT TCTCACTG		
			ACC AC GA AGAGTGAC		
			CCG__ _ CA		
GAM377	SNTB1	3'	TGGTGTAGAATGATTCCA 22013	GTCT	CT
			TGGAATCAT TCT CACTG		
			ACCTTAGTA AGA GTGGT		
			____ T_		
GAM377	CPSF2	3'	AGAAAAGACATGCTCCA 30861	AT	C
			TGGA CATGTCTT TCT		
			ACCT GTACAGAA AGA		
			C_ A		
GAM377	KIAA1183	3'	GGGGAAGAGATGATTCCA 31337	G	
			TGGAATCAT TCTTCTCT		
			ACCTTAGTA AGAAGGGG		
			G		
GAM377	MAPK6	3'	CAGTGAGACTGTACATAATTGC 8626	G C	CTTC
	A		TG AAT ATGT TCTCACTG		
			AC TTA TACA AGAGTGAC		
			G A TGTC		
GAM377	MGC21636	5'	CAGTGAAAAATGTGATTCCA 29647	C	CTC
			TGGAATCATGT TT TCACTG		
			ACCTTAGTGTA AA AGTGAC		
			A ____		
GAM377	POPX1	3'	CAGTGAGAAGTGCAACATCCA 17119	ATCA	_ TC
			TGGA TGT CT TCTCACTG		
			ACCT ACG GA AGAGTGAC		
			ACA_ T _		
GAM377	WDR9	3'	AGGCCTTGAAGACATGATTCC 21032	TCTCA	
			GGAATCATGTCTTC CT		
			CCTTAGTACAGAAG GA		
			TTCCG		
GAM377	LOC170217	5'	CAGTATGGGGACATGTTCCA 40178	T	TCTC
			TGGAA CATGTCTTC ACTG		

		ACCTT GTACAGGGG TGAC		
		— TA__		
GAM377	LOC170218 5'	CAGTATGGGGACATGTTCCA 40180	T	TCTC
		TGGAA CATGTCTTC ACTG		
		ACCTT GTACAGGGG TGAC		
		— TA__		
GAM377	LOC170372 3'	CAGTGAGACTGTACATAATTGC 37539	G C	CTTC
	A	TG AAT ATGT TCTCACTG		
		AC TTA TACA AGAGTGAC		
		G A TGTC		
GAM377	LOC219914 5'	CAGTGAGAGACCAAGAACCCA 44814	AA A	TCT
		TGG TC TG TCTCTCACTG		
		ACC AG AC AGAGAGTGAC		
		CA A C__		
GAM377	LOC91750 3'	CAGCAAGAGAAGAATCTGCTCT 33288	ATCATG	CA
	A	TGGA TCTTCTCT CTG		
		ATCT AGAAGAGA GAC		
		CGTCTA AC		
GAM377	LOC92096 3'	AGTGAGAGTGGCGCCCCA 33775	AATCA	TT
		TGG TGTC CTCTCACT		
		ACC GCGG GAGAGTGA		
		CC__ T_		
GAM378	IMPACT 3'	ATAATCCCTCTGATTCCACTA 20501	AAT	CCT
		TGGTGGAATCA GG ATTAT		
		ATCACCTTAGT CC TAATA		
		CT_ C__		
GAM379	GUCY1B2 3'	GATTTGTAATGAGTACA 10335	AGACC	
		TGTAC CATTACAAATC		
		ACATG GTAATGTTTAG		
		A__		
GAM379	MTMR8 3'	CGATTTGTAATAAACTGAGTT 17744	ACCC_____	
	GTACAA	ACAG ATTACAAATC G		
		TGTT TAATGTTTAG C		
		GAGTCAAAA		
GAM379	MTR 3'	GATCTGTAGGGACTTGTACAA 5797	AC A	A
		TTGTACAG CC TTACA ATC		
		AACATGTT GG GATGT TAG		
		CA _ C		
GAM379	RNTRE 3'	TTGTAATAAACCAAGCTGTACA 16190	ACCC_____	
	AT	ATTGTACAG ATTACAA		

			TAACATGTC	TAATGTT	
			GAACCAAA		
GAM379	RP42	3'	TGTACATAGTCTGTACAATA	21804	CCAT
			TATTGTACAGAC	TACA	
			ATAACATGTCTG	ATGT	
			ATAC		
GAM379	SFRP1	3'	GATTTGTAAAGCTTTACAATA	8933	C ACCCA
			TATTGTA AG	TTACAAATC	
			ATAACAT TC	AATGTTTAG	
			T GA__		
GAM379	SFRS1	3'	TGTAATACGCTGTACAGTA	13804	ACCC
			TATTGTACAG	ATTACA	
			ATGACATGTC	TAATGT	
			GCA_		
GAM379	TFAP2C	3'	TAATGGGGTCTGTAAATA	9222	G _
			TATT TACAGACCC	ATTA	
			ATAA ATGTCTGGG	TAAT	
			_	G	
GAM379	FLJ20054	3'	AATGCAATCTGTATAATA	21130	CC_
			TATTGTACAGA	CATT	
			ATAATATGTCT	GTAA	
			AAC		
GAM379	HRD1	3'	ATTTGTAAATATTGTACAA	34469	ACCCA
			TTGTACAG	TTACAAAT	
			AACATGTT	AATGTTTA	
			ATA__		
GAM379	PAK7	3'	ATTTGTAAATTTTCTGTACGAT	34510	CCC
	A		TATTGTACAGA	ATTACAAAT	
			ATAGCATGTCT	TAATGTTTA	
			TTT		
GAM379	R3HDM	3'	ATTTGCAAGGCTGTACAATG	17659	A CATTA
			TATTGTACAG CC	CAAAT	
			GTAACATGTC GG	GTTTA	
			_ AAC__		
GAM379	LOC146229	3'	TAGTGAATCTGTACAGTA	38114	CC
			TATTGTACAGA	CATTA	
			ATGACATGTCT	GTGAT	
			AA		
GAM380	CLTC	3'	AAAGAGCACCATGATTCCA	11268	AAATATAA
			TGGAATCATGG	CTTT	

ACCTTAGTACC GAAA
 ACGA____
 GAM380 SPAG6 3' CAAAGTTATATTGTGATACTCA 14818 _ A GGA
 TG G ATCAT AATATAACTTTG
 || ||||| |||||
 AC C TAGTG TTATATTGAAAC
 T A ____
 GAM380 ZNF144 3' CAAAGCTTTAGGCATGATTCCA 13990 GAAA TAA
 TGGAATCATG TA CTTTG
 ||||| || |||||
 ACCTTAGTAC AT GAAAC
 GG__ TTC
 GAM380 LOC114971 3' AAAGTTACATTCCTGA 36204 T A
 TCA GGAAAT TAACTTT
 || ||||| |||||
 AGT CCTTTA ATTGAAA
 _ C
 GAM381 AGT 3' CCCCCAGTCTCCAC 5469 A TA
 GTGGGA GATTGGG GG
 ||||| ||||| ||
 CACCCT CTGACCC CC

 GAM381 ASGR2 5' ATCCTACCCAGGCCACCAC 28129 GAAGA
 GTGG TTGGGTAGGAT
 ||| |||||
 CACC GACCCATCCTA
 ACCG_
 GAM381 AXUD1 3' CCTGCCCCCTCCACTTCC 26919 A AAGATT
 A AAGTGGG GGGTAGG
 | ||||| |||||
 C TTCACCT CCGTCC
 C CC____
 GAM381 C20orf1 3' ACCCTCTCCCCACTTTT 14427 A TT
 AAAAGTGGG AGA GGGT
 ||||| ||| |||
 TTTTCACCC TCT CCCA
 C ____
 GAM381 CD4 3' ACCCTTCCTCACCATTCC 6217 A _ A TT
 A AAGTGG GA GA GGGT
 | ||||| || || |||
 C TTCACC CT CT CCCA
 C A C T_
 GAM381 EGR1 3' ATCCTTTCTGCCCCACTTCC 7691 A A TT
 A AAGTGGG AGA GGGT
 | ||||| ||| |||
 C TTCACCC TCT CCTA
 C G TT
 GAM381 ELK1 3' ATCTCCCCCACCTCCCCACTTT 11728 A AT TA
 T AAAAGTGGG AG TGGG GGAT
 ||||| || ||| |||

			TTTTCACCC TC ACCC TCTA		
			C C_ CC		
GAM381	ERBB4	3'	CCTGCTCCAATTTCCCCAC 11744	A	_
			GTGGG AGATTGG GTAGG		
			CACCC TTTAACC CGTCC		
			C T		
GAM381	GFI1	3'	CCCCACAGTCCTTCCCATTTC 11769	A	_ _ TA
			A AAGTGGGAAG ATTG GG GG		
			C TTTACCCTTC TGAC CC CC		
			C C A _		
GAM381	GNB1	3'	CTTACCCCTTTCCAC 7850	ATT	
			GTGGGAAG GGGTAGG		
			CACCTTTC CCCATTC		

GAM381	HLF	3'	CCTGCCTCGCCCCACTTTT 7903	AAGATT	
			AAAAGTGGG GGGTAGG		
			TTTTCACCC TCCGTCC		
			CCGC_		
GAM381	HMGN1	3'	ATCCACCTCATCCCATTTC 11412	A TTG A	
			AAAAGTGGGA GA GGT GGAT		
			TTTTTACCCT CT CCA CCTA		
			A _ C		
GAM381	HUNK	3'	CCTTCCACTTCCCACTTCC 15948	A	AT T
			A AAGTGGGAAG TGGG AGG		
			C TTCACCCTTC ACCT TCC		
			C _ _		
GAM381	MYO1C	3'	CCTGCAATCTCCCAC 30696	A GG	
			GTGGGA GATT GTAGG		
			CACCCT CTAA CGTCC		

GAM381	PMX1	3'	CCTGTCCTCTTCCCAGTT 22914	G	TT GT
			AA TGGGAAGA GG AGG		
			TT ACCCTTCT CC TCC		
			G _ TG		
GAM381	PMX1	3'	CCTGTCCTCTTCCCAGTT 13779	G	TT GT
			AA TGGGAAGA GG AGG		
			TT ACCCTTCT CC TCC		
			G _ TG		
GAM381	RET	3'	ATCCTTTCCCTTACCCAC 21783	_	ATT T
			GTGGG AAG GGG AGGAT		

			CACCC TTC CCT TCCTA		
			A _ T		
GAM381	SMARCD1	3'	CCTATCTCTTCCCAC	29142	TTG
			GTGGGAAGA GGTAGG		
			CACCCTTCT CTATCC		

GAM381	SMARCD1	3'	CCTATCTCTTCCCAC	9044	TTG
			GTGGGAAGA GGTAGG		
			CACCCTTCT CTATCC		

GAM381	UBE2I	5'	CCTAGCTGTGCCCCCACTTT	9353	AAGAT G
			AAAGTGGG TGG TAGG		
			TTTCACCC GTC ATCC		
			CCCGT G		
GAM381	UBE2L3	3'	CTTGCCACTCCCACTTT	9359	AGATTG
			AAAGTGGGA GGTAGG		
			TTTCACCCT CCGTTC		
			CA_____		
GAM381	WNT1	3'	CCCATCTCTCCCACTTCC	11896	A _ T
			A AAGTGGGA AGAT GGG		
			C TTCACCCT TCTA CCC		
			C C _		
GAM381	ZIC1	5'	CCCCCCCACCACTTTT	9447	AAGAT TA
			AAAAGTGGG TGGG GG		
			TTTTCACCC ACCC CC		
			_____ CC		
GAM381	DKFZp547G183	3'	CCTAATCCCCTCACTTTT	20788	AA
			AAAAGTGGG GATTGGG		
			TTTTCACTC CTAATCC		
			CC		
GAM381	FLJ12783	3'	ATCCTACTTCTACCCCCAC	25416	A__ TTG
			GTGGG AGA GGTAGGAT		
			CACCC TCT TCATCCTA		
			CCA _		
GAM381	FLJ13102	3'	CCCACCCGCCTCTTCCCCTTT	24342	T T_ A
			AAAG GGGAAGA TGGGT GG		
			TTTC CCCTTCT GCCCA CC		
			_ CC C		
GAM381	FLJ13848	3'	ATCCCACCCTCTGCCCAACT	24133	_ A TT A
			AGT GGG AGA GGGT GGAT		

TCA CCC TCT CCCA CCTA
 A G _ C
 GAM381 FLJ13993 3' TGCCTACCTTCCCCTT 30328 AT
 AAGTGGGAAG TGGGTA
 ||||| |||||
 TTCACCCTTC ATCCGT
 C_
 GAM381 FLJ22944 3' TTTACATCTTCCCCTTTT 24785 TGG
 AAAAGTGGGAAGAT GTAGG
 ||||| |||||
 TTTTCACCCTTCTA CATT

 GAM381 FLJ32334 3' TCTGAGCCCCCCTTTT 29370 AAGATT A_
 AAAAGTGGG GGGT GGA
 ||||| ||| |||
 TTTTCACCC CCCG TCT
 _____ AG
 GAM381 GTPBP2 3' ATCCTACCACTCTCACCCCACT 21172 A__ TTG
 TT AAAGTGGG AGA GGTAGGAT
 ||||| ||| |||||
 TTTTCACCC TCT CCATCCTA
 CAC CA_
 GAM381 HSPC065 3' ATCCTACCTTCCCCCAC 15449 AA TT
 GTGGG GA GGGTAGGAT
 |||| || |||||
 CACCC CT TCCATCCTA
 C_ _
 GAM381 IMPACT 3' CCTCCCCCCCATT TTTT 20502 AAGATT T
 AAAAGTGGG GGG AGG
 ||||| ||| |||
 TTTTACCC CCC TCC
 _____ C
 GAM381 KIAA0258 3' ATCCATGTCACCTTCCCAC 16643 AT GTA
 GTGGGAAG TGG GGAT
 ||||| ||| |||
 CACCCTTT ACT CCTA
 CC GTA
 GAM381 KIAA0853 3' ACCCCTAAAATCTTACCCAC 17436 _ _
 GTGGG AAGATT GGGT
 |||| ||||| |||
 CACCC TTCTAA CCCA
 A AATC
 GAM381 KIAA1111 3' ATCCGATCCTCCCCTTCC 46019 A T A
 A AAG GGG AATTGGGT
 | ||| ||| |||||
 C TTC CCCT CTAGCCTA
 C _ C
 GAM381 KIAA1854 3' ACCCATCTCCCCCTTCC 35521 A T A T
 A AAG GGG AGAT GGGT
 | ||| ||| |||||

C TTC CCC TCTA CCCA
 C _ C _
 GAM381 KIAA1887 5' CCTGGCCCTTCCCACT 37714 ATT G
 AGTGGGAAG GG TAGG
 ||||| ||||
 TCACCCTTC CC GTCC
 _ G
 GAM381 MGC17330 3' CCTACCACTCCCCGCTTTT 27460 AA TTG
 AAAAGTGGG GA GGTAGG
 ||||| || ||||
 TTTTCGCCC CT CCATCC
 C_ CA_
 GAM381 MGC2541 3' TCCTCACCTTCCCACTTT 27965 AGATT _
 AAAGTGGGA GGGT AGGA
 ||||| ||| ||||
 TTTCACCTT CCCA TCCT
 _ C
 GAM381 P66 3' ACCCTTTCTTCTCCCCATTTT 21842 _ TT
 AAAGTGGG AAGA GGT
 ||||| ||| ||||
 TTTTACCC TTCT CCCA
 CTC TT
 GAM381 STK38L 3' CCCACATCGCTCCCCTTTT 34288 T A_ _
 AAAAG GGGG GAT TGGG
 |||| ||| ||| ||||
 TTTTC CCCT CTA ACCC
 _ CG C
 GAM381 LOC112868 5' ATCCTCACGTCTCCCACTTTT 36076 A TGG _
 AAAAGTGGGA GAT GT AGGAT
 ||||| ||| || ||||
 TTTTCACCCT CTG CA TCCTA
 _ _ C
 GAM381 LOC126528 5' TCCTTCCCTCCCCGCTTT 36845 AAGATT T
 AAAGTGGG GGG AGGA
 ||||| ||| ||||
 TTTTCGCCC CCC TCCT
 CT_ T
 GAM381 LOC126661 5' CCCAGTGTTGCATCCCCACTTC 36849 A _ G
 C A AAGTGGG AA ATTGGG
 | ||||| || |||||
 C TTCACCC TT TGACCC
 C CTACG G
 GAM381 LOC127534 3' CCCAGCTTCCTCCCCTTTT 37166 T_ A
 AAAAG GGGGAG TTGGG
 |||| ||||| ||||
 TTTTC TCCTTC GACCC
 CCC _
 GAM381 LOC144100 3' CCCCCAAGGGTCTTCCCAC 37677 _ TA
 GTGGGAAGAT TGGG GG
 ||||| ||| ||

CACCCCTTCTG ACCC CC
GGA _
GAM381 LOC144289 5' TCCCACCCATCCTCTTTT 40397 T AGAT A
AAAAG GGGG TGGGT GGA
||||| ||| ||||| |||
TTTTTC TCCT ACCCA CCT
_ _ _ C
GAM381 LOC145468 3' CCTGCCCCGCCCCACTTT 36547 AAGATT
AAAGTGGG GGGTAGG
||||||| |||||
TTTCACCC CCCGTCC
GC _
GAM381 LOC145854 3' ATCCCACCTCATCCCATT TTTT 38005 A TTG A
AAAAGTGGGA GA GGT GGAT
||||||| || ||| |||||
TTTTTACCCT CT CCA CCTA
A _ _ C
GAM381 LOC150150 5' CCTGTCCCCTGCCCACT 41135 A ATT _
AGTGGG AG GGG TAGG
||||| || ||| |||||
TCACCC TC CCC GTCC
G _ _ T
GAM381 LOC150155 3' CCTGCCCCGCCCCACTTT 35088 AAGATT
AAAGTGGG GGGTAGG
||||||| |||||
TTTCACCC CCCGTCC
GC _
GAM381 LOC150299 3' ATCTTTGTCAATCTCCCCACTT 41180 A GT
T AAAGTGGG AGATTGG AGGAT
||||||| ||||| |||||
TTTCACCC TCTAACT TTCTA
C GT
GAM381 LOC158956 3' ATCCCACCTCATCCCCTTTT 33096 A TTG A
AAAAGTGGGA GA GGT GGAT
||||||| || ||| |||||
TTTTTACCCT CT CCA CCTA
A _ _ C
GAM381 LOC163412 5' ACCCAGAGCATCTCCCACTTCC 39949 A A _
A AAGTGGGA GAT TGGGT
| ||||| ||| |||||
C TTCACCCT CTA ACCCA
C _ CGAG
GAM381 LOC256222 5' ACCCACCTTCTCACTTCC 46425 A AT
A AAGTGGGAAG TGGGT
| ||||| |||||
C TTCACTCTTC ACCCA
C C_
GAM381 LOC51170 3' ATCCTACCCATTGCCACT 18362 G GAT
AGTGG AA TGGGTAGGAT
||||| || |||||

			TCACC TT ACCCATCCTA			
			G _			
GAM381	LOC90288	3'	TAAGCAATCCTCCCCTTCA 31114	A	A	GG
			A AAGTGGGA GATTG TA			
			A TTCACCCT CTAAC AT			
			C C GA			
GAM382	PTPRC	3'	CTAACGTACATTCAACAGATCA 28150	A		TAAT
			TGAT TGTTGAATGT TTAG			
			ACTA ACAACTTACA AATC			
			G TGC_			
GAM382	PTPRC	3'	CTAAATTAACATTGGGAAATC 8719	ATG	G	
			GAT TT AATGTTAATTTAG			
			CTA GG TTACAATTAAATC			
			AA_ G			
GAM382	PTPRC	3'	CTAAATTAACATTGGGAAATC 28145	ATG	G	
			GAT TT AATGTTAATTTAG			
			CTA GG TTACAATTAAATC			
			AA_ G			
GAM382	KIAA1712	3'	AAATCAACTCAATATATCA 33536		AT	A
			TGATATGTTGA GTT ATTT			
			ACTATATAACT CAA TAAA			
			_ C			
GAM383	KIF5C	3'	TGGCTGCTTTCTCTAACCA 10859	A	_	G
			TG TTAGAGAA GCAG TA			
			AC AATCTCTT CGTC GT			
			C T G			
GAM383	MCP	3'	ACTTGGCTTCTTTAACCA 8204	A	_	
			TG TTAGAGAAGC AGGT			
			AC AATTTCTTCG TTCA			
			C G			
GAM383	SLA	3'	ATTCGCATCTTCTCTATCCA 13596	AT		CAG A
			TG TAGAGAAG GT GAAT			
			AC ATCTCTTC CG CTTA			
			CT TA_ _			
GAM383	SORCS1	3'	ATTCTACCTGCATTTC AATTA 27481	A	A	
			TGATT GAGA GCAGGTAGAAT			
			ATTAA CTTT CGTCCATCTTA			
			_ A			
GAM383	TNFAIP1	3'	ATCTTAGCTTCTTTAATCA 22111		_	
			TGATTAGAGAAGC AGGT			

			ACTAATTTCTTCG TCTA		
			AT		
GAM383	AASDHPPT	3'	TTTACCCCTCTAATTA 17724	AAGCA	
			TGATTAGAG GGTAGA		
			ATTAATCTC CCATTT		
			C____		
GAM383	DDM36	3'	TCTGCATCCTTCTCTAACA 21954	A CAG	
			TG TTAGAGAAG GTAGA		
			AC AATCTCTTC CGTCT		
			CTA		
GAM383	FLJ10853	3'	ATTCTACCTTCATCCTACCCA 20213	AT A AGC	
			TG TAG GA AGGTAGAAT		
			AC ATC CT TCCATCTTA		
			CC _ ACT		
GAM383	FLJ14146	3'	GCTCATGCTTCTCTAATCA 24035	__	
			TGATTAGAGAAGCA GGT		
			ACTAATCTCTTCGT TCG		
			AC		
GAM383	KIAA0534	3'	ATTCTACCCACCTATGGTC 35380	G AAGCA	
			GATTA AG GGTAGAAT		
			CTGGT TC CCATCTTA		
			A CAC__		
GAM383	KIAA1918	3'	ATTCTACCTTTTTCTAACA 36213	A GC	
			TG TTAGAGAA AGGTAGAAT		
			AC AATCTTTT TCCATCTTA		
			CT		
GAM383	MYO5C	3'	TTACTTTTCGCTCTCTAATCA 20818	A __	
			TGATTAGAGA GC AGGTAG		
			ACTAATCTCT CG TTCATT		
			CT		
GAM383	SEMA4G	5'	ATTCTACCCACCTCTATGCA 45409	AT AAGCA	
			TG TAGAG GGTAGAAT		
			AC ATCTC CCATCTTA		
			GT CAC__		
GAM383	LOC152580	5'	CTACCTGCCTCCCATCA 41522	TA_ AA	
			TGAT GAG GCAGGTAG		
			ACTA CTC CGTCCATC		
			CCC __		
GAM383	LOC91660	5'	ATATACCTTTCTAATCA 33207	AAGC GA	
			TGATTAGAG AGGTA AT		

			ACTAATCTT TCCAT TA	
			_____ A_	
GAM383	LOC91660	5'	TCACAGTCTCTCTAATCA 33210	AG AG A
			TGATTAGAGA C GT GA	
			ACTAATCTCT G CA CT	
			CT A_ _	
GAM384	BDKRB2	3'	CCAAAATCACACAGCATTAC 6237	ATTCAATC
			GTAATGTTGTT TTTGG	
			CATTACGACAA AAACC	
			CACTA_____	
GAM384	GIT2	3'	CCAAAGATCAAACACAGCATT 16601	TATTCA
			AATGTTGT ATCTTTGG	
			TTACGACA TAGAAACC	
			CAAAC_	
GAM384	GIT2	3'	CCAAAGATCAAACACAGCATT 27683	TATTCA
			AATGTTGT ATCTTTGG	
			TTACGACA TAGAAACC	
			CAAAC_	
GAM384	GIT2	3'	CCAAAGATCAAACACAGCATT 27696	TATTCA
			AATGTTGT ATCTTTGG	
			TTACGACA TAGAAACC	
			CAAAC_	
GAM384	PP1628	5'	CCAAAGGATGCAACAACAT 24855	ATT A
			ATGTTGTT CA TCTTTGG	
			TACAACAA GT GGAAACC	
			C_ A	
GAM384	LOC154282	3'	CAAAGGTCAACAACAT 41697	ATTCA
			ATGTTGTT ATCTTTG	
			TACAACAA TGGAAAC	
			C_____	
GAM385	LIPA	3'	ATCTATATTCATGAGCTCTCAA 5745	_ TATGC
			TTGAGAG TCATGAAT AGAT	
			AACTCTC AGTACTTA TCTA	
			G TA_____	
GAM385	DKFZP434E2135	3'	CTGAGTCAAGACTCTCAA 25113	A ATTATG
			TTGAGAGTC TGA CAG	
			AACTCTCAG ACT GTC	
			A GA_____	
GAM385	FLJ10232	3'	CTGCAGCAGTGA CTCTCAA 19773	GAATTA
			TTGAGAGTCAT TGCAG	

AACTCTCAGTG ACGTC
 ACG____
 GAM385 FLJ10687 3' ATCTGCATAATGTTCACTGCCA 20007 AG CATGA
 A TTG AGT ATTATGCAGAT
 ||| ||| |||||
 AAC TCA TAATACGTCTA
 CG CTTG_
 GAM385 FLJ10813 3' TCTGCATAATTCTACTT 20167 CAT
 GAGT GAATTATGCAGA
 |||| |||||
 TTCA CTTAATACGTCT
 T_
 GAM385 FLJ13912 3' ATCTGCATAACTCAGCAGTCAA 23027 GA CA A
 TTGA GT TGA TTATGCAGAT
 |||| || ||| |||||
 AACT CG ACT AATACGTCTA
 GA _ C
 GAM385 FLJ20519 3' ATAAATTACGACTCTCAA 19537 A A
 TTGAGAGTC TGA TTAT
 ||||| ||| |||
 AACTCTCAG ATT AATA
 C A
 GAM385 KIAA0217 3' ATCTGTGAAACCCAAACTCTCA 33276 CA AA A
 A TTGAGAGT TG TT TGCAGAT
 ||||| || ||| |||||
 AACTCTCA AC AA GTGTCTA
 A_ CC A
 GAM385 KIAA0417 3' ATCTGCATCTGCTGACCTCAA 35287 A TGAATT
 TTGAG GTCA ATGCAGAT
 |||| ||| |||||
 AACTC CAGT TACGTCTA
 _ CGTC_
 GAM385 KIAA0451 5' CTGCTTTACCCTCATAATTCTC 16806 C ATTAT_
 AA TTGAGAGT ATGA GCAG
 ||||| ||| |||
 AACTCTTA TACT CGTC
 A CCCATTT
 GAM385 KIAA1500 3' CTGATTTCTTGA CTCTCAA 32066 T TTATG
 TTGAGAGTCA GAA CAG
 ||||| ||| |||
 AACTCTCAGT CTT GTC
 T TA_
 GAM385 OCLM 5' TCTCGTAATTCAACAACCCT 22762 A CA C
 AG GT TGAATTATG AGA
 || || ||||| |||
 TC CA ACTTAATGC TCT
 C AC _
 GAM385 LOC151475 5' CTGCCTCATGACTCCCA 41357 A ATTAT
 TG GAGTCATGA GCAG
 || ||||| |||

			AC CTCAGTACT	CGTC	
			C	C	
GAM386	ESRRBL1	3'	AGGATAAATGAATGATG	19739	GAC
			CATCATT TGTTTATCCT		
			GTAGTAA GTAAATAGGA		
GAM386	GDF8	3'	GATAAACTGATGCTA	11766	TTGACT C
			TAGCATCA GTTTAT C		
			ATCGTAGT CAAATA G		
				A	
GAM386	HS3ST4	3'	GAGGAAGGCTAGTCAATAAGCT	36369	ATC _ A
	A		TAGC ATTGACT GTTT TCCTC		
			ATCG TAACTGA CGGA AGGAG		
			AA_ T _		
GAM386	MEF2C	3'	GATAAACAGAAATGCTG	8211	CATTGA
			TAGCAT CTGTTTATC		
			GTCGTA GACAAATAG		
			AA_____		
GAM386	SIP	3'	GATGGGTTTTTAATGATACTA	15757	C CT TT
			TAG ATCATTGA G TATC		
			ATC TAGTAATT T GTAG		
			A TT GG		
GAM386	DKFZp434C0328	3'	GAGGATAAACAGGACAAT	19013	A_
			ATTG CTGTTTATCCTC		
			TAAC GACAAATAGGAG		
			AG		
GAM386	FLJ10307	3'	GAGGATAAGCTAACGATGCTG	19813	A ACT
			TAGCATC TTG GTTTATCCTC		
			GTCGTAG AAT CGAATAGGAG		
			C _____		
GAM386	KIAA0237	3'	AGGAGTTCACAATGATGC	16437	AC TTTA
			GCATCATTG TG TCCT		
			CGTAGTAAC AC AGGA		
			_ TTG_		
GAM386	KIAA1466	3'	ATAAACAACGTGGTGCTA	35602	TGAC
			TAGCATCAT TGTTTAT		
			ATCGTGGTG ACAAATA		
			TCA_		
GAM386	Kv6.3	3'	AGGATGCCAATGATGC	28563	ACTGTT
			GCATCATTG TATCCT		

			CGTAGTAAC	GTAGGA	
			C_____		
GAM386	LOC145566	5'	GAGGATGTTTCAATGATGCT	37898	CTGTT
			AGCATCATTGA	TATCCTC	
			TCGTAGTAACT	GTAGGAG	
			TT____		
GAM386	LOC220766	5'	GATAAACAAGATGCTG	43653	ATTGAC
			TAGCATC	TGTTTATC	
			GTCGTAG	ACAAATAG	
			A_____		
GAM386	LOC253959	5'	AAACAAGAAAATGATGTTA	45507	GA _
			TAGCATCATT	CT GTTT	
			ATTGTAGTAA	GA CAAA	
			AA A		
GAM386	LOC257438	3'	GAGGATAAGCTAACGATGCTG	45107	A ACT
			TAGCATC TTG	GTTTATCCTC	
			GTCGTAG AAT	CGAATAGGAG	
			C ____		
GAM386	LOC91012	5'	GATAAACATCACTTGAGC	32283	A T_ C
			GC TCA	TGA TGTTTATC	
			CG AGT	ACT ACAAATAG	
			_ TC _		
GAM387	ADAM11	3'	ACATTTACAGGAGGCCCGGA	8206	C GGCGATC
			TCCG GGGC	GTAAATGT	
			AGGC CCCG	CATTTACA	
			_ GAGGA__		
GAM387	ADAM11	3'	ACATTTACAGGAGGCCCGGA	22239	C GGCGATC
			TCCG GGGC	GTAAATGT	
			AGGC CCCG	CATTTACA	
			_ GAGGA__		
GAM387	FLJ10206	5'	ACCTTCCCCCGCCCGCGGA	19766	C_ TC
			TCCGCGGGCGG	GA GT	
			AGGCGCCCGCC	CT CA	
			CC TC		
GAM388	LRR2	5'	CTCTGCGGTGTAAACAGCCGCG	23704	AGCGAC
			CGCGGT	TACACCGCAGAG	
			GCGCCG	ATGTGGCGTCTC	
			ACAA__		
GAM389	ATP2A2	3'	ATGAGCGTCGCACAGACA	7400	C C GG
			TG CT	GTGCGACGC AT	

AC GA CACGCTGCG TA
 A _ AG
 GAM389 GNB2 5' CATCCGCGCCGCGCCGC 11777 CT T A
 GC CG GCG CGCGGATG
 || || || || || || || ||
 CG GC CGC GCGCCTAC
 CC _ C
 GAM389 HDAC4 3' ATTCAGTTGACACGAGGCA 12660 _ GC
 TGCCTCGTG CGAC GGAT
 || || || || || || || ||
 ACGGAGCAC GTTG CTTA
 A A_
 GAM389 FLJ20699 3' GATTCATCAGGGCAGGAAGCA 19618 C G GACGCG
 TGC TC TGC GATGAATC
 || || || || || || || ||
 ACG AG ACG CTA CTTAG
 A G GGA_
 GAM389 MGC15937 5' ATTCATTTTGACCACGAGGCA 27948 CGA C
 TGCCTCGTG CG GGATGAAT
 || || || || || || || ||
 ACGGAGCAC GT TTTACTTA
 CA _ _
 GAM390 ALPPL2 3' GCACCCATACCTAGGACCCC 34139 CC CT A_
 GG GG CTAGGTATG GC
 || || || || || || || ||
 CC CC GATCCATAC CG
 _ AG CCA
 GAM390 EFNB1 3' CCTCCCAGAGCAGCCA 10708 CG A TAT C
 TGGC GCTCT GG GAG G
 || || || || || || || ||
 ACCG CGAGA CC CTC C
 A _ _ _ A
 GAM390 OGG1 5' GCAGAGAGCCCAGTGCCGGCCA 18809 T A ATGA_
 TGGCCGGC CT GGT GC
 || || || || || || || ||
 ACCGGCCG GA CCG CG
 T C AGAGA
 GAM390 OGG1 5' GCAGAGAGCCCAGTGCCGGCCA 8392 T A ATGA_
 TGGCCGGC CT GGT GC
 || || || || || || || ||
 ACCGGCCG GA CCG CG
 T C AGAGA
 GAM390 OGG1 5' GCAGAGAGCCCAGTGCCGGCCA 18814 T A ATGA_
 TGGCCGGC CT GGT GC
 || || || || || || || ||
 ACCGGCCG GA CCG CG
 T C AGAGA
 GAM390 ALK7 5' GCGCCCACTGACTAGAGCCA 37297 CC _ A A
 ACC GG GCTCTAG GT TG GCGC
 || || || || || || || ||

CC CCGAGATC CA AC CGCG
 AA AGT C C
 GAM390 KIAA1193 3' CGCAGGGCAGAGCCGGCCA 33581 AG ATGA
 TGGCCGGCTCT GT GCG
 ||||| || ||
 ACCGGCCGAGA CG CGC
 _ GGA_
 GAM390 MGC2835 3' GCCTGACCCAGGCCGGCCA 23505 T A ATGA
 TGGCCGGC CT GGT GC
 ||||| || || ||
 ACCGGCCG GA CCA CG
 _ C GTC_
 GAM390 LOC124044 3' GCAGGCCTAAGCCGGCCA 37431 C ATGA
 TGGCCGGCT TAGGT GC
 ||||| || || ||
 ACCGGCCGA ATCCG CG
 _ GA_
 GAM390 LOC256158 5' GCACTGAACCAGGCCGGCCA 46628 T A ATG C
 TGGCCGGC CT GGT AG GC
 ||||| || || || ||
 ACCGGCCG GA CCA TC CG
 _ _ AG_ A
 GAM391 CX3CR1 3' TCCAATCTAACCACATCA 34981 G A
 TGA GTGGTTAGATTG GG
 || ||||| || ||
 ACT CACCAATCTAAC CT
 A _
 GAM391 TRIM14 3' CGCACCTCACCACCATCA 16667 _ TTAGAT CA
 TGA GGTGG TGAGGG CG
 || |||| || || || ||
 ACT CCACC ACTCCC GC
 A CC_ AC
 GAM391 APBA2BP 3' TGCCCTCATCCCACCCA 25278 A TTA T
 TG GGTGG GAT GAGGGCA
 || |||| || |||||
 AC CCACC CTA CTCCCGT
 _ _ _
 GAM391 FLJ13241 3' TGCCCTCAGTGACACCTCA 24711 GTTAG
 TGAGGTG ATTGAGGGCA
 ||||| |||||
 ACTCCAC TGA CTCCCGT
 AG_
 GAM391 KIAA0914 5' TGCCCCCAACCCAGCTTA 17037 G TTAGA A
 TGAG TGG TTG GGGCA
 ||| || || |||||
 ATTC ACC AAC CCCGT
 G C_ C
 GAM391 KIAA1796 5' TGCCCTCAACAGCCCC 43966 T AGA
 GG GGT TTGAGGGCA
 || |||| |||||

CC CCGA AACTCCCGT
 _ C_
 GAM391 SEPT3 3' CCCTCAACCGTTCTCA 21181 _ TAGAT
 TGAGG TGGT TGAGGG
 ||||| |||| |||||
 ACTCT GCCA ACTCCC
 T ____
 GAM391 LOC116437 3' TGCCCTCAAATGCACCCA 36583 A GTTAGA
 TG GGTG TTGAGGGCA
 || |||| |||||
 AC CCAC AACTCCCGT
 _ GTA_
 GAM391 LOC222134 5' TGTCATCCAACCCCTCA 45172 T A TGAG
 TGAGG GGTT GAT GGCA
 ||||| |||| ||||
 ACTCC CCAA CTA CTGT
 _ C ____
 GAM392 LOC125704 3' CGCCAACCTCCTCCAAGCCAC 36799 TTG_ C
 GT TGGAGGAG TGGCG
 || ||||| |||||
 CA ACCTCCTC ACCGC
 CCGA A
 GAM393 AS3 3' AGGTACGGCGGCGAAGTG 18048 CTA _
 CACT TGT GCCGTACCT
 |||| ||||| |||||
 GTGA GCG CGGCATGGA
 A_ G
 GAM393 CIT 5' ACGGCACATAGAGATGAA 34561 CA
 TTCA CTCTATGTGCCGT
 |||| ||||| |||||
 AAGT GAGATACACGGCA
 A_
 GAM393 FMR1 3' ATGGCACAGGGCATGAA 7774 CA AT
 TTCA CTCT GTGCCGT
 |||| |||| |||||
 AAGT GGA CACGGTA
 AC _
 GAM393 RDX 3' CACAATGGAGTGTGTAAG 8807 _ _
 CTT CACACTCTAT GTG
 ||||| ||||| |||||
 GAA GTGTGAGGTA CAC
 T A
 GAM393 C20orf130 5' AGGTACGGCGGCAATGTGAGG 30935 CTCTA _
 CTTACA TGT GCCGTACCT
 ||||| ||||| |||||
 GGAGTGT ACG CGGCATGGA
 A_ G
 GAM393 CDK5RAP3 5' GGCACAGTCTGTGAGTGGGAAG 24853 A TA_
 CTTCA CACTC TGTGCC
 ||||| ||||| |||||

			GAAG GTGAG ACACGG		
			G TGTCTG		
GAM393	CXYorf1	5'	AGGTACAGCACATAGGCCAGGA 39902	ACAC	C
		G	CTTC TCTATGTGC GTACCT		
			GAGG GGATACACG CATGGA		
			ACC_ A		
GAM393	FLJ12704	3'	AGGAATGACACAGAGCATGGAG 24562	CA AT C A	
			CTTCA CTCT GTG CGT CCT		
			GAGGT GAGA CAC GTA GGA		
			AC _ A A		
GAM393	HCA4	3'	GTTTTGCCATAGAGTGTGA 38026	T CGT	
			TCACACTCTATG GC AC		
			AGTGTGAGATAC CG TG		
			_ TTT		
GAM393	KIAA0427	3'	GGACCAGAGTGTGAAG 16576	AT G	
			CTTCACACTCT GT CC		
			GAAGTGTGAGA CA GG		
			C_ _		
GAM393	MSTP028	3'	GTATGAATGAGTGTGAAG 25695	TAT GC	
			CTTCACACTC GT CGTAC		
			GAAGTGTGAG TA GTATG		
			_ A_		
GAM393	LOC120939	5'	TATGGCACAGAGCATTGAA 37514	CA_ AT	
			TTCA CTCT GTGCCGTA		
			AAGT GAGA CACGGTAT		
			TAC _		
GAM393	LOC149301	3'	AGGTATATACATAGAATGT 38688	C CC	
			ACA TCTATGTG GTACCT		
			TGT AGATACAT TATGGA		
			A A_		
GAM393	LOC152274	3'	AGGCACAGCACTTACAAGGGTG 39229	AT_ C A	
		TGAAG	CTTCACACTCT GTGC GT CCT		
			GAAGTGTGGGA CACG CA GGA		
			ACATT A C		
GAM393	LOC200093	5'	AGGTACAGCACATAGGCCAGGA 31594	ACAC C	
		G	CTTC TCTATGTGC GTACCT		
			GAGG GGATACACG CATGGA		
			ACC_ A		
GAM394	ARNT2	3'	CTGAGCCTTCGTTCTTCAG 16935	CC CCGGC	
			CTGA AAC AAGGCTCAG		

			GA	CT	TTG	TTCCGAGTC		
				TC	C			
GAM394	CRACC	3'	CTGAGCTTACACTAATTGGTCA	22155		CCCGGCA		
	GA		TCTGACCAA	AGGCTCAG				
			AGACTGGTT	TTCGAGTC				
			AATCACA					
GAM394	DFFB	3'	CTGAACCCTGCTCCGTTGGTCA	42241		CC	A	C
	G		CTGACCAAC	GGCA GG TCAG				
			GA	CTGGTTG TCGT CC AGTC				
			CC	C A				
GAM394	G6PT1	5'	TGAGCCTCTGGCTGCCAGA	7201		AC	AC	CA
			TCTG	CA CCGG AGGCTCA				
			AGAC	GT GGTC TCCGAGT				
			C	C				
GAM394	HD	3'	CTGAGCCTCTCTCGGTCA	7894		AACCC	CA	
			TGACC	GG AGGCTCAG				
			ACTGG	TC TCCGAGTC				
			C					
GAM394	VCL	3'	TGAGCCTGGCTGGCACAGA	9407		ACCAAC	A	
			TCTG	CCGGC AGGCTCA				
			AGAC	GGTCG TCCGAGT				
			AC					
GAM394	VCL	3'	TGAGCCTGGCTGGCACAGA	15196		ACCAAC	A	
			TCTG	CCGGC AGGCTCA				
			AGAC	GGTCG TCCGAGT				
			AC					
GAM394	DKFZp547C176	5'	TGAGCCTACCGCCGCCAGA	33383		ACCAACC	A	
			TCTG	CGGC AGGCTCA				
			AGAC	GCCG TCCGAGT				
			C					
GAM394	FLJ10815	3'	CTGTGTGGGCTGGGCTGGTCAG	20171		A	AAG	T
	A		TCTGACCA	CCCGGC GC CAG				
			AGACTGGT	GGGTCG TG GTC				
			C	GG				
GAM394	FLJ20320	3'	CTGAGCCTTGTGACTTGAGCAG	19382		AC	CC	G
	A		TCTG	CAA CG CAAGGCTCAG				
			AGAC	GTT GT GTTCCGAGTC				
			GA	CA				
GAM394	FLJ23191	5'	CTGAGCCTCCAGGAGCTGCCAG	23802		ACCAA	C	CA
	A		TCTG	CC GG AGGCTCAG				

			AGAC	GG CC	TCCGAGTC		
			CGTCGA	A	__		
GAM394	KIAA0449	3'	AGCCTTTGAGGTGGTCAGA	19050		A	_ GC
			TCTGACCA CC CG	AAGGCT			
			AGACTGGT GG GT	TTCCGA			
			_ A	__			
GAM394	TIP47	3'	CTGAGCCTCACCCCTATCAGTCA	12417		CAACCC	CA
	G		CTGAC	GG AGGCTCAG			
			GACTG	CC TCCGAGTC			
			ACTATC	AC			
GAM394	LOC145757	5'	AGCTGCTCCCGGGTTGCCAGA	37969		AC	CAA_
			TCTG CAACCCGG	GGCT			
			AGAC GTTGGGCC	TCGA			
			C_	CTCG			
GAM394	LOC146481	3'	CTGAGCCTGTCAGTGGGTCAGA	38176		A CC	A
			TCTGACC AC	GGCA GGCTCAG			
			AGACTGG TG	CTGT CCGAGTC			
			G A_	_			
GAM394	LOC90333	3'	CTGGGTTTCACCGTGTAGCCA	31224		ACC C	CA
	GA		TCTG AAC CGG	AGGCTCAG			
			AGAC TTG GCC	TTTGGGTC			
			CGA T	AC			
GAM395	GIT2	3'	TTGGCAAATCGCACCTTA	16606		C	CTA
			TAAGGTGCG AT	CCAA			
			ATTCCACGC TA	GGTT			
			_ AAC				
GAM395	GIT2	3'	TTGGCAAATCGCACCTTA	27688		C	CTA
			TAAGGTGCG AT	CCAA			
			ATTCCACGC TA	GGTT			
			_ AAC				
GAM395	GIT2	3'	TTGGCAAATCGCACCTTA	27701		C	CTA
			TAAGGTGCG AT	CCAA			
			ATTCCACGC TA	GGTT			
			_ AAC				
GAM395	KIAA1196	3'	CCTTGATGTTTAGCACTTTA	30819		__	TACC
			TAAGGTGC GCATC	AAGG			
			ATTCACG TG	TAG TTCC			
			ATT	__			
GAM395	ZFP36L2	3'	ATGCCTTGATAGTTAGCCCT	13752		T GCAT	C
			AGG GC	CTA CAAGGCAT			

			TCC CG	GAT GTTCCGTA			
			_ ATT_	A			
GAM396	THY1	3'	AGGAGACAGGAAGCCTCAA	12975	A	A	
			TTGA GCTTCCTG CTCCT				
			AACT CGAAGGAC GAGGA				
			C	A			
GAM396	DKFZp547I224	5'	AACAGAGCAGCCGGAAGCTCC	21471	A	A C A	
	AA		TTG AGCTTCCTG CT CT TGTT				
			AAC TCGAAGGGC GA GA ACAA				
			C	C C G			
GAM396	GTPBP5	3'	GTGGGAGCCAGGAAGCCTCAG	32576	A	A	
			TTGA GCTTCCTG CTCCTAT				
			GACT CGAAGGAC GAGGGTG				
			C	C			
GAM396	LOC145845	3'	AACATGTCGTCAGAACTT	40615	C	TCC	
			AAG TTCCTGAC TATGTT				
			TTC AAGGACTG GTACAA				
			A	CT_			
GAM397	SLC22A1LS	5'	CATGAAACCCCCACCCCCAC	13962	A CAA	G	
			GTGG GG GGGTTT ATG				
			CACC CC CCCAAA TAC				
			C ACC	G			
GAM397	ARHGEF2	3'	GTGGAACCTTGCCCCCA	11091	A	G	
			TGG GGCAAGGGTTT AT				
			ACC CCGTTCCCAAG TG				
			C	G			
GAM397	FLJ12681	3'	CAAACCTCGCCCCACA	23035	A A		
			TGTGG GGC AGGGTTTG				
			ACACC CCG TCCCAAAC				
			_ C				
GAM397	FLJ30213	3'	CAACCCCTCCCCTGCCTCCAC	29608	_____	T	
			GTGGAGGCA AGGG TTG				
			CACCTCCGT TCCC AAC				
			CCCC	C			
GAM397	LOC153688	3'	AACATCAAGGCCACCACA	41651	A AAGGG		
			TGTGG GGC TTTGATGTT				
			ACACC CCG GAACTACAA				
			A	_____			
GAM397	LOC222066	3'	AACAGAGACCCTGCCTCGACA	44552	G A	GA	
			TGT GAGGCA GGGTTT TGTT				

ACA CTCCGT CCCAGA ACAA
 G _ G_
 GAM397 LOC91464 5' AAGGTGGACCCCTGCCTCCA 32871 A G G
 TGGAGGCA GGGTTT AT TT
 ||||| ||||| || ||
 ACCTCCGT CCCAGG TG AA
 C _ G
 GAM398 CYP46 3' CGCCTGCTTCACACCCCTCA 13483 TACA C_
 TGAGGGGT AAGC GCG
 ||||| ||| |||
 ACTCCCCA TTCG CGC
 CAC_ TC
 GAM398 RALBP1 3' GCTCACTTTGTACCCCTCA 13663 T CC_
 TGAGGGGT ACAAAG GC
 ||||| ||||| ||
 ACTCCCCA TGT TTC CG
 _ ACT
 GAM398 C22orf19 3' GAACACGGCTCACTGCCGCCTC 9775 _ TACAA C
 A TGAGG GGT AGCCG GTTC
 ||||| ||| ||||| |||||
 ACTCC CCG TCGGC CAAG
 G TCAC_ A
 GAM399 DAZL 3' TGTCCAGAAGAGTCA 33802 TG TC
 TGACTCTT CTG GACA
 ||||| ||| |||||
 ACTGAGAA GAC CTGT
 _ _
 GAM399 EXO1 5' AAGGTGTCAACAGGGTAGTTA 28181 _ TTG C
 TGACT CT CTGT GACACCTT
 ||||| || ||| |||||
 ATTGA GG GACA CTGTGGAA
 T _ A
 GAM399 FOLR1 5' AAGGTGCAGGGGGCAAAGG 18782 G GA
 TCTTTGCT TC CACCTT
 ||||| || |||||
 GGAAACGG GG GTGGAA
 G AC
 GAM399 PPP2CA 3' AAGGATAGCAGCAAACAATCA 8581 CTC CGACA
 TGA TTTGCTGT CCTT
 ||| ||||| |||
 ACT AAACGACG GGAA
 AAC ATA_
 GAM399 TARBP2 3' AAGGCACAGGGCAAGGAGCCA 28626 A GTCGACA
 TG CTCTTTGCT CCTT
 || ||||| |||
 AC GAGGAACGG GGAA
 C GACAC_
 GAM399 FLJ20136 3' TGTGAAGCAAAGGTCA 19233 T G G
 TGAC CTTTGCT TC ACA
 ||||| ||||| || |||

ACTG GAAACGA AG TGT

GAM399 KIAA0433 3' AAGGTACCAGATGTAAGAGTCA 17545 T T GAC_
TGACTCTT GC GTC ACCTT
||||||| || ||| |||||
ACTGAGAA TG TAG TGGAA
_ _ ACCA
GAM399 KIAA0446 3' AAGGTGTCAATGGGGAGTGTCA 34143 T G C
TGAC CTTT CTGT GACACCTT
||| ||| ||| |||||
ACTG GAGG GGTA CTGTGGAA
T _ A
GAM399 KIAA1826 5' AGGGCCAGCAAAGAATTA 33375 C TCGACA
TGA TCTTTGCTG CCT
|| ||||| |||
ATT AGAAACGAC GGA
A CG____
GAM399 KIF13B 3' AAGGCGCCAACAGAGTAGTC 40309 _ C T ACA
GACT CTTTG TG CG CCTT
||| ||||| || |||
CTGA GAGAC AC GC GGAA
T A C ____
GAM399 KIF13B 3' AAGGCGCCAACAGAGTAGTC 17581 _ C T ACA
GACT CTTTG TG CG CCTT
||| ||||| || |||
CTGA GAGAC AC GC GGAA
T A C ____
GAM399 LOC219940 5' AAGGCACTTGAGCAAAGGTCA 44830 T G CA_
TGAC CTTTGCT TCGA CCTT
||| ||||| ||| |||
ACTG GAAACGA GGTT GGAA
_ _ CAC
GAM399 LOC253675 5' AAGGTGTTACAAAGAGCA 46262 A CTGTC
TG CTCTTTG GACACCTT
|| ||||| |||||
AC GAGAAAC TTGTGGAA
_ A____
GAM399 LOC255919 3' GTGATACAGCAAAAAGCCA 45557 A C CGA
TG CT TTTGCTGT CAC
|| ||||| |||
AC GA AAACGACA GTG
C A TA_
GAM399 LOC91012 5' AAGGTAAGTGGGCAAAGA 32279 GT AC_
TCTTTGCT CG ACCTT
||||||| || |||||
AGAAACGG GT TGGAA
_ GAA
GAM399 LOC92539 3' AAGGTCACCAACAGCAAAGA 34496 CGAC_
TCTTTGCTGT ACCTT
||||||| |||||

			AGAAACGACA	TGGAA		
			ACCAC			
GAM400	COL4A6	3'	CACAACTGTCTTAGACTGC	7581	TTAT	A A
			GCAGTCTGA	GACA TT TG		
			CGTCAGATT	CTGT AA AC		
			_____	C C		
GAM400	COL4A6	3'	CACAACTGTCTTAGACTGC	27357	TTAT	A A
			GCAGTCTGA	GACA TT TG		
			CGTCAGATT	CTGT AA AC		
			_____	C C		
GAM400	TNFRSF10B	3'	CCACAATTGTCACATGAC	9936	_ ATTA	A
			GTC TG	TGACAATT TGG		
			CAG AC	ACTGTTAA ACC		
			T _____	C		
GAM400	LOC154084	5'	GTTGCCAGAATCAGACTGC	41684		A A
			GCAGTCTGATT	TG CAAT		
			CGTCAGACTAA	AC GTTG		
			_____	G C		
GAM401	AKT1	3'	TCTCCGGGTGTGGCCTCA	11654	ATCA A	A
			TGAG	GC TGCACCCG AGA		
			ACTC	CG GTGTGGGC TCT		
			_____	_____	C	
GAM401	ATP7A	3'	TTCTTCATGTAGTCTGCTGATC	5501	T _ CC	
	TCA		TGAGATCAGCA	GC AC GAAGAA		
			ACTCTAGTCGT	TG TG CTTCTT		
			_____	C A TA		
GAM401	CBLB	5'	TTCTTCGGGAGCGAGCTGTTCT	10553	T A A	
	CA		TGAGA CAGC	TGC CCCGAAGAA		
			ACTCT	GTCG GCG GGGCTTCTT		
			_____	T A A		
GAM401	OPA1	3'	TTCTTCTTTTTAGCTGATCTCA	28325	ATGCACCC	
			TGAGATCAGC	GAAGAA		
			ACTCTAGTCG	CTTCTT		
			ATTTT	_____		
GAM401	OPA1	3'	TTCTTCTTTTTAGCTGATCTCA	28333	ATGCACCC	
			TGAGATCAGC	GAAGAA		
			ACTCTAGTCG	CTTCTT		
			ATTTT	_____		
GAM401	OPA1	3'	TTCTTCTTTTTAGCTGATCTCA	28341	ATGCACCC	
			TGAGATCAGC	GAAGAA		

			ACTCTAGTCG	CTTCTT		
			ATTTTT__			
GAM401	OPA1	3'	TTCTTCTTTTTAGCTGATCTCA	28349	ATGCACCC	
			TGAGATCAGC	GAAGAA		
			ACTCTAGTCG	CTTCTT		
			ATTTTT__			
GAM401	OPA1	3'	TTCTTCTTTTTAGCTGATCTCA	28357	ATGCACCC	
			TGAGATCAGC	GAAGAA		
			ACTCTAGTCG	CTTCTT		
			ATTTTT__			
GAM401	TIRAP	5'	TTCCTCAGCTGGTCATGCTGAG	27479	A C C__ A	
	CTCA		TGAG TCAGCATG ACC	GA GAA		
			ACTC AGTCGTAC TGG	CT CTT		
			G _ TCGA C			
GAM401	DKFZP434P1750	3'	TCCTCGCCAGCTGCTGATC	17794	T ACC A	
			GATCAGCA GC	CGA GA		
			CTAGTCGT CG	GCT CT		
			_ ACC C			
GAM401	HCA3	5'	TCTCCGACTGATCGCTGATCTC	28951	ATG CC A	
	A		TGAGATCAGC	CA CG AGA		
			ACTCTAGTCG	GT GC TCT		
			CTA CA C			
GAM401	KIAA0876	3'	TCTTCGGGTACAACCCTGA	32300	CA_ C	
			TCAG TG	ACCCGAAGA		
			AGTC AC	TGGGCTTCT		
			CCA A			
GAM401	MGC12981	3'	TTCTCCGACATGGCTACGTGAT	26143	GCAT ACC__ A	
	CTCA		TGAGATCA GC	CG AGAA		
			ACTCTAGT CG	GC TCTT		
			GCAT GTACA C			
GAM401	NAG14	3'	TCTTCTAAATGCTGATTCA	22706	A GCACCC	
			TGAG TCAGCAT	GAAGA		
			ACTT AGTCGTA	CTTCT		
			_ AAT__			
GAM401	ST7L	3'	TCTTCACCACTGATCTC	28979	CA CACCC	
			GAGATCAG TG	GAAGA		
			CTCTAGTC AC	CTTCT		
			_ CA__			
GAM401	ST7L	3'	TCTTCACCACTGATCTC	29210	CA CACCC	
			GAGATCAG TG	GAAGA		

CTCTAGTC AC CTTCT
 _ CA_
 GAM401 ST7L 3' TCTTCACCACTGATCTC 19337 CA CACCC
 GAGATCAG TG GAAGA
 ||||| || ||||
 CTCTAGTC AC CTTCT
 _ CA_
 GAM401 TA-PP2C 3' TCTTTGCCACTGATCTCA 29285 CAT CCCG
 TGAGATCAG GCA AAGA
 ||||| || ||||
 ACTCTAGTC CGT TTCT
 AC_ _
 GAM401 LOC90593 3' TCAAGTGGGTCCCTGATCTC 31766 CATGC AA_
 GAGATCAG ACCCG GA
 ||||| |||| ||
 CTCTAGTC TGGGT CT
 CC_ GAA
 GAM402 HUS1 3' CTAGAGAGCTGGCCCAGCCA 43790 AAC A AA_
 TGGC TGGGCCA GTT TAG
 ||| ||||| ||| |||
 ACCG ACCCGGT CGA ATC
 _ _ GAG
 GAM402 NDRG1 3' TCCATTAACCACTGGCCGGTTG 29970 G A_ A
 CCA TGGCAACTGG CCA GTTAAT GA
 ||||| ||| ||||| ||
 ACCGTTGGCC GGT CAATTA CT
 _ GAC C
 GAM402 HSPC138 5' TCTTGCCGCTGGCCCAGTCACT 18538 CA A TAAT
 A TGG ACTGGGCCA GT AGA
 ||| ||||| || |||
 ATC TGACCCGGT CG TCT
 AC _ CCGT
 GAM402 HSPC251 3' ATTAACCTCGCTCCCA 18584 CAACT C
 TGG GGGC AAGTTAAT
 ||| ||| |||||
 ACC CTCG TTCAATTA
 _ C
 GAM402 IDN3 3' TCTTTAGCTTAGCCCAGTTTCC 28512 C C T
 A TGG AACTGGGC AAGTTAA AGA
 ||| ||||| ||||| |||
 ACC TTGACCCG TTCGATT TCT
 T A _
 GAM402 KIAA0284 3' TCTGGTGCCAACACAGTTGCCA 31620 GGCCAA TAA
 TGGCAACTG GT TAGA
 ||||| || ||||
 ACCGTTGAC CG GTCT
 ACAAC_ TG_
 GAM402 KIAA0844 3' TCTAAAGTAACTGGCCCCAGTCT 17285 CA A A_
 CCA TGG ACTGGGCCA GTTA TAGA
 ||| ||||| ||| ||||

ACC TGACCCGGT CAAT ATCT
 TC _ GAA
 GAM402 KIAA1068 3' GACTGGCCAGTCTCCA 17645 CA A
 TGG ACTGGGCCA GTT
 ||| ||||| |||
 ACC TGACCCGGT CAG
 TC _
 GAM402 KIAA1169 5' TGGCCCCGGCCAGTTCCCA 19566 C AA_
 TGG AACTGGGCC GTTA
 ||| ||||| |||
 ACC TTGACCCGG CGGT
 C CCC
 GAM402 KIAA1305 3' CTGGTCTAGCCCAGGTTGCCA 24682 _ CA TTAA
 TGGCAAC TGGGC AG TAG
 ||||| |||| || |||
 ACCGTTG ACCCG TC GTC
 G A_ TG_
 GAM402 KIAA1881 3' CTGATGGCTCAACCCAGTCCCA 45656 CA CCA A
 TGG ACTGGG AGTTA TAG
 ||| ||||| ||||| |||
 ACC TGACCC TCGGT GTC
 C_ AAC A
 GAM402 KIAA1932 3' TCTACCAGGACAAGGCCAGTC 36351 CA AA AA_
 CCA TGG ACTGGGCC GTT TAGA
 ||| ||||| ||| |||
 ACC TGACCCGG CAG ATCT
 C_ AA GACC
 GAM402 PB1 3' TCTATTA ACTCAGAGGCTCA 19983 A_
 TGGGCC AGTTAATAGA
 ||||| ||||| |||
 ACTCGG TCAATTATCT
 AGAC
 GAM402 ZDHC8 3' GGCTTGGCCCACTGCCA 31963 AC
 TGGCA TGGGCCAAGTT
 ||||| ||||| |||
 ACCGT ACCCGGTTCTGG
 C_
 GAM402 LOC145547 3' CTGGTCTAGCCCAGGTTGCCA 37892 _ CA TTAA
 TGGCAAC TGGGC AG TAG
 ||||| |||| || |||
 ACCGTTG ACCCG TC GTC
 G A_ TG_
 GAM402 LOC152765 5' CTATGGGGCCCACTGCCA 39314 A AAGTTA
 TGGCA CTGGGCC ATAG
 ||||| ||||| |||
 ACCGT GACCCGG TATC
 _ GG_
 GAM402 LOC161635 5' GGCTTGGCCCACTGCCA 46185 CAA
 TGG CTGGGCCAAGTT
 ||| ||||| |||||

ACC GACCCGGTTCGG
 TCC
 GAM402 LOC253842 3' CTGTCTAGCCAGTTCCCA 46504 C CA TTA
 TGG AACTGGGC AG ATAG
 ||| ||||| || |||
 ACC TTGACCCG TC TGTC
 C A_ _
 GAM402 LOC91149 3' AACAGTGACCACAGTTGCCA 32452 _ C A_
 TGGCAACTG GG CA GTT
 ||||| || || |||
 ACCGTTGAC CC GT CAA
 A A GA
 GAM403 CDK5R2 3' TTTGTGTGTCTGCATCTCCATC 10044 A GT_
 TTA TAGGATG AGATGCAG TATAAA
 ||||| ||||| |||||
 ATTCTAC TCTACGTC GTGTTT
 C TGT
 GAM403 WHN 3' TTTATTCCCCCATCTTCATCC 9651 CA TT
 GGATGAAGATG GG ATAAA
 ||||| || |||||
 CCTACTTCTAC CC TATTT
 C_ CT
 GAM403 APOL4 3' TTTGTGACCCACACCCACACCC 24980 A AAGA CA
 TA TAGG TG TG GGTTATAAA
 ||| || || |||||
 ATCC AC AC CCAGTGTTT
 C ACCC AC
 GAM403 DCOHM 3' TATAACCTCACCATCC 25849 AAGA C
 GGATG TG AGGTTATA
 |||| || |||||
 CCTAC AC TCCAATAT
 C_ _
 GAM403 FLJ22028 3' TTTATAACCTGAAATCATCT 24287 AGATG
 GGATGA CAGGTTATAAA
 |||| |||||
 TCTACT GTCCAATATTT
 AAA_
 GAM403 KIAA0441 3' TTATAATGCCCTCCATCC 16716 A AT GG
 GGATG AG GCA TTATAA
 |||| || || |||||
 CCTAC TC CGT AATATT
 C C_ _
 GAM403 RNF34 3' TTATTTCCCCTTCATCCTA 24770 ATGCA TT
 TAGGATGAAG GG ATAA
 ||||| || |||
 ATCCTACTTC CC TATT
 C_ TT
 GAM403 STX12 3' TGATTGCCCTTCATCC 32984 AT G
 GGATGAAG GCAG TTA
 ||||| ||| |||

CCTACTTC CGTT AGT
 C_ _
 GAM403 LOC146733 5' ACACTCCATCTTCACCCT 40725 A C _
 AGG TGAAGATG AG GT
 ||| ||||| || ||
 TCC ACTTCTAC TC CA
 C C A
 GAM403 LOC219686 3' TTTATATAGATATCTTCATGCC 43678 _ CAGGT
 GG ATGAAGATG TATAAA
 || ||||| |||||
 CC TACTTCTAT ATATTT
 G AGAT_
 GAM404 FBXL11 3' CACTTCCATTGGTCTCCAGGCC 14680 AA G T__
 CCAA TTG GCCTGGGGGA TA GAAGTG
 ||| ||||| || |||||
 AAC CGGACCTCT GT CTTCAC
 CC G TAC
 GAM404 GALNT1 3' CACTCCATACTCAAATATGCTT 21723 C GG_ A
 CA TGAAGC TG GAGTATG AGTG
 ||||| || ||||| |||||
 ACTTCG AT CTCATAC TCAC
 T AAA C
 GAM404 RABGGTA 5' CACTTCTCTCCTCAGACTTCAA 10930 C TAT
 TTGAAG CTGGGGAG GAAGTG
 ||||| ||||| |||||
 AACTTC GACTCCTC CTTCAC
 A T__
 GAM404 RGS3 5' CAGACTCCCCAGGGCTTCAA 22087 _ A
 TTGAAGCC TGGGGAGT TG
 ||||| ||||| ||
 AACTTCGG ACCCCTCA AC
 G G
 GAM404 DKFZP434H132 5' CACCCTCTCCAGGCCTCAA 36446 A TA
 TTGA GCCTGGGGAG TG
 ||| ||||| ||
 AACT CGGACCTCTC AC
 C CC
 GAM404 KIAA1600 3' CACTTCATACAAGGAAACTTC 35392 ____ GGGGA
 GA TGAAG CCT GTATGAAGTG
 |||| ||| |||||
 GCTTC GGA CATACTTCAC
 AAAA A____
 GAM404 MGC2628 3' ATGCACCCCCAGGCTTCAA 23508 A_
 TTGAAGCCTGGGG GTAT
 ||||| ||||| |||||
 AACTTCGGACCCC CGTA
 CA
 GAM404 OSBPL3 3' CACTTCCCTCCCCAGGCCCAA 17815 AA TAT
 TTG GCCTGGGGAG GAAGTG
 ||| ||||| |||||

			AAC CGGACCCCTC CTTCAC			
			CC C_			
GAM404	SYT12	3'	TCTACTCCCCGGACCTCAA 45431	AGC	T	
			TTGA CTGGGGAGTA GA			
			AACT GGCCCCTCAT CT			
			CCA _			
GAM404	LOC124976	3'	CACCTGTGCCCCCAGGCTCAA 36782	A	A	GAA
			TTGA GCCTGGGG GTAT GTG			
			AACT CGGACCCC CGTG CAC			
			_ _ TC_			
GAM404	LOC148114	5'	CACCCAAGCCCCCAGGCCCA 38465	AA	A	A AA
	A		TTG GCCTGGGG GT TG GTG			
			AAC CGGACCCC CG AC CAC			
			CC C A C_			
GAM404	LOC254428	3'	CACCCACACTCCCACCTCTTT 45715	CCTG	A	AA
			GAAG GGGAGT TG GTG			
			TTTC CCCTCA AC CAC			
			TCCA C CC			
GAM404	LOC254945	5'	CACTCCAGTGTTCAGCCCCA 46304	AA C	GTA	A
	A		TTG GC TGGGGA TG AGTG			
			AAC CG ACCCTT AC TCAC			
			CC _ GTG C			
GAM405	TOSO	5'	ACGAGGATTCCTCATCGTC 11935	A	GCCT	C
			GA CGA GA ATCCTCGT			
			CT GCT CT TAGGAGCA			
			_ ACTC T			
GAM405	LOC152283	5'	ACGAGGATTACATCGTCCTCA 41484	A	GCCTGAC	
			TGAG ACGA ATCCTCGT			
			ACTC TGCT TAGGAGCA			
			C ACAT_			
GAM405	LOC255002	5'	GTGTCAGGCTCATTCCA 46270	A	C	
			TG GAA GAGCCTGACAT			
			AC CTT CTCGGACTGTG			
			C A			
GAM405	LOC92017	5'	ACGAGGGTGGCCACCTCTCA 33707	ACGA_	TGAC	
			TGAGA GCC ATCCTCGT			
			ACTCT CGG TGGGAGCA			
			CCACC _			
GAM406	DLEC1	3'	CCCACCTGTGTTCTCA 14270	CATCCA		
			TGAGGAACACGGG TGGG			

ACTCCTTGTGTCC ACCC

GAM406 ESRRB 5' GCCCATGGAGCACTGTCCTCA 33438 ACA _ A
TGAGGA CGG GC TCCATGGGC
||||| ||| || |||||
ACTCCT GTC CG AGGTACCCG
_ A _

GAM406 KLF4 5' GCCCATGGCCGCGCGCTCC 10429 ACA G AT
GGA CG GC CCATGGGC
||| ||| |||||
CCT GC CG GGTACCCG
CGC G CC

GAM406 NTSR1 3' CCCCCTAACCCATGTTTCTCA 8367 C CATCCAT
TGAGGAACA GGG GGG
||||||| ||| |||
ACTCTTTGT CCC CCC
A AATCC_

GAM406 PLA2G2D 3' CCCTCTACCCTGTTCTCA 14768 C CATCCAT
TGAGGAACA GGG GGG
||||||| ||| |||
ACTCCTTGT CCC CCC
_ ATCT_

GAM406 RAG2 3' GCCCATGAACAAGTTAGTTTCT 39987 ACGGGCATC
CA TGAGGAAC CATGGGC
||||||| |||||
ACTCTTTG GTACCCG
ATTGAACAA

GAM406 SORCS2 3' CCCAGTGCCCATGGTTCCTCA 21874 AC_ CCA
TGAGGAAC GGGCAT TGGG
||||||| ||||| |||||
ACTCCTTG CCCGTG ACCC
GTA _

GAM406 TEM5 3' GCCCACAGGCGGATGTTCCCCA 26520 A CGG ATCCA
TG GGAACA GC TGGGC
|| ||||| || |||||
AC CCTTGT CG ACCCG
C AGG GAC_

GAM406 B3GALT1 5' GCCCATGGACAATCTCCACCTC 21972 AACAC GCA
A TGAGG GG TCCATGGGC
||||| || |||||
ACTCC CT AGGTACCCG
ACCT_ AAC

GAM406 FLJ23816 5' CCGCTGCCTGTGCCCCCA 29478 A AA TCCA
TG GG CACGGGCA TGG
|| || ||||| |||
AC CC GTGTCCGT GCC
C CC C_

GAM406 FLJ31737 3' CCCATGGAGTGCTCTCCA 29589 A ACAC _
TG GGA GGGCA TCCATGGG
|| ||| ||||| |||||

			AC CCT CTCGT AGGTACCC		
			— ——— G		
GAM406	GLTP	3'	GCCCCTGGCCTGTGTCCCCCA 18556	A A	ATC T
			TG GG ACACGGGC CA GGGC		
			AC CC TGTGTCCG GT CCCG		
			C C — C		
GAM406	KIAA0828	3'	GCCCATAGACTACAGTTCTTCA 39515		ACG CA C
			TGAGGAAC GG TC ATGGGC		
			ACTTCTTG TC AG TACCCG		
			ACA — A		
GAM406	PLAGL2	3'	CCCACCCCGTCTGTGTCCCCCA 34875	A A	ATCCA
			TG GG ACACGGGC TGGG		
			AC CC TGTGTCTG ACCC		
			C C CCCC_		
GAM406	RASD2	3'	GCCCACCTCCTGACCGCGTTCC 15607		A G TCCA_
	TCA		TGAGGAAC CGG CA TGGGC		
			ACTCCTTG GCC GT ACCCG		
			C A CCTCC		
GAM406	LOC200205	3'	GCCCATCTCCCATGTTTC 42737	C	CATCC
			GGAACA GGG ATGGGC		
			CTTTGT CCC TACCCG		
			A TC_		
GAM406	LOC204084	5'	CCCATGGGACTTTCCTCA 43084		CACG CA
			TGAGGAA GG TCCATGGG		
			ACTCCTT TC GGGTACCC		
			— A_		
GAM406	LOC221632	3'	CCCATGGATGGCTGTTCTCC 45036	AC	G
			GGA ACGG CATCCATGGG		
			CCT TGTC GTAGGTACCC		
			CT G		
GAM406	LOC90768	3'	CCCACAGCCCGTGTTCCCG 31985	A	ATCCA
			TG GGAACACGGGC TGGG		
			GC CCTTGTGCCCG ACCC		
			— AC_		
GAM407	PAX2	5'	AGTCGTGCGCCCCCGCC 10137	A A	
			GGC GG GGCGCACGATT		
			CCG CC CCGCGTGCTGA		
			C C		
GAM407	PAX2	5'	AGTCGTGCGCCCCCGCC 10143	A A	
			GGC GG GGCGCACGATT		

			CCG CC CCGCGTGCTGA		
			C C		
GAM407	CDCA4	3'	CACGGAGGGTGCGCCTGCCGCC 19659	A _	GA TA
	A		TGGC GG AGGCGCAC TT TG		
			ACCG CC TCCGCGTG AG AC		
			_ G GG GC		
GAM407	KIAA0397	5'	TCGGCGCCGCCTCCTGCCA 30895	_ A_	
			TGGCAGGAGGCG C CGA		
			ACCGTCCTCCGC G GCT		
			C CG		
GAM407	KIAA1036	3'	AGGTACCATCGCCTCCTGCCA 17123	CACG_	
			TGGCAGGAGGCG ATTT		
			ACCGTCCTCCGC TGGA		
			TACCA		
GAM407	MAPK8IP2	3'	AAGTGATGCCCTCCTGCCA 18551	C CG	
			TGGCAGGAGG GCA ATTT		
			ACCGTCCTCC CGT TGAA		
			_ AG		
GAM407	MAPK8IP2	3'	AAGTGATGCCCTCCTGCCA 14703	C CG	
			TGGCAGGAGG GCA ATTT		
			ACCGTCCTCC CGT TGAA		
			_ AG		
GAM407	MAPK8IP2	3'	AAGTGATGCCCTCCTGCCA 29154	C CG	
			TGGCAGGAGG GCA ATTT		
			ACCGTCCTCC CGT TGAA		
			_ AG		
GAM407	MCPR	5'	TCGCACGCCTTCCTGCCA 22908	_ CA	
			TGGCAGGA GGCG CGA		
			ACCGTCCT CCGC GCT		
			T AC		
GAM407	LOC159121	5'	TTGCTGTGCCTCCCACCA 42066	CA _	
			TGG GGAGGCGCA CGA		
			ACC CCTCCGTGT GTT		
			AC C		
GAM407	LOC163682	5'	GTGGTGCCGCCTCCTGCCA 42099	_ G	
			TGGCAGGAGGCG CAC AT		
			ACCGTCCTCCGC GTG TG		
			C G		
GAM407	LOC51068	3'	CATAAATATCTTCCTACCA 18059	C CGCACG	
			TGG AGGAGG ATTTATG		

			ACC TCCTTC TAAATAC		
			A TA_____		
GAM407	LOC92335	3'	ATCTTAGCGCCTCCTGCCA 34192	AC_	
			TGGCAGGAGGCGC GAT		
			ACCGTCCTCCGCG CTA		
			ATT		
GAM408	AKAP6	3'	AACCCTGAAGATAATCAA 10488	_	
			TTGGTTATCTT GGGGTT		
			AACTAATAGAA TCCCAA		
			G		
GAM408	ARHGEF11	5'	CAATCCTGATCAAGACACCAA 16638	TA GG	
			TTGGT TCTTG GTTAGGATTG		
			AACCA AGAAC TAGTCCTAAC		
			C_ _		
GAM408	LOC149157	3'	CAATCCTAAGCAAAAATAAC 38657	C GGGG	
			GTTAT TT TTAGGATTG		
			CAATA AA AATCCTAAC		
			A ACG_		
GAM409	FCRH1	3'	AGCACAGAACTCCAGCCCC 27498	AGCTC _ A	
			GG GCTGG GTTCTGT CT		
			CC CGACC CAAGACA GA		
			C_ T C		
GAM409	SOX4	3'	AGAACCCAGCGCACCCCTC 9073	AGCT	
			GAGG CGCTGGGTTCT		
			CTCC GCGACCCAAGA		
			CCAC		
GAM409	TIMELESS	3'	AGGACCCAGAAGCTCCTC 10005	CG	
			GAGGAGCT CTGGGTTCT		
			CTCCTCGA GACCCAGGA		
			A_		
GAM409	FLJ10508	5'	AACTGCGCCAAGAGCTCCTC 19889	GC _ TC	
			GAGGAGCTC TGG GT TGT		
			CTCCTCGAG ACC CG ACA		
			A_ G TC		
GAM409	FLJ10724	3'	TACAAAAGTTTTGAGCTCTTC 20054	CT G C	
			GAGGAGCTCG GG TT TGTA		
			CTTCTCGAGT TT AA ACAT		
			T_ G A		
GAM409	FLJ11320	3'	AGCACAAACAAGCAAGCTCCTT 20425	C GG C A	
			GAGGAGCT GCT GTT TGT CT		

			TTCCTCGA CGA CAA ACA GA		
			A A_ _ C		
GAM409	FLJ13912	3'	ACAGAATGGCTCCTC 23026	CGCTGG	
			GAGGAGCT GTTCTGT		
			CTCCTCGG TAAGACA		

GAM409	FLJ32356	3'	GCACAGCCAGAGACAGCCCC 29492	A GCTG_ _ C	
			TC GAGG GCTC GGT TGT		
			CTCC CGAG CCGA ACG		
			C ACAGAGA C		
GAM409	NUDT11	3'	AGTACACACAGCTAGCTCCTC 30139	C GTTC	
			GAGGAGCT GCTG TGTACT		
			CTCCTCGA CGAC ACATGA		
			T AC_ _		
GAM409	LOC256997	5'	GCACAGCCACAGAGAGCTCCTC 45651	G _ C	
			GAGGAGCTC CTG GGT TGT		
			CTCCTCGAG GAC CCGA ACG		
			A A C		
GAM410	CHST1	5'	AGCAGTCCCTCTTTGACCTCA 9729	A CA A	
			TGAG TCAAAGAG ACT CT		
			ACTC AGTTTCTC TGA GA		
			C CC C		
GAM410	FLJ11539	3'	AGTAGTGGACTCGACTCA 24084	A AAA CAA	
			TGAG TC GAG CTACTACT		
			ACTC AG CTC GGTGATGA		
			_ _ _ A_		
GAM410	FLJ23511	3'	AGTAATGTATTTTGATCTCA 25964	A AC	
			TGAGATCAAAG GCA TACT		
			ACTCTAGTTTT TGT ATGA		
			A A_		
GAM410	PRO1866	5'	AGTCTTTGGCCACCTCTGATCT 20578	A A_ AACT_	
			CA TGAGATCA AG GC ACT		
			ACTCTAGT TC CG TGA		
			C CAC GTTC		
GAM411	NUMA1	3'	CTTCCCCAGACTTGCACTG 44881	_ TTAAA	
			TAGTGCAAG CT GAAG		
			GTCACGTTC GA CTTC		
			A CCC_ _		
GAM411	FLJ14642	3'	TATCTTCTCTGCTGTCACACTG 26595	CA_ TTTTAA	
			TAGTG AGC AGAAGATA		

			GTCAC TCG TCTTCTAT		
			ACTG TC_____		
GAM411	KIAA1084	3'	TATCCCCTTTAAAGGAGACATT 17139	CAAG	AA
	A		TAGTG CTTTAAAG GATA		
			ATTAC GGAAATTTCT CTAT		
			AGA_ CC		
GAM412	DFNA5	3'	CTGCTTGGGACCCTAGCTATA 10655	CA	AGA
			TAT CTA TCCCAGGTAG		
			ATA GAT AGGGTTCGTC		
			TC CCC		
GAM412	ATP6V1B2	3'	CTACCTGGGTCTCTCAGTG 7413	A	AT
			CACT AG CCCAGGTAG		
			GTGA TC GGGTCCATC		
			C CT		
GAM412	FLJ11053	3'	TCTACCTGGAGATAGTG 42778	AGA	_
			CACTA TC CCAGGTAGA		
			GTGAT AG GGTCCATCT		
			____ A		
GAM412	KIAA0478	3'	TCTGCTTGTATCCCAGTGATA 16988	AA	CC
			TATCACT GAT CAGGTAGA		
			ATAGTGA CTA GTTCGTCT		
			CC T_		
GAM412	KIAA1404	3'	TCCACCTAGGGCCACCTAGTGG 31052	AGAT_	_ A
	TA		TATCACTA CCC AGGT GA		
			ATGGTGAT GGG TCCA CT		
			CCACC A C		
GAM412	LANCL2	3'	TCTAGGGTCTATCCTAGTGATA 20780	_____	C
			TATCACTA AGATCC AGG		
			ATAGTGAT TCTGGG TCT		
			CCTA A		
GAM412	OS-9	3'	ACCTGCCCTTAGTGATG 13682	ATCC	
			TATCACTAAG CAGGT		
			GTAGTGATTC GTCCA		
			CC_		
GAM412	PRO1483	5'	CTATTAGTAACCTTAGTGATA 20660	ATCCCA	
			TATCACTAAG GGTAG		
			ATAGTGATTC TTATC		
			CAATGA		
GAM412	RASD2	3'	CCTAAGGAACCTTAGTGAT 15604	A_	C_
			ATCACTAAG TCC AGG		

			TAGTGATTC AGG TCC		
			CA AA		
GAM412	LOC132332	3'	CCTGTGACTGATTTTAGTGATA 37486	C_____	
			TATCACTAAGATC CAGG		
			ATAGTGATTTTAG GTCC		
			TCAGT		
GAM412	LOC92148	5'	TCCACCTGAAACTTGGTGAT 33910	ATCC A	
			ATCACTAAG CAGGT GA		
			TAGTGGTTC GTCCA CT		
			AAA_ C		
GAM413	EIF2C1	3'	CTTATTCCTCTCTGTCCA 14502	A TATGTT	
			TGGA AGAG GAATAAG		
			ACCT TCTC CTTATTC		
			G TC_____		
GAM413	GPR81	3'	CCTTAATTTATACTCTCTC 26282	A TTGAA	
			GA AGAGTATG TAAGG		
			CT TCTCATAT ATTCC		
			C TTA_____		
GAM413	KCNA5	3'	CCATTTTCTCTATTCTTTCCA 30028	TGTT TAA	
			TGGAAAGAGTA GAA GG		
			ACCTTTCTTAT CTT CC		
			CT__ TTA		
GAM413	LPIN1	3'	CTTATTCTCTCTTTCT 33467	TATGTT	
			GGAAAGAG GAATAAG		
			TCTTTCTC CTTATTC		
			T_____		
GAM413	PLAG1	3'	CCTTATTTTAGGACCCTTTCC 8520	A ATGTT	
			GGAAAG GT GAATAAGG		
			CCTTTC CA TTTATTCC		
			C GGAT_		
GAM413	YWHAG	3'	CTTATTCAGCCTTATCCA 14855	AA TAT	
			TGGA GAG GTTGAATAAG		
			ACCT TTC CGACTTATTC		
			A_ ____		
GAM413	C1orf22	3'	CCTTATTTGCAATACTTTTCCC 24837	A GTT	
	A		TGG AAGAGTAT GAATAAGG		
			ACC TTTTCATA TTTATTCC		
			C ACG		
GAM413	FLJ10246	3'	CCTCTTCCATACTCTCCG 19785	A TT TA	
			TGGAA GAGTATG GAA AGG		

GCCTT CTCATAC CTT TCC
 _ _ C_
 GAM413 FLJ10276 3' CTGAGACAACATACTCTGTCCA 19791 A AATA
 TGGA AGAGTATGTTG AG
 ||| ||||| ||
 ACCT TCTCATACAAC TC
 G AGAG
 GAM413 FLJ12700 3' TCACCAGGACATTCTTTCCA 24415 A__ T
 TGGAAAGAGT TG TGA
 ||||| ||||
 ACCTTTCTTA AC ACT
 CAGG C
 GAM413 G2 3' CCTTATGTTTGATACTCTCTC 33112 A GTTGA
 GA AGAGTAT ATAAGG
 || ||||| ||||
 CT TCTCATA TATTCC
 C GTTTG
 GAM413 KIAA1655 3' CTCATTCCCTTCTTTCCA 33087 TATGTT A
 TGGAAAGAG GAAT AG
 ||||| ||||
 ACCTTTCTT CTTA TC
 CC__ C
 GAM413 MOCS3 3' CCTTATTTTCCACCTCCCCCA 15829 AAA TA TT
 TGG GAG TG GAATAAGG
 ||| ||| || |||||
 ACC CTC AC TTTATTCC
 CC_ C_ CT
 GAM413 P66 3' CCCCATTTTCATACTCTTCCCA 21843 A TT AA
 TGG AAGAGTATG GAAT GG
 ||| ||||| ||||
 ACC TTCTCATAC TTTA CC
 C T_ CC
 GAM413 PRO0529 5' TCATACTGTACTCTCCCCA 15301 AA _ _
 TGG AGAGTAT GT TGA
 ||| ||||| ||||
 ACC TCTCATG CA ACT
 CC T T
 GAM413 RA-GEF-2 3' CCTTGAGAGGACATACTTTTCC 18465 A GAA_
 A TGGAA GAGTATGTT TAAGG
 ||||| ||||| ||||
 ACCTT TTCATACAG GTTCC
 _ GAGA
 GAM413 ZNF17 3' CCTTATTCCTCACTCCATCCA 40067 AA AT TT
 TGGAGAGT G GAATAAGG
 |||| |||| | |||||
 ACCT CTCA C CTTATTCC
 AC _ TC
 GAM413 LOC128077 3' CCTTATTCCTTCTCTGCCTCCA 36916 A__ TATGTT
 TGGAGAGG GAATAAGG
 |||| |||| |||||

			ACCT TCTC CTTATTCC		
			CCG TTC__		
GAM413	LOC149127 3'	CCTTCAAAACATACTCATCTCC 40949	AA_ GAAT		
	A	TGGA GAGTATGTT AAGG			
		ACCT CTCATACAA TTCC			
		CTA AAC_			
GAM413	LOC150630 5'	CCTTAATAGCATACCCTCCA 41239	AA A AA		
		TGGA G GTATGTTG TAAGG			
		ACCT C C ATACGAT ATTCC			
		_ C A_			
GAM413	LOC169021 5'	CCTCACAGTATAGTCTTTCCA 40258	G AATA		
		TGGAAAGA TATGTTG AGG			
		ACCTTTCT ATATGAC TCC			
		G AC_			
GAM413	LOC221687 3'	CCTTGAGACACACTCTTTCC 44306	A GAA		
		GGAAAGAGT TGTT TAAGG			
		CCTTTCTCA ACAG GTTCC			
		C A_			
GAM414	ALDH1B1 3'	AGCCAAGAACACCCTT 6346	CAACT		
		AAGGGTGTTCT TGGCT			
		TTCCCAACAAGA ACCGA			
GAM414	CYP7A1 3'	CAGGACTGCAGAACACCCT 6421	_ A_		
		AGGGTGTTCT CA CTTG			
		TCCCACAAGA GT GGAC			
		C CA			
GAM414	EN2 3'	TCAAAATTGTGAACACCC 7147	T C_		
		GGGTGTTT CAA TTGG			
		CCCACAAG GTT AACT			
		T AA			
GAM414	GLUD1 3'	GTGGGCTGAAAACATCCTT 11775	C ACTTG		
		AAGGGTGTT TCA GCTCAT			
		TTCTACAA AGT CGGGTG			
		A _			
GAM414	ODF2 5'	GTGGATGAGAACACCC 8388	AC G		
		GGGTGTTTCTCA TT GC			
		CCCACAAGAGT AG TG			
		_ G			
GAM414	SIM2 3'	TGTGCTGAGAACACCC 14314	ACTTG T		
		GGGTGTTTCTCA GC CA			

CCCACAAGAGT CG GT
 _____ T
 GAM414 ZNF278 3' AGCTCAGCTGTTGAGGACACCC 25771 — —
 GGGTGTCTCAAC TTG GCT
 ||||| ||| |||
 CCCACAGGAGTTG GAC CGA
 TC T
 GAM414 ZNF278 3' AGCTCAGCTGTTGAGGACACCC 25780 — —
 GGGTGTCTCAAC TTG GCT
 ||||| ||| |||
 CCCACAGGAGTTG GAC CGA
 TC T
 GAM414 ZNF278 3' AGCTCAGCTGTTGAGGACACCC 15622 — —
 GGGTGTCTCAAC TTG GCT
 ||||| ||| |||
 CCCACAGGAGTTG GAC CGA
 TC T
 GAM414 ERMAP 3' GTCATTGAGAAACACCCT 20608 — CT
 AGGGTGT CTCAA TGGC
 ||||| ||| |||
 TCCCACAA GAGTT ACTG
 A —
 GAM414 FLJ20373 3' CTGAAATTGGAACACCCTT 19426 T C_TG
 AAGGGTGTTC CAA T G
 ||||| ||| | |
 TTCCCACAAG GTT A C
 — AA GT
 GAM414 SPTLC2 3' ATGAGCCAAGATCACACC 11274 TCTCAA
 GGTGT CTTGGCTCAT
 |||| |||||
 CCACA GAACCGAGTA
 CTA—
 GAM414 LOC91170 5' GTTGGTGCTGAGAACAGCCTT 32481 G AC_TG
 AAGG TGTTCTCA T GC
 ||| ||||| | ||
 TTCC ACAAGAGT G TG
 G CGT GT
 GAM415 EGFL4 3' ATGGTGAAACCCCATGTCTA 30962 C —
 TAG ACATGGGGTT CACTAT
 ||| ||||| |||||
 ATC TGTACCCCAA GTGGTA
 — A
 GAM415 NRCAM 3' AAATAGTGAACCTTTTCTACGT 11446 ACAT_
 GC GGGGTTCACTATTT
 || |||||
 TG TTTCAAGTGATAAA
 CATCT
 GAM415 ARPP-21 3' AAATAGTGAATAAGGTGC 18419 ATGGG
 GCAC GTTCACTATTT
 ||| |||||

			CGTG	TAAGTGATAAA		
			GAA	___		
GAM415	B3GNT7	3'	AAATAGCTTATGGCCCTGTGC	35237	TG	CA___
			GCACA GGGTT	CTATTT		
			CGTGT CCCGG	GATAAA		
			___	TATTC		
GAM415	FLJ11722	3'	AGTGAAACCCCATGTCTA	24519	C	___
			TAG ACATGGGGTT	CACT		
			ATC TGTACCCCAA	GTGA		
			___	A		
GAM415	FLJ20006	3'	ATGGCGAAACCCCATCGCTA	19118	AC	___A
			TAGC ATGGGGTT	C CTAT		
			ATCG TACCCCAA	G GGTA		
			C_	A C		
GAM415	FLJ20958	3'	AAATAGTGGCATTGCATG	22645	G	___
			CATG GGT TCACTATTT			
			GTAC TTA GGTGATAAA			
			G	C		
GAM415	GLTP	3'	ATGGTGAAACCCCATCGCTA	18554	AC	___
			TAGC ATGGGGTT	CACTAT		
			ATCG TACCCCAA	GTGGTA		
			C_	A		
GAM415	KIAA1001	3'	ATGGTGAAACCCCATCGCTA	17323	AC	___
			TAGC ATGGGGTT	CACTAT		
			ATCG TACCCCAA	GTGGTA		
			C_	A		
GAM415	KIAA1160	3'	ATGGTGAAACCCCATGTCTA	21850	C	___
			TAG ACATGGGGTT	CACTAT		
			ATC TGTACCCCAA	GTGGTA		
			___	A		
GAM415	KIAA1430	3'	AAATAGTGGTATGCATGTGT	39356	GGGT	
			GCACATG	TCACTATTT		
			TGTGTAC	GGTGATAAA		
			GTAT			
GAM415	LRP15	5'	AAATAATGAAGAGACACATGTG	27509	GGG___	C
	TTA		TAGCACATG	TTCA TATTT		
			ATTGTGTAC	AAGT ATAAA		
			ACAGAG	A		
GAM415	PTD002	3'	AAATAGTGAGTAGTATGGT	18227	A	GG
			GC CATG GTTCACTATTT			

			TG GTAT TGAGTGATAAA		
			— GA		
GAM415	LOC120400	5'	AGTGCATTCTGTGCTA 37219	TG	T
			TAGCACA GGGT CACT		
			ATCGTGT CTTA GTGA		
			— C		
GAM415	LOC221399	5'	AATAGTGGGGAGTGCTA 45047	ATG	GGG
			TAGCAC TTCACTATT		
			ATCGTG GGGTGATAA		
			AG—		
GAM416	FLNB	3'	ATTTGTGACCTGAACCTGA 31139	ATC	C CTT
			TCAG CA GG TCGCAAAT		
			AGTC GT CC AGTGTTTA		
			CAA _ —		
GAM416	LOC143310	3'	CATCTGCAATGGTTGTGGACCT 37606	A	TTC A
	G		CAG TCCACGGCT GCA ATG		
			GTC AGGTGTTGG CGT TAC		
			C TAA C		
GAM416	LOC92719	3'	CATTTGTGCCCCACTGACCTGA 34847	A	CAC CTTT
			TCAG TC GG CGCAAATG		
			AGTC AG CC GTGTTTAC		
			C TCA CC—		
GAM417	CAPN10	3'	TGAAAGACCTGAAACTC 23358	C	ACC
			GAG TTCAGGTCTT TCA		
			CTC AAGTCCAGAA AGT		
			A —		
GAM417	CAPN10	3'	TGAAAGACCTGAAACTC 23357	C	ACC
			GAG TTCAGGTCTT TCA		
			CTC AAGTCCAGAA AGT		
			A —		
GAM417	HTR2A	3'	CTTGAGCCCAGAAGCTCA 6236	A	TCTTAC
			TGAGCTTC GG CTCAAG		
			ACTCGAAG CC GAGTTC		
			A C—		
GAM417	RAB11A	3'	CTTGATCACTTGAAGCTCA 11033		CTTACC
			TGAGCTTCAGGT TCAAG		
			ACTCGAAGTTCA AGTTC		
			CT—		
GAM417	DDX28	5'	ACTTGAAATAAACCTGAAG 20407	C	CC
			CTTCAGGT TTA TCAAGT		

GAAGTCCA AAT AGTTCA
A AA

GAM417 FLJ11608 3' ACTTGAGGCCATTGAAGCTGCA 23775 _ GTCTTA
TG AGCTTCAG CCTCAAGT
|| ||||| |||||
AC TCGAAGTT GGAGTTCA
G ACC__

GAM417 HGC6.1.1 3' ACCTGAGGTGGCTGAGGCTCA 15683 GTC A
TGAGCTTCAG TTACCTCA GT
||||||| ||||| ||
ACTCGGAGTC GGTGGAGT CA
__ C

GAM417 KIAA0417 3' TGAGATTTTGTGAAGTTCA 35293 ____
TGAGCTTCAG GTCTTA
||||||| |||||
ACTTGAAGTT TAGAGT
GTTT

GAM417 KIAA0766 3' GGAAGACCTGAAAGCCA 16742 A _ A
TG GCTT CAGGTCTT CC
|| ||| ||||| ||
AC CGAA GTCCAGAA GG
_ A _

GAM417 LOC146733 5' AGGTCAGTGAAGCTCA 40726 GGT T
TGAGCTTCA CT ACCT
||||||| || |||
ACTCGAAGT GA TGGA
__ C

GAM417 LOC254431 5' ACTTGAGATTTCTGAAGCGCA 46289 A TCTTAC
TG GCTTCAGG CTCAAGT
|| ||||| |||||
AC CGAAGTCC GAGTTCA
G TTTA__

GAM417 LOC92539 5' ACTTGAGGTTACAAAGCTCA 34498 CAG CTT
TGAGCTT GT ACCTCAAGT
||||| || |||||
ACTCGAA CA TGGAGTTCA
A__ T__

GAM418 LCP1 3' CAAAGAATTCCAAAGCAAAACC 8082 C_ CAT
GGTT GCTTTG TTCTTTG
||| ||||| |||||
CCAA CGAAAC AAGAAAC
AA CTT

GAM418 SON 3' CAAAGAAGGCAATAAGGAACCC 27745 G _ A
A TGGGTTC CTT TGC TTTCTTTG
||||| ||| || |||||
ACCCAAG GAA ACG GAAGAAAC
_ TA _

GAM418 SON 3' CAAAGAAGGCAATAAGGAACCC 29041 G _ A
A TGGGTTC CTT TGC TTTCTTTG
||||| ||| || |||||

ACCCAAG GAA ACG GAAGAAAC
 _ TA _
 GAM418 DKFZP564B1162 5' CAAAAAATGCAAAAACC 25334 CGC C
 GGTT TTTGCATTT TTTG
 ||| ||||| |||
 CCAA AAACGTAAA AAAC
 _ A
 GAM418 SH3BGRL2 3' GCAAAGAAATACAGGAGACC 25531 CGC C
 GGTT TTTG ATTTCTTTGC
 ||| ||| |||||
 CCAG GGAC TAAAGAAACG
 A _ A
 GAM418 LOC138389 5' CAAAGAAACGTGGAATCCA 37504 GCTT A
 TGGGTTT TGC TTTCTTTG
 ||||| || |||||
 ACCTAAG GTG AAAGAAAC
 _ C
 GAM418 LOC90246 3' CAAAGAAATGGAGACCC 30999 CGCTT G
 GGGTT T CATTCTTTG
 |||| | |||||
 CCCAG A GTAAAGAAAC
 _ G
 GAM419 AXL 3' CAAGACTCTAGAGTCCAA 22442 G T A
 TTGGAT CT GA GTCTTG
 ||||| || |||||
 AACCTG GA CT CAGAAC
 A T _
 GAM419 AXL 3' CAAGACTCTAGAGTCCAA 7421 G T A
 TTGGAT CT GA GTCTTG
 ||||| || |||||
 AACCTG GA CT CAGAAC
 A T _
 GAM419 BCL2A1 5' TCAAGACTTTGCTCTCCA 10256 T_ TT
 TGGA GC GAAGTCTTGA
 ||| || |||||
 ACCT CG TTTCAGAACT
 CT _
 GAM419 BHMT2 3' TTCAAGACCAGCCTGACCAA 19117 AT_ TGAA
 TTGG GCT GTCTTGAA
 ||| || |||||
 AACC CGA CAGAACTT
 AGTC C_
 GAM419 CARKL 3' TTCAAGACCAGCCTGACCAA 14940 AT_ TGAA
 TTGG GCT GTCTTGAA
 ||| || |||||
 AACC CGA CAGAACTT
 AGTC C_
 GAM419 GLS 3' TTCAAGACTTCAAATACAA 17112 GATGC
 TTG TTGAAGTCTTGAA
 || |||||

AAC AACTTCAGAACTT
 ATA__
 GAM419 KCNS2 3' AAGACCTTCAAGCTTCCAA 33896 T _
 TTGGA GCTTGAAG TCTT
 ||||| ||||| |||||
 AACCT CGAACTTC AGAA
 T C
 GAM419 MSN 3' TTCAAGACCTTCACCAA 30230 ATGCT _
 TTGG TGAAG TCTTGAA
 |||| ||||| |||||
 AACC ACTTC AGAACTT
 _ C
 GAM419 NRL 3' TTCAAGATTTCAATATCCAA 12839 C
 TTGGATG TTGAAGTCTTGAA
 ||||| ||||| |||||
 AACCTAT AACTTTAGAACTT
 _
 GAM419 PHKB 3' TTCAAGACCAGCCCAGCCAA 5838 AT__ TGAA
 TTGG GCT GTCTTGAA
 |||| || |||||
 AACC CGA CAGAACTT
 GACC C__
 GAM419 RANBP9 5' TTCGAGCCACGCATCCAA 11996 T AA T
 TTGGATGC TG G CTTGAA
 ||||| || |||||
 AACCTACG AC C GAGCTT
 C _ _
 GAM419 SMG1 3' TCAGCCTCAGGCATCCAA 17481 A CT
 TTGGATGCTTGA GT TGA
 ||||| ||||| |||||
 AACCTACGGACT CG ACT
 C _
 GAM419 TNFSF15 3' TTCAAGACCAGCCTGACCAA 11602 AT__ TGAA
 TTGG GCT GTCTTGAA
 |||| || |||||
 AACC CGA CAGAACTT
 AGTC C__
 GAM419 VNN1 3' TCAAGACTCCAATAGACA 11039 GA C A
 TG TG TTG AGTCTTGA
 || || || |||||
 AC AT AAC TCAGAACT
 AG _ C
 GAM419 AP1GBP1 3' TTCAAGGTGAGTAGCTTCCAA 27881 T TGAA
 TTGGA GCT GTCTTGAA
 ||||| || |||||
 AACCT CGA TGGAACCTT
 T TGAG
 GAM419 BC022889 5' TTCAAGATGACAGATCCAA 40687 G T AA
 TTGGAT CT G GTCTTGAA
 ||||| || |||||

AACCTA GA C TAGAACTT
 _ _ AG
 GAM419 C1QTNF2 3' TTCAAGACCAGCCTGACCAA 25653 AT__ TGAA
 TTGG GCT GTCTTGAA
 |||| ||| |||||
 AACC CGA CAGAACTT
 AGTC C__
 GAM419 C20orf12 3' TTCAAGACCAGCCTGACCAA 19962 AT__ TGAA
 TTGG GCT GTCTTGAA
 |||| ||| |||||
 AACC CGA CAGAACTT
 AGTC C__
 GAM419 C20orf177 3' TTCAAGACCAGCCTGACCAA 31130 AT__ TGAA
 TTGG GCT GTCTTGAA
 |||| ||| |||||
 AACC CGA CAGAACTT
 AGTC C__
 GAM419 CUL4A 3' TCAAGACTTCAACCTGCA 9642 ____
 TGC TTGAAGTCTTGA
 ||| |||||
 ACG AACTTCAGAACT
 TCC
 GAM419 DIO2 3' TCAAGACTTCTCCAGGCCCA 15172 AT ____
 TGG GCTT GAAGTCTTGA
 ||| |||| |||||
 ACC CGGA CTTCAGAACT
 __ CCT
 GAM419 DIO2 3' TCAAGACTTCTCCAGGCCCA 6461 AT ____
 TGG GCTT GAAGTCTTGA
 ||| |||| |||||
 ACC CGGA CTTCAGAACT
 __ CCT
 GAM419 FLJ10330 3' TTCAAGCCTCAAGCTTCCAA 19833 T A T
 TTGGA GCTTGA G CTTGAA
 |||| ||||| |||||
 AACCT CGAACT C GAACTT
 T C_
 GAM419 FLJ12660 3' TTCAAGACCAGCCTGACCAA 24788 AT__ TGAA
 TTGG GCT GTCTTGAA
 |||| ||| |||||
 AACC CGA CAGAACTT
 AGTC C__
 GAM419 FLJ12876 3' TCCTGGAACCAAGCATCCA 22988 AAG T_
 TGGATGCTTG TCT GA
 ||||| ||| ||
 ACCTACGAAC AGG CT
 CA_ TC
 GAM419 FLJ20006 3' TTCAAGACCAGCCTGACCAA 19120 AT__ TGAA
 TTGG GCT GTCTTGAA
 |||| ||| |||||

			AACC CGA CAGAACTT		
			AGTC C__		
GAM419	FLJ21240	3'	TTCAAGACCAGCCTGACCAA	24281	AT__ TGAA
			TTGG GCT GTCTTGAA		
			AACC CGA CAGAACTT		
			AGTC C__		
GAM419	KIAA0255	3'	CAAGCCAAGCATCCA	16414	AA T
			TGGATGCTTG G CTTG		
			ACCTACGAAC C GAAC		
			— —		
GAM419	KIAA0268	3'	TTCATTGGCTTCAAAATCCAA	34689	GC T_
			TTGGAT TTGAAGTC TGAA		
			AACCTA AACTTCGG ACTT		
			A_ TT		
GAM419	KIAA1126	3'	TTCAAGACTTCAAGAACA	35612	GATG
			TG CTTGAAGTCTTGAA		
			AC GAACTTCAGAACTT		
			AA__		
GAM419	KIAA1473	3'	TTCAAGACCAGCCTGACCAA	34998	AT__ TGAA
			TTGG GCT GTCTTGAA		
			AACC CGA CAGAACTT		
			AGTC C__		
GAM419	KIAA1649	3'	CAAGAGAGCATCCAG	33255	GAAG
			TTGGATGCTT TCTTG		
			GACCTACGAG AGAAC		
			— —		
GAM419	KIAA1649	3'	CAAGAGAGCATCCAG	26103	GAAG
			TTGGATGCTT TCTTG		
			GACCTACGAG AGAAC		
			— —		
GAM419	KLHL8	3'	TTCAAGACCAGCCTGACCAA	31479	AT__ TGAA
			TTGG GCT GTCTTGAA		
			AACC CGA CAGAACTT		
			AGTC C__		
GAM419	MRPL35	3'	CAGAGCCTCAGCATCCAA	18734	T A TC
			TTGGATGCT GA G TTG		
			AACCTACGA CT C GAC		
			_ C GA		
GAM419	PDZD2	3'	TTCAAGACTGGTCAGTCCAA	39399	GCTTGA
			TTGGAT AGTCTTGAA		

AACCTG TCAGAACTT
ACTGG_
GAM419 PRO0478 5' TTCAAGACCAGCCTGACCAA 15398 AT__ TGAA
TTGG GCT GTCTTGAA
|||| ||| |||||
AACC CGA CAGAACTT
AGTC C__
GAM419 SARM 3' ACTTTAACATGCATCCAA 17452 ____
TTGGATGC TTGAAGT
||||| |||||
AACCTACG AATTTCA
TAC
GAM419 SSFA2 3' TTCAGAGCTTGAAGCATCCAA 36515 G TC
TTGGATGCTT AAG TTGAA
||||||| ||| |||||
AACCTACGAA TTC GACTT
G GA
GAM419 TRIM22 3' TCAAGACTATATCTAA 12719 CTTGA
TTGGATG AGTCTTGA
||||| |||||
AATCTAT TCAGAACT
A__
GAM419 ZNF347 3' TTCAAGACCAGCCTGACCAA 26320 AT__ TGAA
TTGG GCT GTCTTGAA
|||| ||| |||||
AACC CGA CAGAACTT
AGTC C__
GAM419 LOC119504 5' TTCAAGACCAGCCTGACCAA 36616 AT__ TGAA
TTGG GCT GTCTTGAA
|||| ||| |||||
AACC CGA CAGAACTT
AGTC C__
GAM419 LOC126382 5' CAAGATTTGGCTCCAA 37456 T TG
TTGGA GCT AAGTCTTG
|||| ||| |||||
AACCT CGG TTTAGAAC
- -
GAM419 LOC128977 3' CAAGAGCAGGAGCATCTAA 36948 GAAG
TTGGATGCTT TCTTG
||||||| |||||
AATCTACGAG AGAAC
GACG
GAM419 LOC131744 3' TTCAAGACCAGCCTGACCAA 37359 AT__ TGAA
TTGG GCT GTCTTGAA
|||| ||| |||||
AACC CGA CAGAACTT
AGTC C__
GAM419 LOC144465 3' TTCAAGACCAGCCTGACCAA 37753 AT__ TGAA
TTGG GCT GTCTTGAA
|||| ||| |||||

		AACC CGA CAGAACTT	
		AGTC C__	
GAM419	LOC145216 3'	TTCAAGACCAGCCTGACCAA 40510	AT__ TGAA
		TTGG GCT GTCTTGAA	
		AACC CGA CAGAACTT	
		AGTC C__	
GAM419	LOC148894 5'	TCAAGACTTCCTCCAG 40921	TGCTT
		TTGGA GAAGTCTTGA	
		GACCT CTCAGAACT	
		C__	
GAM419	LOC148932 3'	TCCTGAGCCAAGCATCCAA 38625	AAG TT
		TTGGATGCTTG TC GA	
		AACCTACGAAC AG CT	
		CG_ TC	
GAM419	LOC149113 3'	TTCAAGACCAGCCTAGCCAA 38642	AT__ TGAA
		TTGG GCT GTCTTGAA	
		AACC CGA CAGAACTT	
		GATC C__	
GAM419	LOC150630 3'	TTCAAGACCAGCCTGACCAA 41244	AT__ TGAA
		TTGG GCT GTCTTGAA	
		AACC CGA CAGAACTT	
		AGTC C__	
GAM419	LOC154403 3'	TTCAAGACCAGCCTAGCCAA 39470	AT__ TGAA
		TTGG GCT GTCTTGAA	
		AACC CGA CAGAACTT	
		GATC C__	
GAM419	LOC154992 3'	TTCAAGACCAGCCTAGCCAA 39520	AT__ TGAA
		TTGG GCT GTCTTGAA	
		AACC CGA CAGAACTT	
		GATC C__	
GAM419	LOC196812 3'	TTCAAACTAGTATCTAA 43140	TGA C
		TTGGATGCT AGT TTGAA	
		AATCTATGA TCA AACTT	
		__ A	
GAM419	LOC199858 5'	TCTGAATCAGCATCCAA 42643	T AG TT
		TTGGATGCT GA TC GA	
		AACCTACGA CT AG CT	
		_ A_ T_	
GAM419	LOC201868 3'	TTCAAGACCAGCCTAGCCAA 42923	AT__ TGAA
		TTGG GCT GTCTTGAA	

		AACC CGA CAGAACTT	
		GATC C__	
GAM419	LOC201911 3'	TTCAAGACCAGCCTGACCAA 43391	AT__ TGAA
		TTGG GCT GTCTTGAA	
		AACC CGA CAGAACTT	
		AGTC C__	
GAM419	LOC219722 5'	TTCAAGACTAGCCTGACCAA 44713	AT__ TGA
		TTGG GCT AGTCTTGAA	
		AACC CGA TCAGAACTT	
		AGTC ____	
GAM419	LOC221431 3'	TCATGATTCAAGATCCAA 44226	G G T
		TTGGAT CTTGAA TC TGA	
		AACCTA GAACTT AG ACT	
		_ _ T	
GAM419	LOC254531 5'	TTCAAGACCAGCCTGACCAA 45541	AT__ TGAA
		TTGG GCT GTCTTGAA	
		AACC CGA CAGAACTT	
		AGTC C__	
GAM419	LOC90594 3'	TCAAGACTTCAAATGCAT 31775	__
		ATGC TTGAAGTCTTGA	
		TACG AACTTCAGAACT	
		TA	
GAM419	LOC90918 5'	TTCAAGACCAGCCTGACCAA 32178	AT__ TGAA
		TTGG GCT GTCTTGAA	
		AACC CGA CAGAACTT	
		AGTC C__	
GAM420	CNTN3 3'	AAATGCAGTGATTATGCATGT 33131	ATT A
		ACAT TAG TACTGCATTT	
		TGTA ATT GTGACGTAAA	
		CGT A	
GAM420	HMOX1 3'	AAATGCAGTATTTTGTGTGT 7909	T TT
	T	AACACA AT AGATACTGCATTT	
		TTGTGT TG TTTATGACGTAAA	
		_ TT	
GAM420	NCOA4 3'	AAATGCAGCATCTTTGTG 11921	TATTT A
		CACA AGAT CTGCATTT	
		GTGT TCTA GACGTAAA	
		T__ C	
GAM420	NEUROD1 3'	AAATGCAGTCCAGAATAAGTG 8322	A AGAT
		CAC TATTT ACTGCATTT	

			GTG ATAAG TGACGTAAA		
			A ACC_		
GAM420	PDE4D	3'	AAATGCAATATCTGGGTACTGT 36424	_	C
			ACA TATTTAGATA TGCATTT		
			TGT ATGGGTCTAT ACGTAAA		
			C A		
GAM420	APOL6	3'	TGTGTATCTAAACATATGT 24973	_	T
			ACATAT TTAGATAC GCA		
			TGTATA AATCTATG TGT		
			CA _		
GAM420	DKFZP761L0424	3'	AAATGCAGTAAGCATGTGTT 43891		A TAGA
			AACACAT TT TACTGCATTT		
			TTGTGTA GA ATGACGTAAA		
			C _		
GAM420	FLJ20312	3'	AATGCAGTATGGGACTAT 19372	T AG	
			ATA TT ATACTGCATT		
			TAT AG TATGACGTAA		
			C GG		
GAM420	KIAA1950	3'	AAATGCAAAGGGACAAGTATGT 44481		AGATAC_
			GTT AACACATATTT TGCATTT		
			TTGTGTATGAA ACGTAAA		
			CAGGGAA		
GAM420	MGC5391	3'	AAATGCAGTATCTTCAGAATG 26470	ATTT_	
			CAT AGATACTGCATTT		
			GTA TCTATGACGTAAA		
			AGACT		
GAM420	RYBP	5'	AAATGCAGCATCTGCGATGTG 29907	ATT A	
			CACAT TAGAT CTGCATTT		
			GTGTA GTCTA GACGTAAA		
			GC_ C		
GAM420	LOC255533	5'	AATGCAGTAGGCAAATGT 46328	AGA	
			ATATTT TACTGCATT		
			TGTAAA ATGACGTAA		
			CGG		
GAM421	MEF2C	3'	CCCTTGACAATCTTGTCAGCAA 8210	A TTA T	
			TTGCTGACAA ATT CAG GG		
			AACGACTGTT TAA GTT CC		
			C CA_ C		
GAM421	SALL1	3'	CTGCTGGAAAATTTTATCAGCA 8880	C A TG	
			A TTGCTGA AAAATTTT CAG G		

AACGACT TTTTAAAA GTC C
 A G GT
 GAM421 ENAH 3' CCCTATAAATCTGGTCAGCAA 20126 AAAAT C T
 TTGCTGAC TTTA AG GG
 ||||| ||| ||
 AACGACTG AAAT TC CC
 GTCT_ A _
 GAM421 KIAA0556 3' CCACTATGGTGGGCTCCGTCAG 34249 AAAAT ____
 CA TGCTGAC TTTAC AGTGG
 ||||| ||| ||||
 ACGACTG GGGTG TCACC
 CCTC_ GTA
 GAM421 KIAA0648 3' TCCACTGTAGGGTCATCCGCAA 40220 T CAAA
 TTGC GA ATTTTACAGTGGA
 ||| || |||||
 AACG CT TGGGATGTCACCT
 C AC_
 GAM421 LOC143465 5' CCACTGTGATTCTCAACAA 40361 C CAAAATT
 TTG TGA TTACAGTGG
 ||| ||| |||||
 AAC ACT AGTGTACC
 A CTT____
 GAM421 LOC147599 3' CCACTGCTGGGTATCTGTCAGC 40847 AA_ TA
 AA TTGCTGACA ATTT CAGTGG
 ||||| ||| |||||
 AACGACTGT TGGG GTCACC
 CTA TC
 GAM422 PUM1 3' CCATATGTGTATAATTAACA 16147 GC C CAT
 TG TAA TATACACAT TGG
 || ||| ||||| |||
 AC ATT ATATGTGTA ACC
 A_ A T_
 GAM422 SOX13 3' CCCAACTCGATGGGCACAGCCA 12241 AA ATACA A_
 GCCA TGGCT CT CATC TTGGG
 |||| || ||| ||||
 ACCGA GA GTAG AACCC
 CC CACGG CTC
 GAM422 DSCR1L1 3' CCAATATATACATGGTTAGCCA 12428 ACACATC
 TGGCTAACTAT ATTGG
 ||||| ||| ||||
 ACCGATTGGTA TAACC
 CATATA_
 GAM423 COG6 3' ATCCAACCAACTACACATTTTA 36067 CAC A AA
 TAGAATG GG TGG TTGGAT
 ||||| || ||| |||||
 ATTTTAC TC ACC AACCTA
 ACA A _
 GAM423 PCDH19 3' ATCCAATTACTGTGCCTTCTA 31860 T ATGG
 TAGAA GCACGG AATTGGAT
 |||| ||||| |||||

		ATCTT CGTGTC TTAACCTA		
		C A__		
GAM423	LOC146108 3'	TCCCTCTCATCCATGCATTCTA 38064	C	_ ATT
		TAGAATGCA GGATG GA GGA		
		ATCTTACGT CCTAC CT CCT		
		A T C__		
GAM423	LOC151126 3'	TCCAACTGGGTGTATTCTA 39058	__	A
		TAGAATGCAC GG TGG A		
		ATCTTATGTG TC ACCT		
		GG A		
GAM424	SUV39H2 3'	CAAGACATTTGCCAAATGTATT 23974	A	A
	A	TAATGCATTTGG AGGT TCTTG		
		ATTATGTAAACC TTTA AGAAC		
		G C		
GAM424	FLJ13340 3'	AAGAACCAAATGCACTGT 27704	A	AAGGTA
		ATA TGCATTTGG TCTT		
		TGT ACGTAAACC AGAA		
		C A__		
GAM424	TBDN100 3'	AAGAACCAAATGCACTGT 24693	A	AAGGTA
		ATA TGCATTTGG TCTT		
		TGT ACGTAAACC AGAA		
		C A__		
GAM424	YAP1 3'	ATCTTCCAAAGCACTAT 12749	A	A
		ATA TGC TTTGGAAGGT		
		TAT ACG AAACCTTCTA		
		C _		
GAM424	LOC143153 3'	ACGTTCCAAATACATTAT 37577	C	G
		ATAATG ATTTGGAA GT		
		TATTAC TAAACCTT CA		
		A G		
GAM424	LOC143154 3'	ACGTTCCAAATACATTAT 37584	C	G
		ATAATG ATTTGGAA GT		
		TATTAC TAAACCTT CA		
		A G		
GAM424	LOC144571 3'	ATCTATTCCAAATCATTA 40440	C	__
		TAATG ATTTGGA AGGT		
		ATTAC TAAACCT TCTA		
		_ TA		
GAM424	LOC146346 5'	GCCTTCCAAAGTGCATTA 38137	_	
		TAATGCATTT GGAAGGT		

			ATTACGTGAA CCTTCCG		
			A		
GAM424	LOC219294	3'	ACGTTCCAAATACATTAT 44685	C	G
			ATAATG ATTTGGAA GT		
			TATTAC TAAACCTT CA		
			A G		
GAM424	LOC219295	3'	ACGTTCCAAATACATTAT 44680	C	G
			ATAATG ATTTGGAA GT		
			TATTAC TAAACCTT CA		
			A G		
GAM424	LOC219790	3'	ATATCCCCAAATGCTTAT 43904	T	AA
			ATAA GCATTTGG GGTAT		
			TATT CGTAAACC CTATA		
			_ C_		
GAM424	LOC221687	3'	CAAGATACAGCTAAATACATTT 44303	T	C AAG
	A		A AATG ATTTGG GTATCTTG		
			A TTAC TAAATC CATAGAAC		
			T A GA_		
GAM424	LOC83690	3'	AAGGTGCCAAATGCAT 25483	GGAA	
			ATGCATTT GGTATCTT		
			TACGTAAA CCGTGGAA		

GAM425	APBB2	3'	GCTCTTTGACACATGGACA 35879	GTGA	
			TGTTTCATGTG AGAGAGC		
			ACAGGTACAC TTTCTCG		
			AG_		
GAM425	NRCAM	3'	GCCCTCTCATACTATGAACAT 11451	TG	A A
			ATGTTTCATG GTGA GAG GC		
			TACAAGTAT TACT CTC CG		
			CA _ C		
GAM425	PTPN18	3'	GCTCTCCTCACCACACAGCA 15703	CA	A
			TGTT TGTGGTGA GAGAGC		
			ACGA ACACCACT CTCTCG		
			C_ C		
GAM425	KIAA1598	3'	CTCTCCTCACCACAACTTATTA 20329	TTCA	A
			TAATG TGTGGTGA GAGAG		
			ATTAT ACACCACT CTCTC		
			TCA_ C		
GAM425	LOC196500	3'	CTCTCTCCCTCATGAACA 42390	T T	A
			TGTTTCATG GG GA GAGAG		

			ACAAGTAC CC CT CTCTC		
			T _ _		
GAM425	LOC219855	3'	CTCTTTATTGAACATTA 43996	TGTG	
			TAATGTTCA GTGAAGAG		
			ATTACAAGT TATTTCTC		

GAM425	LOC221814	5'	CTCTCTGGCAAGAACATTA 45092	A GGTGA	
			TAATGTTT TGT AGAGAG		
			ATTACAAG ACG TCTCTC		
			A G_____		
GAM426	CASQ2	3'	TCAGCTGGCTTCCTAGC 6904	AAT AG	
			GCTAGGA AG GGCTGA		
			CGATCCT TC TCGACT		
			____ GG		
GAM426	NEK6	3'	CGCAACTTCCTAGCGTGA 15740	ATAGAGG T	
			TCACGCTAGGAA GC G		
			AGTGCGATCCTT CG C		
			CAA_____ T		
GAM426	PRKG2	3'	TGGCACCATTTCCTAAAGT 12942	GC AGA _	
			AC TAGGAAAT GG GCTG		
			TG ATCCTTTA CC CGGT		
			AA _____ A		
GAM426	WHN	3'	CAGCTTTCCCCAGGGTGA 9648	G A AAATA	
			TCAC CT GG GAGGGCTG		
			AGTG GA CC CTTTCGAC		
			G C _____		
GAM426	ALLC	5'	TCAGCGATGCTTATTTCTAGC 20497	AT AGG_	
			GCTAGGAA AG GCTGA		
			CGATCTTT TC CGACT		
			AT GTAG		
GAM426	ELF1	3'	TCAGGTTATTTCTAATGT 35402	C GAG G	
			ACG TAGGAAATA G CTGA		
			TGT ATCCTTTAT T GACT		
			A _____ G		
GAM426	EPN3	5'	TCAGCCCTCCACCTCCGGCG 19668	A AATA	
			CGCT GGA GAGGGCTGA		
			GCGG CCT CTCCCGACT		
			_ CCAC		
GAM426	FLJ11806	5'	CCACTTGCCATTTCCTAGCGCGA 24216	A ATA_ _	
			TC CGCTAGGAA GAG GG		

AG GCGATCCTT TTC CC
 C ACCG A
 GAM426 FLJ20294 3' CAGCCCTCCACCTCTCGGGGA 19343 A_ CT AAATA
 TC CG AGG GAGGGCTG
 || || || |||||
 AG GC TCC CTCCCGAC
 GG TC AC__
 GAM426 FLJ23462 3' CAGCCCTCTGCCTGGC 24264 AAA
 GCTAGG TAGAGGGCTG
 ||||| |||||
 CGGTCC GTCTCCCGAC

 GAM426 KIAA1202 3' CAGCCCTCTACCCTGGATGT 35639 _ AAA
 ACG CTAGG TAGAGGGCTG
 ||| ||||| |||||
 TGT GGTCC ATCTCCCGAC
 A C__
 GAM426 MGC2452 5' TCAGTATTATTTCTAAAATGA 26374 CGC GAGG
 TCA TAGGAAATA GCTGA
 ||| ||||| |||||
 AGT ATCCTTTAT TGA CT
 AAA TA__
 GAM426 P115 3' TCAGCCCTCCATCTAATGTGA 9812 C AAATA
 TCACG TAGG GAGGGCTGA
 ||||| ||||| |||||
 AGTGT ATCT CTCCCGACT
 A AC__
 GAM426 SSR1 3' TCAGCCCTCCTCATTCTA 9115 ATA_
 TAGGAA GAGGGCTGA
 ||||| |||||
 ATCCTT CTCCCGACT
 ACTC
 GAM426 TSGA14 3' TCAGCTTTCCCCTAGCATGG 20795 C AAATA
 TCA GCTAGG GAGGGCTGA
 ||| ||||| |||||
 GGT CGATCC CTTTCGACT
 A C__
 GAM426 LOC146337 3' TCAGCCCTAACCCCAAGTGTGA 40692 A AAATAG
 TCACGCT GG AGGGCTGA
 ||||| || |||||
 AGTGTGA CC TCCCGACT
 C CAA__
 GAM427 ALDH3A2 3' ACCCAGCCCTGTCTGTGA 34339 ATT CCA
 TAACAGACA GCT GGT
 ||||| ||| |||
 ATTGTCTGT CGA CCA
 CC_ C__
 GAM427 CANX 3' AAGACCTGAAAATATGTCTG 42275 _ GCTC
 CAGACA ATT CAGGTCTT
 ||||| ||| |||||

GTCTGT TAA GTCCAGAA
 A AA__
 GAM427 ITGB1 3' AAGAACCGAGCAATTTTCTG 7976 C CA _
 CAGA AATTGCTC GGT CTT
 |||| ||||| ||||
 GTCT TTAACGAG CCA GAA
 T _ A
 GAM427 PIP5K1A 3' AAGACCTGGAACAAGATTCTG 9601 CAA C
 CAGA TTG TCCAGGTCTT
 |||| || |||||
 GTCT AAC AGGTCCAGAA
 TAG A
 GAM427 USH3A 3' ACCTGGAGCAGCTGCTG 27559 A A
 CAG CA TTGCTCCAGGT
 ||| || |||||
 GTC GT GACGAGGTCCA
 _ C
 GAM427 ZNF189 3' AGACCTGGAGTCTATGCT 9503 A ATT
 AG CA GCTCCAGGTCT
 || || |||||
 TC GT TGAGGTCCAGA
 _ ATC
 GAM427 FLJ10546 5' ACCTGGAGACTCTCTGTTA 29911 CAATTG
 TAACAGA CTCCAGGT
 ||||| |||||
 ATTGTCT GAGGTCCA
 CTCA__
 GAM427 FLJ23563 3' ACCTGTTGTCTGTTA 33558 TTGCTC
 TAACAGACAA CAGGT
 ||||| ||||
 ATTGTCTGTT GTCCA

 GAM427 LOC115294 3' ACCTGGAGAAAGTTATCTGT 36142 C G_
 ACAGA AATT CTCCAGGT
 |||| ||| |||||
 TGTCT TTGA GAGGTCCA
 A AA
 GAM427 LOC150606 3' ACTTTCAGAGCAATTATCT 41233 C C_
 AGA AATTGCTC AGGT
 || ||||| ||||
 TCT TTAACGAG TTCA
 A ACT
 GAM427 LOC206426 3' AAGACCTGGAACAAGATTCTG 43113 CAA C
 CAGA TTG TCCAGGTCTT
 |||| || |||||
 GTCT AAC AGGTCCAGAA
 TAG A
 GAM427 LOC55901 5' AAGACCTGGGATTTTGTC 20749 TTG T
 GACAA C CCAGGTCTT
 |||| | |||||

CTGTT G GGTCCAGAA
TTA _

GAM428 PMX1 3' GGCTAATTCTAAGCAC 13782 CAAGC CC
GTGCTTAG GA TAGCC
||||||| || |||||
CACGAATC TT ATCGG
_____ A_

GAM428 PMX1 3' GGCTAATTCTAAGCAC 22917 CAAGC CC
GTGCTTAG GA TAGCC
||||||| || |||||
CACGAATC TT ATCGG
_____ A_

GAM428 ZNF2 3' CTAGCACTTACTGAGCAC 22069 C CGAC
GTGCTTAG AAG CTAG
||||||| ||| |||||
CACGAGTC TTC GATC
A AC_

GAM428 DIS3 3' CTGACTACTTCCCTTGCTAATC 17299 C C CC C
AC GTG TTAGCAAG GA TAG CAG
||| ||||| || ||| |||||
CAC AATCGTTC CT ATC GTC
T C TC A

GAM428 FLJ22329 3' GCCAGCTCTTGCTAAGCA 23957 CGAC A
TGCTTAGCAAG CT GC
||||||| || ||
ACGAATCGTTC GA CG
TC_ C

GAM428 LEC3 3' GCTAGGTCGCGGCAGCA 17571 TA AA
TGCT GC GCGACCTAGC
|||| || ||||| |||||
ACGA CG CGCTGGATCG
_ G_

GAM428 SP192 5' GGCCAGGTTACTTAAGCAC 22298 GCA CG A
GTGCTTA AG ACCT GCC
|||||| || ||||| |||||
CACGAAT TC TGGA CGG
_ AT C

GAM428 LOC144667 3' GCTCCAGCCTGCTGAGCAC 40451 A GACCT
GTGCTTAGCA GC AGC
||||||| || |||
CACGAGTCGT CG TCG
C ACCC_

GAM428 LOC151996 5' TGGCCAGGTCAGAAGCAT 41416 AGCAAGC A
GTGCTT GACCT GCCA
||||| ||||| |||||
TACGAA CTGGA CGGT
GA_ C

GAM428 LOC256113 5' CTGGCTAAGCGGTCTTAAGCAC 46260 CAAGC _
GTGCTTAG GACC TAGCCAG
||||||| ||||| |||||

CACGAATT CTGG ATCGGTC
_____ CGA
GAM429 ANGPT1 5' GGTCTAGAATATGTACACGCAG 6815 TCA C__
CT AGCTGCGT ACA TCTAGACC
||||||| ||| |||||||
TCGACGCA TGT AGATCTGG
CA_ ATA
GAM429 ANGPT1 5' GGTCTAGAATATGTACACGCAG 29290 TCA C__
CT AGCTGCGT ACA TCTAGACC
||||||| ||| |||||||
TCGACGCA TGT AGATCTGG
CA_ ATA
GAM429 DDX3 3' GATTGTTGAACGCAGCTT 7034 C
AAGCTGCGTTCAACA TC
||||||| ||| ||
TTCGACGCAAGTTGT AG
T
GAM429 RBBP9 3' GTCCAGAGTGTTAGCTTAGAGC 34743 GC__ C A
T AGCT GTT AACACTCT GAC
||| ||| ||||||| |||
TCGA CGA TTGTGAGA CTG
GATT _ C
GAM429 USP11 5' GGTCTAGAGCATGGCCAGC 11021 C T ACA
GCTG GT CA CTCTAGACC
||| ||| ||| |||||||
CGAC CG GT GAGATCTGG
_ _ AC_
GAM429 DKFZP564O0463 3' GGTCTAGAATAGGTTGGCA 15444 GTT AC__
TGC CAAC TCTAGACC
||| ||| |||||||
ACG GTTG AGATCTGG
_ GATA
GAM429 ELF4 5' GGTCCAGCCCAGAATGCAGC 7125 AACACT A
GCTGCGTTC CT GACC
||||||| || |||
CGACGTAAG GA CTGG
ACCC_ C
GAM429 FLJ20716 3' GTCAGGCTGAACGCAGC 19632 ACAC A
GCTGCGTTCA TCT GAC
||||||| ||| |||
CGACGCAAGT GGA CTG
C__ _
GAM429 HCC-4 3' GTCCAGACTGAACGCAGC 28898 ACAC A
GCTGCGTTCA TCT GAC
||||||| ||| |||
CGACGCAAGT AGA CTG
C__ C
GAM429 IKKE 3' GTTTCATGTTGAACACAGCT 15205 C CTCT
AGCTG GTTCAACA AGAC
||||| ||||||| |||

			TCGAC CAAGTTGT TTTG		
			A AC__		
GAM429	KIAA0794	3'	GGGTGTTGGACACAGCTT	39183	C
			AAGCTG GTTCAACACTC		
			TTCGAC CAGGTTGTGGG		
			A		
GAM429	KIAA1522	3'	GTCTAGAAGAGGCAGC	32420	G AACAC
			GCTGC TTC TCTAGAC		
			CGACG GAG AGATCTG		
			_ A__		
GAM429	LOC146315	5'	TCCAGAGTGTTGCCAG	30534	C TT A
			CTG G CAACACTCT GA		
			GAC C GTTGTGAGA CT		
			_ _ C		
GAM429	LOC146515	5'	GTCCTTTGAGCGCAGCT	38195	CACTCTA
			AGCTGCGTTCAA GAC		
			TCGACGCGAGTT CTG		
			TC__		
GAM429	LOC221025	3'	TCTAGAAAACCAGCTT	44746	C CAACAC
			AAGCTG GTT TCTAGA		
			TTCGAC CAA AGATCT		
			_ A__		
GAM429	LOC92661	3'	GTCTGGGCACTGACGCAGCT	34726	T ACAC
			AGCTGCGT CA TCTAGAC		
			TCGACGCA GT GGGTCTG		
			_ CAC_		
GAM430	ADORA3	5'	TGCTCCCACCTGATCCTGCACT	6333	A_ CTC
	G		CAGTGCA GTTA TGGGAGCA		
			GTCACGT TAGT ACCCTCGT		
			CC CC_		
GAM430	BAK1	3'	TTGCTCCCAACCCATTCACT	44176	C GTTACTC
			AGTG AA TGGGAGCAA		
			TCAC TT ACCCTCGTT		
			_ ACCCA_		
GAM430	BGN	3'	TGCCCCCAAACCTGTACTG	7438	A ACTC A
			CAGTGCA GTT TGGG GCA		
			GTCATGT CAA ACCC CGT		
			C _ C		
GAM430	CNTN2	3'	GCTCCCAGACGGCCTTGGA	11524	G TTAC
			CAGT CAAG TCTGGGAGC		

			GTCA GTTC AGACCCTCG		
			G CGGC		
GAM430	E2F1	3'	TGCTCCCAGAATCTGGTGCTCT 41120	T	AGTTAC
	G		CAG GCA TCTGGGAGCA		
			GTC CGT AGACCCTCGT		
			T GGTCTA		
GAM430	FUT6	3'	TGCTCCCAGAGACCTTCCAC 5652	C	TTA
			GTG AAG CTCTGGGAGCA		
			CAC TTC GAGACCCTCGT		
			C CA_		
GAM430	GRAF	3'	TGCTCCCACCCTTGCCTG 17447	T	TTACTC
			CAG GCAAG TGGGAGCA		
			GTC CGTTC ACCCTCGT		
			_ CC_		
GAM430	HCN4	3'	TGCCCCCAGAAAGGGGCTGCCC 11980	T	A TA_ A
	TG		CAG GCA GT C TCTGGG GCA		
			GTC CGT CG G AGACCC CGT		
			C _ GG AA C		
GAM430	MADD	3'	CTCCCAGAAGACCAAAGT 9787	GCAA	AC
			CAGT GTT TCTGGGAG		
			GTCA CAG AGACCCTC		
			AAC_ A_		
GAM430	MADD	3'	CTCCCAGAAGACCAAAGT 28252	GCAA	AC
			CAGT GTT TCTGGGAG		
			GTCA CAG AGACCCTC		
			AAC_ A_		
GAM430	MADD	3'	CTCCCAGAAGACCAAAGT 28257	GCAA	AC
			CAGT GTT TCTGGGAG		
			GTCA CAG AGACCCTC		
			AAC_ A_		
GAM430	MADD	3'	CTCCCAGAAGACCAAAGT 28236	GCAA	AC
			CAGT GTT TCTGGGAG		
			GTCA CAG AGACCCTC		
			AAC_ A_		
GAM430	MADD	3'	CTCCCAGAAGACCAAAGT 28242	GCAA	AC
			CAGT GTT TCTGGGAG		
			GTCA CAG AGACCCTC		
			AAC_ A_		
GAM430	MADD	3'	CTCCCAGAAGACCAAAGT 28247	GCAA	AC
			CAGT GTT TCTGGGAG		

GTCA CAG AGACCCTC
 AAC_ A_
 GAM430 PROX1 5' CCAGAATCACTTGCACTG 8648 TAC
 CAGTGCAAGT TCTGG
 ||||| ||||
 GTCACGTTCA AGACC
 CTA
 GAM430 RNPEPL1 3' CTCCCAGCTCTCTTGCACTG 20160 TTACT
 CAGTGCAAG CTGGGAG
 ||||| |||||
 GTCACGTTC GACCCTC
 TCTC_
 GAM430 SH3BP2 3' TTGCCCCACACTAACTTGCCCT 8954 T CTC A
 G CAG GCAAGTTA TGGG GCAA
 || ||||| ||| ||||
 GTC CGTTCAAT ACCC CGTT
 C CAC _
 GAM430 SLC7A5 3' TTGCTACGACAGACTTGCACTG 9579 TTAC GG_
 CAGTGCAAG TCTG AGCAA
 ||||| ||| ||||
 GTCACGTTC AGAC TCGTT
 _ AGCA
 GAM430 TRPM8 3' CTGAGAAGCAACTTGCACTT 23516 A _ G
 AGTGCAAGTT CT CT GG
 ||||| || || ||
 TTACGTTCAA GA GA TC
 C A G
 GAM430 USH3A 3' CTGAGAAATAACTTGCTCTG 27561 T C_ G
 CAG GCAAGTTA TCT GG
 || ||||| ||| ||
 GTC CGTTCAAT AGA TC
 T AA G
 GAM430 XPR1 3' TCAGGAGACAACCTTGCACT 11124 A_ GG
 GTGCAAGTT CTCT GA
 ||||| ||| ||
 CACGTTCAA GAGG CT
 CA A_
 GAM430 AF311304 3' TTGCATTTTAGCACTTGCACT 25262 TACT _
 AGTGCAAGT CTGGGA GCAA
 ||||| ||||| ||||
 TCACGTTCA GATTTT CGTT
 C_ A
 GAM430 DKFZP566G1424 5' GCTCCCAGAACAGGCAC 41115 AA TAC
 GTGC GT TCTGGGAGC
 ||| || |||||
 CACG CA AGACCCTCG
 GA _
 GAM430 FBX30 3' TGCTCCCAGTCTCTCGCTCTG 27044 T A TTACT
 CAG GC AG CTGGGAGCA
 ||| || |||||

GTC CG TC GACCCTCGT
 T C TCT__
 GAM430 FLJ12242 3' CCCAGCCATTTGCATTG 23995 TACT
 CAGTGCAAGT CTGGG
 ||||| ||||
 GTTACGTTTA GACCC
 CC__
 GAM430 FLJ20294 3' TGCTCCCAGAGGCCGGGCAACT 19354 _ AAGTTA
 G CAGT GC CTCTGGGAGCA
 ||| || |||||
 GTCA CG GAGACCCTCGT
 A GGCCG_
 GAM430 FLJ21742 3' TGCTCCCAGCCTTCACTG 25914 C TTACT
 CAGTG AAG CTGGGAGCA
 |||| || |||||
 GTCAC TTC GACCCTCGT
 _ C__
 GAM430 FLJ22215 3' TGCTCCCACACCTGCGC 46284 A TACTC
 GTGCA GT TGGGAGCA
 |||| || |||||
 CGCGT CA ACCCTCGT
 C C__
 GAM430 HEMK 3' CTCCCAGGTAGCACTG 18269 AAGT T
 CAGTGC TAC CTGGGAG
 |||| || |||||
 GTCACG ATG GACCCTC
 _ _
 GAM430 KIAA0182 3' TTGCTCCCAAGGGCCCTCAC 35648 CA TTA TC
 GTG AG C TGGGAGCAA
 ||| || | |||||
 CAC TC G ACCCTCGTT
 _ CCG GA
 GAM430 KIAA0323 3' CCCAAAGACAGCTTGCAC 31690 A_ C
 GTGCAAGTT CT TGGG
 ||||| || |||
 CACGTTCGA GA ACCC
 CA A
 GAM430 KIAA0415 3' TGCTCCCAGGCAACACTG 44479 CAA TACT
 CAGTG GT CTGGGAGCA
 |||| || |||||
 GTCAC CG GACCCTCGT
 AA_ _
 GAM430 KIAA0420 3' TTGCTGAGAGCAACTTGCA 31732 A GGG
 TGCAAGTT CTCT AGCAA
 ||||| ||| ||||
 ACGTTCAA GAGA TCGTT
 C G_
 GAM430 KIAA0556 3' CTCCCAGAACCGCAGCTG 34250 _ AA TAC
 CAG TGC GT TCTGGGAG
 ||| ||| || |||||

GTC ACG CA AGACCCTC
 G C_ ____
 GAM430 KIAA1950 3' GCTCCCAGGGGCCTGCAC 44490 A TA
 GTGCA GT CTCTGGGAGC
 ||||| || |||||
 CACGT CG GGGACCCTCG
 C ____
 GAM430 KRT6IRS 3' TGCTCCCATACACCTGGCACTG 27253 A TTA
 CAGTGC AG TGGGAGCA
 ||||| || |||||
 GTCACG TC ACCCTCGT
 G CACAT_
 GAM430 MATR3 3' CTTAAGACAACCTTGCAC 20820 AC GG
 GTGCAAGTT TCT GAG
 ||||| || |||||
 CACGTTCAA AGA TTC
 C_ A_
 GAM430 MGC35558 3' TGCTCCCAGAGTCACTCA 29620 A T
 C AGT ACTCTGGGAGCA
 | ||| |||||
 A TCA TGAGACCCTCGT
 C C
 GAM430 MGC4415 3' TGCCCCCAGAACTTTTGGATAC 25572 ____ TTAC A
 TG CAGTG CAAG TCTGGG GCA
 ||||| ||||| |||||
 GTCAT GTTT AGACCC CGT
 AG TCA_ C
 GAM430 RAB3IL1 3' GCTCCCAAACCGCTG 15064 CAA ACTC
 CAGTG GTT TGGGAGC
 ||||| || |||||
 GTCGC CAA ACCCTCG
 ____ A____
 GAM430 SFRS5 3' TGGGAGCAACTGTAAATAACTT 13806 CTC_____ GGAG
 GCCCTG GCAAGTTA TG CA
 ||||| || |||||
 CGTTCAAT AC GT
 AAATGTCIIIA GAGG
 GAM430 TAF5L 3' TGCTCCCACGTCCTGCACTG 15752 AGTT TC
 CAGTGCA AC TGGGAGCA
 ||||| || |||||
 GTCACGT TG ACCCTCGT
 CC_ C_
 GAM430 LOC150157 5' TGCTCCCAGAGCCTGAGCAT 41146 A_ TTA
 GTGC AG CTCTGGGAGCA
 ||||| || |||||
 TACG TC GAGACCCTCGT
 AG C_
 GAM430 LOC152756 3' TTGCCAAAGTAATTACACT 41552 CA C G
 AGTG AGTTACT TGG AG
 ||||| ||||| |||||

		TCAC TTAATGA ACC TT		
		A_ A G		
GAM430	LOC196890 5'	TGCTCCCAGAGCCTGAGCAT 43157	A_ TTA	
		GTGC AG CTCTGGGAGCA		
		TACG TC GAGACCCTCGT		
		AG C__		
GAM430	LOC202934 3'	TCACTGACAGCTTGCACTG 43466	AC TGG	
		CAGTGCAAGTT TC GA		
		GTCACGTTCGA AG CT		
		C_ TCA		
GAM430	LOC253675 3'	TGCTCCCAGAGACACTG 46268	CAAGTTA	
		CAGTG CTCTGGGAGCA		
		GTCAC GAGACCCTCGT		
		A_____		
GAM430	LOC255465 3'	TCACTGACAGCTTGCACTG 46458	AC TGG	
		CAGTGCAAGTT TC GA		
		GTCACGTTCGA AG CT		
		C_ TCA		
GAM430	LOC257354 3'	TTGCTGAGAGCAACTTGCA 45585	A GGG	
		TGCAAGTT CTCT AGCAA		
		ACGTTCAA GAGA TCGTT		
		C G__		
GAM430	LOC90075 5'	TCAGAGTACTCACACTG 30741	CA T	
		CAGTG AGT ACTCTGG		
		GTCAC TCA TGAGACT		
		AC _		
GAM430	LOC90362 5'	GCTCCCAGGCTGCAC 31297	A TACT	
		GTGCA GT CTGGGAGC		
		CACGT CG GACCCTCG		
		- - - - -		
GAM430	LOC91461 3'	TGTGGAGGGAGTGACTTGCACT 32870	GGGA	
	G	CAGTGCAAGTTACTCT GCA		
		GTCACGTTCAGTGAGG TGT		
		GAGG		
GAM430	LOC93259 5'	CTCCCAGAGCAACCCTGGGC 35557	G A_ A	
		GT CA GTT CTCTGGGAG		
		CG GT CAA GAGACCCTC		
		G CC C		
GAM431	BCL2L2 3'	CTAGAATACAGTCTGGGTCCCA 10261	C A CTCCCG	
	CA	TG GG ACCCAGAC TTAG		

AC CC TGGGTCTG GATC
 A C ACATAA
 GAM431 C8orf13 3' GGAGACCTGGGTTCCCA 39655 C AC
 TG GGAACCCAG CTCC
 || ||||| ||||
 AC CCTTGGGTC GAGG
 _ CA
 GAM431 OPRL1 3' AACGGGAGGATGGCTTC 6613 C GA
 GAA CCA CCTCCCGTT
 ||| ||| |||||
 CTT GGT GGAGGGCAA
 C A_
 GAM432 CELSR2 3' TGCCCTCATACGCCA 7109 C TT
 TGGCGTATGA GG GCA
 ||||| || |||
 ACCGCATACT CC CGT
 _ C_
 GAM432 EGLN2 5' TGTGGACGCCGTCATCCGCCA 28022 T T CA
 TGGCG ATGACGGT G CACA
 |||| ||||| | ||||
 ACCGC TACTGCCG C GTGT
 C _AG
 GAM432 FZD1 3' CTATGTCTGTCATACGCTA 9594 TTGC C
 TGGCGTATGACGG ACA AG
 ||||| ||| ||
 ATCGCATACTGTC TGT TC
 _ A
 GAM432 ATP6V1EL2 5' TCTGTGTGCAGACTCCCAACGC 27941 A AC _
 CA TGGCGT TG GGT TGCACACAGA
 |||| || ||| |||||
 ACCGCA AC TCA ACGTGTGTCT
 _ CC G
 GAM432 FLJ00001 3' TGTGCAACAACCACATGCCA 39789 A ACG
 TGGCGT TG GTTGCACA
 |||| || |||||
 ACCGTA AC CAACGTGT
 C CAA
 GAM432 KIAA0628 3' TGTGTAACCACCGCCA 16676 TA AC
 TGGCG TG GGTTGCACA
 |||| || |||||
 ACCGC AC CCAATGTGT
 C_ CA
 GAM432 KIAA0652 3' TCTGTGTGCCCTGCCCATCACC 16411 CGTA C_ T_
 A TGG TGA GGT GCACACAGA
 ||| ||| ||| |||||
 ACC ACT CCG CGTGTGTCT
 _ AC TCC
 GAM432 KIAA1389 3' TCTGTGTAGCACCATTACCA 34570 CGTA C_ T_
 TGG TGA GGT GC ACACAGA
 ||| ||| ||| |||||

ACC ACT CCA CG TGTGTCT
 _____ TA _ A
 GAM432 KIAA1889 3' GTGGGACCGTCATCACCA 36390 CGT G
 TGG ATGACGGTT CAC
 ||| ||||| |||
 ACC TACTGCCAG GTG
 AC_ G
 GAM432 MGC29654 5' GTGCAACCTCACCGCCA 33094 TA C
 TGGCG TGA GGTTGCAC
 |||| | |||||
 ACCGC ACT CCAACGTG
 C_ _
 GAM433 BCL10 3' CACCTCAGCCTCTCAAGTAA 10007 CA TT_
 TTGCT AGAGGCTG TG
 |||| ||||| ||
 AATGA TCTCCGAC AC
 AC TCC
 GAM433 LZTR1 3' TGGCTTCAGCCCCTTGAGCAG 13642 A TTTGA
 TTGCTCAAG GGCTG CA
 ||||| |||| |
 GACGAGTTC CCGAC GT
 C TTCG_
 GAM433 PCDH11X 3' TCAAACAGAATTTTAAGGAA 26793 G C GG
 TT CT AAGA CTGTTTGA
 || || |||| |||||
 AA GA TTTT GACAACT
 G A AA
 GAM433 PCDH11X 3' TCAAACAGAATTTTAAGGAA 26808 G C GG
 TT CT AAGA CTGTTTGA
 || || |||| |||||
 AA GA TTTT GACAACT
 G A AA
 GAM433 PCDH11Y 3' TCAAACAGAATTTTAAGGAA 26826 G C GG
 TT CT AAGA CTGTTTGA
 || || |||| |||||
 AA GA TTTT GACAACT
 G A AA
 GAM433 RAB1A 3' TGTATCAAACAGCACAAGCAG 34791 CAAGAG C
 TTGCT GCTGTTTGA ACA
 |||| | ||||| |||
 GACGA CGACAACT TGT
 ACA_ A
 GAM433 TBXA2R 3' GTGCCTCAGCCTCCCGAGCAG 6727 AA TTTGA
 TTGCTC GAGGCTG CAC
 |||| | |||| |
 GACGAG CTCCGAC GTG
 CC TCC_
 GAM433 C21orf18 3' CGGACAGCCCCTTGAACA 18898 C A
 TG TCAAG GGCTGTTG
 || |||| |||||

			AC AGTTC CCGACAGGC		
			A C		
GAM433	CASP9	3'	CACGTGGCCTCTTGAGCAG 6899	TG	T
			TTGCTCAAGAGGC T TG		
			GACGAGTTCTCCG G AC		
			GT C		
GAM433	FLJ20813	3'	TGTCAAACCTTTTTTTGTACAA 19680	CT	CT
			TTG CAAGAGG GTTTGACA		
			AAC GTTTTTT CAAACTGT		
			AT T_		
GAM433	GPR64	3'	CATACAGTGCCTTTGAGCAA 12316	A	_ T
			TTGCTCA GAGGC TGT TG		
			AACGAGT TTCCG ACA AC		
			_ TG T		
GAM433	HTGN29	3'	TGTGTCAAGAAATCTTGGCAA 21433	T	GGCTG
			TTGC CAAGA TTTGACACA		
			AACG GTTCT GAACTGTGT		
			_ AAA_		
GAM433	KIAA0352	3'	TGTCAAGCCCTTAAGCAA 16827	C A	GTT
			TTGCT AAG GGCT TGACA		
			AACGA TTC CCGA ACTGT		
			A _ _		
GAM433	KIAA0757	3'	TATTCAGCTCTTGAGCAA 12672	G	TT
			TTGCTCAAGAG CTG TG		
			AACGAGTTCTC GAC AT		
			_ TT		
GAM433	KIAA1796	3'	TGTGTCAAACTACTTAGCAA 43967	CAA	GCTG
			TTGCT GAG TTTGACACA		
			AACGA TTC AAACGTGTGT		
			_ ATCA		
GAM433	RNO2	5'	GTGTCTCAGCCTCCTGAGCAG 27127	A	TTT
			TTGCTCA GAGGCTG GACAC		
			GACGAGT CTCCGAC CTGTG		
			C T_		
GAM433	ZNF17	3'	CATCCAGCCTCTTGACAA 40066	C	TT
			TTG TCAAGAGGCTG TG		
			AAC AGTTCTCCGAC AC		
			_ CT		
GAM433	LOC145601	3'	CAGACAGCCCCCTGTGCAA 40540	T	AGA
			TTGC CA GGCTGTTTG		

		AACG GT CCGACAGAC		
		T CCC		
GAM433	LOC155340 5'	TGTGGGCAGCGCCCTGAACAA 36319	C A A T TGA	
		TTG TCA G GGC GTT CACA		
		AAC AGT C CCG CGA GTGT		
		A _ _ _ CGG		
GAM433	LOC256598 5'	GTGGGCAGCACCCCTGAACAA 46099	C AGAG TGA	
		TTG TCA GCTGTT CAC		
		AAC AGT CGACGG GTG		
		A CCCA _ _ _		
GAM433	LOC257463 3'	CACCTCAGCCTCCTGAACAG 35207	C A TT_	
		TTG TCA GAGGCTG TG		
		GAC AGT CTCCGAC AC		
		A C TCC		
GAM433	LOC83693 3'	GTGTGGTGCCTTTGAGCAA 25497	A TGTTTG	
		TTGCTCA GAGGC ACAC		
		AACGAGT TTCCG TGTG		
		_ TGG_ _		
GAM434	KIAA0441 3'	TATATTGGACAGCATGGGCCA 16712	ATCAA T	
		TGGCCCATGC CTA TATA		
		ACCGGGTACG GGT ATAT		
		ACA_ _ T		
GAM434	KIAA0555 3'	ATAGGGAACATGGGCCA 16679	CA AA	
		TGGCCCATG TC CTAT		
		ACCGGGTAC AG GATA		
		A_ G_		
GAM434	Rab11-FIP2 3'	TGTAATCTGATGCATGAATCA 17103	CC ACT	
		TGG CATGCATCA ATTATA		
		ACT GTACGTAGT TAATGT		
		AA C_		
GAM434	LOC152992 3'	ATAATTTCTGACATGGGCCA 39348	CA ACT_	
		TGGCCCATG TCA ATTAT		
		ACCGGGTAC AGT TAATA		
		_ CCTT		
GAM434	LOC221830 3'	TGGTAATCAATGCATGGCCA 44438	C CAAC	
		TGGCC ATGCAT TATTA		
		ACCGG TACGTA ATGGT		
		_ ACTA		
GAM435	ARHGDI A 3'	CCAGGCTCTCAGTGCCACCACC 10514	AA A_ CA	
	C	GGGT TG AT AGAGCCTGG		

			CCCA AC TG TCTCGGACC		
			CC CG AC		
GAM435	CRHR1	3'	CCAGGCTCCCTGACCACCCTG 10607	AATGAA A_	
			TAGGGT TCA GAGCCTGG		
			GTCCCA AGT CTCGGACC		
			CC_ CC		
GAM435	MYCBP	3'	CATCTAACTCATTACCTTA 14723	ATCA GCC	
			TAGGGTAATGA AGA TG		
			ATTCCATTACT TCT AC		
			CAA_ _		
GAM435	PPP2R4	3'	CAGGCTCCTTTTCACCCTG 30374	AAT TCAA	
			TAGGGT GAA GAGCCTG		
			GTCCCA CTT CTCGGAC		
			_ TTC_		
GAM435	C5orf4	3'	CCAGGCTCCTTCACCACCC 26179	AA TCAA	
			GGGT TGAA GAGCCTGG		
			CCCA ACTT CTCGGACC		
			CC C_		
GAM435	DNAL4	3'	CCAGGCTCTCAACCGTCTCCCT 12306	TA AATCA	
			AGGG ATG AGAGCCTGG		
			TCCC TGC TCTCGGACC		
			TC CAAC_		
GAM435	HAPIP	3'	CAGGCTCCTGCTGCCCTA 10067	ATGAAT A	
			TAGGGTA CA GAGCCTG		
			ATCCCGT GT CTCGGAC		
			C_ C		
GAM435	MGC15416	3'	CCAGGCCCTGCCAGGTTCCAC 28787	AAT A_ A	
	CC		GGGT GAATC AG GCCTGG		
			CCCA CTTGG TC CGGACC		
			CC_ ACCG C		
GAM435	SLC25A18	3'	CAGGCTCTTGACACCCC 25561	AA AAT	
			GGGT TG CAAGAGCCTG		
			CCCA AC GTTCTCGGAC		
			C_ _		
GAM435	SLC39A3	3'	CAGGCTCTCAGTCACCCCT 29356	TAA ATCA	
			AGGG TGA AGAGCCTG		
			TCCC ACT TCTCGGAC		
			C_ GAC_		
GAM435	LOC127534	3'	CCAGGCTCACCCATCACCC 37165	A AATCAA	
			GGGT ATG GAGCCTGG		

		CCCA TAC	CTCGGACC		
		C CCA__			
GAM435	LOC132617 5'	CAGGCTCCTCGTCACCC	37370	A	ATCAA
		GGGT ATGA	GAGCCTG		
		CCCA TGCT	CTCGGAC		
		C C__			
GAM435	LOC91040 5'	CCAGGCTCCCAACTCCACCCT	32314	AAT	ATCAA
		AGGGT GA	GAGCCTGG		
		TCCCA CT	CTCGGACC		
		C__ CAACC			
GAM436	PAG 3'	ATTCCTGTGGTTCATCCCA	20508	A	_
		TGG ATGAACTACAG	AAT		
		ACC TACTTGGTGTC	TTA		
		C C			
GAM436	C20orf50 5'	CGAATTGTCCGTGCTCACTCCA	34717	A AC	A A
		TGGA TGA	TAC GA TAATTCG		
		ACCT ACT	GTG CT GTTAAGC		
		C C_ C _			
GAM436	KIAA1336 3'	CGAATTATTCCAGGTAGATCC	35802	ATGAA	A__
		GGA CTAC	GAATAATTCG		
		CCT GATG	CTTATTAAGC		
		A__ GAC			
GAM436	PRDM10 3'	TATTCTGCACATTCATTCCA	21498	CTA_	
		TGGAATGAA	CAGAATA		
		ACCTTACTT	GTCTTAT		
		ACAC			
GAM436	TFIP11 3'	GAGTTCTCTGTAGTTCCTCCA	14450	AT	AT
		TGGA GAACTACAGA	AATTC		
		ACCT CTTGATGTCT	TTGAG		
		C_ C_			
GAM436	LOC158364 5'	ATTCCAGAGTTCATTCCA	39814	ACA	
		TGGAATGAACT	GAAT		
		ACCTTACTTGA	CTTA		
		GAC			
GAM436	LOC253613 5'	ATTCCAGAGTTCATTCCA	46010	ACA	
		TGGAATGAACT	GAAT		
		ACCTTACTTGA	CTTA		
		GAC			
GAM437	SULT1C1 3'	CTGGCAATTCCAAACAATGT	6721	CTCT	_
		ACATTGTT	TGG TTGCCAG		

			TGTAACAA ACC AACGGTC		
			_____ TT		
GAM437	HRIHFB2436	5'	GCAAAGAACAAATGTAC 15667	CTTGG	
			GTACATTGTTCT TTGC		
			CATGTAACAAGA AACG		

GAM437	LOC139065	5'	GCCAAGAGAAAAATATAC 37327	C G	
			GTA ATT TTCTCTTGGT		
			CAT TAA AAGAGAACCG		
			A A		
GAM437	LOC151584	3'	CCAGAGAGAACAAATGTAT 41375	_	
			GTACATTGTTCTCT TGG		
			TATGTAACAAGAGA ACC		
			G		
GAM437	LOC222166	3'	CTGTTTCATAAGAGCACAATGT 45155	T GTTGC	
			AC GTACATTGT CTCTTG CAG		
			CATGTAACA GAGAAT GTC		
			C ACTTT		
GAM438	ADH5	3'	ACCCAAGTCTGCTTCTGTGAT 6323	AACTTATC	
			ATCACA GACTTGGGT		
			TAGTGT CTGAACCCA		
			CTTCGT__		
GAM438	ENG	3'	ACCCAAGTCCCTGTCATTTG 5590	CT_ TC	
			CAAA TA GACTTGGGT		
			GTTT GT CTGAACCCA		
			ACT CC		
GAM438	PPP4R2	5'	CCATGGATACGCTTGTGATC 21256	ACT GACT	
			GATCACAA TATC TGG		
			CTAGTGTT ATAG ACC		
			CGC GT__		
GAM438	LOC200854	5'	CCATGGATACGCTTGTGATC 42252	ACT GACT	
			GATCACAA TATC TGG		
			CTAGTGTT ATAG ACC		
			CGC GT__		
GAM438	LOC253187	5'	ACCCAAAAAGGTAAGTTT 46392	GAC	
			AAACTTATC TTGGGT		
			TTTGAATGG AACCCA		
			AAA		
GAM439	GAC1	3'	GGGCCAGATGCCCTGCCA 13039	A	
			TGGCAGG CGTCTGGCTC		

			ACCGTCC GTAGACCGGG		
			C		
GAM439	GRAF	3'	TGACAGAGCCAGACTCC 17446	C	
			GGA GTCTGGCTCTGTCA		
			CCT CAGACCGAGACAGT		
			—		
GAM439	NFIB	3'	GTGACAGAGCCATGAGCCAGCC 12121	A	ACGTC
	A		TGGC GG TGGCTCTGTCA		
			ACCG CC ACCGAGACAGTG		
			A GAGT_		
GAM439	SMG1	3'	GCGAGGTCAGACATCCACCA 17478	CA	C TC
			TGG GGA GTCTGGC TGT		
			ACC CCT CAGACTG GCG		
			A_ A GA		
GAM439	BRD4	3'	CGGACAGACGTCCCGCCA 27775	A	GC
			TGGC GGACGTCTG TCTG		
			ACCG CCTGCAGAC AGGC		
			C —		
GAM439	DARS	3'	TGACAGAGCGAGACCCTGCC 7030	AC	G
			GGCAGG GTCT GCTCTGTCA		
			CCGTCC CAGA CGAGACAGT		
			— G		
GAM439	FLJ14641	3'	TGACAGAGCCAAACTCC 26590	C	C
			GGA GT TGGCTCTGTCA		
			CCT CA ACCGAGACAGT		
			— A		
GAM439	KIAA1056	3'	TGACAGAGCCAGACTCC 17049	C	
			GGA GTCTGGCTCTGTCA		
			CCT CAGACCGAGACAGT		
			—		
GAM439	KIAA1854	3'	ACAGAGCCAGATCAGAACCCA 35520		CAGGAC
			TGG GTCTGGCTCTGT		
			ACC TAGACCGAGACA		
			CAAGAC		
GAM439	MGC15631	3'	ACAGAGCCAGACCCTGACT 26488	—	AC
			GG CAGG GTCTGGCTCTGT		
			TC GTCC CAGACCGAGACA		
			A —		
GAM439	SAMHD1	3'	TGACAGAGGAATCCCCCA 30736	CA	CG TGG
			TGG GGA TC CTCTGTCA		

ACC CCT AG GAGACAGT
 C_ A_ ____
 GAM439 WBSR23 5' GACAGAGCCAGACCCT 24639 AC
 AGG GTCTGGCTCTGTC
 ||| |||||
 TCC CAGACCGAGACAG

 GAM439 LOC162333 5' TGACAGAGCCAAGTTGGC 42136 AG GTC
 GC GAC TGGCTCTGTCA
 || ||| |||||
 CG TTG ACCGAGACAGT
 G_ A_
 GAM439 LOC220003 5' CAGGCCAGACACCCCA 44051 CA AC T
 TGG GG GTCTGGC CTG
 ||| || ||||| |||
 ACC CC CAGACCG GAC
 ____ A_ _
 GAM440 AMFR 3' GCACCTACCCAGGTTCCATAC 29066 CCG_____ GCAC
 CA GGTATGGAATC AG C
 ||||| || |
 CCATACCTTGG TC G
 ACCCCIIIA CACG
 GAM440 CHGA 5' TAGGTGCCCGGCCCCACACC 6939 A AATC A
 GGT TGG CCG GGCACCTA
 ||| ||| ||| |||||
 CCA ACC GGC CCGTGGAT
 C CC_ _
 GAM440 FLJ10842 3' AGGTGCCTCAGCCATCCCA 20187 T AATCCC
 TGG ATGG GAGGCACCT
 ||| ||| |||||
 ACC TACC CTCCGTGGA
 C GA____
 GAM440 FLJ22969 3' TAGGTGCCCTGCATTCCACCCA 34067 TA CC A
 TGG TGGAAT CG GGCACCTA
 ||| ||||| ||| |||||
 ACC ACCTTA GT CCGTGGAT
 C_ C_ C
 GAM440 FLJ23510 5' GTACCTCGGGACATCCATCA 24052 T A_ C
 G ATGGA TCCCGAGG AC
 | |||| ||||| ||
 A TACCT AGGGCTCC TG
 C AC A
 GAM440 FLJ23519 3' AGGCGCCCGTCACCACACCA 25971 A AATCC A A
 TGGT TGG CG GGC CCT
 |||| ||| || ||| |||
 ACCA ACC GC CCG GGA
 C ACT_ _ C
 GAM440 KIAA0961 3' AGGCGCCCGCCACCACACCA 17071 A AATCC A A
 TGGT TGG CG GGC CCT
 |||| ||| || ||| |||

ACCA ACC GC CCG GGA
 C ACC__ _ C
 GAM440 KIAA1265 3' TAGGTGCCCTGTTCTCCTACCA 35034 T ATCC A
 TGGTA GGA CG GGCACCTA
 ||||| ||| || |||||
 ACCAT CCT GT CCGTGGAT
 _ CTT_ C
 GAM440 SLC6A14 3' AGGTGCCCCGCCACCACACCA 14100 A AATCC A
 TGGT TGG CG GGCACCT
 ||||| ||| || |||||
 ACCA ACC GC CCGTGGGA
 C ACC__ _
 GAM440 TP53INP1 3' AGGTTGGGATTACCACACCA 36114 A _ AGGC
 TGGT TGG AATCCCG ACCT
 ||||| ||| ||||| |||||
 ACCA ACC TTAGGGT TGGA
 C A ____
 GAM440 TP53INP1 3' AGGTTGGGATTACCACACCA 27103 A _ AGGC
 TGGT TGG AATCCCG ACCT
 ||||| ||| ||||| |||||
 ACCA ACC TTAGGGT TGGA
 C A ____
 GAM440 VPS39 3' TAGATGCCTCGGAGAGCATCA 31472 AA_ _ C
 TGG TC CCGAGGCA CTA
 ||| || ||||| |||
 ACT AG GGCTCCGT GAT
 ACG A A
 GAM440 LOC147429 3' AGGCACCTACAGGAAAAATTTTC 38335 ____ CG____ GCAC
 ATACCA ATGGAA TCC AG CT
 ||||| ||| || |||
 TACTTT AGG TC GA
 AAAA ACIIIA CACG
 GAM440 LOC154007 3' GCACCTACAGAGGAATCCATAC 39455 A CG____ GCAC
 CA GGTATGGA TCC AG C
 ||||| ||| ||| |
 CCATACCT AGG TC G
 A AGACIIIA CACG
 GAM440 LOC196337 5' CCTGCAGGATTCCATCCA 42358 T CG_
 TGG ATGGAATCC AGG
 ||| ||||| |||
 ACC TACCTTAGG TCC
 _ ACG
 GAM440 LOC200197 3' AGGTGCCTTCTCCACCCA 42730 TA ATCCC
 TGG TGGA GAGGCACCT
 ||| ||||| |||||
 ACC ACCT TTCCGTGGA
 C_ C____
 GAM440 LOC200681 5' TGCCTCCATCTCCATACCA 43341 ATCCC
 TGGTATGGA GAGGCA
 ||||| |||||

			ACCATACCT CTCCGT		
			CTAC_		
GAM440	LOC221583	5'	GCCCGAGACCCATACCA 44245	AA C A	
			TGGTATGG TC CG GGC		
			ACCATACC AG GC CCG		
			C_ A _		
GAM440	LOC51301	3'	AGGTGTCCAAAATTCCATAC 18670	CCCGA	
			GTATGGAAT GGCACCT		
			CATACCTTA CTGTGGA		
			AAAC_		
GAM441	CCNT2	3'	GTATACTGACAACTGTTTACA 27770	T GGC T	
			TGTAAACA TTG CA TATAC		
			ACATTTGT AAC GT ATATG		
			C A_ C		
GAM441	EDNRA	3'	GGCATTTTCCCAGATGTTTACA 32056	_____	
			TGTAAACATTTGG GCC		
			ACATTTGTAGACC CGG		
			CTTTTA		
GAM441	GRB10	3'	ATGGGTCCCCAAATGTTCCCA 11785	TA ____	
			TG AACATTTGGG CCAT		
			AC TTGTAAACCC GGTA		
			CC CTG		
GAM441	HTR4	3'	ATAATGGCCTCCTTGTTTACAC 6540	A TTT	
			GT AACA GGGCCATTAT		
			CA TTGT TCCGGTAATA		
			C TCC		
GAM441	JAG1	3'	GGTATAATAGGCTCTGCCTGAC 5712	AAACATTT _	
	A		TGT GGGCC ATTATACC		
			ACA CTCGG TAATATGG		
			GTCCGT_ A		
GAM441	DKFZP434P1750	3'	GGTGAACCCAATGTTTACA 17793	T ____	
			TGTAAACATT GGG CCATT		
			ACATTTGTAA CCC GGTGG		
			_ AA		
GAM441	NCUBE1	3'	GGTATAATCTAAGAATTGTTTA 18094	____ GCC	
	CA		TGTAAACA TTTGG ATTATACC		
			ACATTTGT GAATC TAATATGG		
			TAA ____		
GAM441	NS1-BP	3'	GGTATTTTCTCCAAATGTTTACAC 35914	A CCATT	
			GT AACATTTGGG ATACC		

			CA TTGTAAACCT	TATGG		
			C	CTTT_		
GAM441	LOC132720	3'	GTATAAAACCAAATGCTTA	37028	A	GCCA
			TAA CATTG	TTATAC		
			ATT GTAAACC	AATATG		
			C	AA__		
GAM441	LOC146957	3'	TGTAAACTCCAAATGTTTACA	38283		CCA
			TGTAAACATTTGGG	TTATA		
			ACATTTGTAAACCT	AATGT		
			CA_			
GAM441	LOC158014	5'	ATAATGGTTTTCTGTCTAC	39688	A	TTT
			GTA ACA	GGGCCATTAT		
			CAT TGT	TTTGGTAATA		
			C	CT_		
GAM441	LOC51339	3'	GGTATAAAACCAGATGTTTACA	18770		GCCA
			TGTAAACATTTGG	TTATACC		
			ACATTTGTAGACC	AATATGG		
			AA__			
GAM442	KAL1	3'	TCATCAAAAATATTGTCATC	5719	A	_
			GATGACAATATT	TT ATGA		
			CTACTGTTATAA	AA TACT		
			A	C		
GAM442	SYT4	3'	AGTCTTCATTTAATTTATTGTC	31292		TTATT_
			GACAATA	ATGAAGACT		
			CTGTTAT	TACTTCTGA		
			TTAATT			
GAM442	KIAA0895	3'	AGTCTTCATTTCTTTATATTGT	44544		TATT__
	CA		TGACAATAT	ATGAAGACT		
			ACTGTTATA	TACTTCTGA		
			TTTCTT			
GAM442	LOC161589	5'	TTATATCAACATTGTCATC	40024	A	AT
			GATGACAAT	TT TATGA		
			CTACTGTTA	AA ATATT		
			C	CT		
GAM443	CNP	3'	AACACAAGGTGGGCAGGG	26976		ATA
			TCCTGCCTATT	TGTT		
			GGGACGGGTGG	ACAA		
			AAC			
GAM443	NCOA4	3'	AGCAAATAGGCCAAAAGA	11922	CC	ATA
			TCT TGCCTATT	TGTT		

AGA ACGGATAA ACGA
AA ____

GAM443 TFE3 3' AACATGTAGGGCAAGAGG 13274 C AT
TCTC TGCCT TATATGTT
||||| |||||
GGAG ACGGG ATGTACAA
A ____

GAM443 VPS26 3' TTTTAACATATGTGTTTGAGA 11329 CT CTAT
TCTC GC TATATGTTAAAA
||||| || |||||
AGAG TG GTATACAATTTT
TT T____

GAM443 CARD6 3' TATCATATAGTAAGCAGAAGA 26322 C C T
TCT CTGC TATTATATG TA
||||| ||||| ||
AGA GACG ATGATATAC AT
A A T

GAM443 DKFZp761K1423 5' TTTTAACACATAAATGAGGGGA 20475 GCCTA A
TCTCCT TTAT TGTAAAAA
||||| |||||
AGGGGA AATA ACAATTTT
GTA__ C

GAM443 KIAA0090 3' TTTTAACATAACCTGGGAGAAG 42655 C G TTA
A TCT CT CCTA TATGTTAAAA
||||| |||||
AGA GA GGGT ATACAATTTT
A _ CCA

GAM443 KIAA0543 3' TTAACCATGGGCAGGA 34180 TATAT
TCCTGCCTAT GTTAA
||||| |||||
AGGACGGGTA CAATT
C____

GAM443 LY75 3' TTTTAACATGTGTAAACAGAG 8152 C CC T
A TCTC TG TA TATATGTTAAAA
||||| || |||||
AGAG AC AT GTGTACAATTTT
_ AA T

GAM443 LOC146179 5' TTTTATGCAAAGTAGGCAG 38077 ATA _
CTGCCTATT TGT TAAAA
||||| |||||
GACGGATGA ACG ATTTT
A__ T

GAM443 LOC221399 5' TTTAACATATAATATAGCAG 45053 C_
CTGC TATTATATGTTAAA
||||| |||||
GACG ATAATATACAATTT
AT

GAM444 DLG5 5' GACTGACTTCTACCACACACTC 40336 A T T
GAG TGT TG TAGAAGTCAGTC
||||| |||||

CTC ACA AC ATCTTCAGTCAG
 _ C C
 GAM444 FCGR2A 3' GACTAACCTCTAACAAACAAATT 38699 GA T A C
 A TGA TGTT GTTAGA GT AGTC
 ||| |||| ||||| || ||||
 ATT ACAA CAATCT CA TCAG
 AA _ C A
 GAM444 LYPLA1 3' ACTAACTTCTAAGATGATTTC 13027 _ TG C
 TGAGAT GTT TTAGAAGT AGT
 ||||| ||| ||||| ||||
 ACTTTA TAG AATCTTCA TCA
 G _ A
 GAM444 PDYN 3' ACTGACTTCCTGAACTCCCA 23652 A T TTA
 TG GA GTTTG GAAGTCAGT
 || || |||| ||||| |||||
 AC CT CAAGT CTTTCAGTCA
 C _ C _
 GAM444 SKI 3' GACTAACTTCTAAAAGC 8988 G C
 GTTT TTAGAAGT AGTC
 |||| ||||| ||||
 CGAA AATCTTCA TCAG
 _ A
 GAM444 KIAA0652 3' GACTGACTCCTGCAGCA 16408 T T A
 TGTT GT AG AGTCAGTC
 |||| || || ||||| |||||
 ACGA CG TC TCAGTCAG
 _ _ C
 GAM444 MGC2452 5' GACCATGTAACAAATACCTCA 26369 A GAA_
 TGAG TGTTTGTTA GTC
 |||| ||||| |||
 ACTC ATAAACAAT CAG
 C GTAC
 GAM444 PLA2G6 3' ACTGACTCCCCCATCAGCTCA 33029 A TT TTA A
 TGAG TG TG GA GTCAGT
 |||| || || ||||| |||||
 ACTC AC AC CT CAGTCA
 G T_ CCC _
 GAM444 LOC145447 5' GACCGACCAGCCCAAGAAACAT 37861 G AGAA_ A
 CTCA TGAGATGTTT TT GTC GTC
 ||||| || ||| ||||
 ACTCTACAAA AA CAG CAG
 G CCGAC C
 GAM444 LOC149711 5' GACCTCACAAACATCTCA 41071 TA A
 TGAGATGTTTGT GA GTC
 ||||| || |||
 ACTCTACAAACA CT CAG
 _ C
 GAM444 LOC253786 3' GACTCAACAAACATCCA 46363 A A A
 TG GATGTTTGT GA GTC
 || ||||| || |||

AC CTACAAACAA CT CAG

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      - - -
GAM445 ANXA4 3' AGAAAAC TTTT TGTGCT 31444 TAT A
      AGCACAG GA TTTTCT
      ||||| || |||||
      TCGTGTT TT AAAAGA
      TT_ C
GAM445 APC 3' AGAATTTT TGTATGCTGTA 5480 C T
      TACAGCA AGTA GAATTTT
      ||||| ||| |||||
      ATGTCGT TCGT TTTAAGA
      A T
GAM445 CENTD1 3' AGAAATCTCAAAC TGTACTGTA 29197 C A AT
      TACAG ACAGT TGA TTTCT
      |||| |||| || ||||
      ATGTC TGTCA ACT AAAGA
      A A CT
GAM445 CENTD1 3' AGAAATCTCAAAC TGTACTGTA 17560 C A AT
      TACAG ACAGT TGA TTTCT
      |||| |||| || ||||
      ATGTC TGTCA ACT AAAGA
      A A CT
GAM445 CLOCK 3' AGAAAATTCTACCTGGCT 11331 A TAT
      AGC CAG GAATTTTCT
      ||| ||| |||||
      TCG GTC CTTAAAAGA
      _ CAT
GAM445 GNB1 3' AGAAAGATCTCTGTGCTGTA 7847 TAT A
      TACAGCACAG GA TTTTCT
      ||||| || |||||
      ATGTCGTGTC CT GAAAGA
      T_ A
GAM445 JAK2 3' AGAAAATTCATAACGTGT 11416 AG
      GCAC TATGAATTTTCT
      ||| |||||
      TGTG ATACTTAAAAGA
      CA
GAM445 JAM3 3' AGGGAAC TCATACTGTCT 26552 C A TT
      AG ACAGTATGA TT CT
      || ||||| || ||
      TC TGTCATACT AA GA
      _ C GG
GAM445 P2RY6 3' AGAAAATGGGAGCTGTGCT 10352 ATGA
      AGCACAGT ATTTTCT
      ||||| |||||
      TCGTGTCG TAAAAGA
      AGGG
GAM445 PKIA 3' AGAAAATGGCTGTGCTG 13698 ATGA
      CAGCACAGT ATTTTCT
      ||||| |||||
```

GTCGTGTCG TAAAAGA
 G____
 GAM445 RBBP5 3' AGAATTTAAATACTGTGCTTA 11484 C GAATT
 A AGCACAGTAT TTCT
 | ||||| |||
 A TCGTGTGCATA AAGA
 T AATT
 GAM445 ALS2CR3 3' AGAAAAATGTTGTGCTGTA 17408 GTATGA
 TACAGCACA ATTTTCT
 ||||| |||||
 ATGTCGTGT TAAAAGA
 TG____
 GAM445 DKFZp566D133 3' AGAAAAATCACTGTGCTG 35543 AT A
 CAGCACAGT GA TTTTCT
 ||||| || |||||
 GTCGTGTCA CT AAAAGA
 _ A
 GAM445 DKFZp761O0113 5' AGAAAATTCATATTGTGT 20445
 GCACAGTATGAATTTTCT
 ||||| ||||| |||||
 TGTGTTATACTTAAAAGA
 GAM445 FLJ10330 3' AAAGTAATGCTGTGCTG 19830 GA
 CAGCACAGTAT ATTTT
 ||||| |||||
 GTCGTGTGCGTA TGAAA
 A_
 GAM445 FLJ10525 3' AGAAAATTTTACTGTGCTGTG 19913 T
 TACAGCACAGTA GAATTTTCT
 ||||| ||||| |||||
 GTGTCGTGTCAT TTAAAAGA
 -
 GAM445 FLJ14457 3' AGAAAATTCATACCTG 26541 CACA
 CAG GTATGAATTTTCT
 || ||||| |||||
 GTC CATACTTAAAAGA
 -
 GAM445 FLJ20273 3' AAAATTTGTATGCTGTA 21112 CAG TG
 TACAGCA TA AATTTT
 ||||| || |||||
 ATGTCGT AT TTAAAA
 _ GT
 GAM445 FLJ20986 3' AGAAAATATTCATGCATGC 23726 CA _
 GCA GTATGAAT TTTCT
 || ||||| |||||
 CGT CGTACTTA AAAGA
 A_ TA
 GAM445 KIAA0408 3' AGATTCATACTTTACTGTA 16230 CAC
 TACAG AGTATGAATT
 |||| ||||| |||||

			ATGTC TCATACTTAGA		
			ATT		
GAM445	KIAA0676	3'	GAAATTACACTGTGCTCA 17392	C	ATG
			A AGCACAGT AATTTT		
			A TCGTGTCA TTAAAG		
			C CA_		
GAM445	KIAA0844	3'	AGAAAATTCATCTGTGC 17282	T	
			GCACAG ATGAATTTTCT		
			CGTGTG TACTTAAAAGA		
			—		
GAM445	KIAA1327	3'	AAAAGATATGCATGTGCTGTA 35761	—	AA
			TACAGCACA GTATG TTTT		
			ATGTCGTGT CGTAT AAAA		
			A AG		
GAM445	KIAA1500	3'	AGAAAATTCATAAAAATGTA 32063	GCACAG	
			TACA TATGAATTTTCT		
			ATGT AACTTAAAAGA		
			AAAA_		
GAM445	KIAA1617	3'	AGAAACCTCACGCCATGCTGTA 43940	CA TA	AT
			TACAGCA G TGA TTTCT		
			ATGTCGT C ACT AAAGA		
			AC GC CC		
GAM445	KIAA1826	3'	AGAACTTACTGTGCTG 33374	TGAAT	
			CAGCACAGTA TTTCT		
			GTCGTGTCAT AAAGA		
			TC_		
GAM445	MGC4737	5'	AGAAAATTCAGCGCTACAGC 25503	AC_ A_	
			GC AGT TGAATTTTCT		
			CG TCG ACTTAAAAGA		
			ACA CG		
GAM445	NDRG4	3'	AGAAAGAGTTAACTGTGCTG 21695	A A_	
			CAGCACAGT TGA TTTTCT		
			GTCGTGTCA ATT GAAAGA		
			_ GA		
GAM445	NDRG4	3'	AGAAAGAGTTAACTGTGCTG 23210	A A_	
			CAGCACAGT TGA TTTTCT		
			GTCGTGTCA ATT GAAAGA		
			_ GA		
GAM445	SHAPY	3'	AGAAAATTCGTGGCTGTGC 29015	AT_	
			GCACAGT GAATTTTCT		

			CGTGTCTG CTTAAAAGA	
			GTGT	
GAM445	SMOC1	3'	GAGATTTATATGCTGTA 22698	CAG
			TACAGCA TATGAATTTT	
			ATGTCGT ATATTTAGAG	
GAM445	SSR3	3'	AAAATGTCTTGCAATGTGCTGT 13968	__ T _
	A		TACAGCACA GTA GA ATTTT	
			ATGTCGTGT CGT CT TAAAA	
			AA T G	
GAM445	USP22	3'	AAAATTCCAATGACTGTGCTGT 33749	AT__
	G		TACAGCACAGT GAATTTT	
			GTGTCGTGTCA CTTAAAA	
			GTAAC	
GAM445	YAP1	3'	AAAATGCAATCACTGTGTTGTA 12747	_ GA_
			TACAGCACAGT AT ATTTT	
			ATGTTGTGTCA TA TAAAA	
			C ACG	
GAM445	LOC147358	5'	AGAAAATTCAGCTGATTACTG 30166	CA__ A
			CAG CAGT TGAATTTTCT	
			GTC GTCG ACTTAAAAGA	
			ATTA _	
GAM445	LOC151647	3'	AAAATTCATCCTGCTG 39153	CA T
			CAGCA G ATGAATTTT	
			GTCGT C TACTTAAAA	
			_ C	
GAM445	LOC163255	3'	AGAAAATTCATACTGATGT 40105	_
			GCA CAGTATGAATTTTCT	
			TGT GTCATACTTAAAAGA	
			A	
GAM445	LOC163255	3'	AGAAAATTCATACTGGTGTA 40106	G A
			TACA C CAGTATGAATTTTCT	
			ATGT G GTCATACTTAAAAGA	
GAM445	LOC163255	3'	AGAAAATTCATACGGGTGT 40104	A_
			GCAC GTATGAATTTTCT	
			TGTG CATACTTAAAAGA	
			GG	
GAM445	LOC200132	3'	AGAAAATTAGCAATGCTGTA 42709	CA ATG
			TACAGCA GT AATTTTCT	

		ATGTCGT CG TTAAAAGA		
		AA A__		
GAM445	LOC201164 3'	AAAATTCAATTGAAGCTGTA 42526	A_ A	
		TACAGC CAGT TGAATTTT		
		ATGTCG GTTA ACTTAAAA		
		AA _		
GAM445	LOC201895 3'	AGAAAATTAGAACCACGCTGTA 42925	ACA ATG	
		TACAGC GT AATTTTCT		
		ATGTCG CA TTAAAAGA		
		CAC AGA		
GAM445	LOC203523 3'	AGAAAATTTTCATTTGTGCTG 43052	T _	
		CAGCACAG ATGAA TTTTCT		
		GTCGTGTT TACTT AAAAGA		
		_ T		
GAM445	LOC219690 3'	AGAATCTCAACGTGCTGTA 44704	A A ATT	
		TACAGCAC GT TGA TTCT		
		ATGTCGTG CA ACT AAGA		
		_ _ CT_		
GAM445	LOC253959 3'	AGAAAAATCACTGTGCTG 45509	AT A	
		CAGCACAGT GA TTTTCT		
		GTCGTGTCA CT AAAAGA		
		_ A		
GAM446	TMEM2 3'	CTTTAAAGCCTTGCAGGAA 15041	G TTTTG	
		TTC CTGCAAG TTAAAG		
		AAG GACGTTC AAATTTC		
		_ CG__		
GAM446	KIAA0660 3'	TCTTTAAACAATTCTGTGAGC 14659	_ A TT	
		GCT GCA G TTGTTTAAAGA		
		CGA TGT C AACAAATTTCT		
		G _ TT		
GAM446	LOC219940 5'	CTTAAGGCACTTGGAGC 44832	G TTT A	
		GCT CAAGT GTTT AAG		
		CGA GTTCA CGGA TTC		
		G _ _ A		
GAM446	LOC90750 3'	CTCTAAACAAATGCATGC 31967	_ AGT A	
		GC TGCA TTTGTTTA AG		
		CG ACGT AAACAAAT TC		
		T _ _ C		
GAM447	ATP1A2 3'	ACCAGATCCTTTTCCATCCAC 6363	TT C__	
	TCCA	GGAGTGGGG TGGAGA	CTGGT	

CCTCACCCCT ACCTTT GACCA
 — TCCTA
 GAM447 DNMT3L 5' ACTGAGGTCCCCAAACCCCACC 15015 A A _
 CC GG GTGGGGTTTGG GACCT GGT
 || ||||| |||| ||
 CC CACCCCAAACC CTGGA TCA
 C C G
 GAM447 DXS1283E 3' CTCCCCTAAACCCCACCCCA 35062 A _
 TGG GTGGGGTTT GGAG
 || ||||| ||
 ACC CACCCCAAA CCTC
 C TCC
 GAM447 NPTX1 3' ACCAGATCTAGCCCCACCCTCA 8351 _ TT _ C
 CTCCA TGGAGTG GGGT GG AGA CTGGT
 ||||| ||| || |||||
 ACCTCAC CCCA CC TCT GACCA
 T CC GA A
 GAM447 FLJ12057 5' ACCAGAGACCCAGACCCCACTC 24123 AGAC
 CA TGGAGTGGGGTTTGG CTGGT
 ||||| ||||
 ACCTCACCCAGACC GACCA
 CAGA
 GAM447 FLJ14075 3' CCAGATCTCCAAGAACTC 24374 GGGGT C
 GAGT TTGGAGA CTGG
 ||| ||||| ||
 CTCA AACCTCT GACC
 AG_ A
 GAM447 SCAM-1 3' ACCAGACCCCAAGTCCCCCACC 12349 A _ AGAC
 CC GG GTGGGG TTTGG CTGGT
 || ||||| ||||
 CC CACCCC GAACC GACCA
 C CT CCA_
 GAM447 LOC138639 3' ACCAAGCCTTATTCCCACTCC 37138 TTTG ACC
 GGAGTGGGG GAG TGGT
 ||||| || ||
 CCTCACCCCT TTC ACCA
 TA_ CGA
 GAM448 GPR30 5' TGCCAGGCTCACTTCA 7253 A AT
 TGGA TGAGCCTG GCA
 ||| ||||| ||
 ACTT ACTCGGAC CGT
 C _
 GAM448 FLJ11273 3' ATAAAGTGGTACAGACTCATTA 20393 G C A _
 CA TG AATGAG CTG TGC ACTTTAT
 || ||||| || || |||||
 AC TTA CTC GAC ATG TGAAATA
 A A _ G
 GAM448 FLJ12650 3' AGGACATCAGGCCCATCCCA 23721 A A CA
 TGG ATG GCCTGATG CT
 ||| || ||||| ||

		ACC TAC CGGACTAC GA		
		C C AG		
GAM448	KIAA0090 3'	AAAGTATCATCAGAATCATCCC 42648	A GC C_	
	A	TGG ATGA CTGATG ACTTT		
		ACC TACT GACTAC TGAAA		
		C AA TA		
GAM448	LOC124045 3'	AGGGTGCACCAGGCCACCCCA 37435	AA A A	
		TGG TG GCCTG TGCACTTT		
		ACC AC CGGAC ACGTGGGA		
		CC C C		
GAM448	LOC124045 3'	AGGGTGCACCAGGCCCGCCCCA 37436	AA A A	
		TGG TG GCCTG TGCACTTT		
		ACC GC CGGAC ACGTGGGA		
		CC C C		
GAM448	LOC124045 3'	AGGGTGCACCAGGCCCGCCCCA 37437	AA A A	
		TGG TG GCCTG TGCACTTT		
		ACC GC CGGAC ACGTGGGA		
		CC C C		
GAM448	LOC124045 3'	AGGGTGCACCAGGGCCACCCCA 37438	AA A GA_	
		TGG TG GCCT TGCACTTT		
		ACC AC CGGG ACGTGGGA		
		CC _ ACC		
GAM448	LOC131873 3'	ATAAAACACATCAGGTTTGCTT 37362	AT CAC	
	CA	TGGA GAGCCTGATG TTTAT		
		ACTT TTTGGACTAC AAATA		
		CG ACA		
GAM449	ACADL 3'	ACTGGCAAGATCACTA 7311	CAC T	
		TAGTGATC TG CCAGT		
		ATCACTAG AC GGTCA		
		A_ _		
GAM449	KCND2 3'	ACTGGATATATCACTATG 14606	CCAC	
		CATAGTGAT TGTCCAGT		
		GTATCACTA ATAGGTCA		
		T_ _		
GAM449	LNK 3'	ACTGGACAGTAGACATCATGA 11969	A A C	
		TCAT GTG TC ACTGTCCAGT		
		AGTA TAC AG TGACAGGTCA		
		C _ A		
GAM449	RARB 3'	TTGTTCAATCACTATGAA 6694	CCAC TC	
		TTCATAGTGAT TG CAG		

			AAGTATCACTA AC GTT		
			____ TT		
GAM449	RARB	3'	TTGTTCAATCACTATGAA 18240	CCAC TC	
			TTCATAGTGAT TG CAG		
			AAGTATCACTA AC GTT		
			____ TT		
GAM449	SLC7A6	3'	ACTGGACAATGTTACGCTAGAA 10124	A ATC C	
			TTC TAGTG CA TGTCCAGT		
			AAG ATCGC GT ACAGGTCA		
			_ ATT A		
GAM449	CNNM1	3'	GGCGGGTGGATCACTTGAA 21609	T GT	
			TTCA AGTGATCCACT CC		
			AAGT TCACTAGGTGG GG		
			_ GC		
GAM449	FLJ11181	5'	ACTGAATTTAGCACTATGAA 20363	ATCCACT C	
			TTCATAGTG GT CAGT		
			AAGTATCAC TA GTCA		
			GATT__ A		
GAM449	FLJ13576	5'	GGCCGAGTCAGATCACTAT 22862	C_ _ T	
			ATAGTGATC ACT G CC		
			TATCACTAG TGA C GG		
			AC G C		
GAM449	FLJ20079	3'	ACTGGGGAGAAATACTATGAA 19165	ATCCA G	
			TTCATAGTG CT TCCAGT		
			AAGTATCAT GA GGGTCA		
			AAA__ G		
GAM449	KIAA1163	3'	ACTAGACAATGATCATTA 38555	CAC C	
			TAGTGATC TGTC AGT		
			ATTACTAG ACAG TCA		
			TA_ A		
GAM449	KIAA1189	3'	ACCAGACAATGAATGAACTATG 35649	G_ C C CA	
	AA		TTCATAGT AT CA TGTC GT		
			AAGTATCA TA GT ACAG CA		
			AG A A AC		
GAM449	LOC148166	5'	ACCAGACAGTGGGAATATTA 38478	A CA	
			TAGTG TCCACTGTC GT		
			ATTAT AGGTGACAG CA		
			A AC		
GAM449	LOC150596	3'	ACTGTTGAGGATCACTCTGAA 38994	T ACTGTC	
			TTCA AGTGATCC CAGT		

			AAGT TCACTAGG	GTCA		
			C	AGTT__		
GAM450	COL5A1	5'	GCCCGTGGGCGAGCGCGCC	5556	A TT	AA
			GG GT CTCGCCCCAC GC			
			CC CG GAGCGGGTG CG			
			G C_ CC			
GAM450	IL2RB	3'	GCTTGTGGACAAGGCTCC	6574	CTCGC	
			GGAGTTT CCACAAGC			
			CCTCGGA GGTGTTCG			
			ACA__			
GAM450	NBS1	3'	GCTTGCAGGTGGAAGTCC	34438	TC CA	
			GGAGTTTC GCC CAAGC			
			CCTCAAGG TGG GTTCG			
			__ AC			
GAM450	PTAFR	3'	GCCTGTGGGCGCATACTACAGT	6658	CGG TTCT	A
	A		TAC AGT CGCCCACA GC			
			ATG TCA GCGGGTGT CG			
			ACA TAC_ C			
GAM450	AF020591	3'	GCTCATGGGCAAGAACTCT	15826	C CA	
			GGAGTTTCT GCCCA AGC			
			TCTCAAAGA CGGGT TCG			
			A AC			
GAM450	ITPK1	5'	GCCTGTGGGCGATTTCCTCCGG	15481	TTTC	A
			CCGGAG TCGCCCACA GC			
			GGCCTC AGCGGGTGT CG			
			CTTT C			
GAM450	PDE4DIP	3'	GCTTGGAAGAACTCC	16052	CG CA	
			GGAGTTTCT CCCA AGC			
			CCTCAAAGA GGGT TCG			
			A_ __			
GAM451	DGKG	3'	CACCCCTAACAGAGCCAGTGC	7025	TG AA__	CCGC
			G C TTTGT TAGGGGTG			
			C G AGACA ATCCCCAC			
			GT ACCG ____			
GAM451	FLJ13955	3'	CACCTTTTTAAAAAATTGCACA	24108	GTCCGCT	
			TGTGCAATTT AGGGGTG			
			ACACGTTAAA TTTCCAC			
			AAATT__			
GAM451	KIAA0356	3'	ACCCCCAGCGGATGCACA	32890	ATTTG	A
			TGTGCA TCCGCT GGGGT			

			ACACGT	AGGCGA	CCCCA		
			_____	C			
GAM451	RASD2	3'	ACCCCCAGCACACACACA	15598	CAATT	CC	A
			TGTG	TGT	GCT	GGGGT	
			ACAC	ACA	CGA	CCCCA	
			_____	CA	C		
GAM452	TRIP15	3'	CTAAACGTACAACATCATAGTA	10430	AATCTG		_
			TACTATGAT	GCGTT	AG		
			ATGATACTA	TGCAA	TC		
			CAACA	_	A		
GAM452	FLJ10901	3'	TTCTAACGTTTTTTTCATCATAG	20234	AATCT		
		T	ACTATGAT	GGCGTTAGAA			
			TGATACTA	TTGCAATCTT			
			CTTTT				
GAM452	GW112	3'	TCTAACGCCTTCATGGTA	13133	TAATCT		
			TACTATGA	GGCGTTAGA			
			ATGGTACT	CCGCAATCT			
			T_____				
GAM452	KIAA0976	3'	GACCCCGATTATCACAG	17166	A	T	C
			CT	TGATAATC	GG	GTT	
			GA	ACTATTAG	CC	CAG	
			C	C	_		
GAM452	LOC245771	5'	TTCTAACGTTTTTTTCATCATAG	44639	AATCT		
		T	ACTATGAT	GGCGTTAGAA			
			TGATACTA	TTGCAATCTT			
			CTTTT				
GAM453	ALDH3B2	3'	ACCCGCCTCCAACGGGTCAC	6355	G	A	A
			GTGA	CCCGTTG	AG	CGG	GT
			CACT	GGGCAAC	TC	GCC	CA
			_	C	C	_	
GAM453	FLJ20813	3'	AACTCCACCTCCCGGGTTCAC	19677	TT	A	AC
			GTGAGCCCG	GA	G	GGAGTT	
			CACTTGGGC	CT	C	CCTCAA	
			C_	_	CA		
GAM453	LOC149650	3'	TAACCCCGTCTTCTTTTTCAC	38795	CCCGTT		A
			GTGAG	GAAGACGG	GTTA		
			CACTT	CTTCTGCC	CAAT		
			TTT_____	C			
GAM453	LOC150397	3'	ACTCCGCCTGGCCTTAC	38958	CGTTGA		A
			GTGAGCC	AG	CGGAGT		

CATTCGG TC GCCTCA
 _____ C
 GAM453 LOC161823 3' ACGTGTCTTCAACTGACTCAC 40029 CCC GA
 GTGAG GTTGAAGACG GT
 |||| ||||| ||
 CACTC CAACTTCTGT CA
 AGT G_
 GAM454 LNK 3' CATAACAGTTTCTTAACCT 11971 A TCAGT
 AGGTT GAG TTGTTATG
 |||| || |||||
 TCCAA TTC GACAATAC
 _ TTT_
 GAM454 KIAA0265 3' ACAGATAACTCAAACCT 34618 A CA
 AGGTT GAGT GTTTGT
 |||| || |||||
 TCCAA CTCA TAGACA
 A A_
 GAM454 KIAA0960 3' GCATAACAAATAAACTCTAAGC 44519 G CA
 T AG TTAGAGT GTTTGTTATGC
 || ||||| |||||
 TC AATCTCA TAAACAATACG
 G AA
 GAM454 LOC138428 5' GCATAACAAGGCCTCCCAACC 37133 A_ TCAG
 GGTT GAG TTTGTTATGC
 ||| || |||||
 CCAA CTC GAACAATACG
 CC CG_
 GAM454 LOC152048 3' TACCCTGACTCTCACCTG 41427 T TT
 CAGGT AGAGTCAG TG
 |||| ||||| ||
 GTCCA TCTCAGTC AT
 C CC
 GAM455 EPHB3 3' TCCAGCAGGGGATCCCCAC 10737 AC A_
 GTG GGATTCT CTGGA
 || ||||| ||||
 CAC CCTAGGG GACCT
 C_ GAC
 GAM455 KIAA0222 3' CCAGCAGCCTCCACCTGTGA 16045 AC TT A
 TCACGGGTG GGA CT CTGG
 ||||| || ||||
 AGTGTCCAC CCT GA GACC
 _ CC C
 GAM455 MGC10818 3' TCCAATAAAATAAGCTACCTGT 24943 ACGG C C
 GA TCACGGGTG ATT TA TGGA
 ||||| || ||||
 AGTGTCCAT TAA AT ACCT
 CGAA A A
 GAM456 RGS17 3' ATACTGTGTTTAGTACACT 14791 TAGTTG
 AGTGTACTA ACAGTAT
 ||||| |||||

			TCACATGAT	TGTCATA	
			TTG__		
GAM456	ZNF387	3'	ATACTGTTTCTCCAAACACTTA	16172	ACTAT TT
			TAAGTGT	AG GACAGTAT	
			ATTCACA	TC TTGTCATA	
			AACC_ T_		
GAM457	CASQ2	3'	AGTCTCACATATTCATCA	6903	TACA
			TGATGAATAT	AGATT	
			ACTACTTATA	TCTGA	
			CAC_		
GAM457	KIAA1715	3'	CTTCTAATCTTGGCCTCCATCA	33792	AATATTA
			TGATG	CAAGATTAGAAG	
			ACTAC	GTTCTAATCTTC	
			CTCCG__		
GAM457	PRO0097	5'	CTTCTTACATAATATTTATCA	15365	CAAGATT
			TGATGAATATTA	AGAAG	
			ACTATTTATAAT	TCTTC	
			ACAT__		
GAM457	LOC143915	3'	TCCAATCATATATTCATCA	40380	TACAA A
			TGATGAATAT	GATT GA	
			ACTACTTATA	CTAA CT	
			TA__ C		
GAM457	LOC170063	3'	TCTATAAATATGTAATATCATC	42188	A AGAT__
	A		TGATGA TATTACA	TAGA	
			ACTACT ATAATGT	ATCT	
			ATAAAT		
GAM457	LOC90268	3'	CTCATCAGTAATATTCACCA	31041	A AA T
			TG TGAATATTAC	GAT AG	
			AC ACTTATAATG	CTA TC	
			C A_ C		
GAM458	HSD17B1	5'	GTAACCATGGTCATGTGA	5996	TTA A
			TCGCATGAT	TATG TTAC	
			AGTGTACTG	GTAC AATG	
			__ C		
GAM458	ITM2B	3'	TAATCATATATATGC	22541	ATT
			GCATG	TATATGATTA	
			CGTAT	ATATACTAAT	
			__		
GAM458	PIGR	3'	AATCACCTTCAGAATCATGTCG	35935	ATA__
	A		TCG CATGATTT	TGATT	

			AGC GTACTAAG	ACTAA		
			T	ACTTCC		
GAM458	RHD	3'	AATCATGTGCTTCATAGA	18214	GC	TT
			TC ATGA TATATGATT			
			AG TACT GTGTACTAA			
			A_ TC			
GAM458	RHD	3'	AATCATGTGCTTCATAGA	18334	GC	TT
			TC ATGA TATATGATT			
			AG TACT GTGTACTAA			
			A_ TC			
GAM458	AMOTL1	3'	CATGTGTACATCATGCGA	36463		T__
			TCGCATGAT TATATG			
			AGCGTACTA GTGTAC			
			CAT			
GAM458	DKFZP434C1715	3'	GTAATCATATACATAGTCA	41675		__
			TGATT TATATGATTAC			
			ACTGA ATATACTAATG			
			TAC			
GAM458	GFR	3'	GTAATCATATAAGGCCAT	14639		A_
			ATG TTTATATGATTAC			
			TAC GAATATACTAATG			
			CG			
GAM458	SLC7A11	3'	GTAATCATATCTACATGC	15645		ATTT
			GCATG ATATGATTAC			
			CGTAC TATACTAATG			
			ATC_			
GAM458	USP24	3'	GTAGTCTTAAATCATGTGA	43819		TAT
			TCGCATGATTTA GATTAC			
			AGTGTACTAAAT CTGATG			
			T__			
GAM458	LOC205251	5'	TAATCAGTGAATCATAGA	43590	GC	A
			TC ATGATTTAT TGATTA			
			AG TACTAAGTG ACTAAT			
			A_ _			
GAM458	LOC254251	3'	TAATCATATATACGTGT	45899		ATT
			GCATG TATATGATTA			
			TGTGC ATATACTAAT			
			AT_			
GAM459	CELSR1	3'	TGTATATATATTGCATTCG	15519		AA__
			CGAATG ATATATACA			

			GCTTAC TATATATGT		
			GTTA		
GAM459	NBEA	3'	ATAGATGTACATATTGTGTCG 45490	ATGA	A
			CGA AATAT TACATCTAT		
			GCT TTATA ATGTAGATA		
			GTG_ C		
GAM459	SCN3A	3'	ATAGATGTTTTTTTTTATTC 13797	TATAT	
			GAATGAAA ACATCTAT		
			CTTATTTT TG TAGATA		
			TTTT_		
GAM459	UBL3	3'	AGATTATATATTTCCCTC 13963	AT	C
			GA GAAATATATA ATCT		
			CT CTTTATATAT TAGA		
			CC _		
GAM459	WT1	3'	TTATAGATGTACATACCTC 23668	AA	A
			GA TAT TACATCTATAA		
			CT ATA ATGTAGATATT		
			CC C		
GAM459	WT1	3'	TTATAGATGTACATACCTC 23672	AA	A
			GA TAT TACATCTATAA		
			CT ATA ATGTAGATATT		
			CC C		
GAM459	WT1	3'	TTATAGATGTACATACCTC 23676	AA	A
			GA TAT TACATCTATAA		
			CT ATA ATGTAGATATT		
			CC C		
GAM459	WT1	3'	TTATAGATGTACATACCTC 5952	AA	A
			GA TAT TACATCTATAA		
			CT ATA ATGTAGATATT		
			CC C		
GAM459	ATP10D	5'	TGGACAAATATATTTTCATT 36202	ACA	
			GAATGAAATATAT TCTA		
			CTTACTTTATATA AGGT		
			AAC		
GAM459	C1QTNF7	3'	ATGTTTGTATATATTCCTC 25663	A	A TC
			GA TGAA TATATACA TAT		
			CT ACTT ATATATGT GTA		
			C _ TT		
GAM459	HELO1	3'	TTATAAATGTATGTCTTCATT 22385	AT	C
			AATGAA ATATACAT TATAA		

			TTACTT TGTATGTA ATATT		
			C_ A		
GAM459	KIAA1203	3'	AGACGTTACATTTTCATTCG 35466	A T A	
			CGAATGAAAT TA AC TCT		
			GCTTACTTTA AT TG AGA		
			C _ C		
GAM459	MGC14161	3'	ATAGATGTATATTATTTTG 26715	_	
			TGAAATA TATACATCTAT		
			GTTTTAT ATATGTAGATA		
			T		
GAM459	PANK	3'	TTATAAATGTAGTGTTCATTG 28717	G A C	
	G		C AATGAAATAT TACAT TATAA		
			G TTACTTTGTG ATGTA ATATT		
			G _ A		
GAM459	LOC133686	3'	TTATAGATGAATGCTTTCATTT 37058	TA A	
	G		CGAATGAAA TAT CATCTATAA		
			GTTTACTTT GTA GTAGATATT		
			C_ A		
GAM460	CNP	3'	AACACAAGGTGGGCAGGG 26976	ATA	
			TCCTGCCTATT TGTT		
			GGGACGGGTGG ACAA		
			AAC		
GAM460	NCOA4	3'	AGCAAATAGGC AAAAGA 11922	CC ATA	
			TCT TGCCTATT TGTT		
			AGA ACGGATAA ACGA		
			AA _		
GAM460	TFE3	3'	AACATGTAGGGCAAGAGG 13274	C AT	
			TCTC TGCCT TATATGTT		
			GGAG ACGGG ATGTACAA		
			A _		
GAM460	VPS26	3'	TTTTAACATATGTGTTTGAGA 11329	CT CTAT	
			TCTC GC TATATGTTAAAA		
			AGAG TG GTATACAATTTT		
			TT T_		
GAM460	CARD6	3'	TATCATATAGTAAGCAGAAGA 26322	C C T	
			TCT CTGC TATTATATG TA		
			AGA GACG ATGATATAC AT		
			A A T		
GAM460	DKFZp761K1423	5'	TTTTAACACATAAATGAGGGGA 20475	GCCTA A	
			TCTCCT TTAT TGTAAAA		

AGGGGA AATA ACAATTTT
 GTA__ C
 GAM460 KIAA0090 3' TTTTAACATAACCTGGGAGAAG 42655 C G TTA
 A TCT CT CCTA TATGTAAAA
 ||| || ||| |||||
 AGA GA GGGT ATACAATTTT
 A _ CCA
 GAM460 KIAA0543 3' TTAACCATGGGCAGGA 34180 TATAT
 TCCTGCCTAT GTTAA
 ||||| |||
 AGGACGGGTA CAATT
 C____
 GAM460 LY75 3' TTTTAACATGTGTTAAACAGAG 8152 C CC T
 A TCTC TG TA TATATGTAAAA
 ||| || |||||
 AGAG AC AT GTGTACAATTTT
 _ AA T
 GAM460 LOC146179 5' TTTTATGCAAAGTAGGCAG 38077 ATA _
 CTGCCTATT TGT TAAAA
 ||||| ||| |||
 GACGGATGA ACG ATTTT
 A__ T
 GAM460 LOC221399 5' TTAAACATATAATATAGCAG 45053 C_
 CTGC TATTATATGTAAAA
 ||| |||||
 GACG ATAATATACAATTT
 AT
 GAM461 FLJ14009 5' ATTATCAGGGCATTCTA 24112 C TTC
 TAGAA GCTCT GATGAT
 |||| ||| |||||
 ATCTT CGGGA CTATTA
 A ____
 GAM461 KIAA0332 3' ATCAAATGAAAGAGCATTTC 31416 C A_
 GAA GCTCTTTTCG TGAT
 || ||||| |||
 CTT CGAGAAAGT ACTA
 A AA
 GAM461 PRO1768 3' ATCATTGAAAAGCGCCCTG 15323 AA C
 TAG CGCT TTTTCGATGAT
 || ||| |||||
 GTC GCGA AAAGTTACTA
 CC _
 GAM462 HTR6 5' ATCACTCCCTTGCCGTCCA 6548 A TA AGTGA
 TG A GCGAG GAGTGAT
 || ||| |||||
 AC T CGTTC CTCACTA
 C GC C____
 GAM462 CECR7 5' CACCGTCGCTCTCCTACCCA 38876 AA C GA
 TG TAG GAGAGTGA GTG
 || ||| ||||| |||

AC ATC CTCTCGCT CAC
 CC _ GC
 GAM462 KIAA1203 3' CACTCTCATCTGCTCA 35467 T G G
 A AGC AGA TGAGAGTG
 | ||| ||| ||| ||| |||
 A TCG TCT ACTCTCAC
 C _ _
 GAM462 KIAA1535 3' CACCCTCACTCTGCCTGTC 38763 ATA G A
 GA GC AGAGTGAG GTG
 || || ||| ||| ||| |||
 CT CG TCTCACTC CAC
 GTC _ C
 GAM462 KIAA1894 3' CACTCTATCTGCCATTCA 36560 A G GTG
 TGAAT GC AGA AGAGTG
 |||| || ||| ||||
 ACTTA CG TCT TCTCAC
 C _ A_
 GAM462 LOC151171 5' ATCACTCTCGGGGCCGCCATTTC 39065 A AGAG
 GAAT GCG TGAGAGTGAT
 |||| ||| ||| ||| ||| |||
 CTTA CGC GCTCTCACTA
 C CGGG
 GAM463 EXO1 5' CTGAGATATGTACACAGTCATT 9797 GCGGAAC
 AATGAC ACATATCTCAG
 |||| ||| ||| ||| ||| |||
 TTAGTG TGTATAGAGTC
 ACACA_
 GAM463 EXO1 5' CTGAGATATGTACACAGTCATT 12644 GCGGAAC
 AATGAC ACATATCTCAG
 |||| ||| ||| ||| ||| |||
 TTAGTG TGTATAGAGTC
 ACACA_
 GAM463 EXO1 5' CTGAGATATGTACACAGTCATT 28183 GCGGAAC
 AATGAC ACATATCTCAG
 |||| ||| ||| ||| ||| |||
 TTAGTG TGTATAGAGTC
 ACACA_
 GAM463 TNFSF4 3' CTGAGATACGCACTCAGCTCCA 9333 AC G ACACA
 T ATG GC GA TATCTCAG
 || ||| ||| ||| ||| |||
 TAC CG CT ATAGAGTC
 CT A CACGC
 GAM463 KIAA0237 3' CTGAAATGTCTCCACGTC 16447 C AC ATC
 GACG GGA ACAT TCAG
 |||| ||| ||| ||| ||| |||
 CTGC CCT TGTA AGTC
 A C_ A_
 GAM463 KIAA0863 5' CTGGGATACACTCCAAGTCA 45634 GC ACACA
 TGAC GGA TATCTCAG
 |||| ||| ||| ||| ||| |||

			ACTG CCT ATAGGGTC		
			AA CAC__		
GAM463	KIAA1165	3'	CTGAGATATGCAAAATACTCAT 33474	CGCGGAACA	
		T	AATGA CATATCTCAG		
			TTACT GTATAGAGTC		
			CATAAAAC_		
GAM463	P2RX5	3'	AGATATGTATTCTCTGACA 8408	A C C	
			TG CG GGAA ACATATCT		
			AC GT TCTT TGTATAGA		
			A C A		
GAM464	COL4A4	3'	TCATTTGACCCATTTGA 5555	TT CAAA	
			TTA TGG GTCAAATGA		
			AGT ACC CAGTTTACT		
			TT ____		
GAM464	CYP51	3'	TCATCGCTCTTGCCAAATAA 6438	_ CAA	
			TTATTTGGCAA AGT ATGA		
			AATAAACCGTT TCG TACT		
			C C__		
GAM464	DDEF2	3'	TCATTTGACTGGAAAAAATAA 9968	GGCAA_	
			TTATTT AGTCAAATGA		
			AATAAA TCAGTTTACT		
			AAAAGG		
GAM464	HIP2	3'	TCATTTGACTTCTCAATAA 11815	T CA	
			TTATT GG AAGTCAAATGA		
			AATAA TC TTCAGTTTACT		
			C ____		
GAM464	ISL1	3'	TCATTGCCTTGCCAAA 7960	A CA	
			TTTGGCAA GT AATGA		
			AAACCGTT CG TTACT		
			C ____		
GAM464	OGT	3'	CATCTGGTGCCAAATGA 9661	AAG A	
			TTATTTGGCA TCA ATG		
			AGTAAACCGT GGT TAC		
			____ C		
GAM464	PAFAH1B1	3'	TCATGACACATTTGCCAAAT 6012	_ CAA	
			ATTTGGCAAA GT ATGA		
			TAAACCGTTT CA TACT		
			A CAG		
GAM464	PLS1	3'	TCATTTGACCCCTTCCAAATA 8541	CAAA_	
			TATTTGG GTCAAATGA		

			ATAAACC CAGTTTACT		
			TTCCC		
GAM464	RASA1	3'	CATTTGACTGTTCAATGA 22904	TG	AA
			TTATT GCA GTCAAATG		
			AGTAA TGT CAGTTTAC		
			CT _		
GAM464	SERPINB9	3'	TCATTTTTATGGCCAAATAA 10367	AAAGTC	
			TTATTTGGC AAATGA		
			AATAAACCG TTTACT		
			GTATT_		
GAM464	SHOC2	3'	TCACTGGATTTTACCAAGTAA 14307	C	AAA
			TTATTTGG AAAGTC TGA		
			AATGAACC TTTTAG ACT		
			A GTC		
GAM464	FLJ10895	3'	TCATCTATGGACTTGCCAAA 21160	A	AA__
			TTTGGCAA GTC ATGA		
			AAACCGTT CAG TACT		
			_ GTATC		
GAM464	FLJ20038	3'	TCATTTAATTCAAATGCCAAAT 19142	A__	C
	AG		TTATTTGGCA AGT AAATGA		
			GATAAACCGT TTA TTTACT		
			AAAC A		
GAM464	FLJ23560	3'	TCATCTAACTCAAGCCAAGTAA 23997	AA_	CAA
			TTATTTGGC AGT ATGA		
			AATGAACCG TCA TACT		
			AAC ATC		
GAM464	GFR	3'	TCATCTGTATAATTGCCAAATG 14641	AGT__	A
	A		TTATTTGGCAA CA ATGA		
			AGTAAACCGTT GT TACT		
			AATAT C		
GAM464	KIAA0258	3'	CATTCAGCCTTTGCCAAA 16645	_CA	
			TTTGGCAAAG T AATG		
			AAACCGTTTC G TTAC		
			C AC		
GAM464	KIAA0982	3'	TCATTTTGATTTTACAAATAA 15250	GC	_
			TTATTTG AAAGTCAAA TGA		
			AATAAAC TTTTAGTTT ACT		
			A_ T		
GAM464	KIAA1077	3'	TCATTTGACCTTGCCAGCTGA 36097	T	A
			TTA TTGGCAA GTCAAATGA		

			AGT GACCGTT CAGTTTACT	
			C C	
GAM464	KIAA1962	3'	TCATTTGACCTTTCAGA 39834	C A
			TTTGG AA GTCAAATGA	
			AGACT TT CAGTTTACT	
			_ C	
GAM464	MGC23980	3'	CATTTGACTTTAAGTAA 29605	GCA
			TTATTTG AAGTCAAATG	
			AATGAAT TTCAGTTTAC	
			—	
GAM464	RALGPS1A	3'	TGTATTTTGACCAAATAA 16020	_ _
			TTATTTGG CAAAGT CA	
			AATAAACC GTTTTA GT	
			A T	
GAM464	TSLRP	5'	CATTTGGGTGGGTGCCAAAT 14853	AAG__
			ATTTGGCA TCAAATG	
			TAAACCGT GGTTTAC	
			GGGTG	
GAM464	UBE1C	3'	TCATTTGAGTACCCAAATA 10108	CAAAG
			TATTTGG TCAAATGA	
			ATAAACC AGTTTACT	
			CATG_	
GAM464	LOC144453	3'	CACAGTGATTTAGCCAAATAA 37745	A AA_
			TTATTTGGC AAGTCA TG	
			AATAAACCG TTTAGT AC	
			A GAC	
GAM464	LOC144571	3'	TCATTTTGTGCCAAATGA 40442	AAGTC
			TTATTTGGCA AAATGA	
			AGTAAACCGT TTTACT	
			GTT_	
GAM464	LOC145547	3'	TCATTTGACTCCAGCCAA 37896	AA_
			TTGGC AGTCAAATGA	
			AACCG TCAGTTTACT	
			ACC	
GAM464	LOC145608	5'	TCACTTATTTTGCTAAATAA 40542	C A
			TTATTTGGCAAAGT AA TGA	
			AATAAATCGTTTTA TT ACT	
			_ C	
GAM464	LOC221692	3'	CATTTAACCTCTGCTAGAT 44296	A C
			ATTTGGCA AGT AAATG	

TAGATCGT TCA TTTAC
 C A
 GAM464 LOC253443 3' TCAGTGTTTTGCCAATTAA 45884 T T AA
 TTA TTGGCAAAG CA TGA
 ||| ||||| || |||
 AAT AACCGTTTT GT ACT
 T _ G_
 GAM465 GLI2 5' GAAACGCTACCAGCAGATTCTG 24935 C AA_____ GAAA
 AG TCAGAATC GCT TG C
 ||||| || || |
 AGTCTTAG CGA GC G
 A CCATC||| AAAG
 GAM465 PAH 5' GTTCCCAGGCTTCTGAGA 5824 T GCTAAT A
 TCTCAGAA CC GGAA C
 ||||| || ||| |
 AGAGTCTT GG CCTT G
 C AC_____ C
 GAM465 XT3 3' CCATTCTGTTCTATTCTGAGA 21444 CC_ T
 TCTCAGAAT GC AATGG
 ||||| || ||||
 AGAGTCTTA TG TTACC
 TCT C
 GAM465 DKFZp762M136 3' CGTTGCACAGAAATTCTGAGA 32302 CCG AA GA
 TCTCAGAAT CT TG AACG
 ||||| || || ||||
 AGAGTCTTA GA AC TTGC
 AA_ C_ G_
 GAM465 FLJ20156 5' CGTTTCCATGGTAACCCTGAG 19247 AATCC A
 CTCAG GCTA TGGAAACG
 |||| ||| |||||
 GAGTC TGGT ACCTTTGC
 CCAA_ _
 GAM465 FLJ20489 3' CGTTTCCATTCTGCCTTCTCAG 19505 C TCC T_
 A TCT AGAA GC AATGGAAACG
 || ||| || |||||
 AGA TCTT CG TTACCTTTGC
 C C_ TC
 GAM465 GRIP1 5' CGCAGTCAGGAATTCTGAGA 34963 _ _ AA_
 TCTCAGAAT CC GCT TG
 ||||| || || ||
 AGAGTCTTA GG TGA GC
 A AC C|||
 GAM465 HT002 3' CGTCTCCAAAGCCAGGATTCTG 15279 _ AA A
 AGG TCTCAGAATCC GCT TGGA ACG
 ||||| || ||| |||
 GGAGTCTTAGG CGA ACCT TGC
 AC A_ C
 GAM465 KIAA0469 3' GAAACGCACTGCAGAGATTCTG 16892 C_ TAA_____ GAAA
 AGA TCAGAATC GC TG C
 ||||| || || |

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AGTCTTAG CG GC G
AGA TCACIII AAAG
GAM465 KIAA1554 3' TTCCCTTAAATTCTGAG 45615 CCGC T
CTCAGAAT TAA GGAA
||||| ||| |||
GAGTCTTA ATT CCTT
A__ C
GAM465 LOC146272 5' CGTTTCCATCCTGTTTCTGTGA 38119 T TCC TA_
TC CAGAA GC ATGGAAACG
|| ||| || |||||
AG GTCTT TG TACCTTTGC
T __ TCC
GAM465 LOC92078 3' TCCACCAGCGGATTCTGAGA 33747 AA
TCTCAGAATCCGCT TGGA
||||||| |||
AGAGTCTTAGGCGA ACCT
CC
GAM466 BCL2 3' CTATTTGTGAGCAAAGGTG 6256 G C
TA CTTTGC CACAAATAG
|| ||| |||||
GT GAAACG GTGTTTATC
G A
GAM466 BCL7A 3' ATTTGTGTTGCTGCTGTA 21988 TTTGCC
TACAGTAGC CACAAAT
||||| |||
ATGTCGTCG GTGTTTA
TT__
GAM466 BCLG 3' GTGGAGCCAAGCTACTGTA 25052 T _
TACAGTAGCTT GC CCAC
||||||| |||
ATGTCATCGAA CG GGTG
C A
GAM466 NDP 3' TATTTGTGGGTGTGCTAT 5809 TT
GTAGC TGCCCACAAATA
|||| |||||
TATCG GTGGGTGTTTAT
T_
GAM466 TRPS1 3' TTTTGGGCAAACTACTCA 15361 C C C
A AGTAG TTTGCCCA AAA
| ||| ||||| |||
A TCATC AAACGGGT TTT
C A T
GAM466 FLJ12595 3' TTGAAGATAAAGCTACTGTA 24558 CCCA
TACAGTAGCTTTG CAA
||||||| |||
ATGTCATCGAAAT GTT
AGAA
GAM466 KIAA1078 3' TATTTGTGATCTACTGT 32473 CTTTGCC
ACAGTAG CACAAATA
||||| |||||

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			TGTCATC	GTGTTTAT		
			TA_____			
GAM466	PSMF1	3'	TGTAGGTAAGCAAGCTACTGTA	13690	_____	C
			TACAGTAGCTT	TGCC ACA		
			ATGTCATCGAA	ATGG TGT		
			CGA	A		
GAM466	LOC144195	3'	TATTTAATAAAGCTACTCA	30266	C	CCCAC
			A AGTAGCTTTG	AAATA		
			A TCATCGAAAT	TTTAT		
			C	AA_____		
GAM467	NEDD4	3'	TCAAGGAACTTGCAAA	34693	C	TTCAA
			TTTGCAAG TC	CTTGA		
			AAACGTTC AG	GAAC T		
			A	_____		
GAM467	TMEPAI	3'	CAAGCTAAGAGAGCTTGCAAA	21405		CAA_
			TTTGCAAGCTCTT	CTTG		
			AAACGTTCGAGAG	GAAC		
			AATC			
GAM467	DKFZp761G2113	5'	CGTCTCCACAAGAGTTTACAAA	34642	C	CAACTT
			TTTG AAGCTCTT	GACG		
			AAAC TTTGAGAA	CTGC		
			A	CACCT_		
GAM467	FLJ12517	3'	TCATGTGAAGTGCTTGCAAA	23270	T	ACT
			TTTGCAAGC CTTCA	TGA		
			AAACGTTCG GAAGT	ACT		
			T	GT_		
GAM467	MGC15437	3'	GAGCAAAGAACTTGCAAA	26688	C	CAA
			TTTGCAAG TCTT	CTT		
			AAACGTTC AGAA	GAG		
			A	AC_		
GAM467	LOC144893	5'	CGCCAGGCTGAGAACTTGCAAA	40458	C	T A A
			TTTGCAAG TCT CA	CTTG CG		
			AAACGTTC AGA GT	GGAC GC		
			A	_ C C		
GAM467	LOC221596	5'	GAGATGGAAGAACTTGCAAA	44174	C	AA_
			TTTGCAAG TCTTC	CTT		
			AAACGTTC AGAAG	GAG		
			A	GTA		
GAM467	LOC57821	5'	TCAATGTGAAGAGCTTAGAA	22151	GC	AC
			TTT AAGCTCTTCA	TTGA		

				AAG TTCGAGAAGT AACT			
				A_ GT			
GAM468	RAB20	3'	ACCACGTCCTACAACTCTGACA	19462	C _	ATAG	
			TG CA AGTTG GGGACGTGGT				
			AC GT TCAAC TCCTGCACCA				
			A C A__				
GAM469	CABC1	5'	GGCACTCAAGCTGGGCCA	21541		CC ATCACC	
			TGGCCCAGCT AG GCC				
			ACCGGGTCGA TC CGG				
			AC A__				
GAM469	FBXL11	3'	GCAGAGGACTGGGCCA	14682	C	AGA ACC	
			TGGCCCAG TCC TC GC				
			ACCGGGTC AGG AG CG				
			_ _ A_				
GAM469	MAP3K1	5'	CGGAGTGTGGAGCTGGACCA	33682	C	G CA	
			TGG CCAGCTCCA AT CCG				
			ACC GGTCTGAGGT TG GGC				
			A G A_				
GAM469	AWP1	5'	CGGCGGTGGCGGAGCCGGAGC	21078	_ A	AGA	
			GC CC GCTCC TCACCGCCG				
			CG GG CGAGG GGTGGCGGC				
			A C C_				
GAM469	DCNP1	5'	GCAGTGATCTGTCACTGACCA	28385	CC	CTC C	
			TGG CAG CAGATCAC GC				
			ACC GTC GTCTAGTG CG				
			A_ ACT A				
GAM469	DDX34	3'	GCACGTGTGAGCTGGGCCA	16163		CAGAT C_	
			TGGCCCAGCTC CAC GC				
			ACCGGGTCGAG GTG CG				
			T__ CA				
GAM469	DREV1 CC	5'	CGGCGGTGATCCGAGCGAGCGG	18108	CA__	CA	
			GGCC GCTC GATCACCGCCG				
			CCGG CGAG CTAGTGGCGGC				
			CGAG C_				
GAM469	FLJ10209 CA	5'	CGAGCGCTCCCCAGATCTGGGC	19768	C	CAGATCAC	_
			TGGCCCAG TC CGC CG				
			ACCGGGTC AG GCG GC				
			T ACCCTC_ A				
GAM469	FLJ20401	5'	GTGAGCTGGAGCTGGGCCA	19448		A	
			TGGCCCAGCTCCAG TCAC				

			ACCGGGTCGAGGTC AGTG		
			G		
GAM469	FLJ22529	3'	GCGGGTAGCTCCTGGGGCTGAG 24170	C	ATCA__
		CCA	TGGC CAGCTCCAG CCGC		
			ACCG GTCGGGGTC GGCG		
			A CTCGATG		
GAM469	LCHN	5'	GGCGCCTGGAGCTGGGC 41729	ATCAC	
			GCCCAGCTCCAG CGCC		
			CGGGTCGAGGTC GCGG		
			C__		
GAM469	MGC3113	3'	GCGGAGCCTTGGAGCTGAGCC 23469	C	ATCA
			GGC CAGCTCCAG CCGC		
			CCG GTCGAGGTT GGCG		
			A CCGA		
GAM469	MUC16	5'	GCTGTATTTGGAGCTGAGCCA 30356	C	C C
			TGGC CAGCTCCAGAT AC GC		
			ACCG GTCGAGGTTTA TG CG		
			A _ T		
GAM469	MYH7B	3'	TGGAGCTGCAGCTGGGCCA 34909	C	ATCA
			TGGCCAGCT CAG CCG		
			ACCGGGTCGA GTC GGT		
			C GA__		
GAM469	PCTAIRE2BP	5'	GGCGGCAGGAGCTGGGCC 34952	AGATCA	
			GGCCCAGCTCC CCGCC		
			CCGGGTCGAGG GGCGG		
			AC__		
GAM469	SEC8	3'	GCAATGCACTGACTGGGCCA 22362	CTC	AT CC
			TGGCCCAG CAG CA GC		
			ACCGGGTC GTC GT CG		
			A__ AC AA		
GAM469	SIMRP7	3'	GCCAGCTGGAGCTGGCCCA 44372	C	ATCACC
			TGG CCAGCTCCAG GC		
			ACC GGTCGAGGTC CG		
			C GAC__		
GAM469	SS-56	5'	CGGCAGCTTCTGACGCTGGGCC 29990	TC	TCACC
		A	TGGCCCAGC CAGA GCCG		
			ACCGGGTCG GTCT CGGC		
			CA TCGA_		
GAM469	LOC222962	3'	GCAGTGATGCCAGCTGGGC 44631	CCAG	C
			GCCCAGCT ATCAC GC		

CGGGTCGA TAGTG CG
 CCG_ A
 GAM469 LOC255975 5' CGGTTCCTGGAGCTGGGC 45889 ATC
 GCCCAGCTCCAG ACCG
 ||||| |||
 CGGGTCGAGGTC TGGC
 CT_
 GAM469 LOC256401 5' GGCGGTCGAGCTGGGCC 45947 CAGATC
 GGCCCAGCTC ACCGCC
 ||||| ||||
 CCGGGTCGAG TGGCGG
 C_____
 GAM469 LOC90249 3' GTGCCTGGAGCCTGGGCCA 31014 _ AT
 TGGCCCAG CTCCAG CAC
 ||||| ||||| |||
 ACCGGGTC GAGGTC GTG
 C C_
 GAM470 EPM2A 3' TCTCATTATCTCCATGATA 12228 T TTTTAC
 TATCATGGA GTA GAGA
 ||||| ||| ||||
 ATAGTACCT TAT CTCT
 C TA_____
 GAM470 KIAA1493 3' TCTCACAAAATACAGATATG 32094 GA AC
 CATG TGTATTTT GAGA
 ||| ||||| ||||
 GTAT ACATAAAA CTCT
 AG CA
 GAM470 KR18 3' GTCTCAGTAGGATACTCCAT 27119 T _
 ATGGA GTATTTTAC GAGAC
 |||| ||||| ||||
 TACCT CATAGGATG CTCTG
 _ A
 GAM470 LOC169166 3' GTCTCATAAAATATCATAAAGA 40272 ATGG _ C
 TA TATC ATG TATTTTA GAGAC
 ||| ||| ||||| ||||
 ATAG TAC ATAAAAT CTCTG
 AAA_ T A
 GAM470 LOC200301 5' GTCTCCCCTAGAAACACATCCA 42783 A AC____
 TGG TCATGGATGT TTTT GAGAC
 ||||| ||| ||||
 GGTACCTACA AAAG CTCTG
 C ATCCC
 GAM471 BMP1 3' GATGCCACCTTCCTTGTCCCC 12770 TTA TG AA
 GGG G A AAGGTGGCATC
 ||| ||| ||||| ||||
 CCC T T TTCCACCGTAG
 C__ GT CC
 GAM471 DPYSL2 3' CACCGAGCCTCATTAACCCA 7061 AAAA_
 TGGGTTAGTGA GGTG
 ||||| |||

ACCCAATTACT CCAC
 CCGAG
 GAM471 IKBKG 3' GATGCCACCTGGAGCCCCACCC 9711 TA_ GAAAA
 A TGGGT GT AGGTGGCATC
 |||| || |||||
 ACCCA CG TCCACCGTAG
 CCC AGG__
 GAM471 MYEOV 5' GATGCCATCCCCACTGAACCCA 29001 _ AAAAA
 TGGGT TAGTG GGTGGCATC
 |||| |||| |||||
 ACCCA GTCAC CTACCGTAG
 A CC__
 GAM471 PDGFRB 3' ACCTCTTTCACTACCCA 32812 T A
 TGGGT AGTGAAA AGGT
 |||| |||| ||||
 ACCCA TCACTTT TCCA
 _ C
 GAM471 SULT1C1 3' ATGCCACCCTTTTGAAGCCC 6719 AG AA
 GGGTT TGAAA GGTGGCAT
 |||| |||| |||||
 CCCGA GTTTT CCACCGTA
 AG C_
 GAM471 DKFZP566B183 3' CTCCTTCTCCACTAACCCA 17767 AAA T
 TGGGTTAGTG AAGG GG
 ||||| ||||
 ACCCAATCAC TTCC TC
 CTC T
 GAM471 DNAM-1 3' ATTTTTCCTCCACTACCCA 13336 T _
 TGGGT AGTG AAAAAGGT
 |||| |||| |||||
 ACCCA TCAC TTTTTTTA
 _ C
 GAM471 FLJ10751 3' GCCTCCTCCCTAACCCA 20093 T AAAA T
 TGGGTTAG GA GG GGC
 ||||| || ||||
 ACCCAATC CT CC CCG
 C ____ T
 GAM471 FLJ10751 3' GCCTCCTCCCTAACCCA 20192 T AAAA T
 TGGGTTAG GA GG GGC
 ||||| || ||||
 ACCCAATC CT CC CCG
 C ____ T
 GAM471 GNG4 3' ATGCCACCTCTTCCTGCTCCC 10806 T_ T AA
 GGG TAG GAA AGGTGGCAT
 || |||| |||||
 CCC GTC CTT TCCACCGTA
 TC _ C_
 GAM471 KIAA1538 3' GATGCCACCCTCCCTGAACCC 35429 _ T AAAA
 GGGT TAG GA GGTGGCATC
 |||| |||| |||||

CCCA GTC CT CCACCGTAG
 A C C___
 GAM471 LEC3 3' ATGCCACCTCGTTTAACC 17565 TGAAAA
 GGTTAG AGGTGGCAT
 ||||| |||||
 CCAATT TCCACCGTA
 TGC___
 GAM471 SNRK 3' ATGGCACCTTTTAACTAACCCA 19307 GA G
 TGGGTTAGT AAAAGGTG CAT
 ||||| ||||| ||
 ACCCAATCA TTTTCCAC GTA
 A_ G
 GAM471 LOC151195 3' CCACCTTTCCTGCTCA 39075 T T AA
 TGGGT AG GAA AGGTGG
 |||| || || |||||
 ACTCG TC CTT TCCACC
 _ _ _
 GAM471 LOC201952 5' GCCTCTTCCACCCACCCA 43395 TA AAA T
 TGGGT GTG AAGG GGC
 |||| || |||||
 ACCCA CAC TTCT CCG
 CC C_ _
 GAM471 LOC222183 3' GCTCCTCCACTGACCCA 45186 AAAA T
 TGGGTTAGTG AGG GGC
 ||||| || |||||
 ACCCAGTCAC TCC TCG
 C_ _
 GAM472 FBXO9 5' TTTCACCTGTTTTCTGCA 27260 CAAT C
 TGCGGGAG ACAG GAAA
 ||||| |||||
 ACGTCCTT TGTC CTTT
 T_ A
 GAM472 FLJ14950 3' GCTGGAACCATTTCTCCCGCA 26674 C A____
 TGCGGGAG AAT CAGC
 ||||| || |||||
 ACGCCCTC TTA GTCG
 T CCAAG
 GAM472 FLJ22362 5' AGGCCGCCGCACTGCCTCCCGC 23103 _ ATACA AAA
 A TGCGGGAG CA GCG CCT
 ||||| || |||||
 ACGCCCTC GT CGC GGA
 C CACGC C_
 GAM472 KIAA0427 3' GGGCTCGCATTGTTCCCGCA 16578 ACA AA
 TGCGGGAGCAAT GCGA CC
 ||||| ||||| |||||
 ACGCCCTTGTTA CGCT GG
 _ CG
 GAM472 KIAA0478 3' GCTTTTATTGCTCCCACA 16981 C C_
 TG GGGAGCAATA AGC
 || ||||| |||||

AC CCCTCGTTAT TCG
 A TT
 GAM472 KIAA1530 3' AGGTCTCACTGTGTTGCCACG 33730 _ A C A
 CG GG GCAATACAG GA ACCT
 || || ||||| || ||||
 GC CC CGTTGTGTC CT TGGA
 A _ A C
 GAM472 LOC145676 5' TGCTGCATTGCTCCAGCA 37921 G A
 TGC GGAGCAAT CAGCG
 ||| ||||| ||||
 ACG CCTCGTTA GTCGT
 A C
 GAM472 LOC220575 3' AGGTCTCGCCATATTGCTC 37527 CA A
 GAGCAATA GCGA ACCT
 ||||| ||| |||
 CTCGTTAT CGCT TGGA
 AC C
 GAM472 LOC91547 3' AGATTTCGCCATATTGCTC 33002 CA C
 GAGCAATA GCGAAA CT
 ||||| ||||| ||
 CTCGTTAT CGCTTT GA
 AC A
 GAM473 DRD1 5' CCAAACGCACCCCGGCGA 6465 A GC
 TC CCGGGGTGCG TGG
 || ||||| |||
 AG GGCCCCACGC ACC
 C AA
 GAM473 F2R 3' ACACTCTTTCCCCGCACCCC 7719 CT__
 GGGGTGCGG GGAGTGT
 ||||| |||||
 CCCCACGCC TCTACA
 CCTT
 GAM473 AGTRL2 5' GACACTCCAGAGGCCCTG 11646 T GG
 CGGGG GC CTGGAGTGTC
 |||| || |||||
 GTCCC CG GACCTCACAG
 _ GA
 GAM473 FLJ10540 3' GACACTCCAGCATGCTAGTGA 19928 CG G GGC
 TCAC G GTGC TGGAGTGTC
 ||| | ||| |||||
 AGTG C TACG ACCTCACAG
 AT G ____
 GAM473 FLJ13852 3' GACACTCCTCCCTCCCCAGTGA 23341 C TGC CT
 TCAC GGGG GG GGAGTGTC
 ||| ||| || |||||
 AGTG CCCC CC CCTCACAG
 A T__ CT
 GAM474 ADD1 3' CCCACTGAGGCCCTACTG 15471 A__ GCA
 CAG GGCTTCA GTGGG
 || ||||| ||||

GTC CCGGAGT CACCC
 ATCC ____
 GAM474 HIP1 3' TCCCGGCGGAAAGCCTCTGT 11812 _ A AG
 ACAGAGGCTT C GC TGGGA
 ||||| || ||
 TGTCTCCGAA G CG GCCCT
 A G ____
 GAM474 HOXC13 3' CCCACTGCCTCCCCTGTT 30014 A CTTCA
 AACAG GG GCAGTGGG
 |||| || |||||
 TTGTC CC CGTCACCC
 _ CTC____
 GAM474 JRK 3' TTCCACTGAAACCTCTGTT 41841 CTTCAG
 AACAGAGG CAGTGGGA
 ||||| |||||
 TTGTCTCC GTCACCTT
 AAA____
 GAM474 KLHL3 3' CCCACTACTGCTTTCCCTGT 42269 A CTT_ C
 ACAG GG CAG AGTGGG
 ||| || || |||||
 TGTC CC GTC TCACCC
 _ TTTC A
 GAM474 MAP1A 3' TCCCACTGCTATACTGTTCTAC 8186 _ _ TTC____
 TG CAG AGG C AGCAGTGGGA
 ||| ||| |||||
 GTC TCT G TCGTCACCCT
 A T TCATA
 GAM474 NEURL 3' GTCCCACTATGGGTCTC 10415 T GC
 GAGGCT CA AGTGGGAC
 |||| || |||||
 CTCTGG GT TCACCCTG
 _ A_
 GAM474 OVOL1 3' TCCCACTGCCCCCGCCTCTCA 10900 C TTCA
 A AGAGGC GCAGTGGGA
 | |||| |||||
 A TCTCCG CGTCACCCT
 C CCCC
 GAM474 UGT1A1 3' GTCCACCGCTGCCCCTACTG 6082 _ CTT A
 CAG AGG CAGC GTGGGAC
 ||| ||| ||| |||||
 GTC TCC GTCG CACCCTG
 A CC_ C
 GAM474 UGT1A4 3' GTCCACCGCTGCCCCTACTG 13980 _ CTT A
 CAG AGG CAGC GTGGGAC
 ||| ||| ||| |||||
 GTC TCC GTCG CACCCTG
 A CC_ C
 GAM474 UGT1A9 3' GTCCACCGCTGCCCCTACTG 22016 _ CTT A
 CAG AGG CAGC GTGGGAC
 ||| ||| ||| |||||

GTC TCC GTCG CACCCTG
 A CC_ C
 GAM474 C9orf14 5' GTCCCACTGCTAACAAGCC 41910 C__
 GGCTT AGCAGTGGGAC
 ||||| |||||
 CCGAA TCGTCACCCTG
 CAA
 GAM474 CGI-01 3' GTTCCCTGCTGAAGCCCCT 18056 A T
 AG GGCTTCAGCAG GGGAC
 || ||||| |||||
 TC CCGAAGTCGTC CCTTG
 C _
 GAM474 DKFZp434C0923 3' CCCACGCAGCCCCTGTT 19063 A TCA A
 AACAG GGCT GC GTGGG
 ||||| ||||| || |||||
 TTGTC CCGA CG CACCC
 C _ _
 GAM474 DNAJC5 3' CCCACCAGGCCCTCTGTTG 30811 _ CAGCA
 TAACAGAGG CTT GTGGG
 ||||| ||||| |||||
 GTTGTCTCC GGA CACCC
 C C__
 GAM474 FLJ23584 3' TCCCTGCAAAGCCTCT 23822 CA T
 AGAGGCTT GCAG GGG
 ||||| ||||| |||||
 TCTCCGAA CGTC CCT
 A_ _
 GAM474 HYA22 3' TCCCATTGCAGCCTC 12389 TCA
 GAGGCT GCAGTGGGA
 ||||| |||||
 CTCCGA CGTTACCCT
 _
 GAM474 KIAA0237 3' CCCACTGCTGCCCTCTG 16443 CTT
 CAGAGG CAGCAGTGGG
 ||||| |||||
 GTCTCC GTCGTCACCC
 C__
 GAM474 KIAA1546 3' TTCACTGAAGCCTATG 33717 G GCA
 CA AGGCTTCA GTGGG
 || ||||| |||||
 GT TCCGAAGT CACTT
 A _
 GAM474 LBP-9 3' TCCCACTGCTGATTATTG 15881 AGGCT
 CAG TCAGCAGTGGGA
 ||| |||||
 GTT AGTCGTCACCCT
 ATT__
 GAM474 NINJ2 3' CCCACTGCTTCCTTCTG 18602 CTC
 CAGAGG AGCAGTGGG
 ||||| |||||

			GTCTTC	TCGTCACCC		
			CT__			
GAM474	PDZD2	5'	TCCCATCAGGCCTCTGT	39396		CAGCA
			ACAGAGGCTT	GTGGGA		
			TGTCTCCGGA	TACCCT		
			C____			
GAM474	PKMYT1	5'	GTCCCACCACTGAAGCTGTTG	10398	A	CA
			CAG GGCTTCAG	GTGGGAC		
			GTT TCGAAGTC	CACCCTG		
			G	AC		
GAM474	PRKWNK2	3'	CTCAGCTGAAGCCCCT	43520	A	AG
			AG GGCTTCAGC	TGGG		
			TC CCGAAGTCG	ACTC		
			C	__		
GAM474	SFXN2	3'	CCCACTGCCACATACCTCTGTT	36602		CTTCA_
			AACAGAGG	GCAGTGGG		
			TTGTCTCC	CGTCACCC		
			ATACAC			
GAM474	SNPH	5'	CCTGCTCCTGAAGCCTCTGT	16292		C TG
			ACAGAGGCTTCAG	AG GG		
			TGTCTCCGAAGTC	TC CC		
			C	GT		
GAM474	LOC147599	3'	TCCCACTGCTGGGTATCTGT	40848	G	T
			ACAGA GCT	CAGCAGTGGGA		
			TGTCT TGG	GTCGTCACCCT		
			A	__		
GAM474	LOC150383	3'	TCCCACTGCTTGCCTGCT	38947	_	TTC
			AG AGGC	AGCAGTGGGA		
			TC TCCG	TCGTCACCCT		
			G	T__		
GAM474	LOC151836	5'	TCCCACTGCGCCCCTG	41391	A	TTCA
			CAG GGC	GCAGTGGGA		
			GTC CCG	CGTCACCCT		
			C	____		
GAM474	LOC221421	3'	TCCCACTGTCCCCTGT	44325	A	CTTCA
			ACAG GG	GCAGTGGGA		
			TGTC CC	TGTCACCCT		
			C	____		
GAM474	LOC255196	5'	TCCCACTACTGATCAGTACTG	46415	AG	_ C
			CAG GCT	TCAG AGTGGGA		

GTC TGA AGTC TCACCCT
 A_ CT A
 GAM474 LOC256337 3' TCGGCAAGCTGGAGCCTCTGTT 45422 A_ G
 A TAACAGAGGCTTCAGC GT GG
 ||||| || ||
 ATTGTCTCCGAGGTCG CG CT
 AA G
 GAM475 ARHGEF6 3' AGTTTTCTATTTCCCA 33843 T CA
 TG GGGAAA GGAAGGCT
 || |||| |||||
 AC CCCTTT TCTTTTGA
 _ A_
 GAM475 ARHGEF6 3' TGAACCCAACTTTTCCCA 33850 T C GAA C
 TG GGGAAA AG GG TCA
 || |||| || || ||
 AC CCCTTT TC CC AGT
 _ _ AAC A
 GAM475 ATP1A2 3' TGAACCTTCCTGTCTCCCA 6371 A C
 TGGGA ACAGGAAGG TCA
 |||| ||||| ||
 ACCCT TGTCTTCC AGT
 C A
 GAM475 CALB1 3' TGAGCTATAATGTTTCCCTCA 11370 T GGAA
 TG GGGAAACA GGCTCA
 || ||||| ||||
 AC CCCTTTGT TCGAGT
 T AATA
 GAM475 E2F3 3' AGCTTTTCCCCATTTCCATA 7666 CA__
 TGTGGGAAA GGAAGGCT
 ||||| |||||
 ATACCCTTT CTTTTCGA
 ACCC
 GAM475 EGLN1 5' AGCCTAGCACCCCACTTTCCAC 22580 ACA A____
 A TGTGGGAA GG AGGCT
 ||||| || ||||
 ACACCTTT CC TCCGA
 CAC CACGA
 GAM475 HIP1 3' TGAGCCATGATTTCCAC 11813 _ GGAA
 GTGGGAAA CA GGCTCA
 ||||| || ||||
 CACCCTTT GT CCGAGT
 A A____
 GAM475 HLCS 5' TGAGATTTCTGTTCCCCAC 5993 A GG
 GTGGG AACAGGAA CTCA
 |||| ||||| ||||
 CACCC TTGTCTTT GAGT
 C A_
 GAM475 IL1A 3' AGCCTTCCTGCCGCA 31306 GAAA
 TGTGG CAGGAAGGCT
 |||| ||||| ||||

ACGCC GTCCTTCCGA

GAM475 MAP3K7IP1 3' TGAGTTAGACTATTTCCCACA 12763 C GAA
TGTGGGAAA AG GGCTCA
||||||| || |||||
ACACCCTTT TC TTGAGT
A AGA

GAM475 MAPT 3' GAGCCCCCTGTCCTTCCCAC 12542 _ AA
GTGGGAA ACAGG GGCTC
||||| |||| |
CACCTT TGTCC CCGAG
CC C_

GAM475 MAPT 3' GAGCCCCCTGTCCTTCCCAC 18830 _ AA
GTGGGAA ACAGG GGCTC
||||| |||| |
CACCTT TGTCC CCGAG
CC C_

GAM475 MAPT 3' GAGCCCCCTGTCCTTCCCAC 18836 _ AA
GTGGGAA ACAGG GGCTC
||||| |||| |
CACCTT TGTCC CCGAG
CC C_

GAM475 MAPT 3' GAGCCCCCTGTCCTTCCCAC 18842 _ AA
GTGGGAA ACAGG GGCTC
||||| |||| |
CACCTT TGTCC CCGAG
CC C_

GAM475 PFAH1B1 3' AGCTTCTATTTTCCACA 6006 C AA
TGTGGGAAA AGG GGCT
||||||| ||| |||
ACACCTTTT TCT TCGA
A _

GAM475 POU2AF1 3' TGAGCTGTCAGTTCCCACA 12894 ACAG A
TGTGGGAA GA GGCTCA
|||||| | |||||
ACACCCTT CT TCGAGT
GA_ G

GAM475 PRDM2 3' AGTTTTCTGTTTCCCAC 14530
GTGGGAAACAGGAAGGCT
|||||||
CACCTTTGTCCTTTTGA

GAM475 SFRP1 3' GAGCCTTTGTTTTTCTCCACA 8932 _ CAG
TGTGG GAAA GAAGGCTC
|||| | |||||
ACACCCTT TTTCCGAG
T TTG

GAM475 SHMT1 3' TGAACCTGGCTTTCTCACA 10375 AC GA C
TGTGGGAA AG AGG TCA
|||||| | ||| |||

			ACACTCTT TC TCC AGT		
			__ GG A		
GAM475	SORBS1	3'	TGAGTTACCTCTTCCCACA 17690	AC	AA
			TGTGGGAA AGG GGCTCA		
			ACACCCTT TCC TTGAGT		
			C_ A_		
GAM475	SPR	3'	TGAACCTTTTTGCCCCAC 9094	AAA	C
			GTGGG CAGGAAGG TCA		
			CACCC GTTTTCC AGT		
			CC_ A		
GAM475	TOP1	3'	GAGTCCATTTCACACA 9296	CA	AAG
			TGTGGGAAA GG GCTC		
			ACACCCTT CC TGAG		
			A_ _		
GAM475	TPK1	3'	GAGGTTCTTTCCACACA 22779	ACA	GG
			TGTGGGAA GGAA CTC		
			ACACCCTT TCTT GAG		
			_ G_		
GAM475	WHSC1L1	5'	GAGCCTTCCTCTTCCCGCA 19409	AC	
			TGTGGGAA AGGAAGGCTC		
			ACGCCCTT TCCTCCGAG		
			C_		
GAM475	WHSC1L1	5'	GAGCCTTCCTCTTCCCGCA 23316	AC	
			TGTGGGAA AGGAAGGCTC		
			ACGCCCTT TCCTCCGAG		
			C_		
GAM475	C1QR1	3'	GAGCCCTCCTATTTTCACA 14335	GG	AC A
			TGTG AA AGGA GGCTC		
			ACAC TT TCCT CCGAG		
			TT A_ C		
GAM475	C20orf4	3'	GGGCCCTTCCACACA 17772	AAC	AA
			TGTGGGA AGG GGCTC		
			ACACCCT TCC CCGGG		
			_ _		
GAM475	CAMKK2	3'	AGCCTTTCGTGTTTTTCCACA 13309	_ _	
			TGTGGGAAA CA GGAAGGCT		
			ACACCTTTT GT CTTTCCGA		
			T G		
GAM475	CTAGE-1	3'	TGAGCCAGGCATCCATTTCAC 22910	ACA	A_
	A		TGTGGGAA GGA GGCTCA		

			ACACCTTT CCT CCGAGT	
			A_ ACGGA	
GAM475	FBXO9	3'	AGCATTTTATTTCCCGCA 27255	C AG
			TGTGGGAAA AGGA GCT	
			ACGCCCTTT TTTT CGA	
			A A_	
GAM475	FLJ13322	3'	TGAGCCTTCCTAGGGTTT 24061	___
			AAAC AGGAAGGCTCA	
			TTTG TCCTCCGAGT	
			GGA	
GAM475	FLJ13646	3'	TGAACTTTGTTTCCCA 23815	GG GC
			TGGGAAACA AAG TCA	
			ACCCTTTGT TTC AGT	
			_ A_	
GAM475	FLJ20188	3'	TGGGAAGCCTAGTTCCACACA 19277	AC AAGG
			TGTGGGAA AGG CTCA	
			ACACCCTT TCC GGGT	
			GA GAA_	
GAM475	FLJ21032	3'	TGAGATTCTATTTCCACA 24403	ACA GG
			TGTGGGAA GGAA CTCA	
			ACACCTTT TCTT GAGT	
			A_ A_	
GAM475	FLJ23306	3'	GAGCCTTTTCTCCCCA 23733	T AACA
			TG GGGA GGAAGGCTC	
			AC CCCT TTTCCGAG	
			_ C_	
GAM475	FYCO1	5'	TGAGCCTTCCTCTGGACCCA 23716	AAAC_
			TGGG AGGAAGGCTCA	
			ACCC TCCTTCCGAGT	
			AGGTC	
GAM475	GMPPB	5'	GAGCCCCGGTTTTCCCAT 45816	CA_ AA
			GTGGGAAA GG GGCTC	
			TACCCTTT CC CCGAG	
			TGG _	
GAM475	HCC-4	3'	GGCCCTCCCTGTTTCCACA 28897	G AA_
			TGTGG AAACAGG GGCT	
			ACACC TTTGTCC CCGG	
			_ CTC	
GAM475	HM74	3'	GGCCTTCTTCCACACA 12637	AACA
			TGTGGGA GGAAGGCT	

ACACCCT TCTTCCGG

GAM475 HSPC063 5' AGCTCCTCTTCCCACA 15438 AC AG
TGTGGGAA AGGA GCT
||||||| ||| |||
ACACCCTT TCCT CGA
C_ _

GAM475 KIAA0247 3' CATGAGCCCTCAGACCACTTGC 16372 A AA_____ III
TTCCCACA AA CAGG GGCTCA TG
|| ||| ||||| ||
TT GTTC CCGAGT AC
C ACCAGACTC III

GAM475 KIAA0668 3' GAGCTTGCTTTCCACA 33049 A GGAA
TGTGGGAA CA GGCTC
||||||| || |||||
ACACCTTT GT TCGAG
C _____

GAM475 KIAA0669 3' TGAGCCTTCCTATCACA 16628 GAAAC
TGTGG AGGAAGGCTCA
||||| |||||
ACACT TCCTTCCGAGT
A_____

GAM475 KIAA0710 3' TGAGCCTGAGTCTTTCCACA 16994 _ AGGA
TGTGGGAA AC AGGCTCA
||||||| || |||||
ACACCTTT TG TCCGAGT
C AG__

GAM475 KIAA0720 3' TGAATCTGCCCAGTTCCCACA 31237 ACA A GC
TGTGGGAA GG AG TCA
||||||| || || |||
ACACCCTT CC TC AGT
GAC G TA

GAM475 KIAA1045 3' TGAGCCCAGCCTTCCCCA 35203 T AAC AA_
TG GGGA AGG GGCTCA
|| ||| ||| |||||
AC CCCT TCC CCGAGT
_ _ GAC

GAM475 KIAA1045 3' TGAGCCTTCTTGCCCCA 35204 AAA
TGGG CAGGAAGGCTCA
||| |||||
ACCC GTTCTTCCGAGT
CG_

GAM475 KIAA1332 3' TGAGTGATGTTTCCATA 35261 GGAAG
TGTGGGAAACA GCTCA
||||||| |||||
ATACCCTTTGT TGAGT
AG_____

GAM475 KIAA1337 3' AGCCCCTGTCTTTCCCAC 35982 _ AA
GTGGGAA ACAGG GGCT
||||||| ||||| |||||

			CACCCTT TGTCC CCGA		
			TC _		
GAM475	KIAA1393	3'	AGATTTCCATTCCCACA 35683	ACA	G
			TGTGGGAA GGAAG CT		
			ACACCCTT CCTTT GA		
			A_ A		
GAM475	KIAA1854	3'	GAGTGTGCGTTCCCACA 35532	AAC _	AG
			TGTGGGA AG GA GCTC		
			ACACCCT TC CT TGAG		
			_ G G_		
GAM475	KIAA1889	3'	AGCTCTGATTCCCACA 36385	A	GAA
			TGTGGGAA CAG GGCT		
			ACACCCTT GTC TCGA		
			A _		
GAM475	LYPLA2	3'	GAGCCCCTGTCCCCAC 14130	AA	AA
			GTGGG ACAGG GGCTC		
			CACCC TGTCC CCGAG		
			C_ _		
GAM475	MAB21L2	5'	TGAGCCTTGATCCCTCA 13153	T	AA GGA
			TG GGA CA AGGCTCA		
			AC CCCT GT TCCGAGT		
			T AG _		
GAM475	MGC2654	3'	GGCCTCCTTCCCACA 23555	AAC	A
			TGTGGGA AGGA GGCT		
			ACACCCT TCCT CCGG		
			_ _		
GAM475	PCANAP7	5'	GGTTTCCTGTCCCCCA 44839	T	AA G
			TG GGG ACAGGAAG CT		
			AC CCC TGTCTTT GG		
			_ CC _		
GAM475	PTDSS2	3'	GAGCCTTCCTTTCACACA 25077	G	AC
			TGTG GAA AGGAAGGCTC		
			ACAC CTT TCCTTCGAG		
			A _		
GAM475	LOC115330	3'	TGAAGTTTCCTTTTCCCACA 28812	C	GC
			TGTGGGAAA AGGAAG TCA		
			ACACCCTTT TCCTTT AGT		
			T GA		
GAM475	LOC124446	5'	GAGCCTCAGTTTCCCTCA 36751	T	AG A
			TG GGGAAC GA GGCTC		

		AC CCCTTTG CT CCGAG		
		T A_ _		
GAM475	LOC126299 5'	AGCCCCTCTTCCCACA 36817	AC	AA
		TGTGGGAA AGG GGCT		
		ACACCCTT TCC CCGA		
		C_ _		
GAM475	LOC133584 3'	TGAAC TTCACATTTCCCACA 37047	CAG	GC
		TGTGGGAAA GAAG TCA		
		ACACCCTTT CTTC AGT		
		ACA A_		
GAM475	LOC144347 3'	TGAGCCTTCCTCCCCCCTCA 37725	T	AAAC
		TG GGG AGGAAGGCTCA		
		AC CCC TCCTTCCGAGT		
		T CCC_		
GAM475	LOC147991 5'	TGAGCCTCAGTTTCCACA 38437	ACAG	A
		TGTGGGAA GA GGCTCA		
		ACACCTTT CT CCGAGT		
		GA_ _		
GAM475	LOC149175 3'	GGCCTCCTTCCCACA 38661	AAC	A
		TGTGGGA AGGA GGCT		
		ACACCCT TCCT CCGG		
		— —		
GAM475	LOC149301 3'	AGCCTTCTTTCCCCA 38687	T	ACA
		TG GGGAA GGAAGGCT		
		AC CCCTT TCTTCCGA		
		— —		
GAM475	LOC151584 5'	AGTCTTTTTTCCCACA 41374	ACAG	
		TGTGGGAA GAAGGCT		
		ACACCCTT TTTCTGA		
		— —		
GAM475	LOC158835 3'	TGAGTCCTGCTTCCTACA 39896	A	AAG
		TGTGGGAA CAGG GCTCA		
		ACATCCTT GTCC TGAGT		
		C _		
GAM475	LOC164397 5'	TGGGACCAACTTCCCACA 40155	AACA	AA _
		TGTGGGA GG GG CTCA		
		ACACCCT TC CC GGGT		
		— AA A		
GAM475	LOC166929 5'	AGCTTCTTTCCCACA 40224	ACA	G
		TGTGGGAA GGAAG CT		

ACACCCTT TCTTC GA

GAM475 LOC169026 3' AGCCTCATTTTCCACA 40262 CAG A
TGTGGGAAA GA GGCT
||||||| || |||
ACACCTTTT CT CCGA

A_ _

GAM475 LOC201194 3' TGAGCCTTCTTGCTCCACA 43219 AAA
TGTGGG CAGGAAGGCTCA
||||| |||||
ACACCT GTTCTTCCGAGT

C_

GAM475 LOC221683 5' GGCCTTCCTGCCTCCCACA 45005 AA
TGTGGGA CAGGAAGGCT
||||| |||||
ACACCCT GTCCTTCCGG

CC

GAM475 LOC222488 3' AGCTGCCCATTTCTTACA 45301 CA AA
TGTGGGAAA GG GGCT
||||||| || |||
ACATCCTTT CC TCGA

A_ CG

GAM475 LOC253613 3' AGCCCTGCTTCCCGCA 46008 A AAG
TGTGGGAA CAGG GCT
||||||| ||| |||
ACGCCCTT GTCC CGA

C _

GAM475 LOC254423 3' TGAACCTTCCTGTGCCAC 46530 GAA C
GTGG ACAGGAAGG TCA
||| ||||| |||
CACC TGTCTTCC AGT

G_ A

GAM475 LOC255045 3' TGAACCTTTGTTTCCCA 46035 GG GC
TGGGAAACA AAG TCA
||||||| ||| |||
ACCCTTTGT TTC AGT

_ A_

GAM475 LOC257153 5' GAGGCTGTTTCTCACA 45826 GAAGG
TGTGGGAAACAG CTC
||||||| |||
ACACTCTTTGTC GAG

G_

GAM475 LOC51667 3' TGACCTTCCTGCTTCCCAC 18198 A C
GTGGGAA CAGGAAGG TCA
||||| ||||| |||
CACCTT GTCCTTCC AGT

C _

GAM475 LOC55901 5' TGAGCCTTCCCGTCCGC 20750 AAACA
GTGGG GGAAGGCTCA
||||| |||||

			CGCCT CCTCCGAGT		
			GC__		
GAM476	BRF1	3'	CATCCAAGGACCCTCCAAGGCT 7255	G CTT	A__
	G		CAGCCTTGG AG GGTC GATG		
			GTCGGAACC TC CCAG CTAC		
			_ __ GAAC		
GAM476	CX3CR1	3'	TGAGCACTCCCAAGTCT 34982	C	CT G
			AG CTTGGGAG TG TCA		
			TC GAACCCTC AC AGT		
			T _ G		
GAM476	GRLF1	3'	CATCTGCACACACCCCCAAGGT 38409	AGCT	GT
			GCCTTGGG TG CAGATG		
			TGGAACCC AC GTCTAC		
			CCAC AC		
GAM476	KCNC3	3'	ATCTGATTCCCAAGGGC 11420	_	AGCTT
			GCC TTGGG GGTCAGAT		
			CGG AACCC TTAGTCTA		
			G C__		
GAM476	KCNJ10	3'	CATCTGACGGATTCCCAAAGGC 8024	_	C G
			GCCTT GGGAG TT GTCAGATG		
			CGGAA CCCTT AG CAGTCTAC		
			A _ G		
GAM476	LTBP2	3'	ATCCACCCTCCCAAGCTG 6004	C	CTT CA
			CAGC TTGGGAG GGT GAT		
			GTCG AACCCCTC CCA CTA		
			_ __ C_		
GAM476	ODF2	5'	CAACTGCCAACCCCAAAGCT 8385	C	AGC T A
			AGC TTGGG TTGG CAG TG		
			TCG AACCC AACCC GTC AC		
			A C_ _ A		
GAM476	PRX	3'	GGTCTCAGCCCCCAAGGCTG 21941	A T_	GT
			CAGCCTTGGG GCT G C		
			GTCGGAACCC CGA C G		
			C CT TG		
GAM476	RPL10	3'	CTGACCAAAGGTCTAGGCT 12623	TG G	_
			AGCCT GGA CTT GGTCAG		
			TCGGA TCT GAA CCAGTC		
			_ G A		
GAM476	CNNM1	3'	CATCTGCTTCCCCCAAGGC 21606	AGCTT	T
			GCCTTGGG GG CAGATG		

CGGAACCC TC GTCTAC
CCT__ _

GAM476 DKFZP434N1511 3' CATCTGCACTGGCCCCCAAGGT 43934 A A T _
CA C GCCTTGGG GCT GGT CAGATG
| ||||| ||| ||| |||||
A TGGAACCC CGG TCA GTCTAC
C C _ C

GAM476 FLJ12770 3' CATCCCAGAGCCTCCCAAGGCT 25884 _ _ TCA
G CAGCCTTGGGAG CT TGG GATG
||||||| || ||| |||||
GTCGGAACCCTC GA ACC CTAC
C G _

GAM476 FLJ13964 3' CATCTTAATGTCCCAAGGC 25901 GC GTC
GCCTTGGGA TTG AGATG
||||||| ||| |||||
CGGAACCCT AAT TCTAC
GT _

GAM476 FLJ20040 3' CTGACCAAGCCCGGG 21065 TG A
CCT GG GCTTGGTCAG
||| || |||||
GGG CC CGAACCAGTC

GAM476 FLJ22551 5' ACCTCTGCCCCAAGGCTG 24025 A TT_
CAGCCTTGGG GC GGT
||||||| || |||
GTCGGAACCC CG CCA
_ TCT

GAM476 KIAA0084 3' CTGAGCCCTCCCAGGGC 33805 CTT _
GCCTTGGGAG GG TCAG
||||||| || |||||
CGGGACCCTC CC AGTC
_ G

GAM476 KIAA0806 3' ATCTGACCGCACCAAGGT 16779 GA TT
GCCTTGG GC GGTCAGAT
||||||| || |||||
TGGAACC CG CCAGTCTA
A _

GAM476 KIAA1950 3' ACCCAGCTTCCAAGGCTG 44483 T
CAGCCTTGGGAGCT GGT
||||||| |||
GTCGGAACCTTCGA CCA
C

GAM476 PPFIA4 3' CTAACCCTCATCCAGGGCT 34819 _ CTT C
AGCCTTGG GAG GGT AG
||||||| ||| ||| ||
TCGGGACC CTC CCA TC
TA _ A

GAM476 SSB-3 3' CATCTCTTGCTCCCGAGGCTG 28100 TT TC
CAGCCTTGGGAGC GG AGATG
||||||| || |||||

GTCGGAGCCCTCG TC TCTAC
 T_ _
 GAM476 LOC115051 3' CCGGGGTCCTCCCAGGGCTG 30159 _
 CAGCCTTGGGAG CTTGG
 ||||| ||||
 GTCGGGACCCTC GGGCC
 CTG
 GAM476 LOC127845 5' ACCCGGAAAGCCCCCAGGCTG 36911 T A _
 CAGCCT GGG GCTT GGT
 ||||| || |||| ||
 GTCGGA CCC CGAA CCA
 C C AGGC
 GAM476 LOC158056 5' CTGGACCCCCAAGGCT 39714 AGCTT _
 AGCCTTGGG GGTC AG
 ||||| |||| ||
 TCGGAACCC CCAG TC
 _ G
 GAM476 LOC196955 5' ACCCTGGCTCCCAAGGCT 37927 T_
 AGCCTTGGGAGCT GGT
 ||||| |||| ||
 TCGGAACCCTCGG CCA
 TC
 GAM476 LOC256158 5' CATCCAGCTGCTCCCAGGCTG 46619 T TT CA
 CAGCCT GGGAGC GGT GATG
 ||||| |||| || ||||
 GTCGGA CCCTCG TCG CTAC
 _ _ AC
 GAM477 ADCY9 3' AGGATGCCACCTGTCCCCCA 6791 A T G G
 TG GG ACAGGTGGG TAT TCT
 || || ||||| || ||||
 AC CC TGTCCACCC GTA GGA
 C C _ _
 GAM477 BACE 3' AGACATCTCCTCACCCC 14414 TACA T_
 GG GGTGGGG ATGTCT
 || ||||| |||||
 CC CCACTCC TACAGA
 _ TC
 GAM477 BACE 3' AGACATCTCCTCACCCC 29082 TACA T_
 GG GGTGGGG ATGTCT
 || ||||| |||||
 CC CCACTCC TACAGA
 _ TC
 GAM477 FASN 3' CATCCCCACCCCACCCCA 10315 A ACA T
 TG GGT GGTGGGG ATG
 || || ||||| ||||
 AC CCA CCACCCC TAC
 C CC_ _
 GAM477 FGFR1 3' CAGACACCACCCCCACCCCA 22449 A ACA T A_
 TG GGT GG GGGGT TGTCTG
 || || ||||| |||||

AC CCA CC CCCC ACAGAC
 C _ _ CC
 GAM477 COAS3 3' CAGACACCTTCCCCACCCATA 29120 CA TA_
 CC GGTA GGTGGGG TGTCTG
 ||| ||||| |||||
 CCAT CCACCCC ACAGAC
 AC CTTCC
 GAM477 FLJ00058 5' ACACACCCCACCCCGTTTTTC 38507 T A_ A
 GAGG AC GGTGGGGT TGT
 ||| || ||||| |||
 CTTT TG CCACCCCA ACA
 T CC C
 GAM477 KIAA0446 3' CAGTTCCCCCACCCTCACCCC 34147 A ACA TATGT
 A TG GGT GGTGGGG CTG
 || ||| ||||| |||
 AC CCA CCACCCC GAC
 C CTC CTT_
 GAM477 KIAA0563 5' TACCCACCCCTACCCCA 16844 A CA
 TG GGTA GGTGGGGTA
 || ||| |||||
 AC CCAT CCACCCCAT
 C C_
 GAM477 KIAA1550 3' AGACATACACATGCACTCA 33066 _ ACAG GG
 TGAG GT GTG GTATGTCT
 ||| || ||| |||||
 ACTC CG TAC CATA CAGA
 A _ _ A_
 GAM477 KIAA1884 3' AGACACACTCACACTCTCA 36290 GTACA _ A
 TGAG GGTG GGGT TGTCT
 ||| ||| ||| |||||
 ACTC TCAC CTCA ACAGA
 _ _ A C
 GAM477 MGC12921 3' CAGAGCGGCCACCCCCACCTCA 31898 ACA T _ ATG
 TGAGGT GG GG GGT TCTG
 ||||| || ||| |||
 ACTCCA CC CC CCG AGAC
 C _ _ A GCG
 GAM477 RA-GEF-2 3' CAGACATACCCATTTGGATGAC 18463 A A _ G
 CCCA TG GGT CAGGTGGG TATGTCTG
 || ||| ||||| |||||
 AC CCA GTTTACCC ATACAGAC
 C GTAG _
 GAM477 LOC147071 5' TACCCACCCCTACCCCA 36139 A CA
 TG GGTA GGTGGGGTA
 || ||| |||||
 AC CCAT CCACCCCAT
 C C_
 GAM477 LOC154141 5' CAGACATAATAACTACACTCA 41686 _ ACA GGGG
 TGAG GT GGT TATGTCTG
 ||| || ||| |||||

			ACTC CA TCA ATACAGAC		
			A _ _ _ ATA_		
GAM477	LOC201173	5'	TACCCACCCCTACCCCA	42218	A CA
			TG GGTA GGTGGGGTA		
			AC CCAT CCACCCCAT		
			C C_		
GAM477	LOC201220	5'	TACCCACCCCTACCCCA	42227	A CA
			TG GGTA GGTGGGGTA		
			AC CCAT CCACCCCAT		
			C C_		
GAM478	ATP7B	3'	AGCCAGGGAGCTTGCCACACTC	5504	CGACCT
			GAG CAAGCTCCCTGGCT		
			CTC GTTCGAGGGACCGA		
			ACACC_		
GAM478	MEN1	3'	AGCCCGGGGAGCCTAGGACCAC	28300	CGA_ CAA _
		TCA	TGAG CCT GCTCCCTGG CT		
			ACTC GGA CGAGGGGCC GA		
			ACCA TC_ C		
GAM478	MEN1	3'	AGCCCGGGGAGCCTAGGACCAC	5773	CGA_ CAA _
		TCA	TGAG CCT GCTCCCTGG CT		
			ACTC GGA CGAGGGGCC GA		
			ACCA TC_ C		
GAM478	MEN1	3'	AGCCCGGGGAGCCTAGGACCAC	28287	CGA_ CAA _
		TCA	TGAG CCT GCTCCCTGG CT		
			ACTC GGA CGAGGGGCC GA		
			ACCA TC_ C		
GAM478	MEN1	3'	AGCCCGGGGAGCCTAGGACCAC	28289	CGA_ CAA _
		TCA	TGAG CCT GCTCCCTGG CT		
			ACTC GGA CGAGGGGCC GA		
			ACCA TC_ C		
GAM478	MEN1	3'	AGCCCGGGGAGCCTAGGACCAC	28291	CGA_ CAA _
		TCA	TGAG CCT GCTCCCTGG CT		
			ACTC GGA CGAGGGGCC GA		
			ACCA TC_ C		
GAM478	MEN1	3'	AGCCCGGGGAGCCTAGGACCAC	28293	CGA_ CAA _
		TCA	TGAG CCT GCTCCCTGG CT		
			ACTC GGA CGAGGGGCC GA		
			ACCA TC_ C		
GAM478	MEN1	3'	AGCCCGGGGAGCCTAGGACCAC	28296	CGA_ CAA _
		TCA	TGAG CCT GCTCCCTGG CT		

ACTC GGA CGAGGGGCC GA
 ACCA TC_ C
 GAM478 BCAA 5' CCAGGGAGCCCCGAGCGGCCGC 18508 A _ AA
 GCG CC TC GCTCCCTGG
 ||| || || |||||
 CGC GG AG CGAGGGACC
 C CG CC
 GAM478 DKFZp762E1511 3' AGCCAGGGAGAGTGAGTC 29930 C AG
 GAC TCA CTCCCTGGCT
 ||| ||| |||||
 CTG AGT GAGGGACCGA
 _ GA
 GAM478 FLJ20312 5' AGTTCCGAGCTTGAAGTCACT 19375 C C CCT
 AG GAC TCAAGCTC GGCT
 || ||| ||||| |||
 TC CTG AGTTCGAG TTGA
 A A CC_
 GAM478 KIAA1239 3' AGCCAGGGAGGTGGTAGCCCA 35339 A G TCAAG
 TG GC ACC CTCCCTGGCT
 || ||| |||||
 AC CG TGG GAGGGACCGA
 C A TG_
 GAM478 PPIL3 5' AGCATTGCTTGAGGTTGCCCA 28393 A TCCCTG
 TG GCGACCTCAAGC GCT
 || ||||| |||
 AC CGTTGGAGTTCG CGA
 C TTA_
 GAM478 LOC144962 5' GCCAGGGAGCCCAGGCTC 37791 GAC CAA
 GAGC CT GCTCCCTGGC
 ||| || |||||
 CTCG GA CGAGGGACCG
 _ CC_
 GAM478 LOC150397 3' CCAGGGAGCTTGAAGAGCT 38960 GACC
 AGC TCAAGCTCCCTGG
 ||| |||||
 TCG AGTTCGAGGGACC
 AGA_
 GAM478 LOC152359 3' CCAGAGAGCCTGAAGTTGCTCA 41493 C A C
 TGAGCGAC TCA GCTC CTGG
 ||||| ||| ||| |||
 ACTCGTTG AGT CGAG GACC
 A C A
 GAM478 LOC220522 3' AGCCAGGGAAGCAGCCGCTC 30351 AC CAA _
 GAGCG CT GCT CCCTGGCT
 |||| || ||| |||||
 CTCGC GA CGA GGGACCGA
 C_ _ A
 GAM479 ABCC1 3' GCGCCCAGGGAGGAGTCAGT 11440 C A_
 ACTGACTCC CCCTG CGT
 ||||| |||| |||

			TGACTGAGG GGGAC GCG		
			A CC		
GAM479	ABCC1	3'	GCGCCCAGGGAGGAGTCAGT 21284	C	A_
			ACTGACTCC CCCTG CGT		
			TGACTGAGG GGGAC GCG		
			A CC		
GAM479	ABCC1	3'	GCGCCCAGGGAGGAGTCAGT 21288	C	A_
			ACTGACTCC CCCTG CGT		
			TGACTGAGG GGGAC GCG		
			A CC		
GAM479	FVT1	3'	AATACGTCAGATTGGACCAAGTG 7791	AC	CCC
			CACTG TCC CTGACGTATT		
			GTGAC AGG GACTGCATAA		
			C_ TTA		
GAM479	CCR5	3'	GTCAGAGAGGAGTCAGAGA 6186	A	CCC
			TC CTGACTCC CTGAC		
			AG GACTGAGG GACTG		
			A AGA		
GAM479	KIAA1265	3'	TGCTCAAAGGAAAGTCAGTGG 35035	CC	CC C
			TCACTGACT CC TGA GTA		
			GGTGACTGA GG ACT CGT		
			AA AA _		
GAM479	PDZD2	3'	AATACTGTAGGAAGTCAGTG 39386	CCCC	AC
			CACTGACT CCTG GTATT		
			GTGACTGA GGAT CATAA		
			A__ GT		
GAM479	LOC150372	5'	TGGCAGGAGGACAGTCAGTGA 38943	CC	_ A
			TCACTGACT CC CCTG CG		
			AGTGACTGA GG GGAC GT		
			CA A G		
GAM480	MYOZ1	5'	CCCCAGGGAGAGCTGACCA 22213	C	G A
			TGG CAGTTCTCC CT GGGG		
			ACC GTCGAGAGG GA CCCC		
			A _ _		
GAM480	BIRC8	5'	CCCCGAGAGAGCTGGCCA 27195	CGCTA	
			TGGCCAGTTCTC GGGG		
			ACCGGTCGAGAG CCCC		
			AG__		
GAM480	DKFZp762M136	3'	CCCAGCAAAGAACTGGC 32301	CC	A
			GCCAGTTCT GCT GGG		

CCGTCAAGA CGA CCC
 AA _
 GAM480 FLJ20449 3' CCAGCAGCGAAAAAGCTGGCCA 19485 CTC_ AGG
 TGGCCAGTT CGCT GG
 ||||| ||| ||
 ACCGGTCGA GCGA CC
 AAAA CGA
 GAM481 ADCY7 3' GGCCGGGAAGCCAGTCTCC 6785 CT G
 GGAGAT TGGT TCCCGGCC
 |||| ||| |||||
 CCTCTG ACCG AGGGCCGG
 _ A
 GAM481 BACH2 3' GTTAAGACACCAAAAACTCC 22380 ATC CC
 GGAG TTGGTGTC GGC
 ||| ||||| |||
 CCTC AACCACAG TTG
 AAA AA
 GAM481 BCL6 5' GAGAGCTGACACCAAGTCCTCC 7430 AT CC C
 GGAG CTTGGTGTC GGC CTC
 ||| ||||| ||| |||
 CCTC GAACCACAG TCG GAG
 CT _ A
 GAM481 HNRPF 5' GCCACACCCAAGATCACC 11415 A _ CCC
 GG GATCTTGG TGT GGC
 || ||||| ||| |||
 CC CTAGAACC ACA CCG
 A C _
 GAM481 IHPK3 5' GAGAGCCAGGAGCCCTTCAAGG 27658 TG_ C C
 TCTCC GGAGATCTTGG TCC GGC CTC
 ||||| ||| ||| |||
 CCTCTGGA ACT AGG CCG GAG
 TCCCG A A
 GAM481 NAV2 3' GAGCTGCGGGAACACCGAGACC 30205 AGA _ GCC
 CC GG TCTTGGTGT CCCG CTC
 || ||||| ||| |||
 CC AGAGCCACA GGGC GAG
 CC_ A GTC
 GAM481 NKX3A 3' GAGGGCCGGGCCAGGAGAATCT 12826 _ TGT
 CC GGAGA TCTTGG CCCGGCCCTC
 |||| |||| |||||
 CCTCT AGGACC GGGCCGGGAG
 AAG _
 GAM481 CBX6 3' GAGGGCCTGGACCCAGATCTCC 15576 T T C
 GGAGATCT GG GTCC GGCCCTC
 ||||| || ||| |||||
 CCTCTAGA CC CAGG CCGGGAG
 _ _ T
 GAM481 EVI5 3' AGAGCCAAGATTTTAACCTAGA 12207 T _ CC C
 TCTCC GGAGATCT GGT GTC GGC CT
 ||||| ||| ||| ||| ||

CCTCTAGA CCA TAG CCG GA
 T ATTT AA A
 GAM481 FLJ20967 3' GGGACACCAAGGATCTCC 22615 _
 GGAGATC TTGGTGTCCC
 ||||| |||||
 CCTCTAG AACCACAGGG
 G
 GAM481 FLJ31978 3' GAGGGCCGAGGGAGAAGATTCC 29489 A GGTG _
 GGAG TCTT TCC CGGCCCTC
 ||| ||| || |||||
 CCTT AGAA GGG GCCGGGAG
 _ GA_ A
 GAM481 KIAA0960 3' GAGTTTCTACCAAGATCTCC 44518 TCCC CC
 GGAGATCTTGGTG GG CTC
 ||||| || |||
 CCTCTAGAACCAT CT GAG
 _ TT
 GAM481 MGC35521 3' GAGGTCCCCAAGATCTCC 29703 TGTCCC C
 GGAGATCTTGG GG CCTC
 ||||| || |||
 CCTCTAGAACC CC GGAG
 _ T
 GAM481 RASD2 3' GAAGGCCAGATGAGAAAGGTCT 15606 GG_ CC C
 CC GGAGATCTT TGTC GGCC TC
 ||||| ||| ||| ||
 CCTCTGGAA GTAG CCGG AG
 AGA A_ A
 GAM481 LOC126432 5' GAGGCGAGAACCAAGATCCC 36841 A G C GC
 GG GATCTTGGT TC CG CCTC
 || ||||| || |||
 CC CTAGAACCA AG GC GGAG
 _ _ A _
 GAM481 LOC144866 5' CCAGGATACTGATACTCC 40475 _ TT C
 GGAG ATC GGTGTCC GG
 ||| || ||||| ||
 CCTC TAG TCATAGG CC
 A _ A
 GAM481 LOC146316 5' GAGGGCCAAGGGCTGGAACCTC 30525 A_ TGGT C_
 C GGAG TCT GTCC GGCCCTC
 ||| || ||| |||||
 CCTC AGG CGGG CCGGGAG
 CA T_ AA
 GAM481 LOC150481 3' GAGGGCCGGGATTGATC 38981 TTGGT
 GATC GTCCCGGCCCTC
 ||| |||||
 CTAG TAGGGCCGGGAG
 T_
 GAM481 LOC64744 3' GAGGGCCGGGACAGCTTTCCTC 30951 TCTT _
 TC GAGA GG TGTCCCGGCCCTC
 ||| || |||||

CTCT TC ACAGGGCCGGGAG
 CCTT G
 GAM481 LOC91266 5' GCCAGGCACAGATCCC 32602 A TG T C
 GG GATCT GTG CC GGC
 || |||| ||| ||||
 CC CTAGA CAC GG CCG
 _ _ _ A
 GAM482 C1orf1 3' CATTTTCAGACACTCCTCAGCA 6874 CA CGCC _
 TGT AGGAG TGT TGGAATG
 ||| |||| ||| |||||
 ACG TCCTC ACA ACTTTAC
 AC _ _ G
 GAM482 CSE1L 5' CATTCCTGGCCCCGCCCCCTGC 30990 T A A CCT _
 A TG CA GG GCG GTT GGAATG
 || |||| ||| |||||
 AC GT CC CGC CGG CCTTAC
 _ C C CC_ T
 GAM482 GJB3 3' TCCTTATGCGCACTCTCAACA 23441 CA _ A C TT
 TGT AG G GCGC TG GGA
 ||| || |||| || |||
 ACA TC C CGCG AT CCT
 AC T A T T_
 GAM482 PRKWINK3 3' CATTCCAAATTGCTACCCAACA 30855 CAA _ CCTG
 TGT GG AGCG TTGGAATG
 ||| || |||| |||||
 ACA CC TCGT AACCTTAC
 AC_ A TA__
 GAM482 RNMT 3' ATTCCCCGCCCTCTGACA 9878 _ A CCTGTT
 TGTCA AGG GCG GGAAT
 ||||| |||| |||||
 ACAGT TCC CGC CCTTA
 C _ C____
 GAM482 C20orf126 3' CAACAGGCACTTCCAACA 25134 CAA C
 TGT GGAG GCCTGTTG
 ||| |||| |||||
 ACA CTTT CGGACAAC
 ACC A
 GAM482 FLJ12987 3' TTAACACTTCTTGACA 24807 CGCC
 TGTCAAGGAG TGTTGG
 ||||| |||||
 ACAGTTCTTC ACAATT

 GAM482 PRDM8 5' CCAACACCTCTTGACA 21490 G CGCC
 TGTCAAG AG TGTTGG
 ||||| || |||||
 ACAGTTC TC ACAACC
 _ C____
 GAM482 SEMA5A 5' CACCAGCGCTCCTCGCA 10103 CA C T
 TGT AGGAGCGC TG TG
 ||| ||||| || ||

ACG TCCTCGCG AC AC
 C_ _ C
 GAM482 TU12B1-TY 3' CATTCCATGGGCTCCTTGCCA 18644 T G TGT
 TG CAAGGAGC CC TGGAATG
 || ||||| || |||||
 AC GTTCCTCG GG ACCTTAC
 C _ T_
 GAM482 LOC167040 5' TCCCCAAGGGGCCCTTGACA 42202 A G GTT
 TGTCAAGG GC CCT GGA
 ||||| || ||| |||
 ACAGTTCC CG GGA CCT
 C G ACC
 GAM482 LOC91050 3' TTTGAGAGGCGCTCCTTGCA 32340 T G TG
 TG CAAGGAGCGCCT T GA
 || ||||| ||| ||
 AC GTTCCTCGCGGA A TT
 _ G GT
 GAM483 NAPG 5' ACACCGCACTGCCAATAT 46249 C AGA CC
 ATAT GG AG GCGGTGT
 ||| || || |||||
 TATA CC TC CGCCACA
 A G_ A_
 GAM483 LOC196955 5' AACACCGCTCAGGCCTGA 37925 AGAA ____
 TCGG GCC GCGGTGTT
 ||| || |||||
 AGTC CGG CGCCACAA
 ____ ACT
 GAM484 C5R1 3' CCAGCCTCCCCCAATG 7473 C G G
 CATTG GGGGAG G TGG
 |||| ||||| |||
 GTAAC CCCCTC C ACC
 _ _ G
 GAM484 CYLN2 3' CCTCCCCTCCCCACAGTG 9423 C T
 CATTG GGGGAGGGG GG
 |||| ||||| ||
 GTGAC CCCCTCCCC CC
 A T
 GAM484 DXS1283E 3' CTGGGTCCCTCCCACAA 35065 CG TGG
 TTG GGGAGGGG TCCGG
 || ||||| ||||
 AAC CCCTCCCT GGGTC
 A_ _
 GAM484 RNH 5' CCACCCCTCCCCGCATTG 8845 T
 CA TGCGGGGAGGGGTGG
 || ||||| |||||
 GT ACGCCCCTCCCCACC
 T
 GAM484 RNH 5' CCACCCCTCCCCGCATTG 29994 T
 CA TGCGGGGAGGGGTGG
 || ||||| |||||

GT ACGCCCCTCCCCACC
T
GAM484 C20orf55 3' CCCTCCTCCCCTCCCCAAT 25406 C T TCC
ATTG GGGGAGGGG GG GGG
||||| |||
TAAC CCCCTCCCC CC CCC
_ T T_
GAM484 EDR2 3' CCAGACACCCCTCCCCGCACTG 30337 T G C
CA TGC GGGGAGGGGTG TC GG
|| ||||| ||
GT ACGCCCCTCCCCAC AG CC
C _ A
GAM484 FLJ14800 3' CCCTGGCCCCCTCCCCGTAA 26621 TG C
TTGCGGGGAGGGG GTC GGG
||||| |||
AATGCCCTCCCC CGG CCC
_ T
GAM484 FLJ23342 3' CCCGGACCACCCCTCATCCAGA 23897 GC _
TG CATT GGG GAGGGGTGGTCCGGG
||||| |||||
GTAG CCT CTCCCCACCAGGCC
A_ A
GAM484 FLJ23519 5' CCACCCCTCCCCGCATTG 25975 T
CA TGC GGGGAGGGGTGG
|| |||||
GT ACGCCCCTCCCCACC
T
GAM484 FLJ23519 5' CCACCCCTCCCCGCATTG 34308 T
CA TGC GGGGAGGGGTGG
|| |||||
GT ACGCCCCTCCCCACC
T
GAM484 KIAA0570 3' CCCACCAGGTCCCTCCCACAA 16253 CG _ CC
TTG GGGAGGGG TGGT GGG
||| ||||| |||
AAC CCCTCCCT ACCA CCC
A_ GG _
GAM484 KIAA0607 3' CCCAGACTTCCTCCCC 35925 GT C
GGGGAGGG GGTC GGG
||||| |||
CCCCTCCT TCAG CCC
_ A
GAM484 KIAA0674 5' CCCAGCTTCCTCCCCGCAA 30398 GT CC
TTGCGGGGAGGG GGT GGG
||||| |||
AACGCCCTCCT TCG CCC
_ A_
GAM484 KIAA1473 3' CCCAGCTTGGCCTCCCCGCAATG 34996 G GGT CC
CATTGCGGG AGG GGT GGG
||||| ||| |||

GTAACGCCC TCC TCG CCC
 _ GGT A_
 GAM484 P450RAI-2 3' CCCGGACCTGTACCCCCTCCCC 21267 C T____
 CCAA TTG GGGGAGGGG GGTCCGGG
 ||| ||||| |||||
 AAC CCCCTCCCC CCAGGCCC
 C CATGT
 GAM484 LOC112868 3' CCCAGACCCTGTGTCCCCCA 36078 C GG_ T C
 TG GGGGA GG GGTC GGG
 || |||| || |||| ||
 AC CCCCT TC CCAG CCC
 _ GTG _ A
 GAM484 LOC51644 3' CCCAGAACTTCCTCCCCACAA 18131 C TGG C
 TTG GGGGAGGGG TC GGG
 ||| ||||| || |||
 AAC CCCCTCCTT AG CCC
 A CA_ A
 GAM485 LOC200014 3' TCTATCTTCAGGAAACCCT 42695 T CGCGA C
 AG GGT CT GAAGATAGA
 || ||| || |||||
 TC CCA GA CTTCTATCT
 _ AAG_ _
 GAM486 BACE2 3' CAGCGTCGCCCCCGTGACCCT 29092 TCCGCT
 AGGGTTACG GCGACGCTG
 ||||| |||||
 TCCCAGTGC CGCTGCGAC
 CCC____
 GAM486 LOC254314 5' CAGCATAAAGCAAATGTAACCC 46150 CC GCGAC
 T AGGGTTACGT GCT GCTG
 ||||| ||| |||
 TCCCAATGTA CGA CGAC
 AA AATA_
 GAM487 IFNAR2 3' CCCGAAGAGGACTACAGC 6554 CATC C
 GCT GTAG CCTCTTCGGG
 ||| ||| |||||
 CGA CATC GGAGAAGCCC
 _ A
 GAM487 FLJ14621 5' CCCGAAGAAGAGCCAGAATGAG 26578 _ GTA C _
 CTCAT C GC CT CTTCGGG
 |||| | || |||||
 GAGTA G CG GA GAAGCCC
 A AC_ A A
 GAM487 FLJ22169 3' CCCGAAGAGGGCTCGGAGGATG 23521 GT____
 AGC GCTCATC AGCCCTCTTCGGG
 ||||| |||||
 CGAGTAG TCGGGAGAAGCCC
 GAGGC
 GAM487 RBAK 3' CCCGAAGAATGTAACAAGAAGC 22140 CATC A CC
 A TGCT GT GC TCTTCGGG
 ||| || |||||

ACGA CA TG AGAAGCCC
 AGAA A TA
 GAM488 CDK10 3' TTCCCCACCAACCGCA 27558 TAT T
 TGC GGTGGTGGG GAA
 ||| ||||| |||
 ACG CCACCACCC CTT

 GAM488 CISH 3' GCTGGTTTGAGGGCCACCACTG 29705 TA GGG
 CA TGC TGGTGGT TGAACCAGC
 ||| ||||| |||||
 ACG ACCACCG GTTTGGTCG
 TC GGA
 GAM488 CISH 3' GCTGGTTTGAGGGCCACCACTG 14972 TA GGG
 CA TGC TGGTGGT TGAACCAGC
 ||| ||||| |||||
 ACG ACCACCG GTTTGGTCG
 TC GGA
 GAM488 DNC11 3' ACCCAAATTCACCACAGCA 43775 A
 TGCT TGGTGG TGGGT
 ||| ||||| |||
 ACGA ACCACT ACCCA
 C TAAA
 GAM488 MHC2TA 3' GCTGGTCCACTCAGTCCATAGC 5780 TGG A
 A TGCTATGG TGGGTG ACCAGC
 ||||| ||||| |||||
 ACGATACC ACTCAC TGGTCG
 TG_ C
 GAM488 POU2AF1 3' CTGGCTCACCCACCTGCTAATA 12891 _ _ A
 GCA TGCTAT GGT GGTGGGTGA CCAG
 ||||| ||| ||||| |||||
 ACGATA TCG CCACCCACT GGTC
 A T C
 GAM488 SCD 3' TTCAAGCCCCACCACATAGCA 11497 G
 TGCTATG TGGTGGG TGAA
 ||||| ||||| |||
 ACGATAC ACCACCC ACTT
 _ CGA
 GAM488 SLC6A8 3' GCTCACCTCTGGTAGCCATAGC 12151
 A TGCTATGGT GGTGGGT
 ||||| |||||
 ACGATACCG CCACTCG
 ATGGTCT
 GAM488 SUFU 3' CTGGCCTTCCCCCACCACAGCA 18253 A T TGAA
 TGCT TGGTGG GGG CCAG
 ||| ||||| ||| |||
 ACGA ACCACC CCC GGTC
 C _ TTCC
 GAM488 DCTN4 3' GCTAGTCAGTATGCACCACCAC 33667 A G A_ C
 AG CT TGGTGGTG GTG AC AGC
 || ||||| ||| || |||

			GA ACCACCAC TAT TG TCG		
			C G GAC A		
GAM488	DKFZP434P0111	3'	GCTAACCTTGGCCACCACCA 33458	G ACC_	
			TGGTGGTGG TGA AGC		
			ACCACCACC GTT TCG		
			G CCAA		
GAM488	EFA6R	3'	GCTAGCATCAGCACCACCTATAG 17625	__ AACC	
	CA		TGCTATGGTGGTG GGTG AGC		
			ACGATATCACCAC CTAC TCG		
			GA GA__		
GAM488	HEMK	3'	TCCCCACCACCACCAGCA 18273	A_ T	
			TGCT TGGTGGTGGG GA		
			ACGA ACCACCACCC CT		
			CC _		
GAM488	KIAA1615	3'	CTGGTTATATTCCACCATAACA 34085	C TGG A	
			TG TATGGTGG GTGA CCAG		
			AC ATACCACC TATT GGTC		
			A TTA _		
GAM488	UQCR	3'	GCTAGCTCCTCCCACCTCAGCA 13711	AT T T ACC	
			TGCT GGTGG GGG GA AGC		
			ACGA CCACC CTC CT TCG		
			CT _ _ CGA		
GAM488	ZF5128	3'	GCCAGTTCACCCACAGATCA 15670	G_ CA	
			TGGT GTGGGTGAAC GC		
			ACTA CACCCACTTG CG		
			GA AC		
GAM488	LOC152273	5'	GCTGGCTGCATTCCACCATAGC 39247	TG AA_	
			GCTATGGTGG GGTG CCAGC		
			CGATACCACC TTAC GGTCG		
			_ GTC		
GAM488	LOC157381	5'	CTAATCATTCACCACAGCA 41790	ATG ACC	
			TGCT GTGGTGGGTGA AG		
			ACGA CACCACTTACT TC		
			_ AA_		
GAM488	LOC157753	3'	GCTGGTTCTCACACCAGCAGCA 39661	AT G GGT	
			TGCT G TGGTG GAACCAGC		
			ACGA C ACCAC CTTGGTCG		
			_ G ACT		
GAM488	LOC221250	5'	GCCTCGCCACCATCAGCA 44121	_ _	
			TGCT ATGGTGGTG GGT		

			ACGA TACCACCGC CCG	
			C T	
GAM489	ABR	3'	ACTTGAAAGACTGCAATA 6747	A C_
			TATTGCAG TC TCGGGT	
			ATAACGTC AG AGTTCA	
			_ AA	
GAM489	ABR	3'	ACTTGAAAGACTGCAATA 22492	A C_
			TATTGCAG TC TCGGGT	
			ATAACGTC AG AGTTCA	
			_ AA	
GAM489	APOL1	3'	ACATTGGAGCCTGCAATA 9731	ATC G
			TATTGCAG CTC GGTGT	
			ATAACGTC GAG TTACA	
			C_ G	
GAM489	FGFR2	3'	ACACCCACTCACTTTGCAATA 5637	TCCTC_
			TATTGCAGA GGGTGT	
			ATAACGTTT CCCACA	
			CACTCA	
GAM489	FGFR2	3'	ACACCCACTCACTTTGCAATA 23233	TCCTC_
			TATTGCAGA GGGTGT	
			ATAACGTTT CCCACA	
			CACTCA	
GAM489	FGFR2	3'	ACACCCACTCACTTTGCAATA 23240	TCCTC_
			TATTGCAGA GGGTGT	
			ATAACGTTT CCCACA	
			CACTCA	
GAM489	FGFR2	3'	ACACCCACTCACTTTGCAATA 23287	TCCTC_
			TATTGCAGA GGGTGT	
			ATAACGTTT CCCACA	
			CACTCA	
GAM489	FGFR2	3'	ACACCCACTCACTTTGCAATA 23293	TCCTC_
			TATTGCAGA GGGTGT	
			ATAACGTTT CCCACA	
			CACTCA	
GAM489	FGFR2	3'	ACACCCACTCACTTTGCAATA 23299	TCCTC_
			TATTGCAGA GGGTGT	
			ATAACGTTT CCCACA	
			CACTCA	
GAM489	HDAC4	3'	GGACACCCAGCGTGCAA 12666	GATC C
			TTGCA CT GGGTGTCC	

			AACGT GA CCCACAGG	
			GC__ _	
GAM489	HTRA3	3'	ACACCCATCTGCAGTA 42937	CCTC
			TATTGCAGAT GGGTGT	
			ATGACGTCTA CCCACA	

GAM489	APOL2	3'	AACTGGAGCCTGCAATA 25158	ATC G
			TATTGCAG CTC GGTGT	
			ATAACGTC GAG TCACA	
			C__ G	
GAM489	FLJ10900	5'	ACAGCAAAGGATTTGCAA 32668	CGG _
			TTGCAGATCCT G TGT	
			AACGTTTAGGA C ACA	
			AA_ G	
GAM489	FLJ12154	5'	GCACAGGATCTGCAA 22465	CGG
			TTGCAGATCCT GTGT	
			AACGTCTAGGA CACG	

GAM489	GIT2	3'	ATGTTTGAGGACCTGCAATA 27682	A TG
			TATTGCAG TCCTCGGG T	
			ATAACGTC AGGAGTTT A	
			C GT	
GAM489	GIT2	3'	ATGTTTGAGGACCTGCAATA 27695	A TG
			TATTGCAG TCCTCGGG T	
			ATAACGTC AGGAGTTT A	
			C GT	
GAM489	GIT2	3'	ATGTTTGAGGACCTGCAATA 16600	A TG
			TATTGCAG TCCTCGGG T	
			ATAACGTC AGGAGTTT A	
			C GT	
GAM489	KIAA0084	3'	GGACACCCTGGGCTACAA 33806	C A TC
			TTG AG TCC GGGTGTCC	
			AAC TC GGG CCCACAGG	
			A _ T_	
GAM489	KIAA0157	3'	GACACTTTATCTGCAA 25898	CCTC
			TTGCAGAT GGGTGT	
			AACGTCTA TTCACAG	
			T__	
GAM489	KIAA0258	3'	ACCCAGGAGCTGCAATA 16640	A C
			TATTGCAG TCCT GGGT	

			ATAACGTC AGGA CCCA		
			G _		
GAM489	SSB-3	3'	GA	28103	A CG T
			TATTGCAG TCCT GG GTC		
			ATAACGTC AGGA TT CAG		
			_ AA _		
GAM489	LOC143173	5'	GGAGCCGTGAGGATCCACAGTA	30270	CA _ G
			TATTG GATCCTCG GGT TCC		
			ATGAC CTAGGAGT CCG AGG		
			AC G _		
GAM489	LOC144266	5'	GGAGTTTGAGGACATGCAATA	37710	GA GG G
			TATTGCA TCCTCG T TCC		
			ATAACGT AGGAGT G AGG		
			AC TT _		
GAM489	LOC145188	3'	ACAATGTGGGACGCTGCAATA	37809	A_ CGGG
			TATTGCAG TCCT TGT		
			ATAACGTC AGGG ACA		
			GC TGTA		
GAM489	LOC151701	5'	GGCAAGAATCTGCAAT	41386	C CGGG
			ATTGCAGAT CT TGTC		
			TAACGTCTA GA ACGG		
			A _ _ _		
GAM489	LOC92912	3'	GGTTACAAGGATTTGCAATA	35084	CGG T
			TATTGCAGATCCT GTG CC		
			ATAACGTTTAGGA CAT GG		
			A _ T		
GAM490	ADCY2	3'	ACCTCTCATCAGCCCAGGTCCC	32432	T C GT_
	A		TGGGA CCTGGGC TGG GAGGT		
			ACCCT GGACCCG ACT CTCCA		
			_ _ ACT		
GAM490	MYO3A	5'	GCCCAGGCCAGGGCCCCA	30196	AT
			TGGG CCTGGGCCTGGGT		
			ACCC GGACCCGGACCCG		
			CG		
GAM490	PLA2G2D	3'	ACCTCACCCAGATATCATCC	14766	TCC GC_
			GGA TGG CTGGGTGAGGT		
			CCT ACT GACCCACTCCA		
			_ ATA		
GAM490	DKFZP564O0423	3'	ACCCAACACCAGAATCCCA	44062	C GCC
			TGGGAT CTGG TGGGT		

ACCCTA GACC ACCCA
 A ACA
 GAM490 FLJ14564 3' ACTCAGGCCAGGTCCCA 37594 T
 TGGGA CCTGGGCCTGGGT
 |||| |||||
 ACCCT GGACCCGGACTCA

 —
 GAM490 KIAA0514 3' ACCTAGGAGCCCAGGACCCC 16201 A —
 GGG TCCTGGGC CTGGGT
 || ||||| |||||
 CCC AGGACCCG GATCCA
 C AG
 GAM490 KIAA1522 3' CCCACCCCCTAGGATCC 32417 CCT A
 GGATCCTGGG GGGTG GG
 ||||| |||||
 CCTAGGATCC CCCAC CC
 — C
 GAM490 KIAA1535 3' GCCCAGGCCCATGACCCCA 38766 A C
 TGGG TC TGGGCCTGGGT
 |||| || |||||
 ACCC AG ACCCGGACCCG
 C T
 GAM490 KIAA1656 3' ACCTGGTCAAGGCCAGGATCCC 32725 G G TG
 A TGGGATCCTGG CCT GG AGGT
 ||||| ||||| |||||
 ACCCTAGGACC GGA CT TCCA
 — A GG
 GAM490 MAD4 3' CCCAACCCTGGATCCCA 13169 T CC
 TGGGATCC GGG TGGG
 ||||| |||||
 ACCCTAGG CCC ACCC
 T A_
 GAM490 NKX2B 3' CCCAGGCCAGGCCCA 8342 AT
 TGGG CCTGGGCCTGGG
 |||| |||||
 ACCC GGACCCGGACCC
 C_
 GAM490 TOM1 3' ACCCTGCAGCCCAGGTCCCA 11984 AT CT_
 TGGG CCTGGGC GGGT
 |||| ||||| |||||
 ACCC GGACCCG CCA
 CT ACGT
 GAM490 TP53TG3 3' ACCCCACCCAGGCTGCTTCCCA 17668 TCCTG A
 TGGGA GGCCTGGGTG GGT
 |||| ||||| |||||
 ACCCT TCGGACCCAC CCA
 TCG_ C
 GAM490 LOC149267 3' CCTCACCCAAGAAACCCCC 28830 ATCCT GC_ _
 GGG GG CT GGGTGAGG
 || || || |||||

CCC CC GA CCCACTCC
 _____ AAA A
 GAM490 LOC150960 5' CCTCACCCAACGATCCC 39030 CTGGGCC
 GGGATC TGGGTGAGG
 ||||| |||||
 CCCTAG ACCCACTCC
 CA_____

GAM490 LOC164714 3' CACTGAGGCCAGGCTCCCA 42175 T G
 TGGGA CCTGGGCCT GTG
 ||||| ||||| |||||
 ACCCT GGACCCGGA TCAC
 C G

GAM490 LOC203292 3' ACCTCACCGTGCAGGAATCCCA 43499 _ G CTG
 TGGGAT CCTG GC GGTGAGGT
 ||||| ||||| |||||
 ACCCTA GGAC TG CCACTCCA
 A G ____

GAM490 LOC257364 3' GTCCAAACCCAGGATCTCA 45524 CC
 TGGGATCCTGGG TGGGT
 ||||| |||||
 ACTCTAGGACCC ACCTG
 AA

GAM491 CSNK1G2 3' GCCTCGGCTAACCAAAATGCTG 7007 ____ CTG
 CACC TGCGGCG TGG GGC GC
 ||||| ||| ||| ||
 ACGTCGT ACC TCG CG
 AAA AA||| GCTC

GAM491 KIAA0669 5' AGCCAAGGCCTGCTGACCGCGC 16624 _ TG C
 CGA TCGGTGCGG CG GGGCCT GGCT
 ||||| || ||||| |||||
 AGCCGCGCC GT TCCGGA CCGA
 A CG A

GAM491 ZFP36L2 5' AGCCCGGCCACGCCGCCCC 13751 T GG TC
 GG GCGGCGT GGCC GGCT
 || ||||| ||||| |||||
 CC CGCCGCA CCGG CCGA
 C _ C_

GAM491 LOC147929 5' GCCAAGGCCCCGCACCCA 38421 C C C
 TG GG GTGGGGCCT GGC
 || || ||||| ||||| |||||
 AC CC CGCCCCGGA CCG
 _ A A

GAM492 APG5L 5' GCTGCCAGGGATCCG 11264 CTA AC
 CGGATCCC TG GCAGC
 ||||| || |||||
 GCCTAGGG AC CGTCG

GAM492 CARD4 3' GCGCCAAGACTCAGGGGATCGG 12740 G A_____ A
 CCG ATCCCCT TG CGC
 ||| ||||| || |||

GGC TAGGGGA AC GCG
_ CTCAGA C
GAM492 CYLN2 3' GTGGAGGCAGAGGGGATCCGG 9424 A ACGCA
CCGGATCCCCT TG GC
||||||| || ||
GGCCTAGGGGA AC TG
G GGAGG
GAM492 DNASE1 5' TGCCTGTGCAGGATCCGG 11716 CCTA A _
CCGGATCC TG CGCAG CA
||||| || ||||| ||
GGCCTAGG AC GTGTC GT
_ _ C
GAM492 KCNN4 5' GTGCTGCGAGGTGGGGGACCC 8039 A GA
GG TCCCCTAT CGCAGCAC
|| ||||| |||||
CC AGGGGGTG GCGTCGTG
C GA
GAM492 ARL8 5' GCCGCGGTGGGGGACCCGG 44764 A GA A
CCGG TCCCCTAT CGC GC
||| ||||| ||| ||
GGCC AGGGGGTG GCG CG
C _ C
GAM492 C17orf31 3' GTACCGTGTAGGGGAGCC 19007 A G CA
GG TCCCCTAT ACG GC
|| ||||| ||| ||
CC AGGGGATG TGC TG
G _ CA
GAM492 DGKD 3' GTGCTGTGGGCCAGGGAATCC 29887 C ATGA
GGAT CCCT CGCAGCAC
||| ||| |||||
CCTA GGA GTGTCGTG
A CCGG
GAM492 KIAA1649 3' GTGCTACGCAGGTGAGGGGATC 26110 A__ A C
CGG CCGGATCCCCT TG CG AGCAC
||||||| || |||||
GGCCTAGGGGA AC GC TCGTG
GTGG _ A
GAM492 MBC3205 5' GTGCTGCGGATTGAGGTCCCGG 27225 ATCC ATGA_
CCGG CCT CGCAGCAC
||| ||| |||||
GGCC GGA GCGTCGTG
CT__ GTTAG
GAM492 TOB2 3' GTGCTGCGCTCTTGGGCC 45769 ATC TAT _
GG CCC GA CGCAGCAC
|| ||| || |||||
CC GGG CT GCGTCGTG
C__ TT_ C
GAM492 TOM1 3' GCTGCAGTGGGATCTGG 11987 _ ATGAC
CCGGATCCC CT GCAGC
||||||| || |||||

GGTCTAGGG GA CGTCG
T _____
GAM492 LOC144667 5' TGCTTACTCAGGGATCCGG 40452 CTA CGC
CCGGATCCC TGA AGCA
||||||| ||| ||||
GGCCTAGGG ACT TCGT
_____ CAT
GAM492 LOC220370 3' GTGCTGTGCAGCAAGGAGCCC 44599 A_ CCTA A
GG TCC TG CGCAGCAC
|| ||| || |||||
CC AGG AC GTGTCGTG
CG AACG _
GAM492 LOC222255 5' GCACCGCGCGGGGAACCCGG 45272 A_ TAT A A_
CCGG TCCCC G CGC GC
|||| |||| | ||| ||
GGCC AGGGG C GCG CG
CA _____ CCA
GAM492 LOC253070 3' GCGCTAGGAGGGGTCCGG 46354 T A_ A
CCGGA CCCCT TG CGC
|||| |||| || |||
GGCCT GGGGA AT GCG
_ GG C
GAM492 LOC257054 3' GTGCTGCGGGCGAGGGCCCCGG 45783 ATC ATGA
CCGG CCCT CGCAGCAC
|||| |||| |||||
GGCC GGGA GCGTCGTG
CC_ GCGG
GAM492 LOC93259 5' CTGCTTCCAGGGGGTCC 35558 AT C
GGATCCCCT GA GCAG
||||||| || ||||
CCTGGGGGA CT CGTC
C_ T
GAM493 EIF1A 5' TCCCTCGTGTGCGCCCTCGGA 42726 ACAGA CCA
TCC GCGACGCGA GGA
||| ||||| |||
AGG CGCTGTGCT CCT
CTCCC C_
GAM493 FCGR2A 3' TTCCTATGCCCTCTCTGTGGA 38701 CGAC ACC
TCCACAGAG GCG AGGAA
||||||| ||| ||||
AGGTGTCTC CGT TCCTT
TCC_ A_
GAM493 FCN2 3' CCTGACTGTGCTCTGTG 17952 GAC AC
CACAGAGC GCG CAGG
||||||| ||| ||||
GTGTCTCG TGT GTCC
_____ CA
GAM493 PYGB 3' CCAGGCAGCGGCTCTGTGGA 8766 GA GA A
TCCACAGAGC CGC CC GG
||||||| ||| || ||

AGGTGTCTCG GCG GG CC
 _ AC A
 GAM493 SLC22A5 5' CCTGGTCGTGCGCCCTATG 9025 C A A
 CA AG GCG CGCGACCAGG
 || ||| |||||
 GT TC CGC GTGCTGGTCC
 A C _
 GAM493 SLC9A6 3' TTCCTGGTTGCACTCTGTAGA 13054 C CGAC
 TC ACAGAG GCGACCAGGAA
 || ||||| |||||
 AG TGTCTC CGTTGGTCCTT
 A A _
 GAM493 SRGAP1 3' CCTGTGTTCTCCTCTGTGGA 35756 C CGC _
 TCCACAGAG GA GAC CAGG
 ||||| || |||
 AGGTGTCTC CT TTG GTCC
 _ C _ T
 GAM493 TRPC6 3' TTCCTTCTTGCTGCTCTGTGG 10981 AC CC
 A TCCACAGAGCG GCGA AGGAA
 ||||| ||| |||||
 AGGTGTCTCGT CGTT TCCTT
 C _ CT
 GAM493 C7orf13 5' TCCTGGCCCTTCTCTGTGGA 26344 CGACGCGA
 TCCACAGAG CCAGGA
 ||||| |||||
 AGGTGTCTC GGTCTT
 TTCCC _
 GAM493 DKFZp547E052 3' TTCCTGGTGCTTGTGTTCCATG 26032 CA AC _ G
 CA GAGCG GC ACCAGGAA
 || |||| |||||
 GT CTTGT CG TGGTCCTT
 AC GTT _
 GAM493 DKFZP761I2123 3' TCCCAAGTTCCCCTGCTCTGTG 25464 ACGC CA _
 CACAGAGCG GAC GGA
 ||||| ||| |||
 GTGTCTCGT TTG CCT
 CCCC AAC
 GAM493 FLJ14082 3' CCCGGTGGGTCATTCTGTGGA 24608 C G G A
 TCCACAGAG GAC C ACC GG
 ||||| ||| ||| ||
 AGGTGTCTT CTG G TGG CC
 A G _ C
 GAM493 FLJ22169 5' TCCTGGTCAGCTGCGTGGA 23524 AGA AC _
 TCCAC GCG GC GACCAGGA
 |||| ||| |||||
 AGGTG CGT CG CTGGTCCT
 _ _ A
 GAM493 KIAA0133 3' TCCTGTGTTAGCTCTGTG 16609 _ GACC
 CACAGAGC GACGC AGGA
 ||||| |||| |||

		GTGTCTCG TTGTG TCCT	
		A ____	
GAM493	KIAA0152 3'	TTCCCATCCTCTCTGTGGA 16341	C CGC CCA
		TCCACAGAG GA GA GGAA	
		AGGTGTCTC CT CT CCTT	
		T C__ AC_	
GAM493	KIAA1858 3'	CCTGAGATGGTCCACTCTGTGG 33329	C_ G AC_
		CCACAGAG GAC CG CAGG	
		GGTGTCTC CTG GT GTCC	
		AC _ AGA	
GAM493	LRP1B 3'	TTCCCAGTCACATCCATTTTGT 20641	C_ CGC CA
	GGA	TCCACAGAG GA GAC GGAA	
		AGGTGTTTT CT CTG CCTT	
		AC ACA AC	
GAM493	PIGQ 3'	CCTGGAGAGGTCGCTTTGTG 10399	GCGA
		CACAGAGCGAC CCAGG	
		GTGTTTCGCTG GGTCC	
		GAGA	
GAM493	SNPH 5'	TCCTGGTCCTGCTCCAGGA 16302	ACA ACGC
		TCC GAGCG GACCAGGA	
		AGG CTCGT CTGGTCCT	
		AC_ C__	
GAM493	THEA 3'	CCTGGTTGCAGCCACGTAGA 32950	C AGA GAC
		TC AC GC GCGACCAGG	
		AG TG CG CGTTGGTCC	
		A CAC A__	
GAM493	LOC115110 5'	TCCTGGTCACGATCTGGTGA 35513	CA GCGA C
		TC CAGA CG GACCAGGA	
		AG GTCT GC CTGGTCCT	
		TG A__ A	
GAM493	LOC147138 5'	TTCCTGGTCACCCTGCCTCGGA 38309	AC A ACGC
		TCC AG GCG GACCAGGAA	
		AGG TC CGT CTGGTCCTT	
		C_ _ CCCA	
GAM493	LOC151121 5'	TCCTGGTCCTGTTCTCTG 39053	C C
		CAGAG GACG GACCAGGA	
		GTCTC TTGT CTGGTCCT	
		_ C	
GAM493	LOC157280 3'	CCCGGCTGTGGCGCTTCTGTGG 36592	_ A A A
	A	TCCACAGA GCG CGCG CC GG	

		AGGTGTCT CGC GTGT GG CC	
		T G C C	
GAM493	LOC158857 5'	TCCTGAAGCCATCTGTGGA 42032	GCGAC GAC
		TCCACAGA GC CAGGA	
		AGGTGTCT CG GTCCT	
		AC__ AA_	
GAM493	LOC159049 5'	TCCTGAAGCCATCTGTGGA 42058	GCGAC GAC
		TCCACAGA GC CAGGA	
		AGGTGTCT CG GTCCT	
		AC__ AA_	
GAM493	LOC170261 5'	CCTGGTTGGGCGGCCCTG 40183	A GA _
		CAG GC CGC GACCAGG	
		GTC CG GCG TTGGTCC	
		C _ GG	
GAM493	LOC205952 5'	TCCTGGTTTGGCGCTTTGTG 43611	A C
		CACAGAGCG CG GACCAGGA	
		GTGTTTCGC GT TTGGTCCT	
		G _	
GAM493	LOC221756 3'	TTCCTGTCCTCTGCTCTGTGGA 44242	ACGC C
		TCCACAGAGCG GAC AGGAA	
		AGGTGTCTCGT CTG TCCTT	
		CTC_ _	
GAM493	LOC255448 3'	CCCGGCTGTGGCGCTTCTGTGG 45402	_ A A A
	A	TCCACAGA GCG CGCG CC GG	
		AGGTGTCT CGC GTGT GG CC	
		T G C C	
GAM493	LOC256586 5'	CCCGGCTCCCTCGCTCTGCAGG 45513	A_ CGC _ A
		CC CAGAGCGA GA CC GG	
		GG GTCTCGCT CT GG CC	
		AC CC_ C C	
GAM493	LOC257051 5'	CCTGGTTGGGCGGCCCTG 46083	A GA _
		CAG GC CGC GACCAGG	
		GTC CG GCG TTGGTCC	
		C _ GG	
GAM493	LOC91344 5'	TCCTGGCAGCTCTGTGG 32678	GACGCGA
		CCACAGAGC CCAGGA	
		GGTGTCTCG GGCCT	
		AC_____	
GAM494	ATP11A 3'	ACCCACGCCGCACCTCATCCGT 37801	AA C AC_ AC
	GCA	TGCA GA GAGG GC GGGT	

ACGT CT CTCC CG CCCA
 GC A ACGC CA
 GAM494 ATP7A 3' TGCATCCTTGTCTTGCA 5497 A C
 TGCAA GACGAGGA GCA
 ||||| ||||| |||
 ACGTT CTGTTCTCT CGT
 C A
 GAM494 BPAG1 3' ACCCACACGCAGTCTTTGCA 17809 GAGGA CAC
 TGCAAAGAC CG GGGT
 ||||| || |||
 ACGTTTCTG GC CCCA
 AC__ ACA
 GAM494 EPHA8 3' ACCAGGCCACCCCTCGTCTCTG 21742 A AC__ ACG
 C GCA AGACGAGG GC GGT
 ||| ||||| || |||
 CGT TCTGCTCC CG CCA
 C CACC GA_
 GAM494 WDR1 3' TCATGACCCTCGTCTCTGCA 18956 A ACG C
 TGCA AGACGAGG CA GG
 ||| ||||| || |||
 ACGT TCTGCTCC GT CT
 C CA_ A
 GAM494 FLJ10781 3' TACCCAACTGTCACCATCTTTG 20138 CGAG CAC
 CA TGCAAAGA GACG GGGTA
 ||||| ||| |||||
 ACGTTTCT CTGT CCCAT
 ACCA CAA
 GAM494 FLJ10781 3' ACCAAACTGTCACCATCTTTGC 20131 CGAG CACG
 A TGCAAAGA GACG GGT
 ||||| ||| |||
 ACGTTTCT CTGT CCA
 ACCA CAAA
 GAM494 HRH3 3' ACCCGTGCCACGCGCTCTGCA 14106 A A AGGAC
 TGCA AG CG GCACGGGT
 ||| || || |||||
 ACGT TC GC CGTGCCCA
 C _ GCAC_
 GAM494 KIAA0450 5' ACCCATCTGTTCTCGTC 16025 C C__
 GACGAGGA GCA GGGT
 ||||| || |||
 CTGCTCCT TGT CCCA
 _ CTA
 GAM494 KIAA1492 3' CTGGCCACCATCATCTTTGCA 32226 C _ AC A
 TGCAAAGA GA GG GC CGG
 ||||| || || |||
 ACGTTTCT CT CC CG GTC
 A A AC _
 GAM494 RIN3 3' ACCCACCCCATCCTCGGTCTTT 24229 _ CGCAC_
 GCA TGCAAAGAC GAGGA GGGT
 ||||| |||| |||

ACGTTTCTG CTCCT CCCA
 G ACCCCA
 GAM494 LOC115110 3' TACCCGCCTGTGTCGCTTTTGC 35512 AGAC _ _
 A TGCAA GAG GACGCA CGGGTA
 |||| | |||| ||||
 ACGTT TTC CTGTGT GCCCAT
 _ G CC
 GAM494 LOC196500 3' ACCCACCTCGTTTCCGCA 42384 AA ACGCAC
 TGC AGACGAGG GGGT
 || ||||| ||
 ACG TTTGCTCC CCCA
 CC A _
 GAM494 LOC197287 3' ACCCACGCCGCACCTCATCCGT 30520 AA C AC_ AC
 GCA TGCA GA GAGG GC GGGT
 ||| || ||| ||
 ACGT CT CTCC CG CCCA
 GC A ACGC CA
 GAM494 LOC91782 3' ACCCGTGCACCTGTCCTGC 33335 AA G AC
 GCA GAC AGG GCACGGGT
 || ||| || |||||
 CGT CTG TCC CGTGCCCA
 C_ _ A_
 GAM495 FLJ22056 5' CACACCGGTGACGCCGACGG 22867 A TT A A
 TC TCGGCGTC CC GG TGTG
 || ||||| || ||||
 GG AGCCGCAG GG CC ACAC
 C T_ _ _
 GAM495 FLJ30567 3' TCACATCCCAGAAGAACT 29631 CG CA
 GG TCTTC GGATGTGA
 || |||| |||||
 TC AGAAG CCTACACT
 AA AC
 GAM495 LOC150142 5' TCACATCCTGACCCCGCCGGCG 38855 AT TCTTC
 A TC CGGCG CAGGATGTGA
 || |||| |||||
 AG GCCGC GTCCTACACT
 CG CCCA_
 GAM495 LOC199858 3' TCACATCCCAACTCCAATG 42642 C C CTTCCA
 CAT GG GT GGATGTGA
 ||| || |||||
 GTA CC CA CCTACACT
 A T AC_
 GAM496 ACADSB 3' TTATTATTGCACTTTATCCTGA 7316 A AC T
 TCAGGA AA GGTGT GTAATAA
 ||||| || |||| |||||
 AGTCCT TT TCACG TATTATT
 A _ T
 GAM496 COLQ 3' CATCACCATTTTTCCTGA 12233 C T
 TCAGGAAAAA GGTG TG
 ||||| |||| ||

			AGTCCTTTTT CCAC AC	
			A T	
GAM496	COLQ	3'	CATCACCATTTTCTGA 27865	C T
			TCAGGAAAAA GGTG TG	
			AGTCCTTTTT CCAC AC	
			A T	
GAM496	COLQ	3'	CATCACCATTTTCTGA 27859	C T
			TCAGGAAAAA GGTG TG	
			AGTCCTTTTT CCAC AC	
			A T	
GAM496	COLQ	3'	CATCACCATTTTCTGA 27853	C T
			TCAGGAAAAA GGTG TG	
			AGTCCTTTTT CCAC AC	
			A T	
GAM496	COLQ	3'	CATCACCATTTTCTGA 27862	C T
			TCAGGAAAAA GGTG TG	
			AGTCCTTTTT CCAC AC	
			A T	
GAM496	COLQ	3'	CATCACCATTTTCTGA 27856	C T
			TCAGGAAAAA GGTG TG	
			AGTCCTTTTT CCAC AC	
			A T	
GAM496	FRAP1	3'	CATCACGTTTTTCTGA 11404	G T
			TCAGGAAAAACG TG TG	
			AGTCTTTTTTGC AC AC	
			_ T	
GAM496	GALNT1	3'	ATTAAGACATTTTCTGA 21722	ACG G
			TCAGGAAAA GTGTT TAAT	
			AGTCCTTTT TACAG ATTA	
			_ A	
GAM496	LFG	3'	CGGCCTCCCGTCTTCTGA 37693	A T_
			TCAGGAAA ACGG GTTG	
			AGTCCTTT TGCC CGGC	
			C CTC	
GAM496	PCDHA9	3'	ACTACATGTTATGTTCTGA 15208	_ G T
			TCAGGAAA AACG TGT GT	
			AGTCCTTT TTGT ACA CA	
			GTA _ T	
GAM496	RP2	3'	ACAACATCCGCCTCCTGG 13789	AAAA _
			TCAGGA CGG TGTTGT	

			GGTCCT	GCC ACAACA		
			CC_	T		
GAM496	SRGAP1	5'	TATTACATTCTTTCCTGA	35759	AAAC	TGT
			TCAGGAA	GG TGTAAATA		
			AGTCCTT	TC ACATTAT		
			____	TT_		
GAM496	SURF4	3'	ACACACCACTTTCCTGA	27011	AAC	T
			TCAGGAAA	GGTGT GT		
			AGTCCTTT	CCACA CA		
			CA_	_		
GAM496	ABLIM	3'	ACAGAACCCTTTTCCTGA	8111	AC	G
			TCAGGAAAA	GGT TTGT		
			AGTCCTTTT	CCA GACA		
			C_	A		
GAM496	ABLIM	3'	ACAGAACCCTTTTCCTGA	13544	AC	G
			TCAGGAAAA	GGT TTGT		
			AGTCCTTTT	CCA GACA		
			C_	A		
GAM496	AKAP11	3'	ATTACGTTTTTCATTTTTTCTGA	18367	C	TGT
			TCAGGAAAAA	GG TGTAAAT		
			AGTCTTTTTT	CT GCATTA		
			A	TTT		
GAM496	DKFZP761C169	3'	TGCAACATTTCTCTGA	33679	_	AAACG
			TCAG GAA	GTGTTGTA		
			AGTC CTT	TACAACGT		
			T	_____		
GAM496	FLJ10737	3'	ACAATAAACCTTTCCTGA	20064	AAC	__
			TCAGGAAA	GGT GTTGT		
			AGTCCTTT	CCA TAACA		
			__	AA		
GAM496	FLJ11273	3'	ATTACAACAAGTTTCTC	20394	A	GG
			GA AAAC	TGTTGTAAT		
			CT TTTG	ACAACATTA		
			C	A_		
GAM496	FLJ11710	3'	TTATCATGATGCTGTCCCTCCT	24278	AAA	TG A
	GA		TCAGGA	ACGGTGT TATAA		
			AGTCCT	TGTCGTA A TATT		
			CCC	GT C		
GAM496	FLJ20189	3'	ATTATAACATTCTTCC	19280	AAAC	
			GGAA	GGTGTGTAAT		

			CCTT TTACAATATTA		
			C___		
GAM496	FLJ20668	3'	TACTGACACATTTTCCTGA	19589	CG _
			TCAGGAAAAA GTGTT GTA		
			AGTCCTTTTT CACAG CAT		
			A_ T		
GAM496	FLJ20694	3'	ATTACTGCCCTTTTCCTGA	19606	AC T T
			TCAGGAAAAA GG GT GTAAT		
			AGTCCTTTTT CC CG CATTA		
			___ _ T		
GAM496	FXYD3	3'	TTATTACAAGATCTTTCC	12594	AAC G
			GGAAA GGT TTGTAATAA		
			CCTTT CTA AACATTATT		
			___ G		
GAM496	FXYD3	3'	TTATTACAAGATCTTTCC	22437	AAC G
			GGAAA GGT TTGTAATAA		
			CCTTT CTA AACATTATT		
			___ G		
GAM496	HZFW1	3'	TACAGTACTTCCTGA	24916	AAAAC
			TCAGGA GGTGTTGTA		
			AGTCCT TCATGACAT		

GAM496	KIAA0237	3'	TGCAGCATCTTTCCT	16456	AAC
			AGGAAA GGTGTTGTA		
			TCCTTT CTACGACGT		

GAM496	KIAA0435	5'	TACTCACCACCATTTCCTGA	16723	AAC_ TT
			TCAGGAAA GGTG GTA		
			AGTCCTTT CCAC CAT		
			ACCA T_		
GAM496	KIAA1729	3'	ATAGTGCTTTTTTCCTGA	42948	AC TG
			TCAGGAAAAA GG TTGT		
			AGTCCTTTTT TC GATA		
			___ GT		
GAM496	MGC10960	3'	TATTGTGACGCTCTCCCTGA	26384	AAAAAC TG
			TCAGG GGTGT TAATA		
			AGTCC TCGCA GTTAT		
			CTC___ GT		
GAM496	MGC2865	3'	CACCGTCCGCTTTTCCTGA	26166	_____
			TCAGGAAAAA ACGGTG		

			AGTCCTTTT TGCCAC	
			CGCC	
GAM496	RAB39	3'	TATTACTCATTTCCTTGA 37647	ACG TT
			TCAGGAAAA GTG GTAATA	
			AGTTCTTTT TAC CATTAT	
			___ T_	
GAM496	TCL6	3'	ATTACAAGTAATTCTTTTCCTG 21767	ACGG _
	A		TCAGGAAAA TG TTGTAAT	
			AGTCCTTTT AT AACATTA	
			CTTA G	
GAM496	TCL6	3'	ATTACAAGTAATTCTTTTCCTG 21774	ACGG _
	A		TCAGGAAAA TG TTGTAAT	
			AGTCCTTTT AT AACATTA	
			CTTA G	
GAM496	TRIM36	3'	TTATTACATATCAGGTTTTCCT 20785	AC_ T
	GA		TCAGGAAAA GGTGT GTAATAA	
			AGTCCTTTT CTATA CATTATT	
			GGA _	
GAM496	LOC127428	5'	CAGGGCTGCTTTTCCTGA 36897	A G
			TCAGGAAAA CGGT TTG	
			AGTCCTTTT GTCG GAC	
			C G	
GAM496	LOC139331	5'	ATTACAACATCTGCTGA 37341	GAAAAAC
			TCAG GGTGTTGTAAT	
			AGTC CTACAACATTA	
			GT_____	
GAM496	LOC147991	5'	CATCACTAGCAATTTTCCTGA 38435	AC___ T
			TCAGGAAAA GGTG TG	
			AGTCCTTTT TCAC AC	
			AACGA T	
GAM496	LOC149267	5'	TTATTACACTGTCTGCTCCTGA 28834	AAA_ T
			TCAGGA ACGGTGT GTAA	
			AGTCCT TGTCACA TATT	
			CGTC T	
GAM496	LOC162333	5'	TTATTACAACGATCTCCTGG 42141	AAAAC _
			TCAGGA GGT GTTGTAATAA	
			GGTCCT CTA CAACATTATT	
			___ G	
GAM496	LOC219673	5'	TTATTATGTCACCTTTCCT 44695	AAC T
			AGGAAA GGTG TGTAATAA	

			TCCTTT CCAC GTATTATT		
			____ T		
GAM496	LOC221301	3'	TATTCACCATTTTCCCTG 44129	A C TT	
			CAGG AAAA GGTG GTA		
			GTCC TTTT CCAC TAT		
			C A T_		
GAM496	LOC221421	3'	CACCAGTTTCCCTTTCCTGA 44321	_____ _	
			TCAGGAAA AAC GGTG		
			AGTCCTTT TTG CCAC		
			CCCT A		
GAM496	LOC90321	3'	TAGCACACACTTTTCCTGA 31212	ACG_	
			TCAGGAAAA GTGTTG		
			AGTCCTTTT CACGAT		
			CACA		
GAM497	APP	3'	TTGCTGCTTCTGCTATATTTGT 6092	TTTTCAA_	
	GAT		ATCACAAATAT CAGCAA		
			TAGTGTTTATA GTCGTT		
			TCGTCTTC		
GAM497	BRPF1	3'	TGCTGTTGTAAATACTGT 36175	AA TT	
			ACA TATTT CAACAGCA		
			TGT ATAAA GTTGTCGT		
			C_ T_		
GAM497	CREB1	3'	TGCTGTACTGCAATATTTGGAT 10602	A TTTCA	
			ATC CAAATATT ACAGCA		
			TAG GTTTATAA TGTCGT		
			CGTCA		
GAM497	DGKB	3'	CTGTTGAAGGTGTTTCATGG 44448	CA T	
			TCA AATATTTT CAACAG		
			GGT TTGTGGAA GTTGTC		
			AC _		
GAM497	EMS1	3'	GCTGTCCTGGCATTGTGG 28868	A TTTCA	
			TCACAAAT TT ACAGC		
			GGTGTTTA GG TGTCG		
			C TCC_		
GAM497	EMS1	3'	GCTGTCCTGGCATTGTGG 11737	A TTTCA	
			TCACAAAT TT ACAGC		
			GGTGTTTA GG TGTCG		
			C TCC_		
GAM497	FLNB	3'	CTGTCGGGAGCATTTGTGA 31144	AT TT A	
			TCACAAAT TT C ACAG		

			AGTGTTTA GA G TGTC		
			C_ GG C		
GAM497	FXVD6	3'	TTGCTGTTCTCTGTATCGTGAT 22554	AA	TTTTTC
			ATCAC ATAT AACAGCAA		
			TAGTG TATG TTGTCGTT		
			C_ TCTC_		
GAM497	PIK3R3	3'	TTGCTGTTGGGCACACCTGGAT 30609	A	AATATTT
			ATC CA TTCAACAGCAA		
			TAG GT GGGTTGTCGTT		
			_ CCACAC_		
GAM497	PPP3CA	3'	TTGCTGAATTAAATATTTATGA 6648	C	TTCAA
			TCA AAATATTT CAGCAA		
			AGT TTTATAAA GTCGTT		
			A TTAA_		
GAM497	PTPRC	3'	CTGTGGAAAAATATTTAAGAT 8720	AC	A
			ATC AAATATTTTTC ACAG		
			TAG TTTATAAAAAG TGTC		
			AA G		
GAM497	PTPRC	3'	CTGTGGAAAAATATTTAAGAT 28146	AC	A
			ATC AAATATTTTTC ACAG		
			TAG TTTATAAAAAG TGTC		
			AA G		
GAM497	ROCK2	3'	CTGGTAAAGACATTTGTGAT 32840	A	CAA
			ATCACAAAT TTTT CAG		
			TAGTGTTTA AGAAA GTC		
			C TG_		
GAM497	SDC2	3'	TGCTGTAAAGCAAAATATTTGT 33328		TCA__
	GA		TCACAAATATTTT ACAGCA		
			AGTGTTTATAAAA TGTCGT		
			CGAAA		
GAM497	TIMM8A	3'	CTGGAGAAAAATATCTGT 10288	A	AA
			ACA ATATTTTTC CAG		
			TGT TATAAAAAG GTC		
			C AG		
GAM497	UTY	3'	TTGCCTGAAAATATTTGTGA 13983	T	ACA
			TCACAAATATTTT CA GCAA		
			AGTGTTTATAAAA GT CGTT		
			_ C_		
GAM497	AOP2	3'	TTGCTATAAAAAAATTTGTGAT 11342	A	CAAC
			ATCACAAAT TTTT AGCAA		

				TAGTGTTTA AAAAA TCGTT		
				A TA__		
GAM497	AUTL1	3'	TTGCTGTTGAACCTTTTATGA 26651	C TATTT		
			TCA AAA TTCAACAGCAA			
			AGT TTT AAGTTGTCGTT			
			A TCC__			
GAM497	FLJ10719	3'	TGCTACTGAAAAATGGCTG 31341	AA AC		
			CA TATTTTCA AGCA			
			GT GTAAAAAGT TCGT			
			CG CA			
GAM497	FLJ12586	3'	TTGCCATGTTGAAAATGTTT 23884	T _		
			AAATATTTT CAACA GCAA			
			TTTGTA AAA GTTGT CGTT			
			_ AC			
GAM497	KIAA1309	3'	TTGCTGTTGAGGTA ACTTG 27265	ATATT		
			CAA TTTCAACAGCAA			
			GTT GGAGTTGTCGTT			
			CAAT_			
GAM497	MDN1	3'	TGTTGTTGATGTAATTTGTGA 31411	ATTTT		
			TCACAAAT TCAACAGCA			
			AGTGTTTA AGTTGTTGT			
			ATGT_			
GAM497	MGC16385	3'	TTGCCGTTGAAAAATACAGTG 29663	AAA A		
			CAC TATTTTCAAC GCAA			
			GTG ATAAAAAGTTG CGTT			
			AC_ C			
GAM497	NET-6	3'	GTTGCTGAAAAATATTTG 15741	A		
			CAAATATTTTCA CAGC			
			GTTTATAAAAAGT GTTG			
			C			
GAM497	PRO0246	5'	TTGCTATGGTCTGAATATTTGT 15382	TTCAAC_		
	G		CACAAATATTT AGCAA			
			GTGTTTATAAG TCGTT			
			TCTGGTA			
GAM497	SYPL	3'	TTGCTGTTGCCTTATTTTGTGAT 44647	C TTTT		
			ATCA AAATA CAACAGCAA			
			TAGT TTTAT GTTGTCGTT			
			T TCC__			
GAM497	VEZATIN	3'	TGCTGTTTTATTTGTGG 19072	TTTTTC		
			TCACAAATA AACAGCA			

GGTGTTTAT TTGTCGT
T____
GAM497 LOC122525 3' CTGTGCAAAAATGTTTGT 37421 CA
ACAAATATTTTT ACAG
||||||| |||
TGTTTGTA AAAA TGTC
CG
GAM497 LOC147495 3' TTGCGTGGAAGTATCTGT 40840 A A A
ACA ATATTTTTC AC GCAA
||| ||||| || |||
TGT TATGAAAAG TG CGTT
C G _
GAM497 LOC148254 3' TTGCTGTTTGTCTTTGCTTGTG 38506 A TTTTTC
AT ATCACAA TA AACAGCAA
||||| || |||||
TAGTGTT GT TTGTCGTT
C TTCTGT
GAM497 LOC196411 3' TTGCTGCTGAAAGATGTCTGTG 42367 A A
CACA ATATTTTTCAGCAA
||||| ||||| |||||
GTGT TG TAGAAAGT GTCGTT
C C
GAM498 ANK1 3' TCACGCAAGGTCCACACTCATT 30289 ACT AGAAA_
CCA TGAATGAGT GA GTGA
||||||| || |||
ACCTTACTCA CT CACT
CAC GGAACG
GAM498 CNTN3 3' CACTTTCTCCAATACTTGT 33133 TG C A
A AGTA TG AGAAAGTG
| ||||| |||||
T TCAT AC TCTTTCAC
GT A C
GAM498 COL1A1 3' TCACTTTCCACCCTCTCTCCA 5539 AT TAC AA
TGGA GAG TG GAAAGTGA
||||| || |||||
ACCT CTC AC CTTTCACT
CT CC_ _
GAM498 HAS3 3' CACTTTCTTCAAAGCCA 11803 A AC
TG GT TGAAGAAAGTG
|| || |||||
AC CG ACTTCTTTCAC
_ AA
GAM498 PPP1R12B 3' TCACCCTCTTCAGTCACCTC 25797 T_ AA
GAG ACTGAAGA GTGA
||| ||||| |||
CTC TGACTTCT CACT
CAC CC
GAM498 PTP4A2 5' TCACTTTCCCATCACA CTCA 27832 AC A_
TGAGT TGA GAAAGTGA
||||| ||| |||||

			ACTCA ACT CTTTCACT		
			C_ ACCC		
GAM498	PTP4A2	5'	TCACTTTCCCCATCACACTCA 9555	AC A__	
			TGAGT TGA GAAAGTGA		
			ACTCA ACT CTTTCACT		
			C_ ACCC		
GAM498	SLC9A1	5'	TCACTTTCTCAGCCAAAGGTC 34859	ATGAGTA A	
	C		GGA CTGA GAAAGTGA		
			CCT GACT CTTTCACT		
			GGAAACC C		
GAM498	USH3A	5'	TCACTTTCTGACCATGCCCA 27565	A_ A ACTGAA	
			TGG ATG GT GAAAGTGA		
			ACC TAC CA CTTTCACT		
			CG _ GTC__		
GAM498	VDR	3'	CACCCCCTTCAGTGCCACCA 5944	AA A AAA	
			TGG TG GTACTGAAG GTG		
			ACC AC CGTGA CTTC CAC		
			_ C CCC		
GAM498	20D7-FC4	3'	CAC TTTCTTCTCCATTC 30537	AGTACT	
			GAATG GAAGAAAGTG		
			CTTAC CTTCTTTCAC		
			CT__		
GAM498	CITED2	3'	CAC TTTCTCCAGTGCTCA 12725	A	
			TGAGTACTG AGAAAGTG		
			ACTCGTGAC TCTTTCAC		
			C		
GAM498	DKFZP434L187	5'	TCACTTTCTGTAGCTCCCTCC 34124	AT ACTGA	
	A		TGGA GAGT AGAAAGTGA		
			ACCT CTCG TCTTTCACT		
			CC ATTG_		
GAM498	FLJ13868	3'	ACCTCTGCTCATTCCA 22955	ACTGA AA	
			TGGAATGAGT AGA GT		
			ACCTTACTCG TCT CA		
			_ C_		
GAM498	FLJ20070	3'	TCCTCAGCACTCATTCTA 19161	A A	
			TGGAATGAGT CTGA GA		
			ATCTTACTCA GACT CT		
			C C		
GAM498	FLJ20154	5'	CACCAGGGGCAATGCTCATTCC 36104	C AAGAAA	
	A		TGGAATGAGTA TG GTG		

ACCTTACTCGT AC CAC
 A GGGGAC
 GAM498 HSNV1 3' TCTCCATCACTCATTCCA 18967 AC A
 TGAATGAGT TG AGA
 ||||| ||||
 ACCTTACTCA AC TCT
 CT C
 GAM498 KIAA0237 3' CACTTTCTTCATAGACTC 16440 AC_
 GAGT TGAAGAAAGTG
 ||| |||||
 CTCA ACTTCTTTCAC
 GAT
 GAM498 KIAA0286 3' CACTTTCCTTTCCCACTCA 33903 ACT _
 TGAGT GAAG AAAGTG
 |||| ||| |||||
 ACTCA TTTC TTTCAC
 CCC C
 GAM498 PDZ-GEF1 3' ACACAGTATCATTCCA 15521 G AAGAAA
 TGAATGA TACTG GT
 ||||| |||| ||
 ACCTTACT ATGAC CA
 _ A____
 GAM498 LOC151610 3' TCACTTTCCCTCACCCATCCC 39138 A A ACTGAA
 GG ATG GT GAAAGTGA
 || ||| || |||||
 CC TAC CA CTTTCACT
 C C CTCCC_
 GAM498 LOC163231 5' TCACTCTCACCCACTCATTG 40100 ACTGAA A
 GAATGAGT GA AGTGA
 ||||| || |||||
 CTTACTCA CT TCACT
 CCCA__ C
 GAM498 LOC163231 5' TCACTCTCTCCCACTCATTG 40101 ACT A A
 GAATGAGT GA GA AGTGA
 ||||| || || |||||
 CTTACTCA CT CT TCACT
 CC_ _ C
 GAM498 LOC219401 3' TCACCTTCTTGGACTCGTTCCA 44594 A G A
 TGAATGAGT CT AAGAA GTGA
 ||||| || |||| ||||
 ACCTTGCTCA GG TTCTT CACT
 _ _ C
 GAM498 LOC254973 5' CACCTTCTTCAGAGACTCA 46077 A_ A
 TGAGT CTGAAGAA GTG
 |||| ||||| |||
 ACTCA GACTTCTT CAC
 GA C
 GAM499 PLDN 5' AGACGACGATATCAGCG 14743 GAC A
 TGTTGAT ATC TCGTCT
 ||||| || |||||

			GCGACTA TAG AGCAGA		
			___ C		
GAM499	DKFZp547A023	3'	AGACCAGCCTCATCAACATA	35942	CATCATC
			TATGTTGATGA GTCT		
			ATACAACTACT CAGA		
			CCGAC__		
GAM499	FLJ13902	3'	ACGATGATGATGAACA	23950	G GA
			TGTT AT CATCATCGT		
			ACAA TA GTAGTAGCA		
			G __		
GAM499	KIAA0429	3'	AGGGGTACATCGTCAACATA	16464	CATC G
			TATGTTGATGA ATC TCT		
			ATACAACTGCT TGG GGA		
			ACA_ _		
GAM499	KIAA0446	5'	GGGCTACATGTGCATCAACATA	34151	_ CATC
			TATGTTGATG ACAT GTCT		
			ATACAACTAC TGTA CGGG		
			G CAT_		
GAM499	LOC143888	3'	AGACAATACAGTTATTAACATA	37665	ATC C
			TATGTTGATGAC AT GTCT		
			ATACAATTATTG TA CAGA		
			ACA A		
GAM499	LOC254266	5'	AGACGATGACCACAGCATA	46480	A ACA
			TATGTTG TG TCATCGTCT		
			ATACGAC AC AGTAGCAGA		
			_ C__		
GAM500	AP1M1	3'	CAGGGGACACACCTGCCAAA	26244	ACG__
			TTTGGCAGGT CCTTG		
			AAACCGTCCA GGGAC		
			CACAG		
GAM500	ARPP-21	5'	GAGCTGCCTGCCAAA	18420	CGCCTT
			TTTGGCAGGTA GCTC		
			AAACCGTCCGT CGAG		

GAM500	JM4	3'	CTGGAGCAAGGCACTCTCAA	14079	CA AC
			TTTGG GGT GCCTTGCTCCAG		
			AAACT TCA CGGAACGAGGTC		
			C_ _		
GAM500	MGC4309	3'	CTGGGCACAAGCCACCTGCCAA	23569	AC CT_ T
	A		TTTGGCAGGT GC TGC CCAG		

			AAACCGTCCA CG ACG GGTC	
			C_ AAC _	
GAM500	TED	3'	CTGGATATGCCACCCCTGCCA 17917	TAC__ CT C
	AA		TTTGGCAGG GC TG TCCAG	
			AAACCGTCC CG AT AGGTC	
			CCACC T_ _	
GAM500	ZNF273	5'	TGGAGCAAAACCTTACAAA 39509	GC ACGCC
			TTTG AGGT TTGCTCCA	
			AAAC TCCA AACGAGGT	
			AT A____	
GAM500	LOC145934	5'	GGCTTGGCACCCGCCAAA 40626	A AC TT
			TTTGGC GGT GCC GCT	
			AAACCG CCA CGG CGG	
			C _ TT	
GAM500	LOC256444	5'	GGCTTGGCACCCGCCAAA 46199	A AC TT
			TTTGGC GGT GCC GCT	
			AAACCG CCA CGG CGG	
			C _ TT	
GAM500	LOC257484	5'	GGACACACCTGCCAAG 42815	ACGCCT C
			TTTGGCAGGT TG TCC	
			GAACCGTCCA AC AGG	
			C_____	
GAM501	EIF4EBP2	3'	CCCGGTCTCAGTCGTCAT 10301	AAT TAA A
			ATGAC CT GAGACC GG	
			TACTG GA CTCTGG CC	
			CT_ _ C	
GAM501	SUV39H1	3'	ACCTGGTCCACGTGGATTGTC 9147	TAAGA
			GACAATCT GACCAGGT	
			CTGTTAGG CTGGTCCA	
			TGCAC	
GAM501	CLDN8	3'	ACCTGAGTCAAAATTGTCAT 14443	C AAGA _
			ATGACAAT TT GAC CAGGT	
			TACTGTTA AA CTG GTCCA	
			A _ A	
GAM501	FLJ11267	3'	ACCCATAATTGAGATTGCCATA 21223	A GAGACCA
			TATG CAATCTTAA GGT	
			ATAC GTTAGAGTT CCA	
			C AATAC__	
GAM501	KIAA0090	3'	ACCTGGCCCATAAATTGTCATA 42649	C AGAGA
			TATGACAAT TTA CCAGGT	

ATACTGTTA AAT GGTCCA
 _ ACCC_
 GAM501 LOC221687 5' CCTGGCATAAGATTGCA 44305 A AGAGA
 TG CAATCTTA CCAGG
 || ||||| ||||
 AC GTTAGAAT GGTCC
 _ AC_
 GAM501 LOC253769 5' CCTGGTCTCTGGCTGTC 46429 AT TTA
 GACA C AGAGACCAGG
 ||| | |||||
 CTGT G TCTCTGGTCC
 CG_
 GAM502 CDC14B 3' TAAAAACCACCCAAACACT 27171 CA_
 AGTGTTTGG GTTTTTA
 ||||| |||||
 TCACAAACC CAAAAAT
 CAC
 GAM502 LHFPL2 3' TAAAAACTACCTAAACACT 34661 _ C
 AGTGTTT GG AGTTTTTA
 ||||| || |||||
 TCACAAA CC TCAAAAAT
 T A
 GAM502 LOC115343 5' CAACGCTCGGAAACCGCCAGAC 35665 A AC_
 AC GTGTTTGGC GTTTTT CGTTG
 ||||| ||||| ||||
 CACAGACCG CAAAGG GCAAC
 C CTC
 GAM503 ADAMTS1 3' GGACATTGAGATCACTTGTC 13851 C GTGCTG
 GACAAG GA CAATGTCC
 ||||| || |||||
 CTGTTC CT GTTACAGG
 A AGA_
 GAM503 FZD8 3' GACATTTTCTGGCTTGTC 25624 G TGCTGC
 TGACAAGC AG AATGTC
 ||||| || |||||
 ACTGTTCG TC TTACAG
 G TT_
 GAM503 HD 3' GACGAGGACACTCGCTTGCCG 7895 A _ GCAA
 TG CAAGCGAGTG CT TGTC
 || ||||| || ||||
 GC GTTCGCTCAC GG GCAG
 C A A_
 GAM503 XRCC2 3' GTTGCAGCACTGCCCATCA 11903 CAA G
 TGA GC AGTGCTGCAAT
 || | |||||
 ACT CG TCACGACGTTG
 ACC_
 GAM503 C20orf59 3' TGCAGCGCCCGCCTGCCA 22626 A A A
 TG CA GCG GTGCTGCA
 || || || |||||

			AC GT CGC CGCGACGT		
			C C C		
GAM503	TJP2	3'	ACACTGCAGTCAGATCCTGTTA 29980	A C G_ _ A	
			TGACA G GA TG CTGCA TGT		
			ATTGT C CT AC GACGT ACA		
			_ _ AG T C		
GAM504	NFATC1	3'	TCCAGCACGAGCACCCACT 12816	C T CCCGC	
			AG GGGTGCTC TGT GGA		
			TC CCCACGAG ACG CCT		
			A C A_ _		
GAM504	TBL2	3'	TCCAACGAGAGCACCCGC 26871	CCCGC	
			GCGGGTGCTCTTGT GGA		
			CGCCACGAGAGCA CCT		
			A_ _		
GAM504	DKFZp586i021	3'	CCCGGCAGAGCACCCGC 26022	TGTC C	
			GCGGGTGCTCT CCG GG		
			CGCCACGAGA GGC CC		
			C_ _ _		
GAM504	FLJ22362	5'	CTCCGCAGACCCGCGCCCGCT 23104	TCTT CC	
			AGCGGGTGTC GTC GCGGAG		
			TCGCCCGCG CAG CGCCTC		
			CC_ _ A_		
GAM504	JM11	3'	CCACAGGAGGGGACCCG 27328	TG CGC	
			CGGGTGCTCT TCC GG		
			GCCACGGGG AGG CC		
			_ _ ACA		
GAM504	JM11	3'	CCACAGGAGGGGACCCG 27329	TG CGC	
			CGGGTGCTCT TCC GG		
			GCCACGGGG AGG CC		
			_ _ ACA		
GAM504	LOC163944	5'	CTGAACCAAGAGCACCCACT 42101	C TCCCG	
			AG GGGTGCTCTTG CGG		
			TC CCCACGAGAAC GTC		
			A CAA_ _		
GAM504	LOC96597	5'	CCGCGGGAGGTCTCACCAACT 33230	CG CT_ TG	
			AG GGTG CT TCCGCGG		
			TC CCAC GG AGGGCGCC		
			AA TCT _		
GAM505	ABCC3	3'	TGCACTCTTCAGGAAAACGTG 21295	C CTTTC	
			TACGT TTCCTGGA GCA		

			GTGCA AAGGACTT	CGT		
			A	CTCA_		
GAM505	SH3BP4	5'	TGCGGCTGTACCAGGAAGA	15856	_	TT
			TCTTCCTGG AC	TCGCA		
			AGAAGGACC TG	GGCGT		
			A	TC		
GAM505	CRSP3	3'	TTGCGAAAGACTTGAAAAC	30413	C	CT A
			GT TTC	GG CTTTCGCAA		
			CA AAG	TC GAAAGCGTT		
			A	T_ A		
GAM505	EVI5	3'	GCTAAGGTCCAAGAAAC	12211	C	C C
			GT TTC	TGGACTTT GC		
			CA AAG	ACCTGGAA CG		
			_	A T		
GAM505	FLJ14888	3'	TTGCGAAGGTTAGAAGA	26657		CTG
			TCTTC	GACTTTCGCAA		
			AGAAG	TTGGAAGCGTT		
			A_			
GAM505	KIAA1058	3'	GTTGCAAGAAAGGAAAAC	40013	C	GGA TC
			GT TTCCT	CTT GCAAC		
			CA AAGGA	GAA CGTTG		
			A	AA_ _		
GAM505	NBR2	5'	GCTGGAAGCCCAGGAAGCAC	12425	_	A _
			GT CTCCTGG	CTTTC GC		
			CA GAAGGACC	GAAGG CG		
			C	C T		
GAM505	PIP3-E	3'	AAAGACTCCAGGAAGCGTA	33174	T	_
			TACG CTCCTGGA	CTTT		
			ATGC GAAGGACCT	GAAA		
			_	CA		
GAM505	LOC158969	5'	GTTGCAAATAAGGAAGATGTA	39923		GGAC C
			TACGTCTTCCT	TTT GCAAC		
			ATGTAGAAGGA	AAA CGTTG		
			AT_ _			
GAM505	LOC196510	3'	GCTGGGGCCCAGGAAGAGTA	42396	G	A TC
			TAC TCTTCCTGG	CTT GC		
			ATG AGAAGGACC	GGG CG		
			_	C GT		
GAM505	LOC199986	3'	GCCAGGGTCCAGAAAGAC	43272	C	C
			GTCTT	CTGGACTTT GC		

CAGAA GACCTGGGA CG
 A C
 GAM505 LOC200220 3' GCTGGGGCCCAGGAAGAGTA 42745 G A TC
 TAC TCTTCCTGG CTT GC
 ||| ||||| ||| ||
 ATG AGAAGGACC GGG CG
 _ C GT
 GAM506 ADPRT 3' CATAGACTAGTCCTATGGA 7323 G G ACC
 TC CA AGGA AGTCTATG
 || || ||| |||||
 AG GT TCCT TCAGATAC
 _ A GA_
 GAM506 FGA 3' CATAAACTATATTCTGTGA 6120 GAACC C
 TCGCAGAG AGT TATG
 ||||| ||| |||
 AGTGTCTT TCA ATAC
 ATA_ A
 GAM506 KIAA0993 3' CATAAACTAATTATTTCTCTGG 32079 G CC_ C
 ATA TATC CAGAGGAA AGT TATG
 ||| ||||| ||| |||
 ATAG GTCTCTTT TCA ATAC
 _ ATTAA A
 GAM507 C20orf126 3' AATCTGGCCATGAAAACCTC 25133 A C G CT
 GAG TTT C ATG GCCAGATT
 ||| ||| ||| |||||
 CTC AAA G TAC CGGTCTAA
 C A_ _
 GAM507 PIP5K2B 3' GGTCAACACCAGAGATCTCA 9615 CGA C _
 TGAGATTTC TG TG CC
 ||||| ||| ||
 ACTCTAGAG AC AC GG
 ACC A T
 GAM507 ZDHHC2 3' AATCTGCTTCAAGAAATCTCA 18484 CGA CT C
 TGAGATTTC TG GC AGATT
 ||||| || || |||
 ACTCTAAAG AC CG TCTAA
 A_ TT _
 GAM507 LOC150142 5' AATCTGGAGACCAGAAATCCA 38848 A CGATG G
 TG GATTTC CT CCAGATT
 || ||||| || |||||
 AC CTAAAG GA GGTCTAA
 _ ACCA_ _
 GAM507 LOC219988 5' GTCAGCATCGGAATCTCA 44046 T _
 TGAGATT CCGATGCTG C
 ||||| ||||| |
 ACTCTAA GGCTACGAC G
 _ T
 GAM508 ADAMTS3 3' AAGAGATAAGTGCATCATGA 15508 CA TC
 TCA ATGC GCTTATCTCTT
 ||| ||| |||||

			AGT TACG TGAATAGAGAA	
			AC _	
GAM508	CA12	3'	AAGAGATATACATTGTGATA 6877	CTCGCT
			TATCACAATG TATCTCTT	
			ATAGTGTTAC ATAGAGAA	
			AT____	
GAM508	CYP19	3'	AAGAGATAACTGTAAATGTGA 5559	ATGCT C
			TCACA CG TTATCTCTT	
			AGTGT GT AATAGAGAA	
			AAAT_ C	
GAM508	CYP19	3'	AAGAGATAACTGTAAATGTGA 25269	ATGCT C
			TCACA CG TTATCTCTT	
			AGTGT GT AATAGAGAA	
			AAAT_ C	
GAM508	NORE1	3'	AAGAGATAAGGGTGTATTATGA 25439	C_ T G
			TCA AATGC C CTTATCTCTT	
			AGT TTGTG G GAATAGAGAA	
			AT _ _	
GAM508	SELE	3'	AAGAGTTCTTAAGGATTGTGAT 6051	G CGCTTAT
	A		TATCACAAT CT CTCTT	
			ATAGTGTTA GA GAGAA	
			G ATTCTT_	
GAM508	FLJ21945	3'	AGATACCTTGGCATTGTTATA 24866	C CGCT
			TAT ACAATGCT TATCT	
			ATA TGTTACGG ATAGA	
			T TTCC	
GAM508	HNRPU	3'	AAGAGAACCTCAGCATTGTG 25579	CGCTTA
			CACAATGCT TCTCTT	
			GTGTTACGA AGAGAA	
			CTCCA_	
GAM508	HNRPU	3'	AAGAGAACCTCAGCATTGTG 10835	CGCTTA
			CACAATGCT TCTCTT	
			GTGTTACGA AGAGAA	
			CTCCA_	
GAM508	LOC152359	3'	AAGAGGTGCAGAGCATTG 41490	GCT
			CAATGCTC TATCTCTT	
			GTTACGAG GTGGAGAA	
			AC_	
GAM508	LOC91266	5'	AGAAAGCCCTGAGCATTG 32600	_ A
			CAATGCTC GCTT TCT	

			GTTACGAG CGAA AGA		
			TCC _		
GAM509	CTNS	3'	AGCATAGTAACTCCTTTCA 11382	G	CC
			TGAAAGGAGTTA CT GCT		
			ACTTTCCTCAAT GA CGA		
			_ TA		
GAM509	MGAT2	5'	AGAAGCAGCTGCTCCTTTC 8231	T	CC C
			GAAAGGAGT AGCT GCT CT		
			CTTTCCTCG TCGA CGA GA		
			_ _ A		
GAM509	HT001	5'	GGCCAGCTATCTCCTTTCA 33115	T	CC
			TGAAAGGAG TAGCT GCT		
			ACTTTCCTC ATCGA CGG		
			T C_		
GAM509	ZNF226	5'	GAGCGGAACCCTGACTTCTCA 18565	A	C_
			A AGGAGTTAG TCCGCTC		
			A TCTTCAGTC AGGCGAG		
			C CCA		
GAM510	BCL11B	3'	AATATCATAAAGGAGCTGGTG 23157	_	AG C
	A		TCACCAG TCTTT ATGA ATT		
			AGTGGTC AGGAA TACT TAA		
			G AA A		
GAM510	EMX2	3'	CGAATGGTGTTTAAAGAC 42315	GA	
			GTCTTTAGAT CATTCTG		
			CAGAAATTTG GTAAGC		
			TG		
GAM510	PRO2086	5'	AATGTGATATTAAAGACT 15344	_	G
			AGTCTTTAG AT ACATT		
			TCAGAAATT TA TGTA		
			A G		
GAM510	UHRF1	3'	GTCATCTAAAGTCCAGTGA 14953	CAGT	
			TCAC CTTTAGATGAC		
			AGTG GAAATCTACTG		
			ACCT		
GAM510	LOC139331	5'	AATGTCATTTACTGG 37340	CTTT	
			CCAGT AGATGACATT		
			GGTCA TTTACTGTAA		

GAM510	LOC151248	5'	AATGCCAGAGACTGTTGA 39081	C	TAGA A
			TCA CAGTCTT TG CATT		

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AGT GTCAGAG AC GTAA
T   ____ C
GAM511 CDH6 3' CTAATCCTTCTGGCAGATT 11372 GT C
AATCTGCC AGAAGGA TAG
||||||| ||||| |||
TTAGACGG TCTTCCT ATC
      A
GAM511 IRF2 3' TTTTCTACAGCAAATTTA 7957 C C
TAAAT TGC GTAGAAGG
||||| ||| |||||
ATTTA ACG CATCTTTT
      A A
GAM511 SALL1 3' CTAATCTTTCAAAACAGATTTA 8879 CCGTA C
A      TTAAATCTG GAAGGA TAG
||||||| ||||| |||
AATTTAGAC CTTTCT ATC
      AAAA_ A
GAM511 DKFZP547L112 5' AGTCCTTCCACGCCCTAGA 33056 C__ A
TCTG CGT GAAGGACT
||| ||| |||||
AGAT GCA CTTCCTGA
      CCC C
GAM511 TRIM2 3' AGCCCTAAAGCAGATTTAA 17596 CG AA A
TTAAATCTGC TAG GG CT
||||||| ||| |||
AATTTAGACG ATC CC GA
      AA _ _
GAM511 LOC161403 5' CTTCCACACACAGATTTAA 40019 CC_ A
TTAAATCTG GT GAAG
||||||| || |||
AATTTAGAC CA CTTC
      ACA C
GAM511 LOC199926 3' CTAGTCCTTCAACTCACAG 43261 CC_ A
CTG GT GAAGGACTAG
||| || |||||
GAC CA CTTCCTGATC
      ACT A
GAM511 LOC202316 3' CTAGTCCTTCAACTCACAG 43426 CC_ A
CTG GT GAAGGACTAG
||| || |||||
GAC CA CTTCCTGATC
      ACT A
GAM512 RAB1A 3' AGCAGTGTCTGTCACTTTCCA 34787 C _ CA
TGG AAGTGAC GATAC CT
||| ||||| ||||| ||
ACC TTCACTG CTGTG GA
      T T AC
GAM513 LASS2 3' CCAGATTAATGCATAAAGCCAA 33623 CCAC TGGG
TTGGTT GC TAATCTGG
||||| || |||||

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			AACCGA CG ATTAGACC	
			AATA TA__	
GAM513	FLJ14249	3'	CCAGCCCCAGCACAGACCCAA 22798	T CAC TAAT
			TTGG TC GCTGGG CTGG	
			AACC AG CGACCC GACC	
			C ACA C__	
GAM513	FLJ14249	3'	CCAGCCCCAGCACAGACCCAA 28168	T CAC TAAT
			TTGG TC GCTGGG CTGG	
			AACC AG CGACCC GACC	
			C ACA C__	
GAM513	SKIL	5'	CCAGATTATAAGGAGAACCAA 11884	CACG GG
			TTGGTTC CT GTAATCTGG	
			AACCAAG GG TATTAGACC	
			A__ AA	
GAM513	LOC149103	3'	CCAGATTACTGGTTAAAATCCA 38652	TTCCAC TG G
	A		TTGG GC G TAATCTGG	
			AACC TG C ATTAGACC	
			TAAAAT GT _	
GAM514	GAL	5'	CCCAGACCCGCCACCGCACCC 43998	AACA AA
			GGGT GT CGGGTCTGGG	
			CCCA CA GCCCAGACCC	
			CGC_ CC	
GAM514	KCNK4	3'	CCCAGACCCAAGCCTGACCCCA 18714	AA TAAC
			TGGGGT CAG GGGTCTGGG	
			ACCCCA GTC CCCAGACCC	
			_ CGAA	
GAM514	LIMK1	3'	CCTGGACCGCTACTGCCCCCA 18798	TAA A G TG
			TGGGG CAGTA CGG TC GG	
			ACCCC GTCAT GCC AG CC	
			CC_ C _ GT	
GAM514	MMP25	3'	CCCAGACCCGGAACCAGCCC 22821	AACA AA
			GGGT GT CGGGTCTGGG	
			CCCG CA GCCCAGACCC	
			AC__ AG	
GAM514	MSF	3'	CCCAGGCCCTCCACACCCCA 42521	AACAGTAAC
			TGGGGT GGGTCTGGG	
			ACCCCA CCCGGACCC	
			CCACCCT__	
GAM514	PTK7	3'	CCCAGACCCACGTCTTCCCA 8688	TAACA AAC
			TGGGG GT GGGTCTGGG	

			ACCCC CA CCCAGACCC	
			TTCTG ____	
GAM514	RNF4	3'	CCAGGTCAC TGTGCCCA 8840	AACG GT
			TGGGGTAACAGT G CTGG	
			ACCCCGTTGTCA C GACC	
			____ TG	
GAM514	SLC8A2	3'	CCCAGACCCGTTACCCACTACC 32967	ACA_
	CT		GGGGTA GTAACGGGTCTGGG	
			TCCCAT CATTGCCAGACCC	
			CACC	
GAM514	DKFZP727G051	3'	CCCAGACCCACCAGACACCA 34429	G AACA AAC
			TGG GT GT GGGTCTGGG	
			ACC CA CA CCCAGACCC	
			A GAC_ ____	
GAM514	FLJ00007	3'	CCCAGACCCCTGACCACCC 35308	AA_ TAAC
			GGGGT CAG GGGTCTGGG	
			CCCCA GTC CCCAGACCC	
			CCA ____	
GAM514	KIAA0237	3'	CCCAGACCAGCAGTCACCCA 16444	A A AACG
			TGGGGT AC GT GGTCTGGG	
			ACCCCA TG CG CCAGACCC	
			C A A_ ____	
GAM514	KIAA1656	3'	CCTGGGTCAC TGTCCCCCA 32728	T AACG GT TG
			TGGGG AACAGT G C GG	
			ACCCC TTGTCA C G CC	
			C ____ TG GT	
GAM514	LOC112840	3'	CCTCACC ACTATTACCCTA 27956	C AACG CT
			TGGGGTAA AGT GGT GG	
			ATCCCAT TCA CCA CC	
			A ____ CT	
GAM514	LOC115207	3'	CCCAGACCCCTCGCCACTCCA 28807	AACAGTAAC
			TGGGGT GGGTCTGGG	
			ACCTCA CCCAGACCC	
			CCGCTCC_	
GAM514	LOC147136	3'	CCCAGACCCACCTCCTGCCCA 38300	AC TAAC
			TGGGGTA AG GGGTCTGGG	
			ACCCCGT TC CCCAGACCC	
			CC CA_	
GAM514	LOC222031	3'	CCCAGATCCATCCACTCCACCC 45131	AAC AAC_
	CA		TGGGGT AGT GGGTCTGGG	

		ACCCCA TCA CCTAGACCC		
		CC_ CCTA		
GAM514	LOC254556 3'	CCAGGTCAGTGTGCCCCA	45393	AACG GT
		TGGGGTAACAGT G CTGG		
		ACCCCGTTGTCA C GACC		
		____ TG		
GAM514	LOC257428 5'	CCCATATATTCACCAGTTACCC	45261	AGTAACGG C
	CA	TGGGGTAAC GT TGGG		
		ACCCCATTG TA ACCC		
		ACCACTTA T		
GAM514	LOC56965 3'	CTCGTACCACCCCTGTTACCCC	21451	TAACG C
	A	TGGGGTAACAG GGT TGGG		
		ACCCCATTTGTC CCA GCTC		
		CCCA_ T		
GAM515	BCL11B 3'	CTTGAAAATGTTGCAGTA	23162	G C
		TACTGCAA ATTT CAAG		
		ATGACGTT TAAA GTTC		
		G A		
GAM515	HOXA7 3'	TCCCAGCTTGGAATTCTGC	13771	AG C
		GCA ATTTCCAAGC GGGA		
		CGT TAAAGGTTTCG CCCT		
		CT A		
GAM515	DKFZP566G1424 3'	CCCGACTTGAGAGGGCA	41114	AAGA C
		TGC TTTCCAAG CGGG		
		ACG GGAGGTTC GCCC		
		____ A		
GAM515	FLJ11125 3'	CCCGGCTTGAAAATTCA	29977	C A C
		TG AAG TTTC AAGCCGGG		
		AC TTC AAAG TTCGGCCC		
		_ A _		
GAM515	KIAA1465 3'	TTTGAAACCTCGCGGTA	30506	A A
		TACTGC AG TTTCCAAG		
		ATGGCG TC AAAGGTTT		
		C C		
GAM515	KIAA1771 5'	TCCCAGCTTGGAAGCA	38635	AAGA C
		TGC TTTCCAAGC GGGA		
		ACG AAGGGTTCG CCCT		
		____ A		
GAM515	NFAT5 5'	TCCCGGCTCAGGAACAGCAG	28959	AAGAT A_
		CTGC TTCC AGCCGGGA		

			GACG AAGG TCGGCCCT		
			AC__ AC		
GAM515	PCDH17	3'	TCCTGAAAAGACCTTGCAGTA 15814	A	CCAAGC
			TACTGCAAG TTT CGGGA		
			ATGACGTTT AGA GTCCT		
			C AAA__		
GAM515	SSB-3	5'	CCCAGCCTGGGCCTCTCTTGCA 28101	TT__	A C
	G		CTGCAAGA TCCA GC GGG		
			GACGTTCT GGGT CG CCC		
			CTCC C A		
GAM515	LOC152300	3'	CCTGTATTGGAAATCTTGCA 39250	GC	
			TGCAAGATTTCCAA CGGG		
			ACGTTCTAAAGGTT GTCC		
			AT		
GAM515	LOC207089	3'	CCCGGCTTCCCGGACTCCAGCA 43108	AA TT	__
			TGC GA TCC AAGCCGGG		
			ACG CT AGG TTCGGCCC		
			AC C_ CCC		
GAM515	LOC221399	5'	CCCAGCTCATTTTGCAG 45049	TTCCA	C
			CTGCAAGAT AGC GGG		
			GACGTTTTA TCG CCC		
			C__ A		
GAM516	BAZ1B	3'	ATAACCCCAACCAACCGCCA 26192	AG_	
			TGGC GGTGGGGTTGT		
			ACCG CCACCCCAATA		
			CCA		
GAM516	APCL	3'	AAGGAAACCCAGCCCCACCA 12495	CA _	GTA
			TGG GGG TGGGGTT CTT		
			ACC CCC ACCCCAA GAA		
			AC G AG_		
GAM516	FLJ14547	3'	CGAAGACGTGCCCTACCCTACC 26559	C	_ A
	A		TGG AGGGTGGGGT TGT CTTCTG		
			ACC TCCCATCCCG GCA GAAGC		
			A T _		
GAM516	PRAX-1	3'	AAGTGGGGCCCCACCTGCC 11145	G	
			GGCAGGGTGGGGTT TACTT		
			CCGTCCCACCCCGG GTGAA		
			-		
GAM516	SDC3	5'	GCGAACCCCACTCTGCCA 16086	-	
			TGGCAGGGTGGGGTT GT		

ACCGTCTCACCCCAA CG
 G
 GAM516 LOC150577 3' TACAACTCCCACCCACCA 41224 CA _
 TGG GGGTGGG GTTGTA
 ||| ||||| |||||
 ACC CCCACCC CAACAT
 AC T
 GAM516 LOC151162 5' GAAAACCAACCCACCCCTGCCA 41307 TAC
 TGGCAGGGTGGGGTTG TTC
 ||||| ||||| |||
 ACCGTCCCACCCCAAC AAG
 CAA
 GAM516 LOC203377 5' GAAAACCAACCCACCCCTGCCA 43542 TAC
 TGGCAGGGTGGGGTTG TTC
 ||||| ||||| |||
 ACCGTCCCACCCCAAC AAG
 CAA
 GAM517 IL18R1 3' TAAGAGTTTTAATGCCAGTGC 9950 CCAG CT
 GCACTGGCA TA ACTCTTA
 ||||| || |||||
 CGTGACCGT AT TGAGAAT
 A__ TT
 GAM517 LFNG 3' TAAGAGTAACAGCAGCCACCGC 44511 AC ACCA AC
 GC TGGC GT TACTCTTA
 || ||| || |||||
 CG ACCG CA ATGAGAAT
 CC ACGA _
 GAM517 HSPC014 3' TAAGAATAATATTTACTGTGTC 18053 C C__ C
 AGTGC CACTGGCAC AGTA TA TCTTA
 ||||| ||| || |||||
 GTGACTGTG TCAT AT AGAAT
 _ TTATA A
 GAM517 KIAA0261 3' TAAGAACATAGTACGCCAGTGT 33834 ACCA C__
 GCACTGGC GTACTA TCTTA
 ||||| ||||| |||||
 TGTGACCG CATGAT AGAAT
 _ ACA
 GAM517 KIAA1727 3' AGCAGCCACTGGTGCCACTGC 32028 C A_ A
 GCA TGGCACCACT CT CT
 || ||||| || |||
 CGT ACCGTGGTCA GA GA
 C CC C
 GAM517 LOC162333 5' AAGAGGTTGGTGTCAATGC 42120 C GTACTA
 GCA TGGCACCA CTCTT
 || ||||| |||||
 CGT ACTGTGGT GAGAA
 A TG__
 GAM517 LOC90906 5' TAAGAGGGCAGGCAGCAGCAGT 32154 _ A_ A ACTA
 GC GCACTG GC CC GT CTCTTA
 ||||| || ||| |||||

CGTGAC CG GG CG GAGAAT
GA AC A G____

GAM518 ITK 3' TTCAGAAAGATGATTTTACTCA 12079 A G GTTC
TGA GTAAAAT GTT CTGAA
||| ||||| ||| |||||
ACT CATTTTA TAG GACTT
_ G AA__

GAM518 PDGFRB 3' TCAGGAACCATGCCCTTC 32819 TAAA TGT
GAAG ATGGT TCCTGA
|||| ||||| |||||
CTTC TACCA AGGACT
CCCG ____

GAM518 XPR1 3' TTCAAAACAAATATTTACTTCA 11126 ATGG CC
TGAAGTAAA TTGTT TGAA
||||||| ||||| |||||
ACTTCATTT AACAA ACTT
ATA_ A_

GAM518 C5orf7 3' CAGGAACCATTTTCAC 31941 _ TGT
GT AAAATGGT TCCTG
|| ||||| |||||
CA TTTTACCA AGGAC
C ____

GAM518 DT1P1A10 3' CAGGAATGCTGCCTTCCTTCA 30857 TAAAAT ____
TGAAG GGT TGTTCTG
||||| ||| |||||
ACTTC CCG GTAAGGAC
CTT____ TC

GAM518 EML4 3' TTCAGGAACAACCAGAGGTATC 21147 AG AAAA
A
TGA T TGGTTGTTCTGAA
||| | |||||
ACT G ACCAACAAGGACTT
AT GAG_

GAM518 EPB41L1 3' TCAGTTCCATTTTACCTC 34943 A TTGTTC
GA GTAAAATGG CTGA
|| ||||| |||||
CT CATTTTACC GACT
C TT____

GAM518 FLJ10583 3' TTCAAAGTCTTCCATTTTACTT 19951 TTGTTC
AAGTAAAATGG TGAA
||||||| |||||
TTCATTTTACC ACTT
TTCTGAA

GAM518 FLJ20154 5' TCAGCGCTGCCATTTTATTTCA 36107 T TC
TGAAGTAAAATGGT GT CTGA
||||||| ||||| |||||
ACTTTATTTTACCG CG GACT
T C_

GAM518 HSF2 3' TTCAAATGGCCATTTTCTCCA 10838 A T TG CC
TG AG AAAATGGT TT TGAA
|| || ||||| || |||||

			AC TC TTTTACCG AA ACTT		
			C T GT _		
GAM518	KIAA1323	3'	TCAAAAAGGCAACGTTACTTCA	31570	AATG CC_
			TGAAGTAA GTTGTT TGA		
			ACTTCATT CAACGG ACT		
			G_ AAAA		
GAM518	NR6A1	3'	TCAGCTGCCCCTTACTTCA	27182	AAT TGTT
			TGAAGTAA GGT CTGA		
			ACTTCATT CCG GACT		
			CC_ TC_		
GAM518	NR6A1	3'	TCAGCTGCCCCTTACTTCA	27188	AAT TGTT
			TGAAGTAA GGT CTGA		
			ACTTCATT CCG GACT		
			CC_ TC_		
GAM518	NR6A1	3'	TCAGCTGCCCCTTACTTCA	7234	AAT TGTT
			TGAAGTAA GGT CTGA		
			ACTTCATT CCG GACT		
			CC_ TC_		
GAM518	PLAGL2	3'	CAGGAACCCCATCCTTGCTTCA	34874	A_ TT
			TGAAGTAA ATGG GTTCCTG		
			ACTTCGTT TACC CAAGGAC		
			CC C_		
GAM518	LOC158235	5'	TTCAGGAGCTTACATTTTACTC	41925	A GTT
	A		TGA GTAAAATG GTTCCTGAA		
			ACT CATTTTAC CGAGGACTT		
			_ ATT		
GAM518	LOC158434	3'	TTCAAGTGTCAACTTTACTTCA	41988	AAT TTCC_
			TGAAGTAA GGTTG TGAA		
			ACTTCATT TCAAC ACTT		
			_ TGTGA		
GAM518	LOC203350	3'	GGCCAACCATTTAACCTCA	43536	A A TT
			TGA GT AAATGGTTG CC		
			ACT CA TTTACCAAC GG		
			C A C_		
GAM518	LOC219529	3'	TCAGGTCTTCCCATTTTGCCTC	44674	A TTGTT
	A		TGA GTAAAATGG CCTGA		
			ACT CGTTTTACC GGA		
			C CTTCT		
GAM518	LOC253613	3'	AGGGACATTTTATCTCA	46009	AG TGGT
			TGA TAAAA TGTTCCT		

ACT ATTTT ACAGGGA
 CT ____
 GAM518 LOC255252 3' TTCAGGAGATTATATTTCACTC 45549 A A GTTG
 A TGA GT AAATG TTCCTGAA
 ||| || |||| |||||
 ACT CA TTTAT GAGGACTT
 _ C ATTA
 GAM518 LOC90750 3' TCAGGAACAGACCATTCA 31969 A _
 A AATGGT TGTCCTGA
 | |||| |||||
 A TTACCA ACAAGGACT
 C G
 GAM519 SLC1A1 3' CTGTACTTCAGTTCTCATCTTG 10378 C TC__
 TAA TTACAAGATGAG AATT TACAG
 ||||| |||| ||||
 AATGTTCTACTC TTGA ATGTC
 _ CTTC
 GAM519 DKFZP566B183 3' CTGTAAAATTTGTCTCATCTTT 17766 C _ T C
 TAA TTA AAGATGAG CAA TT TACAG
 ||| ||||| ||| || ||||
 AAT TTCTACTC GTT AA ATGTC
 T T T A
 GAM519 FLJ00024 3' AGAAACTGCAGGTTCTCTTG 31886 T ____ A
 A TTACAAGA GA GCA TTTCT
 ||||| || || ||||
 AGTGTCTCT CT CGT AAAGA
 _ TGGA C
 GAM519 RAB3-GAP150 3' CTGTAAAAATGTATTATCTTGT 14789 GCA C
 AA TTACAAGATGA ATTT TACAG
 ||||| |||| ||||
 AATGTTCTATT TAAA ATGTC
 ATG A
 GAM520 SP100 3' TTTAAGCTGCCTGTAC 9085 AC TTA
 GTACA GT AGCTTAA
 |||| || |||||
 CATGT CG TCGAATTT
 C_ ____
 GAM520 CAMKK2 3' GTTTAAGCTTCTCTGTAC 13314 ACGTTT
 GTACA AAGCTTAAAC
 |||| |||||
 CATGT TTCGAATTTG
 CTC____
 GAM520 KIAA0449 3' TTTAAGCCCCATGTTGTAC 19058 TTAA
 GTACAACGT GCTTAA
 ||||| |||||
 CATGTTGTA CGAATTT
 CCC_
 GAM521 NOVA1 3' GTTGACATTTGTTTTTAA 8348 T C
 TTAAAAACAA TG GCGAT
 ||||| || ||||

			AATTTTGTGTT AC CGTTG		
			T A		
GAM521	NOVA1	3'	GTTGCACATTTGTTTTTAA 13217	T C	
			TTAAAAACAA TG GCGAT		
			AATTTTGTGTT AC CGTTG		
			T A		
GAM521	KIAA1078	3'	TTAAATCAGTGCTGTTTTTA 32474	ATT _	
			TAAAAACA GCGC GATTTAA		
			ATTTTGT CGTG CTAAATT		
			_ A		
GAM522	B3GNT5	3'	ATTAAACATCAAAGTTAT 25764	GTTC	
			ATAAC GATGTTTAAT		
			TATTG CTACAAATTA		
			AAA_		
GAM522	LOC154007	3'	TGTAAATTAACATGAAT 39457	G C	
			GTTC ATGTTTAAT TACA		
			TAAG TACAAATTA ATGT		
			_ A		
GAM523	JMJ	5'	AATTCGGATTTATTTCA 11418	_	
			TGAGATAAATCC AGATT		
			ACTTTATTTAGG TTAA		
			C		
GAM523	NRCAM	3'	TGACTGGATTTCCCTCA 11452	AT AT	
			TGAG AAATCCAG TCA		
			ACTC TTTAGGTC AGT		
			CC _		
GAM523	DKFZp564I1922	3'	AATTGAATCTAGAGTCTT 17722	AAA C	
			GAGAT TC AGATTCAATT		
			TTCTG AG TCTAAGTTAA		
			_ A		
GAM523	FLJ10097	3'	AATTGAATATTGTTTTGTCTCA 33988	TCCAG	
			TGAGATAAA ATTCAATT		
			ACTCTGTTT TAAGTTAA		
			TGTTA		
GAM523	FLJ20276	3'	ATTGAATCTGCTCTCA 19327	TAAATC	
			TGAGA CAGATTCAAT		
			ACTCT GTCTAAGTTA		
			C_		
GAM523	KIAA0825	3'	GAGCTGGATTTTCTCA 30592	T A	
			TGAGA AAATCCAG TTC		

GAM523	LOC149153	3'	ATTGACTGGATTTTCCCA	40962	A T	AT
			TG GA AAATCCAG TCAAT			
			AC CT TTTAGGTC AGTTA			
			C T _			
GAM523	LOC200563	5'	AATTGATATTAGATTTGTCTCA	43318		CAGAT
			TGAGATAAATC TCAATT			
			ACTCTGTTTAG AGTTAA			
			ATTAT			
GAM523	LOC219627	3'	AATTGAATCTGGAGAGTC	44272	AAA	
			GAT TCCAGATTCAATT			
			CTG AGGTCTAAGTTAA			
			AG_			
GAM523	LOC221814	3'	AATTGAATCTGCAGCATCT	45088	AAATC	
			AGAT CAGATTCAATT			
			TCTA GTCTAAGTTAA			
			CGAC_			
GAM523	LOC257415	3'	AATTGAATCTGGATACATCT	45957	AA	
			AGAT ATCCAGATTCAATT			
			TCTA TAGGTCTAAGTTAA			
			CA			
GAM524	HNRPK	3'	GGTATGAGTATATACCA	7916	C	CAA
			TGG ATATACTCA GCT			
			ACC TATATGAGT TGG			
			A A_			
GAM524	HNRPK	3'	GGTATGAGTATATACCA	25280	C	CAA
			TGG ATATACTCA GCT			
			ACC TATATGAGT TGG			
			A A_			
GAM524	BHLHB2	3'	AACCAAGCCTTGGCACCGCCA	9752		ATATACTCA _
			TGGC CAAG CTTGGTT			
			ACCG GTTC GAACCAA			
			CCACG_ C			
GAM524	FLJ10546	5'	ACTATGCGAGTATATAACA	29912	GC	ACAA T
			TG ATATACTC GC TGGT			
			AC TATATGAG CG ATCA			
			AA _ T			
GAM525	APPBP2	3'	AAGGACTAACATTTTAAAGTTA	13077	C GC_	C
			A ACT GATGTTAG CCTT			

			A TGA TTACAATC GGAA	
			T ATTT A	
GAM525	CSPG4	3'	AAGGGCTAAACATGCATGTGT 7624	C G _
			ACACA TGC ATGTT AGCCCTT	
			TGTGT ACG TACAA TCGGGAA	
			_ _ A	
GAM525	FLRT2	3'	AAGGGCTATAGATCACATACGT 14876	ACAC C GT_
	TA		TAAC TG GAT TAGCCCTT	
			ATTG AC CTA ATCGGGAA	
			CAT_ A GAT	
GAM525	NEDD4	3'	AACTTTGGAAAGTGTGTTA 34690	G_ T
			TAACACACT CGA GTT	
			ATTGTGTGA GTT CAA	
			AAG T	
GAM525	DOCK3	3'	GGCCATGGTCAGTGTGTT 33039	_ G TTA
			AACACACTG C ATG GCC	
			TTGTGTGAC G TAC CGG	
			T G _	
GAM525	FLJ20457	3'	AAGGGCTATAACATACATGTCA 19495	C C CG _
			A ACA TG ATGT TAGCCCTT	
			A TGT AC TACA ATCGGGAA	
			C _ A_ AT	
GAM525	KIAA0293	3'	GTTTCATCGCAGCATGTT 30397	CA TT
			AACA CTGCGATG AGC	
			TTGT GACGCTAC TTG	
			AC _	
GAM525	KIAA0542	3'	GCACCATCTGCAGTGTGT 32859	_ TTA
			ACACACTGC GATG GC	
			TGTGTGACG CTAC CG	
			T CA_	
GAM525	KIAA1322	3'	AAGGGCCTCGTGCAGTGTGTT 36018	G TTA
			AACACACTGC ATG GCCCTT	
			TTGTGTGACG TGC CGGGAA	
			_ TC_	
GAM525	LOC144559	3'	AACTTCAGCACACGTGTGTTA 37763	_ _ T
			TAACACAC TGC GA GTT	
			ATTGTGTG ACG CT CAA	
			CAC A T	
GAM525	LOC257041	5'	AAGGAACTGTCCGCAGTGTG 46563	ATGT C_
			CACACTGCG TAG CCTT	

			GTGTGACGC	GTC	GGAA		
			CT_	AA			
GAM526	LOC143888	3'	CAACCTTAGAAAAGACAAT	37666	GC	A	
			GTTGT	CTTTTCTAAG	TTG		
			TAACA	GAAAAGATT	C AAC		
			—	C			
GAM527	BLAME	3'	AAGCAGAACATTCCATCCA	21303	TAGATA	_ _	
			TGGA	TGGAG	GT CTGCTT		
			ACCT	ACCTT	CA GACGAA		
			—	A A			
GAM527	LOC123242	5'	CAAACAGACCTCCTGCCCATCC	37240	AGATAT	C	
	A		TGGAT	GGAGGTCTG	TTG		
			ACCTA	CCTCCAGAC	AAC		
			CCCGT_	A			
GAM527	LOC253001	5'	CAAACAGACCTCCTGCCCATCC	46057	AGATAT	C	
	A		TGGAT	GGAGGTCTG	TTG		
			ACCTA	CCTCCAGAC	AAC		
			CCCGT_	A			
GAM527	LOC254413	5'	GGGCCTCCACATCCTCCA	46403	TA	A	
			TGGA	GAT TGGAGGTCT			
			ACCT	CTA ACCTCCGGG			
			C_	C			
GAM528	FAT	3'	TGAACCTAGAGGTGATGTG	11753	C	AGC	
			TACA	CACCTCTA	TCA		
			GTGT	GTGGAGAT	AGT		
			A	CCA			
GAM528	MAP2K1	3'	TGAGCATCAGAGAGTGTACATC	8635	CAC	AA_	
	A		TGATGTACAC	CTCT	GCTCA		
			ACTACATGTG	GAGA	CGAGT		
			A_	CTA			
GAM528	KIAA0561	3'	TGGAGGTGGTGTCA	32767	T		
			TGATG	ACACCACCTCTA			
			ACTAC	TGTGGTGGAGGT			
			—				
GAM528	LOC120105	5'	GGAGAAAATGGGTACATCA	37209	A	C_	
			TGATGTAC	CCA	CTCT		
			ACTACATG	GGT	GAGG		
			_	AAAA			
GAM528	LOC129831	3'	GAGCTTTGAGTGTACAT	36978	CACC	T	
			ATGTACAC	TC AAGCTC			

			TACATGTG AG TTCGAG		
			_____ T		
GAM529	DFFB	3'	CTGGGATTACAGGCACCT 42243	_ A_	
			AGGTGCCTG AGT CAG		
			TCCACGGAC TTA GTC		
			A GG		
GAM529	FGF5	3'	CTGCACCCACCAACCTGTCA 10774	GCC A A	
			TGACAGGT TG GT CAG		
			ACTGTCCA AC CA GTC		
			ACC C C		
GAM529	FGF5	3'	CTGCACCCACCAACCTGTCA 27001	GCC A A	
			TGACAGGT TG GT CAG		
			ACTGTCCA AC CA GTC		
			ACC C C		
GAM529	BMF	3'	CTGCACAAGGGCACCTGCAGCT 27278	A GA A	
	A		TAGCTG CAGGTGCCT GT CAG		
			ATCGAC GTCCACGGG CA GTC		
			— AA C		
GAM529	CHST3	3'	TGAGTACAGCCGCATCACCTGT 10485	— — AGTA	
	CAACT		TGACAGGT GC CTG CA		
			ACTGTCCA CG GAC GT		
			CTA CC ATGA		
GAM529	FLJ10713	3'	GTACAGGCACCTGCCA 20041	A GA	
			TG CAGGTGCCT GTAC		
			AC GTCCACGGA CATG		
			C —		
GAM529	FLJ12363	3'	CTGGGATTACAGGCACCTGTCA 25867	_ A_	
			TGACAGGTGCCTG AGT CAG		
			ACTGTCCACGGAC TTA GTC		
			A GG		
GAM529	FLJ12973	3'	CTGGGATTACAGGCACCTGCCA 24407	A _ A_	
			TG CAGGTGCCTG AGT CAG		
			AC GTCCACGGAC TTA GTC		
			C A GG		
GAM529	FLJ22684	3'	CTGGAATTACAGGCACCTGCCA 24643	A _ A_	
			TG CAGGTGCCTG AGT CAG		
			AC GTCCACGGAC TTA GTC		
			C A AG		
GAM529	FLJ31101	3'	CTGGGATTACAGGCACCTGCCA 19684	A _ A_	
			TG CAGGTGCCTG AGT CAG		

			AC GTCCACGGAC TTA GTC		
			C A GG		
GAM529	KIAA0513	5'	CTGGGATTACAGGCACCTGCCA 16357	A	_ A_
			TG CAGGTGCCTG AGT CAG		
			AC GTCCACGGAC TTA GTC		
			C A GG		
GAM529	MDS018	3'	CTGTACTCAGAATGGGTTTCAG 22402	_ AG	GC
			CTGA C GT CTGAGTACAG		
			GA CT G TA GACTCATGTC		
			T GG A_		
GAM529	MGC11386	3'	CTGCACCCATCAACCTGTCACC 26756	C	GCC A A
	TA		TAG TGACAGGT TG GT CAG		
			ATC ACTGTCCA AC CA GTC		
			C ACT C C		
GAM529	MGC15416	3'	TACACGGCCGACCTGTCGC 28788	T	_ T A
			GC GACAGGT GCC G GTA		
			CG CTGTCCA CGG C CAT		
			_ GC _ A		
GAM529	MGC2474	3'	CTGGAATTACAGGCACCTGCCA 23417	C A	_ A_
	CTA		TAG TG CAGGTGCCTG AGT CAG		
			ATC AC GTCCACGGAC TTA GTC		
			_ C A AG		
GAM529	PRO2389	3'	TGAACAGACCTGTCAGC 31880	GC	AGTA
			GCTGACAGGT CTG CA		
			CGACTGTCCA GAC GT		
			_ AA_		
GAM529	PTPRN2	3'	TCAGCCACACCTGTCAGC 28371	C_	
			GCTGACAGGTG CTGA		
			CGACTGTCCAC GACT		
			ACC		
GAM529	PTPRN2	3'	TCAGCCACACCTGTCAGC 28376	C_	
			GCTGACAGGTG CTGA		
			CGACTGTCCAC GACT		
			ACC		
GAM529	VDU1	3'	CTGGGATTACAGGCACCTGCCA 17381	A	_ A_
			TG CAGGTGCCTG AGT CAG		
			AC GTCCACGGAC TTA GTC		
			C A GG		
GAM529	LOC146909	3'	CTGGGATTACAGGCACCCATCA 38267	CA	_ A_
			TGA GGTGCCTG AGT CAG		

		ACT CCACGGAC TTA GTC		
		AC A GG		
GAM529	LOC152313 3'	CTGTACTCACTAGATGCCAGT 41476	A	GGTGCC
		GCTG CA TGAGTACAG		
		TGAC GT ACTCATGTC		
		C AGATC_		
GAM529	LOC154877 3'	CTGGGATTACAGGCATCTGCCA 41742	A	_ A_
		TG CAGGTGCCTG AGT CAG		
		AC GTCTACGGAC TTA GTC		
		C A GG		
GAM529	LOC169026 3'	CTGCACTCATCAACCTGTCATC 40265	C	GCC A
	TA	TAG TGACAGGT TGAGT CAG		
		ATC ACTGTCCA ACTCA GTC		
		T ACT C		
GAM529	LOC200014 3'	CTGGGATTACAGGCACCCACCA 42691	C	ACA _ A_
	CTA	TAG TG GGTGCCTG AGT CAG		
		ATC AC CCACGGAC TTA GTC		
		_ CAC A GG		
GAM529	LOC254439 3'	ACTGGGCACCATCAGCTA 45432	CA	G
		TAGCTGA GGTGCCT AGT		
		ATCGACT CCACGGG TCA		
		A_ _		
GAM529	LOC57107 3'	CTGGAATTACAGGCACCTGCCA 21649	A	_ A_
		TG CAGGTGCCTG AGT CAG		
		AC GTCCACGGAC TTA GTC		
		C A AG		
GAM530	NT5C2 3'	CTCCTTCTTATCTGTGATA 14527	C	ACAT
		TATCACAGA TAAGGG GAG		
		ATAGTGTCT ATTCTT CTC		
		_ C_		
GAM530	ROCK2 3'	CCTCAGTATTAGTCTGTGA 32838		GGGACA
		TCACAGACTAA TGAGG		
		AGTGTCTGATT ACTCC		
		ATG_		
GAM530	FLJ13852 3'	CCCTGGCTTAGTCTGGATA 23339	A	_____
		TATC CAGACTA AGGG		
		ATAG GTCTGAT TCCC		
		_ TCGG		
GAM530	FLJ23563 5'	CCTCATGTCCTCGCCTCTG 33561	CTAA	
		CAGA GGGACATGAGG		

			GTCT TCCTGTACTCC		
			CCGC		
GAM530	KIAA0161	3'	CTTGAGCCCTCAGCCTGTGATA 16430	A A	ACA
			TATCACAG CT AGGG TGAG		
			ATAGTGTC GA TCCC GTTC		
			C C GA_		
GAM530	LANCL2	3'	CCTCATGTCTGTAACATGTGA 20775	GAC	AG
			TCACA TA GGACATGAGG		
			AGTGT AT TCTGTACTCC		
			ACA G_		
GAM530	MAP	3'	CCTCAGGTTCAACCTGTGATA 23095	ACTAAG	A
			TATCACAG GGAC TGAGG		
			ATAGTGTC CTTG ACTCC		
			CAA_ G		
GAM530	LOC221421	3'	CTCACCCAACCTGTGATG 44322	ACTAA	ACA
			TATCACAG GGG TGAG		
			GTAGTGTC CCC ACTC		
			CAA_ _		
GAM531	KCNS3	5'	TGTGCACCACACATTCCA 8050	A A	
			TGGAATGTGTG TG GCG		
			ACCTTACACAC AC TGT		
			C G		
GAM531	MTMR2	3'	TTGATCACTTTTCAACTTCCA 18246	T G T C	
			TGGAA GT TGA GAG GATCAA		
			ACCTT CA ACT TTC CTAGTT		
			_ _ T A		
GAM531	FLJ10052	3'	CGAATCATCACGCATCCCA 19712	A	G_
			TGG ATGTGTGATGA CG		
			ACC TACGCACTACT GC		
			C AA		
GAM531	G4	5'	TTTGGGGGCCCATACACACCC 43736	AA	A GA
	CA		TGG TGTGTGATG GC TCAAA		
			ACC ACACATTAC CG GGTTT		
			CC C GG		
GAM531	KIAA1246	5'	TTGAAGACACCCACATTCCA 44193	TGA	AGCGA
			TGGAATGTG TG TCAA		
			ACCTTACAC AC AGTT		
			CCC AGA_		
GAM531	RALGPS1A	3'	TCGTGACATCACACACTTCA 16019	A	A_
			TGGA TGTGTGATG GCGA		

		ACTT ACACACTAC TGCT		
		C AG		
GAM531	LOC158337 3'	TTGACCACTGAGTTATCACATC 41961	A _ G_ CGA	
	CCA	TGG ATGTG TGAT AG TCAA		
		ACC TACAC ATTG TC AGTT		
		C T AG ACC		
GAM531	LOC200261 3'	TGATCACTGTGTGCCACACCCC 42752	AA TG _ C	
	A	TGG TGTG ATG AG GATCA		
		ACC ACAC TGT TC CTAGT		
		CC CG G A		
GAM531	LOC203292 5'	TGGGAGCCCATCACACATCC 43503	A A GA	
		GGA TGTGTGATG GC TCA		
		CCT ACACACTAC CG GGT		
		_ C AG		
GAM531	LOC219744 5'	TGATCCCACCACAGCATTCCA 43903	_ A AGC	
		TGGAATG TGTG TG GATCA		
		ACCTTAC ACAC AC CTAGT		
		G C C__		
GAM531	LOC221479 3'	GACCGCCACACATTCC 44289	ATGA A	
		GGAATGTGTG GCG TC		
		CCTTACACAC CGC AG		
		C__ C		
GAM531	LOC257554 5'	TTTGGGGGCCCATACACACCC 46643	AA A GA	
	CA	TGG TGTGTGATG GC TCAAA		
		ACC ACACATTAC CG GGTTT		
		CC C GG		
GAM531	LOC92973 5'	TGATCGTAACACATTC 35188	GATGA	
		GAATGTGT GCGATCA		
		CTTACACA TGCTAGT		
		A__		
GAM532	CMKLR1 5'	ACAGCCACAGCCAGAGGAGCCT 10275	AG_ ATA A C	
		AGGC TC GCT TGGC GT		
		TCCG AG CGA ACCG CA		
		AGG AC_ C A		
GAM532	LENG4 5'	ACGGCCATAGCTGTGGACTCTC 23579	CAG	
	T	AGAGG TCATAGCTATGGCCGT		
		TCTCT GGTGTCGATACCGGCA		
		CA_		
GAM532	LRP4 3'	ACAGCCAGCATGACTGCTTCT 32194	A AT C	
		AGAGGCAGTCAT GCT GGC GT		

			TCTTCGTCAGTA CGA CCG CA		
			— — A		
GAM532	SOX10	3'	TGTAGCTATATCTGCCCCT 13826	A TC	
			AG GGCAG ATAGCTATG		
			TC CCGTC TATCGATGT		
			C TA		
GAM532	FIGN	3'	CCTAAAACTATGACTGCCTTT 45777	CTAT__	
			AGAGGCAGTCATAG GG		
			TTTCCGTCAGTATC CC		
			AAAAAT		
GAM532	KIAA0759	3'	GCCATGCCTGCCTCT 33441	TCATA T	
			AGAGGCAG GC ATGGC		
			TCTCCGTC CG TACCG		
			— —		
GAM532	KIAA1058	3'	CGCCATACACTGCTTC 40012	CATAGC C	
			GAGGCAGT TATGGC G		
			CTTCGTCA ATACCG C		
			C__ A		
GAM532	SNX10	3'	TGTAGACCAGACTGCCTCT 14968	ATAG	
			AGAGGCAGTC CTATG		
			TCTCCGTCAG GATGT		
			ACCA		
GAM532	LOC146714	5'	GGCCGCCAGAACTGCCTCT 40722	CATA TAT	
			AGAGGCAGT GC GGCC		
			TCTCCGTCA CG CCGG		
			AGAC__		
GAM532	LOC150142	5'	GGCCATGCTGCCTCT 38854	CATAGCT	
			AGAGGCAGT ATGGCC		
			TCTCCGTCTG TACCGG		
			—		
GAM532	LOC150696	3'	TGTAGCATGACTGCCTCT 29531	A	
			AGAGGCAGTCAT GCTATG		
			TCTCCGTCAGTA CGATGT		
			—		
GAM532	LOC220980	3'	GCAGCCATCAACTGCCTCT 44738	CATAGCT C	
			AGAGGCAGT ATGGC GT		
			TCTCCGTCA TACCG CG		
			AC__ A		
GAM532	LOC92539	3'	CTGTAGCCAGACTGCCTCT 34504	ATA	
			AGAGGCAGTC GCTATGG		

TCTCCGTCAG CGATGTC
 AC_
 GAM533 AKAP13 3' AGAGCCTTGAATCTACT 43176 _ CTTG G
 AG AGAT CC AAGGCTCT
 || ||| || |||||
 TC TCTA GG TTCCGAGA
 A A__ _
 GAM533 BACH2 5' AGAGCCTTCTCATCTCT 22376 CTTGCC
 AGAGAT GAAGGCTCT
 ||||| |||||
 TCTCTA CTTCCGAGA
 CT____
 GAM533 CNR1 3' TAGAGGATTAGTAAGATCTCT 18165 CG GG
 AGAGATCTTGC AA CTCTA
 ||||| || |||
 TCTCTAGAATG TT GAGAT
 A_ AG
 GAM533 DDX6 3' AGAGCCTTGGCCCTCT 10641 ATCTT G
 AGAG GCC AAGGCTCT
 ||| || |||||
 TCTC CGG TTCCGAGA
 C__ _
 GAM533 DLG5 3' AGAGCTTTGACAAACCTC 40332 ATC C G
 GAG TTG CGAAG CTCT
 || || |||| |||
 CTC AAC GTTTC GAGA
 CA_ A _
 GAM533 EPHB2 3' AGACTAACAGCAGATCTCT 10731 T CGAA C
 AGAGATCT GC GG TCT
 ||||| || |||
 TCTCTAGA CG TC AGA
 _ ACAA _
 GAM533 EXO1 5' AGAGCCTTTAGAGCTCT 28182 A TGCC
 AGAG TCT GAAGGCTCT
 ||| || |||||
 TCTC AGA TTTCCGAGA
 G ____
 GAM533 CNIL 3' TCTATCCAGCAAGATCCT 12354 A C_ _
 AG GATCTTGC GA AGG
 || ||||| || |||
 TC CTAGAACG CT TCT
 _ AC A
 GAM533 DKK2 3' GTTAGAGTTTAACAAAATACTC 15775 _ C CCGA
 GAG AT TTG AGGCTCTAAC
 ||| || |||||
 CTC TA AAC TTTGAGATTG
 A A AA__
 GAM533 FLJ10307 3' AGAACCTCTGGGATCTC 19812 TTG A C
 GAGATC CCG AGG TCT
 ||||| || ||| |||

CTCTAG GGT TCC AGA
 ____ C A
 GAM533 GTF3C1 3' GCCATCTCGGCAGGATCTC 7261 A__
 GAGATCTTGCCGA GGC
 ||||| |||
 CTCTAGGACGGCT CCG
 CTA
 GAM533 HSA277841 3' GCTACTTCGGCAAGACATCT 20634 GA ____
 AGA TCTTGCCGAAG GC
 || ||||| ||
 TCT AGAACGGCTTC CG
 AC AT
 GAM533 KIAA0189 3' GCCAGGTGCAGCAGGATCCCT 16318 A ____ AA_
 AG GATCTTGC CG GGC
 || ||||| || |||
 TC CTAGGACG GT CCG
 C AC GGA
 GAM533 KIAA0552 3' GCCCCTCCCCCAACAAGATCTC 16347 CC____ A_
 T AGAGATCTTG GA GGC
 ||||| || |||
 TCTCTAGAAC CT CCG
 AACCCC CC
 GAM533 KIAA0712 3' GTTAGAGTCGTGGAAAAATCCC 16265 A C G AA
 T AG GAT TT CCG GGCTCTAAC
 || ||| ||| |||||
 TC CTA AA GGT CTGAGATTG
 C A A G_
 GAM533 WWP1 5' TTAGAGCCTGACACCTCT 39191 ATCT CCGA
 AGAG TG AGGCTCTAA
 ||| || |||||
 TCTC AC TCCGAGATT
 C__ AG_
 GAM533 LOC137492 5' AGAGCCTTCCAGGGCCTC 37106 AT CC
 GAG CTTG GAAGGCTCT
 ||| ||| |||||
 CTC GGAC CTTCCGAGA
 CG ____
 GAM533 LOC144776 3' AGACTGACAGCAGATCTCT 37787 T CGAA C
 AGAGATCT GC GG TCT
 ||||| || || |||
 TCTCTAGA CG TC AGA
 _ ACAG _
 GAM533 LOC146420 5' GTCTCAGCAGGATCTCT 40694 C A
 AGAGATCTTGC GA GGC
 ||||| || |||
 TCTCTAGGACG CT CTG
 A _
 GAM533 LOC158402 5' TTAGAGCCTTTGTCCTCT 41978 ATCTTGC
 AGAG CGAAGGCTCTAA
 ||| |||||

TCTC GTTTCCGAGATT
 CT____
 GAM533 LOC257438 3' AGAACCTCTGGGATCTC 45106 TTG A C
 GAGATC CCG AGG TCT
 ||||| ||| ||| |||
 CTCTAG GGT TCC AGA
 ____ C A
 GAM534 FOXD2 5' GGGTGGGGACCGCCGCCA 10790 A ACTTTAA
 TGGCG GC CCCCACCC
 ||||| || |||||
 ACCGC CG GGGGTGGG
 _ CCA____
 GAM534 SDC1 3' CGGGTGGGGCTTGGGGCTC 8887 A TAA
 GAGC CTT CCCCACCCG
 ||| ||| |||||
 CTCG GGG GGGGTGGGC
 _ TTC
 GAM534 CSR1 3' GGGTGGGGCGTTACTGCCA 18360 AGC TTAA
 TGGCG AC CCCCACCC
 ||||| || |||||
 ACCGT TG GGGGTGGG
 CAT C____
 GAM534 DKFZP434P211 3' GGGTTAAATGCCGACCA 15869 _ A C
 TGG CG GCA TTAAACCC
 ||| ||| |||||
 ACC GC CGT AAATTGGG
 A _ A
 GAM534 DKFZP586B2420 3' CGGATGAGATGACAGCTCGCCA 37009 ACT ACCC C
 TGGCGAGC TTA CA CCG
 ||||| ||| |||
 ACCGCTCG AGT GT GGC
 AC_ AGA_ A
 GAM534 FBX30 3' GGTGGGGTTAGGTTCCCA 27042 C ACT
 TGG GAGC TTAACCCACC
 ||| ||| |||||
 ACC CTTG GATTGGGGTGG
 _ _
 GAM534 HSPC043 5' GGTGATTGTGAAGTGCTGACCA 33636 CG ACCC
 TGG AGCACTTTA CACC
 ||| ||||| |||
 ACC TCGTGAAGT GTGG
 AG GTTA
 GAM534 KIAA0495 5' CGGGTGGGATCGTCCTGGCC 31356 G C TTAAAC
 GGC AG AC CCCACCCG
 ||| ||| |||||
 CCG TC TG GGGTGGGC
 G C CTA____
 GAM534 KIAA1243 5' CGGGTAAAGAAGTTAAAGTACC 36471 CGAGC CCC____
 ACCA TGG ACTTTAAC ACCCG
 ||| ||||| |||||

ACC TGAAATTG TGGGC
 ACCA_ AAGAAA
 GAM534 LOC157918 3' GGTGGGGTTGGAGCCCCCA 41898 CGAGCA
 TGG CTTTAACCCCACC
 ||| |||||
 ACC GAGGTTGGGGTGG
 CCC__
 GAM535 PHLDA3 3' TCATGCTACCCACCACCTCA 14760 AT ATA G
 TGAGGT TGG GG GTGA
 ||||| ||| ||
 ACTCCA ACC TC TACT
 CC CA_ G
 GAM535 PIM2 3' TTCCTTCCAATACCCCA 30135 A T
 TG GGTATTGGA AGGGG
 || ||||| ||||
 AC CCATAACCT TCCTT
 C _
 GAM535 DKFZP566G1424 5' GTGGCCTCCAATACCCCA 41116 A TAGG G
 TG GGTATTGGA GGT AT
 || ||||| ||| ||
 AC CCATAACCT CCG TG
 C _ G
 GAM535 FLJ11370 3' TCACTTACCCAATGCCCA 24517 A ATAG
 TG GGTATTGG GGGTGA
 || ||||| ||||
 AC CCGTAACC TTCACT
 C CA_
 GAM535 MIG 3' TCATCTTGTCCCCAACACCCCA 8247 A A ATA_
 TG GGT TTGG GGGGTGA
 || ||| ||| |||||
 AC CCA AACC TTCTACT
 C C CCTG
 GAM535 phospho1 5' CATCCTGCGCCCCAATACCTCA 40059 ATA_
 TGAGGTATTGG GGGGTG
 ||||| ||||
 ACTCCATAACC TCCTAC
 CCGCG
 GAM535 ZNF262 3' TTAAGTGAACACCCAATACCC 11559 A ATAGG_
 A TG GGTATTGG GGTGA
 || ||||| ||||
 AC CCATAACC TCATT
 _ CACAAGAG
 GAM535 LOC144308 3' ATCACCCCGTTCGCCCTCA 40405 TAT TA
 TGAGG TGGA GGGGTGAT
 |||| ||| |||||
 ACTCC GCTT CCCCACTA
 C_ GC
 GAM535 LOC149414 5' ATCACCCCGTGTACATCA 40988 G TT ATA
 TGA GTA GG GGGGTGAT
 ||| ||| || |||||

ACT CAT TC CCCCCTA
 A CG ____
 GAM535 LOC196527 3' TATCACCCGGAAAACCTCA 42401 A GGATAG
 TGAGGT TT GGGTGATA
 ||||| || |||||
 ACTCCA AA CCCACTAT
 _ AGG____
 GAM535 LOC199858 5' ATCACCCCTAGTGACCCA 42629 A ATTGGA
 TG GGT TAGGGGTGAT
 || ||| |||||
 AC CCA ATCCCCACTA
 _ GTG____
 GAM535 LOC222134 5' CATGTCATCCAACCCCTCA 45169 TA A G
 TGAGG TTGGAT GG GTG
 |||| ||||| || |||
 ACTCC AACCTA CT TAC
 CC _ G
 GAM536 AKT1 3' ATGCAACCTCACTATGGTATGC 11649 G TC A A
 TG TAGCATAC GTA GA GTT CAT
 ||||| ||| || ||| |||
 GTCGTATG TAT CT CAA GTA
 G CA C C
 GAM536 KIAA0534 3' ACAGAGATGCCGTATACTA 35376 C GAA
 TAG ATACGGTATC GT
 ||| ||||| || ||
 ATC TATGCCGTAG CA
 A AGA
 GAM537 GPR18 5' AACAGAAGCAACTCAAAG 11783 C GGCC
 CTTTG GG GCTTCTGTT
 |||| || |||||
 GAAAC TC CGAAGACAA
 _ AA____
 GAM537 LOC148894 3' ACAGAAGGGCGCCAAGC 40914 TGC G G
 GCTT GG GCC CTTCTGT
 |||| || ||| |||||
 CGAA CC CGG GAAGACA
 _ G _
 GAM538 ANXA8 3' GCTGGGAGCCCTTTTGTTTTA 7341 CA GA A
 TAAACAAAA GC TC CAGC
 ||||| || || |||
 ATTTTGT TTT CG GG GTCG
 CC A_ _
 GAM538 CERD4 3' GCTGTGGTTAGTATCTTGTT 14347 AACA _
 AACAA GC GATCACAGC
 |||| || |||||
 TTGTT TG TTGGTGTCG
 CTA_ A
 GAM538 COL4A3 3' CTGTATGGTTTTGTTTTGTTTT 25355 _ G C
 G TAAACAAAACA GC AT ACAG
 ||||| || || |||

			GTTTTGTTTTGT TG TA TGTC		
			TT G _		
GAM538	COL4A3	3'	CTGTATGGTTTTGTTTTGTTTT 25361	___	G C
	G		TAAACAAAACA GC AT ACAG		
			GTTTTGTTTTGT TG TA TGTC		
			TT G _		
GAM538	COL4A3	3'	CTGTATGGTTTTGTTTTGTTTT 5548	___	G C
	G		TAAACAAAACA GC AT ACAG		
			GTTTTGTTTTGT TG TA TGTC		
			TT G _		
GAM538	DCK	3'	CTGTGATTACTCTTTGCTTTG 6442	A	AC CG
			TAAA CAAA AG ATCACAG		
			GTTT GTTT TC TAGTGTC		
			C C_ AT		
GAM538	DUSP5	3'	CTGTGATTTTTGTTTTTA 10685	C	C
			A AAAACAG GATCACAG		
			A TTTTGTT TTAGTGTC		
			T T		
GAM538	EIF1AY	3'	CTGGGGTGCCATTTTGTTTT 11045	CA	AT A
			AAACAAAA GCG C CAG		
			TTTTGTTTT CGT G GTC		
			AC GG _		
GAM538	EML1	3'	CTGTGATTTCTGTTTTGTTT 30037		C
			AAACAAAACAG GATCACAG		
			TTTGTTTTGTC TTAGTGTC		
			T		
GAM538	FGFR1	3'	GCTACTTTTGCTGTTTTATTTT 6209	C	TCAC
			AAAA AAAACAGCGA AGC		
			TTTT TTTTGTCGTT TCG		
			A TTCA		
GAM538	FGFR1	3'	GCTACTTTTGCTGTTTTATTTT 23374	C	TCAC
			AAAA AAAACAGCGA AGC		
			TTTT TTTTGTCGTT TCG		
			A TTCA		
GAM538	FGFR1	3'	GCTACTTTTGCTGTTTTATTTT 17980	C	TCAC
			AAAA AAAACAGCGA AGC		
			TTTT TTTTGTCGTT TCG		
			A TTCA		
GAM538	GPC4	3'	CTGTGATCTCGCCTTGTTT 7177	AACA	___
			AAACAA GCGA TCACAG		

			TTTGTT CGCT AGTGTC		
			C___ CT		
GAM538	HDAC4	3'	GGTCCCTGTTTTGCTTTA 12667	A	C
			TAAA CAAAACAG GATC		
			ATTT GTTTTGTC CTGG		
			C C		
GAM538	ITCH	3'	CTGTGATTCCTTCATTGTTTTA 25563	AAC	C
			TAAAACAA AG GATCACAG		
			ATTTTGTT TC TTAGTGTC		
			ACT C		
GAM538	LIPA	3'	GCTGTGATTTGACACGTTTTA 5746	AAAA	GC
			TAAAAC CA GATCACAGC		
			ATTTTG GT TTAGTGTCG		
			CACA _		
GAM538	NRAS	3'	GCTGTGATCAGTGATTTTCA 8362	C	CA _
			A AAAA GC GATCACAGC		
			A TTTT TG CTAGTGTCG		
			C AG A		
GAM538	OSR1	3'	CTGTGTTCTTGTTTTGTTCA 11591	A	C T
			A AACAAAACAG GA CACAG		
			A TTGTTTTGTT CT GTGTC		
			C _ T		
GAM538	PLXNA2	3'	CTGTTTTTTGTTTTGTTTTA 24814	C	TC
			TAAAACAAAACAG GA ACAG		
			ATTTTGTTTTGTT TT TGTC		
			T _		
GAM538	SLC22A5	3'	GCTGTAATGTGGGTTTTGTTTT 9027	A_	ATC
	A		TAAAACAAAAC GCG ACAGC		
			ATTTTGTTTTG TGT TGTCG		
			GG AA_		
GAM538	TGFBR2	3'	CTGTGGCTTGTTTTGTTT 9240	_	GAT
			AAACAAAACA GC CACAG		
			TTTGTTTTGT CG GTGTC		
			T _		
GAM538	TTN	5'	CTGTGTAGTTTTGTTTT 28503	AGCGAT	
			AAACAAAAC CACAG		
			TTTTGTTTTG GTGTC		
			AT_		
GAM538	TTN	5'	CTGTGTAGTTTTGTTTT 28505	AGCGAT	
			AAACAAAAC CACAG		

			TTTTGTTTTG	GTGTC		
			AT____			
GAM538	TTN	5'	CTGTGTAGTTTTGTTTT	28508	AGCGAT	
			AAAACAAAAC	CACAG		
			TTTTGTTTTG	GTGTC		
			AT____			
GAM538	TTN	5'	CTGTGTAGTTTTGTTTT	28518	AGCGAT	
			AAAACAAAAC	CACAG		
			TTTTGTTTTG	GTGTC		
			AT____			
GAM538	BIRC5	3'	CTGTGCTCCTGTTTTGTCTTG	6837	A C T	
			TAA ACAAACAG GA CACAG			
			GTT TGTGTTTGTC CT GTGTC			
			C _ C			
GAM538	CHORDC1	3'	CTGTAATCTTTTGTTTTG	14437	C_ C	
			CAAAACAG GAT ACAG			
			GTTTTGTT CTA TGTC			
			TT A			
GAM538	DKFZP434C0826	5'	GCTTTGGCTGTTTTGT	40845	GAT C	
			ACAAAACAGC CA AGC			
			TGTTTTGTGCG GT TCG			
			___ T			
GAM538	DKFZp566H0824	5'	GCTGTCCTTGTTCTGTTTTG	18977	___ TC	
			CAAAACAG CGA ACAGC			
			GTTTTGTC GTT TGTCG			
			TT CC			
GAM538	DNAJB4	5'	CTGGGGACGCTGTTTTCTTTTA	13904	C A A_	
			TAAAA AAAACAGCG TC CAG			
			ATTTT TTTTGTGCGC AG GTC			
			C _ GG			
GAM538	FLJ00026	3'	GCTGTATAGTTATTTTGTGTTT	32428	C_ GATC	
	A		TAAACAAAA AGC ACAGC			
			ATTTTGTGTTT TTG TGTCG			
			TA ATA_			
GAM538	FLJ10081	3'	GCTGTGATGGTTCTGTTTTTA	19724	C _ G	
			A AAAACAG C ATCACAGC			
			A TTTTGTC G TAGTGTCG			
			T TT G			
GAM538	FLJ10702	3'	CTGTGTGTGATTTTGTGTT	20027	CA AT	
			AAACAAAA GCG CACAG			

		TTTGTTTT TGT GTGTC		
		AG _		
GAM538	FLJ11850 3'	GCTGTGGTGTCTTGTT 22950	AAC G	
		AACAA AGC ATCACAGC		
		TTGTT TTG TGGTGTCG		
		CT_ _		
GAM538	FLJ13187 3'	GCTCTCTCTGTTTTGTT 23870	C TCAC	
		AACAAAACAG GA AGC		
		TTGTTTTGTC CT TCG		
		T CTC_		
GAM538	FLJ20232 3'	CTGTGATAGCATGTTTCA 21083	A _ G	
		C AAACA GC ATCACAG		
		A TTTGT CG TAGTGTC		
		C A A		
GAM538	KIAA0229 3'	CTGCTCGCTTTGTTTT 44399	AAC TCA	
		AAAACAA AGCGA CAG		
		TTTTGTT TCGCT GTC		
		_ C_		
GAM538	KIAA0258 3'	TGTGGGCCTTTTTGTTTTA 16652	CA GA	
		TAAACAAAA GC TCACA		
		ATTTTGTTTT CG GGTGT		
		TC _		
GAM538	KIAA0276 3'	GTGAGAGCTGTTTTGTTTT 35137	GA	
		AAAACAAAACAGC TCAC		
		TTTTGTTTTGTCG AGTG		
		AG		
GAM538	KIAA0322 3'	CTGTTCTGTTTTGTTT 44560	CGATC	
		AAACAAAACAG ACAG		
		TTTGTTTTGTC TGTC		
		T_		
GAM538	KIAA0515 3'	CTTTGAGGCTTTTTGTTTTA 31924	C GA C	
		TAAACAAAA AGC TCA AG		
		ATTTTGTTTT TCG AGT TC		
		_ G_ T		
GAM538	KIAA0660 3'	CTGTTATTTGCTGATTTTGTTT 14657	_ TC_	
	TA	TAAACAAAA CAGCGA ACAG		
		ATTTTGTTTT GTCGTT TGTC		
		A TAT		
GAM538	KIAA0876 3'	GCTGTTTTTTTGTTGTTGTTTT 32298	AA TC_	
	A	TAAACA ACAGCGA ACAGC		

			ATTTTGT TGTTGTT TGTCG	
			— TTTT	
GAM538	KIAA0993	3'	GCTGTGGGCAACTGTTTTGTT 32081	CGA_
			AACAAAACAG TCACAGC	
			TTGTTTTGTC GGTGTCG	
			AACG	
GAM538	KIAA1023	3'	GCTGCAGTGTGGTTTTGTT 19092	A ATCA
			AACAAAAC GCG CAGC	
			TTGTTTTG TGT GTCG	
			G GAC_	
GAM538	KIAA1265	3'	TGTGCAGCTAGCTTTGTTTTA 35036	AC_ GAT
			TAAACAAA AGC CACA	
			ATTTTGTTT TCG GTGT	
			CGA AC_	
GAM538	KIAA1493	3'	GCTGTGGTTGTCTCGTTT 32091	_ _
			AAAC AG CGATCACAGC	
			TTTG TC GTTGGTGTCG	
			C T	
GAM538	KIAA1804	3'	CTATGATTGCTTTGTGTTCA 34587	A AAAC C
			A AACA AGCGATCA AG	
			A TTGT TCGTTAGT TC	
			C GTT_ A	
GAM538	MGC2452	5'	GCTGTGTTTTGTTTTGTTT 26372	CGAT
			AAACAAAACAG CACAGC	
			TTTGTTTTGTT GTGTCG	
			TT_	
GAM538	MGC2477	5'	CTGTTTTGCTTTGTTTT 23542	AAC TC
			AAAACAA AGCGA ACAG	
			TTTTGTT TCGTT TGTC	
			_ T_	
GAM538	NUDT11	3'	CTGTGGTTATGTTGTTTT 30141	_
			AAAACAGC GATCACAG	
			TTTTGTTG TTGGTGTC	
			TA	
GAM538	SEC14L1	3'	GCTGTGATCACCTGCCTTTG 8902	A_ C_
			CAAA CAG GATCACAGC	
			GTTT GTC CTAGTGTCG	
			CC CA	
GAM538	SP2	5'	GCAGTGTCTTGTTTTGTTTTA 9081	C T A
			TAAACAAAACAG GA CAC GC	

		ATTTTGTTTTGTT CT GTG CG	
		— — A	
GAM538	SRPK1	3' TGAGGCTTTTTTGTTTTA 9110	C GA
		TAAACAAAA AGC TCA	
		ATTTTGTTTT TCG AGT	
		T G_	
GAM538	LOC134266	3' TGA CTGGCTAGTTTTGTTTT 37072	_ GA_
		AAACAAAAC AGC TCA	
		TTTTGTTTTG TCG AGT	
		A GTC	
GAM538	LOC142972	3' GCTGGGAGCCCTTTTGTTTTA 32478	CA GA A
		TAAACAAAA GC TC CAGC	
		ATTTTGTTTT CG GG GTCG	
		CC A_ _	
GAM538	LOC145439	5' CTGTGTTTCTGCCTTGTTTTA 37864	AA C T
		TAAACAA CAG GA CACAG	
		ATTTTGTT GTC TT GTGTC	
		CC T _	
GAM538	LOC147165	3' CTGTGTTTTGCAGCATTTTGTT 40814	CA__ T_
	TTA	TAAACAAAA GCGA CACAG	
		ATTTTGTTTT CGTT GTGTC	
		ACGA TT	
GAM538	LOC199232	3' CTGTGTGGTTTTGTTTT 42879	AGCGAT
		AAACAAAAC CACAG	
		TTTTGTTTTG GTGTC	
		GT_____	
GAM538	LOC200609	5' CTGCTGATCTGTTTTGT 43328	GC _
		ACAAAACA GATCA CAG	
		TGTTTTGT CTAGT GTC	
		_ C	
GAM538	LOC200933	3' GCTGTATGTATGTTTTGTTTTA 43363	_ ATC
		TAAACAAAACA GCG ACAGC	
		ATTTTGTTTTGT TGT TGTCG	
		A A_	
GAM538	LOC253664	3' CTGTTTTTTGTTTTGTTTTG 45449	C TC
		TAAACAAAACAG GA ACAG	
		GTTTTGTTTTGTT TT TGTC	
		T _	
GAM538	LOC51026	3' TGATTGCACTATTTTGTTTT 18144	CA__
		AAACAAAA GCGATCA	

			TTTTGTTTT CGTTAGT	
			ATCA	
GAM538	LOC91351	3'	GCTGATTCAACTGTTTTGTT 32696	C_ TCA
			AACAAAACAG GA CAGC	
			TTGTTTTGTC CT GTCG	
			AA TA_	
GAM538	LOC93512	3'	CTGTGTTTTGCAGCATTTTGTT 35878	CA__ T_
			TTA TAAACAAAA GCGA CACAG	
			ATTTTGTTTT CGTT GTGTC	
			ACGA TT	
GAM539	CDH6	3'	ACCTCAAATCCACCCATATG 11371	TATA A
			CATATGGGTGG GA GGT	
			GTATACCCACC CT CCA	
			TAAA _	
GAM539	GABRE	3'	ACCTTCTAGACCACATGATA 11406	ATGG A
			TATCAT GTGGT TAGAAGGT	
			ATAGTA CACCA ATCTTCCA	
			_____ G	
GAM539	GABRE	3'	ACCTTCTAGACCACATGATA 22508	ATGG A
			TATCAT GTGGT TAGAAGGT	
			ATAGTA CACCA ATCTTCCA	
			_____ G	
GAM539	GABRE	3'	ACCTTCTAGACCACATGATA 22512	ATGG A
			TATCAT GTGGT TAGAAGGT	
			ATAGTA CACCA ATCTTCCA	
			_____ G	
GAM539	GABRE	3'	ACCTTCTAGACCACATGATA 22527	ATGG A
			TATCAT GTGGT TAGAAGGT	
			ATAGTA CACCA ATCTTCCA	
			_____ G	
GAM539	LTB4R	5'	CCTTCTCCTATATGATA 6405	TGGTAT
			TATCATATGGG AGAAGG	
			ATAGTATATCC TCTTCC	

GAM539	PIM2	3'	ACCTCCTACTACCACCACA 30132	_ _ A
			TG GGTGGTA TAG AGGT	
			AC CCACCAT ATC TCCA	
			A C C	
GAM540	NCK1	3'	ATTTGTCACAGGCCATTGTA 12809	AT__
			TACAATGGCC ATAAGT	

			ATGTTACCGG TGTTTA		
			ACAC		
GAM540	OSBPL11	3'	CTGTTGTTTATCAGCCATTGTA 23046	CAT	GT_
			TACAATGGC ATAA ATAG		
			ATGTTACCG TATT TGTC		
			AC_ TGT		
GAM540	THEA	3'	ATCCATACCTATATGTGGC 32948	A__	A
			GCCATATA GTAT GAT		
			CGGTGTAT CATA CTA		
			ATC C		
GAM540	LOC199796	5'	ATCTACACAGAAGCCATTGTG 36805	CATATAA	A
			TACAATGGC GT TAGAT		
			GTGTTACCG CA ATCTA		
			AAGA__ C		
GAM541	HSA249128	3'	AGAGATATTTTTAGTATATGA 19023	TTTTCG	
			TCATATATTTAA ATCTCT		
			AGTATATGATTT TAGAGA		
			TTA__		
GAM541	KIAA1005	3'	GTTGAAAACCTTAGTATATGA 35779	A	
			TCATATATTAA TTTTCGAT		
			AGTATATGATT AAAAGTTG		
			C		
GAM542	EDNRA	3'	TTGTAATCATGTTACCATTACA 32060	A__	
			TGTAATGGTGATA TACAA		
			ACATTACCATTGT ATGTT		
			ACTA		
GAM542	FCMD	3'	AGATTTTGTAGGGACCCATTA 13571	TGATAA	
			TAATGG TACAAAATCT		
			ATTACC ATGTTTTAGA		
			CAGGG_		
GAM542	ING1	3'	ATTTTGTATTATTGTTCTCAC 12060	AAT TG	
			GT GG ATAATACAAAAT		
			CA TT TATTATGTTTTA		
			CTC GT		
GAM542	DKFZP434C1715	3'	AGATTTTGTATCATGCCAT 41671	G A	
			ATGGT AT ATACAAAATCT		
			TACCG TA TATGTTTTAGA		
			_ C		
GAM542	OSBPL1A	3'	GATTTTAATCACCATTACA 27906	AATAC	
			TGTAATGGTGAT AAAATC		

			ACATTACCACTA	TTTTAG		
			A_____			
GAM542	OSBPL1A	3'	GATTTTAATCACCATTACA	28423	AATAC	
			TGTAATGGTGAT	AAAATC		
			ACATTACCACTA	TTTTAG		
			A_____			
GAM542	OSBPL1A	3'	GATTTTAATCACCATTACA	19771	AATAC	
			TGTAATGGTGAT	AAAATC		
			ACATTACCACTA	TTTTAG		
			A_____			
GAM542	SEC24A	3'	ATTTTGTTAACTATTACA	40232	GATAAT	
			TGTAATGGT	ACAAAAT		
			ACATTATCA	TGTTTTA		
			AT_____			
GAM542	LOC220038	5'	AGATTCTGTATTATCCT	44079	T	A
			GG GATAATACA AATCT			
			TC CTATTATGT TTAGA			
			— C			
GAM543	C1D	3'	CTGAGGATTTTAACATTGTGAT	13031	ATCA	A
	A		TATCACAAT	AGAATT TCAG		
			ATAGTGTTA	TTTTAG AGTC		
			CAA_ G			
GAM543	SGK	3'	CTGATAATTGTATGTATTGT	12139	CAAG	
			ACAATAT	AATTATCAG		
			TGTTATG	TTAATAGTC		
			TATG			
GAM543	C12orf22	3'	GGTTCTTTACATTGTGATA	25130	ATC	
			TATCACAAT	AAGAATT		
			ATAGTGTTA	TTCTTGG		
			CAT			
GAM543	GG2-1	3'	GATTGGTCTTGATATTGAGATA	15678	A	ATT
			TATC CAATATCAAGA	ATC		
			ATAG GTTATAGTTCT	TAG		
			A GGT			
GAM543	HT008	3'	GATGTTCCCATATTGTGA	30072	CAA	T
			TCACAATAT	GAAT ATC		
			AGTGTTATA	CTTG TAG		
			CCC _			
GAM543	KIAA0820	3'	CTGATTGCTCTGATATTGT	34218	A	ATT
			ACAATATCA	GA ATCAG		

			TGTTATAGT CT TAGTC		
			_ CGT		
GAM543	TCL6	3'	CTGATAAAACAGATTGTGATA 15766	ATCAAGAA	
			TATCACAAT TTATCAG		
			ATAGTGTTA AATAGTC		
			GACAA__		
GAM543	TCL6	3'	CTGATAAAACAGATTGTGATA 21760	ATCAAGAA	
			TATCACAAT TTATCAG		
			ATAGTGTTA AATAGTC		
			GACAA__		
GAM543	LOC153684	5'	GATATCCTTGATATTGGA 41650	A AAT	
			TC CAATATCAAG TATC		
			AG GTTATAGTTC ATAG		
			_ CT_		
GAM543	LOC154792	5'	TAATTTCTTATATTGTGATA 41728	C _	
			TATCACAATAT AAG AATTA		
			ATAGTGTTATA TTC TTAAT		
			_ CT		
GAM544	PDX1	3'	CCAAGAAACATATGTTATA 9547	ACA	
			TATAACATG TTTTTTGG		
			ATATTGTAT AAAGAACC		
			AC_		
GAM544	S164	3'	CCAACCTGAAATGTCTGTTATA 30483	T TT C	
			TATAACA GACATTTT GG TGG		
			ATATTGT CTGTAAAG CC ACC		
			_ T_ A		
GAM544	LOC153338	3'	CCAACCAAAAGATCATGCTA 41610	A CA C	
			TA CATGA TTTTTTGG TGG		
			AT GTACT AGAAAACC ACC		
			C _ A		
GAM544	LOC220936	3'	CCAAGAATGTCTTGTGCTA 43930	A T T	
			TAT ACA GACATTTT GG		
			ATA TGT CTGTAAGAA CC		
			C T _		
GAM544	LOC92973	5'	CCAGAAAATGCCATGTTA 35184	A	
			TAACATG CATTTTTTGG		
			ATTGTAC GTAAAAGACC		
			C		
GAM545	SIRT5	5'	AATGGAAATGTTTCTAA 14547	TGATT	
			TTAGA CATTTCCATT		

			AATCT	GTAAAGGTAA		
			TTT__			
GAM545	C20orf106	3'	AATGGAAATGATATCATC	28090	—	
			GATGAT TCATTTCCATT			
			CTACTA AGTAAAGGTAA			
			T			
GAM545	LOC151248	5'	AATGGAAATGAGGTGTATTTA	39082	AT__	
			TAGATG TCATTTCCATT			
			ATTTAT AGTAAAGGTAA			
			GTGG			
GAM545	LOC90408	5'	AATGGAGACCCATCTAA	31393	ATTCA	
			TTAGATG TTTCCATT			
			AATCTAC AGAGGTAA			
			CC__			
GAM546	CCRL1	3'	GAATAACACTCTGCTGTA	18632	T A	
			TACA CAGA TGTTATTT			
			ATGT GTCT ACAATAAG			
			C C			
GAM546	LOC200845	5'	AAATACCATTCTGATGTA	42862	T	
			TACATCAGAATG TATTT			
			ATGTAGTCTTAC ATAAA			
			C			
GAM546	LOC221975	3'	GAAAACACTCTGATGTA	44497	A AT	
			TACATCAGA TGTT TTC			
			ATGTAGTCT ACAA AAG			
			C _			
GAM547	ASPH	3'	TATCACTATAGATCATAGTTA	26224	GG TACAA	
			TAGCTATGA TGT TGATA			
			ATTGATACT ATA ACTAT			
			AG TC__			
GAM547	ASPH	3'	TATCACTATAGATCATAGTTA	26228	GG TACAA	
			TAGCTATGA TGT TGATA			
			ATTGATACT ATA ACTAT			
			AG TC__			
GAM547	CAPZA1	3'	ATCATTTATTGCATCTCATAAC	35946	C TAC_	
	TA		TAG TATGAGGTGT AATGAT			
			ATC ATACTCTACG TTACTA			
			A TTAT			
GAM547	SLC17A4	3'	ATCATTGTTTTCCCTCACAG	11998	A TGTT	
			CT TGAGG ACAATGAT			

GA ACTCC TGTTACTA
 C CTTT
 GAM547 C20orf110 3' CACTTGGGCACTTCACAGC 38833 A A _
 GCT TGAGGTGTT CAA TG
 ||| ||||| ||| ||
 CGA ACTTCACGG GTT AC
 C _ C
 GAM547 ZNF323 3' ATCATTGCAACCTTATTAGGC 25168 _ GTTA
 GCT ATGAGGT CAATGAT
 ||| ||||| |||||
 CGG TATTCCA GTTACTA
 AT AC_
 GAM547 LOC149619 5' ATCATTATAACATCTTCA 41027 _ C
 TGA GGTGTGA AATGAT
 ||| ||||| |||||
 ACT CTACAAT TACTA
 T A
 GAM548 KIAA0857 3' AGCCTTTGTTGTCCTCCCATCC 33120 C_ A T _
 ATCCA TGGATGGA GAG ACA CAA GCT
 ||||| ||| ||| ||| |||
 ACCTACCT CTC TGT GTT CGA
 ACC C T TC
 GAM548 VIPR1 3' GAGCTGCCCTCCTTGTCCACCC 10992 A AACATCA
 A TGG TGGACGAG AGCTC
 ||| ||||| |||||
 ACC ACCTGTTC TCGAG
 C CTCCCG_
 GAM548 C16orf5 5' GAGCCCTGCCTGTTCCCTGTCC 15053 A_ T_ A_
 ATCCA TGGATGGACG GAACA CA GCTC
 ||||| |||| || ||||
 ACCTACCTGT CTTGT GT CGAG
 CC CC CC
 GAM548 KIAA0427 3' GATCGTCCTGTCCATCCA 16575 A AC
 TGGATGGACG GA ATC
 ||||| || |||
 ACCTACCTGT CT TAG
 C GC
 GAM548 KIAA1163 3' GAGCTCAACATTCCATTCCATC 38559 CGA CATCA
 CA TGGATGGA GAA AGCTC
 ||||| || |||||
 ACCTACCT CTT TCGAG
 TAC ACAAC
 GAM548 KIAA1889 3' TGATTACTTTTCATCCATCCA 36391 C AC_
 TGGATGGA GAGA ATCA
 ||||| |||| |||||
 ACCTACCT CTTT TAGT
 A CAT
 GAM548 MGC5139 5' GAAATTCCTGTCCATCCA 36678 A CA
 TGGATGGACG GAA TC
 ||||| ||| ||

ACCTACCTGT CTT AG
 C AA
 GAM548 PRO2435 5' GACTGTGCTTCATCCATCCA 20602 C A_ _
 TGGATGGA GAG ACA TC
 ||||| ||| ||| ||
 ACCTACCT CTT TGT AG
 A CG C
 GAM548 TREX1 5' GAGCTTGACACCCTCGCGTCAC 27338 _ GA AACAA
 A TG GATG CGAG TCAAGCTC
 || ||| ||| |||||
 AC CTGC GCTC AGTTCGAG
 A _ CCAC
 GAM548 LOC113146 3' GAGTTGTCATTCTCATCTATCC 36128 C CATCA
 A TGGATGGA GAGAA AGCTC
 ||||| |||| ||||
 ACCTATCT CTCTT TTGAG
 A ACTG_
 GAM548 LOC90826 5' AGCTTGATGCTCTCAGTC 32049 _ A
 GAC GAGA CATCAAGCT
 ||| ||| |||||
 CTG CTCT GTAGTTCGA
 A C
 GAM548 LOC92822 3' AGCACCTTCTCGTCCACCA 34984 A CATCAA
 TGG TGGACGAGAA GCT
 ||| ||||| |||
 ACC ACCTGCTCTT CGA
 _ CCA_
 GAM549 ACADSB 3' ATCAGAAAATATTCAATACAG 7312 C TTCATC
 CTG ATTGG TTTCTGAT
 ||| |||| |||||
 GAC TAACT AAAGACTA
 A TATA_
 GAM549 AVPR1A 5' GAAAATGAACCAACACA 6375 CA C
 TG TTGGTTTCAT TTTC
 || ||||| ||||
 AC AACCAAGTA AAAG
 AC _
 GAM549 TAL1 3' GATCAGAAAAATGGAGCAA 9170 G C
 TTG TTCAT TTTCTGATC
 ||| |||| |||||
 AAC AGGTA AAAGACTAG
 G A
 GAM549 CDH26 3' GATCAGCCATCTTGAACCAAAG 22371 A TCTTT_
 CA TGC TTGGTTCA CTGATC
 ||| ||||| ||||
 ACG AACCAAGT GACTAG
 A TCTACC
 GAM549 FLJ12587 3' CAGAAAGGTGACCAAGACAG 22849 CA T
 CTG TTGGT CATCTTTCTG
 ||| |||| |||||

			GAC AACCA GTGGAAAGAC			
			AG _			
GAM549	FLJ20073	3'	ATCAGAAAAATTTGAACACAG	19163	_	TC__
			TTG GTTCA TTTCTGAT			
			GAC CAAGT AAAGACTA			
			A TTAA			
GAM549	MGC15875	5'	AGAAATGAACCACCGCA	26746	AT	CT
			TGC TGGTTCAT TTCT			
			ACG ACCAAGTA AAGA			
			CC _			
GAM549	MGC2654	3'	ATCAGAAGCTCACCAAAGCA	23553	A	TCATC
			TGC TTGGT TTTCTGAT			
			ACG AACCA GAAGACTA			
			A CTC_			
GAM549	LOC255251	5'	AGAAATGAACCACCGCA	45907	AT	CT
			TGC TGGTTCAT TTCT			
			ACG ACCAAGTA AAGA			
			CC _			
GAM550	CROT	3'	GCTACTTGAAGGCTGA	22124	T	T
			TCAG CCTTCAAGTA GC			
			AGTC GGAAGTTCAT CG			
			_ _			
GAM550	FSTL3	3'	TGACGATATCCTGGAAGGACTG	12472	A T	CG
	A		TCAGTCCTTC AG ATG CGTCA			
			AGTCAGGAAG TC TAT GCAGT			
			G C A_			
GAM550	GOT1	3'	GACACTTGCAGGACTGA	7867	T	ATGCGC
			TCAGTCCT CAAGT GTC			
			AGTCAGGA GTTCA CAG			
			C _			
GAM550	STCH	3'	TGAACTATACTTGAAGGAC	13836		CGCG
			GTCCTTCAAGTATG TCA			
			CAGGAAGTTCATAT AGT			
			CA_			
GAM550	C9orf14	5'	TGAACTTTAGCACTTGAAGAAC	41911	C	AT GCG_
	TGA		TCAGT CTTCAAGT GC TCA			
			AGTCA GAAGTTCA CG AGT			
			A _ ATTTCA			
GAM550	DKFZp547A023	5'	GTTTATACTTGAGGACTGA	35944	T	C
			TCAGTCCT CAAGTATG GC			

			AGTCAGGA GTTCATAT TG		
			— T		
GAM550	HTR3A	5'	GATCCAGCTGAAGGACTGA 6537	AGTAT GC_	
			TCAGTCCTTCA GC GTC		
			AGTCAGGAAGT CG TAG		
			— ACC		
GAM551	SLC4A4	3'	TTCTGTCACTCAAGACACA 9840	G C GCA	
			TGTGT CT GA GTGGCGGAA		
			ACACA GA CT CACTGTCTT		
			— A —		
GAM551	C20orf13	3'	TCGTGCACTGCTCGAGACACA 19300	G _	
			TGTGT CTCGAGCAGTG GCGG		
			ACACA GAGCTCGTCAC TGCT		
			— G		
GAM551	DNAJC5	3'	CCTGGCTCGAGCACACA 30813	AGT	
			TGTGTGCTCGAGC GG		
			ACACACGAGCTCG CC		
			GT_		
GAM551	FLJ10737	3'	TCCGCTGTGTCCCGAGCACAC 20067	A_ G	
			GTGTGCTCG GCA TGGCGGA		
			CACACGAGC TGT GTCGCCT		
			CC _		
GAM551	FLJ20079	3'	ATTTCATATTGCTCAAACACAC 19167	CTC GC	
	A		TGTGTG GAGCAGTG GGAAT		
			ACACAC CTCGTTAT CTTTA		
			AAA A_		
GAM551	FLJ32499	3'	TTCTCATTGCTGAGCACACA 29422	G C	
			TGTGTGCTC AGCAGTGG GGA		
			ACACACGAG TCGTTACT CTT		
			— —		
GAM551	GABBR1	3'	TCACGCTCAGCACACA 22426	C A	
			TGTGTGCT GAGC GTGG		
			ACACACGA CTCG CACT		
			— —		
GAM551	GABBR1	3'	TCACGCTCAGCACACA 7208	C A	
			TGTGTGCT GAGC GTGG		
			ACACACGA CTCG CACT		
			— —		
GAM551	KIAA0555	3'	ATTCCGTCTGCTCCAACACACA 16682	CTC TG	
			TGTGTG GAGCAG GCGGAAT		

			ACACAC CTCGTC TGCCTTA		
			AAC _		
GAM551	NR4A3	5'	CCGCTCCCTCACTCGAACACAC 13844	C	C_ T_
	A		TGTGTG TCGAG AG GGCGG		
			ACACAC AGCTC TC TCGCC		
			A AC CC		
GAM551	SH3BGRL2	3'	CCCCTGGTACTCAGCACACA 25528	C	CAGT_ C
			TGTGTGCT GAG GG GG		
			ACACACGA CTC CC CC		
			_ ATGGT _		
GAM551	LOC128989	3'	TCCTGCGTGTGCACAAGCACAC 36946	CGA	GTG _
	A		TGTGTGCT GCA GC GGA		
			ACACACGA CGT CG CCT		
			ACA GTG T		
GAM551	LOC149276	3'	CCTCCTACTCAGCACACA 40975	C	CAGT C
			TGTGTGCT GAG GG GG		
			ACACACGA CTC CC CC		
			_ AT_ T		
GAM552	APAF1	5'	GTCTCCCAGTCTTGTCCCGG 6829	C_	
			CCGGGATAAGAC GGAGAC		
			GGCCCTGTTCTG CCTCTG		
			AC		
GAM552	APAF1	5'	GTCTCCCAGTCTTGTCCCGG 14868	C_	
			CCGGGATAAGAC GGAGAC		
			GGCCCTGTTCTG CCTCTG		
			AC		
GAM552	GALNT2	3'	TGTCTTCCTCCCCGGCGG 10801	A	ATA ACC
			CC CCGGG AG GGAGACA		
			GG GGCCC TC CTTCTGT		
			C C_ _		
GAM552	HMGA2	5'	GTGCCCGACCTATCCCGGCGG 9569	A	AGAC AG
			CC CCGGGATA CGG AC		
			GG GGCCCTAT GCC TG		
			C CCCA CG		
GAM552	LOH11CR2A	3'	GTGTCTCATATACCCTATCCTG 15990	AGACCG_	
	GTGG		CCACCGGGATA GAGACAC		
			GGTGGTCCTAT CTCTGTG		
			CCCATATA		
GAM552	PTPRJ	5'	TGTCTCCGGGGAAGCCCGGGG 8732	A	ATAAGA
			CC CCGGG CCGGAGACA		

			GG GGCCC	GGCCTCTGT		
			— GAAGG—			
GAM552	RPS6KA2	3'	GTCCCAGGTACCCGGTGG	22106	ATAAG	— A
			CCACCGGG	ACC GG GAC		
			GGTGGCCC	TGG CC CTG		
			A—	A —		
GAM552	SDC4	3'	GTGTCTCCTCCTGACCCAGTG	8892	C ATA ACC	
	G		CCAC GGG	AG GGAGACAC		
			GGTG CCC	TC CCTCTGTG		
			A CAG	CT—		
GAM552	DKFZp762E1312	5'	TCTCCGGAAAGAGTCCTGGTG	20453	AAGA—	
			CACCGGGAT	CCGGAGA		
			GTGGTCCTG	GGCCTCT		
			AGAAA			
GAM552	FLJ14082	3'	TGTCCTTCTGCCTCCCCGGTGG	24613	ATA—	CC A
			CCACCGGG	AGA GG GACA		
			GGTGGCCC	TCT TC CTGT		
			CTCCG	— —		
GAM552	FLJ20297	5'	GTGCCTATTTTCATCCTGGTGG	19652	A CC AG	
			CCACCGGGAT	AGA GG AC		
			GGTGGTCCTA	TTT CC TG		
			C AT	G—		
GAM552	FLJ20366	3'	GTACCCGTTCTTATCCTAGTGG	19419	CG	C AG
			CCAC GGATAAGA	CGG AC		
			GGTG CCTATTCT	GCC TG		
			AT	T CA		
GAM552	KIAA0014	3'	TGTCCCCAGTCCTGGTCA	16119	C	AAGACC A
			C ACCGGGAT	GG GACA		
			A TGGTCCTG	CC CTGT		
			C	AC— —		
GAM552	KIAA1274	3'	TCTCTCTGTGCCGG	43914	A CC	
			CCGGGATA	GA GGAGA		
			GGCCCTGT	CT TCTCT		
			— C—			
GAM552	P450RAI-2	3'	GTGCCTCTGCCTTATCCCTGGT	21270	—	AC A
	GG		CCACC GGGATAAG	CGGAG CAC		
			GGTGG CCCTATTC	GTCTC GTG		
			T	C— C		
GAM552	SBBI26	3'	TGTCTCTGTTTTATCCAGTGG	20832	CG	C
			CCAC GGATAAGAC	GGAGACA		

GGTG CCTATTTTG TCTCTGT
A_ _
GAM552 SDCCAG3 3' GTGTTTTCCAGTCCCATCCC 13436 AA C _
GGGAT GAC GGAGA CAC
|||| ||| ||||| ||
CCCTA CTG CCTTT GTG
CC A T
GAM552 STX1B2 3' TGTCTTTGTTACCCCAGGGG 27456 A _ A GAC
CC CC GGG TAA CGGAGACA
|| ||| ||| |||||
GG GG CCC ATT GTTTCTGT
_ A C _
GAM552 LOC120839 5' GTCTCCGGCTGCACCGAGTGG 37415 _ GATA A
CCAC CGG AG CCGGAGAC
|||| ||| || |||||
GGTG GCC TC GGCCTCTG
A ACG_ _
GAM552 LOC150245 5' GTGTCTCCCCTGAGCCCGGTG 41163 ATA ACC
CACCGGG AG GGAGACAC
||||| || |||||
GTGGCCC TC CCTCTGTG
GAG C_
GAM552 LOC150776 5' GTGCCTATTTTCATCCTGGTGG 31678 A CC AG
CCACCGGGAT AGA GG AC
||||||| ||| || ||
GGTGGTCCTA TTT CC TG
C AT G_
GAM552 LOC151610 3' GTCTGCATCATCCTGGTGG 39137 AA CCGG
CCACCGGGAT GA AGAC
||||||| || |||
GGTGGTCCTA CT TCTG
_ ACG_
GAM552 LOC199848 5' CGGTGCCTTCCCCGGTGG 43251 AT _
CCACCGGG AAG ACCG
|||||| ||| |||
GGTGGCCC TTC TGGC
C_ CG
GAM552 LOC220045 3' GTGTCTCCAAGCTTCCCAGTG 44862 C TA ACC
CAC GGGA AG GGAGACAC
||| ||| || |||||
GTG CCCT TC CCTCTGTG
A _ GAA
GAM552 LOC91097 5' GTGTCTCCAGGGAACCCACGG 32370 _ ATAAGA _
CCG GG CC GGAGACAC
||| || || |||||
GGC CC GG CCTCTGTG
A CAAG_ A
GAM553 NDRG3 3' TAAGATTCTTTGATCCCGAC 22848 AA A A
GTC GAT TAGGGAA TCTTA
||| ||| ||||| |||||

			CAG CTA GTTTCTT AGAAT		
			CC _ _		
GAM553	NDRG3	3'	TAAGATTCTTTGATCCCGAC 25724	AA A A	
			GTC GAT TAGGGAA TCTTA		
			CAG CTA GTTTCTT AGAAT		
			CC _ _		
GAM553	RABEX5	3'	TAAGATCTATTAAGCTTGACA 15840	AT__ GGAA	
			TGTCAAG ATAG ATCTTA		
			ACAGTTC TATC TAGAAT		
			GAAT ____		
GAM553	LOC115073	3'	AAGATTTACATCTTTACA 36234	C ATAGG	
			TGT AAGAT GAAATCTT		
			ACA TTCTA CTTTAGAA		
			T CA__		
GAM553	LOC147072	3'	TAAGACTTTCCATCTTGGCA 30299	ATA A	
			TGTCAAGAT GGGAA TCTTA		
			ACGGTTCTA CCTTT AGAAT		
			__ C		
GAM553	LOC148085	5'	AGGATTATATCTTGA 40867	GGGAA	
			TCAAGATATA ATCTT		
			AGTTCTATAT TAGGA		

GAM554	EPHA8	3'	ATGTGGGTGATGGTGGATGA 21743	C G T TG T	
			TCA CC ACCA T C CCACAT		
			AGT GG TGGT A G GGTGTA		
			A _ _ GT _		
GAM554	HUNK	3'	ATGTGGAGCAAACCTTGAGG 15945	_ CCA	
			CC CGA TTTGCTCCACAT		
			GG GTT AAACGAGGTGTA		
			A C__		
GAM554	ITGA11	3'	ATGTGGAGACTGATGGCCAGG 14512	GA_ TG_	
			CC CCATT CTCCACAT		
			GG GGTAG GAGGTGTA		
			ACC TCA		
GAM554	NOL3	3'	TGGAGCAAGGGGAGGGTGA 10064	GA A	
			TCACCC CC TTTGCTCCA		
			AGTGGG GG GAACGAGGT		
			AG _		
GAM554	RECQL5	3'	ATGTGGAGCAAAGTGTCAGTGA 10447	CC CA	
			TCAC GAC TTTGCTCCACAT		

AGTG CTG AAACGAGGTGTA
 A_ TG
 GAM554 SMARCD2 3' ATGTGGAGGCCAGGGTAAGGTG 9050 CG ATTTG
 A TCACC ACC CTCCACAT
 ||||| ||| |||||
 AGTGG TGG GAGGTGTA
 AA GACCG
 GAM554 TMC1 5' GTGGAGTGGTCTGGTGA 28933 C ATTT
 TCACC GACC GCTCCAC
 ||||| ||||| |||||
 AGTGG CTGG TGAGGTG
 T ____
 GAM554 BBX 5' ATGTGGAGCAGTGTACAGTGA 21504 CCG CAT
 TCAC AC TTGCTCCACAT
 ||||| || |||||
 AGTG TG GACGAGGTGTA
 ACA T__
 GAM554 EPHA7 5' GTGGAGCAGCCGATCGGGGA 10724 A CCAT
 TC CCCGA TTGCTCCAC
 || ||||| |||||
 AG GGGCT GACGAGGTG
 _ AGCC
 GAM554 FLJ14213 3' ATGTGGAGGTTTATGGGTGA 24251 ACCATTG
 TCACCCG CTCCACAT
 ||||| |||||
 AGTGGGT GAGGTGTA
 ATTTG__
 GAM554 FLJ20004 3' GTGGGATGGCGAGTGA 45646 C A TGCT
 TCAC CG CCATT CCAC
 ||||| || ||||| |||||
 AGTG GC GG TAG GGTG
 A _ ____
 GAM554 FLJ20378 3' ATGTGGACGTGGGTGGGTGA 19434 A TTGC
 TCACCCG CCAT TCCACAT
 ||||| ||||| |||||
 AGTGGGT GGTG AGGTGTA
 G C__
 GAM554 KIAA0711 5' TGTGAAGTGAGTGGGTGA 16961 GACC TG C
 TCACCC ATT CT CACA
 ||||| ||| || |||||
 AGTGGG TGA GA GTGT
 ____ GT A
 GAM554 KIAA0992 3' ATGTAGAGCAAGTTGAAAATGG 18158 ACC__ C
 CCG ATTTGCTC ACAT
 ||| ||||| |||||
 GGT TGAACGAG TGTA
 AAAAGT A
 GAM554 KIAA1130 3' ATGTGGAGATGGGACAGTGGGT 31280 A__ ATTTG
 GA TCACCCG CC CTCCACAT
 ||||| || |||||

			AGTGGGT GG GAGGTGTA	
			GACA GTA__	
GAM554	LRRN3	5'	GTGTGACAACTGATCGGGTGA 34401	C T C _
			TCACCCGA CA TTG TC CAC	
			AGTGGGCT GT AAC AG GTG	
			A C _ T	
GAM554	MGC22014	3'	ATGTGGCCACACGGTGGATGA 32216	C G ATT CT
			TCA CC ACC TG CCACAT	
			AGT GG TGG AC GGTGTA	
			A _ CAC C_	
GAM554	MGC3248	3'	ATGTGGATGCATTAGTCAGGTG 26236	C CATT _
	G		TCACC GAC TGC TCCACAT	
			GGTGG CTG ACG AGGTGTA	
			A ATT_ T	
GAM554	PDZD2	3'	ATGTGGAGCAAATGGAATGGT 39388	CGA
			ACC CCATTTGCTCCACAT	
			TGG GGTAACGAGGTGTA	
			TAA	
GAM554	PRO2859	5'	ATGTGGAACAAATGGAGTGA 20615	CCGA C
			TCAC CCATTTG TCCACAT	
			AGTG GGTAAC AGGTGTA	
			A__ A	
GAM554	PSKH1	3'	ATGTGGCCCCACAGTAGGTGA 33867	CG CATT CT
			TCACC AC TG CCACAT	
			AGTGG TG AC GGTGTA	
			A_ AC_ CC	
GAM554	LOC123242	5'	ATGTGGAGCAGGGCCACGTGA 37239	CCGA AT
			TCAC CC TTGCTCCACAT	
			AGTG GG GACGAGGTGTA	
			CACC _	
GAM554	LOC127703	3'	GCAAGATCCTGGTGGGTGA 36908	G ____
			TCACCC ACCA TTTGC	
			AGTGGG TGGT GAACG	
			_ CCTA	
GAM554	LOC157273	3'	ATGTAAGGCCTTGGTAAGTGA 41781	CCG TTT CC
			TCAC ACCA GCT ACAT	
			AGTG TGGT CGG TGTA	
			AA_ TC_ AA	
GAM554	LOC221463	3'	TGGAGAGAGGTGGCAGGTGA 44204	CGA G_
			TCACC CCATTT CTCCA	

AGTGG GGTGGA GAGGT
 AC_ GA
 GAM554 LOC253001 5' ATGTGGAGCAGGGCCACGTGA 46056 CCGA AT
 TCAC CC TTGCTCCACAT
 ||| || |||||
 AGTG GG GACGAGGTGTA
 CACC _
 GAM554 LOC56965 3' GAGGATGGTCAGGTGG 21453 C TG
 TCACC GACCATT CTC
 |||| ||||| ||
 GGTGG CTGGTAG GAG
 A _
 GAM555 PTK2B 5' GACTGCAATGTGCCGATCTTA 10312 ACA GATG
 TAAGATCG ACGT AGTC
 ||||| ||| |||
 ATTCTAGC TGTA TCAG
 CG_ ACG_
 GAM555 FLJ10583 5' ACTTGGAGTTGTGACCTT 19949 A GTGA
 AAG TCGACAAC TGAGT
 || ||||| ||||
 TTC AGCTGTTG GTTCA
 C AG_
 GAM555 MGC4562 5' ACTCATTACGTGATC 28496 GACA
 GATC ACGTGATGAGT
 ||| |||||
 CTAG TGCATTACTCA
 _
 GAM555 TMLHE 3' ACTCATCAGTGTGGTAATC 20062 CG A _
 GAT AC ACG TGATGAGT
 || || || |||||
 CTA TG TGT ACTACTCA
 A_ G G
 GAM555 LOC139673 3' ACTCTTATCGTCATCTTA 37403 C AAC T
 TAAGAT GAC GTGA GAGT
 ||||| || ||| |||
 ATTCTA CTG TATT CTCA
 _ C_ _
 GAM556 ABL2 5' CGGGTGCGGAGCCGCCGGTGG 14229 AA GG G
 CCACCGGC CTC GCG TCG
 ||||| || ||| |||
 GGTGGCCG GAG CGT GGC
 CC G_ G
 GAM556 ATP5J 5' CGACCGCCCAAGGCAACGGAGG 7406 A GCAA C
 CC CCG CT GGGCGGTCG
 || || || |||||
 GG GGC GA CCCGCCAGC
 A AACG A
 GAM556 CDH6 5' GCGACCGCGGCGGCGGCGGCGG 11374 A G A A T G_
 CC CCG C C CG GCGGTGCG
 || ||| | || |||||

			GG GGC G G GC CGCCAGCG		
			C _ GC _ GG		
GAM556	DMD	5'	GCAAGTCAAGTTACTGGTGG 10233	C	CG GGTC
			CCACCGG AACT GGC GC		
			GGTGGTC TTGA CTG CG		
			A A_ AA__		
GAM556	DMD	5'	GCAAGTCAAGTTACTGGTGG 10194	C	CG GGTC
			CCACCGG AACT GGC GC		
			GGTGGTC TTGA CTG CG		
			A A_ AA__		
GAM556	DMD	5'	GCAAGTCAAGTTACTGGTGG 10221	C	CG GGTC
			CCACCGG AACT GGC GC		
			GGTGGTC TTGA CTG CG		
			A A_ AA__		
GAM556	MAML1	3'	GCAACCAGCCTGAGTCGCGGTG 16499	G A	_ C
			CACCG C ACTCGGGC GGT GC		
			GTGGC G TGAGTCCG CCA CG		
			_ C A A		
GAM556	NRG2	5'	ACCTCCCCGGGCTGCCGGTGG 11318	A	C_
			CCACCGGCA CTCGGG GGT		
			GGTGGCCGT GGGCCC CCA		
			C CT		
GAM556	NRG2	5'	ACCTCCCCGGGCTGCCGGTGG 15144	A	C_
			CCACCGGCA CTCGGG GGT		
			GGTGGCCGT GGGCCC CCA		
			C CT		
GAM556	NRG2	5'	ACCTCCCCGGGCTGCCGGTGG 15143	A	C_
			CCACCGGCA CTCGGG GGT		
			GGTGGCCGT GGGCCC CCA		
			C CT		
GAM556	NRG2	5'	ACCTCCCCGGGCTGCCGGTGG 15145	A	C_
			CCACCGGCA CTCGGG GGT		
			GGTGGCCGT GGGCCC CCA		
			C CT		
GAM556	NRG2	5'	ACCTCCCCGGGCTGCCGGTGG 15146	A	C_
			CCACCGGCA CTCGGG GGT		
			GGTGGCCGT GGGCCC CCA		
			C CT		
GAM556	NRG2	5'	ACCTCCCCGGGCTGCCGGTGG 15147	A	C_
			CCACCGGCA CTCGGG GGT		

GGTGGCCGT GGGCCC CCA
C CT
GAM556 CGRP-RCP 5' CGAGGCTACGAGCTGCCCCGATG 15823 C _ A _ GG
G CCA CGG CA CTCG GGC TCG
||| ||| || ||| ||| |||
GGT GCC GT GAGC TCG AGC
A C C A G_
GAM556 FLJ10748 5' CGCCAAGTAGCCGGTGG 20086 A CG
CCACCGGC ACT GGCG
||||||| ||| |||
GGTGGCCG TGA CCGC
A A_
GAM556 FLJ10925 5' CGACCACGCTGCCTGTGG 20259 C ACT GGC
CCAC GGCA CG GGTCG
||||| ||| ||| |||
GGTG CCGT GC CCAGC
T C _ A _
GAM556 FLJ20315 3' GCAACCAGCTGCTGCCTGTGG 19379 C ACTCG _ C
CCAC GGCA GGC GGT GC
||||| ||| ||| |||
GGTG CCGT TCG CCA CG
T CG _ A A
GAM556 LGI3 5' GCGGTAGCAGCTGCCGGTGG 29279 A CGG GG
CCACCGGCA CT GC TCGC
||||||| || ||| |||
GGTGGCCGT GA CG GGCG
C _ AT
GAM556 MKNK1 5' CGACCGCTCCCCGGCGG 9792 A CAACTC
CC CCGG GGGCGGTCTG
|| ||| |||||
GG GGCC CTCGCCAGC
C C _
GAM556 PM5 5' GCGGGACCCGGCTGCCGGCGG 30497 A A T CGG
CC CCGGCA C CGGG TCGC
|| ||||| | ||| |||
GG GGCCGT G GCCC GGCG
C C _ AG_
GAM556 PTPN4 5' CGACCGCTGCGGCGGCGG 8707 A GCAAC _
CC CCG TCG GGCGGTCTG
|| ||| ||| |||||
GG GGC GGC TCGCCAGC
C _ G
GAM556 LOC145748 5' GCGGGTCGCGAGTCGCCGGT 40579 A _ GG
ACCGGC ACTCG GGC TCGC
||||| ||||| ||| |||
TGGCCG TGAGC CTG GGCG
C G _
GAM556 LOC151445 3' CGCTCGATTGCCAGTGG 34419 C C
CCAC GGCAA TCGGGCG
||||| ||||| |||||

GGTG CCGTT AGCTCGC
A _
GAM556 LOC163682 3' GCGACCGCTGGGTGCCAGG 42096 _ A G
CC GGCA CTCGG CGGTCGC
|| ||| |||| |||||
GG CCGT GGGTC GCCAGCG
A _ _
GAM556 LOC197003 3' GCCTGGCCTGAGTCACCAAGTG 42444 C CA _
CAC GG ACTCGGGC GGT
||| || ||||| |||
GTG CC TGAGTCCG CCG
A AC GT
GAM556 LOC221975 5' CGACCACCGCGGCCGCCGG 44495 AAC _ C
CCGGC TCG GG GGTCG
|||| ||| || ||||
GGCCG GGC CC CCAGC
CC_ G A
GAM556 LOC254712 5' GCAACTTAGCGAAGCTGCCGGT 45912 A _ GGC C
G CACCGGCA CT CG GGT GC
||||| || || ||| ||
GTGGCCGT GA GC TCA CG
C A GAT A
GAM556 LOC93538 5' CGAGCGGAATTCCGGCGG 35923 A C C GGG G
CC CCGG AA TC CG TCG
|| ||| || || |||
GG GGCC TT AG GC AGC
C _ A _ G
GAM557 phospho1 5' CGGCTCAGACGCACATCA 40063 _ C
TGATGTGCGTC GA GCCG
||||||| || |||
ACTACACGCAG CT CGGC
A _
GAM558 ATF7 3' TCTTTTTCATCTATTTGCA 13727 GTTCGA
TGCAAA GTGAAAAAGA
||||| |||||
ACGTTT TACTTTTCT
ATC_
GAM558 BACE 3' TTCCTCTGGAGCTTTGCA 14422 G T_
TGCAAAGTTC AG GAA
||||||| || |||
ACGTTTCGAG TC CTT
G TC
GAM558 BACE 3' TTCCTCTGGAGCTTTGCA 29090 G T_
TGCAAAGTTC AG GAA
||||||| || |||
ACGTTTCGAG TC CTT
G TC
GAM558 CLCN4 3' TCTTTTTCACCGTTTTT 7574 TT A
AAG CG GTGAAAAAGA
||| || |||||

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          TTT GC CACTTTTTCT
          TT _
GAM558 EGLN1  5' CTCTTTCAC TTGATTG  22583  AGT    A
          CAA TCGAGTGAAA AG
          ||| ||||| ||
          GTT AGTTCAC TTT TC
          _ C
GAM558 FGF2   3' TCTTTTTTCACGCATTTGC  7743   GTTCGA
          GCAAA GTGAAAAAGA
          |||| |||||
          CGTTT CACTTTTTCT
          ACG_
GAM558 GJA1   3' TCTTTTTTCATCCACTTGCA  5680   A TC GT
          TGCAA GT GA GAAAAAGA
          |||| || || |||||
          ACGTT CA CT CTTTTTCT
          _ C_ AC
GAM558 HPSE   3' TCTTTTTTCAGAGCTTCTCA  13481  CA    GAG
          TG AAGTTC TGAAAAAGA
          || ||||| |||||
          AC TTCGAG ACTTTTTTCT
          TC _
GAM558 MGAT2  3' TCTTTTTTATCTGAAACTTTGTA 8234   CG TG
          TGCAAAGTT AG AAAAAGA
          ||||| || |||||
          ATGTTTCAA TC TTTTTTCT
          AG TA
GAM558 MLLT2  3' TCTTTTTTCATTGAAACTTT  12573  CG
          AAAGTT AGTGAAAAAGA
          |||| |||||
          TTTCAA TTA CTTTTTCT
          AG
GAM558 NCOA6IP 3' TCTTTTTTCACTCATAGAAT  24228  _
          GTTC GAGTGAAAAAGA
          ||| |||||
          TAAG CTCACTTTTTCT
          ATA
GAM558 RASA1  3' TCTTGATATCTCGAACTTTCA  22906  C    TGAAA
          TG AAAGTTCGAG AAGA
          || ||||| |||
          AC TTTCAAGCTC TTCT
          _ TATAG
GAM558 RNASE4 3' TCTTTTTTCTGAAACTTTG  8838   CG T
          CAAAGTT AG GAAAAAGA
          |||| || |||||
          GTTTCAA TC CTTTTTCT
          AG _
GAM558 SUFU   3' TCTCTTTCAC TTTGGTTTTCG  18259  GT C    A
          GCAAA T GAGTGAAA AGA
          |||| | ||||| |||

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CGTTT G TTCACTTT TCT
TG T C

GAM558 TSLP 5' CTTTTCTCGTAACTTTGC 28849 _ TGA
GCAAAGTT CGAG AAAAG
||||| ||| ||||
CGTTTCAA GCTC TTTTC
AT _

GAM558 UBL1 3' CTTTTTCAGGACATTGCA 9378 A GAG
TGCAA GTTC TGAAAAAG
||||| ||| |||||||
ACGTT CAGG ACTTTTTC
A _

GAM558 VHL 3' CTTTTTCATTTAAC TTT 6161 C
AAAGTT GAGTGAAAAAG
||||| |||||||||
TTTCAA TTTACTTTTTC

GAM558 ARFD1 3' TTTTCACTAATTTTGC 7375 CG
GCAAAGTT AGTGAAAA
||||| |||||||
CGTTTTAA TCACTTTT

GAM558 BRD4 3' TCTTTTCTGCGACTTTG 15595 G GT
CAAAGTTC A GAAAAAGA
||||| | |||||||
GTTTCAGG T CTTTTTCT
G _

GAM558 DJ667H12.2 3' TCTTCTCACCGAACTTTG 21218 A AA
CAAAGTTCG GTGA AAGA
||||| ||| |||
GTTTCAAGC CACT TTCT
_ C _

GAM558 DKFZp547I224 5' CTTTTTCATTCCCCTTT 21476 TTC
AAAG GAGTGAAAAAG
||| |||||||||
TTTC CTTACTTTTTC
CC _

GAM558 DKFZP566K1924 3' TCTTCTTCACTTGAAC TTTGTA 36523 A
TGCAAAGTTCGAGTGAA AAGA
||||||||||| |||
ATGTTTCAAGTTCAC TTTCT
C

GAM558 DKFZP586C1619 3' CTTGCCCTCGAATTCTGCA 31019 A TGAAA
TGCA AGTTCGAG AAG
||| ||||||| |||
ACGT TTAAGCTC TTC
C CCG _

GAM558 DRCTNNB1A 3' TCTTTTTCACTGTGACTGCA 26317 AA CG
TGCA GTT AGTGAAAAAGA
||| ||| |||||||||

			ACGT CAG TCACTTTTCT		
			— TG		
GAM558	ELL2	3'	TCTTTTCCATTTTACTTTGC 14369	TC	A
			GCAAAGT GAGTG AAAAGA		
			CGTTTCA TTTAC TTTTCT		
			T_ C		
GAM558	FLJ10199	3'	TCCTTTTCACTCCGAATCGC 35286	AAA	_ A
			GC GTTCG AGTGAAAA GA		
			CG TAAGC TCACTTTT CT		
			C_ C C		
GAM558	FLJ12650	3'	TTTTCACCTGGGACCTTGCA 23723	A	G
			TGCAA GTTC AGTGAAAA		
			ACGTT CAGG TCACTTTT		
			C G		
GAM558	FLJ13189	3'	TCTTTTTTTAACTTTGC 24333	CGAGT	
			GCAAAGTT GAAAAAGA		
			CGTTTCAA TTTTTTCT		
			AT__		
GAM558	FLJ14054	3'	TCTTTTTTCAGTTGTCTTT 23786	TT	G
			AAAG CGA TGAAAAAGA		
			TTTC GTT ACTTTTTTCT		
			T_ G		
GAM558	FLJ20093	3'	TCTTTTTCAATGAAGCTTTGCA 19205	CGAG	
			TGCAAAGTT TGAAAAAGA		
			ACGTTTCGA ACTTTTTTCT		
			AGTA		
GAM558	FLJ20793	3'	TTTTCACAGCTTTGTA 44111	CGA	
			TGCAAAGTT GTGAAAA		
			ATGTTTCGA CACTTTT		
			—		
GAM558	KIAA0367	3'	CTTTTCCACTTTGCA 33419	TCGAGT	
			TGCAAAGT GAAAAAG		
			ACGTTTCA CTTTTTC		
			C_		
GAM558	NFAT5	3'	TCTTTTTCACTTTACTTT 13378	TC	
			AAAGT GAGTGAAAAAGA		
			TTTCA TTCACTTTTTTCT		
			T_		
GAM558	PRO1386	5'	TTTTCACCTCACTCTGC 25293	A	TC
			GCA AGT GAGTGAAAA		

			CGT TCA TTCACTTTT		
			C C_		
GAM558	RRN3	3'	TCTTTTCCAGGGCTTTGTA	20490	GAG A
			TGCAAAGTTC TG AAAAGA		
			ATGTTTCGGG AC TTTTCT		
			___ C		
GAM558	TP53INP1	3'	CTTTTTCATACATTGCA	27107	A TCGA
			TGCAA GT GTGAAAAAG		
			ACGTT CA TACTTTTTC		
			A ____		
GAM558	TP53INP1	3'	CTTTTTCATACATTGCA	36117	A TCGA
			TGCAA GT GTGAAAAAG		
			ACGTT CA TACTTTTTC		
			A ____		
GAM558	LOC120376	5'	TTTCACTTGTTTTTTACA	37414	C TT
			TG AAAG CGAGTGAAA		
			AC TTTT GTTCACTTT		
			A TT		
GAM558	LOC120892	3'	TCTCTTTCATTGTTACTTTGTA	36649	TCG A
			TGCAAAGT AGTGAAA AGA		
			ATGTTTCA TTACTTT TCT		
			TTG C		
GAM558	LOC130612	5'	CTCTTTCACTCAGAAGC	36998	AAAG _ A
			GC TTC GAGTGAAA AG		
			CG AAG CTCACTTT TC		
			___ A C		
GAM558	LOC145828	5'	TTTTTTTGTTTGGAACCCTGCA	40613	AA G TG
			TGCA GTTC AG AAAAAG		
			ACGT CAAG TT TTTTTT		
			CC G GT		
GAM558	LOC147341	3'	TCTTTTTCACCTTTTCTTGTA	40828	A TTCGA
			TGCAA G GTGAAAAAGA		
			ATGTT C CACTTTTCT		
			_ TTTTC		
GAM558	LOC149175	3'	CTTCTAGTTTTGAACTCTGCA	38660	A TGAAA
			TGCA AGTTCGAG AAG		
			ACGT TCAAGTTT TTC		
			C TGATC		
GAM558	LOC149650	3'	TCTTTTTCACACTAGCTCTG	38797	A CGA
			CA AGTT GTGAAAAAGA		

		GT TCGA CACTTTTTCT	
		C TCA	
GAM558	LOC152762 3'	TTTTCACCTTCTGGACCGC 39308	AAA _
		GC GTTC GAGTGAAAA	
		CG CAGG TTCACCTTT	
		C_ TC	
GAM558	LOC196528 3'	CTCTTTCACCTTGAACCTTGTA 42406	A _ A
		TGCAA GTTCGAG TGAAA AG	
		ATGTT CAAGTTC ACTTT TC	
		_ C C	
GAM558	LOC221876 5'	TCTTTCCTCACTCAGTTTTGCA 45080	GT C AA
		TGCAAA T GAGTG AAAGA	
		ACGTTT A CTCAC TTTCT	
		TG_ CC	
GAM558	LOC254042 3'	TCTTTGTATCTGAACTTTGCA 45794	G TGAA
		TGCAAAGTTC AG AAAGA	
		ACGTTTCAAG TC TTTCT	
		_ TATG	
GAM558	LOC255446 5'	TCTTTTTCAACAGAACTTCACA 46409	CA GAG
		TG AAGTTC TGAAAAAGA	
		AC TTCAAG ACTTTTTCT	
		AC ACA	
GAM558	LOC257017 5'	TCTTTTTTAATAAGAACTTTGC 46500	_ GAGTG
		GCAAAGTT C AAAAAGA	
		CGTTTCAA G TTTTCT	
		A AATAA	
GAM558	LOC51644 3'	TCTTTTTTCATTCTTCTTGCA 18132	A TTC
		TGCAA G GAGTGAAAAAGA	
		ACGTT C CTTACTTTTTCT	
		_ TT_	
GAM558	LOC92360 3'	TCTTTTTTCACCTTCTTGCA 34241	A TTC
		GCAA G GAGTGAAAAAGA	
		CGTT C TTCACCTTTTTCT	
		_ T_	
GAM559	DKC1 3'	GTTTTCTTGTTGATCTCATG 7044	CT AG
		CATG GT AACAAGAAAAC	
		GTAC TA TTGTTCTTTTG	
		TC G_	
GAM559	GRM6 3'	TTTTCCTGTTTTTTTGCATG 6513	TGT A
		CATGC AGAACA GAAAA	

			GTACG TTTTGT CTTT		
			TTT C		
GAM559	NCOA6	5'	TCTGTGTACCTGCAGCAT 15294	A_ _	
			ATGCTGTAG ACA AGA		
			TACGACGTC TGT TCT		
			CA G		
GAM559	SLC11A3	3'	TCTTTCTACAGTATGA 15943	CA	
			TCATGCTGTAGAA AGA		
			AGTATGACATCTT TCT		
			—		
GAM559	ESDN	3'	TTTTCTTGTTCATGA 28156	CTGTA	
			TCATG GAACAAGAAAA		
			AGTAC TTTGTTCTTTT		
			C_		
GAM559	FLJ20445	3'	TTTTCTTGTTACAGTA 19484	A	
			TGCTGT GAACAAGAAAA		
			ATGACA CTTGTTCTTTT		
			—		
GAM559	FLJ23510	5'	GTTTCCTTGTTCTATTTACAGTA 24054	— A	
			TGCTG TAGAACAAG AAAC		
			ATGAC ATCTTGTTT TTTG		
			TTT C		
GAM559	KIAA0179	3'	GTTTTCTATTTACGCATGATA 32366	T ACA	
			TATCATGC GTAGA AGAAAAC		
			ATAGTACG CATTT TCTTTTG		
			— A_		
GAM559	KIAA1535	3'	TTCCTGTTCTGTAGCAT 38769	_ A	
			ATGCTGTAG AACA GAA		
			TACGATGTC TTGT CTT		
			C C		
GAM559	Kv6.3	3'	TTTTTTCATTCTACAGCAT 28568	CA	
			ATGCTGTAGAA AGAAAA		
			TACGACATCTT TTTTTT		
			AC		
GAM559	PFTK1	3'	TTTTCTTGTAACATGATA 14757	CTGTAGA	
			TATCATG ACAAGAAAA		
			ATAGTAC TGTTCTTTT		
			AA_		
GAM559	LOC139522	5'	TTTTCTTGGGTGAGCATGA 37345	GTAGAA	
			TCATGCT CAAGAAAA		

			AGTACGA	GTTCTTTT	
			GTGG__		
GAM559	LOC196485	3'	GTTTTCTTGCTCCTGTGGATG	42381	G TG AA_
			CAT C TAG CAAGAAAAC		
			GTA G GTC GTTCTTTTG		
			_GT CTC		
GAM559	LOC202986	3'	GTTTTCTTGCTCCTGTGGATG	43472	G TG AA_
			CAT C TAG CAAGAAAAC		
			GTA G GTC GTTCTTTTG		
			_GT CTC		
GAM559	LOC203378	3'	GTTTTCTTGCCAGCCATGA	43556	_ TAGAA
			TCATG CTG CAAGAAAAC		
			AGTAC GAC GTTCTTTTG		
			C C__		
GAM559	LOC257106	3'	TCTCCTCTGCAGCATGA	45679	ACA
			TCATGCTGTAGA AGA		
			AGTACGACGTCT TCT		
			CC_		
GAM560	SB52	3'	ACTCAAATAAAGCGTGTAAATA	28733	A GCAGC
			TATTACAC CTTTA GT		
			ATAATGTG GAAAT CA		
			C AAAC		
GAM560	UHRF2	3'	AACACAGCTTCTAAAGTGTG	36353	C _
			CACACTTTAG AGC GTGTT		
			GTGTGAAATC TCG CACAA		
			T A		
GAM560	LOC50999	3'	GTTGTACTTAAGTGTGTAA	18117	TA__
			TTACACACTT GCAGC		
			AATGTGTGAA TGTTG		
			TTCA		
GAM561	BLAME	3'	CCACTATTCATAAAGTATTAAC	21305	C_ TCA C
	CAA		TTGGTTAATAT TATG AG GG		
			AACCAATTATG ATAC TC CC		
			AA TTA A		
GAM561	LOC90342	5'	CTGGACATAGACATCAAC	31252	A A A
			GTT AT TCTATGTC AG		
			CAA TA AGATACAG TC		
			C C G		
GAM562	BCRP2	3'	TGTGCGCTTATTGTCTCA	31278	A _
			TGA ACAATAAGCG ATA		

			ACT TGTTATTCGC TGT		
			C G		
GAM562	FOXO1A	3'	ATAATTCTTTGCTCTTGTTTCA 7757	TA	TA
			TGAAACAA AGCGA AATTAT		
			ACTTTGTT TCGTT TTAATA		
			C_ TC		
GAM562	IL20RA	3'	ATAATTTAGTAGGGGCTTATTG 15789	A	GA_____
			TCTC GA ACAATAAGC TAAATTAT		
			CT TGTTATTCG ATTTAATA		
			C GGGATG		
GAM562	TACTILE	3'	ATAATAAGTGCTTATTGTTT 12408	ATAA	
			AAACAATAAGCG ATTAT		
			TTTGTATTTCGT TAATA		
			GAA_		
GAM563	NR2F2	5'	AAACTAACCAACCTCAAC 22001	T	AGAT
			GTTG AGG GTTAGTTTT		
			CAAC TCC CAATCAAAA		
			_ AAC_		
GAM564	DOCK1	3'	AATGATTATCCATATGTGTT 7050	TAAT_	
			AACACATAT ATCATT		
			TTGTGTATA TAGTAA		
			CCTAT		
GAM564	LOC146452	3'	ATCAAATGAATATGTGT 38162	TAATA	C
			ACACATAT TCATT GAT		
			TGTGTATA AGTAA CTA		
			_____ A		
GAM565	ALDH1A3	3'	AGCTGTAATTCACCTTA 6352	AG	A
			TAAAGT ATTACAG CT		
			ATTTCA TAATGTC GA		
			CT _		
GAM565	GFAP	3'	TAGGTAGTGCCCTATTTTA 7816	ATTACAG	
			TAAAGTAG ACTACCTA		
			ATTTTATC TGATGGAT		
			CCG_____		
GAM565	PPP2R5E	3'	AGGTAGTCCTGGTACTCCTTTA 12920	T	ATTA _
			TAAAG AG CAG ACTACCT		
			ATTTTC TC GTC TGATGGA		
			C ATG_ C		
GAM565	PREB	3'	TAGGTAGTCTACCCTTACCTTG 15038	A	ATTAC
			TAA GTAG AGACTACCTA		

			GTT CATT TCTGATGGAT		
			C CCCA_		
GAM565	ZNF24	3'	TAGGTACTGTAATCTAC 13838	AC	
			GTAGATTACAG TACCTA		
			CATCTAATGTC ATGGAT		
			—		
GAM565	FLJ22028	3'	TAGGTAAGTTATCTACTT 24286	TACA _	
			AAGTAGAT GACT ACCTA		
			TTCATCTA TTGA TGGAT		
			— A		
GAM565	KIAA0626	3'	TTAGGTAGGAGTGATGCCACTT 22315	AG_ AGA	
	TA		TAAAGT ATTAC CTACCTAA		
			ATTTCA TAGTG GATGGATT		
			CCG AG_		
GAM565	KIAA0794	3'	TAGGTTTTTCATCTACTTTA 39184	TACA CT	
			TAAAGTAGAT GA ACCTA		
			ATTTTCATCTA CT TGGAT		
			— TT		
GAM565	LOC157421	5'	AGGTAGTTCAGTCCACT 41793	A ACA	
			AGT GATT GACTACCT		
			TCA CTGA TTGATGGA		
			C C_		
GAM565	LOC257048	3'	AGGTAGCCTGAACCTTTG 46027	AGATTA A	
			TAAAGT CAG CTACCT		
			GTTTCA GTC GATGGA		
			A_ C		
GAM565	LOC84549	3'	AGGCAGTCTGTGGCCTCCT 26255	T AT A	
			AG AG TACAGACT CCT		
			TC TC GTGTCTGA GGA		
			C CG C		
GAM566	CYP51	3'	AACTCTTGTTAGTTTACTGTT 6435	_ C C	
			AACAGTAAAC AC GG AGTT		
			TTGTCATTTG TG TC TCAA		
			A T _		
GAM566	MASP1	3'	AACCCATCGGTCCTACTGTT 29157	AAC CA_	
			AACAGTA ACCGG GTT		
			TTGTCAT TGGCT CAA		
			CC_ ACC		
GAM566	PRKWINK3	3'	AATTGCTACCCAACATTACTGT 30854	ACACC_	
	T		AACAGTAA GGCAGTT		

		TTGTCATT	TCGTTAA	
		ACAACCCA		
GAM566	FLJ10199	3' AACAAAGTTTGTGTTTGCTGT	35284	C_ A_
		ACAGTAAACAC GGC GTT		
		TGTCGTTTGTG TTG CAA		
		TT AA		
GAM566	KIAA0981	3' AACACGTGGGCATTTATTGTT	30794	CA G A_
		AACAGTAAA CC GC GTT		
		TTGTTATTT GG TG CAA		
		AC G CA		
GAM566	MGC4832	3' AAATATAAAGGTGTTTGCT	29697	GGCAGT
		AGTAAACACC TATTT		
		TCGTTTGTGG ATAAA		
		AAAT__		
GAM566	UBE2D1	3' AATTGAGCACTGTTTACTGTT	9345	CCGG_
		AACAGTAAACA CAGTT		
		TTGTCATTTGT GTTAA		
		CACGA		
GAM566	ZFP106	3' AATAACTGCAGTTTAT	22828	ACCG
		GTAAAC GCAGTTATT		
		TATTTG CGTCAATAA		
		A__		
GAM566	LOC145739	3' TTGCTACAGTATTTACTGTT	37966	C C__
		AACAGTAAA AC GGCAG		
		TTGTCATTT TG TCGTT		
		A ACA		
GAM566	LOC147990	3' AAATAACTTTTGTGTTTATT	40862	CG C
		AGTAAACAC G AGTTATTT		
		TTATTTGTG T TCAATAAA		
		TT_		
GAM566	LOC162239	3' ATAAGTGTCAACTGTT	40049	AAACACC
		AACAGT GGCAGTTAT		
		TTGTCA CTGTCAATA		
		A_____		
GAM566	LOC221395	3' AAATAATTGTTATGTTTCTGTT	44182	T CC
		AACAG AAACA GGCAGTTATTT		
		TTGTC TTTGT TTGTTAATAAA		
		_ A_		
GAM566	LOC254778	3' AACACAATGGTTCTTACTGTT	45975	AC GCA_
		AACAGTAA ACCG GTT		

TTGTCATT TGGT CAA
 CT AACAA
 GAM566 LOC51026 3' AAATAACTTTTGATAATGTTTA 18139 C___ C
 CT AGTAAACA CGG AGTTATTT
 ||||| || |||||
 TCATTTGT GTT TCAATAAA
 AATA T
 GAM567 ATP1A2 3' TGTACTTAATAACACTTCA 6372 A CTTAC
 TGAAGT TTA TAAGTACA
 ||||| || |||||
 ACTTCA AAT ATTCATGT
 C A___
 GAM567 WHSC1 3' TGCACTTAGAATGATGTAATAT 14252 A _ _ A
 TCCA TG AGTATTAC TTA CTAAGT CA
 || ||||| || ||||| ||
 AC TTATAATG AGT GATTCA GT
 C T AA C
 GAM567 ZNF146 5' GTGAAGGTAGCAATACTTCA 13996 A T AAG
 TGAAGTATT CT ACT TAC
 ||||| || || |||||
 ACTTCATAA GA TGG GTG
 C _ AA_
 GAM567 ARFD1 3' TGTGCATAAATAATACTTC 7374 C CTAA
 GAAGTATTA TTA GTACA
 ||||| || |||||
 CTTCATAAT AAT CGTGT
 A A___
 GAM567 BART1 3' TTGTACCATGAGTAAACTTCA 14426 A CTAA
 TGAAGT TTA CTTA GTACAA
 ||||| ||||| |||||
 ACTTCA AATGAGT CATGTT
 A AC_
 GAM567 FLJ20093 3' TTGTACTTTTTTTATATACTTC 19206 TACTTACT
 A TGAAGTAT AAGTACAA
 ||||| |||||
 ACTTCATA TTCATGTT
 TATTTTT_
 GAM567 KIAA0763 3' ACTTAGTGTGTTCCCTTCA 16966 TATT T
 TGAAG AC TACTAAGT
 |||| |||||
 ACTTC TG GTGATTCA
 CT_ T
 GAM567 ZNF387 3' TTGTACTTAGCAAATAC 16181 ACTTA
 GTATT CTAAGTACAA
 |||| |||||
 CATAA GATTCATGTT
 AC_
 GAM567 LOC221830 3' TGCTTCAAGTAATACTTC 44437 ACT
 GAAGTATTACTT AAGTA
 ||||| |||||

			CTTCATAATGAA	TTCGT		
			C__			
GAM567	LOC222493	5'	TGCAAGGAAGAAATACTTCA	45302	A	A AA
			TGAAGTATT CTT CT	GTA		
			ACTTCATAA GAA GG	CGT		
			A _ AA			
GAM568	FGFR1	5'	GCTTGAAAAGCCGCGGAAC	6210	A	ATA
			GTT CGCGGCTT	TCAAGC		
			CAA GCGCCGAA	AGTTCG		
			G A__			
GAM568	FGFR1	5'	GCTTGAAAAGCCGCGGAAC	17981	A	ATA
			GTT CGCGGCTT	TCAAGC		
			CAA GCGCCGAA	AGTTCG		
			G A__			
GAM568	FGFR1	5'	GCTTGAAAAGCCGCGGAAC	23363	A	ATA
			GTT CGCGGCTT	TCAAGC		
			CAA GCGCCGAA	AGTTCG		
			G A__			
GAM568	FGFR1	5'	GCTTGAAAAGCCGCGGAAC	23367	A	ATA
			GTT CGCGGCTT	TCAAGC		
			CAA GCGCCGAA	AGTTCG		
			G A__			
GAM568	FGFR1	5'	GCTTGAAAAGCCGCGGAAC	23378	A	ATA
			GTT CGCGGCTT	TCAAGC		
			CAA GCGCCGAA	AGTTCG		
			G A__			
GAM568	FGFR1	5'	GCTTGAAAAGCCGCGGAAC	23375	A	ATA
			GTT CGCGGCTT	TCAAGC		
			CAA GCGCCGAA	AGTTCG		
			G A__			
GAM568	KIAA0757	3'	GTGATGCCACGTAACCTTA	12671	C	_
			TAAGTTACG GGC	TTAT		
			ATTCAATGC CCG	AGTG		
			A T			
GAM569	GALGT	3'	CCTGCCAGGAATTTCCAA	7210		CCATTA
			TTGGAAATTTCT	AGG		
			AACCTTTAAGGA	TCC		
			CCG__			
GAM569	HOXC10	3'	CCTTAATGGAGAAAAAAACC	30720	AAA	____
			TAATAA	TATTGG	TTTCTCCATTAAGG	

			ATAATC	AAAGAGGTAATTCC		
			CAAAAAA			
GAM569	SMARCD1	3'	CCTTAATGGAGAAACGGGCC	9048	AAA_	
			GG TTTCTCCATTAAGG			
			CC AAAGAGGTAATTCC			
			GGGC			
GAM569	SMARCD1	3'	CCTTAATGGAGAAACGGGCC	29146	AAA_	
			GG TTTCTCCATTAAGG			
			CC AAAGAGGTAATTCC			
			GGGC			
GAM569	LOC149117	3'	CCTTAATGAAACAGTATCCAA	40954	A TCTC	
			TTGGA ATT CATTAAGG			
			AACCT TGA GTAATTCC			
			A CAAA			
GAM569	LOC149628	3'	CCTCATGGGAAGCTTCCAATAA	38791	A T TA	
			TTATTGGAA TTTC CCAT AGG			
			AATAACCTT GAAG GGTA TCC			
			C _ C_			
GAM570	B3GALT2	3'	CACAATTCTAGGATGAA	9871	T AATC	
			TTCATCCTG GAA GTG			
			AAGTAGGAT CTT CAC			
			_ AA_			
GAM571	FLJ12448	3'	CAAACTTAGAGTGATTTGGA	23156	GA A	
			TTCAAG CATTCTAA TTTTG			
			AGGTTT GTGAGATT AAAAC			
			A_ C			
GAM571	KIAA0293	3'	CAAAATTTAGATAACCTTTGAA	30393	ACAT	
			TTCAAGG TCTAAATTTTG			
			AAGTTTC AGATTTAAAAC			
			CAAT			
GAM571	LOC152245	5'	CAAAATTTAGAATTTGGCC	41448	AC_	
			GG ATTCTAAATTTTG			
			CC TAAGATTTAAAAC			
			GGTT			
GAM572	KIAA1948	5'	CACATTTCTAAAAAACAGG	40078	GCGGTC	
			CTTG TAGGAAATGTG			
			GGAC ATCCTTTACAC			
			AAAAAA			
GAM572	RASD2	3'	CACACCTCCTAGACCACGCC	15599	_ AA	
			GGC GGTCTAGGA TGTG			

			CCG CCAGATCCT ACAC		
			CA CC		
GAM573	ZNF268	3'	ATTCACAGCTTGTTATACATCA 31498		ATTCGACA
			TGATGTATGA TGAAT		
			ACTACATATT ACTTA		
			GTTTCGAC_		
GAM573	KIAA0970	3'	CATCAGAATTCATAATCA 17203	G	GAC
			TGAT TATGAATTC ATG		
			ACTA ATACTTAAG TAC		
			_ AC_		
GAM573	TBC1D2	5'	TCACCTCCAGCCCATACATCA 20467		AA C CA
			TGATGTATG TT GA TGA		
			ACTACATAC GA CT ACT		
			CC C CC		
GAM573	LOC92283	3'	ATTCACACCTTATTCAACATCA 34092	A	TCGACA
			TGATGT TGAAT TGAAT		
			ACTACA ACTTA ACTTA		
			_ TTCCAC		
GAM574	CLN5	5'	ATTACATTTTCAGCTCTCA 13225	AAC	C
			TGAGAGCT ATG TAAT		
			ACTCTCGA TAC ATTA		
			CTT _		
GAM574	FLJ13646	3'	ATATATTAGGTCAGCTCTTA 23810	A	ATG
			TGAGAGCT AC CTAATATAT		
			ATTCTCGA TG GATTATATA		
			C _		
GAM574	KIAA1615	3'	ATATATTAACATGGCTTCA 34081	G	TAA C
			TGA AGC CATG TAATATAT		
			ACT TCG GTAC ATTATATA		
			_ _ A		
GAM574	SLC21A14	3'	TATATATTAGCTGTACTC 18891	CTA	T
			GAG ACA GCTAATATATA		
			CTC TGT CGATTATATAT		
			A_ _		
GAM574	LOC146229	3'	TATTCAGTGAATGCCAGCTCTC 38115	AA	_ _
	A		TGAGAGCT CAT GCT AATA		
			ACTCTCGA GTA TGA TTAT		
			CC AG C		
GAM574	LOC92405	3'	ATACATTAGCATGTAAATT 34303	GC	A
			GA TAACATGCTAAT TAT		

			TT ATTGTACGATTA ATA		
			AA C		
GAM575	CNTNAP2	3'	TCTTTCTTCTAAAACGG 15422	A T	
			CCGTTTTA AAG AAAGA		
			GGCAAAT TTC TTTCT		
			C _		
GAM575	EIF1A	3'	GTTCTTCACCTCTAAGATGGG 42723	AAA A	
			CCCGTTTTA GT AAGAAC		
			GGGTAGAAT CA TTCTTG		
			CTC C		
GAM575	HHEX	3'	TTCTTTACTTTTATATG 8595	TT	
			CGT TAAAAGTAAAGAA		
			GTA ATTTTCATTTCTT		
			T_		
GAM575	DKFZp547H025	3'	GTTCTTTGTAAATAAAACAGG 21372	C AAAG	
			CC GTTTTA TAAAGAAC		
			GG CAAAT GTTTCTTG		
			A AAAT		
GAM575	DKFZp761B0514	3'	CTTCACTTCCCGAGGGCGGGTG 26050	AA__ A	
			TACCCGTTTT AAGT AAG		
			GTGGGCGGGA TTCA TTC		
			GCCC C		
GAM575	EIF2S1	3'	GTTCTTTATAACAAAACAGGG 10299	_ AAAA	
			CCC GTTTT GTAAAGAAC		
			GGG CAAAA TATTTCTTG		
			A CAA_		
GAM575	KIAA0008	5'	GTTCTTTACTTTTTGTTTGG 16461	TTTT	
			CCG AAAAGTAAAGAAC		
			GGT TTTTCATTTCTTG		
			TTGT		
GAM575	KIAA1673	3'	CTTTACTTTTAATACAGG 35026	C T	
			CC GT TTAAGTAAAG		
			GG CA AATTTTCATTTC		
			A T		
GAM575	KIAA1911	3'	CTCTACTTTTAAAGGGT 36392	GT A	
			ACCC TTAAAAGTA AG		
			TGGG AAATTTTCAT TC		
			_ C		
GAM575	SSR3	3'	TTCTTTACTTTTCTTTGGTG 13974	CGTTTT	
			TACC AAAAGTAAAGAA		

			GTGG	TTTTCATTTCTT		
			TTTC__			
GAM575	LOC147341	5'	TTTCCTCTTAAACGGGTG	40829	A	T
			TACCCGTTTTTAA	AG AAA		
			GTGGGCAAAATT	TC TTT		
			C	C		
GAM575	LOC148195	3'	CTTCTTTTTAAAGAGGTA	40875	CG	T
			TACC	TTTTAAAG AAAG		
			ATGG	AAAATTTTC TTTC		
			AG	_		
GAM575	LOC158819	5'	GTTCTTTACCTTTACTTGG	42028	TTT	A
			CCG	TAAA GTAAAGAAC		
			GGT	ATTT CATTTCTTG		
			TC_	C		
GAM575	LOC51026	3'	GTTCTTTACAGGAGTTTAAAC	18141	A	_____
		G	CGTTTTAAA	GTAAAGAAC		
			GCAAATTT	CATTTCTTG		
			GAGGA			
GAM575	LOC91035	5'	GTTCTCCAAACGCTCTAAAC	32291	AAA_	AA_____
		GGG	CCCGTTTTA	GT AGAAC		
			GGGCAAAAT	CA TCTTG		
			CTCG	AAACC		
GAM576	SORD	3'	AGTAAGAGGACTACTCAGCA	9069	A	A TC _
			TG	CTGA TGGTC CT ACT		
			AC	GA CT ATCAG GA TGA		
			_	C GA A		
GAM576	WT1	3'	AAGAATTTTACCATTCAGTTA	23666	CTCCTAC	
			TGACTGAATGGT	TCTT		
			ATTGACTTACCA	AGAA		
			TTTTA__			
GAM576	WT1	3'	AAGAATTTTACCATTCAGTTA	5950	CTCCTAC	
			TGACTGAATGGT	TCTT		
			ATTGACTTACCA	AGAA		
			TTTTA__			
GAM576	WT1	3'	AAGAATTTTACCATTCAGTTA	23670	CTCCTAC	
			TGACTGAATGGT	TCTT		
			ATTGACTTACCA	AGAA		
			TTTTA__			
GAM576	WT1	3'	AAGAATTTTACCATTCAGTTA	23674	CTCCTAC	
			TGACTGAATGGT	TCTT		

ATTGACTTACCA AGAA
 TTTTA__
 GAM576 DCAMKL1 3' AAAAGTAAGATTTTCAGTCA 11110 TG CC C
 TGA CTG GAA GTCT TACT TT
 ||||| ||| ||| ||
 ACTGACTT TAGA ATGA AA
 _ _ A
 GAM576 FLJ11011 3' AGTAAAACCATTCATCA 20290 C CTCC
 TGA TGAATGGT TACT
 || ||||| |||
 ACT ACTTACCA ATGA
 A AA_
 GAM576 FLJ20802 3' AAGAGTAAATCCAAGTCA 19673 GAA TCTCC
 TGA CTG TGG TACTCTT
 ||| || |||||
 ACTGA ACC ATGAGAA
 _ TAA_
 GAM576 KIAA1396 3' GAAATGTAGAAAAACCTTCAGC 31547 A T CTC_ TC
 CA TG CTGAA GGT CTAC TTC
 || |||| ||| ||| |||
 AC GACTT CCA GATG AAG
 C _ AAAA TA
 GAM576 LOC116166 3' AGTAAGAGGACTACTCAGCA 30059 A A TC _
 TG CTGA TGGTC CT ACT
 || ||| |||| || |||
 AC GACT ATCAG GA TGA
 _ C GA A
 GAM576 LOC201696 3' GAAGAATAATAATCCATTCAAGT 31624 TCTCC C
 ACTGAATGG TA TCTTC
 ||||| || |||||
 TGA CTTACC AT AGAAG
 TAATA A
 GAM576 LOC254266 5' AAGAGCAGGAGGCCAGGCA 46479 AA A
 TG TGGTCTCCT CTCTT
 || ||||| |||||
 AC ACCGGAGGA GAGAA
 GG C
 GAM577 TOX 3' AGTTGCTAAGCACTTA 16325 TAA C
 TAAGTGCTT AGCG GCT
 ||||| ||| |||
 ATTCACGAA TCGT TGA
 _ _
 GAM577 UBL3 3' ATGTGCCTGTTTAAAGCACT 13965 G C T
 AGTGCTTTAAA CG GC ACAT
 ||||| || || |||
 TCACGAAATTT GT CG TGTA
 _ C _
 GAM577 DKFZP547E2110 3' GTAATGAAAGCACTTA 43731 AAAGCG C
 TAAGTGCTTT CG TAC
 ||||| || |||

ATTCACGAAA GT ATG
 _____ A
 GAM577 FLJ10352 3' TAGTGTGCTTCAAAACATT 25828 C A
 AGTG TTT AAGCGCGCTA
 |||| ||| |||||
 TTAC AAA TTCGTGTGAT
 A C
 GAM577 KIAA1028 3' TGCACCTTTTAAAGCACT 44166 C__
 AGTGCTTTAAAG GCG
 ||||| |||
 TCACGAAATTTT CGT
 CCA
 GAM578 CAMK4 3' GGTAAGAAATTGAAGTATCCTT 7482 AG ACCCT
 AAG TACT ATTTCTTACC
 || ||| |||||
 TTC ATGA TAAAGAATGG
 CT AGT__
 GAM578 DSCR1L1 3' TAAGAAATGGAAAGACTC 12431 A ACC
 GAGT CT CTATTTCTTA
 |||| || |||||
 CTCA GA GGTAAGAAT
 _ AA_
 GAM578 FLJ13646 3' TAAGAACTGGAGCAAGTACTCT 23814 ACC_ T
 T AAGAGTACT CTA TTCTTA
 ||||| ||| |||||
 TTCTCATGA GGT AAGAAT
 ACGA C
 GAM578 FLJ14106 3' AAGAAATAGGGGCCCTGCT 24663 CTA_
 AGTA CCCTATTTCTT
 ||| |||||
 TCGT GGGATAAAGAA
 CCGG
 GAM578 KIAA0515 3' GTAAGAAACAAGGAAATCACTC 31928 ACTAC A_
 GAGT CCT TTTCTTAC
 ||| || |||||
 CTCA GGA AAAGAATG
 CTAAA AC
 GAM578 KIAA1554 3' GGTAAGAGATAAACAGTAACCC 45612 A _ ACCC
 TT AAG GT ACT TATTTCTTACC
 ||| ||| |||||
 TTC CA TGA ATAGAGAATGG
 C A CAA_
 GAM578 ST13 3' AAATAAGGTAGTACTTTT 10032 C
 AAGAGTACTACC TATTT
 ||||| |||||
 TTTTCATGATGG ATAAA
 A
 GAM578 ST13 3' GGTAATTGTAGGGTAATAC 10033 C TTC
 GTA TACCCTAT TTACC
 ||| ||||| |||||

			CAT ATGGGATG AATGG		
			A TT_		
GAM578	LOC150933	3'	AGGAGGTGAGGGCAATACTC 41270	CTA _	
			GAGTA CCCT ATTTCTT		
			CTCAT GGGG TGGAGGA		
			AAC G		
GAM578	LOC157798	5'	TAAGAAATAGCATTTTACTCT 41851	CTACC	
			AGAGTA CTATTTCTTA		
			TCTCAT GATAAAGAAT		
			TTTAC		
GAM578	LOC163590	3'	GGTAAGAGTTTGTAGACTCTT 29652	A CCTAT	
			AAGAGT CTAC TTCTTACC		
			TTCTCA GATG GAGAATGG		
			_ TTT_		
GAM578	LOC255045	3'	TAAGAACTGGAGCAAGTACTCT 46034	ACC_ T	
		T	AAGAGTACT CTA TTCTTA		
			TTCTCATGA GGT AAGAAT		
			ACGA C		
GAM578	LOC51134	5'	AAGGAGTGGGAAATACCCTT 18207	A CTAC	
			AAG GTA CCTATTTCTT		
			TTC CAT GGGTGAGGAA		
			C AAA_		
GAM579	ADD3	3'	GAGAATTTTATTCTCAATAC 18818	TAC_ CC	
	CT		AGGT GGAAATAAAAA CTC		
			TCCA TCTTTATTTT GAG		
			TAAC AA		
GAM579	ABT1	3'	AGGGCCTTTATTTCCAACCT 15028	AC AA	
			GGTT GGAAATAAA CCCT		
			TCAA CCTTTATTT GGGA		
			_ CC		
GAM579	FLJ21144	3'	TTTTTATTTCCACAACCT 23039	AC	
			AGGTT GGAAATAAAAA		
			TCCAA CCTTTATTTT		
			CA		
GAM579	FLJ22551	5'	AGGCTGATCCCCGTAACCTA 24026	AA AAAAAC	
			TAGGTTACGG AT CCT		
			ATCCAATGCC TA GGA		
			CC GTC_		
GAM579	KIAA0594	3'	AGGGTTTTTAAAGAATAACCT 32384	CGGAAA	
			AGGTTA TAAAAACCCT		

			TCCAAT	ATTTTGGGA		
			AAGAA_			
GAM579	KIAA1877	3'	GGCTTTTATTTCCAACC	32883	AC	A
			GGTT GGAAATAAAA CC			
			CCAA CCTTTATTTT GG			
			— C			
GAM579	TRAF3	3'	GAGGGTCCCACAGACGTAACCT	30045		GAAATAAAA
	G		TAGGTTACG ACCCTC			
			GTCCAATGC TGGGAG			
			AGACACCC_			
GAM580	SLC15A1	3'	ACATTGGTCATCTTCCCTA	11520	T	ATA C
			TAGG AAGATGAT CAA GT			
			ATCC TTCTACTG GTT CA			
			C — A			
GAM580	FLJ10846	3'	TACATTATATCATTACCTG	20201	AG	CAAC
			TAGGTA ATGATATA GTA			
			GTCCAT TACTATAT CAT			
			— TA_			
GAM581	CASP8AP2	3'	AAATATGTATAATTATGATG	14429		C_
			TATCATAA TACATATTT			
			GTAGTATT ATGTATAAA			
			AAT			
GAM581	DAPP1	3'	GAAATATGTAATAATGATA	15732	AAC	
			TATCAT TACATATTTT			
			ATAGTA ATGTATAAAG			
			ATA			
GAM581	FLJ10483	3'	TGTAGGAAATGCCTTGTGATA	19878		CTACA
			TATCATAA TATTCCTACA			
			ATAGTGTT GTAAAGGATGT			
			CC_			
GAM581	FLJ10936	3'	TGTAGGAAATAAAAGTGATGAT	20272	A	ACA
	A		TATCAT ACT TATTCCTACA			
			ATAGTA TGA ATAAAGGATGT			
			G AA_			
GAM581	KIAA0798	3'	GTAGGAAATAAACTTGATA	16070		TAACTACA
			TATCA TATTCCTAC			
			ATAGT ATAAAGGATG			
			TCAA_			
GAM581	TERA	3'	TGTACTGTATGTAGTCATG	22207	A	TTCC
			CAT ACTACATAT TACA			

			GTA TGATGTATG ATGT		
			C TC__		
GAM581	ZNF84	3'	AGGAAATGCAATTATGATA 9478	CTACA	
			TATCATAA TATTTCT		
			ATAGTATT GTAAAGGA		
			AAC__		
GAM581	LOC127255	3'	TAGGAAATAGAATTATGA 29774	CTACA	
			TCATAA TATTTCTA		
			AGTATT ATAAAGGAT		
			TAAG_		
GAM581	LOC90317	3'	TGTAGCAATGCAGTTATGA 31208	A ATTTC	
			TCATAACT CAT CTACA		
			AGTATTGA GTA GATGT		
			C AC__		
GAM581	LOC93070	3'	TGTAGGAAATAAAAGTGATGAT 35327	A ACA	
	A		TATCAT ACT TATTTCTACA		
			ATAGTA TGA ATAAAGGATGT		
			G AA_		
GAM582	MTIF2	5'	ATATCCTAGCGGCGAAACA 8289	A ATGTAT	
			TGTT TGCC CTAGGATAT		
			ACAA GCGG GATCCTATA		
			A C_____		
GAM582	ZNF202	3'	ATATCCTAAAGACTGCTCAACA 9507	AT CAT ATC	
			TGTT GC GT TAGGATAT		
			ACAA CG CA ATCCTATA		
			CT T__ GAA		
GAM582	CG012	3'	ATATCCTTTTCAAGCATAACA 40484	CA TATCT	
			TGTTATGC TG AGGATAT		
			ACAATACG AC TCCTATA		
			A_ TTT__		
GAM582	DKFZP564C196	3'	ATCCTAGAAGGCTAACA 34710	T ATGTA	
			TGTTA GCC TCTAGGAT		
			ACAAT CGG AGATCCTA		
			_ A_____		
GAM582	POLR2D	3'	ATCCCCAGGCATAACA 11228	A TATCTA	
			TGTTATGCC TG GGAT		
			ACAATACGG AC CCTA		
			_ C_____		
GAM582	TPARL	3'	ATATCAATAACATGGCACAACA 20542	A ATCTAG	
			TGTT TGCCATGT GATAT		

			ACAA ACGGTACA	CTATA		
			C	ATAA__		
GAM583	IL12RB2	5'	TCCTGATGGCTGTCAACA	7281	A	AAATA
			TGTT ACAGCTATCA	GGA		
			ACAA TGTCGGTAGT	CCT		
			C	C__		
GAM583	FLJ00024	5'	ATTTTGCTAACTGTTAACA	31887	C T	
			TGTTAACAG TA CAAAAT			
			ACAATTGTC AT GTTTTA			
			A C			
GAM583	LOC121536	3'	ATGTTGGTTTGATACTGTTAAC	36663	C	A G
		A	TGTTAACAG TATCAA TAG AT			
			ACAATTGTC ATAGTTT GTT TA			
			_ G G			
GAM583	LOC221322	5'	ATCCTATTGACCGAAGCTGTCA	44152	A	A AA__
		A	TT ACAGCT TC AATAGGAT			
			AA TGTCGA AG TTATCCTA			
			C _ CCAG			
GAM584	DSP	3'	TGTATTAGGAGAAAATTACC	10678	TGTA	
			GGTA TTCTCCTAATACA			
			CCAT AAGAGGATTATGT			
			TAA_			
GAM584	RAI2	5'	TATTAGGAGATATCTAT	22350	TGTAT	
			ATAGGTA TCTCCTAATA			
			TATCTAT AGAGGATTAT			

GAM584	DYRK4	5'	TGTATCAGGAGAATCAAGCT	32123	A T	A
			GGT TG ATTCTCCT ATACA			
			TCG AC TAAGAGGA TATGT			
			A _ C			
GAM584	FLJ21032	3'	GTATTAGGTGCATACATAT	24401	TCT	
			GTATGTAT CCTAATAC			
			TATACATA GGATTATG			
			CGT			
GAM584	LOC219942	3'	GTATCAGGAAGGTACCTGT	44826	GTATTC	A
			ATAGGTAT TCCT ATAC			
			TGTCCATG AGGA TATG			
			GA__ C			
GAM584	LOC221288	3'	TGTATCAGAAATGCATACCT	44973	CTC	A
			AGGTATGTATT CT ATACA			

			TCCATACGTAA	GA TATGT		
			A__ C			
GAM585	EGFL5	5'	ACAGAGTCAGCCCCTGGGCCA	41875	_	TATATATA C
			TGGCC AGGG	ACTC GT		
			ACCGG TCCC	TGAG CA		
			G CGAC__	A		
GAM585	LOC165552	3'	ACGAAGCTCCAGAATCCTGGCC	40131		ATATATAA C
	A		TGGCCAGGGT	CT CGT		
			ACCGGTCCTA	GA GCA		
			AGACCTC_	A		
GAM585	LOC200132	3'	TGGCTATATACCCTGACCA	42710	C	TAACT
			TGG CAGGGTATATA	CCG		
			ACC GTCCCATATAT	GGT		
			A C__			
GAM585	LOC93380	3'	AGTTGTGTAACCGTGACCA	35724	C G A	
			TGG CA GGT TATATAACT			
			ACC GT CCA ATGTGTTGA			
			A G _			
GAM586	ACCN2	3'	GGCAGGAACTAAAACCTCA	21297	CAAT	A
			TGAGGTTT	TTCCT CT		
			ACTCCAAA	AAGGA GG		
			ATC_	C		
GAM586	COX11	3'	AGTTCTGTTGAAATCTCA	10592	TTCCT	
			TGAGGTTTCAAT	ACT		
			ACTCTAAAGTTG	TGA		
			TCT__			
GAM586	NORE1	3'	TCGTCACCAAACCTGGAACCTCA	25443	A	CCTACT
			TGAGGTTTCA TTT	CGA		
			ACTCCAAGGT AAA	GCT		
			C CCACT_			
GAM586	SLC14A1	3'	TCTGGTATGGAATTTGAAACCC	17996	A T _	C
	CA		TG GGTTTCAA TTCC TACT GA			
			AC CCAAAGTT AAGG ATGG CT			
			C T T T			
GAM586	C6orf26	3'	TCAAGTAGGAACACCCCA	24929	A	TTCAAT C
			TG GGT	TTCCTACT GA		
			AC CCA	AAGGATGA CT		
			C C__	A		
GAM586	FLJ20188	3'	AGGAAACTGAAAGCCCCA	19275	A _	A
			TG GGTTT CA TTTCT			

AC CCGAA GT AAAGGA
 C A C
 GAM586 LOC221143 3' TCGATGAATTTAAACCTCA 44945 C CCTAC
 TGAGGTTT AATTT TCGA
 ||||| |||| ||||
 ACTCCAAA TTAAG AGCT
 T T____
 GAM586 LOC253918 5' TTCAAGTGGTGCTGAATCCTCA 46042 T ATTTC C
 TGAGG TTCA CTACT GAA
 |||| |||| |||| ||||
 ACTCC AAGT GGTGA CTT
 T CGT__ A
 GAM587 DSC3 3' ACAAAAACATTTTAAACTT 7652 AGCAG
 AGGT AAAATGTTTTGT
 ||| |||||
 TTCA TTTTACAAAAACA
 AAA__
 GAM587 DSC3 3' ACAAAAACATTTTAAACTT 23663 AGCAG
 AGGT AAAATGTTTTGT
 ||| |||||
 TTCA TTTTACAAAAACA
 AAA__
 GAM587 FXYD6 3' CAAAAACCTTGCTTCCTTA 22547 T AAAAT
 TAAGG AGCAG GTTTTTG
 |||| |||| |||||
 ATTCC TCGTT CAAAAAC
 T C____
 GAM587 SLC14A1 5' GGGCATCTCCTGCTACTT 17995 AAA
 AGGTAGCAG ATGTTT
 ||||| |||||
 TTCATCGTC TACGGG
 CTC
 GAM587 C8orf4 3' AGCATTTTGCTGCTACCTTA 21324 _
 TAAGGTAGCAG AAAATGTT
 ||||| |||||
 ATTCCATCGTC TTTTACGA
 G
 GAM587 FLJ10700 3' ACAAAAACAAAATCTACCTTA 20018 CAGAAAA
 TAAGGTAG TGTTTTGT
 ||||| |||||
 ATTCCATC ACAAAAACA
 TAAA__
 GAM587 FLJ20276 3' ACAAAAACATTTTCTTCTTCT 19326 T C
 AGG AG AGAAAATGTTTTGT
 ||| || |||||
 TCT TC TCTTTTACAAAAACA
 _ T
 GAM587 FLJ21839 3' ACAGGGACCTGCCACC 22405 A AAAAT
 GGT GCAG GTTTTTGT
 ||| |||| |||||

			CCA CGTC CAGGGACA		
			C _____		
GAM587	LOC163682	5'	ACAAAGATCCCCTACTGCCT 42082	C	AAAAT
			AGGTAG AG GTTTTTGT		
			TCCGTC TC TAGAAACA		
			A CCC__		
GAM587	LOC169026	3'	ACAAAAACATTGAGTTGACC 40259	_	A_ AA
			GGT AGC GA ATGTTTTTGT		
			CCA TTG CT TACAAAAACA		
			G AG __		
GAM588	ATF5	3'	ATGTCTATGCCCGTCACATA 14320	AA	TGAA
			TATGTGACG CATA GCAT		
			ATACACTGC GTAT TGTA		
			CC C__		
GAM588	FKBP9	3'	CATGCTTTTCCAGCTCATCACA 45144	C	ACATAT
			TGTGA GA GAAGCATG		
			ACACT CT TTTCGTAC		
			A CGACCT		
GAM589	BCL7A	3'	GCGGCTACACATTCCA 21994	C	CATC
			TGGAATGTG AGCC GC		
			ACCTTACAC TCGG CG		
			A _____		
GAM589	DGUOK	3'	CGATGGTCCTACACATTCCA 28135	C	C_
			TGGAATGTG AG CCATCG		
			ACCTTACAC TC GGTAGC		
			A CT		
GAM589	DSCR1	3'	GCGACGAGGACGCATTCCA 10675	CAG	CA_
			TGGAATGTG CC TCGC		
			ACCTTACGC GG AGCG		
			A__ AGC		
GAM589	IL2RB	3'	TGCAATGGCTCAAACAACATTC 6575	GC_____	C C
	CA		TGGAATGT AGCC AT GCA		
			ACCTTACA TCGG TA CGT		
			ACAAAC _ A		
GAM589	P4HB	3'	CGGGGGCTGCACACCCA 6628	AA	A
			TGG TGTGCAGCCC TCG		
			ACC ACACGTCGGG GGC		
			C_ _		
GAM589	PARN	3'	TGCAAAAAGAGCTGACATTCCA 8444	G	CCATC__
			TGGAATGT CAGC GCA		

			ACCTTACA GTCG	CGT		
			_ AGAAAAA			
GAM589	PPAT	3'	TGCGATAACTGAACATTTCCA	8551	_ G CCC	
			TGGAA TGT CAG ATCGCA			
			ACCTT ACA GTC TAGCGT			
			T A AA_			
GAM589	A4GALT	5'	TGCAATGGGCTGCCCAGGCT	18896	AA T C	
			GG TG GCAGCCCAT GCA			
			TC AC CGTCGGGTA CGT			
			GG C A			
GAM589	FLJ20309	3'	TGAGATCACTGACATTCCA	19371	G CCC G	
			TGGAATGT CAG ATC CA			
			ACCTTACA GTC TAG GT			
			_ AC_ A			
GAM589	FLJ21916	3'	TGCCTATGCTGACATTCCA	23384	G CCATC	
			TGGAATGT CAGC GCA			
			ACCTTACA GTCG CGT			
			_ TATC_			
GAM589	KIAA1089	3'	TGCAGGGGCTGCACATCCCA	34142	A ATC	
			TGG ATGTGCAGCCC GCA			
			ACC TACACGTCGGG CGT			
			C GA_			
GAM589	KIAA1538	3'	TGCTTCCTAGCACATTCCA	35433	_ CCCATC	
			TGGAATGTGC AG GCA			
			ACCTTACACG TC CGT			
			A CTT__			
GAM589	SFXN5	3'	TGCGATGGTGCTGCACCCC	29389	AAT _	
			GG GTGCAGC CCATCGCA			
			CC CACGTCG GGTAGCGT			
			C_ T			
GAM589	WDR13	5'	CGGGACGCTCACATTCCA	19552	C CCA	
			TGGAATGTG AGC TCG			
			ACCTTACAC TCG GGC			
			_ CAG			
GAM589	LOC124997	3'	GCGACCTCACATTCTA	36787	C CCCA	
			TGGAATGTG AG TCGC			
			ATCTTACAC TC AGCG			
			_ C__			
GAM589	LOC150174	3'	TGCGATGGCGTTCACGTCCA	38875	A C _	
			TGGA TGTG AGC CCATCGCA			

ACCT GCAC TTG GGTAGCGT
 _ _ C
 GAM589 LOC150213 3' TGCGATGGCGTTCACGTCCA 36962 A C _
 TGGA TGTG AGC CCATCGCA
 |||| |||| || |||||
 ACCT GCAC TTG GGTAGCGT
 _ _ C
 GAM589 LOC150236 5' TGCGATGGCGTTCACGTCCA 38907 A C _
 TGGA TGTG AGC CCATCGCA
 |||| |||| || |||||
 ACCT GCAC TTG GGTAGCGT
 _ _ C
 GAM589 LOC153218 5' TGCGATGAGTCAGCCTCCA 39365 AT GCA C
 TGGA GT GC CATCGCA
 |||| || || |||||
 ACCT CG TG GTAGCGT
 C_ AC_ A
 GAM589 LOC154525 5' TGCGATGGGCCGCACATTTT 41708 A
 GGAATGTGC GCCCATCGCA
 ||||| |||||
 TTTTACACG CGGGTAGCGT
 C
 GAM589 LOC200261 5' GCAAGGCAGCTGCACATCCA 42751 A _ ATC
 TGGA TGTGCAGC CC GC
 |||| ||||| || ||
 ACCT ACACGTCG GG CG
 _ AC AA_
 GAM590 TSN 3' ATATTCTGCTATTGCAGCAATT 10982 C TT
 A TAA TGCTGCGATAGT GGGTAT
 |||| ||||| |||||
 ATT ACGACGTTATCG CTTATA
 A T_
 GAM590 KIAA0318 3' ATACCCAAATACACAGCA 34184 CGATA
 TGCTG GTTTGGGTAT
 |||| |||||
 ACGAC TAAACCCATA
 ACA_
 GAM590 LOC142779 3' ACCCATCTCCGTAGCAGT 37558 AT TT
 ACTGCTGCG AG TGGGT
 ||||| || ||||
 TGACGATGC TC ACCCA
 C_ T_
 GAM590 LOC200609 5' ATACCCAGTTTCACAGCA 43323 C TAGT
 TGCTG GA TTGGGTAT
 |||| || |||||
 ACGAC CT GACCCATA
 A TT_
 GAM591 LOC153196 5' TCTAAGCATTTGGCC 41593 AGAT
 GGT CAAATGCTTAGA
 || |||||

CCG GTTTACGAATCT

GAM591 LOC158014 5' ATTCTAAGCATTTCATACC 39690 GATCA
GGTA AATGCTTAGAAT
|||| |||||||||
CCAT TTACGAATCTTA
AC__

GAM591 LOC158318 5' TTCTAGGCAATCCACC 41959 A CAAA
GGT GAT TGCTTAGAA
||| ||| |||||||
CCA CTA ACGGATCTT
C ____

GAM592 BN51T 3' GGGCTATTATAGATGAAAAGT 42284 _ TACACAA
CAC GTGCAGTTTTCT TCT CCC
||||||| ||| |||
CACGTCAAAAG AGA GGG
T TATTATC

GAM592 CDKN1B 3' GGTTTCATGTAGAGAAAAGCAC 10274 AG T C_
GTGC TTTTCTCT ACA AACC
|||| |||||| ||| |||
CACG AAAAGAGA TGT TTGG
_ _ AC

GAM592 LAMC2 3' GGATGGAAAGACAAACTGCAC 12090 TC ACA A
GTGCAGTTT TCTT CA CC
|||||| ||| |||
CACGTCAAA AGAA GT GG
C_ AG_ A

GAM592 PAG 3' TGTATGGAAAAGCTGCAC 20512 CT T
GTGCAGTTTT C TACA
||||||| | |||
CACGTCGAAA G ATGT
AG T

GAM592 RBL1 3' GGGTTATAAGAAAAAATTGCAC 8802 C CAC
GTGCAGTTTT TCTTA AACCC
||||||| |||| ||||
CACGTTAAAA AGAAT TTGGG
A A__

GAM592 SOCS5 3' GGTTATAACAGAAAAGT 15228 C CAC
CAGTTTTCT TTA AACC
||||||| ||| |||
GTCAAAAGA AAT TTGG
C A__

GAM592 FLJ23017 3' GGGTTCAAGAAAAAAGTGC 23130 C ACAC
GCAGTTTT TCTT AACCC
|||||| ||| ||||
CGTCAAAA AGAA TTGGG
A C__

GAM592 KIAA0354 3' GGCTATGTAAGAGTTAGCAGC 16997 A TT CAA
GC GTT CTCTTACA CC
|| ||| |||||| ||

			CG CGA GAGAATGT GG		
			A TT ATC		
GAM592	KIAA0472	3'	GGGCTGCAAAGTGACAACTGCA 35579	T T	ACA A
		C	GTGCAGTT TC CTT CA CCC		
			CACGTCAA AG GAA GT GGG		
			C T AC_ C		
GAM592	KIAA1297	5'	GGGCTGCGTAAGGGGGTCCAGC 35718	AGTT	A A
		AC	GTGC TTCTCTTAC CA CCC		
			CACG GGGGGAATG GT GGG		
			ACCT C C		
GAM592	L3MBTL2	5'	GGTTACAGGGAAAACCCAC 42793	CA	TACAC
			GTG GTTTTCTCT AACC		
			CAC CAAAAGGGA TTGG		
			CA_		
GAM592	LEC3	5'	GTTGTGGAAACTGCAC 17572	CTCTTA	_
			GTGCAGTTTT CACAA C		
			CACGTCAAAG GTGTT G		
			A		
GAM592	TUSP	3'	GGTAAAGAAGAAACTGCAC 21532	TC	ACACA
			GTGCAGTTT TCTT ACC		
			CACGTCAAA AGAA TGG		
			GA A_		
GAM592	LOC143308	5'	TGGCTAGGAAAAAACTGC 40349	C	CA
			GCAGTTTT TCTTA CA		
			CGTCAAAA AGGAT GT		
			A CG		
GAM592	LOC146136	5'	GGGCCATATGGGAAGCTGCAC 36111		CTTACACAA
			GTGCAGTTTTCT CCC		
			CACGTCGAAGGG GGG		
			TATACC_		
GAM592	LOC150225	3'	GGTTGTGTAAAGCCTGTGGCA 41190	AGTTTT	C
		C	GTGC CT TTACACAACC		
			CACG GA AATGTGTTGG		
			GTGTCC A		
GAM592	LOC152860	3'	GGGCTGTGAAGAGAAAACCTCAC 39325	C	A A
			GTG AGTTTTCTCTT CACA CCC		
			CAC TCAAAGAGAA GTGT GGG		
			_ _ C		
GAM592	LOC158301	5'	GGACCGTGTAAGAGGACACCAC 39810	CA T	AA_
			GTG GT TTCTCTTACAC CC		

		CAC CA AGGAGAATGTG GG	
		__ C CCA	
GAM592	LOC220565 3'	GGGCCGTATGGGAAGCTGCAC 43635	CT ACAA
		GTGCAGTTTTCT TAC CCC	
		CACGTCGAAGGG ATG GGG	
		T_ CC__	
GAM592	LOC221810 3'	GGGCTGTTATTCAGAACACCGC 45085	A T CTTAC A
	AC	GTGC GT TTCT ACA CCC	
		CACG CA AAGA TGT GGG	
		C C CTTAT C	
GAM592	LOC255158 3'	GTAAACAGAAAACCTGCAC 46001	C_
		GTGCAGTTTTCT TTAC	
		CACGTCAAAAGA AATG	
		CA	
GAM592	LOC90538 3'	GGGTATGAAAAAAAAAACTGCA 31657	CTCTTA CA
		TGCAGTTTT CA ACCC	
		ACGTCAAAA GT TGGG	
		AAAAAA A_	
GAM592	LOC93380 3'	GTTGTGTAACCGTGACCAC 35726	CA TTCTC
		GTG GTT TTACACAAC	
		CAC CAG AATGTGTTG	
		__ TGCC__	
GAM593	CBFA2T3 3'	TGCGTTCGCCTCTGGCCC 11694	A
		GGGCCA AGGCGAATGTA	
		CCCGGT TCCGCTTGCGT	
		C	
GAM593	GAS11 3'	GGGATGAATCACCCCTTGGCCCA 7222	A C ATGTA
		TGGGCCAA GG GA ATCCT	
		ACCCGGTT CC CT TAGGG	
		C A AAG__	
GAM593	NID 3'	GGATTACATGCCCATCCCA 8341	CCAAA GA
		TGGG GGC ATGTAATCC	
		ACCC CCG TACATTAGG	
		TAC__ __	
GAM593	NIPSNAP1 3'	GGATTACAGCTCTGCCCA 9703	CAAA GAA
		TGGGC GGC TGTAATCC	
		ACCCG TCG ACATTAGG	
		TC__ __	
GAM593	UBE3A 3'	AGAATTACATTGTATAGCCC 28359	CAAAG G C
		GGGC GC AATGTAAT CT	

			CCCG	TG TTACATTA GA		
			ATA__ _	A		
GAM593	UBE3A	3'	AGAATTACATTGTATAGCCC	28363	CAAAG G	C
			GGGC	GC AATGTAAT CT		
			CCCG	TG TTACATTA GA		
			ATA__ _	A		
GAM593	UBE3A	3'	AGAATTACATTGTATAGCCC	6078	CAAAG G	C
			GGGC	GC AATGTAAT CT		
			CCCG	TG TTACATTA GA		
			ATA__ _	A		
GAM593	XRCC2	3'	AGGATTACAGGCCCGTGCCCA	11900	C AA	GAA
			TGGGC A	GGC TGTAATCCT		
			ACCCG T	CCG ACATTAGGA		
			GC	G		
GAM593	KIAA0141	3'	AGGACCTTTGTGCTCACTTTGG	16584	___	AATGTAA
			CCCA	TGGGCCAAAG GCG TCCT		
			ACCCGGTTTC	CGT AGGA		
			ACT	GTTTCC_		
GAM593	KIAA1550	3'	AGGATTGTCACCTTCACCCCA	33067	CCA	C ATG
			TGGG	AAGG GA TAATCCT		
			ACCC	TTCC CT GTTAGGA		
			CAC	A _		
GAM593	KIAA1956	3'	TGCATTTGCCTCCAGCCCA	38363	CAA	
			TGGGC	AGGCGAATGTA		
			ACCCG	TCCGTTTACGT		
			ACC			
GAM593	MGC17330	3'	AGGATCTGCTCCGCCTTTGGCC	27458	AAT	_
			GGCCAAAGGCG	GTA ATCCT		
			CCGGTTTCCGC	CGT TAGGA		
			CT_	C		
GAM593	NYD-SP11	3'	AGGATCACATTGCATTGACCC	25688	C AG G	A
			GGG CAA	GC AATGT ATCCT		
			CCC GTT	CG TTACA TAGGA		
			A A_ _	C		
GAM593	ZNF33A	3'	AGGATTACAAAGGATTTAGCCT	43895	C	GGCGAA
			GGGC AAA	TGTAATCCT		
			TCCG TTT	ACATTAGGA		
			A	AGGAA_		
GAM593	LOC124602	3'	GATTACATAAATGCCTGGC	36758	AA	A_
			GCCA	GGCG ATGTAATC		

			CGGT CCGT TACATTAG		
			___ AAA		
GAM593	LOC130412	5'	GATCATTGGCCTTTGGACCA 37291	G	G TA
			TGG CCAAAGGC AATG ATC		
			ACC GGTTTCCG TTAC TAG		
			A G ___		
GAM593	LOC203397	3'	GATTACATAAATGCCTGGC 43038	AA	A___
			GCCA GGCG ATGTAATC		
			CGGT CCGT TACATTAG		
			___ AAA		
GAM594	ALS2	3'	TGAAGTTGTAAGAAAAGCTTCC 21931	C	ACGGA CC
	A		TGG AG TCTTACAAC CA		
			ACC TC AGAATGTTG GT		
			T GAAA_ AA		
GAM594	HTRA3	3'	GGAGCTGAGCCCCGCCCTGCCA 42942	A_	AT CAA
			TGGCAG CGG CTTA CC		
			ACCGTC GCC GAGT GG		
			CC CC CGA		
GAM594	KMO	3'	GTTGTGAGCCACCGCTGCCA 9780	A	AT_
			TGGCAG CGG CTTACAAC		
			ACCGTC GCC GAGTGTTG		
			_ ACC		
GAM594	LAMA4	5'	GGGGCTCACCCCAATCCGTCTG 8070		CTTACAA__
	CC		GGCAGACGGAT CCCC		
			CCGTCTGCCTA GGGG		
			ACCCCACTC		
GAM594	TNFRSF10B	3'	TTGTAAGATCCATCTACA 9942	GC	C
			TG AGA GGATCTTACAA		
			AC TCT CCTAGAATGTT		
			A_ A		
GAM594	WNT10B	3'	TGGAGCCATAAGATCTGTATCT 9432	CAG	CAACC
	A		TGG ACGGATCTTA CCA		
			ATC TGTCTAGAAT GGT		
			TA_ ACCGA		
GAM594	CDC14B	3'	TGGGATTATAGGCGTCTGCCA 27176	GAT	C C
			TGGCAGACG CTTA AA CCA		
			ACCGTCTGC GGAT TT GGGT		
			___ A A		
GAM594	CSRP2BP	3'	TGGGGTTGTTGGGCAGCCTGCC 34737	ACGGA	T
	A		TGGCAG TCT ACAACCCA		

ACCGTC GGG TGTTGGGGT
 CGAC_ T
 GAM594 DKFZP434D146 3' TGGGATTGTAAGAGTATGCCA 17874 GACGGA C
 TGGCA TCTTACAA CCCA
 |||| ||||| ||||
 ACCGT AGAATGTT GGGT
 ATG__ A
 GAM594 KIAA0435 5' TGGGATTGTAGGAGTGTGCCA 16726 G GGA C
 TGGCA AC TCTTACAA CCCA
 |||| || ||||| ||||
 ACCGT TG AGGATGTT GGGT
 G __ A
 GAM594 KIAA0444 3' TGGGGAGGTGGATCCTCTGCCA 31247 C T AA
 TGGCAGA GGATCT AC CCCCA
 ||||| ||||| || ||||
 ACCGTCT CCTAGG TG GGGGT
 _ _ GA
 GAM594 KIAA0563 5' TGGGGTTGCAGGTGTGCACCA 16845 CAGA G TA
 TGG CG ATCT CAACCCCA
 || || || || |||||
 ACC GT TGGA GTTGGGGT
 AC__ G C_
 GAM594 PHYHIP 3' GGGGCTGGGGTCCGCCTGCC 16512 A CAA
 GGCAG CGGATCTTA CCCC
 |||| ||||| ||||
 CCGTC GCCTGGGGT GGGG
 C C_
 GAM594 PRO1843 5' GGTTGTAAGAAAGGCTCCCA 20574 C ACGGA
 TGG AG TCTTACAACC
 || || ||||| ||||
 ACC TC AGAATGTTGG
 C GGAA_
 GAM594 RIL 3' GGGGCCGCCGCCGGCCGTCTGC 9798 A TACAA_
 GCAGACGG TCT CCCC
 ||||| || ||||
 CGTCTGCC GGG GGGG
 _ CGCCGCC
 GAM594 TUSP 3' TGAAGTTGTAAGAGTTGTC 21536 A CC
 GACGG TCTTACAAC CA
 |||| ||||| || ||
 CTGTT AGAATGTTG GT
 G AA
 GAM594 LOC144845 5' GGTCAAGTTCCGTCTGCCA 28823 T ACA
 TGGCAGACGGA CTT ACC
 ||||| || ||||
 ACCGTCTGCCT GAA TGG
 T C_
 GAM594 LOC150290 3' TGGGACTACAGATGTTTGCCA 38934 GG TACAAC
 TGGCAGAC ATCT CCCA
 ||||| || ||||

			ACCGTTTG TAGA GGGT	
			__ CATCA_	
GAM594	LOC254423	3'	TGGGGTTGTGGTGGGCATCC 46531	_ _
			GGAT CT TACAACCCCA	
			CCTA GG GTGTTGGGGT	
			C GTG	
GAM595	ABCG1	3'	TGAAGAATGATTCAGGGTA 11352	ATC
			TACTCTGAATCA TCTTCA	
			ATGGGACTTAGT AGAAGT	
			A_	
GAM595	ADORA1	3'	TGAAGAGATACCCACAGAGTG 6330	AATCA
			TACTCTG ATCTCTTCA	
			GTGAGAC TAGAGAAGT	
			ACCCA	
GAM595	CD28	3'	TGAAGAGAGCATCAGAGT 12783	ATCAA
			ACTCTGA TCTCTTCA	
			TGAGACT AGAGAAGT	
			ACG_	
GAM595	CIT	5'	TGAAGAGGAGATCCAGG 34565	A AA
			TCTG ATC TCTCTTCA	
			GGAC TAG GGAGAAGT	
			C A_	
GAM595	CLCA3	3'	TGAAGAGGGACATCAAGTA 11356	C ATCAA
			TACT TGA TCTCTTCA	
			ATGA ACT GGAGAAGT	
			_ ACAG_	
GAM595	CYP19	3'	AAGAACGTGGTCAGAGTA 25268	A ATC
			TACTCTGA TCA TCTT	
			ATGAGACT GGT AGAA	
			_ GCA	
GAM595	CYP19	3'	AAGAACGTGGTCAGAGTA 5558	A ATC
			TACTCTGA TCA TCTT	
			ATGAGACT GGT AGAA	
			_ GCA	
GAM595	FLRT2	3'	TGAAGAGATTGAACCTAGTA 14887	CTGAA
			TACT TCAATCTCTTCA	
			ATGA AGTTAGAGAAGT	
			TCCA_	
GAM595	MDM1	3'	TGAAGAGGCATTTTCAGAGTG 21321	TCAA
			TACTCTGAA TCTCTTCA	

			GTGAGACTT GGAGAAGT		
			TAC_		
GAM595	NXF2	5'	TGAAGAGACTATGCTGAGTG 19459	TGA	CAA
			TACTC AT TCTCTTCA		
			GTGAG TA AGAGAAGT		
			TCG TC_		
GAM595	PCDH7	3'	TGAAAAGAAGTATTCAGAGTA 26218	CAA	C
			TACTCTGAAT TCT TTCA		
			ATGAGACTTA AGA AAGT		
			TGA _		
GAM595	RAD54B	3'	TGAAAAGATTGAAGAG 28678	GAA	C
			CTCT TCAATCT TTCA		
			GAGA AGTTAGA AAGT		
			_ A		
GAM595	SLC2A3	3'	AAGAGAGGTTATAGAGTA 13814	_	AA
			TACTCTG AATC TCTCTT		
			ATGAGAT TTGG AGAGAA		
			A _		
GAM595	TRPC5	3'	TGAAGAGATTTCAAAG 14850	C	TCA
			CT TGAA ATCTCTTCA		
			GA ACTT TAGAGAAGT		
			A _		
GAM595	WHSC1	3'	GAAGGCTTTGATTTAGAGTA 14250		TC
			TACTCTGAATCAA TCTTC		
			ATGAGATTTAGTT GGAAG		
			TC		
GAM595	AAK1	3'	TGAAGCCTAGACATTCAGAG 17145	CAA	_
			CTCTGAAT TCT CTTCA		
			GAGACTTA AGA GAAGT		
			C_ TCC		
GAM595	AF020591	5'	AAGAGACCCGTTTCAGAGT 15825	CAA	
			ACTCTGAAT TCTCTT		
			TGAGACTTG AGAGAA		
			CCC		
GAM595	BFAR	3'	TGAAGAGTTGCTAGGATTCAGA 30480	AAT	_____
	GTA		TACTCTGAATC CTCTTCA		
			ATGAGACTTAG GAGAAGT		
			GATCGTT		
GAM595	C15orf5	3'	TGAGGATTTTGATTCAGA 25215	TC	
			TCTGAATCAA TCTTCA		

			AGACTTAGTT AGGAGT		
			TT		
GAM595	CED-6	3'	TGAAAATGTGACTTAGAGTA	18434	A ATCTC
			TACTCTGA TCA TTCA		
			ATGAGATT AGT AAGT		
			C GTAA_		
GAM595	DKFZP761C169	5'	AGGGGATTATTCAAAGTA	33677	C C
			TACT TGAAT AATCTCTT		
			ATGA ACTTA TTAGGGGA		
			A _		
GAM595	DKFZP761C169	5'	TGAAGAGATTGAAAGA	33678	GAA
			TCT TCAATCTCTTCA		
			AGA AGTTAGAGAAGT		
			A_		
GAM595	FLJ10579	3'	AAGAGGGATCAGAGTG	19943	A AA
			TACTCTGA TC TCTCTT		
			GTGAGACT AG GGAGAA		
			_ _		
GAM595	FLJ10956	3'	TGAAGAGATTCGTCTAGAG	20278	A C
			CTCTG AT AATCTCTTCA		
			GAGAT TG TTAGAGAAGT		
			C C		
GAM595	FLJ11125	3'	TGAAGAGATGGTTCAGA	29978	A
			TCTGAATCA TCTCTTCA		
			AGACTTGGT AGAGAAGT		
			_		
GAM595	FLJ20294	3'	TGAAGGTGAGGGTTCAGAGTA	19352	AA _
			TACTCTGAATC TC TCTTCA		
			ATGAGACTTGG AG GGAAGT		
			G_ T		
GAM595	FLJ21034	3'	TGAAGAGATGGATATCAAGTA	24484	C _ A
			TACT TGA ATC ATCTCTTCA		
			ATGA ACT TAG TAGAGAAGT		
			_ A G		
GAM595	FLJ23584	5'	TGAAGAGATCCAGGTA	23823	T AATCA
			TAC CTG ATCTCTTCA		
			ATG GAC TAGAGAAGT		
			_ C_		
GAM595	FLJ30213	3'	TGAAGAGGCACTTTCGAGTA	29609	T TCAA
			TACTC GAA TCTCTTCA		

			ATGAG CTT GGAGAAGT		
			_ TCAC		
GAM595	KIAA0089	3'	TGAAGAGATTTTGGTGAGGA	34670	GA _
			TCT ATCA ATCTCTTCA		
			AGG TGGT TAGAGAAGT		
			AG TT		
GAM595	KIAA1155	3'	TGAAGAGGCTGCCAAAGTA	31201	C AAT AT
			TACT TG CA CTCTTCA		
			ATGA AC GT GAGAAGT		
			A C_ CG		
GAM595	KIAA1276	5'	TGAAGGAGAGGATTCAGGTA	33020	T AA_ T
			TAC CTGAATC TC CTTCA		
			ATG GACTTAG AG GAAGT		
			_ GAG _		
GAM595	KIAA1712	3'	TGAAGAGATTACCTAGAG	33540	AATC
			CTCTG AATCTCTTCA		
			GAGAT TTAGAGAAGT		
			CCA_		
GAM595	KIAA1775	3'	TGAAGAGACAATTCAGGG	26945	CAA
			CTCTGAAT TCTCTTCA		
			GGGACTTA AGAGAAGT		
			AC_		
GAM595	MSP	3'	TGAAGAGACTGGACAAAGT	25762	C AA A
			ACT TG TCA TCTCTTCA		
			TGA AC GGT AGAGAAGT		
			A A_ C		
GAM595	MYOZ2	3'	TGAAGACCTATTCAGAGT	18694	CAATC
			ACTCTGAAT TCTTCA		
			TGAGACTTA AGAAGT		
			TCC_		
GAM595	PAK2	5'	TGAAGAGATTATGGAG	33063	AATC
			CTCTG AATCTCTTCA		
			GAGGT TTAGAGAAGT		
			A_		
GAM595	PRO1430	5'	TGAAGAGACTGAGGTGCAGA	20678	AA_ A
			TCTG TCA TCTCTTCA		
			AGAC AGT AGAGAAGT		
			GTGG C		
GAM595	SIAT4A	5'	TGAAGAACTGAGGTTTCAGAG	8982	AATC_
			CTCTGAATC TCTTCA		

		GAGACTTGG AGAAGT	
		AGTCAA	
GAM595	TOPBP1	3' TGAAGAATTCTGCTTCAGAGTA 13888	T ATC_
		TACTCTGAA CA TCTTCA	
		ATGAGACTT GT AGAAGT	
		C CTTA	
GAM595	LOC126603	5' TGAAGGACATTCAGAG 37152	CAA T
		CTCTGAAT TC CTTCA	
		GAGACTTA AG GAAGT	
		C _ _	
GAM595	LOC129676	5' TGAAGAACTCAGACTCAGAGTG 37289	A AATC_
		TACTCTGA TC TCTTCA	
		GTGAGACT AG AGAAGT	
		C ACTCA	
GAM595	LOC143914	5' TGAAGAGAGATCTTAGAG 37637	_ AA
		CTCTGA ATC TCTCTTCA	
		GAGATT TAG AGAGAAGT	
		C _	
GAM595	LOC144195	3' AAGAGAGGTTATAGAGTA 30264	_ AA
		TACTCTG AATC TCTCTT	
		ATGAGAT TTGG AGAGAA	
		A _	
GAM595	LOC149707	5' TGAAGAAATAAGTTCAGAG 38803	CA C
		CTCTGAAT AT TCTTCA	
		GAGACTTG TA AGAAGT	
		AA A	
GAM595	LOC150848	3' AGGGATTGACCAGAGTA 41252	AA
		TACTCTG TCAATCTCT	
		ATGAGAC AGTTAGGGA	
		C_	
GAM595	LOC150960	3' TGAAGAGACTGAGAGT 39032	TGAA A
		ACTC TCA TCTCTTCA	
		TGAG AGT AGAGAAGT	
		_ _ C	
GAM595	LOC154789	5' TGAAGAGACATTGTTTCAGAG 39488	T _
		CTCTGAA CAA TCTCTTCA	
		GAGACTT GTT AGAGAAGT	
		_ AC	
GAM595	LOC157226	5' TGAAGAGACTGTGGAGT 31979	AAT A
		ACTCTG CA TCTCTTCA	

			TGAGGT GT AGAGAAGT		
			___ C		
GAM595	LOC158062	3'	TGAAAAGACATCAGAGTA 41916	ATCAA	C
			TACTCTGA TCT TTCA		
			ATGAGACT AGA AAGT		
			AC___ A		
GAM595	LOC200227	5'	TGAAGAAATAAGTTCAGAG 42748	CA	C
			CTCTGAAT AT TCTTCA		
			GAGACTTG TA AGAAGT		
			AA A		
GAM595	LOC200273	3'	GAAGACCAGACAGATTCAGAG 35029	AA	___
			CTCTGAATC TC TCTTC		
			GAGACTTAG AG AGAAG		
			AC ACC		
GAM595	LOC256529	5'	TGAAAGCGGATTCAGAG 46590	AAT	C
			CTCTGAATC CT TTCA		
			GAGACTTAG GA AAGT		
			GC_ _		
GAM595	LOC51068	3'	AAGAGATTGAGCAAGTG 18057	C	AA
			TACT TG TCAATCTCTT		
			GTGA AC AGTTAGAGAA		
			_ G_		
GAM595	LOC91496	5'	AAGAGATCGTTAGAGTG 32914	ATCA	
			TACTCTGA ATCTCTT		
			GTGAGATT TAGAGAA		
			GC_		
GAM596	CPD	3'	ATTAATGTATCAGTTATCCCA 6983	A	___
			TG GATAGCTGA ATTGAT		
			AC CTATTGACT TAATTA		
			C ATG		
GAM596	DVL3	3'	ATTTATTCAGCTACATCA 10689	GA	T
			TGA TAGCTGAAT GAT		
			ACT ATCGACTTA TTA		
			AC T		
GAM596	RTN3	3'	AGTCTTACTCAGCTATCCA 36584	A	ATT_
			TG GATAGCTGA GATT		
			AC CTATCGACT CTGA		
			_ CATT		
GAM596	TEM6	3'	TGAATCAAGTGTATTTCA 22964	G	TGAA
			TGAGATA C TTGATTCA		

ACTTTAT G AACTAAGT
 TG
 GAM596 XPR1 3' CATTGGATTTCATGCCATCCCA 11123 A A _ ATT
 TG GAT GC TGA GATTCAATG
 || ||| ||| |||||
 AC CTA CG ACT TTAGGTTAC
 C C T _
 GAM596 MGC29898 3' TGAATCAAAGTTATTCA 29679 A GAA
 TGAG TAGCT TTGATTCA
 ||| ||| |||||
 ACTT ATTGA AACTAAGT

 GAM596 LOC145955 5' ATCATTAGCTATCCCA 40642 A AT
 TG GATAGCTGA TGAT
 || ||||| |||
 AC CTATCGATT ACTA
 C _
 GAM596 LOC152905 3' AGTCTTACTCAGCTATCCA 30330 A ATT_
 TG GATAGCTGA GATT
 || ||||| |||
 AC CTATCGACT CTGA
 _ CATT
 GAM597 CGGBP1 3' AACACCACTTAACAGTA 9737 AAA T
 TGCT TTGA TGGTGTT
 ||| ||| |||||
 ATGA AATT ACCACAA
 C_ C
 GAM598 BCRP2 3' ATAAATGTTATGAAAAGGCAGA 31272 A G_ C
 A TTC TGT TTCATAACA TTAT
 ||| ||| ||||| |||
 AAG ACG AAGTATTGT AATA
 _ GAA A
 GAM598 ESRRG 3' ATAAGCACTGCACATGAGA 32996 TCATAACA
 TTTCATGTGT CTTAT
 ||||| |||
 AGAGTACACG GAATA
 TCAC_
 GAM598 FLJ20147 3' GTGGATTATGAACAAATGAAA 19242 G _
 TTTCAT TGTTCATAA CAC
 ||||| ||||| |||
 AAAGTA ACAAGTATT GTG
 A AG
 GAM598 FLJ22060 3' ATAAGCAATGATACATGAAA 23866 T AACA
 TTTCATGTGT CAT CTTAT
 ||||| ||| |||||
 AAAGTACATA GTA GAATA
 _ AC_
 GAM598 HIC 3' TGTTTATGGACACATGAAA 33496 _
 TTTCATGTGTTTCATAA CA
 ||||| ||||| ||

AAAGTACACAGGTATT GT

T

GAM598 TAF2 3' ATAAGCATTTAAAAACATATGA 9158 CA CA_
AA TTTTCATGTGTT TAA CTTAT

||||||| ||| ||||

AAAGTATACAA ATT GAATA

AA TAC

GAM599 ADD3 3' TGGCTTTGAATTTTAAGCA 18819 C _
TGC TAAAGT TAAAGTCA

||| ||||| |||||

ACG ATTTTA GTTTCGGT

A A

GAM599 CLCN6 3' GTGGTTTGACTCTCCTTAG 22339 AGTTAA
CTAA AGTCAAACCAC

||| |||||

GATT TCAGTTTGGTG

CCTC__

GAM599 CLCN6 3' GTGGTTTGACTCTCCTTAG 22344 AGTTAA
CTAA AGTCAAACCAC

||| |||||

GATT TCAGTTTGGTG

CCTC__

GAM599 CLCN6 3' GTGGTTTGACTCTCCTTAG 6962 AGTTAA
CTAA AGTCAAACCAC

||| |||||

GATT TCAGTTTGGTG

CCTC__

GAM599 DBY 3' TGACTTTAACTTTAGACA 11029 C
TG CTAAAGTTAAAGTCA

|| |||||

AC GATTTCAATTTCAGT

A

GAM599 MAD2L1 3' GTAGTTTGACTCAGTATAGGTA 8171 AAGTTAA C
TGCCTA AGTCAAAC AC

||||| ||||| ||

ATGGAT TCAGTTTG TG

ATGAC__ A

GAM599 ORC4L 3' TGACTTCAACTTTGGCA 31091 T A
TGCC AAAGTT AAGTCA

||| ||||| |||||

ACGG TTTCAA TTCAGT

_ C

GAM599 RBM3 5' GTGGGAGGGCTCAACTTTA 34894 AA AAA
TAAAGTT AGTC CCAC

||||| ||| ||||

ATTTCAA TCGG GGTG

C_ GAG

GAM599 TGFBR1 3' TGGTCTTAACTTTAGGTA 10951 AG
TGCCTAAAGTTAA TCA

||||||| |||

			ATGGATTTC AATT GGT		
			CT		
GAM599	KCNMB2	3'	GTTTGACTTTTCATAAGCA 12447	C AAGTT	
			TGC TA AAAGTCAAAC		
			ACG AT TTTCAGTTTG		
			A ACT__		
GAM599	KIAA1627	3'	GTGGGAGACTTAACTTTAG 39345	A AAA	
			CTAAAGTTAA GTC CCAC		
			GATTTC AATT CAG GGTG		
			_ AG_		
GAM599	LOC152573	3'	GTTTGACTTTTAAAGTTGCA 39289	CT AG	
			TGC AA TTAAAGTCAAAC		
			ACG TT AATTTCAGTTTG		
			_ GA		
GAM599	LOC202451	5'	GTGGTTCTCAAAC TTTAG 43440	AA TCA	
			CTAAAGTT AG AACCAC		
			GATTTC AA TC TTGGTG		
			AC _		
GAM599	LOC253039	3'	TGGTTTGAGAACTTTA 45994	AAAG	
			TAAAGTT TCAAACCA		
			ATTTCAA AGTTTGGT		
			G _		
GAM599	LOC253782	3'	TGGCTAAAATTAAC TTTAG 45800	_	
			CTAAAGTTAA AGTCA		
			GATTTC AATT TCGGT		
			AAAA		
GAM599	LOC91801	3'	TGGAGACTTAACTTTAAGCA 29010	C A AAA	
			TGC TAAAGTTAA GTC CCA		
			ACG ATTTCAATT CAG GGT		
			A _ A _		
GAM600	AICDA	3'	CAGGAATGTCACACACGATGAA 21832	CATAA GA_	
	A		TTTCATTGTG GCA CTG		
			AAAGTAGCAC TGT GAC		
			ACAC_ AAG		
GAM600	F2R	3'	TCAGTCTGCTTAGAAATAA 7724	GCA	
			TTGT TAAGCAGACTGA		
			AATA ATTCGTCTGACT		
			AAG		
GAM600	ROCK2	3'	CAGCCTGCCCAACATAGTGAAA 32837	CATAA A	
			TTTCATTGTG GCAG CTG		

			AAAGTGATAC	CGTC GAC		
			AACC_	C		
GAM600	AP1GBP1	3'	CAGCCTGGCCAACACAATGAAA	27878	CATAAG	A
			TTTCATTGTG	CAG CTG		
			AAAGTAACAC	GTC GAC		
			AACCG_	C		
GAM600	ARSDR1	3'	CAGTCTTTATGCAAATGAAA	18109	G	GC
			TTTCATT	TGCATAA AGACTG		
			AAAGTAA	ACGTATT TCTGAC		
			—	—		
GAM600	FLJ12688	3'	CAGCTGGATGTACAAT	36221	AAG	A
			ATTGTGCAT	CAG CTG		
			TAACATGTA	GTC GAC		
			G_	_		
GAM600	FLJ23042	3'	CAGCCTAGGCAACACAGTGAAA	24795	CATAA	_ A
			TTTCATTGTG	GC AG CTG		
			AAAGTGACAC	CG TC GAC		
			AA_	GA C		
GAM600	KIAA0391	3'	TCAGTCTGCTTATTTTCCAA	16141	TGC_	
			TTG	ATAAGCAGACTGA		
			AAC	TATTCGTCTGACT		
			CTTT			
GAM600	KIAA1364	3'	CAGCCTGGCCAACATAATGAAA	31812	CATAAG	A
			TTTCATTGTG	CAG CTG		
			AAAGTAATAC	GTC GAC		
			AACCG_	C		
GAM600	KIAA1586	5'	CAGCCTGCCCAGTATAGTGAAA	44348	ATAA	A
			TTTCATTGTGC	GCAG CTG		
			AAAGTGATATG	CGTC GAC		
			ACC_	C		
GAM600	MGC13017	3'	CAGCCTGGCCAACACGATGAAA	27945	CATAAG	A
			TTTCATTGTG	CAG CTG		
			AAAGTAGCAC	GTC GAC		
			AACCG_	C		
GAM600	PTPNS1	3'	TCAGTCTGCTCATCCGTAA	28057	C	A
			TTGTG	AT AGCAGACTGA		
			AATGC	TA TCGTCTGACT		
			C	C		
GAM600	RoXaN	3'	CAGCCTGGCCAACATAATGAAA	24601	CATAAG	A
			TTTCATTGTG	CAG CTG		

			AAAGTAATAC	GTC GAC		
			AACCG_	C		
GAM600	LOC148809	5'	CAGCCTGGCCAACACAGTGAAA	38593	CATAAG	A
			TTTCATTGTG	CAG CTG		
			AAAGTGACAC	GTC GAC		
			AACCG_	C		
GAM600	LOC149606	5'	TCTGACCTATGCACAAGAAA	38784	A	AG_
			TTTC TTGTGCATA	CAGA		
			AAAG AACACGTAT	GTCT		
			_	CCA		
GAM600	LOC153579	3'	CAGCCTGGCTAACACAGTGAAA	39403	CATA	_ A
			TTTCATTGTG	AGC AG CTG		
			AAAGTGACAC	TCG TC GAC		
			AA_	G C		
GAM600	LOC200251	5'	CAGCCTGACCAACACGATGAAA	42755	CATAAG	A
			TTTCATTGTG	CAG CTG		
			AAAGTAGCAC	GTC GAC		
			AACCA_	C		
GAM600	LOC202052	3'	CAGCCTGGCCAACACAGTGAAA	43406	CATAAG	A
			TTTCATTGTG	CAG CTG		
			AAAGTGACAC	GTC GAC		
			AACCG_	C		
GAM600	LOC90092	3'	CAGCCTGGCCAACATAATGAAA	30784	CATAAG	A
			TTTCATTGTG	CAG CTG		
			AAAGTAATAC	GTC GAC		
			AACCG_	C		
GAM601	DMD	5'	AAAAACAGATGCCAGTATTCT	10190	AA	CTA
			AGAATACT CA	TGTTTTT		
			TCTTATGA GT	ACAAAAA		
			CC AG_			
GAM601	DMD	5'	AAAAACAGATGCCAGTATTCT	10217	AA	CTA
			AGAATACT CA	TGTTTTT		
			TCTTATGA GT	ACAAAAA		
			CC AG_			
GAM601	DMD	5'	AAAAACAGATGCCAGTATTCT	10229	AA	CTA
			AGAATACT CA	TGTTTTT		
			TCTTATGA GT	ACAAAAA		
			CC AG_			
GAM601	EGR1	3'	AAACAGCAGTCCCAGTATTCTC	7690	AAC	A_
	A		TGAGAATACT ACT	TGTTT		

			ACTCTTATGA TGA ACAAA	
			CCC CG	
GAM601	IL18RAP	5'	AAAACATATGTGATTCTCA 9948	ACTAA _
			TGAGAAT CAC TATGTTTT	
			ACTCTTA GTG ATACAAAA	
			_____ T	
GAM601	NARS	3'	GCATGTCATGTATTCTCA 10889	TAAC T
			TGAGAATAC AC ATGT	
			ACTCTTATG TG TACG	
			TAC_ _	
GAM601	TIRAP	3'	AAAAGCCTGTTAGTATTTTCA 27471	CTAT
			TGAGAATACTAACA GTTTTT	
			ACTTTTATGATTGT CGAAAA	
			C_	
GAM601	FLJ23403	3'	AAAAACATAGTATTAGTGATAC 22611	AA_ C
			TC GAG TACTAA ACTATGTTTTT	
			CTC GTGATT TGATACAAAAA	
			ATA A	
GAM601	KIAA1948	3'	AAAAACTACAATCAGTATTCTC 40074	AACACTAT
			GAGAATACT GTTTTT	
			CTCTTATGA CAAAAA	
			CTAACAT_	
GAM601	LOC142893	5'	AAAAACACAGTCCTTTTATTCT 40320	CTAAC A
			CA TGAGAATA ACT TGTTTTT	
			ACTCTTAT TGA ACAAAAAA	
			TTTCC C	
GAM602	ADRA2A	3'	TACAAGGGCATGGCTCACA 6338	AAT TC
			TGT GCCA TGCTTTTGTA	
			ACA CGGT ACGGGAACAT	
			CT_ _	
GAM602	BCRP2	3'	ACAAAAGTAGCCTTACA 31271	T CATC
			TGTAA GC TGCTTTTGT	
			ACATT CG ATGAAAACA	
			C _	
GAM602	DNAH9	5'	TACAAGGGCAAAGACACTACA 11032	A CCATC
			TGTA TG TGCTTTTGTA	
			ACAT AC ACGGGAACAT	
			C AGAA_	
GAM602	GLRA3	3'	TACAAAAGCAAATTTTGCA 30168	TGCCATC
			TGTAA TGCTTTTGTA	

			ACGTT	ACGAAAACAT		
			TTAA__			
GAM602	IGFBP3	3'	ACATTCAGAGGCATCACA	6196	A A	CTTT
			TGT ATGCC TCTG TGT			
			ACA TACGG AGAC ACA			
			C _ TT__			
GAM602	MGAT2	3'	TACAAGTTTTGAGTTAGCATT	8233	CA__	TGCT
	CA		TGTAATGC TC TTTGTA			
			ACATTACG AG GAACAT			
			ATTG TTTT			
GAM602	THBD	3'	ACCTTAGCTGGCATTACA	5917	TCT	TTT
			TGTAATGCCA GCT GT			
			ACATTACGGT CGA CA			
			__ TTC			
GAM602	ZNF278	3'	CAGGGGCAGAAAACACTACA	15624	A CCA	
			TGTA TG TCTGCTTTTG			
			ACAT AC AGACGGGGAC			
			C AAA			
GAM602	ZNF278	3'	CAGGGGCAGAAAACACTACA	25773	A CCA	
			TGTA TG TCTGCTTTTG			
			ACAT AC AGACGGGGAC			
			C AAA			
GAM602	ZNF278	3'	CAGGGGCAGAAAACACTACA	25782	A CCA	
			TGTA TG TCTGCTTTTG			
			ACAT AC AGACGGGGAC			
			C AAA			
GAM602	C21orf108	3'	AGGGCAGATGCCATCACA	42765	A C	
			TGT ATG CATCTGCTTT			
			ACA TAC GTAGACGGGA			
			C C			
GAM602	DKFZp547H025	3'	TACAACCTGATGGCATT	21373		TGCTT
			TAATGCCATC TTGTA			
			ATTACGGTAG AACAT			
			TCC__			
GAM602	FLJ10044	3'	CAGGAGCAAATTGCACCACA	19710	AA C C	
			TGT TGC AT TGCTTTTG			
			ACA ACG TA ACGAGGAC			
			CC T A			
GAM602	FLJ11164	3'	ACAAAAGCAGATGATGTAC	20354	ATGC	
			GTA CATCTGCTTTTGT			

			CAT GTAGACGAAAACA		
			GTA_		
GAM602	GOLPH2	3'	ACAATAACAATGGCATT	18624	C CTT
			TAATGCCAT TG TTGT		
			ATTACGGTA AC AACA		
			_ AAT		
GAM602	KIAA0420	3'	ACAAAAGCATGATCATTCA	31721	T CC _
			TG AATG ATC TGCTTTTGT		
			AC TTAC TAG ACGAAAACA		
			_ _ T		
GAM602	KIAA1024	3'	TAAGAGCAGTGGCATCACA	34236	A T
			TGT ATGCCA CTGCTTTTG		
			ACA TACGGT GACGAGAAT		
			C _		
GAM602	KIAA1239	3'	ACAGGAAGGGCATTACA	35338	ATCTGC
			TGTAATGCC TTTTGT		
			ACATTACGG AGGACA		
			GA_____		
GAM602	MGC4655	3'	ACAAAAGTCGGGAGCGCCACA	27143	AA CA T
			TGT TGC TC GCTTTTGT		
			ACA GCG GG TGAAAACA		
			CC AG C		
GAM602	POLE3	3'	TACAAAAACAGATGGCAT	18899	C
			ATGCCATCTG TTTTGTA		
			TACGGTAGAC AAAACAT		
			A		
GAM602	ZID	3'	TAGAACAGATGGCACTA	13415	A C
			TA TGCCATCTG TTTTG		
			AT ACGGTAGAC AAGAT		
			C _		
GAM602	LOC123283	3'	ACAAAAGCAGCAGCTACTAC	37424	AT_ CAT
			GTA GC CTGCTTTTGT		
			CAT CG GACGAAAACA		
			CAT AC_		
GAM602	LOC144266	5'	ACATTGGATGGCAATACA	37708	A GCTTT
			TGTA TGCCATCT TGT		
			ACAT ACGGTAGG ACA		
			A TT_____		
GAM602	LOC253782	3'	ACTGAGCAGCATTACA	45795	CATC TT
			TGTAATGC TGCTT GT		

ACATTACG ACGAG CA
 _____ T_
 GAM602 LOC257354 3' ACAAAGCATGATCATTCA 45574 T CC _
 TG AATG ATC TGCTTTTGT
 || ||| ||| |||||
 AC TTAC TAG ACGAAAACA
 _ _ T
 GAM602 LOC51320 3' ACAAAGCAGCTGTGACA 18740 AATGC T
 TGT CA CTGCTTTTGT
 ||| || |||||
 ACA GT GACGAAAACA
 GT__ C
 GAM602 LOC89932 3' ACAGGAAAGACGGGCATTACA 30485 A_ GC
 TGTAATGCC TCT TTTTGT
 ||||| ||| |||||
 ACATTACGG AGA AGGACA
 GC A_
 GAM602 LOC90470 3' TACAAAGTAGATAGCATTATA 31537 C T
 TGTAATGC ATCTGCTTT GTA
 ||||| ||||| |||
 ATATTACG TAGATGAAA CAT
 A _
 GAM603 NEDD4L 3' TCACTCAACAGGTATAGTA 17606 A ACT
 TATTATACCT TTGA TGA
 ||||| ||| |||
 ATGATATGGA AACT ACT
 C C_
 GAM603 DKFZp566D133 3' CTTTATGGTTCAATAAATATA 35546 CC _
 TATA TATTGAACT TGAAG
 ||| ||||| |||||
 ATAT ATAACCTTGG ATTTC
 AA T
 GAM603 MAP2K6 3' GCCTCAAGTTCAATATGG 8644 _ A
 CC TATTGAACTTGA GC
 || ||||| |||
 GG ATAACCTTGAAC CG
 T C
 GAM603 MAP2K6 3' GCCTCAAGTTCAATATGG 25703 _ A
 CC TATTGAACTTGA GC
 || ||||| |||
 GG ATAACCTTGAAC CG
 T C
 GAM603 LOC151068 5' CTCCAAGTTTTGAAGGTATAAT 41297 ATT A
 ATTATACCT GAACTTG AG
 ||||| ||||| |||
 TAATATGGA TTTGAAC TC
 AGT C
 GAM603 LOC253959 3' CTTTATGGTTCAATAAATATA 45512 CC _
 TATA TATTGAACT TGAAG
 ||| ||||| |||||

ATAT ATAACCTTGG ATTTC
 AA T
 GAM604 ASPA 5' AAGTCTCATTACATTTC 5489 CTAGT
 GAAATGT GTGAGACTT
 ||||| |||||
 CTTTACA TACTCTGAA
 TT__
 GAM604 EGLN1 5' TGAAGTCTCTCTATAACAT 22588 C GTGT
 ATGT TA GAGACTTCA
 ||| || |||||
 TACA AT CTCTGAAGT
 _ ATCT
 GAM604 EGR3 3' TGAAATTCTTCACCAACATTTC 29960 CTA T C_
 A TGAAATGT GTG GAGA TTCA
 ||||| ||| ||| |||
 ACTTTACA CAC TTCT AAGT
 AC_ _ TA
 GAM604 IFNAR2 5' AAGTTTAATTAGACACTTCA 6551 A GTGA
 TGAA TGTCTAGT GACTT
 ||| ||||| |||
 ACTT ACAGATTA TTGAA
 C AT__
 GAM604 BAIAP1 3' GAAATCTCTACACATTTC 11138 CTA T C
 TGAAATGT GTG GAGA TTC
 ||||| ||| ||| |||
 ACTTTACA CAT CTCT AAG
 _ _ A
 GAM604 DKFZp762K2015 3' TCTCATAATGGATATCTCA 35885 A G
 TGA ATGTCTA TGTGAGA
 ||| ||||| |||||
 ACT TATAGGT ATACTCT
 C A
 GAM604 FLJ11127 3' TGAAACCAAAGCTAGCATTTC 21109 T GTGAGAC
 TGAAATG CTAGT TTCA
 ||||| ||||| |||
 ACTTTAC GATCG AAGT
 _ AAACCA_
 GAM604 KIAA0391 3' CTCACACTAAACATTTTA 16138 C
 TGAAATGT TAGTGTGAG
 ||||| |||||
 ATTTTACA ATCACACTC
 A
 GAM604 PAI-RBP1 3' TCTAAACTAGACATCTTA 17893 A GTG
 TGA ATGTCTAGT AGA
 ||| ||||| |||
 ATT TACAGATCA TCT
 C AA_
 GAM604 SAD1 5' TGAAGTCTCACGCCTACATTCA 32010 A CTA
 TGAA TGT GTGTGAGACTTCA
 ||| ||| |||||

ACTT ACA CGCACTCTGAAGT
 _ TC_
 GAM604 LOC145868 5' TGAAATCTCACATGTCTAGTTC 40620 ATGTCTA C
 A TGAA GTGTGAGA TTCA
 |||| ||||| ||||
 ACTT TACACTCT AAGT
 GATCTG_ A
 GAM604 LOC152316 3' TGAAGTCTTGGGTTGGACATTT 41454 TG
 CA TGAAATGTCTAG TGAGACTTCA
 ||||| |||||
 ACTTTACAGGTT GTTCTGAAGT
 GG
 GAM604 LOC158230 3' TGAAGTCTCTTGTAACATTCCA 39767 A CTAGTGT
 TG AATGT GAGACTTCA
 || |||| |||||
 AC TTACA CTCTGAAGT
 C ATGTT_
 GAM604 LOC91660 5' GAAATCTCACACATTTTC 33209 CTAGT C
 GAAATGT GTGAGA TTC
 |||| ||||| ||||
 CTTTACA CACTCT AAG
 _ A
 GAM605 ENAH 3' AAGATCACCACGCATTGA 20121 TGCTAA
 TTAATGC TGGTGATCTT
 |||| |||||
 AGTTACG ACCACTAGAA
 C_
 GAM605 ERp44 3' TAAGCCTTTCAACAGCAGCAT 39724 AA TGAT
 ATGCTGCT TGG CTTA
 ||||| || ||||
 TACGACGA ACT GAAT
 CA TTCC
 GAM605 MO25 3' AGTATCACAGCATTAA 18415 GCTAATG _
 TTAATGCT GTGAT CT
 ||||| |||| ||
 AATTACGA CACTA GA
 _ T
 GAM605 LOC150372 5' AAGATCTGCCAGCAGC 38935 AAT _
 GCTGCT GGT GATCTT
 |||| || |||||
 CGACGA CCG CTAGAA
 _ T
 GAM605 LOC219940 5' AAGATTAGGTCCTCAGCAGCAT 44829 AAT _
 ATGCTGCT GG TGATCTT
 ||||| || |||||
 TACGACGA CC ATTAGAA
 CT_ TGG
 GAM605 LOC222166 3' ATCCCAAACAGCATTAG 45149 CTAA T
 TTAATGCTG TGG GAT
 ||||| |||||

			GATTACGAC ACC CTA		
			AA__ _		
GAM605	LOC51133	3'	CAAGCATTAGCAATATTAA 18203	C	G_
			TTAATG TGCTAATG TG		
			AATTAT ACGATTAC AC		
			A GA		
GAM605	LOC92181	3'	GAAGACCACAGCATTAA 33943	CTAA	GA
			TTAATGCTG TGGT TC		
			AATTACGAC ACCA AG		
			_____ GA		
GAM606	GAN	3'	TTATATGCCAGAGGCACC 22565	GTACA	
			GGTGCT GGCATATAA		
			CCACGG CCGTATATT		
			AGA__		
GAM606	GLS	3'	TTTACATGCCTGATGGCACC 17113	A	A
			GGTGCTGT CAGGCAT TAAA		
			CCACGGTA GTCCGTA ATTT		
			_____ C		
GAM606	HUS1	3'	TGTGCCCTCACAGCACCG 43791	ACA	
			CGGTGCTGT GGCATA		
			GCCACGACA CCGTGT		
			CTC		
GAM606	IL20RA	3'	ATATGCACATAGCACTGT 15790	ACAG	
			ACGGTGCTGT GCATAT		
			TGTCACGATA CGTATA		
			CA__		
GAM606	PLS1	3'	ATATGTTTTTCACAGCCCGT 8539	T	AC_
			ACGG GCTGT AGGCATAT		
			TGCC CGACA TTTGTATA		
			_____ CTT		
GAM606	C1orf17	3'	ATCCCATACCAGCACCGT 33851	_	CA C
			ACGGTGCT GTA GG AT		
			TGCCACGA CAT CC TA		
			C AC _		
GAM606	KIAA0894	3'	TTTATATGCCTAATGTTAC 17061	CT	AC
			GTG GT AGGCATATAAA		
			CAT TA TCCGTATATTT		
			TG A_		
GAM606	KIAA1181	3'	TTTATACACCCGGCACC 33925	TACA	CA
			GGTGCTG GG TATAAA		

			CCACGGC CC ATATTT		
			____ AC		
GAM606	NEDD5	3'	TATGTTTGTACACAACACC 10659	C__	
			GGTG TGTACAGGCATA		
			CCAC ACATGTTTGTAT		
			AAC		
GAM606	LOC154525	5'	TTTATATGCCTGTGTCAGC 41709	_	
			GCTG TACAGGCATATAAA		
			CGAC GTGTCCGTATATTT		
			T		
GAM606	LOC221271	3'	TTATATGCCTGCCACAGT 44127	A_	
			GCTGT CAGGCATATAA		
			TGACA GTCCGTATATT		
			CC		
GAM606	LOC253260	3'	TTTATAGATGCAGCACC 45910	CAGGCA	
			GGTGCTGTA TATAAA		
			CCACGACGT ATATTT		
			AG____		
GAM606	LOC90841	5'	TTATATGCCAGTCACACC 32115	C T A	
			GGTG TG AC GGCATATAA		
			CCAC AC TG CCGTATATT		
			_ _ A		
GAM606	LOC91149	3'	TTTTATATGCCTATTATTCAC 32461	CT C_	
			GTG GTA AGGCATATAAAA		
			CAC TAT TCCGTATATTTT		
			T_ TA		
GAM607	PTHR2	3'	TCATGCTGCATCTATATC 11481	C CTACC	
			GA ATAGAT TAGCATGA		
			CT TATCTA GTCGTA		
			A C__		
GAM607	FLJ23017	3'	CATGCTGCTCACTTATGTCA 23129	ATCTACC	
			TGACATAG TAGCATG		
			ACTGTATT GTCGTAC		
			CACTC__		
GAM607	KIAA1622	3'	TCATGCTTAAGCTATGTCA 27767	ATCTACCT	
			TGACATAG AGCATGA		
			ACTGTATC TCGTA		
			GAAT__		
GAM607	LOC145820	3'	ATCAGGATAGTAGATCTAT 37987	C GCA	
			ATAGATCTAC TA TGAT		

TATCTAGATG AT ACTA
 _ AGG
 GAM607 LOC149420 3' ATCACTGATACAGTCTATGTCA 38748 CTACC CA
 TGACATAGAT TAG TGAT
 ||||| ||| |||
 ACTGTATCTG GTC ACTA
 ACATA _
 GAM608 ADAM28 3' TCTCACCAGTATTTGCT 15541 T TAG
 AGC AAATACTG GAGA
 ||| ||||| |||
 TCG TTTATGAC CTCT
 _ CA_
 GAM608 COL4A3 3' CTCTTACCAGTATTTAACTT 25354 C _
 AAG TAAATACTG TAGGAG
 ||| ||||| |||||
 TTC ATTTATGAC ATTCTC
 A C
 GAM608 COL4A3 3' CTCTTACCAGTATTTAACTT 25360 C _
 AAG TAAATACTG TAGGAG
 ||| ||||| |||||
 TTC ATTTATGAC ATTCTC
 A C
 GAM608 COL4A3 3' CTCTTACCAGTATTTAACTT 5547 C _
 AAG TAAATACTG TAGGAG
 ||| ||||| |||||
 TTC ATTTATGAC ATTCTC
 A C
 GAM608 DPH2L1 3' TGTCTCTGCTCCTACATCCAGC 7056 AAATAC _
 T AGCT TGTAGGA GAGACA
 ||| ||||| |||||
 TCGA ACATCCT CTCTGT
 CCT_ CGT
 GAM608 DPYSL2 3' TGTCTCTCTACACATTTTGC 7066 T AC G
 GC AAAT TGTAG AGAGACA
 || ||| ||||| |||||
 CG TTTA ACATC TCTCTGT
 T C_ _
 GAM608 DXS1283E 3' CTCTCTGAGTATTTAGCT 35064 GTA
 AGCTAAATACT GGAGAG
 ||||| |||||
 TCGATTTATGA TCTCTC
 G_
 GAM608 EMP1 3' ATGTCCCTCTTTGGAACAGATA 7131 _ _ A |||
 TTTAGCT AATA CTGT AGGAG GACA T
 ||| ||| ||||| ||| |
 TTAT GACA TTCTC CTGT A
 A AGGT C |||
 GAM608 FCN3 5' TCTCAAAACAGTATTAGCTT 9744 A AG_
 AAGCTAA TACTGT GAGA
 ||||| ||||| |||

TTCGATT ATGACA CTCT
 _ AAA
 GAM608 GLS 3' TGTCTCTCTCTACCCTAGCTT 17111 AATAC TA
 AAGCTA TG GGAGAGACA
 ||||| || |||||
 TTCGAT AC TCTCTCTGT
 CCC_ TC
 GAM608 LZTFL1 3' GTCTCTCCATATTTAG 21601 CTGTA
 CTAAATA GGAGAGAC
 ||||| |||||
 GATTTAT CCTCTCTG
 A____
 GAM608 PRSS16 3' TCTCTCTTATTTAGTCTT 12482 _ CTGTA
 AAG CTAAATA GGAGAGA
 || ||||| |||||
 TTC GATTTAT TCTCTCT
 T _____
 GAM608 SLC20A1 5' GTAGTTTACAGTATTTA 29874 AGAG
 TAAATACTGTAGG AC
 ||||| ||
 ATTTATGACATTT TG
 GA____
 GAM608 TRIM9 3' CTCTCCTGTAGCGTTAGCT 17514 ATA
 AGCTAA CTGTAGGAGAG
 ||||| |||||
 TCGATT GATGTCCTCTC
 GC_
 GAM608 ZNF215 5' GTCTCTCCCTGTCCTAGCT 14912 AAT TGTA
 AGCTA AC GGAGAGAC
 ||||| || |||||
 TCGAT TG CCTCTCTG
 CC_ TC_
 GAM608 APOA5 3' TCTCCTGCATATCCAGC 27540 AA C
 GCT ATA TGTAGGAGA
 || || |||||
 CGA TAT ACGTCCTCT
 CC _
 GAM608 ARHGAP5 3' TGTCTCTCCCAACTGTAAAGTT 37821 A CTGTA
 AGCT AATA GGAGAGACA
 ||||| || |||||
 TTGA TTGT CCTCTCTGT
 A CAAC_
 GAM608 ARHGEF4 3' TGTCTCTCCCTGTTTCAGCT 26875 A CTGTA
 AGCT AATA GGAGAGACA
 ||||| || |||||
 TCGA TTGT CCTCTCTGT
 C C____
 GAM608 ARNTL2 3' TGTCTTTTATACAATTTTTCAGC 21421 TAC G
 T AGCTAAA TGTA GAGAGACA
 ||||| || |||||

TCGATTT ACAT TTTTCTGT
TTA A

GAM608 DKFZP727G051 3' GTCTCTCTGCTGTACCAGCT 34431 AAA T G
AGCT TAC GTAG AGAGAC
|||| ||| ||| |||||
TCGA ATG CGTC TCTCTG
CC_ T _

GAM608 DKFZp761D221 3' TCCTACAGTATTTACTT 26058 C
AAG TAAATACTGTAGGA
||| ||||| |||||
TTC ATTTATGACATCCT

GAM608 FLJ10687 3' TGTCTCTCACTGATTTAGCTT 20012 ACTG _
AAGCTAAAT TAG GAGAGACA
||||||| ||| |||||
TTCGATTTA GTC CTCTCTGT
_ A

GAM608 FLJ13855 3' TGTCTCTGATGGGTATTTGC 23345 T G GG
GC AAATACT TA AGAGACA
|| ||||| || |||||
CG TTTATGG GT TCTCTGT
_ _ AG

GAM608 FLJ20006 3' TGTCTCTCCATTCTCCGAGCT 19119 AAATACT A
T AAGCT GT GGAGAGACA
|||| || |||||
TTCGA TA CCTCTCTGT
GCCTCT_ C

GAM608 FLJ20986 5' TGTCTTCTGAGCACAGTATT 23728 A_ G
AATACTGT GGA AGACA
|||||| ||| |||||
TTATGACA TCT TCTGT
CGAG _

GAM608 KIAA0907 3' GTCCTTTTTCAGTATTTA 17277 T A
TAAATACTG AGGAG GAC
||||||| ||||| |||
ATTTATGAC TTTTC CTG

GAM608 moblak 3' TGTCTCTCAAGGGCACCCAGCT 28312 AAATA_ GTAG
T AAGCT CT GAGAGACA
|||| || |||||
TTCGA GG CTCTCTGT
CCCACG AA_

GAM608 PA26 3' TTCACAGTATTTTGCTT 15809 T A
AAGC AAATACTGT GGA
||| ||||| |||
TTCG TTTATGACA CTT
T _

GAM608 PRO2730 3' TCTCTGCAGTATTAGC 24900 A G
GCTAA TACTGTAG AGA
|||| ||||| |||

CGATT ATGACGTC TCT

GAM608 SSH2 3' TCTCTCCTCATTTTAGTT 31187 TAC T
AGCTAAA TG AGGAGAGA
||||| || |||||
TTGATTT AC TCCTCTCT
T__ _
GAM608 STAF65(gamma) 3' TCTCTCCTCATCCTTTTGC 16927 T TAC T
GC AAA TG AGGAGAGA
|| ||| || |||||
CG TTT AC TCCTCTCT
T CCT _
GAM608 SZF1 3' TGTCTCTCCTCACACTCCAGC 18176 AAATAC _
GCT TGT AGGAGAGACA
||| ||| |||||
CGA ACA TCCTCTCTGT
CCTC__ C
GAM608 LOC134637 3' GTCTCTCATCATTTGCT 37078 T TAC TAG
AGC AAA TG GAGAGAC
||| ||| || |||||
TCG TTT AC CTCTCTG
_ __ TA_
GAM608 LOC136345 3' TGTCTCTCCTGCACACATAGC 37502 AATAC
GCTA TGTAGGAGAGACA
||| |||||
CGAT ACGTCCTCTCTGT
ACAC_
GAM608 LOC147694 3' TTCTACAGTATTTATCTT 38373 C
AAG TAAATACTGTAGGA
||| |||||
TTC ATTTATGACATCTT
T
GAM608 LOC155032 5' TGTCTCTCCTGCACACATAGC 41750 AATAC
GCTA TGTAGGAGAGACA
||| |||||
CGAT ACGTCCTCTCTGT
ACAC_
GAM608 LOC158835 3' TGTCTCTCCTTCTCTAGCT 39897 AATACTGT
AGCTA AGGAGAGACA
||| |||||
TCGAT TCCTCTCTGT
CTCT____
GAM608 LOC199991 5' GTCTCTCCCGAGGATCTGGC 43276 A A GTA
GCTA AT CT GGAGAGAC
||| ||| || |||||
CGGT TA GG CCTCTCTG
C _ AGC
GAM608 LOC255520 3' TCTTCAGTATTTGCTT 45880 T T
AAGC AAATACTG AGGA
||| ||||| |||

TTCG TTTATGAC TTCT

```

GAM608 LOC257358 3' TGTCTCTCCTGCCTTCTGCTT 46391 TAAATACT
                      AAGC   GTAGGAGAGACA
                      |||   |||||
                      TTCG   CGTCCTCTCTGT
                      TCTTC__
GAM608 LOC90485 3' TGTCTCTCTCTGTCACCCAGGC 31556 AAATAC _ _
                      T      AGCT   TG TAG GAGAGACA
                      |||   || ||| |||||
                      TCGG   AC GTC CTCTCTGT
                      ACCC__ T T
GAM609 ADRA2B 3' TCACTGGCATTACCCCCCTGCA 6340 AAAA TT
                      TGTA   GTGG TGCCAGTGA
                      |||   ||| |||||
                      ACGT   CACT ACGGTCACT
                      CCCC   T_
GAM609 CD8A 3' TCACTGATGACTTTTTATA 7530 G TTGC
                      TGTA AAAAAGT GT CAGTGA
                      ||||| || ||||
                      ATATTTTCA TA GTCACT
                      G ____
GAM609 FLJ20509 3' CACTACCACAGTTTTTACA 19522 _ TTGCC
                      TGTA AAAA GTGGT AGTG
                      ||||| ||| |||
                      ACATTTT CACCA TCAC
                      GA ____
GAM609 FLJ21777 3' GTCAGTGCGCCACCTGTCACA 25924 AAAAA TTT _
                      TGT   GTGG GC CAGTGAC
                      ||   ||| || |||||
                      ACA   CACC CG GTCAGTG
                      CTGTC ____ C
GAM609 KIAA1586 5' TCACTAAGAGAACTTTTTACA 44349 GG GCC
                      TGTA AAAAAGT TTT AGTGA
                      ||||| || ||||
                      ACATTTTCA GAG TCACT
                      A_ AA_
GAM609 KIAA1841 3' CACTGAATTAATTTTTACA 39026 G TGC
                      TGTA AAAA TGGTT CAGTG
                      ||||| ||| |||
                      ACATTTT ATTAA GTCAC
                      A ____
GAM609 MGC30052 3' TCACTGAGGCCATATCTTTTCA 29545 _ GC
                      CA      TGTA AAAAAG TGGTTT CAGTGA
                      ||||| ||| ||||
                      ACATTTTTC ACCGGA GTCACT
                      TAT ____
GAM609 NMT1 3' TCACCGAAGCCACTTTCTACA 22049 A GCCA
                      TGTA AAAGTGGTTT GTGA
                      ||| ||||| |||
```


ACAT TTTCACCGAA CACT
 C GC__
 GAM609 NUDT11 3' GCCCTAACCACTTCTTACA 30143 A T__
 TGTA AAGTGGTT GC
 ||||| ||||| ||
 ACATT TTCACCAA CG
 C TCC
 GAM609 P5-1 3' CACTGGCACTTTTCAGCA 13496 AA GGTTT
 TGT AAAGT GCCAGTG
 ||| ||||| |||||
 ACG TTTCA CGGTCAC
 AC ____
 GAM609 SYT13 3' CACCAGCAGATCATCTTT 44887 _ CA
 AAAG TGGTTTGC GTG
 ||||| ||||| |||
 TTTC ACTAGACG CAC
 T AC
 GAM609 LOC130813 3' GTCACTCTTACACACTTTTTTAC 37313 _ TTGCC
 A TGTA AAAAGTG GT AGTGAC
 ||||| ||||| |||||
 ACATTTTTCAC CA TCACTG
 A TTC__
 GAM609 LOC157681 5' CACTAATTATTTTTTACA 39641 TGCC
 TGTA AAAAGTGGTT AGTG
 ||||| ||||| |||||
 ACATTTTTTATTAA TCAC

 GAM610 TNFRSF6B 5' AGACCCTGGTGGGGGAATGACA 18557 A A_ AA_
 TCA TGAT TCATTCTC ACTA TCT
 ||||| ||||| ||||| |||
 ACTA AGTAAGGG TGGT AGA
 C GG CCC
 GAM611 AGMAT 3' CAGACGTGGTGTGGTGACACAC 24106 G _
 GTGTGCAC TATA ACGTCTG
 ||||| ||||| |||||
 CACACGTG GTGT TGCAGAC
 _ GG
 GAM611 KIAA0337 3' CAGACACACACGTACGCACACT 16654 _ ATAAC
 G TAGTGTGC ACGT GTCTG
 ||||| ||||| |||||
 GTCACACG TGCA CAGAC
 CA CACA_
 GAM611 KIAA0544 3' ATGTTACACATGCACACTCA 35110 T C AT_
 A AGTGTGCA GT AACGT
 | ||||| || |||||
 A TCACACGT CA TTGTA
 C A CAC
 GAM611 KIAA0825 3' CAGACGTTATACATATTCAC 30590 TGCAC
 GTG GTATAACGTCTG
 ||| ||||| |||||

			CAC CATATTGCAGAC		
			TTATA		
GAM611	SDC3	3'	CAGACACCATTTGCCACACTAT 16078	CAC TAAC_	
			ATAGTGTG GTA GTCTG		
			TATCACAC CGT CAGAC		
			C_ TACCA		
GAM611	LOC51301	5'	CAGACAATATAAGACACACTAT 18671	CACG AC	
	A		TATAGTGTG TATA GTCTG		
			ATATCACAC ATAT CAGAC		
			AGA_ AA		
GAM612	EVA1	3'	AGCACAGTGCTCCTCCATATCA 12379	CGCCT CAC	
			TGATATGG GGTAC GCT		
			ACTATACC TCGTG CGA		
			TCC_ ACA		
GAM612	DKFZp434E0519	3'	ACACAGAGCCAAACCATATCA 25983	C_ _ _	
			TGATATGG GC CTG GT		
			ACTATACC CG GAC CA		
			AAAC A A		
GAM612	LOC148166	5'	AGCCACCCAGGCGCCCATCA 38480	AT TACCAC	
			TGAT GCGCCTGG GCT		
			ACTA CCGCGGACC CGA		
			C_ CCAC_		
GAM613	C20orf7	3'	AAGTAGAATCACATGTAAC 23571	_ C	
			GTT CGTG GATTCTACTT		
			CAA GTAC CTAAGATGAA		
			T A		
GAM613	EIF3S1	3'	GGTTGCAACGTGACA 31641	TCG	
			TGTCACGT TGCGATT		
			ACAGTGCA ACGTTGG		

GAM614	CYBB	3'	ACCCAGAAACAAAAATCTC 37536	A ACACG	
			GA GATTTTT TTGGGT		
			CTCTAAAAA GACCCA		
			_ CAAA_		
GAM614	HSPC155	5'	ACCCAACGTCTCATCTTC 18539	TTTTAC	
			GAAGAT ACGTTGGGT		
			CTTCTA TGCAACCCA		
			CTC_		
GAM614	LOC158431	3'	ACCCAAAAGGAAAATCTT 41991	ACACG	
			AAGATTTTT TTGGGT		

			TTCTAAAAG AACCCA		
			GAA__		
GAM615	AXIN1	3'	CCCGCCCCGCTTGGCACCA 30514	G	TAAAA
			TGGTG CGGGTG GCGGG		
			ACCAC GTTCGC CGCCC		
			G CCC__		
GAM615	EGFL4	3'	CCAGCCATCCCCGCCACCA 30965	TG	AAAA _
			TGGTGGCGGG T GC GG		
			ACCACCGCCC A CG CC		
			CT C__ A		
GAM615	FMNL	5'	CCCGCCACCGCCACCA 12512	G	TAAAA
			TGGTGGCGG TG GCGGG		
			ACCACCGCC AC CGCCC		
			— ———		
GAM615	FNTB	3'	CCACTTGACACGCCACCATT 7780	GG	AA C
			AATGGTGGC GTGTA AG GG		
			TTACCACG CACGT TC CC		
			— — A		
GAM615	FOXD1	5'	CCCGCCCGGGCCCGCCACC 10778	T	AAAA
			GGTGGCGGG GT GCGGG		
			CCACCGCCC CG CGCCC		
			_ GGCC		
GAM615	KCNN4	5'	CCCGCCCTGCCTGGCCGTCACC 8035	G__	AAA
	A		TGGTGGCGG T GTA GCGGG		
			ACCACTGCC G CGT CGCCC		
			G TC CC_		
GAM615	LY6E	3'	CCCCCTGCACCTCCACC 8146	C	AAA C
			GGTGG GGGTGT AG GGG		
			CCACC TCCACG TC CCC		
			— — C		
GAM615	MADH4	5'	CCCACTCCCCTCGCCACCG 11831	TG	TAAA C
			TGGTGGCGGG AG GGG		
			GCCACCGCTC TC CCC		
			CCC__ A		
GAM615	MAPT	5'	CCCACCTTCTGCCGCCGCCACC 18828	GT	A C_
	A		TGGTGGCGG GTA AAG GGG		
			ACCACCGCC CGT TTC CCC		
			GC C CA		
GAM615	MAPT	5'	CCCACCTTCTGCCGCCGCCACC 12540	GT	A C_
	A		TGGTGGCGG GTA AAG GGG		

			ACCACCGCC CGT TTC CCC		
			GC C CA		
GAM615	MAPT	5'	CCCACCTTCTGCCGCCGCCACC 18834	GT A C_	
	A		TGGTGGCGG GTA AAG GGG		
			ACCACCGCC CGT TTC CCC		
			GC C CA		
GAM615	MAPT	5'	CCCACCTTCTGCCGCCGCCACC 18840	GT A C_	
	A		TGGTGGCGG GTA AAG GGG		
			ACCACCGCC CGT TTC CCC		
			GC C CA		
GAM615	MAZ	5'	CCCGCCTCCGCCGCCACTAT 36325	G TAAAA	
			ATGGTGGCGG TG GCGGG		
			TATCACCGCC GC CGCCC		
			_ CTC_		
GAM615	MSF	5'	CCGCTGCCACCAGCCATC 42523	G TAAA	
			GGTGGC GGTG AGCGG		
			CTACCG CCAC TCGCC		
			A CCG_		
GAM615	NGB	3'	CCCGCCCTCACCCAGCCATC 22233	_ TAAAA	
			GGTGGC GGGTG GCGGG		
			CTACCG CCCAC CGCCC		
			AC TCC_		
GAM615	NPY2R	5'	CCCACCTTCACCCGCCACC 6609	_ TAA C_	
			GGTGG CGGGTG AAG GGG		
			CCACC GCCAC TTC CCC		
			C _ CA		
GAM615	PSCD4	3'	CCCACCCCCACATTTGCACACC 15037	_ AAAAGC	
			GGTG GCGGGTGT GGG		
			CCAC CGTTTACA CCC		
			A CCCCCA		
GAM615	RANBP3	3'	CCGCCCACCCGCCCCCA 9688	T TAAAA	
			TGG GGCGGGTG GCGG		
			ACC CCGCCCAC CGCC		
			C C_		
GAM615	RANBP3	3'	CCGCCCACCCGCCCCCA 14240	T TAAAA	
			TGG GGCGGGTG GCGG		
			ACC CCGCCCAC CGCC		
			C C_		
GAM615	BRUNOL6	5'	CCCGCCCCTTTCCTGCCCGCCC 27420	T TA _	
	CA		TGG GGCGGGTG AAA GCGGG		

ACC CCGCCCGT TTT CGCCC
 _ CC CCC
 GAM615 C1orf2 5' CCCGCTTTTACCCTCCCCACC 13356 C T
 GGTGG GGG GTAAAAGCGGG
 ||||| ||| |||||
 CCACC CTC CATTTTCGCCC
 C C
 GAM615 C1orf2 5' CCCGCTTTTACCCTCCCCACC 45396 C T
 GGTGG GGG GTAAAAGCGGG
 ||||| ||| |||||
 CCACC CTC CATTTTCGCCC
 C C
 GAM615 CLSTN1 5' CCCGCCCTCCCGCCGCCA 17256 TGTAATA
 TGGTGGCGGG GCGGG
 ||||| ||| |||||
 ACCGCCGCC CGCCC
 TCCC__
 GAM615 DKFZP434J193 3' CCAGGCCACCCCCACCA 35164 C TAAAA _
 TGGTGG GGGTG GC GG
 ||||| |||| || ||
 ACCACC CCCAC CG CC
 _ _ GA
 GAM615 DKFZp586I021 5' CCCGCCTTTTCAGCCGTCACCA 26021 G T _
 TGGTGGCGG TG AAAAG CGGG
 ||||| || ||||| |||||
 ACCACTGCC AC TTTTC GCCC
 G _ C
 GAM615 FLJ22215 3' CCGCCCACCGCCACTAT 23118 G TAAAA
 ATGGTGGCGG TG GCGG
 ||||| || |||||
 TATCACCGCC AC CGCC
 _ C__
 GAM615 FLJ22215 5' CCGCCCACCGCCACTAT 46280 G TAAAA
 ATGGTGGCGG TG GCGG
 ||||| || |||||
 TATCACCGCC AC CGCC
 _ C__
 GAM615 FLJ23590 5' CCCGCTTCCTCACCACCCCCAC 23940 C TAA__
 T GGTGG GGGTG AAGCGGG
 ||||| ||||| |||||
 TCACC CCCAC TTCGCC
 _ CACTCC
 GAM615 KIAA0455 3' CCCACTTCTCACCACCGCC 35881 CG__ TAA C
 AT ATGGTGG GGTG AAG GGG
 ||||| ||| ||| |||
 TACCGCC CCAC TTC CCC
 ACCA TC_ A
 GAM615 MCFP 5' CCCGCCTCTACCCCGCCTCCAT 20828 T T AAA
 T AATGG GGC GGG GTA GCGGG
 ||||| ||||| ||| |||||

			TTACC CCGCCC CAT CGCCC		
			T _ CTC		
GAM615	MGC15730	5'	CCGCCGCCCGCCACCG 26701	T AAAA	
			TGGTGGCGGG GT GCGG		
			GCCACCGCCC CG CGCC		
			_ C _		
GAM615	NEDD5	5'	CCGCACTCCCGCCACCA 10657	T AAAA	
			TGGTGGCGGG GT GCGG		
			ACCACCGCCC CA CGCC		
			T _		
GAM615	LOC128710	5'	CCAAACCCCGCCACCAT 36934	T AAAAGC	
			ATGGTGGCGGG GT GG		
			TACCACCGCCC CA CC		
			_ AA _		
GAM615	LOC146381	5'	CCCGCCTTTTTTGCGGCCACCA 38145	GGG _	
		TT	AATGGTGGC TGTA AAA GCGGG		
			TTACCACCG GCGTTTT CGCCC		
			_ TTC		
GAM615	LOC197439	5'	CCCGCCTTTTTTGCGGCCACCA 42517	GGG _	
		TT	AATGGTGGC TGTA AAA GCGGG		
			TTACCACCG GCGTTTT CGCCC		
			_ TTC		
GAM615	LOC245811	5'	CCCACTCTCCACCCCGCCGCA 45070	T AAA_ C	
			TGGTGGCGGG GT AG GGG		
			ACCGCCGCCC CA TC CCC		
			_ CCTC A		
GAM615	LOC92573	5'	CCACTCTGTACCCACCATT 34595	C AA C	
			GGTGG GGGTGTA AG GG		
			TTACC CCCATGT TC CC		
			A C_ A		
GAM616	CPNE3	3'	TGACTTTTACCTTTTACAGCGT 9998	A CAATGT_	
		A	TAC CTGTAAAA GTCA		
			ATG GACATTTT CAGT		
			C CCATTTT		
GAM616	PCDHA9	3'	TTTGATACTTGACAGTG 15216	AAAA T	
			CACTGT CAA GTGTCAAG		
			GTGACA GTT CATAGTTT		
			_ _		
GAM616	SLA	3'	ACAGAAGTGTTACAGTGTA 13595	AA ATG_	
			TAACTGT AACA TGT		

			ATGTGACA TTGT ACA		
			C_ GAAG		
GAM616	ARHGAP10	3'	TGAAATAGCTTTACAGTG	21889	ACAA G
			CACTGTAAA TGT TCA		
			GTGACATTT ATA AGT		
			CG_ A		
GAM616	BAG5	3'	GGTGCTGTTTTACAACGTG	11308	_ AT TG
			CAC TGTA AAAACA G TC		
			GTG ACATTTTGT C GG		
			CA _ GT		
GAM616	C20orf45	3'	CTTGCCTTTATTTTACAGTG	18123	C TGT T
			CACTGTAAAA AA G CAAG		
			GTGACATTTT TT C GTTC		
			A TC_ _		
GAM616	FLJ14437	3'	TTGATATTGCACAGTG	26311	AAAA AT
			CACTGT CA GTGTCAA		
			GTGACA GT TATAGTT		
			C_ _ _		
GAM616	FLJ20725	3'	TATGGTGTTTACAGTGTA	19637	A AT
			TACACTGTAAA CA GTG		
			ATGTGACATTT GT TAT		
			_ GG		
GAM616	KIAA0350	3'	CTTGACATTGGGCCTACACTGT	30667	C AAA_ AT
	A		TACA TGTA CA GTGTCAAG		
			ATGT ACAT GT TACAGTTC		
			C CCGG _		
GAM616	KIAA0947	3'	CTTGACACATTTTGAACA	30849	AA C
			TGT AA AATGTGTCAAG		
			ACA TT TTACACAGTTC		
			AG _		
GAM616	KIAA1322	3'	CTTGACACAGTCACAGTGTA	36026	AAAACAA
			TACACTGT TGTGTCAAG		
			ATGTGACA ACACAGTTC		
			CTG_ _		
GAM616	KIAA1376	5'	CTTGACTTTTTTGTCTTACA	31824	A TGT_
			TGTAA ACAA GTCAAG		
			ACATT TGTT CAGTTC		
			C TTTT		
GAM616	KIAA1870	3'	CACAATTGTCTCTCACAGTGTA	25862	AAA_ _
			TACACTGT ACAAT GTG		

			ATGTGACA	TGTTA CAC	
			CTCTC	A	
GAM616	MBLL39	3'	ATTCATTACCTTACAGTGTA	29569	AAC T
			TACACTGTAA	AATG GT	
			ATGTGACATT	TTAC TA	
			CCA	T	
GAM616	SCYB10	3'	TATATTGTTTTCAGTGTA	7294	T
			TACACTG	AAAACAATGTG	
			ATGTGAC	TTTTGTTATAT	
GAM616	LOC151877	3'	CTTGACACACTGTTACTGT	41396	T AA A
			AC GTA	ACA TGTGTCAAG	
			TG CAT	TGT ACACAGTTC	
			T	__ C	
GAM617	LOC154442	3'	CTCAAAAGAATTA	ACTCT 41706	A_
			AGAGTTAATTTTT	GAG	
			TCTCAATTAAGAA	CTC	
			AA		
GAM617	LOC51279	3'	AATTTATCTCTAAAAAATGGC	18613	A
			GTTA TTTTTAGAGATAAATT		
			CGGT	AAAAATCTCTATTAA	
			A		
GAM617	LOC51336	3'	TTATTTTAAAAATCAGCTCT	18760	A A
			AGAGTT	ATTTTT GAGATAA	
			TCTCGA	TAAAAA TTTTATT	
			C		
GAM618	B4GALT4	3'	ATATGTCTATCAAATACCTCT	9857	CC_ ACCC
			GGAGGTA	GAT AGACATAT	
			TCTCCAT	CTA TCTGTATA	
			AAA	___	
GAM618	MSR1	3'	ATGTCCATTATGTACCTCC	8284	CG CCCA
			GGAGGTAC	ATA GACAT	
			CCTCCATG	TAT CTGTA	
			__	TAC_	
GAM618	SLC12A5	3'	CTGGGTACAGTACCTCC	21854	CGA
			GGAGGTAC	TACCCAG	
			CCTCCATG	ATGGGTC	
			AC_		
GAM619	SLC21A11	5'	GCGACCTCATCTGCCGCAACCG	32207	ACC_ A_ _ C
			GACGGCTA	TCC GC AGA AGG CG C	

		AGG CG TCT TCC GC G		
		CCAA CCG AC A III		
GAM619	LOC151429 3'	CGGCCCTCCCACGGTGGAC 41341	CAA A	
		GTCCACCG GA GGCCG		
		CAGGTGGC CT CCGGC		
		ACC C		
GAM619	LOC153572 5'	CGGCCTTCACGGCGCAGGCGGC 41639	CAC AA_	
		GCCGTC CGC GAAGGCCG		
		CGGCGG GCG CTTCCGGC		
		AC_ GCA		
GAM619	LOC155340 5'	GGTGC GCGGTGACGGCTA 36318	C AAGAAG	
		TAGCCGTC ACCGC GCC		
		ATCGGCAG TGGCG TGG		
		_ CG_		
GAM619	LOC93052 5'	GCCTTCTTGCGGACGGT 35302	ACC	
		GCCGTCC GCAAGAAGGC		
		TGGCAGG CGTTCTTCGG		

GAM620	FLJ10781 3'	CTGTATCGTAGCCGTCCACAA 20136	G CTCGC	
		TTG GGACGGCTAC GCAG		
		AAC CCTGCCGATG TGTC		
		A CTA_		
GAM620	KIAA0182 3'	TGCAGTAGCCTGTCCCCAA 35647	_ CTC	
		TTGGGGAC GGCTAC GCG		
		AACCCCTG CCGATG CGT		
		T A_		
GAM620	LOC151610 3'	CTGCACAAGGGGCCAGTCCCCAA 39135	_ TA CGC	
		TTGGGGAC GGC CCT GCAG		
		AACCCCTG CCG GGA CGTC		
		A _ ACA		
GAM620	LOC157958 3'	GCTGCACCTCTGCAGTCCCCAA 39685	G TACCTCGC	
		TTGGGGAC GC GCAGC		
		AACCCCTG CG CGTCG		
		A TCTCCA_		
GAM621	PABPC1 5'	AGCCGAGACCGACCCGCCCCG 8418	CCTT	
		CGGGC GTCGGTCTCGGT		
		GCCCG CAGCCAGAGCCGA		
		CC_		
GAM621	POLS 3'	CCGAGACCAGCACCCCG 13864	CCCT C	
		CGGG TGT GGTCTCGG		

			GCCC ACG CCAGAGCC		
			C__ A		
GAM621	CD36L2	5'	CCGAAACCGAGTCCGGGCCCGT 12021	TTG_	C
			ACGGGCCC TCGGT TCGG		
			TGCCCCGGG AGCCA AGCC		
			CCTG A		
GAM621	POMT1	3'	AGCCGAGAACCCAGGGCC 14015	TGTC	_
			GGCCCT GGT CTCGGCT		
			CCGGGA CCA GAGCCGA		
			C__ A		
GAM621	Rab11-FIP3	3'	AGCCAAGACCAGCAGGTCCC 16225	C T C	C
			GGG CCT GT GGTCT GGCT		
			CCC GGA CG CCAGA CCGA		
			T _ A A		
GAM622	KCNQ1	3'	CAGAGCAACCCCTGGACCCCA 5722	A	T GGTACG
			TG GGTCCAGG GG TCTG		
			AC CCAGGTCC CC AGAC		
			C _ AACG__		
GAM622	RFX2	3'	CAGCGAGTCCACCTGGACCTC 6270	TA	T
			GAGGTCCAGGTGGGG CG CTG		
			CTCCAGGTCCACCCT GC GAC		
			GA _		
GAM622	FKBP5	3'	CAGACGTGAAAGCCAGAACCTC 10323	CCA	GGGG
	A		TGAGGT GGT TACGTCTG		
			ACTCCA CCG GTGCAGAC		
			AGA AAA_		
GAM622	MGC20576	5'	ACGGTCCCTACCTAGACCCCA 29510	A C	TA
			TG GGTC AGGTGGGG CGT		
			AC CCAG TCCATCCC GCA		
			C A TG		
GAM622	OSBPL5	3'	CAGCTGTTCCACCTGGACCCCA 35987	A	GG C T
			TG GGTCCAGGTGG TA G CTG		
			AC CCAGGTCCACC GT C GAC		
			C TT __		
GAM622	P2RXL1	3'	CAGACGTGGGGAGCCTGACCCC 11927	A C	GGGG
	A		TG GGTC AGGT TACGTCTG		
			AC CCAG TCCG GTGCAGAC		
			C _ AGGG		
GAM622	RA-GEF-2	3'	CAGACATACCCATTTGGAT 18462	G C	
			GTCCAGGTGGG TA GTCTG		

TAGGTTTACCC AT CAGAC

_ A

GAM622 LOC197358 3' CAGCTAGCCCACACAGACCCCA 42507 A CAG G C T
TG GGTG GTGGG TA G CTG
|| ||| |||| || |||
AC CCAG CACCC AT C GAC
C ACA G _ _

GAM623 CLCN7 3' CAGCTTCACACTGGCGCCA 6963 A T GA
TGGC CC GTGTGAGG CTG
|||| || ||||| |||
ACCG GG CACACTTC GAC
C T _

GAM623 NAGA 3' CAGCAGTCCCCTGGCCAGCACC 5798 CAC T G _
GG CTG GT AGGG ACTGCTG
|| ||| || |||| |||||
CC GAC CG TCCC TGACGAC
AC_ _ G C

GAM623 PDAP1 3' CAGCCCCTCATGGCCA 44420 ACCTG A
TGGC TGTGAGGG CTG
|||| ||||| |||
ACCG GTACTCCC GAC
_ C

GAM623 STC1 3' CAGTCCCTTATGAGCGTCA 9133 AC G
TGGC CT TGTGAGGGACTG
|||| || ||||| |||||
ACTG GA GTATTCCCTGAC
C_ _

GAM623 SURF5 3' CAGTCCCTCAGCTTCACCCA 13606 CACCT G
TGG GT TGAGGGACTG
||| || ||||| |||||
ACC CG ACTCCCTGAC
CACTT _

GAM623 C11orf14 3' CAGCTGTTTCAAACAGGTGCCA 21808 GTGA GG T
TGGCACCTGT G AC GCTG
||||||| | || |||
ACCGTGGACA C TG CGAC
AA_ TT T

GAM623 ERp44 3' GGTAGCACACAGGACCA 39723 CA AGGGA
TGG CCTGTGTG CTGCT
|| ||||| |||||
ACC GGACACAC GATGG
A_ _

GAM623 KIAA1091 3' AGCAGTCCCCCAGTGTCA 34538 CTGTG A
TGGCAC TG GGGACTGCT
||||| || ||||| |||
ACTGTG AC CCCTGACGA
_ C

GAM623 PSMF1 3' AGCAGTAGTCACAAAGCCA 13687 ACCTG GGG
TGGC TGTGA ACTGCT
|||| ||||| |||||

ACCG AACT TGACGA
 AA__ GA_
 GAM623 RAB6C 3' AGCAGTCCGACCAAGCC 25832 ACC T GAG
 GGC TG GT GGA CTGCT
 ||| ||| |||||
 CCG AC CA CCTGACGA
 A__ _ G__
 GAM623 WDR9 3' CAGCATTACGACAGGTGCCA 27389 GAG C
 TGGCACCTGTGT GGA TGCTG
 ||||| ||| |||||
 ACCGTGGACACG CTT ACGAC
 A__ _
 GAM623 LOC143943 5' AGCACACCCACAAATGCCA 40381 CCTG A GAC
 TGGCA TGTG GG TGCT
 |||| ||| || |||
 ACCGT ACAC CC ACGA
 AA__ _ AC_
 GAM623 LOC147976 3' GTATCCTCACACAGAGCCA 38426 AC _
 TGGC CTGTGTGAGGG AC
 ||| ||||| ||| ||
 ACCG GACACACTCCT TG
 A__ A
 GAM623 LOC150157 5' CAGCAGTGTGGCTCAGGTGCCA 41141 T GAGGG
 TGGCACCTG GT ACTGCTG
 ||||| || |||||
 ACCGTGGAC CG TGACGAC
 T GTG__
 GAM623 LOC157653 5' AGCAGTCCCTGGGCACCCA 39631 CACCT G_
 TGG GTGT AGGGA CTGCT
 || ||| |||||
 ACC CACG TCCCTGACGA
 _ _ GG
 GAM623 LOC256158 5' TGGCCCCACACAGGTACC 46635 C A A
 GG ACCTGTGTG GGG CTG
 || ||||| ||| |||
 CC TGGACACAC CCC GGT
 A C _
 GAM624 CA2 3' GCTAGTTAAGGCAAATCA 5513 ATCAA G
 TGATTTGCC AA TGGC
 ||||| || |||
 ACTAAACGG TT ATCG
 AA__ G
 GAM624 GALC 3' GGCTCTATGTAGCAAATCA 5662 CAT AA T
 TGATTTGC CA AG GGCC
 ||||| || || |||
 ACTAAACG GT TC TCGG
 AT_ A_ _
 GAM624 PIK3R3 3' GCCACTTGTGGCAAACA 30604 A CAA
 TG TTTGCCAT AAGTGGC
 || ||||| |||||

AC AAACGGTG TTCACCG

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      ———
GAM624 PTPRC  3' TACTTTTGACAACAAATTA 8721      CCA
                TGATTTG TCAAAAGTG
                ||||| |||||
                ATTAAC AGTTTTCAT
                AAC
GAM624 PTPRC  3' TACTTTTGACAACAAATTA 28147     CCA
                TGATTTG TCAAAAGTG
                ||||| |||||
                ATTAAC AGTTTTCAT
                AAC
GAM624 XT3    3' GGCACACTCAATGGCAAACA 21446  A   CAAA  _
                TG TTTGCCAT AGTG GCC
                || ||||| ||| |||
                AC AAACGGTA TCAC CGG
                _ AC_ A
GAM624 ABLIM  3' CCACTTTTGACTAGGTAA 13547  A__
                TTGCC TCAAAAGTGG
                |||| |||||
                AATGG AGTTTTCACC
                ATC
GAM624 ABLIM  3' CCACTTTTGACTAGGTAA 8114   A__
                TTGCC TCAAAAGTGG
                |||| |||||
                AATGG AGTTTTCACC
                ATC
GAM624 AUTL1  3' GGCCACCTGTAAGGCAAATC 26649    AT_ AAA
                GATTTGCC CA GTGGCC
                ||||| || |||||
                CTAAACGG GT CACCGG
                AAT C_
GAM624 DKFZP564A1164 5' GGCCAGTGCGACGGCAAATC 35153    A AAAAG
                GATTTGCC TC TGGCC
                ||||| || |||||
                CTAAACGG AG ACCGG
                C CGTG_
GAM624 DKFZP564K0822 3' GTCTTTTGTAGACAAATTA 45141    C   T
                TGATTTGC ATCAAAAG GGC
                ||||| ||||| |||
                ATTAACG TAGTTTTT CTG
                A   _
GAM624 FLJ14735 3' GCTTTTAAAGGCAAATCA 26609    ATC
                TGATTTGCC AAAAGT
                ||||| |||||
                ACTAAACGG TTTTCG
                AAA
GAM624 G4     5' GGCCACTTTGTAGAAATCA 43734    GCCATCA
                TGATTT AAAGTGGCC
                ||||| |||||
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			ACTAAA	TTTCACCGG		
			GATG__			
GAM624	KCNJ14	3'	GCCAACTGAGTAGCAAATCA	14994	CA_	AAAG
			TGATTTGC TCA TGGC			
			ACTAAACG AGT ACCG			
			ATG CA__			
GAM624	KIAA0470	3'	CCACTTGATGCACAAAT	16776	C_	AA
			ATTTG CATCA AGTGG			
			TAAAC GTAGT TCACC			
			AC _			
GAM624	PRSC	3'	GGCCACTTTACGCAACTCA	13349	T	CATCA
			TGA TTGC AAAGTGGCC			
			ACT AACG TTTCACCGG			
			C CA__			
GAM624	SRF	3'	GGCTGGGGCATGGCAAATCA	9100		CAAAAGT
			TGATTTGCCAT GGCC			
			ACTAAACGGTA TCGG			
			CGGGG__			
GAM624	TM4SF11	3'	GTTACTGAAAGCAAATCA	18086	CA	AAA
			TGATTTGC TCA GTGGC			
			ACTAAACG AGT CATTG			
			AA _			
GAM624	TRIP-Br2	3'	CCACCTTTGTGGTAAACA	16485	A	T A
			TG TTTGCCA CAAA GTGG			
			AC AAATGGT GTTT CACC			
			_ _ C			
GAM624	UBE4B	3'	GGCCAAATGTGGCAAACCA	12682	A	CAAAAG
			TG TTTGCCAT TGGCC			
			AC AAACGGTG ACCGG			
			C TAA__			
GAM624	LOC115219	3'	GGTCGCCAATGGCAAACA	36280	A	CAAAA
			TG TTTGCCAT GTGGCC			
			AC AAACGGTA CGCTGG			
			A AC__			
GAM624	LOC126526	5'	GGCCACTTCCGAGTGGATC	36846	TG CA	AA
			GATT C TC AAGTGGCC			
			CTAG G AG TTCACCGG			
			GT__ CC			
GAM624	LOC143286	5'	TACTTTTGATAGCAGACCA	40355	A	C
			TG TTTGC ATCAAAAGTG			

AC AGACG TAGTTTTTCAT
 C A
 GAM624 LOC165693 5' GCCACTTTTGGCAGA 40187 TCA
 TTTGCCA AAAGTGGC
 ||||| |||||
 AGACGGT TTTCACCG

 GAM624 LOC220020 5' GCCATTTCTGAGGGCAAATCA 44865 A A
 TGATTTGCC TCA AAGTGGC
 ||||| || |||||
 ACTAAACGG AGT TTTACCG
 G C
 GAM624 LOC220766 3' CCACTTGATGCACAAAT 43651 C_ AA
 ATTTG CATCA AGTGG
 |||| |||| ||||
 TAAAC GTAGT TCACC
 AC _
 GAM624 LOC254826 3' GCCAAAGTCCCCAGTGGCAAAT 46434 CAAAAG____
 CA TGATTTGCCAT TGGC
 ||||| ||||
 ACTAAACGGTG ACCG
 ACCCCTGAA
 GAM624 LOC257554 5' GGCCACTTTGTAGAAATCA 46641 GCCATCA
 TGATTT AAAGTGGCC
 |||| |||||
 ACTAAA TTTCACCGG
 GATG____
 GAM624 LOC92568 3' ACCCTTGATGGCTAATCA 34573 T AA
 TGATT GCCATCAA GT
 |||| ||||| ||
 ACTAA CGGTAGTT CA
 T CC
 GAM625 ARNT2 3' CTCCCCACTCCCGGCAGCACTT 16934 A ATT _
 T AAAGTGTT CC GA TGGGGAG
 ||||| || |||||
 TTTCACGA GG CT ACCCCTC
 C CC_ C
 GAM625 OTOF 3' CTCCCCATCCCGGGCACAC 11224 TA ATT
 GTGT CC GATGGGGAG
 ||| || |||||
 CACA GG CTACCCCTC
 CG CC_
 GAM625 RGS3 5' CTCCCCCGGAGCAGCACTTTG 28669 A__ ATTGAT
 CAAAGTGTT CC GGGGAG
 ||||| || |||||
 GTTTCACGA GG CCCCTC
 CGA C____
 GAM625 TCF7 3' TCCCCATTGAGACACTTCA 9194 A ACCAT _
 C AAGTGTT TGA TGGGGA
 | ||||| || |||||

			A TTCACAG	ACT ACCCCT		
			C	_____ T		
GAM625	ABLM	3'	CCAGCCAACAGTAACACTT	8115	CA	A_
			AAGTGTTAC	TTG TGG		
			TTCACAATG	AAC ACC		
			AC	CG		
GAM625	ABLM	3'	CCAGCCAACAGTAACACTT	13548	CA	A_
			AAGTGTTAC	TTG TGG		
			TTCACAATG	AAC ACC		
			AC	CG		
GAM625	COLEC10	3'	CCCTATATAGTCACACTTTG	13145	T	CATTG
			CAAAGTGT	AC ATGGGG		
			GTTTCACA	TG TATCCC		
			C	ATA_		
GAM625	DKFZP564L0864	3'	CTGTCACAGTAACACTTT	35920	CAT	
			AAAGTGTTAC	TGATGG		
			TTTCACAATG	ACTGTC		
			AC	_		
GAM625	FLJ12552	3'	CCCACTAATGGTATCACT	23114	T	A
			AGTG TACCATTG	TGGG		
			TCAC ATGGTAAT	ACCC		
			T	C		
GAM625	FLJ22390	3'	CTCAAAAATGACAACACTT	22958	AC	GA
			AAGTGTT	CATT TGGG		
			TTCACAA	GTAA ACTC		
			CA	AA		
GAM625	KIAA0210	3'	CCCTATGACAACACTTTG	16422	AC	TGAT
			CAAAGTGTT	CAT GGGG		
			GTTTCACAA	GTA TCCC		
			CA	_____		
GAM625	NR1I3	5'	CTCCTTATAATAGACACTTCA	11605	A	ACCATTG
			C AAGTGTT	ATGGGGAG		
			A TTCACAG	TATTCCTC		
			C	ATAA_		
GAM625	SEMA6B	3'	CTCCCCATCAATAAACTCT	25800	T	ACC
			AG GTT	ATTGATGGGGAG		
			TC CAA	TAACACCCCTC		
			T	AA_		
GAM625	SV2	3'	CTCCCCATTTTGTAACACT	16884	CATT	
			AGTGTTAC	GATGGGGAG		

			TCACAATG TTACCCCTC		
			TT__		
GAM625	LOC133814	5'	CTTGTCAATGAAAACACTCTG 37381	A AC TG	
			CA AGTGTT CATTGA GG		
			GT TCACAA GTA ACT TC		
			C AA GT		
GAM625	LOC146227	3'	CTCCCCATAAATACCACCTTG 38088	A T CCATTG	
			CAA GTG TA ATGGGGAG		
			GTT CAC AT TACCCCTC		
			C C AAA__		
GAM625	LOC152674	3'	TCCCCACTCCACACTTT 41539	TACCATT _	
			AAAGTGT GA TGGGGA		
			TTTCACA CT ACCCCT		
			C_____ C		
GAM625	LOC197287	3'	CTCCACACAGTAACATTT 30522	CAT A	
			AAGTGTTAC TG TGGGG		
			TTTACAATG AC ACCTC		
			AC_ _		
GAM626	ADRBK1	3'	CCCGCCTTTTATAAACCTCT 7328	A GGT	
			AGAGGT TTG GGGGCGGG		
			TCTCCA AAT TTCCGCC		
			_ ATT		
GAM626	DHCR24	3'	GCCCACCCCAGCCACCACTGA 16525	A ATT G C	
			TCAG GGT GG TGGGG GGGC		
			AGTC CCA CC ACCCC CCCG		
			A _ G A		
GAM626	FSTL3	3'	GCCCACCCCACCCTGGGGCCCT 12469	A ATT_ C	
	G		CAG GGT GGGTGGGG GGGC		
			GTC CCG CCCACCCC CCCG		
			_ GGGT A		
GAM626	LY6E	3'	GCCCACCCCCTGCACCTC 8147	ATTG T C	
			GAGGT GG GGGG GGGC		
			CTCCA TC CCCC CCCG		
			CG_ _ A		
GAM626	NDUFV3	5'	CCCAGCCAACACCCTGA 22044	A A G	
			TCAG GGT TTGG TGGG		
			AGTC CCA AACC ACCC		
			_ C G		
GAM626	UBTF	3'	GCCCACCCCACCACTTCTG 15497	ATT C	
			CAGAGGT GGGTGGGG GGGC		

GTCTTCA CCCACCCC CCCG
 _____ A
 GAM626 CD109 3' GCCCACCCACCCCAACC 28571 ATT C
 GGT GGGTGGGG GGGC
 ||| ||||| |||
 CCA CCCACCCC CCCG
 AC_ A
 GAM626 DKFZP434N161 3' GCCCACCCCACTCACAAC 38397 GTAT C
 GAG TGGGTGGGG GGGC
 ||| ||||| |||
 CTC ACTCACCCC CCCG
 AC_ A
 GAM626 FLJ12750 3' CCCGCCCCCATACTC 23971 TGGGT
 GAGGTAT GGGGCGGG
 ||||| |||||
 CTCCATA CCCC GCCC
 C____
 GAM626 KIAA0346 5' GCCCACCCCACTGTGGTC 33920 GG_ T C
 TG CAGA TA TGGGTGGGG GGGC
 ||| ||||| |||
 GTCT GT ACCCACCCC CCCG
 GGT C A
 GAM626 KIAA1023 3' CCCGCCCCACCTGCGGTT 19089 GTATT
 GAG GGGTGGGGCGGG
 ||| ||||| |||
 CTT CCCACCCCGCCC
 GGCGT
 GAM626 KIAA1163 3' CCCACCCACACCTGTGA 38556 G AT
 TCA AGGT TGGGTGGG
 ||| ||| |||||
 AGT TCCA ACCCACCC
 G C_
 GAM626 KIAA1465 3' GCCCGCCCCACCGTGGGCTCTG 30503 GTATTG
 G TCAGAG GGTGGGGCGGGC
 ||||| ||||| |||
 GGTCTC CCACCCCGCCCG
 GGGTG_
 GAM626 SCYA14 5' CCCACCTCCAACACCTCCTGA 26773 _ A GTG C
 TCAG AGGT TTGG GGG GGG
 ||| ||| ||| ||| |||
 AGTC TCCA AACC TCC CCC
 C C _ A
 GAM626 SCYA14 5' CCCACCTCCAACACCTCCTGA 10373 _ A GTG C
 TCAG AGGT TTGG GGG GGG
 ||| ||| ||| ||| |||
 AGTC TCCA AACC TCC CCC
 C C _ A
 GAM626 LOC146146 5' GCCCGCCCGCACCAACCCTCTG 38071 TATTG _
 A TCAGAGG GGTG GGGCGGGC
 ||||| ||| |||||

AGTCTCC CCAC CCCGCCCG
 CAA__ G
 GAM626 LOC148697 5' GCCCACCCCATCTAACTTCTGA 38573 AT C
 TCAGAGGT TGGGTGGGG GGGC
 ||||| ||||| |||
 AGTCTTCA ATCTACCCC CCCG
 __ A
 GAM626 LOC155179 3' CCCGCCCCACCCTGCGGTTC 39556 GTATT
 GAG GGGTGGGGCGGG
 || |||||
 CTT CCCACCCCGCCC
 GGCGT
 GAM626 LOC219700 5' GCCCGCTTCCCCAACACCTC 44702 A T
 GAGGT TTGGG GGGGCGGGC
 |||| ||| |||||
 CTCCA AACCC CTTGCCCCG
 C _
 GAM626 LOC220753 3' GCCCACCCACCCAAGATTC 44662 GTA C
 GAG TTGGGTGGGG GGGC
 || ||||| |||
 CTT AACCCACCCC CCCG
 AG_ A
 GAM627 FLJ12294 3' CTCAACCACTGCGGCCTAATCC 24744 C__ GACA
 GGAT GC CAGTGGTTGAG
 ||| || |||||
 CCTA CG GTCACCAACTC
 ATC GC__
 GAM627 LOC255718 5' CTCAACCACCATGGCCCCTGA 46581 ATC GA CA
 TCGG GC CA GTGGTTGAG
 ||| || || |||||
 AGTC CG GT CACCAACTC
 CC_ __ AC
 GAM628 HPS3 3' AAAGATTTCAAACCTCA 26176 CCTGA GG
 TGAGGT TTG GTCTTT
 |||| | |||||
 ACTCCA AAC TAGAAA
 __ TT
 GAM628 MADD 5' AAAGACCTAGAACCCA 28232 A C GATTG
 TG GGT CT GGGTCTTT
 || ||| || |||||
 AC CCA GA TCCAGAAA
 _ A ____
 GAM628 PSCD3 3' AAAGACCCAGGTAAAAGACCCA 10422 A CTG_ TG
 TG GGTC AT GGGTCTTT
 || ||| || |||||
 AC CCAG TG CCCAGAAA
 _ AAAA GA
 GAM628 TCF21 5' GAGACCCAACCAGACCCA 9204 A C ATTG
 TG GGTC TG GGGTCTT
 || ||| || |||||

AC CCAG AC CCCAGAG
 C _ CAA_
 GAM628 DJ37E16.5 3' GGACCCATCAGGACCCCA 21578 A TG
 TG GGTCTGAT GGGTCT
 || ||||| |||||
 AC CCAGGACTA CCCAGG
 C _
 GAM628 DKFZP564O123 3' ACTGAAATCAAGGCCTCA 29903 C GG
 TGAGGTC TGATT GGT
 ||||| ||||| ||
 ACTCCGG ACTAA TCA
 A AG
 GAM628 FLJ10761 3' AGATCCAATCAAACCTCA 20105 CC G
 TGAGGT TGATTGGG TCT
 ||||| ||||| ||||| ||
 ACTCCA ACTAACCT AGA
 A_ _
 GAM628 FLJ23189 3' AAATGCCTCATAACCTCA 24654 CCTGAT C
 TGAGGT TGGGGT TTT
 ||||| ||||| ||||| ||
 ACTCCA ACTCCG AAA
 AT_ _ T
 GAM628 NYD-SP11 3' TGAAAGAGTGAGGATCAAGACC 25692 C GGGG_
 GGTC TGATT TCTTTCA
 ||| ||||| |||||
 CCAG ACTAG AGAAAGT
 A GAGTG
 GAM628 SSH2 3' GAAATTAAAACAGGACCCCA 31184 A A_ GG
 TG GGTCTG TTGG TC
 || ||||| ||||| ||
 AC CCAGGAC AATT AG
 C AA AA
 GAM628 LOC124976 3' CCCCAAGCCAGGACCCCA 36784 A A_
 TG GGTCTG TTGGGG
 || ||||| |||||
 AC CCAGGAC AACCCC
 C CG
 GAM629 ATP2A2 3' AGCCGTCAGCCAAGTC 7398 CG GT
 GAC TGGCTGAC GGCT
 ||| ||||| |||||
 CTG ACCGACTG CCGA
 A_ _
 GAM629 KIAA1643 3' AGGTTCCACGGCAGCCACG 32237 A CT
 CGTGGCTG CGTGG AGCCT
 ||||| ||||| |||||
 GCACCGAC GCACC TTGGA
 G _
 GAM629 MGC10999 3' AGGCTGCAGTGAGCCACAGTC 26089 C G GTG T
 GAC GTGGCT AC GC AGCCT
 ||| ||||| || |||||

			CTG CACCGA TG CG TCGGA		
			A G A__ _		
GAM629	NAF1	3'	GGCCATGCCAGCCACGTC 12702 C A		
			GAC GTGGCTG CGTGGCT		
			CTG CACCGAC GTACCGG		
			_ C		
GAM629	TJP2	3'	AGACTAGCCACTCCTGCCAGG 29981 G T_ C C		
			CC TGGC GA GTGGCTAG CT		
			GG ACCG CT CACCGATC GA		
			_ TC _ A		
GAM629	TSPEAR	3'	AGACCACACCTGCCACGGTC 29595 TGAC _		
			GACCGTGGC GTGG CT		
			CTGGCACCG CACC GA		
			TCCA A		
GAM629	LOC113730	5'	AGGCTGGAGGTCAGCCAC 36182 GTGG		
			GTGGCTGAC CTAGCCT		
			CACCGACTG GGTCGGA		
			GA__		
GAM629	LOC152687	5'	AGGCCTCGGTGATTGAGCCAC 39302 C G A__		
			GTGGCTGA GT GCT GCCT		
			CACCGACT TA TGG CGGA		
			_ G CTC		
GAM629	LOC164582	5'	AGGCATCGTCACCAGCCACGGC 40156 A AC TA_		
			G CCGTGGCTG GTGGC GCCT		
			C GGCACCGAC CACTG CGGA		
			_ _ CTA		
GAM629	LOC220370	3'	AGCTCATGTCAGCCAGGTC 44597 G _		
			GACC TGGCTGACGTG GCT		
			CTGG ACCGACTGTAC CGA		
			_ T		
GAM629	LOC221763	3'	AGCCCATGAATCAGCCGCGGTC 45034 _ _		
			GACCGTGGCTGA CGTGG CT		
			CTGGCGCCGACT GTACC GA		
			AA C		
GAM629	LOC89932	3'	AGGCTAGTTCCAGCCCCAGTC 30486 CGT ACGT		
			GAC GGCTG GGCTAGCCT		
			CTG CCGAC TTGATCGGA		
			ACC C__		
GAM630	GORASP1	3'	ATACAAGGCATCTACCCAGCCC 25644 A A TCGCCA_		
	CA		TG GG CTGG CCTTGTAT		

			AC CC GACC	GGAACATA	
			C _	CATCTAC	
GAM630	TAF1C	3'	ACAAGGTGGGCTGCCCTCA	12234	ACT CG
			TGAGG GGT CCACCTTGT		
			ACTCC TCG GGTGGAACA		
			CG_ _		
GAM630	DRIL2	3'	ACAAGTCTTGAATCAGTCCTCA	13181	_ CCAC
			TGAGGACTGGT CG CTTGT		
			ACTCCTGACTA GT GAACA		
			A TCT_		
GAM630	LOC120114	3'	TATAACAATCCAGTCCTCA	37212	TCGCCACC
			TGAGGACTGG TTGTA		
			ACTCCTGACC AATAT		
			TAAC_		
GAM630	LOC204823	5'	ACAAGGTGATGTCCCCT	43101	ACT T C
			AGG GG CG CACCTTGT		
			TCC CC GT GTGGAACA		
			_ T A		
GAM630	LOC220672	3'	ACACAGTTGCAAACAGTCCTCA	30307	GTC C CT
			TGAGGACTG GC AC TGT		
			ACTCCTGAC CG TG ACA		
			AAA T AC		
GAM630	LOC90841	3'	ACAGTGTGCAAAGACCAGTCCT	32109	GC_ C
	CA		TGAGGACTGGTC CAC TTGT		
			ACTCCTGACCAG GTG GACA		
			AAAC T		
GAM631	DNASE1	5'	GGCCACAGAGCAGTCATG	11714	ATA
			CATGAC CTCTGTGGCC		
			GTACTG GAGACACCGG		
			AC_		
GAM631	EGLN1	5'	CGAGTGCGCGCCGTATG	22582	TCT G
			CATAC GTG CCACTCG		
			GTATG CGC GGTGAGC		
			CC_ _		
GAM631	IFNAR2	3'	AGTGGCGGTGGCTATACCATG	6552	AC CT TG G
			CATG ATA C T GCCACT		
			GTAC TAT G G CGGTGA		
			CA C_ GT G		
GAM631	COL12A1	3'	GCCACAGAAGATGTCATG	27936	AC
			CATGACAT TCTGTGGC		

			GTACTGTA AGACACCG		
			GA		
GAM631	COL12A1	3'	GCCACAGAAGATGTCATG 10589	AC	
			CATGACAT TCTGTGGC		
			GTACTGTA AGACACCG		
			GA		
GAM631	KIAA1023	3'	AGCAGCCACAGGAGATGTCA 19084	AC	CA
			TGACAT TCTGTGGC CT		
			ACTGTA GGACACCG GA		
			GA AC		
GAM631	KIAA1091	3'	TGGCTGGTGGAGTATGTGATG 34543	G	TG_
			CAT ACATACTC T GGCCA		
			GTA TGTATGAG G TCGGT		
			G GT G		
GAM631	NRF	3'	CGAATGACAGTTGAGTATGTC 18986	TG_ GC C	
			GACATACTC TG CA TCG		
			CTGTATGAG AC GT AGC		
			TTG A_ A		
GAM631	LOC148089	3'	CGAGCAGCCGCTGGGACGCCAT 38451	ACATA T	CA
	G		CATG CTC GTGGC CTCG		
			GTAC GGG CGCCG GAGC		
			CGCA_ T AC		
GAM631	LOC148490	5'	CGAACAGCCACAAGCAGCCATG 38546	ACATA C	CAC
			CATG CT TGTGGC TCG		
			GTAC GA ACACCG AGC		
			CGAC_ _ ACA		
GAM631	LOC148764	5'	AGTCCACAGAATACCCATG 38589	ACA C	CC
			CATG TA TCTGTGG ACT		
			GTAC AT AGACACC TGA		
			CC_ A _		
GAM631	LOC155179	3'	AGCAGCCACAGGAGATGTCA 39552	AC	CA
			TGACAT TCTGTGGC CT		
			ACTGTA GGACACCG GA		
			GA AC		
GAM631	LOC91355	5'	AGTGGCCACAAACTGTGTTA 32702	CTC_	
			TGACATA TGTGGCCACT		
			ATTGTGT ACACCGGTGA		
			CAAA		
GAM632	CACNG6	5'	GTCCCTTCCTGGGTACCCCA 25642	A	ACAT
			TGGGGTGCCCA GAAG GGC		

			ACCCCATGGGT CTTC CTG	
			C C__	
GAM632	CHN1	5'	GCCCCATCGGGCACCCCA 7562	AAGAA CAT
			TGGGGTGCCC GA GGC	
			ACCCACGGG CT CCG	
			_____ ACC	
GAM632	EGR3	3'	CACCTCTTCTCAGGCACCCC 29955	CA CA
			GGGGTGCC AGAAGA TG	
			CCCCACGG TCTTCT AC	
			AC CC	
GAM632	FOXE3	3'	GCCGCCCTCGAGCGCCCCA 14472	CCAA A ACA
			TGGGGTGC GA G TGGC	
			ACCCCGCG CT C GCCG	
			AG__ _CC_	
GAM632	FOXM1	3'	CCATCCCGGGCACTCCA 22482	AA AGACA
			TGGGGTGCCC GA TGG	
			ACCTCACGGG CT ACC	
			CC _____	
GAM632	GAL	5'	GCCATGCGGTGAGCGCCCCA 43999	C AGAAGA
			TGGGGTGC CA CATGGC	
			ACCCCGCG GT GTACCG	
			A GGC__	
GAM632	KCNK7	5'	GCCAGTTCCCACAGCACCCCA 27254	CCAAGAA A
			TGGGGTGC GAC TGGC	
			ACCCACG TTG ACCG	
			ACACCC_ _	
GAM632	KCNK7	5'	GCCAGTTCCCACAGCACCCCA 27199	CCAAGAA A
			TGGGGTGC GAC TGGC	
			ACCCACG TTG ACCG	
			ACACCC_ _	
GAM632	KCNK7	5'	GCCAGTTCCCACAGCACCCCA 27200	CCAAGAA A
			TGGGGTGC GAC TGGC	
			ACCCACG TTG ACCG	
			ACACCC_ _	
GAM632	KCNK7	5'	GCCAGTTCCCACAGCACCCCA 12268	CCAAGAA A
			TGGGGTGC GAC TGGC	
			ACCCACG TTG ACCG	
			ACACCC_ _	
GAM632	MFAP4	3'	TGCCACATCCCTGTCACACACC 34329	_ CCCA AA CA
	CA		TGGG GTG AG GA TGGCA	

			ACCC CAC TC CT ACCGT A ACTG C_ AC	
GAM632	MGAT1	3'	GCCCGCTCCCAGGCGCCCCA 8226 TGGGGTGCC GA G GGC ACCCCGCGG CT C CCG ACC _ GC__	CAA A ACAT
GAM632	OCRL	3'	CCATGGCTATTCCAGCACCCCA 5818 TGGGGTGC GAA CATGG ACCCACG CTT GTACC AC__ ATCG	CCAA GA__
GAM632	OCRL	3'	CCATGGCTATTCCAGCACCCCA 7305 TGGGGTGC GAA CATGG ACCCACG CTT GTACC AC__ ATCG	CCAA GA__
GAM632	PCTK1 A	5'	TGCCTTCCTCCCCAAGCACCTC 26911 TGGGGTGC GA GA GGCA ACTCCAG CT CT CCGT AACCC C T__	CCAA_ A CAT
GAM632	SLA2	3'	GCCTCCTGGGCACCCCA 25943 TGGGGTGCCCA GA GGC ACCCACGGGT CT CCG C _____	A AGACAT
GAM632	C11orf11	3'	TGCCCATGGGTCTCTGGGCACCC 44789 GGGTGCCCA GA CATGG CA CCCACGGGT CT GTACC GT C GG_ C	A AGA _
GAM632	CGI-203	5'	CCACGTCTCCCCTGCACCCCA 21675 TGGGGTGC GA GAC TGG ACCCACG CT CTG ACC TCCC _ C	CCAA A A
GAM632	KIAA0222	3'	GCCCCTTCCCTGAGCCACCCCA 16046 TGGGGTG C CA GAAG GGC ACCCAC G GT CTTC CCG C A CC C__	_ C A_ ACAT
GAM632	KIAA1915	5'	TGTCTTCTCAAACACCCCA 36274 TGGGGTG AGAAGACA ACCCAC TCTTCTGT AAAC	CCCA
GAM632	QSCN6	3'	GCCATCTCTAGGCACCTCA 8698 TGGGGTGCC AGA ATGGC 	CAAGA C

			ACTCCACGG	TCT TACCG	
			A___	C	
GAM632	UCK1	3'	TGCTTCCTCTCGGCGCACCCCA	25429	_ A A CAT
			TGGGGTGC CC AGA GA	GGCA	
			ACCCACG GG TCT CT	TCGT	
			C C C	___	
GAM632	LOC149134	5'	TGCCACGTCTGTGATGTGGGCA	40960	AGA___ A
			CCTCA	TGGGGTGCCCA AGAC TGGCA	
			ACTCCACGGGT	TCTG ACCGT	
			GTAGTG	C	
GAM632	LOC149837	3'	TGCCATGTCCCCTCTCATCCTA	41103	CCCA AA
			TGGGGTG AG GACATGGCA		
			ATCCTAC TC CTGTACCGT		
			TC__	CC	
GAM632	LOC151723	5'	TGCTGTGCCCTTGGGCACCCC	40192	AAGA
			GGGGTGCCCAAG CATGGCA		
			CCCCACGGGTTC	GTGTCGT	
			CC__		
GAM632	LOC157653	5'	TGCCCAGCAGTCCCTGGGCACC	39636	A_ AGACAT
			C	GGGTGCCCA GA GGCA	
			CCCACGGGT CT	CCGT	
			CC GACGAC		
GAM632	LOC255397	5'	GCTGGCTCCTGGGCGCCCCA	46566	A A ACAT
			TGGGGTGCCCA GA G	GGC	
			ACCCCGCGGGT CT C	TCG	
			C _ GG__		
GAM632	LOC58525	3'	GCCATGTCAAGGCCCCCA	38458	T CAAGAA
			TGGGG GCC	GACATGGC	
			ACCCC CGG	CTGTACCG	
			C AA__		
GAM633	FGF5	3'	AAATAGCTATAATACCT	26995	CACA C
			AGGTAT TG AGCTATTT		
			TCCATA AT TCGATAAA		
			___	A	
GAM633	HIP1	3'	AAAACAGCTGCATCTGTTACTT	11809	T C A
			AGGTA CA ATGCAGCT TTTT		
			TTCAT GT TACGTCGA AAAA		
			T C	C	
GAM633	TGFBR3	3'	AAAATAAGCTCAGTGATACCT	9246	A C _
			AGGTATCAC TG AGCT ATTTT		

		TCCATAGTG AC TCGA TAAAA	
		— — A	
GAM633	FLJ20413 3'	AAAATAGACAAGTGATACCT 19449	A CAG
		AGGTATCAC TG CTATTTT	
		TCCATAGTG AC GATAAAA	
		A A__	
GAM633	HSPCAL3 3'	AGTGATGCTGTGATACCTTA 37616	T __
		TAAGGTATCACA GCA GCT	
		ATTCCATAGTGT CGT TGA	
		— AG	
GAM633	KIAA0608 3'	AAAATAGCTTTGAAGATACTT 35735	ACATGC
		AGGTATC AGCTATTTT	
		TTCATAG TCGATAAAA	
		AAGTT_	
GAM633	KIAA1026 3'	AAAATAGCTACAGGTAACCCTT 35272	TATC A C
		AAGG AC TG AGCTATTTT	
		TTCC TG AC TCGATAAAA	
		CAA_ G A	
GAM633	LOC220549 5'	TGGCTGCACATATACCTTA 44653	CACA
		TAAGGTAT TGCAGCTA	
		ATTCCATA ACGTCGGT	
		TAC_	
GAM633	LOC51696 3'	AGCCCATGATACCTTA 18306	CA CA
		TAAGGTATCA TG GCT	
		ATTCCATAGT AC CGA	
		— C_	
GAM634	CSPG3 3'	CATGTCTGTTACTCACTTT 10614	C CAA
		AAAGTGAGT AACA GTG	
		TTTCACTCA TTGT TAC	
		— CTG	
GAM634	DAAM2 3'	TTTCACTTGCATCCAACTCCT 44336	T CAACA_
		AG GAGT CAAGTGAAA	
		TC CTCA GTTCACTTT	
		— ACCTAC	
GAM634	ESRRBL1 3'	CACCTGGTGGCTCATTTTT 19741	A A A
		AAAAGTGAGTCA C CA GTG	
		TTTTTACTCGGT G GT CAC	
		— — C	
GAM634	GRB10 3'	TTTGTATTGATCACTTTT 11788	G C
		AAAAGTGA TCAA ACAAG	

			TTTTCACT AGTT TGTTT		
			— A		
GAM634	IL1A	3'	TCACTTGTCTCACTT	31308	TCAAC
			AAGTGAG ACAAGTGA		
			TTCACTC TGTTCACT		
			————		
GAM634	IRTA1	3'	TCACTGGAGACTCACTT	25303	AA CAA
			AAGTGAGTC CA GTGA		
			TTCACTCAG GT CACT		
			AG —		
GAM634	RERE	3'	TTTCACTTGTGTCTGCTCCT	14411	T CA
			AG GAGT ACACAAGTGAAA		
			TC CTCG TGTGTTCACTTT		
			— TC		
GAM634	RNMT	3'	TTCACCTGTGGTAACTCATTTT	9892	CAA A
			AAAGTGAGT CACA GTGAA		
			TTTTACTCA GTGT CACTT		
			ATG C		
GAM634	RU2	5'	TTTACCTGTGGATTTCG	18494	AA A
			TGAGTC CACA GTGAAA		
			GCTTAG GTGT CACTTT		
			— C		
GAM634	TRAM	3'	TCACTTGTGTCACCAGCT	15592	GA CA
			AGT GT ACACAAGTGA		
			TCG CA TGTGTTCACT		
			AC C_		
GAM634	UBE2A	3'	TTCACTTGTGTTGGATTTA	9343	—
			TGAGTC AACACAAGTGAA		
			ATTTAG TTGTGTTCACTT		
			G		
GAM634	ADAMDEC1	3'	TTTCACTTGTCACTTCTACTTT	15824	— CAAC
			AAAGT GAGT ACAAGTGAAA		
			TTTCA CTTA TGTTCACTTT		
			T C_		
GAM634	APCL	3'	CACCCCGAGTCCTGAGCTCACT	12496	— AC AA_
	TT		AAAGTGAG TCA AC GTG		
			TTTCACTC AGT TG CAC		
			G CC AGCCC		
GAM634	ARHGAP8	5'	TCACTTGTGCCAGGCATAC	19274	A AA_
			GTG GTC CACAAGTGA		

			CAT CGG GTGTTCACT		
			A ACC		
GAM634	BCAA	3'	TTTCACTTGTATTGACTT	18514	C
			GAGTCAA ACAAGTGAAA		
			TTCAGTT TGTTCACTTT		
			A		
GAM634	CAMP-GEFII	3'	CACTTGTGCCATCTTCTTT	13880	T TCAA
			AAAG GAG CACAAGTG		
			TTTC TTC GTGTTCAC		
			_ TACC		
GAM634	CKAP4	3'	TCACTTGTCTTCCACTTT	13703	AGTC C
			AAAGTG AA ACAAGTGA		
			TTTCAC TT TGTTCACT		
			C__ C		
GAM634	DKFZp434E0519	3'	TTTCACTTGGCTTGGTGAC	25985	AG CA
			GTG TCAA CAAGTGAAA		
			CAC GGTT GTTCACTTT		
			GT C_		
GAM634	FLJ11078	3'	TCGGTGGTATATGACTCAC	20310	__ A AG
			GTGAGTCA AC CA TGA		
			CACTCAGT TG GT GCT		
			ATA _ G_		
GAM634	FLJ12783	3'	TTCACTCATTGACTCACT	25421	CACA
			AGTGAGTCAA AGTGAA		
			TCACTCAGTT TCACTT		
			AC__		
GAM634	FLJ14327	3'	CACTTGTGTGGCTGCCT	24422	TG A
			AG AGTCA CACAAGTG		
			TC TCGGT GTGTTCAC		
			CG _		
GAM634	FLJ20345	3'	TGGCCTTGACTCACTTTT	19406	CA_
			AAAAGTGAGTCAA CA		
			TTTTCACTCAGTT GT		
			CCG		
GAM634	FLJ21369	3'	TCATTATTGACTCACTTTT	24184	CACA
			AAAAGTGAGTCAA AGTGA		
			TTTTCACTCAGTT TTA		
			A__		
GAM634	FLJ23233	3'	TTCAAATGTGACTCACTTTT	24001	A CAAG
			AAAAGTGAGTCA CA TGAA		

			TTTTCACTCAGT GT ACTT		
			_ AA_		
GAM634	KIAA0993	3'	TCAC TTATTA ACTCTCTTTT 32084	T C CAC	
			AAAAG GAGT AA AAGTGA		
			TTTTC CTCA TT TTCACT		
			T A A_		
GAM634	KIAA1040	3'	TTCAC TTGCTTTTCATTTT 35746	TCAACA	
			AAAAGTGAG CAAGTGAA		
			TTTTTACTT GTTCACTT		
			TC_		
GAM634	KIAA1069	3'	TTTTCACTGTGAATTCAC TTTT 33728	CAA A	
			AAAAGTGAGT CACA GTGAAA		
			TTTTCACTTA GTGT CACTTT		
			A_ _		
GAM634	KIAA1613	3'	TTCCTTG GGGCTAGCTCACTTT 32361	CAACA_ T	
			AAAGTGAGT CAAG GAA		
			TTTCACTCG GTTC CTT		
			ATCGGG _		
GAM634	MGC2550	3'	TTTCACTCACTATTTCACTTT 23500	TCAACACA	
			AAAGTGAG AGTGAAA		
			TTTCACTT TCACTTT		
			TATCAC_		
GAM634	MGC26954	3'	TTTCACTTCTCCTGGCTCACT 29640	ACAC	
			AGTGAGTCA AAGTGAAA		
			TCACTCGGT TTCAC TTT		
			CCTC		
GAM634	PRO0365	3'	TTTCACTTATGTACCATTTT 15391	A CA C	
			AAAAGTG GT ACA AAGTGAAA		
			TTTTTAC CA TGT TTCAC TTT		
			_ _ A		
GAM634	SGP28	3'	TTCAC TAAAATCAGTGACTCAC 12704	A ACACA_	
	TTCC		A AAGTGAGTCA AGTGAA		
			C TTCAC TCACT TCACTT		
			C GACTAAAA		
GAM634	LOC120856	3'	TCACTCATGTTGTGGCTTATTT 36645	_ CA	
			AAGTGAGTCA ACA AGTGA		
			TTTATTCGGT TGT TCACT		
			GT AC		
GAM634	LOC144079	5'	TTCAC TTGCTCCTTCACTTCC 37674	A TCAACA	
			A AAGTGAG CAAGTGAA		

		C TTCAC TT GTTCACTT	
		C CCTC__	
GAM634	LOC146184 5'	CACTTAGTGGGCTGCACTTTT 40660	_ AA _
		AAAAGTG AGTC CAC AAGTG	
		TTTTCAC TCGG GTG TTCAC	
		G _ A	
GAM634	LOC147077 3'	TTCAAGCTGCTGACTCACTTT 38295	A CAAG
		AAAGTGAGTCA CA TGAA	
		TTTCACTCAGT GT ACTT	
		C CGA_	
GAM634	LOC148046 3'	CACTCCTGACCTCAGACTCACT 40865	A AA__ CA
	TCC	A AAGTGAGTC CA AGTG	
		C TTCACTCAG GT TCAC	
		C ACTCCA CC	
GAM634	LOC152674 5'	TTTCACTTACATTATTTCACTT 41541	TCAACAC
		AAGTGAG AAGTGAAA	
		TTCACTT TTCACTTT	
		TATTACA	
GAM634	LOC153222 3'	TCACTTGTATATGGCACAC 39368	A AC_
		GTG GTCA ACAAGTGA	
		CAC CGGT TGTTCACT	
		A ATA	
GAM634	LOC153711 3'	CTTCTGTTAGACTCACTTTT 41669	_ C
		AAAAGTGAGTC AACA AAG	
		TTTTCACTCAG TTGT TTC	
		A C	
GAM634	LOC157624 5'	TTGGCTGTAAC TCACTTTT 41828	CAAC A G
		AAAAGTGAGT ACA GT AA	
		TTTTCACTCA TGT CG TT	
		A__ _ G	
GAM634	LOC157867 5'	CACTCTGTTACTCATTTT 41855	C CA
		AAAGTGAGT AACA AGTG	
		TTTTACTCA TTGT TCAC	
		_ C_	
GAM634	LOC196264 3'	TTTCACTTGTATTGTTTTTCA 42338	T__ C
		TGAG CAA ACAAGTGAAA	
		ACTT GTT TGTTCACTTT	
		TTT A	
GAM634	LOC219899 3'	TTTGTATGTTACTA ACTCACTT 43994	CAAC_ A TG
	TT	AAAAGTGAGT ACA G AA	

			TTTTCACTCA	TGT T TT		
			ATCAT	A GT		
GAM634	LOC253187	5'	TACTTAGTAACTCACTTTT	46394	CAAC	_
			AAAAGTGAGT	AC AAGTG		
			TTTTCACTCA	TG TTCAT		
			A__	A		
GAM634	LOC90750	5'	TTCCTTGCTGACTCATTTCC	31972	A	ACA T
			A AAGTGAGTCA	CAAG GAA		
			C TTTACTCAGT	GTTC CTT		
			C	C__		
GAM634	LOC91133	3'	TTTCAGAATTGACTCATTTCC	32431	A	CACAAG
			A AAGTGAGTCAA	TGAAA		
			C TTTACTCAGTT	ACTTT		
			C	AAG__		
GAM635	MGC5370	3'	AGTAACAAGCCTGTCAAA	26469	A	A
			TTT ACAGGCTTGT	ACT		
			AAA TGTCCGAACA	TGA		
			C	A		
GAM635	LOC139522	5'	CCCTGAAGCCACAAGCCTTG	37344	_	AA A
			CA GGCTTGT	CTTCA GG		
			GT CCGAACA	GAAGT CC		
			T	CC C		
GAM635	LOC158382	5'	CCTTAAAGCTATGAGCCTTTAA	41965	C	TG A C
	A		TTTAA AGGCT	TA CTT AAGG		
			AAATT TCCGA	AT GAA TTCC		
			_	GT C A		
GAM635	LOC219920	3'	CCTTAAAGTTGTAAGCCTTTAA	44805	C	C
	A		TTTAA AGGCTTGTAACTT	AAGG		
			AAATT TCCGAATGTTGAA	TTCC		
			_	A		
GAM635	LOC63928	3'	CCTTGAAGTCTGGACTCTTAA	22637	C G	TGTA
			TTTAA AG CT	ACTTCAAGG		
			AAATT TC GG	TGAAGTTCC		
			C A TC__			
GAM636	G6PC	3'	TTTCTCTATCCCAAGCCAACCA	5661	_	AGCAT
	A		TTGGTTG CT	GATAGAGAAA		
			AACCAAC GA	CTATCTCTTT		
			C ACC__			
GAM636	MS4A2	3'	TTCTCCATCAGCAACCAG	22477	AGCAT	A
			TTGGTTGCT	GAT GAGAA		

			GACCAACGA CTA CTCTT	
			_____ C	
GAM636	OXTR	3'	TTTCTTTATACTAGCAAC 6623	CATG
			GTTGCTAG ATAGAGAAA	
			CAACGATC TATTTCTTT	
			A_____	
GAM636	SERPINB9	3'	CTCCAGCCCCCAGCAACCA 10365	A_____ A ATA
			TGGTTGCT GC TG GAG	
			ACCAACGA CG AC CTC	
			CCCC _ _ _ _	
GAM636	WNT8B	3'	CTTCCTCCTAGCAACCAA 29984	CAT TA
			TTGGTTGCTAG GA GAG	
			AACCAACGATC CT TTC	
			_____ CC	
GAM636	KIAA0976	3'	TTTATCCATACTTAGCAACCAA 17169	CAT_____
			TTGGTTGCTAG GATAGA	
			AACCAACGATT CTATTT	
			CATAC	
GAM636	SMCR7	3'	TCTGTCCATCACCAGCAACCAA 29170	AGCAT_____
			TTGGTTGCT GATAGA	
			AACCAACGA CTGTCT	
			CCACTAC	
GAM636	LOC138307	5'	TCTCTGAGCTGCCAGCAGCCAA 37124	A TGA
			TTGGTTGCT GCA TAGAGA	
			AACCGACGA CGT GTCTCT	
			C CGA	
GAM636	LOC146316	5'	CTCTTCACCAGCAACCAG 30524	AGCA T
			TTGGTTGCT TGA AGAG	
			GACCAACGA ACT TCTC	
			CC_____ _	
GAM636	LOC157226	5'	TCTCCATCACCGCAACCAA 31978	TAGCA A
			TTGGTTGC TGAT GAGA	
			AACCAACG ACTA CTCT	
			CC_____ C	
GAM636	LOC158714	5'	CTACATGCCAGCAACCA 39884	A A
			TGGTTGCT GCATG TAG	
			ACCAACGA CGTAC ATC	
			C _	
GAM636	LOC254082	5'	TTCTCTATCACTCACAAC 46422	CT CA
			GTTG AG TGATAGAGAA	

CAAC TC ACTATCTCTT
 AC _
 GAM636 LOC51634 3' TCCCTGTCCCTAGCAACCA 18101 CAT A
 TGGTTGCTAG GATAG GA
 ||||| |||||
 ACCAACGATC CTGTC CT
 C_ C
 GAM636 LOC92017 3' TTCTAAATCCCAGCAACCAA 33711 AGCAT AG
 TTGGTTGCT GAT AGAA
 ||||| ||| ||||
 AACCAACGA CTA TCTT
 CC_ AA
 GAM637 FREB 3' AATAAAATTCTGTTGTTTGT 26465 TG_
 GC TAACAGAATTTTATT
 || |||||
 TG GTTGTCTTAAAATAA
 TTT
 GAM637 TNFSF10 3' AATAAAATTCTATTACAGT 9899 C
 GCTGTAA AGAATTTTATT
 ||||| |||||
 TGACATT TCTTAAAATAA
 A
 GAM637 KIAA0323 3' AGGTTCTGCTCAGCCTTAA 31687 A TAA
 TTAA GCTG CAGAATTT
 ||| ||| |||||
 AATT CGAC GTCTTGGA
 C TC_
 GAM637 LOC254251 5' AATAAAATTCCCAACAGCTT 45893 AACA
 AAGCTGT GAATTTTATT
 ||||| |||||
 TTCGACA CTTAAAATAA
 ACC_
 GAM638 AKT1 3' CTTGACCTTTTCGACGCTT 11650 ACA T
 AAGC CGAG GGGTCAAG
 ||| ||| |||||
 TTCG GCTT TCCAGTTC
 CA_ T
 GAM638 ARHGAP6 3' AGTACTTGACCCTGAGCGGCGC 6841 ACA AGT_ C
 GC CG GGGTCAAG ACT
 || || ||||| |||
 CG GC CCCAGTTC TGA
 CG_ GAGT A
 GAM638 BSN 3' TGCTTGACCCTCTTGCTT 9521 CACG T
 AAGCA AG GGGTCAAGCA
 |||| |||||
 TTCGT TC CCCAGTTCGT
 _ T
 GAM638 DIO3 3' GTGCTTTGGCCCGGTGCTT 7042 ACGAG _
 AAGCAC TGGGTCAA GCAC
 |||| ||||| |||

TTCGTG GCCCGGTT CGTG
 _____ T
 GAM638 FTH1 5' AGTGCTTGACGGAACCCGGCG 33808 ACA A GGG____
 CT AGC CG GT TCAAGCACT
 ||| ||| |||||
 TCG GC CA GGTTCGTGA
 CG_ C AGGCA
 GAM638 GNRHR 5' GTGCTCAACAGTGTGTTT 5983 GAG GTCA
 AAGCACAC TG AGCAC
 ||||| || ||||
 TTTGTGTG AC TCGTG
 ACA _____
 GAM638 GPR30 3' GCGCCCGCCGTCTGCT 7252 C A CAA
 AGCA ACG GTGGGT GC
 ||||| ||||| ||
 TCGT TGC CGCCCG CG
 C _ _
 GAM638 MYBL1 3' AGTACTTTTGCCCATGTGCT 32041 CGAG C_ C
 AGCACA TGGGT AAG ACT
 ||||| ||||| |||||
 TCGTGT ACCCG TTC TGA
 _____ TT A
 GAM638 NCALD 3' TGCCCAGAGCCCCAGTGTGCTT 25746 GAGT CAA____
 AAGCACAC GGGT GCA
 ||||| ||||| ||
 TTCGTGTG CCG CGT
 AC_ AGACC
 GAM638 SHOX 5' AGCGCTGGTGATCCACCCGCGC 13746 ACA A _ A
 GC GC CG GTGGGTCA AGC CT
 || ||||| ||||| |||||
 CG GC CACCTAGT TCG GA
 CGC C GG C
 GAM638 SHOX 5' AGCGCTGGTGATCCACCCGCGC 6053 ACA A _ A
 GC GC CG GTGGGTCA AGC CT
 || ||||| ||||| |||||
 CG GC CACCTAGT TCG GA
 CGC C GG C
 GAM638 TIMP3 5' GCCCACCCACTCGCGTGC 5931 A CAA
 GCAC CGAGTGGGT GC
 ||||| ||||| ||
 CGTG GCTCACCCA CG
 C CC_
 GAM638 TK2 3' GCACCTGTTGTGTGC 10959 G CAA
 GCACACGA TGGGT GC
 ||||| ||||| ||
 CGTGTGTT GTCCA CG
 _ _
 GAM638 BM-002 3' AGTGCTTGACCTCCTGT 18725 G TG
 AC AG GGTCAAGCACT
 || ||||| |||||

TG TC CCAGTTCGTGA
 _ CT
 GAM638 C1QTNF3 3' AGTGCTTGACCAGTAATGTGGT 25217 A AGTG_
 T AGC CACG GGTCAAGCACT
 ||| ||| |||||
 TTG GTGT CCAGTTCGTGA
 _ AATGA
 GAM638 CHST4 5' TGCTTCCTCATTTGCTT 12339 CACG TC
 AAGCA AGTGGG AAGCA
 |||| ||||| ||||
 TTCGT TTA CTC TTCGT
 _ C_
 GAM638 DKFZp761N1114 3' AGTGCTGTGATTCACACG 38605 A _
 CG GTGGGTCA AGCACT
 || ||||| |||||
 GC CACTTAGT TCGTGA
 A G
 GAM638 FLJ14327 3' GCACCTACTGTGTGCTT 24427 G CAA
 AAGCACAC AGTGGGT GC
 ||||| ||||| ||
 TTCGTGTG TCATCCA CG
 _ _
 GAM638 FLJ23375 3' GCACTTACCGCTGTGCTT 24513 _ A CAA
 AAGCACA CG GTGGGT GC
 ||||| || ||||| ||
 TTCGTGTG GC CATTCA CG
 C _ _
 GAM638 GTPBP2 3' AGTGCTCCGAAGCTGTGTGCT 21171 G GGGTCA
 AGCACAC AGT AGCACT
 ||||| ||| |||||
 TCGTGTG TCG TCGTGA
 _ AAGCC_
 GAM638 KIAA0876 3' AGTGCCTGTGCCCACTCTGTGC 32295 C _ A
 GCACA GAGTGGGT CA GCACT
 |||| ||||| || |||||
 CGTGT CTCACCCG GT CGTGA
 _ T C
 GAM638 KIAA0923 3' AGTGCCTAACCCCTGCTTGT 15239 _ CAA
 ACGAGT GGGT GCACT
 ||||| ||| |||||
 TGTTCG CCGA CGTGA
 T ATC
 GAM638 KLHL6 3' GCCTGACCTTGTGATCTGC 28211 _ AGT A
 GCA CACG GGGTCA GC
 ||| ||| ||||| ||
 CGT GTGT TCCAGT CG
 CTA _ C
 GAM638 MDN1 3' CTTGAAACTGTGTGCT 31409 G GGG
 AGCACAC AGT TCAAG
 ||||| ||| |||||

TCGTGTG TCA AGTTC
 _ A_
 GAM638 MGC10870 5' AGCGCAGGACCACCGCGTGTGC 26080 AGTG AA A
 T AGCACACG GGTC GC CT
 ||||| ||| |||
 TCGTGTGC CCAG CG GA
 GCCA GA C
 GAM638 MGC10981 3' AGTGCTTGGAGGTCCGTGT 26387 AG GGG
 ACACG T TCAAGCACT
 |||| | |||||
 TGTGC G GGTTCGTGA
 CT GA_
 GAM638 RABL4 5' GCCCACCCTCGCGTCT 13730 C A CAA
 AG AC CGAGTGGGT GC
 || ||||| ||
 TC TG GCTCACCCA CG
 _ C CC_
 GAM638 SIRPB1 3' AGTGCTTGACCTTTTTGT 12705 T
 ACGAG GGGTCAAGCACT
 |||| |||||
 TGTTT TCCAGTTCGTGA
 T
 GAM638 UNC5D 3' ACCCTTTTGCTAGTGTGCTT 28110 G ____
 AAGCACAC AGT GGGT
 ||||| || |||
 TTCGTGTG TCG CCCA
 A TTTT
 GAM638 LOC150225 3' GCAGGTGGCCCACACATGTGC 41189 CGA A_
 GCACA GTGGGTCA GC
 |||| ||||| ||
 CGTGT CACCCGGT CG
 ACA GGA
 GAM638 LOC154007 3' TGCTTAGTTCATAGTATGCT 39456 C GA TC
 AGCA AC GTGGG AAGCA
 ||| || |||| ||||
 TCGT TG TACTT TTCGT
 A A_ GA
 GAM638 LOC154222 3' GCACCCGCTCATGTGCT 41692 C CAA
 AGCACA GAGTGGGT GC
 |||| ||||| ||
 TCGTGT CTCGCCCA CG
 A ____
 GAM638 LOC157918 3' AGTGCCTGACCCTGACCTGTCC 41894 C CGAGT A
 T AG ACA GGGTCA GCACT
 || || |||| ||||
 TC TGT CCCAGT CGTGA
 C CCAGT C
 GAM638 LOC157919 5' AGTGCCTGACCCTGACCTGTCC 39681 C CGAGT A
 T AG ACA GGGTCA GCACT
 || || |||| ||||

			TC TGT CCCAGT CGTGA		
			C CCAGT C		
GAM638	LOC201562	3'	GTGCTTGACTGCATGCT 42884	CACGAG _	
			AGCA TG GGTCAAGCAC		
			TCGT AC TCAGTTCGTG		
			_____ G		
GAM638	LOC257106	3'	AGTGCCCAACTCTATAGGCTT 45676	ACAC_ G TCAA	
			AAGC GAGT GG GCACT		
			TTCG CTCA CC CGTGA		
			GATAT A _____		
GAM638	LOC92689	3'	GCACCTACTGTGTGCT 34783	G CAA	
			AGCACAC AGTGGGT GC		
			TCGTGTG TCATCCA CG		

GAM639	GLI2	5'	TGTGCTGCTTTACCGACACAT 24938	AA G	
			ATGT CGGTAAAGCAG CACG		
			TACA GCCATTTCGTC GTGT		
			CA _____		
GAM639	C11orf23	3'	GTGCCTAAACATTACATTG 20303	CG AAAGC	
			TAATGTAA GT AGGCAC		
			GTTACATT CA TCCGTG		
			A_ AA_____		
GAM639	ECE2	3'	CGTGCCTGCCCCACTGTGAC 16198	A AAA	
			GT ACGGT GCAGGCACG		
			CA TGTCA CGTCCGTGC		
			G CCC		
GAM639	FLJ10901	3'	CCTAAGCGTCCTTTACATTA 20230	C TAAA _	
			TAATGTAA GG GC AGG		
			ATTACATT CC CG TCC		
			T TG_ AA		
GAM639	ZNF317	3'	CGCGCCTGCTTTAGAGACA 35636	AACGG A	
			TGT TAAAGCAGGC CG		
			ACA ATTCGTCCG GC		
			GAG_ C		
GAM639	LOC245771	3'	CCTAAGCGTCCTTTACATTA 44635	C TAAA _	
			TAATGTAA GG GC AGG		
			ATTACATT CC CG TCC		
			T TG_ AA		
GAM640	GPRK7	3'	CTGTGTATTACGCAAAGTCCTA 29228	CCAATAC _	
	G		CTAGGACT GTGCG AG		

			GATCCTGA	TATGT TC		
			AACGCAT	G		
GAM640	ITGAL	3'	CTCCCCTGCACTGGAGTCC	7971	ATAC	A__
			GGACTCCA	GTGCG GAG		
			CCTGAGGT	CACGT CTC		
			_____	CCC		
GAM640	ITGB3	3'	CTCTCGCAAGGGAAGTCCT	5707	_ AATACG	
			AGGACT CC	TGCGAGAG		
			TCCTGA GG	ACGCTCTC		
			A GA_____			
GAM640	MYCL1	3'	TTTGATGATTATTGGAGCCCCA	11853	A A	__ G
	G		CT GG CTCCAATA	CGT CGAG		
			GA CC GAGGTTAT	GTA GTTT		
			C C	TA _		
GAM640	SIRT2	3'	CTCCCCAAACTGGGGTCCCAG	24958	A	ATACG C_
			CT GGACTCCA	TG GAG		
			GA CCTGGGGT	AC CTC		
			C	CAAA_ CC		
GAM640	TPD52L2	3'	CTCTCGCACACCGGGGCCCTG	9297	A	AATAC
			TAGG CTCC	GTGCGAGAG		
			GTCC GGGG	CACGCTCTC		
			C	CCA__		
GAM640	ZNF261	3'	TCTTGCATTGGAGGTCCCAG	11563	A	_ ATAC
			CT GGAC TCCA	GTGCGAGA		
			GA CCTG AGGT	TACGTTCT		
			C G	_____		
GAM640	C20orf103	5'	CTCGACACCGAGTCCTAG	14570	CAATAC	_
			CTAGGACTC	GTG CGAG		
			GATCCTGAG	CAC GCTC		
			C_____	A		
GAM640	MGC5242	3'	CTCTTGAGGCTCTGGAGTCC	23464	ATAC	G_
			GGACTCCA	GT CGAGAG		
			CCTGAGGT	CG GTTCTC		
			CT__	GA		
GAM640	SEMA3E	5'	TCTCGCACGCTGCCCTG	14809	ACTC	ATA
			TAGG	CA CGTGCAGAGA		
			GTCC	GT GCACGCTCT		
			CC__	C__		
GAM640	LOC112817	5'	CTCTTTAGTATTGGGATCCCAG	28781	A CT	GTGC
			CT GGA CCAATAC	GAGAG		

			GA CCT GGTTATG TTCTC		
			C AG AT__		
GAM640	LOC147353	3'	CTCCGTGGTGTAAATGAAGTCCC 40834	A	C __ G A
		AG	CT GGACT CA ATAC TGCG GAG		
			GA CCTGA GT TGTG GTGC CTC		
			C A AA _ _		
GAM640	LOC63923	3'	TGCACTATTGGAGCCCTGG 33325	A	C
			CTAGG CTCCAATA GTGCG		
			GGTCC GAGGTTAT CACGT		
			C _		
GAM640	LOC91301	5'	CGTCTGTGTATTGGAGGCC 32647	A_	T__
			GG CTCCAATACG GCG		
			CC GAGGTTATGT TGC		
			CG GTC		
GAM641	PKDREJ	3'	ATCTGGGGAGACAGCAGGATCA 12714	C	CGCCG GA
		CA	TG GATCCTGC CC AGAT		
			AC CTAGGACG GG TCTA		
			A ACAGA GG		
GAM641	CLIC5	5'	GGCAGCGGCAGGAGCGCA 18847	A	C
			TGCG TCCTGCCGC GCC		
			ACGC AGGACGGCG CGG		
			G A		
GAM641	FLJ23360	5'	ATCCCCGGCGGCGGCGGCGG 23334	AT _	AA
		G	CG CC TGCCGCCCG GAT		
			GC GG GCGGCGGCGGC CTA		
			GG C CC		
GAM641	RTP801	5'	TTCAAGCGGCAGGACGCA 21141	A	CGCC
			TGCG TCCTGCCGC GAA		
			ACGC AGGACGGCG CTT		
			_ AA__		
GAM642	ATP7B	3'	ACATTTCCGCTGTCCGTCA 5502	A	CC_
			TGGCGGACA CGG TGT		
			ACTGCCTGT GCC ACA		
			C TTT		
GAM642	B3GAT1	5'	GCGTAGGGGCCGTTGCCCGC 20718	A	GTTC
			GCGG CAACGGCCT ACGC		
			CGCC GTTGCCGGG TGCG		
			C GA__		
GAM642	B3GAT1	5'	GCGTAGGGGCCGTTGCCCGC 27630	A	GTTC
			GCGG CAACGGCCT ACGC		

CGCC GTTGCCGGG TGCG
C GA__

GAM642 BRPF1 3' GCGTAAACAGGCCATCCCACC 36173 C ACAAC C_
A TGG GG GGCCTGTT ACGC
||| || ||||| |||
ACC CC CCGGACAA TGCG
A CTA__ AA

GAM642 EGFL3 3' ACAGGGCCACTGTCCTCCA 31373 C AC _
TGG GGACA GGCC TGT
||| |||| ||| |||
ACC CCTGT CCGG ACA
T CA G

GAM642 KIAA0513 5' CGTGAGCCACTGCCCCCA 16355 C A AC CTGT
TGG GG CA GGC TCACG
||| || ||| |||||
ACC CC GT CCG AGTGC
_ C CA ____

GAM642 LOC149478 5' GCGCCGGAAGAACCGTTGTCTG 38754 CCTG A_
CCA TGGCGGACAACGG TTC CGC
||||||| ||| |||
ACCGTCTGTTGCC AGG GCG
AAGA CC

GAM642 LOC203378 5' GCGTGAACAAGCCAGTCCCGCT 43554 _ AAC C
A TGGCGG AC GGC TGTTACGC
||||| || ||| |||||
ATCGCC TG CCG ACAAGTGCG
C A__ A

GAM642 LOC91179 5' GCAGCCACCGCTGTCCGCCA 32492 A C_
TGGCGGACA CGG CTGT
||||||| ||| |||
ACCGCCTGT GCC GACG
C ACC

GAM643 SMURF1 5' CCAGCAAGCGCCGATCTCC 44411 A G ____
GGAGATCG CGC TG GG
||||||| ||| |||
CCTCTAGC GCG AC CC
C A GA|||

GAM643 FLJ12443 3' GCGCGCACGCGGATCCC 24225 A GA G TC
GG GATC CGCGTG G CGC
|| |||| ||||| | |||
CC CTAG GCGCAC C GCG
_ _ G__

GAM643 KIAA0229 3' GACAGTGCATCGATGCTCC 44401 _ C TGG
GGAG ATCGA GCG GTC
||| ||||| ||| |||
CCTC TAGCT CGT CAG
G A GA__

GAM643 KIAA0674 5' GGACGACACCGATTTCC 30399 ACGC G_
GGAGATCG GTG GTCC
||||||| ||| |||

CCTTTAGC CAC CAGG
 _____ AG
 GAM643 KIAA0712 3' GCAGTTCACATCGATTTCC 16264 CGC GG CC
 GGAGATCGA GTG T GC
 ||||| ||| | ||
 CCTTTAGCT CAC G CG
 A__ TT A_
 GAM643 KIAA1229 3' GCCGCCAACAAAACGTCGATCA 31100 A CG_ _____ TCCG
 CC G GATCGACG TG GG C
 | ||||| || || |
 C CTAGCTGC AC CC G
 A AAA AAI|| GCCT
 GAM643 RNF10 5' GGCGGGGCTCGCGCAACCTCC 16963 ATCGAC _
 GGAG GCGTGGGTCC GCC
 ||| ||||| |||
 CCTC CGCGCTCGGG CGG
 CAA_____ G
 GAM643 SDCCAG43 3' GGTCCACGCGCCGTCTCC 34845 T A T
 GGAGA CG CGCGTGGG CC
 |||| || ||||| ||
 CCTCT GC GCGCACCT GG
 _ C _
 GAM643 SMOC2 5' GGCGCAGGACGCGGCCGATCTC 35835 A_ GGGTC
 C GGAGATCG CGCGT CGCC
 ||||| |||| |||
 CCTCTAGC GCGCA GCGG
 CG GGAC_
 GAM643 STAG2 5' GGCGATTGGCATCGATCTCT 34931 CGC G C
 GGAGATCGA GT GGTC GCC
 ||||| || ||| |||
 TCTCTAGCT CG TTAG CGG
 A__ G _
 GAM643 LOC253981 3' GCGAAGATGGTCTCGATCTCC 45865 C GTGG _
 GGAGATCGA GC GTC CGC
 ||||| || ||| |||
 CCTCTAGCT TG TAG GCG
 C G__ AA
 GAM644 ABCC1 3' AGAGTGAGCAACCAGCTGGA 11438 TG C A
 TC GT GGTT CTCACTCT
 || || ||| |||||
 AG CG CCAA GAGTGAGA
 GT A C
 GAM644 ABCC1 3' AGAGTGAGCAACCAGCTGGA 21282 TG C A
 TC GT GGTT CTCACTCT
 || || ||| |||||
 AG CG CCAA GAGTGAGA
 GT A C
 GAM644 ABCC1 3' AGAGTGAGCAACCAGCTGGA 21286 TG C A
 TC GT GGTT CTCACTCT
 || || ||| |||||

			AG CG CCAA GAGTGAGA		
			GT A C		
GAM644	ANKTM1	3'	AGAGTGAGGAAGAAGCAGAATG 14255	C G_ GGTTA	
	A		TCA TCTG TC CTCACTCT		
			AGT AGAC AG GAGTGAGA		
			A GA AAG__		
GAM644	WVOX	3'	AGAGCAGTCACAACAGAGTGA 18503	GTCG T CA	
			TCACTCTG GT ACT CTCT		
			AGTGAGAC CA TGA GAGA		
			AA__ C C_		
GAM644	DKFZp762E1511	3'	GAGTGAGTCCCCCAGA 29935	TC TT	
			TCTGG GG ACTCACTC		
			AGACC CC TGAGTGAG		
			C_ _		
GAM644	KIAA0534	3'	TGAAAACTGACCAAATGA 35388	CTC AC	
			TCA TGGTCGGTT TCA		
			AGT ACCAGTCAA AGT		
			AA_ A_		
GAM644	KIAA1580	5'	AGAATGAAATAAACAGAGT 34405	CG AC C	
			ACTCTGGT GTT TCA TCT		
			TGAGACCA TAA AGT AGA		
			AA _ A		
GAM644	RAI17	3'	GGTGACACCCAACCAAAGTGA 43863	C C TTACT	
			TCACT TGGT GG CACT		
			AGTGA ACCA CC GTGG		
			A A CACAT		
GAM644	SBB126	3'	AGTAAGCCAGAGTGA 20831	CGG	
			TCACTCTGGT TTACT		
			AGTGAGACCG AATGA		
			—		
GAM644	LOC220018	5'	AGGAGTTTGACCAGATGA 44853	C TT A	
			TCA TCTGGTCGG ACTC CT		
			AGT AGACCAGTT TGAG GA		
			— — —		
GAM644	LOC254251	3'	GAGTAATTGTCAAGTGA 45897	C T	
			TCACT TGG CGGTTACTC		
			AGTGA ACT GTTAATGAG		
			— —		
GAM644	LOC57086	5'	AGTGAATTACCCAGAGTG 21616	TC TAC	
			CACTCTGG GGT TCACT		

			GTGAGACC TTA AGTGA		
			CA ____		
GAM645	ZNF2	3'	ACCAACCATATGAAGTAGGC 22065	G__ C	
			GC TTTCA ATGGTTGGT		
			CG GAAGT TACCAACCA		
			GAT A		
GAM646	ABH	3'	CAGCACCCAGACAAGCCA 30054	TG AGC A	
			TGGCTTGT CTG GGT CTG		
			ACCGAACA GAC CCA GAC		
			____ C		
GAM646	OSR1	3'	AGAACCCAGCAACAAACC 11586	C AGC A	
			GG TTGTTGCTG GGT CT		
			CC AACAACGAC CCA GA		
			A ____ A		
GAM646	KIAA0408	3'	CAGCCTCAGCAACAAACA 16231	GC CGGTA	
			TG TTGTTGCTGAG CTG		
			AC AACAACGACTC GAC		
			A ____ C____		
GAM646	PA26	3'	ACAGCTCAGCAACAACCA 15805	C G	
			TGG TTGTTGCTGAGC GT		
			ACC AACAACGACTCG CA		
			____ A		
GAM646	RENT2	3'	CAACACCGGAACAAGCC 17802	G TGAG AC	
			GGCTTGTT C CGGT TG		
			CCGAACAA G GCCA AC		
			____ CA		
GAM646	RENT2	3'	CAACACCGGAACAAGCC 27908	G TGAG AC	
			GGCTTGTT C CGGT TG		
			CCGAACAA G GCCA AC		
			____ CA		
GAM646	TGOLN2	3'	TCAAAGACTTCAGCAGCAAACC 32027	C GC AC_	
	A		TGG TTGTTGCTGA GGT TGA		
			ACC AACGACGACT TCA ACT		
			A ____ GAA		
GAM646	LOC152245	3'	CAGCATAGCAGCCACAAGCCA 41449	T AGCG A	
			TGGCTTGT GCTG GT CTG		
			ACCGAACA CGAC TA GAC		
			C GA__ C		
GAM646	LOC200933	3'	TCAATATTTAACAACAAGCCA 43364	C GCG C	
			TGGCTTGTTG TGA GTA TGA		

			ACCGAACAACTT TAT ACT	
			A _ A	
GAM647	PIK3R2	3'	TCCATGTTGGGGGTCCTAA 11466	T ATGG
			TTAG GA TTCAACATGGA	
			AATC CT GGGTTGTACCT	
			_ GG_	
GAM647	PTPRC	3'	CCATGTAAATCCCATTTCAT 8718	TTC_
			GTGAATGG AACATGG	
			TACTTACC TTGTACC	
			CTAAA	
GAM647	PTPRC	3'	CCATGTAAATCCCATTTCAT 28144	TTC_
			GTGAATGG AACATGG	
			TACTTACC TTGTACC	
			CTAAA	
GAM647	TAF5	3'	TTCCATGTTCTACTTCAGCTAA 29134	GAAT TC
			TTAGT GGT AACATGGAA	
			AATCG TCA TTGTACCTT	
			ACT_ TC	
GAM647	TAF5	3'	TTCCATGTTCTACTTCAGCTAA 13837	GAAT TC
			TTAGT GGT AACATGGAA	
			AATCG TCA TTGTACCTT	
			ACT_ TC	
GAM647	C1QR1	3'	TCCATATATTCACTAA 14337	GTTCAAC
			TTAGTGAATG ATGGA	
			AATCACTTAT TACCT	
			A _	
GAM647	COP9	3'	TTTCCATACTAAACCAGTTTGT 13536	TG _ CAAC
	TAA		TTAG AA TGGTT ATGGAAA	
			AATT TT ACCAA TACCTTT	
			GT G ATCA	
GAM647	KIAA0061	3'	TTTCCATGCCGAACAACACTCA 33894	ATG AA
			TGA GTTC CATGGAAA	
			ACT CAAG GTACCTTT	
			CAA CC	
GAM647	NAG73	5'	CCATCAGCCATTACTAA 26301	CAAC
			TTAGTGAATGGTT ATGG	
			AATCATTTACCGA TACC	
			C_	
GAM647	P450RAI-2	3'	CCATATTTATTCACTGA 21266	TTCAAC
			TTAGTGAATGG ATGG	

			AGTCACTTATT	TACC	
			TA_____		
GAM647	LOC123242	5'	TTTCCATGTCACAGCTCCAC	37249	AAT CA_
			GTG GGTT ACATGGAAA		
			CAC TCGA TGTACCTTT		
			C_ CAC		
GAM647	LOC253001	5'	TTTCCATGTCACAGCTCCAC	46063	AAT CA_
			GTG GGTT ACATGGAAA		
			CAC TCGA TGTACCTTT		
			C_ CAC		
GAM648	CYP19	3'	CGTATCCATAAAGACCCG	5561	CCC
			CGGGTTT ATGGATACG		
			GCCCAGA TACCTATGC		
			AA_		
GAM648	CYP19	3'	CGTATCCATAAAGACCCG	25271	CCC
			CGGGTTT ATGGATACG		
			GCCCAGA TACCTATGC		
			AA_		
GAM648	HTR4	3'	CCAGTGCAGGAACCCGGTG	6541	C_ _
			CACCGGGTTTC CA TGG		
			GTGGCCCAAGG GT ACC		
			AC G		
GAM648	JRK	5'	CGTGTGGAGTGAGAAACCCG	41835	C GG_
			CGGGTTTC CAT ATACG		
			GCCCAAAG GTG TGTGC		
			A AGG		
GAM648	KLRG1	3'	CGTAATGCAAAAACCCGGT	12392	CC_ GGA
			ACCGGGTTT CAT TACG		
			TGGCCCAA GTA ATGC		
			AAC _		
GAM648	ERp44	3'	TATCAGGAAGCCCAGTG	39725	C CATG
			CAC GGGTTTCC GATA		
			GTG CCCGAAGG CTAT		
			A A_		
GAM648	FLJ10546	3'	G TTCAGGAAACTCAGTG	29914	C CA
			CAC GGGTTTCC TGGAT		
			GTG CTCAAAGG ACTTG		
			A _		
GAM648	FLJ21438	3'	GTCTGAAAAACCTGGTG	30847	CC TG
			CACCGGGTTT CA GAT		

GTGGTCCAAA GT CTG
AA _
GAM648 KIAA1115 5' GTTCCCAGAAACCCAGTG 17228 C CCA AT
CAC GGGTTTC TGG AC
||| ||||| ||| ||
GTG CCCAAAG ACC TG
A _ CT
GAM648 SMARCF1 3' GTGACCGAAAGAACCCGGTG 20522 CCCA A
CACCGGGTTT TGG TAC
||||||| ||| |||
GTGGCCCAAG GCC GTG
AAA_ A
GAM648 LOC90297 5' TCCAGGAAACCCGCTG 31131 C CA
CA CGGGTTTCC TGGA
|| ||||| |||
GT GCCCAAAGG ACCT
C _
GAM648 LOC90785 3' CGTG TAGGAAACCCAGTG 32007 C _
CAC GGGTTTCC CATG
||| ||||| |||
GTG CCCAAAGG GTGC
A AT
GAM649 FOXE3 3' CTTCATCAACCTTCTCTCA 14470 ACCAA AA
TGAGAGAAG TTGA AAG
||||||| ||| |||
ACTCTCTTC AACT TTC
C_ AC
GAM649 LRP8 3' CTTCTTCAATTTCTTTCA 11008 GACCA A
TGAGAGAA ATTGAA AAG
||||||| ||||| |||
ACTTTCTT TAACTT TTC
_ C
GAM649 LRP8 3' CTTCTTCAATTTCTTTCA 27132 GACCA A
TGAGAGAA ATTGAA AAG
||||||| ||||| |||
ACTTTCTT TAACTT TTC
_ C
GAM649 Nrap 3' ACTCCTTTCTTAGTCTTCTTCC 29235 AG CAATT A_
A TG AGAAGAC GAAA AGT
|| ||||| ||| |||
AC TCTTCTG CTTT TCA
CT ATT_ CC
GAM649 TRPS1 3' TCAATTTAGTCTTCTCTCA 15359 C_
TGAGAGAAGAC AATTGA
||||||| |||||
ACTCTCTTCTG TAACT
AT
GAM649 WT1 3' TTCAGTTGATCTTCTTCA 23669 G C
TGA AGAAGA CAATTGAA
||| ||||| |||||

			ACT TCTTCT GTTGA		
			— A		
GAM649	WT1	3'	TTCAGTTGATCTTCTTCA	23673	G C
			TGA AGAAGA CAATTGAA		
			ACT TCTTCT GTTGA		
			— A		
GAM649	WT1	3'	TTCAGTTGATCTTCTTCA	23677	G C
			TGA AGAAGA CAATTGAA		
			ACT TCTTCT GTTGA		
			— A		
GAM649	WT1	3'	TTCAGTTGATCTTCTTCA	5953	G C
			TGA AGAAGA CAATTGAA		
			ACT TCTTCT GTTGA		
			— A		
GAM649	CLIC5	3'	ACTTTTAAAAAGGCCTTCTCTC	18844	A AA GA
	A		TGAGAGAAG CC TT AAAAGT		
			ACTCTCTTC GG AA TTTTCA		
			C AA A_		
GAM649	DAMS	3'	CTTTTCTCCCTTCCTCA	22543	A ACCAATT
			TGAG GAAG GAAAAAG		
			ACTC CTTC CTTTTTC		
			— CCT_____		
GAM649	DRIL2	3'	TCAACTGCGTCTTCTCTCA	13191	_ A
			TGAGAGAAGAC CA TTGA		
			ACTCTCTTCTG GT AACT		
			C C		
GAM649	FLJ13102	3'	TTCGAGGTTTCTCTCA	24346	A AA
			TGAGAGA GACC TTGAA		
			ACTCTCT TTGG AGCTT		
			— —		
GAM649	FLJ20033	3'	TTCAGGTGGTCTTCTACCA	19127	AG A
			TG AGAAGACCA TTGAA		
			AC TCTTCTGGT GACTT		
			CA G		
GAM649	FLJ23441	5'	ACTTTTCAACTTGAACCTTC	23987	AC_ _
			GAAG CAA TTGAAAAAGT		
			CTTC GTT AACTTTTCA		
			CAA C		
GAM649	KIAA1735	3'	CTTGTCAGTTTTCTCTCA	42344	CAAT AA
			TGAGAGAAGAC TGA AAG		

			ACTCTCTTTTG	ACT	TTC	
			_____G_			
GAM649	MGC2452	3'	CTTTT	AGACCTTCTTCA	26368	ACCAATTG
			TGAGAGAAG	AAAAAG		
			ACTTTCTTC	TTTTTC		
			CAGA_____			
GAM649	LOC150225	3'	ACTTTGTGATGGGCTTCTCTCA	41186		A A GAA
			TGAGAGAAG	CC ATT AAAGT		
			ACTCTCTTC	GG TAG TTTCA		
			G TG			
GAM649	LOC157627	3'	TTTAGTATCTTCTCTC	39622		CCA
			GAGAGAAGA	ATTGAA		
			CTCTCTTCT	TGATTT		
			A_			
GAM649	LOC196264	3'	ACTTCTCCTTTGTATTCTCTCA	42330		GAC TT AA
			TGAGAGAA	CAA GA AAGT		
			ACTCTCTT	GTT CT TTCA		
			AT_ TC C_			
GAM649	LOC253832	3'	TTTCATGGTATAGTCTTTC	45499		AG_ AT
			GAGAGA	ACCA TGAAA		
			CTTTCT	TGGT ACTTT		
			GATA _			
GAM649	LOC255082	5'	ACTTCCGGGTTGGCCTTCTCCA	46116		A A GAAA
			TG GAGAAG	CCAATT AAGT		
			AC CTCTTC	GGTTGG TTCA		
			_ C GCC_			
GAM650	CHAC	3'	AATAAGTATCCTACTCAAA	27138		A A
			TTT AGTA	GATACTTATT		
			AAA TCAT	CTATGAATAA		
			C C			
GAM650	HTEX4	5'	AATAAGTATCTTTGGGAAATCT	44212		_ AAGT
	TT		AAAG TTT	AAGATACTTATT		
			TTTC AAA	TTCTATGAATAA		
			T GGGT			
GAM650	HTEX4	5'	AATAAGTATCTTTGGGAAATCT	46648		_ AAGT
	TT		AAAG TTT	AAGATACTTATT		
			TTTC AAA	TTCTATGAATAA		
			T GGGT			
GAM650	HTEX4	5'	AATAAGTATCTTTGGGAAATCT	46717		_ AAGT
	TT		AAAG TTT	AAGATACTTATT		

TTTC AAA TTCTATGAATAA
 T GGGT
 GAM650 KIAA1357 3' AAGTAGAAGCTTAACTT 35627 AAGA
 AAGTTTAAGT TACTT
 ||||| ||||
 TTCAAATTCG ATGAA
 AAG_
 GAM651 DKFZP434I092 3' GCAAATACTTCAGTGCCTGCTA 33674 A A TA
 TGGCA GCAT GA AGTATTTGC
 |||| ||| || |||||
 ATCGT CGTG CT TCATAAACG
 C A _
 GAM651 KIAA0556 3' GCAAATACTTCATGAGCTTAGC 34252 _ A GAT
 GC AAGC TA AAGTATTTGC
 || ||| || |||||
 CG TTCG GT TTCATAAACG
 A A AC_
 GAM651 LIG-1 3' GCAAGTGCCATCCACACTTGC 31951 CATA AA
 GCAAG GAT GTATTTGC
 |||| || |||||
 CGTTC CTA CGTGAACG
 ACAC C_
 GAM651 LOC164382 3' ACTTCCACCTACAGCTTGCCA 42163 A_ AT_
 TGGCAAGC TAG AAGT
 ||||| || |||
 ACCGTTTCG ATC TTCA
 AC CACC
 GAM652 ADAM29 5' ACTCGTCAATACTCCTGTGATC 42261 AAT GTAA
 GATCACAG GTG ACGAGT
 ||||| || |||||
 CTAGTGTC CAT TGCTCA
 CT_ AAC_
 GAM652 NEDD4 3' ACTCATTGGATGATTCTGTGA 34691 GTGG C
 TCACAGAAT TAAA GAGT
 ||||| ||| |||
 AGTGTCTTA GTTT CTCA
 GTAG A
 GAM652 E2F6 3' ACTCATTTACCACTCTGTG 7675 AT C
 CACAGA GTGGTAAA GAGT
 |||| ||||| |||
 GTGTCT CACCATT CTCA
 _ A
 GAM652 ENDOGLYX1 3' ACTCTTCACCACACCCTGTATT 24102 TC AA A C
 C GA ACAG TGTGGT AA GAGT
 || ||| ||||| || |||
 CT TGTC ACACCA TT CTCA
 TA CC C _
 GAM652 FLJ22795 3' ACTCGCCTCTGCTCCTGTGGTC 24687 AAT TG TAAA
 GATCACAG G G CGAGT
 ||||| | | ||||

		CTGGTGTC C C GCTCA		
		CT_ GT TCC_		
GAM652	MGC22014 3'	ACCCGTTTACCGTGCTATAATC 32215	CAC AATG	A
		GAT AG TGGTAAACG GT		
		CTA TC GCCATTTGC CA		
		ATA GT_ C		
GAM652	LOC145717 3'	ACTCGCCTCTGCTCCTGTGGTC 33188	AAT TG TAAA	
		GATCACAG G G CGAGT		
		CTGGTGTC C C GCTCA		
		CT_ GT TCC_		
GAM652	LOC145725 5'	ACTCGCCTCTGCTCCTGTGGTC 37945	AAT TG TAAA	
		GATCACAG G G CGAGT		
		CTGGTGTC C C GCTCA		
		CT_ GT TCC_		
GAM652	LOC145732 5'	ACTCGCCTCTGCTCCTGTGGTC 37954	AAT TG TAAA	
		GATCACAG G G CGAGT		
		CTGGTGTC C C GCTCA		
		CT_ GT TCC_		
GAM652	LOC149076 3'	ACTCATCTATATATTCTGTATC 38636	C	GTAAAC
		GAT ACAGAATGTG GAGT		
		CTA TGTCTTATAT CTCA		
		_ ATCTA_		
GAM652	LOC196326 5'	ACCCGTGGAGCGCACATTCTG 43576	_ AA_ A	
		CAGAATGTG GT ACG GT		
		GTCTTACAC CG TGC CA		
		G AGG C		
GAM652	LOC196957 5'	ACTCGCCTCTGCTCCTGTGGTC 42427	AAT TG TAAA	
		GATCACAG G G CGAGT		
		CTGGTGTC C C GCTCA		
		CT_ GT TCC_		
GAM652	LOC196961 5'	ACTCGCCTCTGCTCCTGTGGTC 42436	AAT TG TAAA	
		GATCACAG G G CGAGT		
		CTGGTGTC C C GCTCA		
		CT_ GT TCC_		
GAM652	LOC197138 5'	ACTCGCCTCTGCTCCTGTGGTC 42454	AAT TG TAAA	
		GATCACAG G G CGAGT		
		CTGGTGTC C C GCTCA		
		CT_ GT TCC_		
GAM652	LOC220537 3'	ACTCGCCTCTGCTCCTGTGGTC 43620	AAT TG TAAA	
		GATCACAG G G CGAGT		

			CTGGTGTC C C GCTCA		
			CT_GT TCC_		
GAM652	LOC245727	5'	ACTCGCCTCTGCTCCTGTGGTC 43795	AAT TG TAAA	
			GATCACAG G G CGAGT		
			CTGGTGTC C C GCTCA		
			CT_GT TCC_		
GAM653	TRPV1	3'	AAACTACAGAACCACATCCCA 20809	CA GCCAATC	
			TGGGATG GGT AGTTT		
			ACCCTAC CCA TCAAA		
			A_ AGACA_		
GAM653	TRPV1	3'	AAACTACAGAACCACATCCCA 27989	CA GCCAATC	
			TGGGATG GGT AGTTT		
			ACCCTAC CCA TCAAA		
			A_ AGACA_		
GAM653	TRPV1	3'	AAACTACAGAACCACATCCCA 27997	CA GCCAATC	
			TGGGATG GGT AGTTT		
			ACCCTAC CCA TCAAA		
			A_ AGACA_		
GAM653	TRPV1	3'	AAACTACAGAACCACATCCCA 28005	CA GCCAATC	
			TGGGATG GGT AGTTT		
			ACCCTAC CCA TCAAA		
			A_ AGACA_		
GAM653	KIAA1557	3'	AACTGATCATGGCTTCCCA 30638	T AG CCA	
			TGGGA GC GTG ATCAGTT		
			ACCCT CG TAC TAGTCAA		
			T G_ _		
GAM653	LOC255147	3'	AAACCAATTGAAAGCGTCCCA 45802	AGGTGC CA	
			TGGGATGC CAAT GTTT		
			ACCCTGCG GTTA CAAA		
			AAA_ AC		
GAM654	CEP2	3'	AATACTCCTTCTTCCTTCA 13649	CAAT C A	
			TGAAGGAAG AG AG TATT		
			ACTTCCTTC TC TC ATAA		
			T_ C _		
GAM654	DKFZP564I052	3'	CTGTGGCATTGCTTCCTT 33138	A_	
			AAGGAAGCAAT GCAG		
			TTCCTTCGTTA TGTC		
			CGG		
GAM654	GMEB2	5'	CTGCCTTGCTTCCTCCA 14741	A TA	
			TG AGGAAGCAA GCAG		

			AC TCCTTCGTT CGTC			
			C C_			
GAM654	KIAA1024	3'	AATATCTGCCATTTTC 34232	GC	A	
			GAA AAT GCAGATATT			
			CTT TTA CGTCTATAA			
			_ C			
GAM654	MGC27434	3'	AATATCTGCTCCTTCC 29681	CAAT		
			GGAAG AGCAGATATT			
			CCTTC TCGTCTATAA			
			C_			
GAM654	TLK2	3'	TTGCAATTGCTTCCCTCA 38276	A	A	
			TGA GGAAGCAAT GCAG			
			ACT CCTTCGTTA CGTT			
			C A			
GAM654	TLK2	3'	TTGCAATTGCTTCCCTCA 13722	A	A	
			TGA GGAAGCAAT GCAG			
			ACT CCTTCGTTA CGTT			
			C A			
GAM654	LOC130951	3'	CTTCCTGTTGCTCCCTCCA 29026	A	A	C_
			TG AGG AGCAATAG AG			
			AC TCC TCGTTGTC TC			
			C C CT			
GAM654	LOC151584	3'	TATGTGCTACCCTTCCTTCA 41377	CAA	G	
			TGAAGGAAG TAGCA ATA			
			ACTTCCTTC ATCGT TAT			
			CC_ G			
GAM654	LOC221410	3'	TTGCTATTACTTCTTTCA 44196	C		
			TGAAGGAAG AATAGCAG			
			ACTTTCTTC TTATCGTT			
			A			
GAM654	LOC257249	5'	TAATATCTGACTGGCCTCC 45904	A	AA	_
			GGA GC TAG CAGATATTA			
			CCT CG GTC GTCTATAAT			
			C _ A			
GAM655	ADRA2A	3'	ACAGGGAAAAGATTTCTGTCCA 6335	AC	TTA	CT
			TG CAGA CTTT TCCCTGT			
			AC GTCT GAAA AGGGACA			
			CT TTA _			
GAM655	AGL	3'	ACAGTTGTGACAGTAATCTG 6296	T	TTCC	
			CAGATTACT TC CTGT			

			GTCTAATGA AG GACA		
			C TGTT		
GAM655	AGL	3'	ACAGTTGTGACAGTAATCTG 6303	T	TTCC
			CAGATTACT TC CTGT		
			GTCTAATGA AG GACA		
			C TGTT		
GAM655	AGL	3'	ACAGTTGTGACAGTAATCTG 5464	T	TTCC
			CAGATTACT TC CTGT		
			GTCTAATGA AG GACA		
			C TGTT		
GAM655	AGL	3'	ACAGTTGTGACAGTAATCTG 6281	T	TTCC
			CAGATTACT TC CTGT		
			GTCTAATGA AG GACA		
			C TGTT		
GAM655	AGL	3'	ACAGTTGTGACAGTAATCTG 6286	T	TTCC
			CAGATTACT TC CTGT		
			GTCTAATGA AG GACA		
			C TGTT		
GAM655	AGL	3'	ACAGTTGTGACAGTAATCTG 6291	T	TTCC
			CAGATTACT TC CTGT		
			GTCTAATGA AG GACA		
			C TGTT		
GAM655	EGFR	3'	ACAAGGAAGAAGCTTGCTGGT 11720	ATTAC	C
			ACCAG TTTCTTCC TGT		
			TGGTC GAAGAAGG ACA		
			GTTC_ A		
GAM655	MAPK4	3'	ACAGCTGAGGAAAGCAATT 8620	A	C_
			GATT CTTTCTTC CTGT		
			TTAA GAAAGGAG GACA		
			C TC		
GAM655	MBNL CA	3'	ACAAAGAAGAAAGCAGCACTGT 22022	C ATTA_	CC
			TGAC AG CTTTCTTC TGT		
			ACTG TC GAAAGAAG ACA		
			_ ACGAC AA		
GAM655	TNFSF8 C	3'	ACAGAGAAGTGGGGAATCCAGT 6914	CA A TT	C
			GAC GATT CT CTTC CTGT		
			CTG CTAA GG GAAG GACA		
			AC G GT A		
GAM655	XCL1	3'	AGGGAGAAAATAATCCAGTC 8886	CA C	T
			GAC GATTA TTTCT CCCT		

			CTG CTAAT AAAGA GGA		
			AC A _		
GAM655	FLJ12056	3'	ACAGGGAAGAAAGTGAAGGT	24468	AGA
			ACC TTACTTTCTTCCCTGT		
			TGG AGTGAAAGAAGGGACA		
			A__		
GAM655	HTMP10	3'	CAGGGAAGCACCTGGCTCA	27047	_ ATTACTTT
			TGA CCAG CTTCCCTG		
			ACT GGTC GAAGGGAC		
			C CAC_____		
GAM655	KIAA0125	5'	ACAGGGAAGAAACTCCTCCGGT	16687	A TTAC
	C		GACC GA TTTCTTCCCTGT		
			CTGG CT AAAGAAGGGACA		
			C CCTC		
GAM655	KIAA0232	3'	ACAGAAAAGAAAGTACCATC	36033	_ CC
			GAT TACTTTCTT CTGT		
			CTA ATGAAAGAA GACA		
			CC AA		
GAM655	KIAA0774	5'	CAAGGAAGAGAATCTGTCA	44088	C TAC C
			TGAC AGAT TTTCTTCC TG		
			ACTG TCTA AGAGAAGG AC		
			_ _ A		
GAM655	KIAA0847	3'	AAGAAAGTAACATGATCA	38045	C GA
			TGA CA TTACTTTCTT		
			ACT GT AATGAAAGAA		
			A AC		
GAM655	SEN7	3'	ACAGAGAAGAAAATAACTTG	21822	A C C
			CAG TTA TTTCTTC CTGT		
			GTT AAT AAAGAAG GACA		
			C A A		
GAM655	LOC158886	5'	ACAAGGAAGAAAAACCTG	40311	A AC C
			CAG TT TTTCTTCC TGT		
			GTC AA AAAGAAGG ACA		
			C _ A		
GAM656	CAPN2	3'	AACAGTCCAAGATTACCATTT	7484	CACA__
			GAATGGTG GACTGTT		
			TTTACCAT CTGACAA		
			TAGAAC		
GAM656	DLST	3'	TGGCTGTGCACATTCTC	7645	G A
			GAGAATG TGCACAG CTG		

CTCTTAC ACGTGTC GGT

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      - -
GAM656 KLHL3  3' CAGGGTGTGCACCCTCTC  42267  AT   GA
      GAGA GGTGCACA CTG
      ||| ||||| ||
      CTCT CCACGTGT GAC
      C_   GG
GAM656 LANCL1 3' TAACAGTCTGTGTTTTCTC  12696  TGGT
      GAGAA GCACAGACTGTTA
      ||| |||||
      CTCTT TGTGTCTGACAAT
      T___
GAM656 MEST   3' TAACAGTCTGAGACTCCTC  34639  AAT  GCA
      GAG GGT CAGACTGTTA
      || || |||||
      CTC TCA GTCTGACAAT
      C_   GA_
GAM656 MYO10  3' TAACAGTCTGCACAGTTTC  14732  ATG   CA
      GAGA GTGCA GACTGTTA
      ||| ||| |||||
      CTTT CACGT CTGACAAT
      GA_   _
GAM656 PIGR   3' CAGGTTGACACCATTCTC  35937  CA   A
      GAGAATGGTG CAG CTG
      ||||| ||| ||
      CTCTTACCAC GTT GAC
      A_   G
GAM656 PSCD4  3' AGTCATGCCCATCTC  15035  T   CA
      GAGAATGG GCA GACT
      ||||| || |||
      CTCTTACC CGT CTGA
      _   A_
GAM656 SLC16A2 3' TAACAGTCTGCTCCCCTC  13271  AAT T  CA
      GAG GG GCA GACTGTTA
      || || || |||||
      CTC CC CGT CTGACAAT
      C_   T   _
GAM656 STCH   3' GTCCTGTACATCATTCTC  13835  C   _
      GAGAATGGTG ACAG AC
      ||||| ||| ||
      CTCTTACTAC TGTC TG
      A   C
GAM656 SULT1C1 3' TAACAGTATGTCACCACTTC  6722  _   C  G
      GAA TGGTG ACA ACTGTTA
      || ||| || |||||
      CTT ACCAC TGT TGACAAT
      C   _   A
GAM656 TPK1   3' TAACAGTCTGCATCATCATC  22781  GA   CA
      GA ATGGTGCA GACTGTTA
      || ||||| |||||
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CT TACTACGT CTGACAAT
 AC ____
 GAM656 YWHAE 3' AACAAATCCGTGGCTGCTCATTC 13612 _ _ _ A C
 TT GAGAATG GT GC AC GA TGTT
 ||||| || || || ||
 TTCTTAC CG CG TG CT ACAA
 T T G C A
 GAM656 ZNF144 3' AGCTCTGCACCATCCTC 13989 A C A
 GAG ATGGTGCA AG CT
 || ||||| || ||
 CTC TACCACGT TC GA
 C C _
 GAM656 APOL4 5' TAACAGTCAGTATCCAGCCTC 24977 AA _ ACA
 GAG TGG TGC GACTGTTA
 || || || |||||
 CTC ACC ATG CTGACAAT
 CG T A _
 GAM656 C20orf30 3' TAACAGTCCTTGGACCATTCT 15432 G CA
 AGAATGGT CA GACTGTTA
 ||||| || |||||
 TCTTACCA GT CTGACAAT
 G TC
 GAM656 FLJ12985 3' AACAGAGGTGAGCACCTTTC 24462 T A GA _
 GAA GGTGC CA CTGTT
 || |||| || ||||
 CTT CCACG GT GACAA
 T A GGA
 GAM656 KIAA0179 3' AACAGTCTGTTTTCTT 32364 TG GTGC
 GAGAA ACAGACTGTT
 |||| |||||
 TTCTT TGTCTGACAA
 T _ _ _
 GAM656 KIAA1877 3' ACGTTCACACCATTCTC 32878 CACA C
 GAGAATGGTG GA TGT
 ||||| || ||
 CTCTTACCAC CT GCA
 A _ T
 GAM656 PRO0767 5' TAACAGTCTTATTCTCATTCTT 15309 TGCAC
 GAGAATGG AGACTGTTA
 ||||| |||||
 TTCTTACT TCTGACAAT
 CTTAT
 GAM656 SPINLW1 3' AACAGTCCACGTGTTCTC 21665 _ CACA
 GAGAATG GTG GACTGTT
 ||||| || |||||
 CTCTTGT CAC CTGACAA
 G _ _ _
 GAM656 LOC138307 5' CAGGCTGCCGTGCACCATCCT 37122 A _ _ A
 AG ATGGTGAC AG CTG
 || ||||| || ||

		TC TACCACGTG TC GAC		
		C CCG G		
GAM656	LOC144182 3'	AACAGTCTTGGCCATTCTC 29166	_	G C
		GAGAA TGGT CA AGACTGTT		
		CTCTT ACCG GT TCTGACAA		
		T _ _		
GAM656	LOC149734 3'	TAAGTGTGTTGCATCATCCTC 41054	A	CAG T
		GAG ATGGTGCA AC GTTA		
		CTC TACTACGT TG CAAT		
		C TG_ T		
GAM656	LOC157983 3'	TAAGGGTTGACACCATTCTC 39687		CACA G
		GAGAATGGTG GACT TTA		
		CTCTTACCAC TTGG AAT		
		AG_ G		
GAM656	LOC158857 5'	AACAGTCTGCAAGATTC 42030	GG	CA
		GAAT TGCA GACTGTT		
		CTTA ACGT CTGACAA		
		GA _		
GAM656	LOC159049 5'	AACAGTCTGCAAGATTC 42056	GG	CA
		GAAT TGCA GACTGTT		
		CTTA ACGT CTGACAA		
		GA _		
GAM656	LOC168283 5'	TAACGGTGGTGCACCATCCT 40240	A	AG
		AG ATGGTGCACTGTTA		
		TC TACCACGTG TGGCAAT		
		C G_		
GAM656	LOC203289 3'	TAAGGGTTGACACCATTCTC 43029		CACA G
		GAGAATGGTG GACT TTA		
		CTCTTACCAC TTGG AAT		
		AG_ G		
GAM656	LOC203378 5'	AACAGTCTCACTTCATTCTT 43545		TGCAC
		GAGAATGG AGACTGTT		
		TTCTTACT TCTGACAA		
		TCAC_		
GAM656	LOC255624 3'	AACAGAGGTGAGCACCTTTC 45350	T	A GA_
		GAA GGTGC CA CTGTT		
		CTT CCACG GT GACAA		
		T A GGA		
GAM656	LOC256544 3'	TAAGGGTTGACACCATTCTC 46016		CACA G
		GAGAATGGTG GACT TTA		

			CTCTTACCAC	TTGG AAT		
			AG__ G			
GAM656	LOC91151	5'	CAATTTGAGCACCATTCTC	27052	A C	
			GAGAATGGTGC CAGA TG			
			CTCTTACCACG GTTT AC			
			A A			
GAM656	LOC92492	5'	TAACAGTCTGTGCTGTCCA	34454	T__	
			TGG GCACAGACTGTTA			
			ACC CGTGTCTGACAAT			
			TGT			
GAM656	LOC92573	5'	CACTCTGTACCCACCATTTC	34594	C__ C	
			GAATGGTG ACAGA TG			
			CTTACCAC TGTCT AC			
			CCA C			
GAM657	LANCL1	3'	CACTGAATTCGAATTTTCATTTTC	12694	A C GA	
			GAAAT AAAT GGAATTT TG			
			CTTTA TTTA CCTTAAG AC			
			C A TC			
GAM657	FAM8A1	3'	GCACTCACCTTCCGATTTTA	18381	TT _	
			TAAAATCGGAA TGA TGC			
			ATTTTAGCCTT ACT ACG			
			CC C			
GAM657	ORC6L	3'	GCATCTTACAGATTTTACTTCA	15620	A GGAATTT	
			TGAA TAAAATC GATGC			
			ACTT ATTTTAG CTACG			
			C ACATT__			
GAM657	STK38L	3'	GCATCAAATTCTTTGGGTATCT	34291	A AAATC	
	C		GA ATA GGAATTTGATGC			
			CT TAT TCTTAAACTACG			
			C GGGTT			
GAM657	ZER6	3'	CATCAAATTCTTATCTTTTC	31741	TAAA C	
			GAAA AT GGAATTTGATG			
			CTTT TA TCTTAAACTAC			
			TC__ T			
GAM657	ZFR	3'	CAGTAGTTCGATTTTTTC	18187	TA TGA	
			GAAA AAATCGGAATT TG			
			CTTT TTTAGCCTTGA AC			
			__ TG_			
GAM657	LOC152765	3'	GCACTGAGCTCCAATTTGTTC	39317	A C A GA	
	CA		TG AATAAAAT GGA TTT TGC			

			AC TTGTTTTTA CCT GAG ACG		
			C A C TC		
GAM657	LOC256401	5'	GCATCAAATGTACATTATTTCA 45946		AATCGGA
			TGAAATAA ATTTGATGC		
			ACTTTATT TAAACTACG		
			ACATG__		
GAM658	CMG2	3'	ACCAGCCTCCTCAGACAA 27716	G	CA
			TTGTT GAGGAGGC GT		
			AACAG CTCCTCCG CA		
			A AC		
GAM658	LOC91664	3'	CTGGCCCAACAAACTA 33214		AGGAG
			TAGTTTGTGG GCCAG		
			ATCAAACAACC CGGTC		

GAM659	ATP1B2	3'	ACTTGTCTGAGCCTCACATC 7389	A	AAGT
			GAT TGAGGCTCA GGT		
			CTA ACTCCGAGT TCA		
			C CTGT		
GAM659	DAB2	3'	ACCACATCCCTTCATATCA 7021		CTCAA
			TGATATGAGG GTGGT		
			ACTATACTTC CACCA		
			CCTA__		
GAM659	KCNAB2	3'	ACCAATGATGAGCCTCATGCCA 9704	A	AAG_
			TG TATGAGGCTCA TGGT		
			AC GTACTCCGAGT ACCA		
			C AGTA		
GAM659	MTA1L1	3'	GTTACCACCTCGAGACTTGTCT 11137	T TG G	AAA
	CA		TGA A AG CTC GTGGTAAC		
			ACT T TC GAG CACCATTG		
			C GT A CTC		
GAM659	NLGN1	3'	TACCACTCTGATTATA 17230	GGC	A
			TATGA TCA AGTGGTA		
			ATATT AGT TCACCAT		
			__ C		
GAM659	OGT	3'	ACCACTTGAGCCTATATCA 9660	G	A
			TGATAT AGGCTCAA GTGGT		
			ACTATA TCCGAGTT CACCA		
			__ __		
GAM659	TRPM6	3'	GCCTTCTGAGCCTCACATC 19203	A	AAGT
			GAT TGAGGCTCA GGT		

CTA ACTCCGAGT CCG
C CTT_

GAM659 VHL 3' GCCACCAGCCTCATTCCA 6162 AT CAAA
TG ATGAGGCT GTGGT
|| ||||| ||||
AC TACTCCGA CACCG
CT C_

GAM659 DKFZp434H2226 5' ATTATTTGGCCTCACATCA 34034 A CA
TGAT TGAGGCT AAGTGGT
|||| ||||| |||||
ACTA ACTCCGG TTTATTA
C _

GAM659 FLJ20758 5' ACTTTGAACCTCAGATCA 19654 A C
TGAT TGAGG TCAAAGT
|||| ||||| |||||
ACTA ACTCC AGTTTCA
G A

GAM659 KIAA0215 5' GTTACCACTCCGACCGGACTCA 16384 TATGA C AA
TGA GG TC AGTGGTAAC
||| ||| |||||
ACT CC AG TCACCATTG
CAGG_ _ CC

GAM659 LOC152317 5' CACTGAGCCTCATACCA 41465 A AA
TG TATGAGGCTCA GTG
|| ||||| |||
AC ATACTCCGAGT CAC
C _

GAM660 LOC92106 5' CCGTAGAATTTTCGCTTCACCGA 28755 ATAAT GGA
TCG AGCGAAAT TATGG
||| ||||| ||||
AGC TCGCTTTA ATGCC
CACT_ AG_

GAM661 TSG 3' ACTTAGTAAAATAATAGGTA 21810 CG _
TACC TTATTTTAC AAGT
|||| ||||| ||||
ATGG AATAAAATG TTCA
AT A

GAM661 ZNF214 5' ACACCCGTGTAGATGGGTA 14910 ATTT AA
TACCCGTT TAC GTGT
||||| ||| |||
ATGGGTAG GTG CACA
AT_ CC

GAM661 ALDH9 5' ACACTTGTAAGTGCTACG 6359 _
CGT TATTTTACAAGTGT
||| ||||| |||||
GCA GTGAAATGTTCA
TC

GAM661 LASP1 3' ACACTTGTAACCCACAGGTG 12790 C TATTT
TACC GT TACAAGTGT
|||| ||| |||||

GTGG CA ATG TTCACA
 A CCC__
 GAM661 LOC121504 3' A CACTTCCTAGATAACGG 36669 TAC
 CCGTTATTT AAGTGT
 ||||| ||||
 GGCAATAGA TTCACA
 TCC
 GAM661 LOC153937 5' A CACTTGTAAGTTCACAGGT 39444 C TAT
 ACC GT TTTACAAGTGT
 ||| || |||||
 TGG CA GAATG TTCACA
 A CTT
 GAM662 CALCR 3' GAGGGGAAAAAATTA ACTGCTC 7479 A A _ G
 CA TG AGTA TTAATTTTT CT CCTC
 || ||| ||||| || |||
 AC TCGT AATTAAAAA GG GGAG
 C C A _
 GAM662 LTA 3' AGGCAAAAAAATTA AATTATTT 6194 _ C
 AAGTAATT AATTTTT TGCCT
 ||||| ||||| ||||
 TTTATTAA TTAAAAA ACGGA
 A A
 GAM662 ZHX1 3' AGGAGAATCAATTCTTCA 14091 T A
 TGAAG AATT ATTTTTCT
 |||| ||| |||||
 ACTTC TTAA TAAGAGGA
 _ C
 GAM662 DKFZP434C1715 3' AGGCAGAAGGATCACTT 41672 AATTA
 AAGT ATTTTTCTGCCT
 |||| |||||
 TTCA TAGGAAGACGGA
 C__
 GAM662 FLJ23556 3' AGGCAGAAGGATCACTT 24318 AATTA
 AAGT ATTTTTCTGCCT
 |||| |||||
 TTCA TAGGAAGACGGA
 C__
 GAM662 IDN3 3' AGGCAGAAAACTTGAAATAC 28510 A_ _
 GTA TTAA TTTTCTGCCT
 || ||| |||||
 CAT AGTT AAAAAGACGGA
 AA C
 GAM662 KIAA1456 3' AGGCAGAAGGATCACTT 33262 AATTA
 AAGT ATTTTTCTGCCT
 |||| |||||
 TTCA TAGGAAGACGGA
 C__
 GAM662 NXPH3 3' AGACAGAAATGTTACTTC 32714 TAATT C
 GAAGTAAT TTTCTG CT
 ||||| ||||| ||

CTTCATTG AAAGAC GA
 T_____ A
 GAM662 PNPASE 3' GAGGCAGAAGAATCACTTCA 35103 AATTA
 TGAAGT ATTTTCTGCCT
 ||||| |||||
 ACTTCA TAAGAAGACGGAG
 C_____

GAM662 ZNF33A 3' AGGCAGAAGAATCACTT 43896 AATTA
 AAGT ATTTTCTGCCT
 ||| |||||
 TTCA TAAGAAGACGGA
 C_____

GAM662 LOC126282 3' AGGCAGGATAATCACTT 36816 A ATTT
 AAGT ATTA TTCTGCCT
 ||| ||| |||||
 TTCA TAAT AGGACGGA
 C _____

GAM662 LOC144583 3' AGGCAGGATAATCACTT 37767 A ATTT
 AAGT ATTA TTCTGCCT
 ||| ||| |||||
 TTCA TAAT AGGACGGA
 C _____

GAM662 LOC145231 3' AGGCAGGCGAATTACTTCA 40518 AATTTT
 TGAAGTAATT TCTGCCT
 ||||| |||||
 ACTTCATTAA GGACGGA
 GC_____

GAM662 LOC147837 3' AGGCAGGATAATCACTT 38392 A ATTT
 AAGT ATTA TTCTGCCT
 ||| ||| |||||
 TTCA TAAT AGGACGGA
 C _____

GAM662 LOC149910 3' GAGACAGAATCTTTAGTTACTT 38827 TTT C
 CA TGAAGTAATTAA TTCTG CTC
 ||||| |||||
 ACTTCATTGATT AAGAC GAG
 TCT A

GAM662 LOC158160 3' AGGCAGAAGGATCACTT 36168 AATTA
 AAGT ATTTTCTGCCT
 ||| |||||
 TTCA TAGGAAGACGGA
 C_____

GAM662 LOC158292 5' AGGCAGAAGAATCACTT 41932 AATTA
 AAGT ATTTTCTGCCT
 ||| |||||
 TTCA TAAGAAGACGGA
 C_____

GAM662 LOC162333 5' GAAGCAGAAGATACTACTTTA 42129 ATTAAT C
 TGAAGTA TTTTCTGC TC
 ||||| ||||| ||

			ATTCAT	AGAAGACG AG		
			CAT__	A		
GAM662	LOC202018	3'	GCTTTAAACTAATTACTTCA	42958	A	TCT
			TGAAGTAATTA TTTT	GC		
			ACTTCATTAAT AAAA	CG		
			C	TTT		
GAM662	LOC219392	5'	GCAGAGGGAACCAGCTTCA	43799	AATTAA	
			TGAAGT	TTTTCTGC		
			ACTTCG	AGGGAGACG		
			ACCA__			
GAM663	BCL7A	3'	ACGTGCTTTCCTATTCTCA	21985	TA	ATTA
			TGAGA AG	AAAGCACGT		
			ACTCT TC	TTTCGTGCA		
			TA C__			
GAM663	CLCN4	5'	GCGTTTTAACTTTATCTCA	7573	A	_
			TGAGATAAG TTAAAA	GC		
			ACTCTATTT AATTTT	CG		
			C	G		
GAM663	ZNF264	3'	GTGCAATTTTATCTCA	9458	AAAA	
			TGAGATAAGATT	GCAC		
			ACTCTATTTTAA	CGTG		

GAM663	DKFZP761F241	3'	ACGTGCTTAGCCTTTATTTCA	25474	ATTA	
			TGAGATAAG	AAGCACGT		
			ACTTTATTT	TTCGTGCA		
			CCGA_			
GAM663	FLJ10008	5'	ACGGCAGCATCTTATCTCA	19690	TAAAA	A
			TGAGATAAGAT	GC CGT		
			ACTCTATTCTA	CG GCA		
			CGA__	_		
GAM663	TSPAN-2	3'	ACATGCTTTTAAATGTCTCA	12279	AGA	C
			TGAGATA	TTAAAAGCA GT		
			ACTCTGT	AATTTTCGT CA		
			A__	A		
GAM663	ZDHC3	3'	ACGTACCTGTGTCTTATCT	18685	TAAA	C_
			AGATAAGAT	AG ACGT		
			TCTATTCTG	TC TGCA		
			TG__	CA		
GAM663	LOC205095	3'	ACATGCCACCTCTTATCTCA	43600	TTAAAA	C
			TGAGATAAGA	GCA GT		

			ACTCTATTCT	CGT CA		
			CCCACC	A		
GAM663	LOC221272	5'	CTTTTAAGGTATTATCTCA	44963	GA__	
			TGAGATAA	TTAAAAG		
			ACTCTATT	AATTTTC		
			ATGG			
GAM663	LOC92078	5'	ACGTGCTTTTATTATATCCA	33739	A A T	
			TG GATA GAT	AAAAGCACGT		
			AC CTAT TTA	TTTTTCGTGCA		
			_ A _			
GAM664	BCMP1	3'	GTGTTTGAATATAAATGAT	25458	AAT	
			ATCATTTATAT	GACAT		
			TAGTAAATATA	TTGTG		
			AGT			
GAM664	FLJ20294	3'	TCATTAAAATGATGACAT	19350	A ATA	
			ATG CATCATTT	TAATGA		
			TAC GTAGTAAA	ATTACT		
			A _			
GAM664	KIAA0446	5'	ATGTCTAATAAATGATGTC	34145	ATAAT	
			GACATCATTTAT	GACAT		
			CTGTAGTAAATA	CTGTA		
			AT__			
GAM664	STARD7	3'	ATGTCATTGTAATGATTTC	29258	C TTA	
			TGA ATCAT	TATAATGACAT		
			ACT TAGTA	ATGTTACTGTA		
			T _			
GAM664	STARD7	3'	ATGTCATTGTAATGATTTC	21354	C TTA	
			TGA ATCAT	TATAATGACAT		
			ACT TAGTA	ATGTTACTGTA		
			T _			
GAM664	STHM	3'	ATGTCACCAACAGGATGATGTC	13176	ATATAA	
	A		TGACATCATTT	TGACAT		
			ACTGTAGTAGG	ACTGTA		
			ACAACC			
GAM664	LOC122786	3'	ATGTCACTGAGTGAATGAT	36698	A A	
			ATCATTTAT TA	TGACAT		
			TAGTAAGTG GT	ACTGTA		
			A C			
GAM664	LOC158696	3'	TTGTTATATAAATGTCATCAT	39881	CAT TG	
			ATGA	CATTTATATAA A		

			TACT GTAAATATATT T		
			ACT GT		
GAM665	ATP11B	3'	ATTTTCAGGTTATGTCAT 39144	AT	
			ATGACATAGCCT GAGT		
			TACTGTATTGGA TTTA		
			CT		
GAM665	BCL2	3'	TATGACTCACATGATGTCAT 6260	A AGCCTA	
			ATG CAT TGAGTCATA		
			TAC GTA ACTCAGTAT		
			_ GTAC_		
GAM665	FBXL5	3'	GATACAGGCATATGTCAT 14461	_ AT A	
			ATGACATA GCCT G GTC		
			TACTGTAT CGGA C TAG		
			A _ A		
GAM665	FBXL5	3'	GATACAGGCATATGTCAT 27303	_ AT A	
			ATGACATA GCCT G GTC		
			TACTGTAT CGGA C TAG		
			A _ A		
GAM665	FGF5	3'	TATGACTCTCTGCTATCCCA 10776	AC CTAT	
			TG ATAGC GAGTCATA		
			AC TATCG CTCAGTAT		
			CC TCT_		
GAM665	FGF5	3'	TATGACTCTCTGCTATCCCA 27003	AC CTAT	
			TG ATAGC GAGTCATA		
			AC TATCG CTCAGTAT		
			CC TCT_		
GAM665	FNTB	3'	TATGACTCAGGATTTATTCA 7782	C CCTA	
			TGA ATAG TGAGTCATA		
			ACT TATT ACTCAGTAT		
			_ TAGG		
GAM665	GNAO1	3'	ATGACCAATCCTATGTCAT 43719	CCTA A	
			ATGACATAG TG GTCAT		
			TACTGTATC AC CAGTA		
			CTA_ _		
GAM665	IL1RN	3'	ATGACTCGTATATGTC 6177	GCC	
			GACATA TATGAGTCAT		
			CTGTAT ATGCTCAGTA		
			—		
GAM665	PPP1CB	3'	GATTGTAAGGCTTATGTCA 8560	_ ATG	
			TGACATA GCCT AGTC		

			ACTGTAT CGGA TTAG		
			T ATG		
GAM665	SELE	3'	TGTGATCAGGCTATGT 6052	ATGA	
			ACATAGCCT GTCATA		
			TGTATCGGA TAGTGT		
			C__		
GAM665	SIM1	3'	TATGGAAATATAGGCTATGT 11512	AG_	
			ACATAGCCTATG TCATA		
			TGTATCGGATAT GGTAT		
			AAA		
GAM665	VSX1	3'	ACTTGATAGGCTATGCAT 15955	A _	
			ATG CATAGCCTAT GAGT		
			TAC GTATCGGATA TTCA		
			_ G		
GAM665	ZNF264	3'	TATGATGGGGTTATGTCA 9459	ATGA	
			TGACATAGCCT GTCATA		
			ACTGTATTGGG TAGTAT		
			G__		
GAM665	DKFZP564O0463	3'	ATGTTCCATAGATTATGTCAT 15441	GC AGT	
			ATGACATA CTATG CAT		
			TACTGTAT GATAC GTA		
			TA CTT		
GAM665	KIAA0226	3'	GAGAATAGGACTACGTCAT 31787	A _ GAG	
			ATGAC TAG CCTAT TC		
			TACTG ATC GGATA AG		
			C A AG_		
GAM665	KIAA0534	3'	ACCATGACTATGTCAT 35377	CC A	
			ATGACATAG TATG GT		
			TACTGTATC GTAC CA		
			A_ _		
GAM665	KIAA1193	3'	ATGACGTGGTGGGCTACGT 33579	A GA_	
			AC TAGCCTAT GTCAT		
			TG ATCGGGTG CAGTA		
			C GTG		
GAM665	KIAA1622	3'	ATGCTTAAGCTATGTCA 27765	CTA T	
			TGACATAGC TGAG CAT		
			ACTGTATCG ATTC GTA		
			A_ _		
GAM665	LOC116064	3'	TATGACTCTCACCCATGTCAT 36496	AGCCTAT	
			ATGACAT GAGTCATA		

			TACTGTA	CTCAGTAT		
			CCCACT_			
GAM666	AKAP13	3'	ACAGAAGTGCTTTCTATT	43175	_	A
			AATAGAAA TACT TCTGT			
			TTATCTTT GTGA AGACA			
			C _			
GAM666	RET	3'	ACAGACGAGTGCCTCCTTTACG	21781	TA AA	A_
	TTA		TAACGTAA GA TACT TCTGT			
			ATTGCATT CT GTGA AGACA			
			TC CC GC			
GAM666	ZDHHC2	3'	ACGGTACATTTCTATTAC	18485		ACTAT
			GTAATAGAAAT CTGT			
			CATTATCTTTA GGCA			
			CAT__			
GAM666	LOC158263	3'	ACAGCTGGTTTCTATTGC	39796	AT	T
			GTAATAGAA ACTA CTGT			
			CGTTATCTT TGGT GACA			
			_ C			
GAM666	LOC221656	3'	ACAGATAGTGTGGGCTTCAC	44291	AAT AA	_
			GT AG ATACTATCTGT			
			CA TC TGTGATAGACA			
			CT_ GGG			
GAM667	G6PC	3'	ACTAATTATATAGTATACCATA	5653	A T C	
			TATG TATA CTA TATAATTAGT			
			ATAC ATAT GAT ATATTAATCA			
			C _ _			
GAM667	SLC16A2	3'	ACTGGAAGAGTAGAATATCATA	13266	A	ATAA
			TATGATAT TCTACT TTAGT			
			ATACTATA AGATGA GGTCA			
			_ GAA_			
GAM667	LOC140139	5'	ACTAATTATAAGAGAATTCATA	37347	TATA	AC
			TATGA TCT TATAATTAGT			
			ATACT AGA ATATTAATCA			
			TA__ GA			
GAM668	GOCAP1	3'	TACTACTAGTAGCAAATA	22940	A T	
			TATTTTGCTA CTA GTAGTA			
			ATAAAACGAT GAT CATCAT			
			_ _			
GAM668	LZTFL1	3'	CTATACCCTTTAGCAAATA	21598	CTA_	
			TATTTTGCTAA TGTA			

		ATAAAACGATT ATATC	
		TCCC	
GAM668	SLC13A1 3'	TTGTAGACAGGTAGCAAAATA 22777	ACTA AG
		TATTTTGCTA TGT TACAA	
		ATAAAACGAT ACA ATGTT	
		GG_ G_	
GAM668	DKFZp547I224 3'	CTGCATGAAC TAATGAGCAAAA 21475	AAC_____
	TA	TATTTTGCT TATGTAG	
		ATAAAACGA GTACGTC	
		GTAATCAA	
GAM668	FLJ12331 3'	TGCAGACAAGTTAGCAAA 24542	A A_
		TTTGCTAACT TGT GTA	
		AAACGATTGA ACA CGT	
		_ GA	
GAM668	FLJ20220 3'	TGCACTCGAGTAATTAGCAAAG 19304	C GT_ A
		TTTTGCTAA TAT AGT CA	
		GAAACGATT ATG TCA GT	
		A AGC C	
GAM668	OSBPL3 3'	TTGTAAAAGTTTAGCAAAATA 17820	_ ATGTAG
		TATTTTGCTAA CT TACAA	
		ATAAAACGATT GA ATGTT	
		T AA_____	
GAM668	TSPAN-3 3'	ATGTAGACTAGCAAAATA 12277	A_
		TATTTTGCTA CTATGT	
		ATAAAACGAT GATGTA	
		CA	
GAM668	LOC122830 3'	GCTACAAC TGAAGCAAAATA 36707	AACTA
		TATTTTGCT TGTAGT	
		ATAAAACGA ACATCG	
		GTCA_	
GAM668	LOC138199 3'	TTGTACTACACAAGTAAAA 37119	AACTA
		TTTTGCT TGTAGTACAA	
		AAAATGA ACATCATGTT	
		AC_____	
GAM668	LOC158357 3'	TTATATAGTTTACAAAATA 39821	CT
		TATTTTG AACTATGTAG	
		ATAAAAC TTGATATATT	
		AT	
GAM668	LOC221687 3'	TTACAAGTTGGCAAAATA 44309	A
		TATTTTGCTAACT TGTAG	

ATAAAACGGTTGA ACATT

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GAM669  PRNP    3' GAAAGCACCATCATCATA  5849  A  A
                _
                TAT ATGAT GTGCTTTT
                ||| |||| |||||
                ATA TACTA CACGAAAG
                C  C
GAM669  TRIM9   3' GAAAAGCCTATCATCATA  27549  A  T
                TAT ATGATAG GCTTTT
                ||| ||||| |||||
                ATA TACTATC CGAAAAG
                C  _
GAM669  pcnp    3' CCAAAAAAAAAAATTAACATTGT 21627  A  GC
                A
                TATAATG TAGT TTTTTTTTGG
                ||||| ||| |||||
                ATGTTAC ATTA AAAAAAAACC
                A  A_
GAM670  AKR1D1  3' ATCAAAGGCAACATATGA  12610  G  GTTTA
                TCA ATGTTGCT  TGAT
                ||| ||||| |||
                AGT TACAACGG  ACTA
                A  AA__
GAM670  C8orf13 3' CATGACTCAGCAACATTGA  39653  A  T_
                TCAG TGTTGCTG TTATG
                ||| ||||| |||
                AGTT ACAACGAC AGTAC
                _  TC
GAM670  CED-6   3' CATCTAAGCATCATCTGAT  18431  T  GTTT
                ATCAGATG TGCT  ATG
                ||||| ||| |||
                TAGTCTAC ACGA  TAC
                T  ATC_
GAM671  STX7    3' TTCAAGTTAAAACTCCCCA  9624  AT
                TGGG GTTTTAACTTGGA
                ||| |||||
                ACCC CAAAATTGAACTT
                CT
GAM672  SPAP1   3' AAAATGTGATTTTTTGACATA  25046  TTA G
                TATGTCAAAA C ACATTTT
                ||||| ||| |||||
                ATACAGTTTT G TGTA AAA
                TA__
GAM672  FENS-1  3' GTAAAATGTGACCGTTTGACAT 21891  ATTACG
                ATGTCAAA  ACATTTTAC
                ||||| |||||
                TACAGTTT  TGTA AAAATG
                GCCAG_
GAM672  FLJ20689 3' GTAAAATGTCTTTTTTGACATG 19703  TTAC
                TATGTCAAAA GACATTTTAC
                ||||| |||||
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GTACAGTTTT CTGTAAAATG
 T____
 GAM672 FLJ20689 3' GTAAAATGTCTTTTTGACATG 19599 TTAC
 TATGTCAAAA GACATTTTAC
 ||||| |||||
 GTACAGTTTT CTGTAAAATG
 T____
 GAM673 LOC146056 3' AGCAACCACATCAGGATCGGAA 38050 A AC A
 TC GATT CGGTTCTGAT GGTT CT
 ||| ||||| ||| ||
 CTAA GCTAGGACTA CCAA GA
 G CA C
 GAM674 DGKB 3' TAGAAATTGAATTAGCATA 44450 CTTTGTG
 TATGCTA CAATTTCTA
 ||||| |||||
 ATACGAT GTTAAAGAT
 TAA____
 GAM674 HGF 3' TAGAAATTTCAAGAGCATA 45226 A TTG C
 TATGCT CT TG AATTTCTA
 ||||| || || |||||
 ATACGA GA AC TTAAAGAT
 _ _ _ T
 GAM674 ZNF192 3' TTAGAAATTTAAATAGCAT 12991 C TGC
 ATGCTA TTTG AATTTCTAA
 ||||| ||| |||||
 TACGAT AAAT TTAAAGATT
 A ____
 GAM674 DKFZP434G1411 3' AGAAATTGCAAGATGTAATATA 44229 C TTTG
 TATG TAC TGCAATTTCT
 ||||| ||| |||||
 ATAT ATG ACGTTAAAGA
 A TAGA
 GAM674 DKFZP762D096 3' AGAAATTACTGATGAAGCAGCA 32664 A TG G ____
 TG TATGCT CTT T CA ATTTCT
 ||||| ||| || |||||
 GTACGA GAA A GT TAAAGA
 C GT _ CAT
 GAM674 N4BP3 3' TTAGAACATATTACAAAGTAGC 32943 CAAT_
 A TGCTACTTTGTG TTCTAA
 ||||| ||| |||||
 ACGATGAAACAT AAGATT
 TATAC
 GAM674 LOC134637 3' TTAGAAATTAGCAAGTAGTGCA 37079 T TTG _
 TA TATGC ACT TGC AATTTCTAA
 ||||| ||| || |||||
 ATACG TGA ACG TTAAAGATT
 _ TGA A
 GAM674 LOC147622 5' AGAAATTGTAACAGCATG 40850 ACTTTG
 TATGCT TGCAATTTCT
 ||||| |||||

			GTACGA	ATGTAAAGA		
			CA_____			
GAM674	LOC151361	5'	TAGCTTTGGCACAAAGCAGCA	41332	A	AATTT
			TGCT CTTTGTGC	CTA		
			ACGA GAAACACG	GAT		
			C	GTTTC		
GAM674	LOC152263	3'	TTAGAAATTGAGACCTGTACAT	41483	C	TTTGTG
	A		TATG TAC	CAATTTCTAA		
			ATAC ATG	GTAAAGATT		
			_	TCCAGA		
GAM674	LOC51580	3'	TTAGAAATTATTATTAGTAGCA	18018		TTGTGC
	T		ATGCTACT	AATTTCTAA		
			TACGATGA	TTAAAGATT		
			TTATTA			
GAM675	ADAM12	3'	CACTTGCAACCTACCTGTT	9543	A	A_
			GGCA GTGGGT	CAAGTG		
			TTGT CATCCA	GTTCAC		
			C	AC		
GAM675	ALOX12B	5'	AGACACCTGCTCACTCACC	6807	CA	CAA C
			GG AGTGGGTA	GTG CT		
			CC TCACTCGT	CAC GA		
			AC	C_ A		
GAM675	ASH1	3'	GCACTTGTAAGTCTGCTGCC	20548	A TG G	
			GGCA G G	TACAAGTGC		
			CCGT C C	ATGTTACAG		
			_	GT A		
GAM675	ATP5J	5'	GCACTTACCCTCCACTTCCTCC	7408	A C	TAC_
			A AGG AAGTGGG	AAGTGC		
			C TCC TTCACCT	TTCACG		
			C _	CCCA		
GAM675	DBY	3'	AGGCACTTGGGAACTTAC	11026	A_	
			GTGGGT	CAAGTGCCT		
			CATTCA	GTTACGGA		
			AGG			
GAM675	HK1	5'	CACCTACCCACACCTGCTTT	27269	A_	CAA
			AAGGCA	GTGGGTA GTG		
			TTTCGT	CACCCAT CAC		
			CCA	C_		
GAM675	HK1	5'	CACCTACCCACACCTGCTTT	27272	A_	CAA
			AAGGCA	GTGGGTA GTG		

TTTTCGT CACCCAT CAC
 CCA C__
 GAM675 HK1 5' CACCTACCCACACCTGCTTT 27275 A__ CAA
 AAGGCA GTGGGTA GTG
 ||||| ||||| ||
 TTTTCGT CACCCAT CAC
 CCA C__
 GAM675 HOXD4 3' GCACTCGTCTTTGCCTT 15981 GTG T A
 AAGGCAA GG AC AGTGC
 ||||| || || |||||
 TTCCGTT TC TG TCACG
 ____ C
 GAM675 KISS1 5' AGGCACTTCTAGGACCTGGCT 8061 AAG AC__
 GGC TGGGT AAGTGCCT
 || |||| |||||
 TCG GTCCA TTCACGGA
 ____ GGATC
 GAM675 ODF2 3' GCACCATCACTTGCTTTT 8387 GTACAA
 AAAGGCAAGTGG GTGC
 ||||| ||||| |||||
 TTTTCGTTCACT CACG
 AC__
 GAM675 P2RY6 5' AGGCACTTGCTAACTCTTGCC 10354 AAGT A__
 T AGGC GGGT CAAGTGCCT
 |||| |||| |||||
 TCCG CTCA GTTCACGGA
 GTT_ ATC
 GAM675 PPP2R2B 3' AGGCACTTCTAACTCACCCC 10922 CAA AC_
 GG GTGGGT AAGTGCCT
 || ||||| |||||
 CC CACTCA TTCACGGA
 C__ ATC
 GAM675 PPP2R5A 3' AGGTGAATTACCCAGCTTGCCT 12908 _ CAAG
 AGGCAAG TGGGTA TGCCT
 ||||| ||||| |||||
 TCCGTTC ACCCAT GTGGA
 G TAA_
 GAM675 SNL 3' GGCAAGCCCCCTTGCCTT 9066 T ACAAG
 AAAGGCAAG GGGT TGCC
 ||||| ||||| |||||
 TTTCCGTTT CCCG ACGG
 C A__
 GAM675 TEM7 3' AGGCACCTGCCAACTACTTGCT 21669 GTA_ A
 TT AAGGCAAGTGG CA GTGCCT
 ||||| ||||| |||||
 TTTTCGTTTCATC GT CACGGA
 AACC C
 GAM675 FBXO27 3' GCACTTGTACCTCCCT 36838 CAAGT
 AGG GGGTACAAGTGC
 || ||||| |||||

TCC TCCATGTTACG
 C____
 GAM675 FLJ10521 3' GCACTTGTGTGTCACCAGCCT 19911 AA GG_
 AGGC GTG TACAAGTGC
 |||| ||| |||||||
 TCCG CAC GTGTTACG
 AC TGT
 GAM675 HBXAP 3' GCACTTGTGCTTTAGCTTT 18656 AAGT
 AAGGC GGGTACAAGTGC
 |||| |||||||||
 TTTCG TTCGTGTTACG
 AT____
 GAM675 HRH4 3' AGGCACTTGCCACCACGCC 22257 AA GTA
 GGC GTGG CAAGTGCCT
 ||| |||| |||||||
 CCG CACC GTTCACGGA
 _ ACC
 GAM675 KIAA0089 3' GCACTTGTATGATGCTTT 34666 AGTGG C
 AAGGCA GTACAAGTG C
 |||| |||||||
 TTTCGT TATGTTAC G
 AG____ A
 GAM675 KIAA0547 3' CACTTGTAGGACTTCCTTT 16695 C GGG
 AAAGG AAGT TACAAGTG
 |||| |||| |||||||
 TTTCC TTCA ATGTTAC
 _ GG_
 GAM675 KIAA1318 3' AGGCACATCCCACCTTACCT 33429 C _ TACAA
 AGG AAG TGGG GTGCCT
 ||| |||| |||||
 TCC TTC ACCC CACGGA
 A C TA____
 GAM675 MGC16175 3' AGACACTTGTGAAACCTTGC 26511 TGGG C
 GCAAG TACAAGTG CT
 |||| |||||||
 CGTTC GTGTTAC GA
 CAAA A
 GAM675 PRO1866 5' CATGTGTACCCACCACCTT 20580 CAA A
 AAGG GTGGGTACA GTG
 |||| |||||||
 TTCC CACCCATGT TAC
 AC____ G
 GAM675 WBSCR22 3' AGGCACTTGCCTCTGCACTTT 18971 _ A T GTA
 AAAG GCA G GG CAAGTGCCT
 |||| ||| | |||||||
 TTTC CGT C CC GTTCACGGA
 A _ T ____
 GAM675 ZNF230 5' AGGCACAATTCCACCTTCCTTT 12994 CAA TACAA
 AAAGG GTGGG GTGCCT
 |||| |||| |||||

TTTCC CACCT CACGGA
 TTC TAA__
 GAM675 LOC145989 3' GGCAAGCCCCCTTGCCTTT 29954 T ACAAG
 AAAGGCAAG GGGT TGCC
 ||||| ||| |||
 TTTCCGTTC CCCG ACGG
 C A____
 GAM675 LOC148018 5' CACTTACAGGGTGCCTACCCC 40090 CAA _____
 GG GTGGGTAC AAGTG
 || ||||| |||
 CC CATCCGTG TTCAC
 C__ GGACA
 GAM675 LOC148223 3' AGGCACTCGCCTGTCCACTTCT 38494 C GT CA__
 GG AAGTGG A AGTGCCT
 || |||| | |||||
 TC TTCACC T TCACGGA
 _ TG CCGC
 GAM675 LOC158401 5' CACCTACCAACTTTGCCT 39836 _ G CAA
 AGGCAA GT GGTA GTG
 |||| | ||| |||
 TCCGTT CA CCAT CAC
 T A C__
 GAM675 LOC203378 3' CATTCCCACTTGGCTT 43549 G TACA
 AAG CAAGTGGG AGTG
 || ||||| |||
 TTC GTTCACCC TTAC
 G _____
 GAM675 LOC220549 5' AGGCACTTAGGCCTCGCCTCC 44648 A AAGT AC
 A AGGC GGGT AAGTGCCT
 | ||| ||| |||||
 C TCCG TCCG TTCACGGA
 C C__ GA
 GAM675 LOC221490 5' AGGCACTTGAGGCCTTGCTT 44985 AGT A_
 AGGCA GGGT CAAGTGCCT
 |||| ||| |||||
 TTCGT TCCG GTTCACGGA
 _ GA
 GAM675 LOC255146 3' AGACACTCCCACTCGCC 45755 A TACA C
 GGC AGTGGG AGTG CT
 || |||| | ||| ||
 CCG TCACCC TCAC GA
 C _ A
 GAM675 LOC255452 3' GGGCACCCCCCACTTGCCTCC 46576 A TACAA
 A AGGCAAGTGGG GTGCCT
 | ||||| |||
 C TCCGTTCACCC CACGGG
 C C____
 GAM675 LOC257000 3' AGGCACCTGTGCCCACCCCT 46271 CAA A
 AGG GTGGGTACA GTGCCT
 || ||||| |||||

			TCC CACCCGTGT CACGGA		
			CC_ C		
GAM675	LOC90785	3'	AGGCACTTGCTGAGCCACGCT 32005	AA	A__
			GGC GTGGGT CAAGTGCCT		
			TCG CACCCG GTTCACGGA		
			_ AGTC		
GAM676	FACL5	3'	AACAGGCTTATTTTCTGTGAA 32105	C	GAG
			TTCACAGAA ATAAG GTT		
			AAGTGTCTT TATTC CAA		
			T GGA		
GAM676	FZD10	3'	AAACCTCACATTTGTGAA 14049	ACATAAG	
			TTCACAGA GAGGTTT		
			AAGTGTTT CTCCAAA		
			ACA__		
GAM676	TACC1	3'	AAACCTTTTGTCTGT 12959	TAA	
			ACAGAACA GGAGGTTT		
			TGTCTTGT TTTCCAAA		
			_		
GAM676	WHSC1	3'	AGCCTCCTGCTCTGTGAA 28457	ACATA	
			TTCACAGA AGGAGGTT		
			AAGTGTCT TCCTCCGA		
			CG__		
GAM676	WHSC1	5'	AGCCTCCTGCTCTGTGAA 28472	ACATA	
			TTCACAGA AGGAGGTT		
			AAGTGTCT TCCTCCGA		
			CG__		
GAM676	WHSC1	3'	AGCCTCCTGCTCTGTGAA 28440	ACATA	
			TTCACAGA AGGAGGTT		
			AAGTGTCT TCCTCCGA		
			CG__		
GAM676	XRCC4	5'	AAAACCTTGATCTGTGAA 22880	A	TAAGG
			TTCACAGA CA AGGTTTT		
			AAGTGTCT GT TCCAAAA		
			A ____		
GAM676	DEPP	3'	AAAGCCCATGTTCTGTGAG 13876	AAGGA	
			TTCACAGAACAT GGTTTT		
			GAGTGTCTTGTA CCGAAA		
			C__		
GAM676	DKFZP761I2123	3'	AAGTTCCCCTGCTCTGTGAA 25462	A TAA	G
			TTCACAGA CA GGAG TT		

			AAGTGTCT GT CCTT AA		
			C CC_ G		
GAM676	FLJ14768	3'	TTCTTTATCCTGTGAA 26616	AAC	
			TTCACAG ATAAGGAG		
			AAGTGTC TATTTCTT		
			C__		
GAM676	GMPPB	5'	GAATCTCCATGTCCCATGAA 45815	CAGA AA	
			TTCA ACAT GGAGGTTT		
			AAGT TGTA CCTCTAAG		
			ACCC _		
GAM676	KIAA0335	3'	CAAAACCTGAAGATGTCCGTGA 16730	A A AAGG	
	A		TTCAC GA CAT AGGTTTTG		
			AAGTG CT GTA TCCAAAAC		
			C _ GAAG		
GAM676	KIAA1553	3'	CAAATTTAATGTGTTCCATGA 44141	CA AGG	
	A		TTCA GAACATA AGGTTTTG		
			AAGT CTTGTGT TTAAAAAC		
			AC AA_		
GAM676	Rpo1-2	3'	CTTCCTTATGTTTCCTGAA 21101	CA	
			TTCA GAACATAAGGAGG		
			AAGT CTTGTATTCCTTC		
			C_		
GAM676	SLC17A6	3'	AAACACTTATTTCTGTGAA 21593	C GAG	
			TTCACAGAA ATAAG GTTT		
			AAGTGTCTT TATTC CAAA		
			_ A_		
GAM676	LOC143392	5'	CAAACCGTAGGAATTCTGTGA 40357	CATAAGGA	
	A		TTCACAGAA GGTTTTG		
			AAGTGTCTT CCAAAC		
			AAGGATG_		
GAM676	LOC148189	5'	AACCTCAGTTCTGTGAA 38482	ATAAG	
			TTCACAGAAC GAGGTT		
			AAGTGTCTTG CTCCAA		
			A__		
GAM676	LOC149271	5'	CAAACCTCCAAGCTTTCTGGA 38678	A CATAA	
	A		TTC CAGAA GGAGGTTTTG		
			AAG GTCTT CCTCCAAAAC		
			_ TCGAA		
GAM676	LOC157623	5'	TCTACTCTATGCTCTGTGAA 39617	A AG _	
			TTCACAGA CATA G AGG		

		AAGTGTCT GTAT C TCT C CT A	
GAM676	LOC203197 3'	CTCCCCCATATTTTGTGAA 43010 TTCACAGAA AT GGAG AAGTGTTTT TA CCTC A CCC	C AA_
GAM677	ADD1 T	3' TCCTTAACCGTGGACTCTTCCT 15469 AAGGAAGA TT T GTTAA GA TTCCTTCT AG G CAATT CT C GT C C	A TG T A
GAM677	ADD1 T	3' TCCTTAACCGTGGACTCTTCCT 15473 AAGGAAGA TT T GTTAA GA TTCCTTCT AG G CAATT CT C GT C C	A TG T A
GAM677	FCGR2A	3' TCTTTAACATCTTCTTTCCT 38700 AGGAA GAA TGTTAAAGA TCCTT CTT ACAATTTCT T CT__	_ TTTGT
GAM677	FXD6 TTA	3' CTTTAACAAAACCTTGCTTCC 22551 TAAGGAAG TTGTAAAG ATTCCTTC AACAATTC GTTCCAAA	AATTTG__
GAM677	HGF	3' TCTTTAATGACTCTTCCT 45229 AGGAAGA GT TTAAAGA TCCTTCT CA AATTTCT __ GT	ATTT TG
GAM677	TRPV1	3' CTTTGGGAACAACTCTTCCTT 28011 AAGGAAGA TTTGTT TTAAAG TTCCTTCT AAACAA GGTTTC C G	A G
GAM677	TRPV1	3' CTTTGGGAACAACTCTTCCTT 27995 AAGGAAGA TTTGTT TTAAAG TTCCTTCT AAACAA GGTTTC C G	A G
GAM677	TRPV1	3' CTTTGGGAACAACTCTTCCTT 28003 AAGGAAGA TTTGTT TTAAAG TTCCTTCT AAACAA GGTTTC C G	A G
GAM677	TRPV1	3' CTTTGGGAACAACTCTTCCTT 20815 AAGGAAGA TTTGTT TTAAAG 	A G

TTCCTTCT AAACAA GGTTC
 C G
 GAM677 DDM36 3' TCTCTAACACGTGACTACCT 21953 A AATT A
 AGG AG TGTTGTTA AGA
 ||| || ||||| |||
 TCC TC GCAACAAT TCT
 A AGT_ C
 GAM677 KIAA0240 3' CTCCTAATCAAATTCTTCTCA 44407 A TTGTTA
 A GGAAGAATTTG AAG
 | ||||| |||
 A TCTTCTTAAAC TTC
 C TAATCC
 GAM677 PDE11A 3' TAATTTTGGATTTTTCCTTA 18868 TT TT
 TAAGGAAGAAT G GTTA
 ||||| |||
 ATTCCTTTTTA T TAAT
 GG TT
 GAM677 LOC146268 3' TCCTTAACACCCTATTCTTCCT 38125 TTGT A
 AGGAAGAAT TGTTAA GA
 ||||| ||||| ||
 TCCTTCTTA ACAATT CT
 TCCC C
 GAM678 FGF7 3' AAATAAAATTTGCTCTAGT 7747 GAAAGG
 ACTAGAGCAAA TATTT
 ||||| |||||
 TGATCTCGTTT ATAAA
 AAA____
 GAM678 ITGA1 3' TCTTTCTTTGCCAGTAA 31792 AGA
 TTACT GCAAAGAAAGG
 |||| |||||
 AATGA CGTTTCTTTCT
 CC_
 GAM678 C20orf64 3' AAATACCTTTCTTCCTTGTA 27309 TA CA
 TTAC GAG AAGAAAGGTATTT
 |||| ||| |||||
 AATG TTC TTCTTTCCATAAA
 _ C_
 GAM678 SIAT8D 3' AAATACCTGCAAAGTGCTCTA 12222 AAGAA_
 TAGAGCA AGGTATTT
 ||||| |||||
 ATCTCGT TCCATAAA
 GAAACG
 GAM678 SNIP1 3' TCTTTCTTTATTCTAATAA 24010 C C
 TTA TAGAG AAAGAAAGG
 ||| ||||| |||||
 AAT ATCTT TTTCTTTCT
 A A
 GAM678 LOC120448 5' GAGTGCTCCTTGCTCTGTAA 37221 T A AAG
 TTAC AGAGCAA GA GTATTT
 |||| ||||| || |||||

AATG TCTCGTT CT CGTGAG
 — C —
 GAM678 LOC145216 3' ACCTTTCTTCTTTGTAG 40504 T CA
 TTAC AGAG AAGAAAGGT
 |||| ||| |||||
 GATG TTTC TTCTTTCCA

 — —
 GAM678 LOC154743 3' TGCACTTCTTTACTCTGGTAA 39481 C AG
 TTACTAGAG AAAGAA GTA
 ||||| ||||| |||
 AATGGTCTC TTTCTT CGT
 A CA
 GAM678 LOC196812 3' CCTCCCTGCTCTAGTAG 43134 AA AA
 TTACTAGAGCA G AGG
 ||||| ||| |||
 GATGATCTCGT C TCC
 — CC
 GAM679 ABL1 3' ACAGCTGGTGCCAAATAGC 11635 T _ AT
 G CTATTTG CA TCAGCTGT
 | ||||| || |||||
 C GATAAAC GT GGTCGACA
 — C —
 GAM679 ABL1 3' ACAGCTGGTGCCAAATAGC 14224 T _ AT
 G CTATTTG CA TCAGCTGT
 | ||||| || |||||
 C GATAAAC GT GGTCGACA
 — C —
 GAM679 P23 3' ACAGCTGACTGATCAGACT 13379 ATTTG AT
 AGTCT CA TCAGCTGT
 |||| || |||||
 TCAGA GT AGTCGACA
 CTA_ C_
 GAM679 PARK2 3' ACAGCCAAATTGCAGAAGA 15155 A CA
 TCT TTTGCAATT GCTGT
 ||| ||||| |||||
 AGA AGACGTTAA CGACA
 — AC
 GAM679 PARK2 3' ACAGCCAAATTGCAGAAGA 10901 A CA
 TCT TTTGCAATT GCTGT
 ||| ||||| |||||
 AGA AGACGTTAA CGACA
 — AC
 GAM679 PARK2 3' ACAGCCAAATTGCAGAAGA 15148 A CA
 TCT TTTGCAATT GCTGT
 ||| ||||| |||||
 AGA AGACGTTAA CGACA
 — AC
 GAM679 SACM2L 5' ACAGCTGGAGTCAAACAACTTA 22882 CTA CAA
 TAAGT TTTG TTCAGCTGT
 |||| ||| |||||

			ATTCA AAAC AGGTCGACA		
			AC_ TG_		
GAM679	SACM2L	5'	ACAGCTGGAGTCAAACAACTTA 27885	CTA	CAA
			TAAGT TTTG TTCAGCTGT		
			ATTCA AAAC AGGTCGACA		
			AC_ TG_		
GAM679	P66	3'	ACAGGAGGAAATAGACTTA 21841	TGCAA	AG
			TAAGTCTATT TTC CTGT		
			ATTCAGATAA AGG GACA		
			_____ AG		
GAM679	LOC146958	3'	ACAGCGCTGCCTGCAAAATAGA 40771	_	ATTCA_
	C		GTCTATTT GCA GCTGT		
			CAGATAAA CGT CGACA		
			A CCGTCG		
GAM680	ATP6V1G2	5'	TCAAAACAGCATCGGCCA 28224	A__	
			TGGCCGATGTTG TGA		
			ACCGGCTACGAC ACT		
			AAA		
GAM680	ITPR2	3'	AGGATCATCAATGCTA 7988	CGAT	
			TGGC GTTGATGATCCT		
			ATCG TAACTACTAGGA		

GAM680	PSA	3'	AGGTCAACATTGACCA 22128	C	TGAT
			TGG CGATGTTGA CCT		
			ACC GTTACAACCT GGA		
			A _____		
GAM680	PSA	3'	AGGTCAACATTGACCA 27737	C	TGAT
			TGG CGATGTTGA CCT		
			ACC GTTACAACCT GGA		
			A _____		
GAM680	DKFZP566N034	3'	AGAATCATCAGTATGTCA 39063	CG	C
			TGGC ATGTTGATGAT CT		
			ACTG TATGACTACTA GA		
			_____ A		
GAM680	LOC146455	5'	AGCATCATCAACATCACCA 38155	CC	C
			TGG GATGTTGATGAT CT		
			ACC CTACAACCTACTA GA		
			A_ C		
GAM681	NKX3A	3'	GGGAGCAAGAGGTGTGCACA 12830	A	CGA G
			TGT CACACCTC CT TC		

ACA GTGTGGAG GA GG
 C AAC G
 GAM681 ASB13 3' AACCGACAGCAGTGTGAAGGTG 24011 T __ A__ A
 TGTCA G ACACACCT C CG CTGTC GTT
 ||||| || |||||
 C TGTGTGGA G GT GACAG CAA
 _ A T GAC C
 GAM681 FLJ20273 3' AACTGGATTGGGGTGTGCACA 21113 A T CTG
 TGT CACACC CCGA TCAGTT
 ||| ||||| |||||
 ACA GTGTGG GGTT GTCAA
 C _ A__
 GAM681 KIAA1336 3' AACTGACTGATAAAGCTGTACA 35799 CAC CCGACT
 TGTACA CT GTCAGTT
 ||||| || |||||
 ACATGT GA CAGTCAA
 C__ AATAGT
 GAM681 LOC161742 3' AACTGACAACATTGTGTATA 40025 CCTCCGAC
 TGTACACA TGTCAGTT
 ||||| |||||
 ATATGTGT ACAGTCAA
 TACA____
 GAM681 LOC255919 3' ACTGACAAGAAGTGTGCA 45554 AC CCGAC
 TGTACAC CT TGTCAGT
 ||||| || |||||
 ACGTGTG GA ACAGTCA
 AA _____
 GAM682 MLLT2 3' GCAAAAGATCTTTCCAAA 12570 T AA
 TTTGG AAAGATCTT TGC
 ||||| ||||| |||||
 AAACC TTTCTAGAA ACG
 _ A_
 GAM682 PROS1 3' ATTAGCATTAAAATAGCTAAA 42255 AAAG C
 TTTGGT AT TTAATGCTAAT
 ||||| || |||||
 AAATCG TA AATTACGATTA
 A__ A
 GAM682 TPMT 3' TATGATAGATCTTTACTAAA 5940 TA_
 TTTGGTAAAGATCT ATG
 ||||| ||||| |||||
 AAATCATTTCTAGA TAT
 TAG
 GAM682 DKFZP566J091 3' TAGCATTTTTTTTTTTCCAAA 25186 T TCTT
 TTTGG AAAGA AATGCTA
 ||||| ||||| |||||
 AAACC TTTT TTACGAT
 _ TTTT
 GAM682 ERAP140 3' AGCATAATTTTCATTACCAAA 37082 A TCTTA
 TTTGGTAA GA ATGCT
 ||||| || |||||

			AAACCATT CT	TACGA	
			A TTAA		
GAM683	NFIA	3'	ATGCCCATTTTTATATGC	34838	C AGT
			GT TG AAAATGGGCAT		
			CG AT TTTTACCCGTA		
			T AT_		
GAM683	SLC20A1	5'	ATGCCCATACGCAGCGTA	29872	T A AAA
			TACG CTG GTA TGGGCAT		
			ATGC GAC CAT ACCCGTA		
			_ G _		
GAM683	FLJ13782	3'	GATGCCCACTTTTCTGGTCAGAC	24438	G _ _
			GTCTGA TA AAA TGGGCATC		
			CAGACT GT TTT ACCCGTAG		
			G C C		
GAM683	FLJ14054	3'	ATGCCACGTACTCAGAGTA	23782	G AAATG
			TAC TCTGAGTA GGCAT		
			ATG AGACTCAT CCGTA		
			_ GCA_		
GAM683	GCN2	5'	ATGCCACCTACCTATCCAGAT	31445	AG AAA_
	GTA		TACGTCTG TA TGGGCAT		
			ATGTAGAC AT ACCCGTA		
			CT CCATCC		
GAM683	KIAA0570	3'	GATGCTCAAGCACTCAAAC	16254	C AAAA
			GT TGAGT TGGGCATC		
			CA ACTCA ACTCGTAG		
			A CGA_		
GAM683	TIP-1	3'	GATGCCCATTTCTACTTTTGA	15967	T_ A
			TC GAGTA AATGGGCATC		
			AG TTCAT TTACCCGTAG		
			TT C		
GAM683	LOC152765	3'	ATGTTTCTACTCAGAC	39313	AAAT
			GTCTGAGTA GGCAT		
			CAGACTCAT TTTGTA		
			C_		
GAM683	LOC163412	5'	GATGCCCATTTCTCAAACGT	39954	C TAA
	A		TACGT TGAG AATGGGCATC		
			ATGCA ACTC TTACCCGTAG		
			A TTA		
GAM684	GNA15	3'	TCGCGGCCCAAGCATCC	30106	ACTT TA
			GGATGTTTGT GT CGA		

			CCTACGAACA CG GCT		
			CC__ GC		
GAM684	FLJ10620	3'	CAGGAACACACATCCTC 19972	T A__	
			GAGGATGT TGT CTTG		
			CTCCTACA ACA GGAC		
			C CAA		
GAM684	HCGIV.9	5'	GCAGACAGACATCCTCT 21057	A T	
			AGAGGATGTTTGT CT GT		
			TCTCCTACAGACA GA CG		
			— —		
GAM684	TRAF3	3'	TCGTAACAAAACAACGTCCCCT 30048	A T AC	
			AG GGATGTT GT TTGTTACGA		
			TC CCTGCAA CA AACAATGCT		
			C _ A_		
GAM684	LOC145255	3'	AGCAGAAACATCCTC 40527	GTAC	
			GAGGATGTTT TTGTT		
			CTCCTACAAA GACGA		
			—		
GAM685	KCNJ14	3'	ATGGAATGCCCCAAGTATT 14993	GTCGCT	
			AATACT GGCATTCCAT		
			TTATGA CCGTAAGGTA		
			ACC__		
GAM685	KIAA0431	3'	GGACTGGGGACAACAGTATTAA 17580	__ G TG CAT	
			TTAATACT GTC C G TCC		
			AATTATGA CAG G C AGG		
			CAA G GT__		
GAM685	KIAA1371	3'	TGAAATGCCATAGTATTA 42909	TCGC C	
			TAATACTG TGGCATT CA		
			ATTATGAT ACCGTAA GT		
			__ A		
GAM686	COX11	3'	TGAAACTGTAGTATCATA 10595	C AAG	
			TATGA TAC ACAGTTTCA		
			ATACT ATG TGTCAAAGT		
			_ A_		
GAM686	GALNT7	3'	TGATCCTGTAATCATGGTA 18880	C A _	
			TACTATGA TACA GA CA		
			ATGGTACT ATGT CT GT		
			A C A		
GAM686	BTBD1	3'	TGAAACTGCATGCAGCCATA 24922	A A AGA	
			TATG CT CA CAGTTTCA		

			ATAC GA GT GTCAAAGT		
			C C AC_		
GAM686	DKFZP564D166	3'	GAAATACAAGTCATAGTA	24990	ACAAGACA
			TACTATGACT GTTTC		
			ATGATACTGA TAAAG		
			ACA_____		
GAM686	FLJ23053	3'	AAACTGTCCTGGTTATG	23205	CAA
			TATGACTA GACAGTTT		
			GTATTGGT CTGTCAAA		
			C_		
GAM686	KHDRBS1	3'	TGAAGAATCTTTCAGTCATAGT	13329	AC CAG
	A		TACTATGACT AAGA TTTCA		
			ATGATACTGA TTCT GAAGT		
			CT AA_		
GAM686	KIAA1393	5'	TGAAACTGGAAAGCCATAG	35690	A ACAAGA
			CTATG CT CAGTTTCA		
			GATAC GA GTCAAAGT		
			C AAG_		
GAM686	PORIMIN	3'	AAGAGGTATGTAGTCACAGTA	27490	A AG AG
			TACT TGA CTACA AC TTT		
			ATGA ACTGATGT TG GAA		
			C A_ GA		
GAM686	RNAH	3'	GAATTTCTTGTAGTCATA	31038	C
			TATGACTACAAGA AGTTT		
			ATACTGATGTTCT TTAAG		
			-		
GAM686	LOC158714	3'	TGAAACTGCTGGTAGAGTCATA	39886	ACA_ A
			TATGACT AG CAGTTTCA		
			ATACTGA TC GTCAAAGT		
			GATGG _		
GAM686	LOC221362	3'	TGAAACTGCTGAAATCATA	45023	CTACA A
			TATGA AG CAGTTTCA		
			ATACT TC GTCAAAGT		
			AAAG_ _		
GAM686	LOC255158	3'	GGAAGTGTCATCATAGTA	46000	CTACAA G
			TACTATGA GACA TTTC		
			ATGATACT CTGT AAGG		
			A_____ G		
GAM687	KIAA0022	3'	AACTCATCACAAATTAATG	17024	CGTTT C
			CATTAATTG TGAG GT		

			GTAATTAAC	ACTC CA		
			ACT__	A		
GAM688	LANGERIN	3'	ATCAAAGTTACTCCAGA	17930	C TAC	
			TTTGG GT	AACTTTGAT		
			AGACC CA	TTGAAACTA		
			T ____			
GAM688	MID1	3'	TAGAGTTGTAAGACCAAA	5956	CG	
			TTTGG TTACAACTTTG			
			AAACC AATGTTGAGAT			
			AG			
GAM688	KIAA0461	3'	TCATGGTTGTAAACCAAA	35076	CG T	
			TTTGG TTACAACT TGA			
			AAACC AATGTTGG ACT			
			A_ T			
GAM688	LOC131000	5'	TTAAAGTTATAACGGCAAA	37350	G C	
			TTTG CGTTA AACTTTGA			
			AAAC GCAAT TTGAAATT			
			G A			
GAM689	NR2E1	3'	ATTGACACAAAGCATTCCA	9277	AA G	
			TGGAATGCTT TG TAAT			
			ACCTTACGAA AC GTTA			
			AC A			
GAM689	SYNGR1	3'	ATTGTGTCATCAAGCATTCC	11059	TAA A	
			GGAATGCT TGGT ATGCAAT			
			CCTTACGA ACTA TGTGTTA			
			__ C			
GAM689	C12orf2	3'	GCATTACTGCACTCCA	40291	A TTAAT	
			TGGA TGC GGTAAATGC			
			ACCT ACG TCATTACG			
			C ____			
GAM689	C20orf21	3'	GCTCCATTAAGTACTCCA	19441	A TAAT	
			TGGA TGCTTAATGG GC			
			ACCT ATGAATTACC CG			
			C T__			
GAM689	MGC17330	3'	ATTGCACTGAGCATTCCA	27459	ATG	
			TGGAATGCTTA GTAAT			
			ACCTTACGAGT CGTTA			
			CA_			
GAM689	LOC150225	3'	TGCATTACATATTCCA	41193	CTTAATG	
			TGGAATG GTAATGCA			

			ACCTTAT	CATTACGT		
			A_____			
GAM689	LOC150481	3'	GCATCACTGCATTCCA	38982	TTAAT	A
			TGGAATGC	GGT ATGC		
			ACCTTACG	TCA TACG		
			_____ C			
GAM689	LOC152316	3'	TGCACCACTGCATTCCA	41455	TTAA	AAT
			TGGAATGC	TGGT GCA		
			ACCTTACG	ACCA CGT		
			TC_____			
GAM689	LOC158191	3'	TTGCATCACTGCATTCCA	39760	TTAAT	A
			TGGAATGC	GGT ATGCAA		
			ACCTTACG	TCA TACGTT		
			_____ C			
GAM689	LOC90072	5'	TTGCACTACTGCATTCCA	30732	TTAAT	A
			TGGAATGC	GGTA TGCAA		
			ACCTTACG	TCAT ACGTT		
			_____ C			
GAM690	EYA2	3'	GGCAGTTCAAGCTGTTGA	11752	G	CGTG
			TC AACAGCTTGAAC	TGCT		
			AG TTGTCGAACTTG	ACGG		

GAM690	SLC35A3	3'	GAGCACACAACAAATGTCAGA	14549	GA	GC AACC
			TC ACA TTG	GTGTGCTC		
			AG TGT AAC	CACACGAG		
			AC A_ AA_			
GAM690	FLJ32499	3'	GAGCACACAGTTGCAGCT	29421	TG	C
			AGCT AAC	GTGTGCTC		
			TCGA TTG	CACACGAG		
			CG	A		
GAM690	KIAA1233	3'	GAGCACACGGTCTCTTTTGTTTC	31590	CTT	_
			GAACAG	GA ACCGTGTGCTC		
			CTTGTT	CT TGGCACACGAG		
			TT_ C			
GAM690	KIAA1910	3'	ACAGCTTCAACTGTTCGA	36284	C	CCG
			TCGAACAG	TTGAA TGT		
			AGCTTGTC	AACTT ACA		
			_ CG_			
GAM690	MGC19556	5'	AGTTGGTTCAAACCTGTTGGA	27313	G	C TGT
			TC AACAG	TTGAACCG GCT		

			AG TTGTC AACTTGGT TGA		
			G A _		
GAM690	LOC150606 5'	ACAATTCAAGCTTTCTGA	41232	C	CCG
		TCGAA AGCTTGAA TGT			
		AGCTT TCGAACTT ACA			
		_ A _			
GAM690	LOC221683 5'	GAGTGTACGCTCAAACCGTTT	45003	AGC	AC TG
		GAAC TTGA CGTG CTC			
		TTTG AACT GCAT GAG			
		CCA C_ GT			
GAM690	LOC93589 3'	AGTTCAAGTTCAAAGCTGTTC	35976	_	CG T
		GAACAGCTT GAAC TG GCT			
		CTTGTCGAA CTTG AC TGA			
		A A_ T			
GAM691	GAD1 3'	ATGCTGCCAACCAGCTTGTCCA	6479	CGC	_
	A	TTGGACAAGCT GTAGCAT			
		AACCTGTTCTGA CGTCGTA			
		CCAAC			
GAM691	FLJ22028 3'	CTACAAGCTTGTCCAA	24284	CGC	
		TTGGACAAGCT GTAG			
		AACCTGTTCTGA CATC			
		A _			
GAM692	CGI-142 3'	ATAATGAATGCTGCATATTA	18145	ACCT	
		TAATATGCA TTCATTGT			
		ATTATACGT AAGTAATA			
		CGT _			
GAM692	FLJ10701 3'	ATGAAATGAAAGGTTGCATAT	20022	G	
		ATATGCAACCTTTCATT TCAT			
		TATACGTTGGAAAGTAA AGTA			
		-			
GAM692	KIAA1363 3'	ACAAATGAAAAGTTGCATA	34331	C	_
		TATGCAAC TTTTCATT GT			
		ATACGTTG AAAGTAA CA			
		A A			
GAM693	CNTNAP2 3'	TGTGACACAATCCTAATA	15423	A	G
		TATTA GGATTGTGTT ACA			
		ATAAT CCTAACACAG TGT			
		- -			
GAM693	PCDHB12 3'	TTTATGTCAAACAATTATGCTT	21003	_	G
	AATA	TATTAAG GATTGT TTGACATAAA			

			ATAATTC	TTAACA	AACTGTATTT	
			GTA	_		
GAM693	PCDHB7	3'	TTTATGTCAAACAATTATGCTT	21009	___	G
	AATA		TATTAAG	GATTGT	TTGACATAAA	
			ATAATTC	TTAACA	AACTGTATTT	
			GTA	_		
GAM693	FLJ21302	3'	TCAGGCATAATCCCTAATA	23185	A	_
			TATTA	GGATTGTGT	TGA	
			ATAAT	CCTAATACG	ACT	
			C	G		
GAM693	FLJ22557	3'	TCACACATCATCCCATCCTTAA	24039	_____	T
	TA		TATTAAGGAT	TGTGT	GA	
			ATAATTCCTA	ACACA	CT	
			CCCTACT	_		
GAM693	KIAA1228	3'	TTTATGCCATGACTGACCTTAA	32448	ATT GT A	
	TA		TATTAAGG	GT TG	CATAAA	
			ATAATTCC	CA AC	GTATTT	
			AGT	GT C		
GAM693	PCDH10	3'	TTTATGTCAACAATATTAAT	26772	GGATTG	
			ATTAA	TGTTGACATAAA		
			TAATT	ACAACTGTATTT		
			ATA	___		
GAM694	ADCY7	3'	CACACGTATCTAACAAACAAAC	6780	CA A AT	
			GTT	TTT TTA	GGTGCGTGTG	
			CAA	AAA AAT	CTATGCACAC	
			AC	C	___	
GAM694	EGFL4	3'	CACACGCATACACACATGAAC	30963	TTATTAATG	
			GTTTCAT	GTGCGTGTG		
			CAAGTA	TACGCACAC		
			CACACA	___		
GAM694	GLS	3'	CACATGCACACAAATGGAC	17105	ATTAATG	
			GTTTCATT	GTGCGTGTG		
			CAGGTAAA	CACGTACAC		
			CA	___		
GAM694	VNN1	3'	CACACACACCAGATAATA	11038	A_ C	
			TATTA	TGGTG	GTGTG	
			ATAAT	ACCAC	CACAC	
			AG	A		
GAM694	LOC56920	3'	ACCATGTAATAAATGAAC	21380	___	
			GTTTCATTTATTA	ATGGT		

CAAGTAAATAAT TACCA
 G
 GAM694 LOC93463 3' CACACACACCACTAATTTCCCT 35850 TTT__ A C
 GAA TTCA ATTA TGGTG GTGTG
 |||| ||| |||| ||||
 AAGT TAAT ACCAC CACAC
 CCCTT C A
 GAM695 ESR1 3' TGTGTTCTACAATTGGC 5602 C ACCCT
 GCCAATTG AG ACACA
 ||||| || ||||
 CGGTTAAC TC TGTGT
 A CT__
 GAM695 KCNK4 3' TGTAGGGTCCGGCGTG 18717 AATTGCA
 CATGCC GACCCTACA
 |||| |||||
 GTGCGG CTGGGATGT
 C____
 GAM695 NEO1 3' TGTGTAGGGCTGGCTCCAGGCA 8319 AATT _ A
 TG CATGCC GC AG CCCTACACA
 |||| || |||||
 GTACGG CG TC GGGATGTGT
 ACCT G _
 GAM695 HDAC9-PENDING 3' TGTGTAGGTTGCAATTGAACAT 16252 C_ AC
 ATG CAATTGCAG CCTACACA
 || ||||| |||||
 TAC GTTAACGTT GGATGTGT
 AA _
 GAM695 KIAA1634 3' TGTGTAGGGTATGCCAGCA 31754 CAATT G
 TGC GCA ACCCTACACA
 || || |||||
 ACG CGT TGGGATGTGT
 ACC__ A
 GAM695 TP53INP1 3' TGTGGTTTCTGCCTAAAATTGG 36120 ____ CC
 CA TGCCAATT GCAGA CTACA
 ||||| |||| ||||
 ACGGTAA CGTCT GGTGT
 AATC TT
 GAM695 TP53INP1 3' TGTGGTTTCTGCCTAAAATTGG 27111 ____ CC
 CA TGCCAATT GCAGA CTACA
 ||||| |||| ||||
 ACGGTAA CGTCT GGTGT
 AATC TT
 GAM695 USP15 3' TGTATTGTAAATTGGCAT 13006 _ ACCC
 ATGCCAATT GCAG TACA
 ||||| || ||||
 TACGGTTAA TGTT ATGT
 A ____
 GAM696 CGTHBA 3' GCCACAAACAGGCTCATA 14361 T A _
 TATGA GCCTGTT TG GGT
 |||| ||||| || |||

ATACT CGGACAA AC CCG
 _ _ A
 GAM696 SORCS2 3' CACACCAGGCGACAGGCACCA 21871 A ATG_ A
 TG TGCCTGTT GGT TG
 || ||||| ||| ||
 AC ACGGACAG CCA AC
 C CGGA C
 GAM696 CHST3 3' CATACATAGACAAGCATCATA 10478 C ATGG
 TATGATGC TGTT GTATG
 ||||| ||| |||||
 ATACTACG ACAG CATAC
 A ATA_
 GAM696 KIAA0205 3' CATATTTAAGCAAACATCA 17004 CC A
 TGATG TGTT TGGGTATG
 |||| ||| |||||
 ACTAC ACGA ATTTATAC
 AA _
 GAM696 MIG-6 3' TCATACCAAGGCCTCATA 21019 T GTTATG
 TATGA GCCT GGTATGA
 |||| ||| |||||
 ATACT CGGA CCATACT
 C A____
 GAM696 STAF65(gamma) 3' ACTGCATAACAGGCACCA 16921 A _
 TG TGCCTGTTATG GGT
 || ||||| ||| |||
 AC ACGGACAATAC TCA
 C G
 GAM696 LOC201685 5' GTCATACCCTACTAAACACCCA 43387 CC AT____
 TG TGTT GGGTATGAC
 || ||| |||||
 AC ACAA CCCATACTG
 CC ATCAT
 GAM697 EMP1 3' GGAAGATGAACCTTTGTCATTA 7135 A ACTGAA
 TAATGACAAA TT TTCC
 ||||| || |||
 ATTACTGTTT AA AAGG
 C GTAG_
 GAM697 MKKS 5' GGAATTACTAATTTGTCATTAA 20833 A CTG
 TTAATGACAAA TTA AATTCC
 ||||| ||| |||||
 AATTACTGTTT AAT TTAAGG
 _ CA_
 GAM697 PCDHA9 3' GAATTCACCTTGTTCTGTCA 15211 A TAC
 TGACA AAT TGAATTC
 |||| ||| |||||
 ACTGT TTG ACTTAAG
 C TTC
 GAM697 TRIM9 3' AATTCATTAGTTTGTTCAT 17512 A C
 ATGACAAA TTA TGAATT
 ||||| ||| |||||

			TACTGTTT GAT ACTTAA		
			— T		
GAM697	FBXO21	3'	AGCTAATCTTGTCAATTA 27320	A	—
			TTAATGACAA ATTA CT		
			AATTACTGTT TAAT GA		
			C C		
GAM697	KIAA0721	3'	GAATTCAGTGAATATTCATTA 45927	CAAAA	
			TTAATGA TTAATGAATTC		
			AATTACT AGTGACTTAAG		
			TATA_		
GAM697	KIAA0721	3'	GAATTCAGTGAATATTCATTA 22320	CAAAA	
			TTAATGA TTAATGAATTC		
			AATTACT AGTGACTTAAG		
			TATA_		
GAM697	LOC142779	3'	GGAATTCAGTCTTTATCATTGA 37560	C ATT	
			TTAATGA AAA ACTGAATTCC		
			AGTTACT TTT TGAAGTAAAG		
			A C_		
GAM697	LOC157798	5'	GAATTCATTCTTTGTCAATTA 41849	ATTACT	
			TAATGACAAA GAATTC		
			ATTACTGTTT TTTAAG		
			CTTAC_		
GAM698	DKFZp547M072	3'	CTGGGCTACAGCAAGCCA 30614	A T ATTAA	
			TG CTTG CTGTG CCAG		
			AC GAAC GACAT GGTC		
			C _ CG_		
GAM698	KIAA1130	3'	TAATCCTGGGAGACAGGTCA 31285	GT_	
			TGACTTGTCT GATTA		
			ACTGGACAGA CTAAT		
			GGGTC		
GAM698	p25	3'	GCCCAATCACAGACAAGCA 13893	A AACCA	
			TG CTTGTCTGTGATT GC		
			AC GAACAGACACTAA CG		
			_ CC_		
GAM698	LOC144501	3'	CTGGTCAATCAGGCTGATCA 40426	CTT GT A	
			TGA GTCT GATT ACCAG		
			ACT CGGA CTAA TGGTC		
			AGT _ C		
GAM698	LOC150333	5'	CGCCCGAGTCCACAGACAA 41198	_ AACCA	
			TTGTCTGTG ATT GCG		

			AACAGACAC TGA CGC		
			C GCC__		
GAM699	AGL	5'	ACAGATTCGAATTTTACTTC 6302	GACA	C
			GAAGTAAAA TTGAA CTGT		
			CTTCATTTT AGCTT GACA		
			A__ A		
GAM699	ATP8B2	3'	CAGCCTGTCCTTTACTTCA 32510	A	TTGAAC
			TGAAGTAAA GACA CTG		
			ACTTCATTT CTGT GAC		
			C CC__		
GAM699	CHRNA2	3'	ACAGATCCATCCTTTTGCTTCA 6400	ACAT	AAC
			TGAAGTAAAAG TG CTGT		
			ACTTCGTTTTT AC GACA		
			CT__ CTA		
GAM699	PAX9	5'	CAGACTTCCTTTTACTTC 12866	ACATT	C_
			GAAGTAAAAG GAA CTG		
			CTTCATTTTC CTT GAC		
			__ CA		
GAM699	TNFSF8	3'	ACAAGTTCAAAGACTTTTACTT 6913	ACA	C
			AAGTAAAAG TTGAAC TGT		
			TTCATTTTC AACTTG ACA		
			AGA A		
GAM699	TTC3	5'	ACAGGAAGATGTCTTTTCTTCA 9313	T	GAA
			TGAAG AAAAGACATT CCTGT		
			ACTTC TTTTCTGTAG GGACA		
			_ AA_		
GAM699	ABCA10	3'	AATGTTTCCTTTTACTTCA 27824	__	
			TGAAGTAAAAG ACATT		
			ACTTCATTTTC TGTA		
			CTT		
GAM699	ADMP	3'	ACTGGAAATTCTTTTACTTCA 29654	C	GAA T
			TGAAGTAAAAGA ATT CC GT		
			ACTTCATTTTCT TAA GG CA		
			_ A__ T		
GAM699	AP1GBP1	3'	ACAGATAATGTCTTTTAATCCA 27876	AAG	AAC
			TG TAAAAGACATTG CTGT		
			AC ATTTTCTGTAAT GACA		
			CTA A__		
GAM699	CLIC2	3'	ACAGGTCTTCATACTTTTACTT 6965	ACAT	__
			AAGTAAAAG TGA ACCTGT		

			TTCATTTTC ACT TGGACA		
			AT__ TC		
GAM699	FLJ10246	3'	ACAGGTTTCATCTTTGACTTCA 19783	A	CAT
			TGAAGT AAAGA TGAACCTGT		
			ACTTCA TTTCT ACTTGGACA		
			G ____		
GAM699	FLJ10701	3'	CAATCGTTTTTTTACTTCA 20023	_	
			TGAAGTAAAAGAC ATTG		
			ACTTCATTTTTTG TAAC		
			C		
GAM699	FLJ14297	3'	AATGTTTCCTTTTACTTCA 24390	__	
			TGAAGTAAAAG ACATT		
			ACTTCATTTTC TGTAAC		
			CTT		
GAM699	FLJ20618	3'	ACAGGCATGTCTTTGACCCCA 19568	AA A	TGAA
			TG GT AAAGACAT CCTGT		
			AC CA TTTCTGTA GGACA		
			CC G C__		
GAM699	KRTHB2	3'	ACAGGCTCACACTGCCCTTACT 26923		AAGACAT_ A
	TTA		TGAAGTAA TGA CCTGT		
			ATTTCACT ACT GGACA		
			CCCGTCAC C		
GAM699	MGC21675	3'	AGGGCCAACCTATTACTTCA 27443	A ACA	AA
			TGAAGTAA AG TTG CCT		
			ACTTCATT TC AAC GGA		
			A C__ CG		
GAM699	SART3	3'	CAGGAAATGCCTTACTTCA 16249	AA A	GAA
			TGAAGTA AG CATT CCTG		
			ACTTCAT TC GTAA GGAC		
			_ C A__		
GAM699	UHRF2	3'	ACAGGTTTCATTTTTTTTA 36354	CAT	
			TAAAAGA TGAACCTGT		
			ATTTTTT ACTTGGACA		
			TT_		
GAM699	LOC147093	3'	CAGGTTCAATGACTTGC 40799	AA A	
			GTA AG CATTGAACCTG		
			CGT TC GTAACCTGGAC		
			_ A		
GAM700	SFRS2IP	3'	AACATGTACCATTAA 11083	TAGA	
			TTAATGGTAT GTGTT		

AATTACCATG TACAA

GAM700 FLJ21477 3' TTTTAACACATTGTATCATTA 24791 TAGA
TTAATGGTAT GTGTTAAAA
||||||| |||||
AATTACTATG CACAATTTT
TTA_

GAM700 LOC220477 5' TAACACCTCACCATTGA 37410 ATT A
TTAATGGT AG GTGTTA
||||| || |||||
AGTTACCA TC CACAAT
C_ _

GAM700 LOC255147 3' TAACACTTTGATCTCATTA 45803 GT
TTAATG ATTAGAGTGTTA
||||| |||||
AATTAC TAGTTTCACAAT
TC

GAM701 C20orf45 3' AAGTGAAATAACATTTTCAGCTA 18120 ATCGC_
TGGCT TATTTCACTT
||||| |||||
ATCGA ATAAAGTGAA
CTTTACA

GAM701 FLJ22060 3' AGTAGCTATAGCCATTA 23865 C
TTAATGGCTAT GCTATT
||||||| |||||
AATTACCGATA CGATGA
T

GAM701 LOC130507 3' AAGTGAAAATATTAGCCTTAA 36996 T TCGCTA
TTAA GGCTA TTTCACTT
||||| |||||
AATT CCGAT AAAGTGAA
_ TATA_

GAM701 LOC152185 3' AAGTGAAATATACAGCCTTAA 29538 T ATCGC
TTAA GGCT TATTTCACTT
||||| |||||
AATT CCGA ATAAAGTGAA
_ CAT_

GAM701 LOC154089 3' AAGTGAAAGAAGCCAGCCAT 39462 ATC A_
ATGGCT GCT TTTCACTT
||||| ||| |||||
TACCGA CGA AAAGTGAA
C_ AG

GAM701 LOC203411 3' AAGTGACTAAGGGCAATAACTC 43564 _C C ATT_
ATTAA TTAATG G TAT GCT TCACTT
||||| ||| ||| |||||
AATTAC C ATA CGG AGTGAA
T A A GAATC

GAM701 LOC51634 3' TGAAACCCTGTAGCCATTA 18104 CGCTA
TTAATGGCTAT TTTCA
||||||| |||||

			AATTACCGATG	AAAGT		
			TCCC_			
GAM701	LOC91923	5'	AAGTGAAACCTTATACCCATTA	33542	C	CGCTA
		A	TTAATGG TAT	TTTCACTT		
			AATTACC ATA	AAAGTGAA		
			C TTCC_			
GAM702	SFRS2IP	3'	AAATATAGGTCTGCACTGCAA	11082	T	G
			TTGCA TGCAGACT	ATGTTT		
			AACGT ACGTCTGG	TATAAA		
			C	A		
GAM702	FLJ13456	3'	ACATCAGTCCACAAGCAA	32795	A	CA
			TTGC TTG	GA CTGATGT		
			AACG AAC	CTGACTACA		
			_ AC			
GAM702	FLJ21276	3'	GTAAAACATGCATTTGCAAT	23903	C	_
			ATTGCAGA TG	ATGTTTTAC		
			TAACGTTT AC	TACAAAATG		
			_ G			
GAM702	KIAA0940	3'	TAAAACGTTC CCAATGCA	17149		CAGACT
			TGCATTG	GATGTTT A		
			ACGTAAC	TTGCAAAAT		
			ACCC_			
GAM702	KIAA1363	3'	AAAACAGAAGTCAATGCAA	34330	GCA	GA
			TTGCATT	GA CT TGTTTT		
			AACGTAA	CTGA ACAAAA		
			_ AG			
GAM702	KRTHB5	3'	AAATGCCGCTGCAATGCAA	8065	AC	AT
			TTGCATTGCAG TG	GTTT		
			AACGTAACGTC GC	TAAA		
			_ CG			
GAM702	MGC12466	3'	AAAACACCTCTGTCAATGTAA	27065	_	CTGA
			TTGCATTG CAGA	TGTTTT		
			AATGTAAC GTCT	ACAAAA		
			T CC_			
GAM702	PCDH17	5'	GCCTCAGCCAGCAATGCAA	15813	AGA	T
			TTGCATTGC	CTGA GT		
			AACGTAACG	GA CT CG		
			ACC	C		
GAM702	UBA2	3'	TAAAACAACACAATGCA	12002	CAGAC	A
			TGCATTG	TG TGTTTTA		

ACGTAAC AC ACAAAT
 _____ A
 GAM702 LOC88523 5' GTAAATTACACCTGCAGTGCAA 26960 AC A T
 TTGCATTGCAG TG TG TTTAC
 ||||| || |||||
 AACGTGACGTC AC AT AAATG
 C_ _ T
 GAM703 CLCN6 3' AAGTGAGCATCTGGGCATT 6958 AGTG
 GATGTT AGATGCTCACTT
 ||||| |||||
 TTACGG TCTACGAGTGAA
 G_
 GAM703 CLCN6 3' AAGTGAGCATCTGGGCATT 22335 AGTG
 GATGTT AGATGCTCACTT
 ||||| |||||
 TTACGG TCTACGAGTGAA
 G_
 GAM703 CLCN6 3' AAGTGAGCATCTGGGCATT 22340 AGTG
 GATGTT AGATGCTCACTT
 ||||| |||||
 TTACGG TCTACGAGTGAA
 G_
 GAM703 SMG1 3' TGAGATCCACCAACATCT 17483 A A G
 AGATGTT GTG GAT CTCA
 ||||| || |||||
 TCTACAA CAC CTA GAGT
 C _ _
 GAM703 LOC150951 5' AGTCACCTCACCAAGCATC 41275 A_ A _
 GATGTT GTGAG TG CT
 ||||| |||| ||||
 CTACGA CACTC AC GA
 AC C T
 GAM704 IL1R1 3' AAAAAGGGCAATAAATGCCC 6561 AA_
 GGG ATTGCCCTTTT
 || |||||
 CCC TAACGGGAAAAA
 GTAAA
 GAM704 PDE4D 3' GAAAAAGGTTTTCCCTTGT 36430 C_ TTGC
 ACA GGGAAA CCTTTTTC
 || ||||| |||||
 TGT CCCTTT GGAAAAAG
 TC TT_
 GAM704 SAS 3' GAAAAAGGAAAGGCCCTTGT 12605 C AAA GC
 ACA GGG TT CCTTTTTC
 || || || |||||
 TGT CCC GA GGAAAAAG
 T CG_ AA
 GAM704 TCF7 3' AAAAAGGGCTGTCCATGT 9190 _ AATT
 ACG GGA GCCCTTTT
 || || |||||

			TGT CCT CGGGAAAAA		
			A GT__		
GAM704	AP3M2	3'	GAAAAAGGAAGACCCGT 13675	AAA GC	
			ACGGG TT CCTTTTTC		
			TGCC AG GGAAAAAG		
			__ AA		
GAM704	DKFZP564I1171	3'	GAAAAGTCCACAATTTCCC 35444	CC__	
			GGGAAATTG CTTTT		
			CCCTTTAAC GAAAAG		
			ACCT		
GAM704	KIAA0433	3'	GAAAAACTATTGATTTCCCATG 17547	C GCCC_	
			CA GGGAAATT TTTTC		
			GT CCCTTTAG AAAAAG		
			A TTATC		
GAM704	KIAA0557	5'	GAAAAAACTCTCTTCCTGTGT 38206	ATTGCCC	
			ACACGGGAA TTTTC		
			TGTGTCCTT AAAAAG		
			CTCTCAA		
GAM704	KIAA1350	3'	GAAAAGGACTAGACCTGTGT 36000	AAATTGC	
			ACACGGG CCTTTTTC		
			TGTGTCC GGAAAAAG		
			AGATCA_		
GAM704	KIAA1557	3'	GAAAAGCCTCAGTTTCC 30640	CC_	
			GGAAATTG CTTTTTC		
			CCTTTGAC GAAAAAG		
			TCC		
GAM704	KIAA1735	3'	GAAAAGGGCTGCCCATGT 42345	C AAATT	
			ACA GGG GCCCTTTTTC		
			TGT CCC CGGGAAAAAG		
			A GT__		
GAM704	MGC5466	3'	AAAAAGGGCAGAAATCACC 36158	_ AA_	
			GG GA TTGCCCTTTT		
			CC CT GACGGGAAAAA		
			A AAA		
GAM704	RAI17	3'	GAAAAGGACAAGAGTCTGTGT 43861	AAA C	
			ACACGGG TTG CCTTTTTC		
			TGTGTCT AAC GGAAAAAG		
			GAG A		
GAM704	SPIB	3'	GAAAAGGGCGTCCC 9092	AAT	
			GGGA TGCCCTTTTTC		

CCCT GCGGGAAAAAG

GAM704 SSFA2 3' AAAAAGGAAAATGGTTTCCC 36514 C___
GGGAAATTG CCTTTTT
||||||| |||||
CCCTTTGGT GGAAAAA

AAAA

GAM704 SSH-3 3' GAAAACAGAGCTTCCCGTG 19535 ATT C _
CACGGGAA GC CT TTTTC
||||||| || |||||
GTGCCCTT CG GA AAAAG

___ A C

GAM704 LOC153474 3' GAAAAGTCCACAATTTCCC 39380 CC___
GGGAAATTG CTTTTT
||||||| |||||
CCCTTTAAC GAAAAG

ACCT

GAM704 LOC200734 3' AAAGCCAAATTTCCCATGT 42839 C GCC
ACA GGGAAATT CTTT
||| ||||| |||
TGT CCCTTTAA GAAA

A ACC

GAM704 LOC202347 3' AAAGAGGGGAGCCCTGTGT 43429 AAA G
ACACGGG TT CCCTTTTT
||||||| || |||||
TGTGTCC GA GGGAGAAA

C__ G

GAM704 LOC89919 3' GAAAAAGGGTGTCCAGT 30463 G AAT
AC GGA TGCCCTTTTTC
|| ||| |||||
TG CCT GTGGGAAAAAG

A ___

GAM704 LOC93550 3' AAAAAGAACATTTTTCCAGTGT 35930 _ T CC
ACAC GGGAAA TG CTTTTT
||| ||||| || |||||
TGTG CCTTTT AC GAAAAA

A T AA

GAM705 ALDH1A3 3' ACAATGCGAGAATGAT 6351 CA AA
ATCA TCTCGCAT TGT
||| ||||| |||
TAGT AGAGCGTA ACA

A_ _

GAM705 C9orf9 3' CAAACATTGTAAAATGTG 21025 CTCGC
CACAT ATAATGTTTG
||||| |||||
GTGTA TGTTACAAAC

AAA__

GAM705 DKFZP727C091 3' TTCAAACATCATATGCCGGA 32909 C _
TCT GCATA ATGTTTGAA
||| ||||| |||||

			AGG CGTAT TACAACTT		
			C AC		
GAM705	ESM1	3'	TTCAAACATCTGAGGCATGAT 13916	CA	CATA
			ATCA TCTCG ATGTTTGAA		
			TAGT GGAGT TACAACTT		
			AC C__		
GAM705	FBXO4	3'	CAAATAGTAAAGAGATGTGAT 27263		GCATAA
			ATCACATCTC TGTTTG		
			TAGTGTAGAG ATAAAC		
			AAATG_		
GAM705	FLJ11273	3'	TTCAAACATTATCATTTAATGT 20396		CTCGC_
			ACAT ATAATGTTTGAA		
			TGTA TATTACAACTT		
			ATTTAC		
GAM705	FLJ21916	3'	TCAAACATTCATGATGGAT 23382	A	TCGCAT
			ATC CATC AATGTTTGA		
			TAG GTAG TTACAACT		
			_ TAC__		
GAM705	LHFPL2	3'	TTCAAACATCTGTGGTGT 34662	TC	TA
			ACATC GCA ATGTTTGAA		
			TGTGG TGT TACAACTT		
			_ C_		
GAM705	SEZ6	5'	TCCAGCTTATGGAGATGTGA 36776	G	T T
			TCACATCTC CATAA GTT GA		
			AGTGTAGAG GTATT CGA CT		
			_ _ C		
GAM705	SIAT8C	5'	TTCAAACATTTAGCAAGCATG 18028	_	C AT
			CAT CT GC AATGTTTGAA		
			GTA GA CG TTACAACTT		
			C A AT		
GAM705	LOC163255	5'	CAAAGCCAGATGTGAT 40107	C	ATAATG
			ATCACATCT GC TTTG		
			TAGTGTAGA CG AAAC		
			C _____		
GAM705	LOC164397	5'	CAAGAGGGTGCAAGATGTGA 40149	C	AATG
			TCACATCT GCAT TTTG		
			AGTGTAGA CGTG GAAC		
			A GGA_		
GAM705	LOC255862	3'	TTCAATTGATGAAGATGTGAT 45341	CG	AATGT
			ATCACATCT CAT TTGAA		

			TAGTGTAGA GTA AACTT	
			A_ GTT__	
GAM705	LOC256176 5'	TCAAACATTAAAATGTG	46171	CTCGCA
		CACAT TAATGTTTGA		
		GTGTA ATTACAAACT		
		AA_____		
GAM705	LOC91050 3'	TCATGACACTAAGATGTGA	32338	CGCA A _
		TCACATCT TA TGTT TGA		
		AGTGTAGA AT ACAG ACT		
		_____ C T		
GAM706	ADAM10 3'	TAACCTTAATGGCACAAAGTCTT	6769	GC__ AAGA
	A	TAAGAC TGC ATTAAGTTA		
		ATTCTG ACG TAATTCAAT		
		AAAC G_____		
GAM706	ZIM2 3'	TAACCTTAATTCTCTTCGTT	17664	CTGCA
		GACG AGAATTAAGTTA		
		TTGC TCTTAATTCAAT		
		TTC_____		
GAM706	LOC221715 5'	TAGCTTTCTTACAGCGTCTT	45018	C TTA
		AAGACGCTG AAGAA AGTTA		
		TTCTGCGAC TTCTT TCGAT		
		A _____		
GAM707	EYA4 3'	GCCGGAGATCTATTTTTTA	10308	C _
		TAA AAATA ATCTCCGGC		
		ATT TTTAT TAGAGGCCG		
		T C		
GAM707	C20orf180 3'	GGCTTTTAATTATTTGTTAT	20496	CTCC
		ATAACAAATAAT GGCC		
		TATTGTTTATTA TCGG		
		ATTT		
GAM707	LOC145474 3'	TGAGAGATTATTCGTTATA	37870	A _
		TATAAC AATAATCTC CG		
		ATATTG TTATTAGAG GT		
		C A		
GAM707	LOC146229 3'	GGCCAGACTGTGTTTGTGA	38112	ATC C
		TAACAAATA TC GGCC		
		ATTGTTTGT AG CCGG		
		GTC A		
GAM707	LOC158382 5'	GGCCAGGAGTTTGTGA	41967	TAAT _
		TAACAAA CTCC GGCC		

		ATTGTTT GAGG CCGG	
		_____ A	
GAM707	LOC163255 5'	GGCCAGCTGGTTTGTAT 40108	AAT CC
		ATAACAAAT CT GGCC	
		TATTGTTTG GA CCGG	
		GTC ____	
GAM707	LOC200420 5'	GGCCGAAGGCTTGTATG 29813	ATAA C
		TATAACAA TCT CGGCC	
		GTATTGTT GGA GCCGG	
		C____ A	
GAM708	ATP7B 3'	TGAGACCACAGTTTACCTCA 5509	CAT A
		TGAGGTAAACT TG TTTCA	
		ACTCCATTTGA AC AGAGT	
		C__ C	
GAM708	EGLN2 3'	GAAATAAAAGTTTACCTCA 18990	CATTG
		TGAGGTAAACT ATTTC	
		ACTCCATTTGA TAAAG	
		AAA__	
GAM708	NDUFA5 3'	TTGAAATTATGGTTAACCTCA 11443	A T T
		TGAGGT AAC CAT GATTTCAA	
		ACTCCA TTG GTA TTAAAGTT	
		A _ _	
GAM708	STXBP1 3'	TGAAACTTGTTTACCTTA 9142	TCATTGA
		TGAGGTAAAC TTTCA	
		ATTCCATTTG AAAGT	
		TTC____	
GAM708	DKFZp434M0331 5'	TGAAATCCTTTTACCTC 19075	CTCATT
		GAGGTAAA GATTTCA	
		CTCCATTT CTAAAGT	
		TTC____	
GAM708	DKFZP547E2110 3'	TTGAAAGAACAAAGTTTACTTC 43733	CATTGA
	A	TGAGGTAAACT TTTCAA	
		ACTTCATTTGA AAAGTT	
		AACAAG	
GAM708	DRIL2 3'	TTGATGCACAGAATTTACCTCA 13193	C AT ATT
		TGAGGTAAA TC TG TCAA	
		ACTCCATTT AG AC AGTT	
		A AC GT_	
GAM708	FLJ12671 5'	GAGATCGAGCTTACCTCA 25243	A ATT
		TGAGGTAA CTC GATTTT	

		ACTCCATT GAG CTAGAG	
		C ____	
GAM708	FLJ12891 3'	TCAAAGTAGTTTACCTCA 24511	CA_
		TGAGGTAAACT TTGA	
		ACTCCATTTGA AACT	
		TGA	
GAM708	H2AFJ 3'	TGGGCATAATAGTTTACCTCA 20238	C AT
		TGAGGTAAACT ATTG TTCA	
		ACTCCATTTGA TAAT GGGT	
		_ AC	
GAM708	KIAA0261 3'	TTGAAAATTGATTTACCTCA 33836	C TTGA
		TGAGGTAAA TCA TTTCAA	
		ACTCCATTT AGT AAAGTT	
		_ TA__	
GAM708	KIAA1045 3'	TGAAATCACCATTCCCCTCA 35202	TA CTCAT
		TGAGG AA TGATTTCA	
		ACTCC TT ACTAAAGT	
		CC ACC__	
GAM708	KIAA1432 5'	TGAAATTGAGTCTGACCTCA 33154	AA_ TTG
		TGAGGT ACTCA ATTTCA	
		ACTCCA TGAGT TAAAGT	
		GTC ____	
GAM708	MGC11034 3'	TGAAATGGATTATTTATCTCA 25473	CTC G
		TGAGGTAAA ATT ATTTCA	
		ACTCTATTT TAG TAAAGT	
		AT_ G	
GAM708	RA-GEF-2 3'	TGAATACAAGTTTACCTCA 18466	CAT AT
		TGAGGTAAACT TG TTCA	
		ACTCCATTTGA AC AAGT	
		__ AT	
GAM708	LOC145844 3'	GAGGTAAAGTTTACTTCA 38000	CAT
		TGAGGTAAACT TGATTTT	
		ACTTCATTTGA ATTGGAG	
		__	
GAM708	LOC147180 5'	TTGAAACCCAGATTTACCTC 40819	C ATTGA
		GAGGTAAA TC TTTCAA	
		CTCCATTT AG AAAGTT	
		_ ACCC_	
GAM708	LOC150933 3'	TTAAAGAGAATTACCTCA 41274	A_ A
		TGAGGTAA CTC TTGA	

ACTCCATT GAG AATT
 AA A
 GAM708 LOC157450 3' TGAAGAGCAGAGCTTACCTCA 35149 A AT A_
 TGAGGTAA CTC TG TTTCA
 ||||| ||| || ||||
 ACTCCATT GAG AC GAAGT
 C _ GA
 GAM708 LOC221486 3' TGAAATCACTTTACCTGCA 43747 _ CTCAT
 TG AGGTAAA TGATTTC
 || ||||| |||||
 AC TCCATTT ACTAAAGT
 G C____
 GAM709 REPS2 5' CAACACAGTTTTACATTGCCCT 11097 C ACA ____
 GA CAG GGCAAT GTGAA TGTG
 || ||||| |||| ||||
 GTC CCGTTA CATTT ACAAC
 _ _ TGAC
 GAM709 TRPM8 3' CAACATTCATATGTTTGC 23514 _ C
 GCAA TA AGTGAATGTTG
 ||| || |||||
 CGTT GT TCACTTACAAC
 T A
 GAM709 LOC199923 3' CAACTGCCTGCAACCGCCGCTG 42667 AATA_ TGAAT
 A TCAGCGGC CAG GTTG
 ||||| ||| ||||
 AGTCGCCG GTC CAAC
 CCAAC CGT____
 GAM710 PRX 3' CTGAGATGAAACTCCCT 21936 CCAAC A
 AGGGA TTCATCTCA G
 |||| ||||| |
 TCCCT AAGTAGAGT C
 CA_ C
 GAM710 PRX 3' TGAGATGAAGCTTCC 21942 GACCAA
 GGAGG CTTCATCTCA
 |||| |||||
 CCTTC GAAGTAGAGT

 GAM710 BRD2 5' TCTTTTGAAGAGTCAGTCCCTC 11576 CA CA TC
 C GGAGGGAC ACTT TC AAGA
 ||||| ||| || ||||
 CCTCCCTG TGAG AG TTCT
 AC A_ TT
 GAM710 FLJ14082 3' TCCTGAGACCCAAGGTTCCCTCC 24612 AACTTCA A
 GGAGGGACC TCTCA GA
 ||||| |||| ||
 CCTCCTTG AGAGT CT
 AACCC_ C
 GAM710 KIAA0444 3' GGGCTGATGGTCCCTCC 31244 ACT T
 GGAGGGACCA TCA CTC
 ||||| ||| |||

CCTCCCTGGT AGT GGG
 ____ C
 GAM710 KIAA0574 3' TCTCTGAGAAAGTAGCCCTCC 34348 ACCA TCA _
 GGAGGG ACT TCTCA AGA
 ||||| || ||||| ||
 CCTCCC TGA AGAGT TCT
 CGA_ ____ C
 GAM710 KIAA1209 3' CTTGAGACTGAGTCTCTCC 30471 CAACT _
 GGAGGGAC TCA TCTCAAG
 ||||| || |||||
 CCTCTCTG AGT AGAGTTC
 ____ C
 GAM710 P450RAI-2 3' TGTGTTGTAATTGGTCCCTCC 21271 CTT TCT
 GGAGGGACCAA CA CA
 ||||| || ||
 CCTCCCTGGTT GT GT
 AAT TGT
 GAM710 RABL4 5' CTTGAGATCAGCCCTCC 13729 ACCAA TC
 GGAGGG CT ATCTCAAG
 ||||| || |||||
 CCTCCC GA TAGAGTTC
 ____ C_
 GAM710 SEC61A1 3' TCTTGAGACCTGATGCCCTCC 14986 ACCAACT _
 GGAGGG TCA TCTCAAGA
 ||||| || |||||
 CCTCCC AGT AGAGTTCT
 GT____ CC
 GAM710 TCL6 5' GGGCAGTTAGTCCTTCC 21776 C TCAT
 GGAGGGAC AACT CTC
 ||||| || ||
 CCTTCCTG TTGA GGG
 A C____
 GAM710 TCL6 5' GGGCAGTTAGTCCTTCC 21778 C TCAT
 GGAGGGAC AACT CTC
 ||||| || ||
 CCTTCCTG TTGA GGG
 A C____
 GAM710 LOC221543 3' CTTGGCTCCAGCTGGTCCCTCC 45012 A TCATC
 GGAGGGACCA CT TCAAG
 ||||| || |||||
 CCTCCCTGGT GA GGTTTC
 C CCTC_
 GAM710 LOC257596 3' CTTGGCTCCAGCTGGTCCCTCC 46753 A TCATC
 GGAGGGACCA CT TCAAG
 ||||| || |||||
 CCTCCCTGGT GA GGTTTC
 C CCTC_
 GAM710 LOC63923 3' CTTGATAATTGGTTCCTCC 33323 CTTTCATC
 GGAGGGACCAA TCAAG
 ||||| || |||||

			CCTCCTTGGTT	AGTTC	
			AAT____		
GAM710	LOC92080	5'	GAGGTGGGACTGGCCTCTCC	33760	A AC
			GGAGGG CCA TTCATCTC		
			CCTCTC GGT GGGTGGAG		
			C CA		
GAM711	ATP2B2	5'	TCCAGACCCTGACACCTCTCA	7404	ATTTAAC
			TGAGGG CAGGGTCTGGA		
			ACTCTC GTCCCAGACCT		
			CACA____		
GAM711	DR1	5'	CCAAACTCATCCTAAATCTCTC	29856	ACCA C
	A		TGAGGGATTTA GGGT TGG		
			ACTCTCTAAAT CTCA ACC		
			CCTA A		
GAM711	E2F1	3'	CCAGACCCTGTGGTCCCTC	41119	TAAC
			GAGGGATT CAGGGTCTGG		
			CTCCCTGG GTCCCAGACC		
			T____		
GAM711	FAAH	3'	CCAGACCCTGGGGCAGCCCCTC	23596	ATTTAA
			GAGGG CCAGGGTCTGG		
			CTCCC GGTCCCAGACC		
			CGACGG		
GAM711	SORBS1	3'	CCAAGACCAAATCCCTCA	17686	AACCAG _
			TGAGGGATTT GGTCT GG		
			ACTCCCTAAA CCAGA CC		
			_____ A		
GAM711	TYRO3	3'	CCGGA CTGACCAAATCACCCA	12985	A _ AACCAG
			TG GG GATT GGTCTGG		
			AC CC CTAAA TCAGGCC		
			_ A CCAG__		
GAM711	UBE2L3	3'	CCAGACCCCGGGCTCGCCTC	9357	_ TTAA A
			GAGG GA CC GGGTCTGG		
			CTCC CT GG CCCAGACC		
			G CG__ C		
GAM711	C1orf34	3'	TCCAGACCACGGGCCAAATCCC	30438	AA AG_
	T		AGGGATTT CC GGTCTGGA		
			TCCCTAAA GG CCAGACCT		
			CC GCA		
GAM711	FLJ13305	5'	TCCAGACCCCGGTAAATCCCAT	43344	_ A A
	CA		TGA GGGATTTA CC GGGTCTGGA		

ACT CCCTAAAT GG CCCAGACCT
 A _ C
 GAM711 KIAA1634 3' CCAGAGATCAATCCCTCA 31753 TAACCA G_
 TGAGGGATT GG TCTGG
 ||||| || ||||
 ACTCCCTAA CT AGACC
 _____ AG
 GAM711 MGC11287 3' TCAGACCAGACCCCTCA 25502 A AACCAG
 TGAGGG TTT GGTCTGG
 ||||| || |||||
 ACTCCC AGA CCAGACT
 C _____
 GAM711 P114-RHO-GEF 3' CCAGACCCTGGCACCCTC 17638 ATTTAA
 GAGGG CCAGGGTCTGG
 |||| |||||
 CTCCC GGTCCCAGACC
 AC_____
 GAM711 PPP1R16B 3' CCAGACTGACGCTGAAATCCCT 30770 AAC ____
 CA TGAGGGATTT CAG GGTCTGG
 ||||| || |||||
 ACTCCCTAAA GTC TCAGACC
 _____ GCAG
 GAM711 RAI16 3' CCAGACCCCAGACCCTCA 22969 A AACCA
 TGAGGG TTT GGGTCTGG
 ||||| || |||||
 ACTCCC AGA CCCAGACC
 _ C_____
 GAM711 TIAM2 3' TCCAGATATGGGTAAATTCCT 14824 AGG
 CA TGAGGGATTTAACC GTCTGGA
 ||||| |||||
 ACTCCTTAAATTGG TAGACCT
 GTA
 GAM711 TIMM9 5' TCCAGACCCTGACCCTCCCTC 14832 TTTAAC
 GAGGGA CAGGGTCTGGA
 |||| |||||
 CTCCCT GTCCCAGACCT
 CCCA_____
 GAM711 LOC112868 3' CCAGACCCTGTGTCCCCCA 36077 A TTAAC
 TG GGGAT CAGGGTCTGG
 || |||| |||||
 AC CCCTG GTCCCAGACC
 C T_____
 GAM711 LOC116228 3' CAGCATCTAACTAAATCCTCA 36534 G ACCA _
 TGAGG ATTTA GGGT CTG
 |||| |||| ||||
 ACTCC TAAAT TCTA GAC
 _ CAA_ C
 GAM711 LOC201910 3' CCTTGGTCAAATCCTTCA 42929 A
 TGAGGGATTT ACCAGGG
 ||||| |||||

ACTTCCTAAA TGGTTCC

C

GAM712 DKFZp566D234 5' AACAGGACCCATATCAAC 30991 C CGA

GTT GATA GTCCTGTT

||| ||| |||||

CAA CTAT CAGGACAA

_ ACC

GAM713 CBFA2T1 3' CTGTGAGGTTTCCCAATGGTGT 10544 T CAA A G

AC CCAT GAAAC TCA CAG

|| ||| ||||| ||| |||

TG GGTA CTTTG AGT GTC

T ACC G _

GAM713 DGAT2 3' TCTGTTATCTCTTGATGAG 26293 C AACATC

CTC ATCAAGA AGCAGA

||| ||||| |||||

GAG TAGTTCT TTGTCT

_ CTA__

GAM713 IL24 3' TCTGCTGATATCTGCAGGGA 13721 ATCA AAC

TCC AGA ATCAGCAGA

||| ||| |||||

AGG TCT TAGTCGTCT

GACG A__

GAM713 MAPRE1 3' CTGGTCTTTCTTGACAGGGT 14707 CA C

ACTC TCAAGAAA ATCAG

|||| ||||| |||||

TGGG AGTTCTTT TGGTC

AC C

GAM713 NEO1 3' CTGCTGATATTCTGCAGGA 8316 ATCA AC

TCC AGAA ATCAGCAG

||| ||| |||||

AGG TCTT TAGTCGTC

ACG_ A_

GAM713 PTER 3' TCTGCTGATCAAAGATGATCAA 25000 CC AGAAAC

G

CT ATCA ATCAGCAGA

|| ||| |||||

GA TAGT TAGTCGTCT

AC AGAAAC

GAM713 RAG1 3' TCCGCTAAGTTTAGATGGAGT 6041 AAG ATC A

ACTCCATC AAAC AGC GA

||||| ||| ||| ||

TGAGGTAG TTTG TCG CT

A__ AA_ C

GAM713 SIRT3 3' TCTGCTGAAGCTCCTAATGGA 14546 CAA AACA

TCCAT GA TCAGCAGA

|||| || |||||

AGGTA CT AGTCGTCT

ATC CGA_

GAM713 SPON1 3' TCTGAATACTTCTTGATGGG 31305 ACATCAG

TCCATCAAGAA CAGA

||||||| |||

			GGGTAGTTCTT	GTCT	
			CATAA__		
GAM713	ZNF74	3'	CTGTTTTCCTTGATGGG	9473	A CATC
			TCCATCAAG AA	AGCAG	
			GGGTAGTTC TT	TTGTC	
			C ____		
GAM713	C21orf69	5'	TTGAGTCTCCCTGGTGGAG	27752	A_ A A
			CTCCATCA GA AC	TCAG	
			GAGGTGGT CT TG	AGTT	
			CC C _		
GAM713	CHK	3'	CTGCCCTTCCTCCTGATGGAGT	6946	A AACATCA
			ACTCCATCA GA	GCAG	
			TGAGGTAGT CT	CGTC	
			C CCTTCC_		
GAM713	DKFZP434N1235	3'	TCTGCTGATGTTTATCTT	25313	__
			AAGA AACATCAGCAGA		
			TTCT TTGTAGTCGTCT		
			AT		
GAM713	DKFZp547H025	3'	TCTAGGAGTCTCTTGATGAG	21376	C A A AGC
			CTC ATCAAGA AC TC	AGA	
			GAG TAGTTCT TG AG	TCT	
			_ C _ GA_		
GAM713	DRIL2	3'	TCTGCTGATGGGAAGGCAGAG	13192	CA AAGAAA
			CTC TC CATCAGCAGA		
			GAG GG GTAGTCGTCT		
			AC AAGG__		
GAM713	FLJ12294	3'	CTGCTGGACTGTTATTTCTTGA	24745	__ _
			TCAAGAA ACA TCAGCAG		
			AGTTCTT TGT GGT	CGTC	
			TAT CA		
GAM713	FLJ12476	5'	TCTGCATAGTTTTGATGAAG	23068	C AACATCA
			CT CATCAAGA	GCAGA	
			GA GTAGTTTT	CGTCT	
			A GATA__		
GAM713	FLJ14525	3'	TCTAATAATGTTTCTTAATGG	26551	C CAGC
			CCAT AAGAAACAT	AGA	
			GGTA TTCTTTGTA	TCT	
			A ATAA		
GAM713	FLJ20511	3'	CTGCTGATAAGAGGGAGGAGT	19528	A AAGAAAC
			ACTCC TC ATCAGCAG		

		TGAGG AG TAGTCGTC	
		G GAGAA__	
GAM713	FLJ23120 3'	CTGCTAATGGGGATGGGGT 41264	AAGAAA C
		ACTCCATC CAT AGCAG	
		TGGGGTAG GTA TCGTC	
		GG__ A	
GAM713	FLJ31951 3'	TCTGCTGATGTTTTATAGAG 29552	C CAA
		CTC AT GAAACATCAGCAGA	
		GAG TA TTTTGTAGTCGTCT	
		A __	
GAM713	KIAA0317 3'	TCTGCTGATACTCCTTGGAG 16798	TCAA AAC
		CTCCA GA ATCAGCAGA	
		GAGGT CT TAGTCGTCT	
		TC__ CA__	
GAM713	KIAA0321 5'	TCCACTGTCTTCCCTGGTGGAG 31269	A_ ACAT CA
		CTCCATCA GAA CAG GA	
		GAGGTGGT CTT GTC CT	
		CC CT__ AC	
GAM713	KIAA0523 3'	TCTGCGAAGGCCCTGATGGAG 33647	AGAAACA A
		CTCCATCA TC GCAGA	
		GAGGTAGT AG CGTCT	
		CCCCGGA _	
GAM713	KIAA1598 3'	CTGATCCTCTTGATGGAG 20330	AAC
		CTCCATCAAGA ATCAG	
		GAGGTAGTTCT TAGTC	
		CC__	
GAM713	KIAA1607 3'	CTGCTGCTGCCTGATGGAG 31914	A AAA T
		CTCCATCA G CA CAGCAG	
		GAGGTAGT C GT GTCGTC	
		_C__ C	
GAM713	KIAA1911 3'	TCTGCTGATACAGTGATAGG 36394	_ AGAAAC
		CC ATCA ATCAGCAGA	
		GG TAGT TAGTCGTCT	
		A GACCA__	
GAM713	MGC10818 3'	GCTTCGCTTTTGATGGAGT 24941	AACATC
		ACTCCATCAAGA AGC	
		TGAGGTAGTTTT TCG	
		CGCT__	
GAM713	MMD 3'	TCTGCTGGAACTCCTGAAGAG 30076	CA A AACA
		CTC TCA GA TCAGCAGA	

			GAG AGT CT	GGTCGTCT		
			A_ C CAAA			
GAM713	RAP2B	3'	TCTGCTGATATTTGTGGA	45862	T	AAAC
			TCCA CAAG	ATCAGCAGA		
			AGGT GTTT	TAGTCGTCT		
			_ A__			
GAM713	SEC15B	3'	TCTGCTGATACCTTGATG	33130		AAAC
			CATCAAG	ATCAGCAGA		
			GTAGTTC	TAGTCGTCT		
			CA__			
GAM713	TRIM26	3'	CTGCTGGTTTTCCCGAGGGA	9500	A AA	AT
			TCC TC	GAAAC CAGCAG		
			AGG AG	CTTTG GTCGTC		
			G CC	_		
GAM713	TU3A	5'	TCTGGGACTTCCCGGTGGAGT	14037	AA	ACA AG
			ACTCCATC	GAA TC CAGA		
			TGAGGTGG	CTT AG GTCT		
			CC C_ G_			
GAM713	ZER6	3'	GATATTTTCTTGATGAAGT	31743	C	C_
			ACT CATCAAGAAA	ATC		
			TGA GTAGTTCTTT	TAG		
			A	TA		
GAM713	ZNF337	3'	CTACTGATGTTTTGATG	33772	GA	C
			CATCAA	AACATCAG AG		
			GTAGTT	TTGTAGTC TC		
			_	A		
GAM713	LOC127702	3'	TCTGCTGGGCCCTGAAGGAG	37184	A	AGAAACA
			CTCC TCA	TCAGCAGA		
			GAGG AGT	GGTCGTCT		
			A CCCG__			
GAM713	LOC146669	3'	CTGCTGATGAATGACCGAGT	38224	CA	AGAAA
			ACTC TCA	CATCAGCAG		
			TGAG AGT	GTAGTCGTC		
			CC AA__			
GAM713	LOC146856	5'	TCTGCTGATATGGAATGGA	40300	_	AAGAAAC
			TCCAT C	ATCAGCAGA		
			AGGTA G	TAGTCGTCT		
			A GTA__			
GAM713	LOC150225	3'	TCTGCTGACGATGAGGCAG	41192	_ A	AGAAACA
			CT CC TCA	TCAGCAGA		

		GA GG AGT AGTCGTCT		
		C _ AGC_____		
GAM713	LOC150406 3'	TCTGCTGAGTGTAATGGA	38965	CAAGAA A
		TCCAT AC TCAGCAGA		
		AGGTA TG AGTCGTCT		
		AATG__ _		
GAM713	LOC152300 3'	TGTTAGTGTTTTTAATGGAG	39253	C C
		CTCCAT AAGAAACAT AGCA		
		GAGGTA TTTTTGTG TTGT		
		A A		
GAM713	LOC154790 5'	GCTGGTGTGACGGAGT	39491	A AAGAA
		ACTCC TC ACATCAGC		
		TGAGG AG TGTGGTCG		
		C C_____		
GAM713	LOC155081 3'	CTGGACCATTCTTGATGGAG	39544	ACA_
		CTCCATCAAGAA TCAG		
		GAGGTAGTTCTT GGTC		
		ACCA		
GAM713	LOC170372 5'	CTACTGATGTTGTTGAT	37540	GA C
		ATCAA AACATCAG AG		
		TAGTT TTGTAGTC TC		
		G_ A		
GAM713	LOC170425 3'	TCTGCTGATGTCCTGACCATGG	37553	CA__ AA
	A	TCCAT AG ACATCAGCAGA		
		AGGTA TC TGTAGTCGTCT		
		CCAG C_		
GAM713	LOC202802 3'	CTGGACCATTCTTGATGGAG	42989	ACA_
		CTCCATCAAGAA TCAG		
		GAGGTAGTTCTT GGTC		
		ACCA		
GAM713	LOC221810 3'	TCTGCTGACATTCCTTGG	45086	A CA
		TCAAG AA TCAGCAGA		
		GGTTC TT AGTCGTCT		
		C AC		
GAM713	LOC222228 3'	CTGGACCATTCTTGATGGAG	45275	ACA_
		CTCCATCAAGAA TCAG		
		GAGGTAGTTCTT GGTC		
		ACCA		
GAM713	LOC222233 3'	CTGGACCATTCTTGATGGAG	45244	ACA_
		CTCCATCAAGAA TCAG		

		GAGGTAGTTCTT	GGTC		
		ACCA			
GAM713	LOC253502	3'	CTGCTGATCCTGACGGA	45381	A A AACA
			TCC TCA GA TCAGCAG		
			AGG AGT CT AGTCGTC		
			C C ____		
GAM713	LOC255242	5'	TCTGCTGGAGTCCTGATGGG	45906	A AACA
			TCCATCA GA TCAGCAGA		
			GGGTAGT CT GGTCGTCT		
			C GA__		
GAM713	LOC257494	3'	CTGCTGGTTTCCCGAGGGA	46687	A AA AT
			TCC TC GAAAC CAGCAG		
			AGG AG CTTTG GTCGTC		
			G CC ____		
GAM713	LOC57115	3'	TCTACTGATGTTTATTAGAG	21663	CATCAAG C
			CTC AAACATCAG AGA		
			GAG TTTGTAGTC TCT		
			ATTA__ A		
GAM714	IGFBP3	3'	TTAGAGTCATTCTCATGCT	6200	C AAA
			AGCATGAGAA TGA TAA		
			TCGTACTCTT ACT ATT		
			_ GAG		
GAM714	SULT1C1	3'	TTGGGTTTCAGTCTCATGC	6723	A AA
			GCATGAGA CTGAA TAA		
			CGTACTCT GACTT GTT		
			_ GG		
GAM714	CGI-142	3'	GATTTATTTTTTTTCCCAGTGC	18148	GA_ CT
			GCAT GAA GAAAATAAATC		
			CGTG CTT TTTTATTTAG		
			ACC ____		
GAM714	FLJ20783	3'	ATTTATTTTCATGTTATGC	19669	GAAC
			GCATGA TGAAAATAAAT		
			CGTATT ACTTTTATTTA		
			GT__		
GAM714	FLJ22625	3'	TTATTATCAGTTCTATGCTA	24043	G A
			TAGCAT AGAACTGA AATAA		
			ATCGTA TCTTGACT TTATT		
			_ A		
GAM714	KIAA1966	3'	ATTTATTTTCAGCTGTCTGC	28495	T GAA
			GCA GA CTGAAAATAAAT		

			CGT CT GACTTTTATTTA		
			_ GTC		
GAM714	LRMP	5'	ATTTTCAGTTTTGCCTGC 12806	TG_	
			GCA AGAACTGAAAAT		
			CGT TTTTGACTTTTA		
			CCG		
GAM714	SV2	3'	TTCACCTTCGTCATGCTG 16887	_ C_	
			TAGCATGA GAA TGAA		
			GTCGTA CT T ACTT		
			G CC		
GAM714	LOC152756	3'	GATTTATTCCAGTGACCTTGCT 41550	TGAGA AA	
	A		TAGCA ACTG AATAAATC		
			ATCGT TGAC TTATTTAG		
			TCCAG C_		
GAM714	LOC84549	3'	ATTTATATAGCTCTCATGT 26256	A AAA	
			GCATGAGA CTG ATAAAT		
			TGTACTCT GAT TATTTA		
			C A_		
GAM715	FLJ11259	3'	GGTTTCAACAAGTCAGGTGA 20386	C CGTC	
			TTACC GACTTGT TGAAATT		
			AGTGG CTGAACA ACTTTGG		
			A _		
GAM715	MGC10946	5'	AATTTCAAGCAAGAGTCG 24946	GTCG	
			CGACTT TCTGAAATT		
			GCTGAG AGACTTTAA		
			AACG		
GAM715	LOC149650	3'	TCCTGAGATAAGTCAGGTAA 38796	C G T_	
			TTACC GACTTGTC TC GA		
			AATGG CTGAATAG AG CT		
			A _ TC		
GAM716	POU3F1	3'	GAAACTTTTCAACAAAACCAA 29830	CC CG CG	
			TTGGT TG TC GAGTTTC		
			AACCA AC AG TTCAAAG		
			AA A_ CT		
GAM716	TMOD	3'	GAAACTCCAGATATCAA 9293	CCTGC C	
			TTGGT GTC GGAGTTTC		
			AACTA TAG CCTCAAAG		
			_ A		
GAM716	ZNF80	5'	GAAACTCCGAACACATCCGA 13987	TCC C C	
			TTGG TG GT CGGAGTTTC		

			AGCC AC CA GCCTCAAAG	
			T__ A A	
GAM716	LOXL4	3'	AGGAGTATAGGACAGAGGACCA 25927	GC GGAGT
	A		TTGGTCCT GTCC TTCCT	
			AACCAGGA CAGG GAGGA	
			GA ATAT_	
GAM716	SFXN2	3'	GGAAATCAACCAGGACCAA 36605	C CCG G
			TTGGTCCTG GT GA TTTCC	
			AACCAGGAC CA CT AAAGG	
			_ A__ _	
GAM716	LOC145814	5'	GAAACTCCGAACACATGC 37986	CC C C
			GT TG GT CGGAGTTTC	
			CG AC CA GCCTCAAAG	
			T_ A A	
GAM716	LOC147042	3'	AGGAAACCCCATCAAGGACCGA 40786	GCGTCC A
			TTGGTCCT GG GTTTCCT	
			AGCCAGGA CC CAAAGGA	
			ACTAC_ _	
GAM716	LOC196540	3'	AGGAGCATGGACACAGGACCAG 43149	C GA T
			TTGGTCCTG GTCCG GTT CCT	
			GACCAGGAC CAGGT CGA GGA	
			A A_ _	
GAM716	LOC51141	3'	AGGAAACTCCAAACAGATCA 34046	C CGTCC
			TGGTC TG GGAGTTTCCT	
			ACTAG AC CCTCAAAGGA	
			_ AAA_	
GAM717	BCL2	3'	CTAAACCTTTTGAAAATCTGC 6255	G C__
	C		GGCAGATTTT TCGGA TTAG	
			CCGTCTAAAA GGTTT AATC	
			_ TCCA	
GAM717	LOC120939	3'	TCCAATGGCCAAAATCTGC 37515	_ _
			GCAGATTTTG TC GGA	
			CGTCTAAAC GG CCT	
			C TAA	
GAM717	LOC143381	3'	ATCCAAGTGACTTTAAATCTGC 37612	T__ GG A
	C		GGCAGATTT GTC ACTT GAT	
			CCGTCTAAA CAG TGAA CTA	
			TTT _ C	
GAM717	LOC257095	5'	ATCTACCAAAACAAGATCTGCC 46312	C__ ACT
	A		TGGCAGATTTTGT GG TAGAT	

ACCGTCTAGAACA CC ATCTA
 AAA ____
 GAM717 LOC51055 5' CTATATCACAAAAACCTGCCA 18044 A_ CG CT
 TGGCAG TTTTGT GA TAG
 ||||| ||||| || |||
 ACCGTC AAAACA CT ATC
 CA ____ AT
 GAM717 LOC92597 3' ATCTAAGTTATGAAATCCAACA 34673 GCA TG CG
 TG GATTT T GACTTAGAT
 || ||||| | |||||
 AC CTAAC A TTGAATCTA
 AAC GT____
 GAM718 FGA 3' AACTTATAATTACAATGCA 6118 TTC A
 TGCATTGTA GTTA GAGTT
 ||||| |||||
 ACGTAACAT TAAT TTCAA
 ____ A
 GAM718 PLAGL2 3' AACTCTTAACAGATGCAGT 34872 TC
 ATTGTAT GTTAAGAGTT
 ||||| |||||
 TGACGTA CAATTCTCAA
 GA
 GAM718 LOC256112 3' AACCTTTTGAATACAATG 46101 TT A
 CATTGTATTCG AAG GTT
 ||||| |||||
 GTAACATAAGT TTC CAA
 T_ _
 GAM718 LOC92979 5' TAACTCTTAATCTTCACAAT 28765 ATTC
 ATTGT GTTAAGAGTTA
 ||||| |||||
 TAACA TAATTCTCAAT
 CTC
 GAM719 FGF4 5' GCACCTCCTCGGTTGCGCAC 7745 G CC _
 GTGCGCAAC GAG GAG TGT
 ||||| |||||
 CACGCGTTG CTC CTC ACG
 G ____ C
 GAM719 NPR1 5' CGCACACTCCAGTTGTTTAC 42233 C _ AGCC A
 GTG GCAAC GG GAGTGT CG
 ||||| |||||
 CAC TGTTG CC CTCACA GC
 T A ____ C
 GAM719 TBR1 3' AACTCCTCCTTGCGCAC 13357 C CC
 GTGCGCAA GGAG GAGTGT
 ||||| |||||
 CACGCGTT CCTC CTCACA
 _ _
 GAM719 KIAA0125 3' AACTTGGGCCCATGCACAC 30342 C AC AG
 GTG GCA GG CCGAGTGT
 ||||| |||||

CAC CGT CC GGTTCACA
A AC G_
GAM720 MSF 3' CCAGGGGAGAATGCAGCCCA 42520 A A_ G C
TGG GT CATTCTCC TC GG
||| || ||||| || ||
ACC CG GTAAGAGG GG CC
_ AC _ A
GAM720 CHST8 5' CCACCGGACAGAGAACTTTCC 22817 TACA C
GGAG TTCTC GTCCGGTGG
|||| |||| |||||
CCTT AAGAG CAGGCCACC
TC_ A
GAM720 KIAA0435 3' CATGACGGAGAATGCCCTCCA 16718 TA CG
TGGAG CATTCTCCGTC GTG
|||| ||||| |||
ACCTC GTAAGAGGCAG TAC
CC _
GAM721 DNMT3B 3' ACAGACATACATTTCTCA 13758 G CAA CA
TGAG AAATGTA TG CTGT
|||| |||| || |||
ACTC TTTACAT AC GACA
_ _ A_
GAM721 OXR1 3' ACAGATGCATATTTCTCA 19731 GTACA _
TGAGGAAAT ATGCA CTGT
||||| |||| |||
ACTCCTTTA TACGT GACA
_ A
GAM721 SRC 3' ACATGTTGTACATTTACCA 11886 AG AT C
TG GAAATGTACA GCA TGT
|| ||||| ||| |||
AC CTTTACATGT TGT ACA
CA _ _
GAM721 SUFU 3' GACAGGGTATCACACATTTCTC 18254 G ACA A
A TGAG AAATGT ATGC CTGTC
|||| |||| ||| |||||
ACTC TTTACA TATG GACAG
_ CAC G
GAM721 FLJ22596 5' GACAGTGCTGGACATTTCTC 24704 ACAAT
AGGAAATGT GCACTGTC
||||| |||||
TCCTTTACA CGTGACAG
GGT_
GAM721 KIAA0229 3' GACAGTGCATCGATGCTCCCCC 44402 AAAT CA_
GG GTA ATGCACTGTC
|| || |||||
CC CGT TACGTGACAG
CCCT AGC
GAM721 KIAA1228 3' GACACCTTGTACTTTTCTCA 32443 T TGCAC
TGAGGAAA GTACAA TGTC
||||| |||| |||

			ACTCCTTT CATGTT	ACAG		
			T	CC__		
GAM721	STX6	3'	ACAGTGCACCGCTGTCCCA	12419	A AAT ACAA	
			TG GGA GT	TGCACTGT		
			AC CCT CG	ACGTGACA		
			_ GT_ CC_			
GAM721	LOC126661	3'	GACAGTAGGAGGCTACCTTTCC	36852	T CAATGC_	
			TCA	TGAGGAAA GTA	ACTGTC	
			ACTCCTTT CAT	TGACAG		
			C CGGAGGA			
GAM721	LOC146823	3'	GCTTCCTGTACATTTCCTCA	40749	AT__	
			TGAGGAAATGTACA	GC		
			ACTCCTTTACATGT	CG		
			CCTT			
GAM721	LOC152018	3'	ACAGTGTAACACTTCTCA	41419	AA ACAA	
			TGAGGA TGT	TGCACTGT		
			ACTCTT ACA	ATGTGACA		
			C_ ____			
GAM721	LOC157278	3'	ACAAAATGACATTCCCTCA	41776	A A ATGCAC	
			TGAGG AATGT CA	TGT		
			ACTCC TTACA GT	ACA		
			C _ AAA__			
GAM721	LOC219855	3'	ACAGTCTTCTCTGTGCATTTC	43995	A ATGC__	
			CCA	TG GGAAATGTACA	ACTGT	
			AC CCTTTACGTGT	TGACA		
			C CTCTTC			
GAM721	LOC255461	3'	ACAAAATGACATTCCCTCA	46462	A A ATGCAC	
			TGAGG AATGT CA	TGT		
			ACTCC TTACA GT	ACA		
			C _ AAA__			
GAM721	LOC255516	3'	ACAAAATGACATTCCCTCA	46468	A A ATGCAC	
			TGAGG AATGT CA	TGT		
			ACTCC TTACA GT	ACA		
			C _ AAA__			
GAM722	BACE	3'	ACTAACCTGGAGACAGTAACA	14413	C T CATGA	
			TGT ACT TC	TAGGTTAGT		
			ACA TGA AG	GTCCAATCA		
			A C AG__			
GAM722	BACE	3'	ACTAACCTGGAGACAGTAACA	29081	C T CATGA	
			TGT ACT TC	TAGGTTAGT		

ACA TGA AG GTCCAATCA
 A C AG____
 GAM722 CHST5 3' ACTCTTCATGGAAAGCAAC 14438 CA TA
 GT CTTTCCATGA GGT
 || ||||| ||
 CA GAAAGGTACT TCA
 AC TC
 GAM722 CHST6 3' ACTCTTCATGGAAAGCAAC 22243 CA TA
 GT CTTTCCATGA GGT
 || ||||| ||
 CA GAAAGGTACT TCA
 AC TC
 GAM722 FMN2 3' ACCAATTATGGAAAGCAAC 38740 CA A
 GT CTTTCCATGAT GGT
 || ||||| ||
 CA GAAAGGTATTA CCA
 AC A
 GAM722 IL20RA 3' ACTAACCTAAAAGAAAATGACA 15788 C CATGA
 TGTCA TTTC TAGGTTAGT
 ||||| |||||
 ACAGT AAAG ATCCAATCA
 A AAA____
 GAM722 PCDHB12 3' TAACTAATAAGTGACA 21002 TCCATG A
 TGTCACCTT AT GGTTA
 ||||| |||||
 ACAGTGAA TA TCAAT
 _____ A
 GAM722 PCDHB7 3' TAACTAATAAGTGACA 21007 TCCATG A
 TGTCACCTT AT GGTTA
 ||||| |||||
 ACAGTGAA TA TCAAT
 _____ A
 GAM722 FLJ22167 3' ACTCTTCATGGAAAGCAAC 23738 CA TA
 GT CTTTCCATGA GGT
 || ||||| ||
 CA GAAAGGTACT TCA
 AC TC
 GAM722 KIAA0737 3' ACTGGGCTACATGGAAAATGAC 16817 C A G
 A TGTCA TTTCCATG TAG TTAGT
 ||||| ||||| |||||
 ACAGT AAAGGTAC ATC GGTC A
 A _ G
 GAM722 SE70-2 5' ACTCATCATGGAAACAACA 22662 CAC AG
 TGT TTTCCATGAT GT
 ||| ||||| ||
 ACA AAAGGTACTA CA
 AC_ CT
 GAM722 LOC112817 3' ACTTGATCAGGAAAAGTGACA 28779 A _
 TGTCACCTTTCC TGAT AGGT
 ||||| ||||| |||||

ACAGTGAAAGG ACTA TTCA
 _ G
 GAM722 LOC112840 3' ACTAACAGTTTTAGAAAGTGA 27954 CAT AG
 TCACTTTC GAT GTTAGT
 ||||| || |||||
 AGTGAAAG TTG CAATCA
 ATT A_
 GAM722 LOC158332 3' ACCTGTCAAAAAATGACA 39822 C CCA
 TGTCA TTT TGATAGGT
 ||||| || |||||
 ACAGT AAA ACTGTCCA
 A AA_
 GAM722 LOC254549 5' CAACCCACAAAGTGACA 46045 CCA ATA A
 TGTCACTTT TG GGTT G
 ||||| || |||||
 ACAGTGAAA AC CCAA C
 C_ C_ C
 GAM723 ALDOA 5' AAGAATTTCTCTGAAGCACCG 5473 GAAGA A
 CGG CA AGGAAATTCTT
 || || |||||
 GCC GT TCCTTTAAGAA
 ACGAA C
 GAM723 KERA 5' AAGAATTTCTTTGCTGGGC 13906 GGGA A
 GC AG CAAAGGAAATTCTT
 || || |||||
 CG TC GTTTCCTTTAAGAA
 GG_ _
 GAM723 PLA2G2D 3' TTTCCCCTGTTTTCCCACA 14775 C AA
 TG GGGAAGACA GGAAA
 || ||||| |||||
 AC CCCTTTTGT CCTTT
 A CC
 GAM723 PODXL 3' AGAACTGGTCTTCTCACA 11870 C AA GAAA
 TG GGGAAGAC AG TTCT
 || ||||| || |||||
 AC CTCTTCTG TC AAGA
 A G_ _
 GAM723 AP3S2 3' GAATATGCTTCCCGCA 12439 A AAGGAA
 TGCGGGAAG CA ATTC
 ||||| || |||||
 ACGCCCTTC GT TAAG
 _ A_
 GAM723 PHYHIP 3' GAACCCTCTTCCTGCA 16509 CAAA AAA
 TGCGGGAAGA GG TTC
 ||||| || |||||
 ACGTCCTTCT CC AAG
 _ C_
 GAM723 LOC136183 5' AAGAATGCTCTTTGTCTTCC 37391 AA
 GGAAGACAAAGG ATTCTT
 ||||| |||||

CCTTCTGTTTCT TAAGAA
 CG
 GAM723 LOC150819 5' AATTTCCCTTTCCCCA 41245 C GACAA
 TG GGGAA AGGAAATT
 || |||| |||||
 AC CCCTT TCCTTTAA

 — ———
 GAM724 APPBP2 3' ATAAGTGGATACAACCACTCTA 13078 ACG A G
 TAGA GGTT GTA TTACTTAT
 ||| ||| ||| |||||
 ATCT CCAA CAT GGTGAATA
 CA_ _ A
 GAM724 BACH1 3' AAGTAACTACACTACCTCA 6853 C TA_
 A GGGT GTAGTTACTT
 | ||| |||||
 A TCCA CATCAATGAA
 C TCA
 GAM724 LOC145371 3' AAGTAATTTACCAGTTCTA 37839 G TAGT
 TAGAAC GGT AGTTACTT
 ||||| ||| |||||
 ATCTTG CCA TTAATGAA
 A T____
 GAM725 APBA1 3' TCTCTGGAAGGCCCTT 34648 A TG
 AAGG GCCTTC CGGAGA
 ||| ||||| |||||
 TTCC CGGAAG GTCTCT
 C _
 GAM725 HDAC5 3' CATCTCTGCAGACCCCTCTCC 29222 A CCT
 A GGAG TCTGCGGAGATG
 | ||| |||||
 C TCTC AGACGTCTCTAC
 C CCC
 GAM725 KCND2 3' CTGTGCAAATAAACTCCTTTTA 14608 CCTTC_ G
 TAAAAGGAG TGCG AG
 ||||| ||| ||
 ATTTTCCTC ACGT TC
 AAATAA G
 GAM725 NDRG1 3' CATCTCCGCATCGCATCCT 29966 _ CTTC
 AGGA GC TGCGGAGATG
 ||| || |||||
 TCCT CG ACGCCTCTAC
 A CT_
 GAM725 KIAA1297 5' CATGCCCAGAAGGCCACC 35710 A_ C AG
 GG GCCTTCTG GG ATG
 || ||||| || |||
 CC CGGAAGAC CC TAC
 AC _ G_
 GAM725 OPRL1 3' CATCCTCCCAAGGCTCC 6615 TC C _
 GGAGCCT TG GGAG ATG
 ||||| || ||| |||

CCTCGGA AC CCTC TAC
 — — C
 GAM725 PPP2R3A 3' ATCTCAGAGACTTCTTTTA 8584 CC GCG
 TAAAAGGAG TTCT GAGAT
 ||||| ||| ||||
 ATTTTCTTC GAGA CTCTA
 A_ —
 GAM725 RA-GEF-2 3' CATCTCCTCAAGGCTCC 18464 TC C
 GGAGCCT TG GGAGATG
 ||||| || |||||
 CCTCGGA AC CCTCTAC
 — T
 GAM725 LOC126961 3' CATCGTATCCAAAAGGCTCTTT 36886 C CGGA_
 T AAAGGAGCCTT TG GATG
 ||||| || ||||
 TTTTCTCGGAA AC CTAC
 A CTATG
 GAM725 LOC201696 3' TTGCCAGAAGGCTCTTTTTA 31627 —
 TAAAAGGAGCCTTCTG CGG
 ||||| ||||| ||||
 ATTTTCTCGGAAGAC GTT
 C
 GAM725 LOC255042 5' CATCCCTCTCAGGCTCCTT 45648 TCTGC A
 AAGGAGCCT GG GATG
 ||||| || ||||
 TTCCTCGGA CC CTAC
 CTCT_ —
 GAM725 LOC257395 3' CATCGTATCCAAAAGGCTCTTT 45694 C CGGA_
 T AAAGGAGCCTT TG GATG
 ||||| || ||||
 TTTTCTCGGAA AC CTAC
 A CTATG
 GAM726 BACH1 3' AAGTAACTACACTACCTCA 6854 C TA_
 A GGGT GTAGTTACTT
 | ||| |||||
 A TCCA CATCAATGAA
 C TCA
 GAM726 SLC4A4 3' AAGTAACTTTGTCCCAGTCCTA 9834 A _ T T
 TAG AC GGG TAG AGTTACTT
 ||| || ||| |||||
 ATC TG CCC GTT TCAATGAA
 C A T _
 GAM726 UC28 3' AAGTAACTGAACCATTC 22278 CG AG
 GAA GGTT TAGTTACTT
 ||| ||| |||||
 CTT CCAA GTCAATGAA
 A_ —
 GAM726 FLJ10933 3' AATAGTTAACCCTTCTA 20267 C TA
 TAGAA GGGTTAG GTT
 |||| ||||| |||

			ATCTT CCAATT TAA		
			— GA		
GAM726	FLJ13659	3'	AGCCTCTAACCCGTCCTG 24831	A	TA
			TAG ACGGGTTAG GTT		
			GTC TGCCCAATC CGA		
			C TC		
GAM726	KIAA1321	3'	AAGTAACTACTTTGGCTC 31191	—	
			GGGTT AGTAGTTACTT		
			CTCGG TCATCAATGAA		
			TT		
GAM726	LOC145371	3'	AAGTAATTTACCAGTTCTA 37840	G	TAGT
			TAGAAC GGT AGTTACTT		
			ATCTTG CCA TTAATGAA		
			A T—		
GAM726	LOC90288	3'	AAGTAACTACTACAGGT 31103	GG	T
			AC GT AGTAGTTACTT		
			TG CA TCATCAATGAA		
			GA _		
GAM727	ADAM19	3'	GCAATACGCCTTTCCAATCTTT 27098		CTCAAACC
	AT		ATAAAG GGCGTATTGC		
			TATTTT CCGCATAACG		
			TAACCTTT		
GAM727	KCNAB1	3'	GCAAGTTTAAATATTTGAGCTT 30547		CCGGCGTA_
	TA		TAAAGCTCAAA TTGC		
			ATTTTCGAGTT AACG		
			ATAAATTTG		
GAM727	PKDREJ	3'	ATGCCACTTTAAGCTTTAT 12715	C	CC
			ATAAAGCT AAA GGCGT		
			TATTTTCA TTT CCGTA		
			A CA		
GAM727	RAD54B	3'	GCACTACAGATTGAGCTTTAT 28676		ACCGGC T
			ATAAAGCTCAA GTA TGC		
			TATTTTCGAGTT CAT ACG		
			AGA__ C		
GAM727	SNX10	3'	GCAATATGTATTTGAGTT 14967	CCG	
			AGCTCAAA GGCGTATTGC		
			TTGAGTTT TGTATAACG		
			A__		
GAM727	LOC115294	3'	TGTCCATATTTGAGCTTTAT 36148		CC__
			ATAAAGCTCAAA GGCG		

		TATTTGAGTTT CTGT	
		ATAC	
GAM727	LOC148254 3'	GCAAGTAGGTTCAAGTTTAT 38503	CA G GTA
		ATAAAGCT AACC GC TTGC	
		TATTTTGA TTGG TG AACG	
		AC A ____	
GAM727	LOC164714 5'	GCAAGAACAGCTTTGAGCTCTA 42181	A ACC _ A_
		TA AGCTCAA GGC GT TTGC	
		AT TCGAGTT TCG CA AACG	
		C ____ A AG	
GAM727	LOC166424 5'	GCAGAGTCAGTTTTGAGCTT 42195	_C GTAT
		AAGCTCAAA C GGC TGC	
		TTCGAGTTT G CTG ACG	
		T A AG__	
GAM727	LOC255096 5'	GCAACGTGGTGGTCCAGCTTTA 46608	CAA G TA
	T	ATAAAGCT ACCG CG TTGC	
		TATTTGCA TGGT GT AACG	
		CC_ G GC	
GAM727	LOC91380 3'	GCAACTGCTATTTGAGTTT 32756	CC TA
		AAGCTCAAA GGCG TTGC	
		TTTGAGTTT TCGT AACG	
		A_ C_	
GAM728	BCL11B 3'	CAAGCACAAGCATTGTG 23159	CGG AC C
		TACAATGCTT GT GCTT G	
		GTGTTACGAA CA CGAA C	
		____ _ A	
GAM728	C20orf64 5'	CCGAAGCGAGCCGAAGCAT 27310	GTA
		ATGCTTCGG CGCTTCGG	
		TACGAAGCC GCGAAGCC	
		GA_	
GAM728	KIAA1958 5'	AGGCCTCAAAGCATTG 39827	C TAC
		CAATGCTT GGG GCTT	
		GTTACGAA CTC CGGA	
		A ____	
GAM729	FLJ10716 3'	GACTGCTGAATCATCATA 20046	AAGCGG
		TATGATGATT AGCGGTC	
		ATACTACTAA TCGTCAG	
		G_____	
GAM729	NTT73 3'	ACCACTCATCATCATA 19822	TAAGCG C
		TATGATGAT GAG GGT	

			ATACTACTA	CTC CCA		
			_____ A			
GAM729	LOC157562	5'	TGACCGCTCCAGTTCTCATCAT	41818	TTA _	
			ATGATGA AGC GGAGCGGTCA			
			TACTACT TTG CCTCGCCAGT			
			C__ A			
GAM730	ABCD1	5'	ACCTGCCTCAACTGCTGCCCCA	5470	A	GTAAT T
			TG GGCAGCAGT GTG GGT			
			AC CCGTCGTCA CGT CCA			
			C ACTC_ _			
GAM730	C14orf1	3'	ACAATCCCTCACTGCTGCCTCA	14027	TAATG_	
			TGAGGCAGCAGTG TGT			
			ACTCCGTCGTCA CACA			
			TCCCTA			
GAM730	DRIL1	3'	ACCACACACTCACCCTCC	11718	C CA TAA	
			GG AG GTG TGTGTGGT			
			CC TC CAC ACACACCA			
			C AC TC_			
GAM730	ICMT	3'	GCACCACTCTGCTGCCCCA	14780	A	T AAT
			TG GGCAGCAG GT GTGT			
			AC CCGTCGTC CA CACG			
			C T C_			
GAM730	UBE2L3	3'	CCACCCACTGCTGCCCCA	9356	A	TAATGT
			TG GGCAGCAGTG GTGG			
			AC CCGTCGTCA CACC			
			C C_			
GAM730	KIAA0329	3'	ACCACACAACACACCACCCCC	16872	A CAGCA AA	
	A		TG GG GTGT TGTGTGGT			
			AC CC CACA ACACACCA			
			_ CACAC CA			
GAM730	KIAA1554	3'	ACGCTTACACCTCTGCCTCA	45607	CA T	
			TGAGGCAG GTGTAA GTGT			
			ACTCCGTC CACATT CGCA			
			TC _			
GAM730	PRDM7	3'	ACCACACACTTGCACACCCC	27566	CAGCA _	
			GG GTGTAA TGTGTGGT			
			CC CACGTT ACACACCA			
			CCA_ C			
GAM730	PRDM9	3'	ACCACACACTTGCACACCCC	21493	CAGCA _	
			GG GTGTAA TGTGTGGT			

			CC CACGTT ACACACCA		
			CCA__ C		
GAM730	RAB40C	3'	CCACACAGCTGCCTCA	22144	AGTGTAA
			TGAGGCAGC	TGTGTGG	
			ACTCCGTCG	ACACACC	
GAM730	SEC8	3'	ACCACACACAGTGATGCCTCA	22359	G G AAT
			TGAGGCA CA TGT	GTGTGGT	
			ACTCCGT GT ACA	CACACCA	
			A G		
GAM730	TMPRSS5	3'	CGCACACCACTGCCTCA	25054	GCA TAA TG
			TGAGGCA GTG	TGTG G	
			ACTCCGT CAC	ACAC C	
			__ C__ GT		
GAM730	LOC149319	5'	CCACCTGCTGCCTCA	38712	TGTAAT T
			TGAGGCAGCAG	GTG G	
			ACTCCGTCGTC	CAC C	
			__ C		
GAM730	LOC254423	5'	ACCACCGGGTCACACTGCTGCC	46528	A G _
	T		AGGCAGCAGTGT AT TG	TGGT	
			TCCGTCGTCACA TG GC	ACCA	
			C G C		
GAM730	LOC89919	5'	ACCACACCTGCACTTCTGCCTC	30461	C AT
	A		TGAGGCAG AGTGTA	GTGTGGT	
			ACTCCGTC TCACGT	CACACCA	
			T C_		
GAM730	LOC91812	5'	ACCACACAGCATCATCGCCCCA	33389	A AGCA AA
			TG GGC	GTGT TGTGTGGT	
			AC CCG	TACG ACACACCA	
			C CTAC		
GAM730	LOC91813	5'	ACCACACAGCATCATCGCCCCA	33393	A AGCA AA
			TG GGC	GTGT TGTGTGGT	
			AC CCG	TACG ACACACCA	
			C CTAC		
GAM731	COG7	3'	CACCACACACCGGACCAC	33577	A ACA
			GTGGTTTG GT	TGGTG	
			CACCAGGC CA	ACCAC	
			_ CAC		
GAM731	FLJ13710	3'	TCACCATGTACTGATGATC	24208	TG_
			GGTT AGTACATGGTGA		

			CTAG TCATGTACCACT		
			TAG		
GAM731	KIAA1486	3'	CCAACTCAAACACTTTT 33461	G	ACA
			AAAAGTG TTTGAGT TGG		
			TTTTCAC AAACCTCA ACC		
			— —		
GAM731	KIAA1954	3'	CACCATGGAAACCAAGTTCC 38095	A G	GAGTA
			A AA TGGTTT CATGGTG		
			C TT ACCAAA GTACCAC		
			C G G —		
GAM731	MGC2541	3'	CCATTACCCAAACCACT 27962	A C	
			AGTGGTTTG GTA ATGG		
			TCACCAAAC CAT TACC		
			C —		
GAM731	SEPT3	3'	CCATTTATCCAAACCACT 21180	AG C	
			AGTGGTTTG TA ATGG		
			TCACCAAAC AT TACC		
			CT T		
GAM731	LOC146958	5'	TCACCATGTCCTTAAACCAT 40775	T	
			GTGGTTTGAG ACATGGTGA		
			TACCAAATTC TGTACCACT		
			C		
GAM732	RP42	3'	CCTGTCATATTACCAAC 21800	ACG	
			GTTG GATATGACAGG		
			CAAC TTATACTGTCC		
			CA_		
GAM732	RS1	3'	CCTGCACCCATCAGCCAA 5876	C ATA A	
			TTGGTTGA GG TG CAGG		
			AACCGACT CC AC GTCC		
			A C_ _		
GAM732	FLJ22940	5'	CCCGCCACACCAACCAACCAAT 23797	AC_ ATA ACA	
	A		TATTGGTTG GG TG GGG		
			ATAACCAAC CC AC CCC		
			CAA AC_ CG_		
GAM732	MAL2	3'	CCCCAGAGACCATTAACCAATA 27468	C ATA_ ACA	
			TATTGGTTGA GG TG GGG		
			ATAACCAATT CC AC CCC		
			A AGAG _		
GAM732	TU3A	3'	CCCTATCATTATTTACCAAGC 14032	GACG T_ C	
	CAATA		TATTGGTT GA ATGA AGGG		

			ATAACCGA	CT	TACT TCCC		
			ACCA	TTAT	A		
GAM733	ABCC3	3'	ATTCCCAACTGAGTGTTA	21290	A	CACTC	
			TAACA CTCAGTTG	GAAT			
			ATTGT GAGTCAAC	CTTA			
			—	C	—		
GAM733	ABCC3	3'	ATTCCCAACTGAGTGTTA	21289	A	CACTC	
			TAACA CTCAGTTG	GAAT			
			ATTGT GAGTCAAC	CTTA			
			—	C	—		
GAM733	NUFIP1	3'	AGTGTTACAACACTGAGTTG	14736		—	
			CAACTCAGTTG	CACT			
			GTTGAGTCAAC	GTGA			
			ATT				
GAM733	PARK2	3'	GATTCAAGTGCAATCCATGT	10905	ACTCA	C	
			ACA	GTTGCACT GAATC			
			TGT	TAACGTGA CTTAG			
			ACC	— A			
GAM733	PARK2	3'	GATTCAAGTGCAATCCATGT	15152	ACTCA	C	
			ACA	GTTGCACT GAATC			
			TGT	TAACGTGA CTTAG			
			ACC	— A			
GAM733	PARK2	3'	GATTCAAGTGCAATCCATGT	15159	ACTCA	C	
			ACA	GTTGCACT GAATC			
			TGT	TAACGTGA CTTAG			
			ACC	— A			
GAM733	ANKT	5'	TGAGGGCAACCAAGTTGTTA	18498	CA	A	
			TAACAACT	GTTGC CTCG			
			ATTGTTGA	CAACG GAGT			
			AC	G			
GAM733	OLFM3	3'	GATTTTCATACAACACTGAGTT	39961		CACTC	
			AACTCAGTTG	GAATC			
			TTGAGTCAAC	TTTAG			
			ATAC	—			
GAM734	APPL	3'	AGAAGGTAACAACACTATGTTGAA	14399	AAC	—	
			TTCAACATG	TGTTAC TTCT			
			AAGTTGTAT	ACAATG AAGA			
			CA	— G			
GAM734	PPP3CB	3'	AAGTCAAGACTGCATGTTGAA	22104	AACT	—	
			TTCAACATG	GTT ACTT			

			AAGTTGTAC CAG TGAA		
			GT__ AAC		
GAM734	ARPP-19	3'	TAGAGTTGGCAGTTAATGCTGA 13423	A G	C
	A		TTCA CAT AACTGTTA TTCTA		
			AAGT GTA TTGACGGT GAGAT		
			C A T		
GAM734	C20orf26	5'	GTAGAAGTTGTTTCATTGCCGAA 34758	AA _	TGTT
			TTC CA TGAAC ACTTCTAC		
			AAG GT ACTTG TGAAGATG		
			CC T T__		
GAM734	CLDN1	3'	AGGAGAAAATCATGTTGAA 22081	ACTG	A
			TTCAACATGA TT CTTCT		
			AAGTTGTACT AA GAGGA		
			AA__ _		
GAM734	FLJ12697	3'	AGTGACAGTCATGTTGAA 44472	A	
			TTCAACATGA CTGTTACT		
			AAGTTGTACT GACAGTGA		
			-		
GAM734	FLJ14154	3'	AGTGTCCAGCCCAGTGTGAA 24270	GAA_ T_	
			TTCAACAT CTG TACT		
			AAGTTGTG GAC GTGA		
			ACCC CT		
GAM734	ICAP-1A	3'	GTAGAAGTCAACTTCATCTGAA 11155	AC CT _	
			TTCA ATGAA GTT ACTTCTAC		
			AAGT TACTT CAA TGAAGATG		
			C_ _ C		
GAM734	KIAA0186	3'	TAGAAATACAATTGATGTTGAA 22037	G C TAC	
			TTCAACAT AA TGT TTCTA		
			AAGTTGTA TT ACA AAGAT		
			G A TA_		
GAM734	KIAA0527	3'	TAGAATCTAAAAATTCATGTTG 45848	CTG C_	
	AA		TTCAACATGAA TTA TTCTA		
			AAGTTGTACTT AAT AAGAT		
			AAA CT		
GAM734	MGC15438	3'	AGAAACGGATTATGTTGAA 26692	A A	
			TTCAACATGA CTGTT CT		
			AAGTTGTATT GGCAA GA		
			A A		
GAM734	PAPOLG	3'	TAGAAGTGGCTGTCATACGTGA 23155	AC_ ACT	
	A		TTCA ATGA GTTACTTCTA		

AAGT TACT CGGTGAAGAT
 GCA GT_
 GAM734 LOC161742 3' GTAAAAGCTTCATGTTGAG 40027 _ G
 TTCAACATGAA CT TTAC
 ||||| || ||||
 GAGTTGTACTT GA AATG
 C A
 GAM735 SPAP1 3' CAATATCACCAAAGTATG 25047 C ACA
 CATACTTTGG GA TGTG
 ||||| || ||||
 GTATGAAACC CT ATAAC
 A ____
 GAM736 TNS 5' CAACGGCTCCACCAGGGTCACC 22899 _ A_ A A
 GG GAT TGG TG AGCCGTTG
 || ||| ||| || |||||
 CC CTG ACC AC TCGGCAAC
 A GG _ C
 GAM736 FLJ21438 5' CAACGGCTCCAAGACTCCCCTT 30844 ATAT ____ A
 C GAGGG GGA TG AGCCGTTG
 |||| ||| || |||||
 CTTCC CCT AC TCGGCAAC
 ____ CAGA C
 GAM736 KIAA1036 3' GCCACCCCTATCCCTCT 17128 T A AA
 AGAGGGATA GG TG GC
 ||||| || || ||
 TCTCCCTAT CC AC CG
 C C ____
 GAM736 KIAA1950 3' CTTTCATCCATACCCTTCT 44488 A
 AGAGGG TATGGATGAAG
 ||||| |||||
 TCTTCC ATACCTACTTC
 C
 GAM736 MGC19556 3' CAACAGCCTGCCCAGATCCCTC 27314 A ATGAA C
 T AGAGGGAT TGG GC GTTG
 ||||| ||| || ||||
 TCTCCCTA ACC CG CAAC
 G CGTC_ A
 GAM736 LOC254428 3' CAACATTTTCCCCATCCCTCT 45714 TA AT CC
 AGAGGGA TGG GAAG GTTG
 ||||| ||| ||| ||||
 TCTCCCT ACC CTTT CAAC
 _ C_ TA
 GAM737 CAPN2 3' TAAAGGACAAAATAAGCTGTTT 7486 AGGAAATA
 AAGCAGCT TCCTTA
 ||||| |||||
 TTTGTCGA AGGAAAT
 ATAAAAC_
 GAM737 CRHR2 3' AAAGGATCAGTTTGGCTGC 7609 AAAT
 GCAGCTAGG ATCCTT
 ||||| |||||

			CGTCGGTTT TAGGAAA		
			GAC_		
GAM737	MBNL	3'	GTAAAGGATATTTTGCTCTGT 22030	CTA	
	T		AGCAG GGAAATATCCTTTAC		
			TTGTC TTTTATAGGAAATG		
			TCG		
GAM737	MEF2C	3'	TAAAGGATGCTAGCCTGC 8212	_	GAAA
			GCAG CTAG TATCCTTTA		
			CGTC GATC GTAGGAAAT		
			C _		
GAM737	OGG1	5'	TAAAGGTCATGTCTCCTAGCT 8393	A	_
			AGCTAGGA ATAT CCTTTA		
			TCGATCCT TGTA GGAAAT		
			C CT		
GAM737	OGG1	5'	TAAAGGTCATGTCTCCTAGCT 18810	A	_
			AGCTAGGA ATAT CCTTTA		
			TCGATCCT TGTA GGAAAT		
			C CT		
GAM737	OGG1	5'	TAAAGGTCATGTCTCCTAGCT 18815	A	_
			AGCTAGGA ATAT CCTTTA		
			TCGATCCT TGTA GGAAAT		
			C CT		
GAM737	PIG8	3'	GTAAAGGAGTGTCCCAGTTGCT 11316	A	AATA
			AGCAGCT GGA TCCTTTAC		
			TCGTTGA CCT AGGAAATG		
			C GTG_		
GAM737	PTER	3'	TAAAAGATATTTCTGCTG 24999	TA	C
			CAGC GGAAATATC TTTA		
			GTCG TCTTTATAG AAAT		
			_ A		
GAM737	RARB	3'	GACATTTTCTAGCTACTT 18239	C	A
			AAG AGCTAGGAAAT TC		
			TTC TCGATCTTTTA AG		
			A C		
GAM737	RARB	3'	GACATTTTCTAGCTACTT 6693	C	A
			AAG AGCTAGGAAAT TC		
			TTC TCGATCTTTTA AG		
			A C		
GAM737	TAZ	3'	AAAGGACCTCAGCTGCTT 5584	_	AAATA
			AAGCAGCT AGG TCCTTT		

TTCGTCGA TCC AGGAAA
 C _____
 GAM737 TXNIP 3' AAAGGAAGCTAGCTGCT 13196 GAAATA
 AGCAGCTAG TCCTTT
 ||||| |||||
 TCGTCGATC AGGAAA
 GA_____
 GAM737 KIAA0935 3' GTAAAGGATATTTGGC 36013 GGA
 GCTA AATATCCTTTAC
 ||| |||||
 CGGT TTATAGGAAATG

 GAM737 KIAA0937 3' TAAAGCCAGCCCCATAGCTGCT 44019 _ AAATATC
 T AAGCAGCTA GG CTTTA
 ||||| || |||||
 TTCGTCGAT CC GAAAT
 A CCGACC_
 GAM737 KIAA1303 3' AGGGACATTTCTAGCCAGCT 32831 A_ A
 AGC GCTAGGAAAT TCCTT
 ||| ||||| |||||
 TCG CGATCCTTTA AGGGA
 AC C
 GAM737 OS-9 3' AGGATATTCCCTGCTGC 13683 T A
 GCAGC AGG AATATCCT
 ||||| ||| |||||
 CGTCG TCC TTATAGGA
 _ C
 GAM737 SFXN2 3' AAAGGCCAATGTCTTCTAGCTG 36601 A ____
 CTT AAGCAGCTAGGA ATAT CCTTT
 ||||| ||||| |||||
 TTCGTCGATCTT TGTA GGAAA
 C ACC
 GAM737 SMCR5 3' GGGATCCCCTAGCTGTCC 29565 A AAAT
 A GCAGCTAGG ATCCT
 | ||||| |||||
 C TGTGATCC TAGGG
 C CC_
 GAM737 SSR1 3' AGAGATATTTCCCAGTTACT 9112 C A _
 AG AGCT GGAAATATC CT
 || ||| ||||| ||
 TC TTGA CCTTTATAG GA
 A C A
 GAM737 STX3A 3' GTAAAGGACATTTGCTTACCTG 10388 C _ A
 CAG TAGG AAAT TCCTTTAC
 ||| ||| ||| |||||
 GTC ATTC TTTA AGGAAATG
 C G C
 GAM737 LOC149842 3' GACATTTCTAGTGCTT 41091 G A
 AAGCA CTAGGAAAT TC
 ||||| ||||| ||

TTCGT GATCCTTTA AG
 — C
 GAM737 LOC221143 3' TAAAGGACATTTCTGGTCTT 44944 CA A
 AAG GCTAGGAAAT TCCTTTA
 ||| ||||| |||||
 TTC TGGTCCTTTA AGGAAAT
 — C
 GAM737 LOC254394 3' TAAAGAATATTTCCCATGC 45930 GCTA C
 GCA GGAAATAT CTTTA
 ||| ||||| |||||
 CGT CCTTTATA GAAAT
 AC — A
 GAM738 EVI2A 5' AGAAAAGAAGTGGTTTATCA 15477 C TG GC
 TGA AAAC C TCTTTTCT
 ||| ||| | |||||
 ACT TTTG G AGAAAAGA
 A GT A_
 GAM738 RECQL5 3' AGAAAAAGCGAGGAAATCAG 10446 CAAA G C
 CTGA CT CGCT TTTTCT
 ||| || ||||| |||||
 GACT GA GCGA AAAAGA
 AAAG _ A
 GAM738 THBS1 3' AGAAAATGCAGTTTTC A 9254 CTC
 TGA AAAGT GCG TTTTCT
 ||| ||||| |||||
 ACT TTTGACGT AAAAGA
 — —
 GAM738 ARHE 3' AGAAAGCACAGTTTGTGAG 11666 G C CTT
 CT ACAAACTG GCT TTCT
 || ||||| ||| |||||
 GA TGTTTGAC CGA AAGA
 G A —
 GAM738 EIF3S1 3' AAGAAAAGCAGTTTGCAG 31640 A GC_
 CTG CAAACTGC TCTT
 ||| ||||| |||||
 GAC GTTTGACG AGAA
 — AAA
 GAM738 FLJ20330 3' AGAAAAGAGCACAGGCTGCA 21058 A AA C
 TG CA CTG GCTCTTTTCT
 || || ||| ||||| |||||
 AC GT GAC CGAGAAAAGA
 _ CG A
 GAM738 KIAA1432 5' CGAGAAAAGAGCCCATTGTCAG 33149 A C C
 CTG CAAA TG GCTCTTTTCTCG
 ||| ||| || ||||| |||||
 GAC GTTT AC CGAGAAAAGAGC
 — _ C
 GAM738 P66 3' GAGATGCCCAAGTTTGTGTCAG 21847 GC_ _
 CTGACAAACT GC TCTT
 ||||| || |||||

			GACTGTTTGA	CG	AGAG			
			ACC	T				
GAM738	PIP5K2A	5'	CGAGCCGAGCGCAGTCTGCCGG	11469		A	A	TTTT
			CTG	CA	ACTGCGCTC	CTCG		
			GGC	GT	TGACGCGAG	GAGC		
			C	C	CC	__		
GAM738	TTY2	5'	AAAGGATCTGCAGAATTTGTCA	42067		__		C_
	G		CTGACAAA	CTGCG	TCTTTT			
			GACTGTTT	GACGT	AGGAAA			
			AA	CT				
GAM738	LOC159148	5'	AAAGGATCTGCAGAATTTGTCA	42074		__		C_
	G		CTGACAAA	CTGCG	TCTTTT			
			GACTGTTT	GACGT	AGGAAA			
			AA	CT				
GAM738	LOC221718	5'	TGGGAAGCAAGTTTGTCA	44981		GC		CTTT
			TGACAAACT	GCT	TCTCG			
			ACTGTTTGA	CGA	AGGGT			
			A_	__				
GAM738	LOC256880	5'	AGGAGCGCAGTTACCAG	46384		ACA		
			CTG	AACTGCGCTCTT				
			GAC	TTGACGCGAGGA				
			CA_					
GAM738	LOC90246	3'	GGGAAAGAGCCCAGCCTGCCA	31001		A	AA	C
			TG	CA	CTG	GCTCTTTTCT		
			AC	GT	GAC	CGAGAAAGGG		
			C	CC	C			
GAM739	IKBK	3'	TTTCCCATCTTTTTGTACCAT	9712		T		TGT
	A		TAT	GTAATA	GA	ATGGGAAA		A
			ATA	CATTGT	TT	TACCCTTT		
			C	TT_	C			
GAM739	MDM4	3'	TTCCATGCACATTTACAATA	8209		T		AA
			TATTGTAA	ATGTG	ATGGGA			
			ATAACATT	TACAC	TACCTT			
			_	G_				
GAM739	PPP2CA	3'	TTTGTATTTACACATATTACAAT	8582				G
			ATTGTAATATGTGAAATG	GAA				
			TAACATTATACACTTTAT	TTT				
			G					
GAM739	SYT1	3'	TTCCAGATTTACACCTACAAT	12173		ATA		G_
	A		TATTGTA	TGTGAAAT	GGAA			

			ATAACAT	ACACTTTA	CCTT		
			CC_	GA			
GAM739	FLJ22167	5'	CCCATCTTCATTATAATA	23739	ATAT	_	
			TATTGTA	GTGAA	ATGGG		
			ATAATAT	TACTT	TACCC		
			_____	C			
GAM739	GTF2E1	3'	TTCCCATCCATCTGTTTACTAC	12039	_____	T	AA
			AATA	TATTGTA	ATA	GTG	ATGGGAA
			ATAACAT	TGT	TAC	TACCCTT	
			CATT	C	C_		
GAM739	KIAA0186	3'	TTTCCCATCCCAAGATCACAAT	22041	A	ATG	AA
			ATTGT	AT	TG	ATGGGAAA	
			TAACA	TA	AC	TACCCTTT	
			C	GA_	CC		
GAM739	KIAA1610	3'	TTTCCCATTCTGCATTAAATA	33343	GTAAT	_	
			TATT	ATGT	GAAATGGGAAA		
			ATAA	TACG	CTTTACCCTTT		
			AT_____	T			
GAM739	PRO2012	3'	TTTCCCATTATACATAACAATA	20683	AA	A	
			TATTGT	TATGTG	AATGGGAAA		
			ATAACA	ATACAT	TTACCCTTT		
			_____	A			
GAM739	LOC145758	5'	TCCCAATCACATTTTACAATA	40588	AAT	AA	
			TATTGT	ATGTGA	TGGGA		
			ATAACA	TACACT	ACCCT		
			CTT	A_			
GAM739	LOC149506	3'	TCCCATTTAATAACTATAATA	41011	ATA	G	
			TATTGTA	TGT	AAATGGGA		
			ATAATAT	ATA	TTTACCCT		
			CA_	A			
GAM739	LOC158014	5'	TTCCAAAAGACTATTACAATA	39697	T	GAAA	
			TATTGTAATA	GT	TGGGA		
			ATAACATTAT	CA	ACCTT		
			_____	GAAA			
GAM739	LOC202316	3'	TTTCCATTACATATTACAA	43428	A		
			TTGTAATATGTGAA	TGGGAA			
			AACATTATACACTT	ACCTTT			

GAM739	LOC254196	3'	TTCCCATTCTTGTACAATA	46478	ATATGT	A	
			TATTGTA	GAA	TGGGAA		

			ATAACAT	CTT ACCCTT	
			GTT__ _		
GAM739	LOC90538	3'	TTTCCCATTTGAATAACTAGAA	31661	G ATA G_
		TA	TATT TA TGT AAATGGGAAA		
			ATAA AT ATA TTTACCCTTT		
			G CA_ AG		
GAM739	LOC91585	3'	TTCCACCTCCATTTCAATA	33078	TAAT T AA
			TATTG ATG GA TGGGAA		
			ATAAC TAC CT ACCCTT		
			TT__ _ CC		
GAM740	FLJ13322	3'	CATTCAAATTCCTCGTC	24057	TAAAGC
			GACG GAATTTTGAATG		
			CTGC CTAAAACTTAC		
			CC__		
GAM740	MGC9912	3'	CATTCAAATGTTTTAC	27950	AAT
			GTAAAGCG TTTGAATG		
			CATTTTGT AACTTAC		

GAM740	NFX1	3'	GCATTCAAAGAGGCTCTTTAC	8326	CGAA_
			GTAAAG TTTTGAATGC		
			CATTTC GAAACTTACG		
			TCGGA		
GAM740	RPS6KA4	3'	GCATTCTGCCTCACTTTATGT	10056	C ATTTT
	CA		TGACGTAAAG GA GAATGC		
			ACTGTATTTC CT TTTACG		
			A CCGTC		
GAM740	LOC255027	3'	CATTCAAGTCAGCTTTCAC	45571	_ GAAT
			GT AAAGC TTTGAATG		
			CA TTTCG GAACTTAC		
			C ACT_		
GAM741	BACE	5'	AGACTTGGGGGCAGGCGCC	14415	GTA
			GGCGC TGTCCCCAAGTCT		
			CCGCG ACGGGGGTTCAGA		
			G_		
GAM741	BACE	5'	AGACTTGGGGGCAGGCGCC	29083	GTA
			GGCGC TGTCCCCAAGTCT		
			CCGCG ACGGGGGTTCAGA		
			G_		
GAM741	SLC25A15	3'	TAGACTTGGGGATGGACAGCT	15528	GC A
			GGC GT TGTCCCCAAGTCTA		

TCG CA GTAGGGGTTTCAGAT
A_ G

GAM741 SMOH 3' TAGACTTGAGGGGCTACCCTG 12162 CGC T _
CAGG GTA GTCCC CAAGTCTA
|||| ||| ||||| |||||
GTCC CAT CGGGG GTTCAGAT
_ _ A

GAM741 HSA243666 3' AGACTTGGGACAACCTGCCTG 19018 C A C
CAGGCG GT TGTCCC AAGTCT
||||| || ||||| |||||
GTCCGT CA ACAGGG TTCAGA

GAM741 LHPP 3' AGACTTGAAGGTGTCATGCCC 22672 C _ GT CC
GG GCGT AT C CAAGTCT
|| ||| || | |||||
CC CGTA TG G GTTCAGA
_ C TG AA

GAM741 RIP60 3' AGACTTGGAGAGACCCGTCTG 15058 C ATG C
CAGGCG GT TC CCAAGTCT
||||| || || |||||
GTCTGC CA AG GGTTTCAGA
C G_ A

GAM741 LOC123624 3' TAGACACAAACATATACGCCT 37253 CG CCCCAA
AGGCG TATGT GTCTA
|||| |||| ||||
TCCGC ATACA CAGAT
AT AACAA_

GAM741 LOC131873 5' AGAAGGGGACATACAGGCC 37361 GC AAG
GGC GTATGTCCCC TCT
||| ||||| |||
CCG CATACAGGGG AGA
GA A_

GAM741 LOC150174 3' AGACCCAGGGTGCGTGCC 38869 TGT CAA
GGCGCGTA CCC GTCT
||||| ||| |||
CCGTGCGT GGG CAGA
_ ACC

GAM741 LOC151979 5' TAGGCGTGAGACACCGCGCCTG 39189 TA CC A
CAGGCGCG TGTC CA GTCTA
||||| ||| || |||||
GTCCGCGC ACAG GT CGGAT
C_ A_ G

GAM741 LOC219397 3' AGACTTGTGATCACGCC 44898 C AT CC
GG GCGT GTC CAAGTCT
|| ||| || |||||
CC CGCA TAG GTTCAGA
_ C_ T_

GAM741 LOC256158 5' AGACTCGGGGCGGTACCTG 46617 CG GTA T A
CAGG C TG CCCC AGTCT
|||| | || |||||

			GTCC G GC GGGG TCAGA	
			AT _ _ C	
GAM741	LOC92223	5'	TAGACTTGAAGAACATGAACCT 33994	CG ATG CC
		G	CAGG CGT TC CAAGTCTA	
			GTCC GTA AG GTTCAGAT	
			AA CA_ AA	
GAM742	BACH2	3'	CAACGACTGTAACAGGTTACAT 22377	AT_
			ATGTAGCCT TAGTTGTTG	
			TACATTGGA GTCAGCAAC	
			CAAT	
GAM742	CORO1C	3'	CAACCAGCGATAGGCCACAT 15629	A A _
			ATGT GCCTATT GTTG TTG	
			TACA CGGATAG CGAC AAC	
			C _ C	
GAM742	DCK	3'	TCAGCATAGTGACTAAACTACA 6444	CCTA TG_
		T	ATGTAG TTAGT T TGCTGA	
			TACATC AATCA G ACGACT	
			A_ GT AT	
GAM742	SFRP1	3'	CAGCAGCAAAAACACTACAT 8927	CCTATTAG
			ATGTAG TTGTTGCTG	
			TACATC AACGACGAC	
			AAA_	
GAM742	CHL1	3'	TCAGGATTCTAATAGCTACAT 13396	C TT G
			ATGTAGC TATTAG GTT CTGA	
			TACATCG ATAATC TAG GACT	
			_ T_ _	
GAM742	CSMD1	3'	CAACAACCTTAGACTGCA 36185	C TT
			TGTAG CTA AGTTGTTG	
			ACGTC GAT TCAACAAC	
			A _	
GAM742	NUDT11	3'	CAGAGCCAACAGGCTATAT 30140	ATTA TTG
			ATGTAGCCT GTTG CTG	
			TATATCGGA CAAC GAC	
			_ CGA	
GAM742	PDE10A	3'	CAGCCTTTTCTAATAGGCTA 13461	TTGTT
			TAGCCTATTAG GCTG	
			ATCGGATAATC CGAC	
			TTTTC	
GAM742	RAP140	3'	CAGCAACGCCAGACTATAT 17553	C ATTA T
			ATGTAG CT GT GTTGCTG	

			TATATC GA CG CAACGAC		
			A C _ _		
GAM742	LOC146488	5'	CAACAACAACTGCTACA 35040	CTATT	C
			TGTAGC AGTTGTTG TG		
			ACATCG TCAACAAC AC		
			_____ A		
GAM742	LOC162083	5'	CAGCAAACACAGGCTGCA 40046	ATTA	TG
			TGTAGCCT GT TTGCTG		
			ACGTCGGA CA AACGAC		
			_____ CA		
GAM743	COX15	3'	CTAGTTCCTCTTTTGATA 27788	C	
			TATCAAAAGA GGAAGTAG		
			ATAGTTTCT CCTTGATC		

GAM743	CSRP1	3'	TCTAGTTCCTGCTTGATG 10278	A_	AC
			TATCAA AG GGAAGTAGA		
			GTAGTT TC CCTTGATCT		
			CG _		
GAM743	EXTL2	3'	GTCTAGTTGTTTGCTTGATA 7163	A_	GA
			TATCAA AGACG ACTAGAC		
			ATAGTT TTTGT TGATCTG		
			CG _		
GAM743	SPOCK	3'	GTCTAGTTCCAAATTTGGTA 31457	AGAC	
			TATCAA GGAAGTAGAC		
			ATGGTTT CCTTGATCTG		
			AAA_		
GAM743	BRD2	5'	TCGGGGACCGTCTTTTGA 11575	AA	A
			TCAAAAGACGG CT GA		
			AGTTTTCTGCC GG CT		
			AG G		
GAM743	FLJ12747	3'	GTCTAGTTTTCACCTTGA 25880	AA	CG
			TCAA GA GAACTAGAC		
			AGTT CT TTTGATCTG		
			CA _		
GAM743	GRIN3A	3'	TCTAGGGTTGTAGCTTTTGATA 28540	_	AA
			TATCAAAAG ACGG CTAGA		
			ATAGTTTTC TGTT GATCT		
			GA GG		
GAM743	HSPC054	3'	CTAGCTCTCTGTCTTGAT 15434	AA	A_
			ATCA AGACGGA CTAG		

			TAGT TCTGTCT GATC		
			— CTC		
GAM743	KIAA0016	3'	GTCTAGTTTCTGCCTCTGAT 16534	AA A	—
			ATCA AG CGGAA CTAGAC		
			TAGT TC GTCTT GATCTG		
			C_ C T		
GAM743	P311	3'	TTTAGCTCTTCTTTTGA 11163	C A	
			TCAAAAGA GGA CTAGA		
			AGTTTTCT TCT GATTT		
			— C		
GAM743	PA26	3'	CTGGCGATCTTTTGATA 15807	— GAA	
			TATCAAAAGA CG CTAG		
			ATAGTTTTCT GC GGTC		
			A —		
GAM743	SFXN5	3'	GTCTGGGTCGTCTTTTGA 29386	AA	
			TCAAAAGACGG CTAGAC		
			AGTTTTCTGCT GGTCTG		
			G_		
GAM743	LOC196027	3'	GTCTACCAGATGTCTTTTGA 42305	GAAC_	
			TCAAAAGACG TAGAC		
			AGTTTTCTGT ATCTG		
			AGACC		
GAM743	LOC81034	3'	TCCAGTTCTTGTTTTTTGG 25070	— A	
			TCAAAAGACG GAACT GA		
			GGTTTTTGT CTTGA CT		
			T C		
GAM744	TPM4	3'	ACAGAAGAGTCTTGTTCCA 9299	C G_	
			TG GAACAAGACTT TGT		
			AC CTTGTTCTGAG ACA		
			— AAG		
GAM744	ZNF135	3'	ACACAAGCCTTTTCACA 9488	C C A	
			TG GAA AAG CTTGTGT		
			AC CTT TTC GAACACA		
			A _ C		
GAM744	DKFZp434C0923	5'	AAAACCAAATGGATCTTGTTC 19060	— C TG G A	
			GCA TGCG AACAAGA T T TG TTTT		
			ACGC TTGTTCT G A AC AAAA		
			C A GT A C		
GAM744	DKFZp566H0824	5'	AAAATCAGCTTGTCTTGTTC 18972	C TT G	
			TG GAACAAGAC GT TGATTTT		

AC CTTGTTCTG CG ACTAAAA
 _ TT _
 GAM744 LOC152106 3' ACAGAAGAGTCTTGTTCCA 34708 C G__
 TG GAACAAGACTT TGT
 || ||||| ||
 AC CTTGTTCTGAG ACA
 _ AAG
 GAM744 LOC255152 5' AAAATCACCAGGCTCACTC 46533 ACA A T
 GA AG CTTG GTGATTTT
 || || ||| |||||
 CT TC GGAC CACTAAAA
 CAC _ _
 GAM745 ABCC1 3' ATATCTGGTCAGAACTGCA 21283 ATGC CAA
 TGCA TCTG CAGATAT
 ||| ||| |||||
 ACGT AGAC GTCTATA
 CA__ TG_
 GAM745 ABCC1 3' ATATCTGGTCAGAACTGCA 21287 ATGC CAA
 TGCA TCTG CAGATAT
 ||| ||| |||||
 ACGT AGAC GTCTATA
 CA__ TG_
 GAM745 ABCC1 3' ATATCTGGTCAGAACTGCA 11439 ATGC CAA
 TGCA TCTG CAGATAT
 ||| ||| |||||
 ACGT AGAC GTCTATA
 CA__ TG_
 GAM745 ZFH4 5' TCAGTTGCAGGCATTACA 24056 C T A
 TG AATGC CTGCAAC GA
 || |||| ||||| ||
 AC TTACG GACGTTG CT
 A _ A
 GAM745 CLIC4 3' GTACATCTGTTGAGCA 15131 TGC A
 TGCTC AACAGAT TAC
 |||| ||||| ||
 ACGAG TTGTCTA ATG
 _ C
 GAM745 FLJ13194 3' ATCTGTTGGAGGACATCCCA 24786 CA CT G
 TG ATG CT CAACAGAT
 || ||| || |||||
 AC TAC GA GTTGTCTA
 CC AG G
 GAM745 KIAA1753 3' TTGCTGCAGAGCTCTGCA 32383 AT A
 TGCA GCTCTGCA CAG
 ||| ||||| ||
 ACGT CGAGACGT GTT
 CT C
 GAM745 KLHL4 3' GTATTTCCACAGAGCATGCA 21196 A CAAC
 TGCA TGCTCTG AGATAT
 ||| ||||| |||||

ACGT ACGAGAC TTTATG
 _ ACC_
 GAM745 LOC200609 5' GTATATCTGTTACAGCTAGTTG 43330 GCT C
 CAAT CTG AACAGATATAC
 ||| ||| |||||
 GTTG GAC TTGTCTATATG
 ATC A
 GAM745 LOC220980 5' TCTATTGCAGAGCACAGCA 44739 AA C
 TGC TGCTCTGCAA AGA
 ||| ||||| |||
 ACG ACGAGACGTT TCT
 AC A
 GAM745 LOC254556 3' GTCTGGTTGCAGAACCTGCA 45394 ATGC _
 TGCA TCTGCAAC AGAT
 ||| ||||| |||
 ACGT AGACGTTG TCTG
 CCA_ G
 GAM745 LOC93538 3' ATATTTGTGCAGAACTGCA 35922 ATGC A
 TGCA TCTGCA CAGATAT
 ||| ||||| |||||
 ACGT AGACGT GTTTATA
 CAA_ _
 GAM746 GRM7 3' TTTGACTGATCAGTGTG 6518 T T
 CAC ACTG TCAGTCAAA
 ||| ||| |||||
 GTG TGAC AGTCAGTTT
 _ T
 GAM746 MGAT5 5' TCCTTTGACTGAAGCATGTATG 8240 C _ _ A
 T ACA TAC TGTT CAGTCAAA GA
 ||| ||| ||| ||||| ||
 TGT ATG ACGA GTCAGTTT CT
 _ T A C
 GAM746 XBP1 3' TCTTTTGACATCCAGCAGT 11533 CA_
 ACTGTT GTCAAAAGA
 ||||| |||||
 TGACGA CAGTTTTCT
 CCTA
 GAM746 DKFZP434B044 3' TCCTTTGACTGATGTTCAAGTGT 25553 ACTGT A
 C GACACT TCAGTCAAA GA
 ||||| ||||| ||
 CTGTGA AGTCAGTTT CT
 CTTGT C
 GAM746 FLJ12806 3' CTTTGTGACTTAACGTCA 23112 ACTACT C
 TGAC GTT AGTCAAAAG
 ||| ||| |||||
 ACTG CAA TCAGTTTTC
 _ _ _ T
 GAM746 FLJ22635 3' CTCCTGAGAGCAGTGGTCA 24716 C AG AA
 A ACTACTGTTC TCA AG
 | ||||| ||| ||

		A TGGTGACGAG AGT TC		
		C _ CC		
GAM746	FLJ23604 3'	CTTTGACTGGAAAGGTCA 24661	ACTACTG	
		TGAC TTCAGTCAAAAG		
		ACTG AGGTCAGTTTTC		
		GAA_		
GAM746	KIAA0557 3'	ACTGACATTATTTAGTGTCA 38202	C_ T	
		TGACACTA TGT CAGT		
		ACTGTGAT ACA GTCA		
		TTATT _		
GAM746	LOC144742 5'	CTCTTGACCAGTAGTGTCA 37777	TTCA A	
		TGACACTACTG GTCAA AG		
		ACTGTGATGAC CAGTT TC		
		_____ C		
GAM746	LOC145842 5'	CTTTGACTGGAAGAGTCA 37997	A ACTG A	
		TGAC CT TTCAGTCAAA G		
		ACTG GA AGGTCAGTTT C		
		A _____ C		
GAM746	LOC153711 3'	CTTCAGGTTGAACAGTAGCTTC 41668	CA GT AA	
	A	TGA CTACTGTTCA C AAG		
		ACT GATGACAAGT G TTC		
		TC TG AC		
GAM746	LOC51008 3'	CTCTTGACTATTGGGAGTAGTG 18064	G C_ A	
		CACTACT TT AGTCAA AG		
		GTGATGA GG TCAGTT TC		
		G TTA C		
GAM747	DLG5 5'	ACACCCCCCAAATAGACTA 40331	A TT	
		TAGTTTATTTTGG GG GTGT		
		ATCAGATAAAACC CC CACA		
		_ C_		
GAM747	FOSB 3'	ACACACAAAACAAACAAAC 13580	AT GAGG	
		GTTT TTTG TTGTGTGT		
		CAAA AAAC AACACACA		
		C_ AA_		
GAM747	LOC130813 3'	ACACACAAACAAAATAAAC 37305	GAGG	
		GTTTATTTTG TTGTGTGT		
		CAAATAAAAC AACACACA		
		A_		
GAM747	LOC202460 5'	ACACACAAGGAATAAAACAAAC 42979	A GAGG	
		GTTT TTTTG TTGTGTGT		

CAAA AAAAT AACACACA
 C AAGG
 GAM747 LOC221895 3' ACATTTCCCCAAAACAAA 44441 A A TT
 TTT TTTTGG GG GTGT
 ||| ||||| || ||||
 AAA AAAACC CC TACA
 C C TT
 GAM748 FLJ11280 5' TCATCACCCAGAGCA 20405 T AAC
 TGCTTTGG GT GATGA
 ||||| || ||||
 ACGAGACC CA CTACT

 GAM748 KIAA0172 5' CTCACCACA ACTCCCAAAGCAT 32410 T_ AACGA
 ATGCTTTGG GT TGAG
 ||||| || ||||
 TACGAAACC CA ACTC
 CT ACACC
 GAM748 SLC17A6 3' CTCATCACTATTTACTAAAGCA 21596 TAAC__
 TGCTTTGGTG GATGAG
 ||||| ||||
 ACGAAATCAT CTACTC
 TTATCA
 GAM748 LOC200488 5' CTCAGGTCCACACCAAAGCTTG 43313 T A_ GA
 AA TTCA GCTTTGGTGT AC TGAG
 ||| ||||| || ||||
 AAGT CGAAACCACA TG ACTC
 T CC G_
 GAM749 ACVR1 3' CATTACCCACGTGACACCACCG 6762 AA _ _
 CGGT TGTCG GTGG TAATG
 ||| |||| |||| ||||
 GCCA ACAGT CACC ATTAC
 CC G C
 GAM749 HK1 3' ACCAGCAGACACTGCCGGG 5689 A GG_
 CCCGGTA TGTC TGGT
 ||||| |||| ||||
 GGGCCGT ACAG ACCA
 C ACG
 GAM749 HK1 3' ACCAGCAGACACTGCCGGG 27267 A GG_
 CCCGGTA TGTC TGGT
 ||||| |||| ||||
 GGGCCGT ACAG ACCA
 C ACG
 GAM749 HK1 3' ACCAGCAGACACTGCCGGG 27270 A GG_
 CCCGGTA TGTC TGGT
 ||||| |||| ||||
 GGGCCGT ACAG ACCA
 C ACG
 GAM749 HK1 3' ACCAGCAGACACTGCCGGG 27273 A GG_
 CCCGGTA TGTC TGGT
 ||||| |||| ||||

			GGGCCGT ACAG ACCA		
			C ACG		
GAM749	HK1	3'	ACCAGCAGACACTGCCGGG	27266	A GG_
			CCCGGTA TGTC TGGT		
			GGGCCGT ACAG ACCA		
			C ACG		
GAM749	ITGAL	3'	CATTACCAGACGGTTCACC	7969	AA__ GG
			GGT TGTC TGGTAATG		
			CCA GCAG ACCATTAC		
			CTTG _		
GAM749	KIF5C	3'	ATTACCACCGACTCGGCC	10852	AAT
			GGT GTCGGTGGTAAT		
			CCG CAGCCACCATTA		
			GCT		
GAM749	SRD5A1	3'	ACCGGGTGACATCACCGGG	6714	A G_
			CCCGGT ATGTCG TGGT		
			GGGCCA TACAGT GCCA		
			C GG		
GAM749	MGC13159	3'	ATTATGTACATTACTGGGTT	26751	CG
			AACCCGGTAATGT GTGGT		
			TTGGGTCATTACA TATTA		
			TG		
GAM749	MGC3020	3'	CATTACCACATCCACACAGGG	23483	G AA TCG
			CCC GT TG GTGGTAATG		
			GGG CA AC CACCATTAC		
			A C_ CTA		
GAM749	LOC146227	5'	ATCACCACCGCCGGCGT	38081	_ TAATGT A
			AC CCGG CGGTGGT AT		
			TG GGCC GCCACCA TA		
			C _ C		
GAM749	LOC151719	5'	ATCACCACCACCGGGT	39161	AATGTC A
			ACCCGGT GGTGGT AT		
			TGGGCCA CCACCA TA		
			_ C		
GAM750	RELN	3'	AGTTGTACAACACCAGCAA	45279	CTA TT
			TTGCTGGTG TAC GCT		
			AACGACCAC ATG TGA		
			AAC T_		
GAM750	SCA7	3'	ACAGCAAGTATCGACAGCAA	5882	GTGCT
			TTGCTG ATACTTGCTGT		

			AACGAC TATGAACGACA		
			AGC__		
GAM750	FLJ20171	3'	ACAGCAAGCAGCATGCAGCA	19260	_ ATA
			TGCTG GTGCT CTTGCTGT		
			ACGAC TACGA GAACGACA		
			G C__		
GAM750	GG2-1	3'	ACAGACCCCAACCACCAGCAATA	15677	CTATACTTG
			TATTGCTGGTG CTGT		
			ATAACGACCAC GACA		
			CAACCCA__		
GAM750	LOC132235	5'	CAGCAAATGCCAGCAAT	37480	GCTATAC
			ATTGCTGGT TTGCTG		
			TAACGACCG AACGAC		
			TA_____		
GAM750	LOC255104	3'	ACAGAGGGGATAACAACAGCAA	45681	G C A TG
			TA TATTGCTG TG TAT CT CTGT		
			ATAACGAC AC ATA GG GACA		
			A A G GA		
GAM751	CX3CR1	3'	CAATTTACTTGCCATTACTCA	34976	AT _ TGT
			TGAGTAAT GCA GT TTG		
			ACTCATTA CGT CA AAC		
			C_ T TTT		
GAM751	OXR1	3'	CTTCATTTTCACATGTTACTCA	19732	CAGTTGTT
			TGAGTAATATG TGAAG		
			ACTCATTGTAC ACTTC		
			ACTTTT__		
GAM751	KIAA1036	3'	AGGCCTCTGCATATTCTCA	17122	T TT
			TGAG AATATGCAG GTTT		
			ACTC TTATACGTC CGGA		
			_ TC		
GAM751	LOC120856	3'	TCAAACAGTGCCAACACTCA	36644	AATAT G
			TGAGT GCA TTGTTTGA		
			ACTCA CGT GACAAACT		
			CAAC_ _		
GAM751	LOC221474	5'	CTTCCGAGCCGCATGTTACTCA	44379	A GTTT
			TGAGTAATATGC GTT GAAG		
			ACTCATTGTACG CGA CTTC		
			C GC__		
GAM752	ATP8A2	3'	AGCCAACCCAAACCCGCGC	44916	C GC
			GCGTG GT TTGGGTTGGCT		

CGCGC CA AACCCAACCGA
C _
GAM752 KIAA1229 3' GCCAACCCAAATGCCCAT 31099 C GC
GTG GT TTGGGTTGGC
||| || |||||
TAC CG AACCCAACCG
C TA
GAM752 KIAA1509 3' AGCTCCGTTAAGCACACAC 30871 C GTT
GTG GTGCTTGG GGCT
||| ||||| |||
CAC CACGAATT TCGA
A GCC
GAM752 Ubc6p 3' GCCAGCCCGCACGCGC 27714 TT _
GTGCGTGC GGGTTGG C
||||| ||||| |
CGCGCACG CCCGACC G
_ C
GAM752 LOC165904 3' GCCAACTGGACACAGCGT 40194 GC C G
GCGT GTG TT GGTTGGC
||| ||| |||||
TGCG CAC AG TCAACCG
A _ _ G
GAM753 EDR1 3' GGTTATAACCTGGTACCA 10702 A C
TGGTATCA GTTA AATC
||||| ||| |||
ACCATGGT CAAT TTGG
C A
GAM753 KIAA1423 3' GCTAGTAACTGTGATACCA 30921 _ AATCAA
TGGTATCA AGTTAC AGC
||||| ||||| |||
ACCATAGT TCAATG TCG
G A _ _
GAM753 LOC149844 5' CGCCTTTCTTGCAACCTGGTAC 38822 A A TC A
CA TGGTATCA GTT CAA AA GCG
||||| ||| ||| |||
ACCATGGT CAA GTT TT CGC
C C CT C
GAM754 RUNX1 3' AGAACAGAGACATTGCCA 7493 T
TGGC AATGTCTCTGTTTT
||| |||||
ACCG TTACAGAGACAAGA
_
GAM754 AGPAT1 5' GAGACAGAGACACAGCCA 13117 AA
TGGCT TGTCTCTGTTTT
||||| |||||
ACCGA ACAGAGACAGAG
C_
GAM754 DKFZP434E2135 5' AGTTAAAACAAAGGACGCTA 25112 TAAT C_
TGGC GTCT TGTTTAACT
||| ||| |||||

			ATCG CAGG ACAAATTGA		
			AA		
GAM754	MPHOSPH10	5'	TAGCTAAAACAGAAACGTAAGG	31204	A_ C A
		CC	GGCT ATGT TCTGTTTTA	CTA	
			CCGG TGCA AGACAAAAT	GAT	
			AA A C		
GAM754	RENT2	3'	GAGGCAGAAACACCAGCC	27909	AA C
			GGCT TGT TCTGTTTT		
			CCGA ACA AGACGGAG		
			CC A		
GAM754	RENT2	3'	GAGGCAGAAACACCAGCC	17803	AA C
			GGCT TGT TCTGTTTT		
			CCGA ACA AGACGGAG		
			CC A		
GAM754	LOC132948	3'	AAAATCTCCAGACATTGCCA	29779	T CT__
			TGGC AATGTCT	GTTTT	
			ACCG TTACAGA	TAAAA	
			— CCTC		
GAM754	LOC146332	3'	TAAAACACAAAAATTAGCCA	38129	GTCTC_
			TGGCTAAT	TGTTTTA	
			ACCGATTA	ACAAAAT	
			AAAAAC		
GAM754	LOC150519	3'	AGTTAAATATTGGGACACTAAC	38987	C A TGT_
		CA	TGG TA TGTCTC	TTTAACT	
			ACC AT ACAGGG	AAATTGA	
			A C TTAT		
GAM754	LOC196446	5'	AGTTGGAAGTCATCAGCCA	42371	A T CTGT
			TGGCT ATG CT	TTTAACT	
			ACCGA TAC GA	AGGTTGA	
			C T ____		
GAM754	LOC90233	3'	TAAAATACAAAAATTAGCCA	28744	GTCTC_
			TGGCTAAT	TGTTTTA	
			ACCGATTA	ATAAAAT	
			AAAAAC		
GAM755	GDI2	3'	CAATGTTATGGCAGGGC	7241	AAT A
			GCCC TTA AACATTG		
			CGGG GGT TTGTAAAC		
			AC_ A		
GAM755	C20orf43	3'	AAGTGAACTGGGCTTTAA	30112	A AAAA
			TTAAAGCCCA	TTT CATT	

AATTTCGGGT AAA GTGAA
 C ____
 GAM755 C20orf82 3' GTTTTAAATAGGCTTTAA 41085 CA
 TTAAAGCC ATTAAAAAC
 ||||| |||||
 AATTTCGG TAAATTTTG
 A_
 GAM755 MGC12966 3' ATGTGTTAAATTGTGCTTTAA 26418 C A
 TTAAAGC CAATTTAA ACAT
 ||||| ||||| |||
 AATTTCG GTTAAATT TGTA
 T G
 GAM756 UBE2L3 3' AATTCTGTCAGCTATCCAA 9354 _ T
 TTGGATAGCT ACAG GTT
 ||||| ||| |||
 AACCTATCGA TGTC TAA
 C T
 GAM756 AMOT 3' TAAAATAACATTGTACATCCAA 28416 AGC
 TTGGAT TACAGTGTTATTTTA
 |||| |||||
 AACCTA ATGTTACAATAAAAT
 C_
 GAM756 FLJ13195 3' AAAAAACAATACAGCTATCCA 23203 ACAG A
 A TTGGATAGCT TGTT TTTT
 ||||| ||| |||
 AACCTATCGA ACAA AAAA
 CATA A
 GAM756 FLJ23132 3' TAAAATAAGAGCTGTAGCTACC 45983 A G_
 AA TTGG TAGCTACAGT TTATTTTA
 ||| ||||| |||||
 AACC ATCGATGTCG AATAAAAT
 AG
 GAM756 HSPC039 3' AATTACACTGTACTACCCAA 18180 A C T
 TTGG TAG TACAGTGT ATT
 ||| ||| ||||| |||
 AACC ATC ATGTCACA TAA
 C _ T
 GAM756 PPFIBP1 3' AGTGTTCACTGTAGCCACC 9685 ATA T_
 GG GCTACAGTG TATT
 || ||||| |||
 CC CGATGTCAC GTGA
 AC_ TT
 GAM756 PRDM8 5' AAAATAACACTACAGTTTCC 21488 T AC
 GGA AGCT AGTGTTATTTT
 ||| ||| |||||
 CCT TTGA TCACAATAAAA
 _ CA
 GAM756 LOC122726 5' AAATAATCCTTAGCTATCCAA 37236 C TG T
 TTGGATAGCTA AG TTA TTT
 ||||| || ||| |||

AACCTATCGAT TC AAT AAA
_ CT C
GAM756 LOC83690 3' TAAAATAATCCTTTAATATCCA 25485 GC C TG
A TTGGATA TA AG TTATTTTA
||||| || || |||||
AACCTAT AT TC AATAAAAT
A_ T CT
GAM757 ZNF207 3' TTAAGAAATCTGACCCAC 9515 ATT CC C
GTGG GTCG GA TTCTTAA
||| ||| || |||||
CACC CAGT CT AAGAATT
_ _ A
GAM757 FLJ23309 3' TTAAGGACAAAGCCAACAATCC 24381 C_ CGAC
AC GTGGATTGT GC TTCTTAA
||||||| || |||||
CACCTAACA CG AGGAATT
AC AAAC
GAM757 SPRY1 5' AAGTGTGTTGGAATCCAC 32429 GTCG TT_
GTGGATT CCGAC CTT
||||| ||| |||
CACCTAA GGTTG GAA
A_ TGT
GAM757 LOC91431 5' TTTAAGAAGTCAAAAGATACCA 28948 AT GCC_
C GTGG TGTC GACTTCTTAAA
||| ||| |||||
CACC ATAG CTGAAGAATTT
_ AAAA
GAM758 PKHD1 3' TGAGAAGTACTGGCAGACA 28945 C AC A
TGTC TGCCA ACTT CTCA
||||| ||| |||
ACAG ACGGT TGAA GAGT
_ CA _
GAM758 RNMT 3' TTGAGTGCCTGGCAGGA 9893 ACACT
TCCTGCCA TACTCAA
||||| |||||
AGGACGGT GTGAGTT
CAC_
GAM758 FLJ23056 3' ATTTGAGTAAGTTTACATGAC 23807 C CC C
A TGTC TG AA ACTTACTCAAAT
||| || || |||||
ACAG AC TT TGAATGAGTTTA
T A_ T
GAM758 IPT 3' ATTTGAGTGAATGGCAGGA 19151 ACAC
TCCTGCCA TTA CTCAAAT
||||| |||||
AGGACGGT AGTGAGTTTA
A_
GAM758 MDS028 3' GTGGTATTGGCAGGATA 20535 C T
TGTCTGCCAA ACT AC
||||||| ||| ||

			ATAGGACGGTT TGG TG		
			A _		
GAM758	LOC137492	5'	GGGGAGCGCAGGCAGGACA 37107	AACA	A
			TGTCCTGCC CTT CTC		
			ACAGGACGG GAG GGG		
			ACGC _		
GAM759	TRPC5	3'	GCTAAGACTGTCATAAAA 14849	C	T
			TTTTATG ACAGTCTT GT		
			AAAATAC TGTCAGAA CG		
			_ T		
GAM759	KIAA0090	3'	CAAAGACTGTGCCTAAAA 42651	T	
			TTTTA GCACAGTCTTTG		
			AAAAT CGTGTGAGAAAC		
			C		
GAM759	LOC138199	3'	TCTAAGAAAACCTATGCGTAAAA 37117	C C G	
			TTTTATGCA AGT TTT TTTAGA		
			AAAATGCGT TCA AAA GAATCT		
			A _ _		
GAM759	LOC254228	3'	AAGCAGTACTGGCATAAAA 45916	A	CT
			TTTTATGC CAGT TTGTTT		
			AAAATACG GTCA GACGAA		
			_ T_		
GAM759	LOC254251	5'	TCTACAAAGAAAACCAGCATAA 45900	ACAG_	TT
	AA		TTTTATGC TCTTTGT AGA		
			AAAATACG AGAAACA TCT		
			ACCAAA _		
GAM760	EPB49	3'	TGGGAATTCCAGCACTAA 7710	AA	AGAG
			TTAGTGCT GAAT CCCG		
			AATCACGA CTTA GGGT		
			C_ A_		
GAM760	F2RL3	3'	GCAACCTCATCCCTCAGCACT 10082	A AATA_	CCC
	AA		TTAGTGCT AG GAG GC		
			AATCACGA TC CTC CG		
			C CCCTA CAA		
GAM760	FLJ11029	5'	TGCAAGCTCCAGGAAGCACTGA 30569	AAGAATA	CC
			TTAGTGCT GAGC GCA		
			AGTCACGA CTCG CGT		
			AGGAC_ AA		
GAM760	FLJ21168	3'	TGTCTTTCATTCCTAGCACTAA 24674	A _	CCC
			TTAGTGCTA GAAT AGAG GCA		

			AATCACGAT CTTA TTTC TGT		
			C C ____		
GAM760	GNG10	3'	GCTTTATTTTAACTAA 10332	C	
			TTAGTG TAAGAATAGAGC		
			AATCAC ATTTTATTTCG		
			A		
GAM760	GR6	5'	CTCTACTCTTAGCACTGA 14283	A	
			TTAGTGCTAAGA TAGAG		
			AGTCACGATTCT ATCTC		
			C		
GAM760	HBOA	3'	GCAGGTCTCTCAGCACTGA 13931	AAGAAT _ C	
			TTAGTGCT AGAG CC GC		
			AGTCACGA TCTC GG CG		
			C_____ T A		
GAM760	KIAA0319	3'	TTCTATTCCCAGGACTAA 16766	G AA	
			TTAGT CT GAATAGAG		
			AATCA GA CTTATCTT		
			G CC		
GAM760	KIAA0472	3'	CTCTATTCTCTGCACTAA 35576	TA	
			TTAGTGC AGAATAGAG		
			AATCACG TCTTATCTC		
			TC		
GAM760	PASK	5'	GCTTTTTCCTCTAGCACTAA 17502	_ AAT	
			TTAGTGCTA AG AGAGC		
			AATCACGAT TC TTTCG		
			C CTT		
GAM760	LOC220883	3'	GCAGGTCTCTCAGCACTGA 43852	AAGAAT _ C	
			TTAGTGCT AGAG CC GC		
			AGTCACGA TCTC GG CG		
			C_____ T A		
GAM760	LOC221662	3'	TGCAATTTTATTCTTAACTA 44390	GC CCC	
	A		TTAGT TAAGAATAGAG GCA		
			AATCA ATTCTTATTTT CGT		
			A_ TAA		
GAM761	GTPBP5	3'	CTTCACGACTGAATGCAC 32575	A G	
			GT CATT AGTCGTGAAG		
			CA GTAA TCAGCACTTC		
			C G		
GAM761	KIAA0625	5'	CAAGATCTCCACGAATATCA 17407	G_ A	
			TGA TCGTG AGATCTTG		

			ACT AGCAC TCTAGAAC		
			ATA C		
GAM761	KIAA1493	3'	CAAAATCTTCACCTTGAGTACA 32087	AG_ ____	C
			ATGTAC TACATTG TC GTGAAGAT TTG		
			ATGTAAC AG CACTTCTA AAC		
			ATG TTC A		
GAM762	APOBEC1	3'	GCAAAAACACCACCAATCAC 12510	CA G_	
			GTGATTGG GTGT TTGC		
			CACTAACC CACA AACG		
			AC AA		
GAM762	CLCN4	3'	ATGCACTTCATACTAGCAATCA 7570	GC T__	
	CA		TGTGATTG AGTGTG TGCAT		
			ACACTAAC TCATAC ACGTA		
			GA TTC		
GAM762	PCDHA1	3'	TATCGGCCACCTGCCAATCACA 20868	_ T C	
			TGTGATTGGCAG TG GTTG ATA		
			ACACTAACCGTC AC CGGC TAT		
			C _ _		
GAM762	PCDHA1	3'	TATCGGCCACCTGCCAATCACA 25387	_ T C	
			TGTGATTGGCAG TG GTTG ATA		
			ACACTAACCGTC AC CGGC TAT		
			C _ _		
GAM762	PCDHA10	3'	TATCGGCCACCTGCCAATCACA 20878	_ T C	
			TGTGATTGGCAG TG GTTG ATA		
			ACACTAACCGTC AC CGGC TAT		
			C _ _		
GAM762	PCDHA10	3'	TATCGGCCACCTGCCAATCACA 25619	_ T C	
			TGTGATTGGCAG TG GTTG ATA		
			ACACTAACCGTC AC CGGC TAT		
			C _ _		
GAM762	PCDHA11	3'	TATCGGCCACCTGCCAATCACA 20889	_ T C	
			TGTGATTGGCAG TG GTTG ATA		
			ACACTAACCGTC AC CGGC TAT		
			C _ _		
GAM762	PCDHA12	3'	TATCGGCCACCTGCCAATCACA 20899	_ T C	
			TGTGATTGGCAG TG GTTG ATA		
			ACACTAACCGTC AC CGGC TAT		
			C _ _		
GAM762	PCDHA13	3'	TATCGGCCACCTGCCAATCACA 20909	_ T C	
			TGTGATTGGCAG TG GTTG ATA		

			ACACTAACCGTC AC CGGC TAT	
			C _ _	
GAM762	PCDHA2	3'	TATCGGCCACCTGCCAATCACA 20919	_ T C
			TGTGATTGGCAG TG GTTG ATA	
			ACACTAACCGTC AC CGGC TAT	
			C _ _	
GAM762	PCDHA3	3'	TATCGGCCACCTGCCAATCACA 20929	_ T C
			TGTGATTGGCAG TG GTTG ATA	
			ACACTAACCGTC AC CGGC TAT	
			C _ _	
GAM762	PCDHA4	3'	TATCGGCCACCTGCCAATCACA 20939	_ T C
			TGTGATTGGCAG TG GTTG ATA	
			ACACTAACCGTC AC CGGC TAT	
			C _ _	
GAM762	PCDHA5	3'	TATCGGCCACCTGCCAATCACA 20949	_ T C
			TGTGATTGGCAG TG GTTG ATA	
			ACACTAACCGTC AC CGGC TAT	
			C _ _	
GAM762	PCDHA6	3'	TATCGGCCACCTGCCAATCACA 20959	_ T C
			TGTGATTGGCAG TG GTTG ATA	
			ACACTAACCGTC AC CGGC TAT	
			C _ _	
GAM762	PCDHA6	3'	TATCGGCCACCTGCCAATCACA 25591	_ T C
			TGTGATTGGCAG TG GTTG ATA	
			ACACTAACCGTC AC CGGC TAT	
			C _ _	
GAM762	PCDHA7	3'	TATCGGCCACCTGCCAATCACA 20969	_ T C
			TGTGATTGGCAG TG GTTG ATA	
			ACACTAACCGTC AC CGGC TAT	
			C _ _	
GAM762	PCDHA8	3'	TATCGGCCACCTGCCAATCACA 20979	_ T C
			TGTGATTGGCAG TG GTTG ATA	
			ACACTAACCGTC AC CGGC TAT	
			C _ _	
GAM762	PCDHA9	3'	TATCGGCCACCTGCCAATCACA 25605	_ T C
			TGTGATTGGCAG TG GTTG ATA	
			ACACTAACCGTC AC CGGC TAT	
			C _ _	
GAM762	PCDHAC1	3'	TATCGGCCACCTGCCAATCACA 20848	_ T C
			TGTGATTGGCAG TG GTTG ATA	

A C A C T A A C C G T C A C C G G C T A T
 C _ _
 GAM762 PCDHAC2 3' TATCGGCCACCTGCCAATCACA 20858 _ T C
 TGTGATTGGCAG TG GTTG ATA
 ||||| || ||| |||
 A C A C T A A C C G T C A C C G G C T A T
 C _ _
 GAM762 CAMTA1 3' ATGCAACAACAACACACA 33718 AT GCA G
 TGTG TG GT TGTTCAT
 ||| || || |||||
 A C A C A C C A A C A A C G T A
 _ A A _
 GAM762 FLJ12121 3' ACACAACGTAGGCCTAATCACA 24537 _ AG____
 TGTGATT GGC TGTGT
 ||||| || |||
 A C A C T A A C C G A C A C A
 T G A T G C A
 GAM762 KIAA0329 3' CAACACACCTCACCTCACA 16876 TT CA__
 TGTGA GG GTGTGTTG
 |||| || |||||
 A C A C T C C C A C A C A A C
 _ A C T C
 GAM762 KIAA0390 3' ACACGGTGCACCAATCTACA 16269 _ _ G
 TGT GATTG GCA TGTGT
 || |||| || |||||
 A C A C T A A C C G T G C A C A
 T C A G
 GAM762 KIAA1550 3' GCATACACACCAACACA 33071 A C A T
 TGTG TTGG GTGTGT GC
 ||| ||| ||||| ||
 A C A C A A C C C A C A T A C G
 _ A _
 GAM762 MBD2 3' GCACACAAGCTCTGCGCCAATC 17946 ____ G _
 A C G T G A T T G G C A G T T G T T G C
 ||||| || ||| |||
 C A C T A A C C G T C G A C A A C G
 C G T C A C
 GAM762 SLAM 3' ACACACTGACCACAGTCACA 8992 ____
 TGTGATTGG CAGTGTGT
 ||||| |||||
 A C A C T G A C C G T C A C A C A
 A C C A
 GAM762 LOC118851 5' CAACATATCAACTCACA 37200 _ GCA
 TGTGA TTG GTGTGTTG
 |||| || |||||
 A C A C T A A C T A T A C A A C
 C _
 GAM762 LOC146890 5' ACACAGGAGGGCTGCTAATCAC 40764 _____
 A T G T G A T T G G C A G T G T G T
 ||||| ||| |||

		ACACTAATCGTCG CACA		
		GGAGGA		
GAM762	LOC157627 3'	TATGCACCACTGCCATCACA 39621	T T T	
		TGTGAT GGCAGTG GT GCATA		
		ACACTA CCGTCAC CA CGTAT		
		— — —		
GAM762	LOC163682 5'	GCATCAACACCGCCACCCACA 42093	AT A GT_	
		TGTG TGGC GTGT TGC		
		ACAC ACCG CACA ACG		
		CC C ACT		
GAM763	MCF2 3'	CAAGTAAAGCACAACATTATG 11840	TACA A_	
		CATAGTGT TGTG TTA CTG		
		GTATTACA ACAC AATGAAC		
		— GA		
GAM763	KIAA0293 3'	AAGCCATCACAAAACACTAT 30392	ACA TA	
		ATAGTGTT TGTGAT CTT		
		TATCACAA AACTA GAA		
		A_ CC		
GAM763	LOC91664 3'	AAGTCTTCAGTAACACTA 33211	ATG TT	
		TAGTGTTAC TGA ACTT		
		ATCACAAATG ACT TGAA		
		— TC		
GAM764	C21orf25 3'	AAGCCAGAAGACGTGCACCCA 31794	T A GG AA	
		TG GGT CATG TTCT CTT		
		AC CCA GTGC AAGA GAA		
		— C AG CC		
GAM765	KCNJ16 3'	ATCAGCTCACCAGTTCAA 20727	T AA TTT	
		TTGA ACT GTG AGCTGAT		
		AACT TGA CAC TCGACTA		
		— C_ —		
GAM765	CG005 3'	AATCAGCACATCACTTAGTTCA 17038	T TTTA	
	A	TTGA ACTAAGTG GCTGATT		
		AACT TGATTCAC CGACTAA		
		— TACA		
GAM765	LOC219401 3'	AATCAGCACTTACTAAACATCA 44584	ACTA TTTA	
	A	TTGAT AGTG GCTGATT		
		AACTA TCAT CGACTAA		
		CAAA TCA_		
GAM765	LOC90462 3'	AATCAGCTTTTCTAAGATCAA 31503	A A TGTTT	
		TTGAT CT AG AGCTGATT		

			AACTA GA TC TCGACTAA	
			_ A TTT_	
GAM766	AK1	3'	GAGCCAAGATTGCGCCACTGCA 6087	AGACCAG
			TGTAGT GATCTTGGCTC	
			ACGTCA TTAGAACCGAG	
			CCGCG_	
GAM766	DMC1	3'	GAGCCAAGATGGCACCCTGCA 13933	AGA_ GGA
			TGTAGT CCA TCTTGGCTC	
			ACGTCA GGT AGAACCGAG	
			CCAC _	
GAM766	DXYS155E	3'	AGCCAAGACCCTTCTGC 11540	CC A
			GTAGA AGG TCTTGGCT	
			CGTCT TCC AGAACCGA	
			_ C	
GAM766	FLRT2	5'	AAGATCCCATACCTACTACA 14875	ACCA_
			TGTAGTAG GGATCTT	
			ACATCATC CCTAGAA	
			CATAC	
GAM766	HRH1	3'	GAGCCAAGATCACGCCACTGCA 6525	AGACCAG
			TGTAGT GATCTTGGCTC	
			ACGTCA CTAGAACCGAG	
			CCGCA_	
GAM766	HUNK	3'	GAGCCAAGATCATGCTACTGCA 15950	ACCAG
			TGTAGTAG GATCTTGGCTC	
			ACGTCATC CTAGAACCGAG	
			GTA_	
GAM766	KCNJ5	3'	GAGCCAAGATCATGCCACTGCA 6588	AGAC G
			TGTAGT CA GATCTTGGCTC	
			ACGTCA GT CTAGAACCGAG	
			CC_ A	
GAM766	LEP	3'	GAGCCAAGATCGCGCCACTGCA 5738	AGACCAG
			TGTAGT GATCTTGGCTC	
			ACGTCA CTAGAACCGAG	
			CCGCG_	
GAM766	NUP62	3'	GAACCAAGATCACACCACTGCA 18628	AGACCAG C
			TGTAGT GATCTTGG TC	
			ACGTCA CTAGAACC AG	
			CCACA_ A	
GAM766	PIM1	3'	AGCCAAGACCTCACACACACA 43754	A AGACC A
			TGT GT AGG TCTTGGCT	

			ACA CA TCC AGAACCGA		
			_ CACAC _		
GAM766	SCAP2	3'	GAGCCAAGATCGCGCCACTGCA 10029	AGACCAG	
			TGTAGT GATCTTGGCTC		
			ACGTCA CTAGAACCGAG		
			CCGCG_		
GAM766	SLC17A5	3'	GAACCAAGATCACGCCACTGCA 14814	AGACCAG	C
			TGTAGT GATCTTGG TC		
			ACGTCA CTAGAACC AG		
			CCGCA_ A		
GAM766	SULT2A1	3'	GAGCCAAGATCGCGCCACTGCA 35540	AGACCAG	
			TGTAGT GATCTTGGCTC		
			ACGTCA CTAGAACCGAG		
			CCGCG_		
GAM766	SUV39H2	3'	GAGCCAAGATCATACCACTGCA 23975	AGACCAG	
			TGTAGT GATCTTGGCTC		
			ACGTCA CTAGAACCGAG		
			CCATA_		
GAM766	TRPM8	3'	GAACCAAGATTGCACCACTGCA 23517	AGACCAG	C
			TGTAGT GATCTTGG TC		
			ACGTCA TTAGAACC AG		
			CCACG_ A		
GAM766	XT3	3'	GAGCCAAGATCATGCCACTCCA 21445	T AGAC G	
			TG AGT CA GATCTTGGCTC		
			AC TCA GT CTAGAACCGAG		
			C CC_ A		
GAM766	ALTE	3'	GAGCCAAGACTACGCCACTGCA 11104	AGACCA A	
			TGTAGT GG TCTTGGCTC		
			ACGTCA TC AGAACCGAG		
			CCGCA_ _		
GAM766	ARNTL2	3'	GAGCCAAGATCGCGCCACTGCA 21414	AGACCAG	
			TGTAGT GATCTTGGCTC		
			ACGTCA CTAGAACCGAG		
			CCGCG_		
GAM766	BIRC1	3'	GAGCCAAGATGGCGCCACTGCA 10886	AGA_ GGA	
			TGTAGT CCA TCTTGGCTC		
			ACGTCA GGT AGAACCGAG		
			CCGC _		
GAM766	BLOV1	3'	GAGCCAAGATCGTACCACTGCA 37521	AG_ CAG	
			TGTAGT AC GATCTTGGCTC		

			ACGTCA TG CTAGAACCGAG	
			CCA ____	
GAM766	C20orf108	3'	GAGCCAAGATCACACCACTGCA 28085	AGACCAG
			TGTAGT GATCTTGGCTC	
			ACGTCA CTAGAACCGAG	
			CCACA__	
GAM766	C9orf5	3'	GAGCCAAGATGGCGCCACTGCA 25714	AGA_ GGA
			TGTAGT CCA TCTTGGCTC	
			ACGTCA GGT AGAACCGAG	
			CCGC ____	
GAM766	cerk	3'	GAGCCAAGATTGCGCCACTGCA 23013	AGACCAG
			TGTAGT GATCTTGGCTC	
			ACGTCA TTAGAACCGAG	
			CCGCG__	
GAM766	CG012	5'	GAGCCAAGATCACACCACTGCA 40488	AGACCAG
			TGTAGT GATCTTGGCTC	
			ACGTCA CTAGAACCGAG	
			CCACA__	
GAM766	COE2	3'	GAGCCAAGATCACGCCACTGCA 32127	AGACCAG
			TGTAGT GATCTTGGCTC	
			ACGTCA CTAGAACCGAG	
			CCGCA__	
GAM766	DDX34	3'	GAGCCAAGATCGTGCCACTGCA 16162	AGAC G
			TGTAGT CA GATCTTGGCTC	
			ACGTCA GT CTAGAACCGAG	
			CC__ G	
GAM766	DIS3	3'	GAGCCAAGATCGCGCCACTGCA 17301	AGACCAG
			TGTAGT GATCTTGGCTC	
			ACGTCA CTAGAACCGAG	
			CCGCG__	
GAM766	DKFZP434I1735	3'	GAGCCAAGATTGTGCCACTGCA 42421	AGAC G
			TGTAGT CA GATCTTGGCTC	
			ACGTCA GT TTAGAACCGAG	
			CC__ G	
GAM766	DKFZP564B1023	3'	GAGCCAAGATCGCACCACTGCA 25343	AGACCAG
			TGTAGT GATCTTGGCTC	
			ACGTCA CTAGAACCGAG	
			CCACG__	
GAM766	DKFZP586D2223	3'	GAGCCAAGATTATGCCACTGCA 20645	AGAC G
			TGTAGT CA GATCTTGGCTC	

		ACGTCA GT TTAGAACCGAG	
		CC__ A	
GAM766	DKFZp586I021 3'	AGCCCGTGGCCTGGCCTGCTAC 26018	A A TT_
	A	TGTAGTAG CCAGG TC GGCT	
		ACATCGTC GGTCC GG CCGA	
		C _ TGC	
GAM766	DKFZp761J139 5'	GAGCCAAGATCGCCCACTGCA 26036	AGACCAG
		TGTAGT GATCTTGGCTC	
		ACGTCA CTAGAACCGAG	
		CCCG__	
GAM766	ERAP140 3'	GAGCCAAGATCGTGCCCACTGCA 37086	AGAC G
		TGTAGT CA GATCTTGGCTC	
		ACGTCA GT CTAGAACCGAG	
		CC__ G	
GAM766	FBXO27 3'	GAACCAAGATCATGCCCACTGCA 36836	AGAC G C
		TGTAGT CA GATCTTGG TC	
		ACGTCA GT CTAGAACC AG	
		CC__ A A	
GAM766	FKBP14 3'	GAGCCAAGATTGTGCCCACTGCA 19645	AGAC G
		TGTAGT CA GATCTTGGCTC	
		ACGTCA GT TTAGAACCGAG	
		CC__ G	
GAM766	FLJ10008 3'	GAGCCAAGATCGCGCCCACTGCA 19692	AGACCAG
		TGTAGT GATCTTGGCTC	
		ACGTCA CTAGAACCGAG	
		CCGCG__	
GAM766	FLJ10650 3'	GAGCCAAGATCACTCCCACTGCA 19986	A CCAG
		TGTAGT GA GATCTTGGCTC	
		ACGTCA CT CTAGAACCGAG	
		C CA__	
GAM766	FLJ10803 3'	GAGCCAAGATCCTGCCCACTGCA 20155	AGAC
		TGTAGT CAGGATCTTGGCTC	
		ACGTCA GTCCTAGAACCGAG	
		CC__	
GAM766	FLJ11151 3'	GAGCCAAGATCATGCCCACTGCA 33706	AGAC G
		TGTAGT CA GATCTTGGCTC	
		ACGTCA GT CTAGAACCGAG	
		CC__ A	
GAM766	FLJ11700 3'	GAGCCAAGATCACACTACTGCA 24367	ACCAG
		TGTAGTAG GATCTTGGCTC	

		ACGTCATC CTAGAACCGAG	
		ACA__	
GAM766	FLJ12800	3' GAGCCAAGATCTCGCCACTGCA 23191	AGACCA
		TGTAGT GGATCTTGGCTC	
		ACGTCA TCTAGAACCGAG	
		CCGC__	
GAM766	FLJ14641	3' GAGCCAAGATCACGCCACTGCA 26587	AGACCAG
		TGTAGT GATCTTGGCTC	
		ACGTCA CTAGAACCGAG	
		CCGCA__	
GAM766	FLJ20013	3' GAGCCAAGATCACGCCACTGCA 19121	AGACCAG
		TGTAGT GATCTTGGCTC	
		ACGTCA CTAGAACCGAG	
		CCGCA__	
GAM766	FLJ20211	3' AGCCAAGATTGCGCCACTGCA 19296	AGACCAG
		TGTAGT GATCTTGGCT	
		ACGTCA TTAGAACCGA	
		CCGCG__	
GAM766	FLJ20783	3' GAGCCAAGATAGTGCCACTGCA 19670	AGAC GG
		TGTAGT CA ATCTTGGCTC	
		ACGTCA GT TAGAACCGAG	
		CC__ GA	
GAM766	FLJ20825	3' GAGCCAAGATCGCGCCACTGCA 19681	AGACCAG
		TGTAGT GATCTTGGCTC	
		ACGTCA CTAGAACCGAG	
		CCGCG__	
GAM766	FLJ21687	3' GAGCCAAGATCGCACCACTGCA 24289	AGACCAG
		TGTAGT GATCTTGGCTC	
		ACGTCA CTAGAACCGAG	
		CCACG__	
GAM766	FLJ21870	3' GAGCCAAGATCACGACACTGCA 23280	AGACCAG
		TGTAGT GATCTTGGCTC	
		ACGTCA CTAGAACCGAG	
		CAGCA__	
GAM766	FLJ22692	3' GAGCCAAGATCGTGCCACTGCA 24645	AGAC G
		TGTAGT CA GATCTTGGCTC	
		ACGTCA GT CTAGAACCGAG	
		CC__ G	
GAM766	FLJ22814	3' GAGCCAAGATCGCGCCACTGCA 24441	AGACCAG
		TGTAGT GATCTTGGCTC	

			ACGTCA	CTAGAACCGAG		
			CCGCG__			
GAM766	FLJ23235	3'	GAACCAAGATCACGCCACTGCA	24488	AGACCAG	C
			TGTAGT	GATCTTGG TC		
			ACGTCA	CTAGAACC AG		
			CCGCA__	A		
GAM766	FLJ31737	3'	GAGCCAAGATCCCGCCACTGCA	29590	AGACCA	
			TGTAGT	GGATCTTGGCTC		
			ACGTCA	CCTAGAACCGAG		
			CCGC__			
GAM766	KIAA0252	3'	GAGCCAAGATCGTGCCACTGCA	31448	AGAC G	
			TGTAGT	CA GATCTTGGCTC		
			ACGTCA	GT CTAGAACCGAG		
			CC__	G		
GAM766	KIAA0266	3'	GAGCCAAGATTGTGCCACTGCA	22310	AGAC G	
			TGTAGT	CA GATCTTGGCTC		
			ACGTCA	GT TTAGAACCGAG		
			CC__	G		
GAM766	KIAA0420	3'	AGTTCCCCTAGTTACTACA	31723	A C ATCTT	
			TGTAGT	GAC AGG GGCT		
			ACATCA	TTG TCC TTGA		
			_ A CC__			
GAM766	KIAA0472	3'	GAGCCAAGATCACACCACTGCA	35578	AGACCAG	
			TGTAGT	GATCTTGGCTC		
			ACGTCA	CTAGAACCGAG		
			CCACA__			
GAM766	KIAA0527	3'	AGATCCTAATCTACTGCA	45841	CC	
			TGTAGTAGA	AGGATCT		
			ACGTCATCT	TCCTAGA		
			AA			
GAM766	KIAA0794	3'	GAGCCAAGATCGCACCATTACA	39181	AGACCAG	
			TGTAGT	GATCTTGGCTC		
			ACATTA	CTAGAACCGAG		
			CCACG__			
GAM766	KIAA1228	3'	GAGCCAAGATCGCACCCTGCA	32444	AGACCAG	
			TGTAGT	GATCTTGGCTC		
			ACGTCA	CTAGAACCGAG		
			CCACG__			
GAM766	KIAA1641	3'	GAGCCAAGATCGTGCCACTGCA	39100	AGAC G	
			TGTAGT	CA GATCTTGGCTC		

		ACGTCA GT CTAGAACCGAG	
		CC__ G	
GAM766	KIAA1871	3' GAGCCAAGATCATGCCACTGCA 30705	AGAC G
		TGTAGT CA GATCTTGGCTC	
		ACGTCA GT CTAGAACCGAG	
		CC__ A	
GAM766	KIAA1872	3' GAGCCAAGATCGTGCCACTGCA 31519	AGAC G
		TGTAGT CA GATCTTGGCTC	
		ACGTCA GT CTAGAACCGAG	
		CC__ G	
GAM766	KIAA1969	3' GAGCCAAGATTGTACCACTGCA 38491	AG_ CAG
		TGTAGT AC GATCTTGGCTC	
		ACGTCA TG TTAGAACCGAG	
		CCA ____	
GAM766	KR18	3' GAGCCAAGATCATGCCACTGCA 27118	AGAC G
		TGTAGT CA GATCTTGGCTC	
		ACGTCA GT CTAGAACCGAG	
		CC__ A	
GAM766	LIM	3' GAGCCAAGATCGTACCACTGCA 13178	AG_ CAG
		TGTAGT AC GATCTTGGCTC	
		ACGTCA TG CTAGAACCGAG	
		CCA ____	
GAM766	LRG	3' GAGCCAAGATCGTGCCACTGCA 27546	AGAC G
		TGTAGT CA GATCTTGGCTC	
		ACGTCA GT CTAGAACCGAG	
		CC__ G	
GAM766	MESDC2	3' GAGCCAAGATCAGGCCACTGCA 35893	AGA AG
		TGTAGT CC GATCTTGGCTC	
		ACGTCA GG CTAGAACCGAG	
		CC_ A_	
GAM766	MGC14407	3' GAGCCAAGACTGTGCCACTGCA 26728	AGAC GA
		TGTAGT CAG TCTTGGCTC	
		ACGTCA GTC AGAACCGAG	
		CCGT ____	
GAM766	MGC2562	3' AGCCAAGATCCTACCACTA 26162	AGACC
		TAGT AGGATCTTGGCT	
		ATCA TCCTAGAACCGA	
		CCA__	
GAM766	MGC2562	3' GAGCCAAGATTGCGCCACTGCA 26164	AGACCAG
		TGTAGT GATCTTGGCTC	

			ACGTCA	TTAGAACCGAG	
			CCGCG__		
GAM766	MGC29891	3'	GAGCCAAGATCGTGCCACTGCA	29437	AGAC G
			TGTAGT	CA GATCTTGGCTC	
			ACGTCA	GT CTAGAACCGAG	
			CC__ G		
GAM766	MGC4840	3'	GAGCCAAGATCACGCCACTGCA	35439	AGACCAG
			TGTAGT	GATCTTGGCTC	
			ACGTCA	CTAGAACCGAG	
			CCGCA__		
GAM766	PRO0478	5'	GAGCCAAGATCACGCCACTGCA	15397	AGACCAG
			TGTAGT	GATCTTGGCTC	
			ACGTCA	CTAGAACCGAG	
			CCGCA__		
GAM766	Rpo1-2	3'	GAGCCAAGATTGTGCCACCACA	21102	A AGAC G
			TGT GT	CA GATCTTGGCTC	
			ACA CA	GT TTAGAACCGAG	
			C CC__ G		
GAM766	Rpo1-2	3'	GAGCCAAGATTGTGCCACTGCA	21103	AGAC G
			TGTAGT	CA GATCTTGGCTC	
			ACGTCA	GT TTAGAACCGAG	
			CC__ G		
GAM766	SAMHD1	3'	GAGCCAAGATCAGGCCACTGCA	30735	AGA AG
			TGTAGT	CC GATCTTGGCTC	
			ACGTCA	GG CTAGAACCGAG	
			CC_ A_		
GAM766	SCN12A	3'	GAGCCAAGATCGTGTCACTGCA	15409	A C G
			TGTAGT	GAC A GATCTTGGCTC	
			ACGTCA	CTG T CTAGAACCGAG	
			_ _ G		
GAM766	SPTLC2	3'	GAGCCAAGATCACACCACTGCA	11281	AGACCAG
			TGTAGT	GATCTTGGCTC	
			ACGTCA	CTAGAACCGAG	
			CCACA__		
GAM766	TRIAD3	3'	GAGCCAAGATTGTGCCACTGCA	45347	AGAC G
			TGTAGT	CA GATCTTGGCTC	
			ACGTCA	GT TTAGAACCGAG	
			CC__ G		
GAM766	WBSCR23	3'	GAGCCAAGATCGCACCACTGCA	24640	AGACCAG
			TGTAGT	GATCTTGGCTC	

			ACGTCA	CTAGAACCGAG	
			CCACG__		
GAM766	WSB1	3'	AGCCAAGATCACACCACTGCA	28615	AGACCAG
			TGTAGT	GATCTTGGCT	
			ACGTCA	CTAGAACCGA	
			CCACA__		
GAM766	WSB1	3'	AGCCAAGATCACACCACTGCA	28621	AGACCAG
			TGTAGT	GATCTTGGCT	
			ACGTCA	CTAGAACCGA	
			CCACA__		
GAM766	ZFP106	3'	GAGCCAAGATCATACTACTGCA	22832	ACCAG
			TGTAGTAG	GATCTTGGCTC	
			ACGTCATC	CTAGAACCGAG	
			ATA__		
GAM766	LOC115129	5'	GAGCCAAGATCATGCCACTGCA	36251	AGAC G
			TGTAGT	CA GATCTTGGCTC	
			ACGTCA	GT CTAGAACCGAG	
			CC__ A		
GAM766	LOC127428	3'	AGCCAAGATTGTACCACTGCA	36896	AG_ CAG
			TGTAGT	AC GATCTTGGCT	
			ACGTCA	TG TTAGAACCGA	
			CCA ____		
GAM766	LOC134147	3'	GAGCCAAGATTGTGCCACTAC	29031	AGAC G
			GTAGT	CA GATCTTGGCTC	
			CATCA	GT TTAGAACCGAG	
			CC__ G		
GAM766	LOC145988	5'	GAGCCAAGATCACGCCACTGCA	38038	AGACCAG
			TGTAGT	GATCTTGGCTC	
			ACGTCA	CTAGAACCGAG	
			CCGCA__		
GAM766	LOC146229	3'	GAGCCAAGATGGCGCCACTACA	38110	AGA_ GGA
			TGTAGT	CCA TCTTGGCTC	
			ACATCA	GGT AGAACCGAG	
			CCGC ____		
GAM766	LOC147837	3'	GAGCCAAGATCGCGCCACTGCA	38393	AGACCAG
			TGTAGT	GATCTTGGCTC	
			ACGTCA	CTAGAACCGAG	
			CCGCG__		
GAM766	LOC148147	3'	GAGCCAAGATCGCGCCACTGCA	38476	AGACCAG
			TGTAGT	GATCTTGGCTC	

	ACGTCA CTAGAACCGAG	
	CCGCG__	
GAM766 LOC148254 3'	GAGCCAAGATCACACCACTGCA 38502	AGACCAG
	TGTAGT GATCTTGGCTC	
	ACGTCA CTAGAACCGAG	
	CCACA__	
GAM766 LOC149705 3'	AGCCAAGACTATGCCACTGCA 41052	AGAC GGA
	TGTAGT CA TCTTGGCT	
	ACGTCA GT AGAACCGA	
	CC__ ATC	
GAM766 LOC150245 3'	GAGCCAAGACCACACCACTGCA 41162	AGACCA A
	TGTAGT GG TCTTGGCTC	
	ACGTCA CC AGAACCGAG	
	CCACA_ _	
GAM766 LOC150481 3'	GAGCCAAGATCGCATCACTGCA 38980	A CCAG
	TGTAGT GA GATCTTGGCTC	
	ACGTCA CT CTAGAACCGAG	
	_ ACG_	
GAM766 LOC151248 3'	GAGCCAAGATCGCGCCACTGCA 39088	AGACCAG
	TGTAGT GATCTTGGCTC	
	ACGTCA CTAGAACCGAG	
	CCGCG__	
GAM766 LOC152426 3'	GAGCCAAGATCGCGCTACTGCA 41499	ACCAG
	TGTAGTAG GATCTTGGCTC	
	ACGTCATC CTAGAACCGAG	
	GCG__	
GAM766 LOC153727 3'	GAGCCAAGATCGTGCCACTGCA 41681	AGAC G
	TGTAGT CA GATCTTGGCTC	
	ACGTCA GT CTAGAACCGAG	
	CC__ G	
GAM766 LOC155006 3'	GAGCCAAGATCATGCCACTGCA 39526	AGAC G
	TGTAGT CA GATCTTGGCTC	
	ACGTCA GT CTAGAACCGAG	
	CC__ A	
GAM766 LOC158088 3'	GAGCCAAGATCGCGCCACTGCA 41917	AGACCAG
	TGTAGT GATCTTGGCTC	
	ACGTCA CTAGAACCGAG	
	CCGCG__	
GAM766 LOC158677 5'	GAGCCAAGATTTTGCCACTGCA 42023	AGAC
	TGTAGT CAGGATCTTGGCTC	

		ACGTCA GTTTTAGAACCGAG		
		CC__		
GAM766	LOC158819 3'	GAGCCAAGATCGTGCCACTGCA 42026	AGAC G	
		TGTAGT CA GATCTTGGCTC		
		ACGTCA GT CTAGAACCGAG		
		CC__ G		
GAM766	LOC159036 3'	GAGCCAAGATCGTGACACTGCA 42054	AGAC G	
		TGTAGT CA GATCTTGGCTC		
		ACGTCA GT CTAGAACCGAG		
		CA__ G		
GAM766	LOC200251 5'	GAGCCAAGATCACACCACTGCA 42756	AGACCAG	
		TGTAGT GATCTTGGCTC		
		ACGTCA CTAGAACCGAG		
		CCACA__		
GAM766	LOC201220 3'	GAGCCAAGATTGCACCACTGCA 42224	AGACCAG	
		TGTAGT GATCTTGGCTC		
		ACGTCA TTAGAACCGAG		
		CCACG__		
GAM766	LOC201895 3'	GAACCAAGATCGCACCACTGCA 42926	AGACCAG	C
		TGTAGT GATCTTGG TC		
		ACGTCA CTAGAACC AG		
		CCACG__ A		
GAM766	LOC203378 3'	GAACCAAGATCATGCCACTGCA 43553	AGAC G	C
		TGTAGT CA GATCTTGG TC		
		ACGTCA GT CTAGAACC AG		
		CC__ A A		
GAM766	LOC220662 3'	GAGCCAAGATTGCGCCGCTACA 43823	AGACCAG	
		TGTAGT GATCTTGGCTC		
		ACATCG TTAGAACCGAG		
		CCGCG__		
GAM766	LOC221477 3'	GAGCCAAGATTGTGCCACTTCA 44254	T AGAC G	
		TG AGT CA GATCTTGGCTC		
		AC TCA GT TTAGAACCGAG		
		T CC__ G		
GAM766	LOC221543 5'	GAGCCAAGACCGCACCACTGCA 45013	AGACCA A	
		TGTAGT GG TCTTGGCTC		
		ACGTCA CC AGAACCGAG		
		CCACG_ _		
GAM766	LOC221755 3'	GAACCAAGATTCCTACTGACA 44386	_ ACCA	C
		TGT AGTAG GGATCTTGG TC		

		ACA TCATC CTTAGAACC AG	
		G _____ A	
GAM766	LOC254122 3'	GAGCCAAGACCCCAATGCTA 45436	GACCA A
		TAGTA GG TCTTGGCTC	
		ATCGT CC AGAACCGAG	
		AACAC C	
GAM766	LOC255196 3'	GAGCCAAGATTGTGCCACTGCA 46413	AGAC G
		TGTAGT CA GATCTTGGCTC	
		ACGTCA GT TTAGAACCGAG	
		CC__ G	
GAM766	LOC257354 3'	AGTTCCCCTAGTTACTACA 45576	A C ATCTT
		TGTAGT GAC AGG GGCT	
		ACATCA TTG TCC TTGA	
		_ A CC__	
GAM766	LOC51336 3'	GAGCCAAGATCATTTACCTCA 18757	TA A CCAG
		TG GT GA GATCTTGGCTC	
		AC CA CT CTAGAACCGAG	
		TC _ TTA_	
GAM766	LOC90979 3'	GAGCCAAGATTGCACCACTGCA 32232	AGACCAG
		TGTAGT GATCTTGGCTC	
		ACGTCA TTAGAACCGAG	
		CCACG__	
GAM766	LOC92078 3'	CCAAGATTGCACTACTGCA 33743	ACCAG
		TGTAGTAG GATCTTGG	
		ACGTCATC TTAGAACC	
		ACG__	
GAM766	LOC92421 3'	GAGCCAAGATCATGCCACTGCA 34310	AGAC G
		TGTAGT CA GATCTTGGCTC	
		ACGTCA GT CTAGAACCGAG	
		CC__ A	
GAM766	LOC92771 3'	GAGCCAAGATCACGCCACTGCA 27249	AGACCAG
		TGTAGT GATCTTGGCTC	
		ACGTCA CTAGAACCGAG	
		CCGCA__	
GAM766	LOC93132 5'	GAGCCAAGATCGTGCCACTGCA 35409	AGAC G
		TGTAGT CA GATCTTGGCTC	
		ACGTCA GT CTAGAACCGAG	
		CC__ G	
GAM767	LOC93587 3'	ATAATAAAAAAAAAAGCCCTTT 35963	T GTC
	AA	TTAAA GGCTTTT TTATTAT	

			AATTT CCGAAAAA AATAATA	
			C AAA	
GAM768	PTPRC	3'	CAAACCTTGACAGTAAATCACAC 28148	CAAA GCGG
	A		TGTG TTAC CAAGTTTG	
			ACAC AATG GTTCAAAC	
			ACTA ACA_	
GAM768	GLP	3'	AGACCCACTAATTTGCACA 20722	CGC CAA
			TGTGCAAATTA GG GTTT	
			ACACGTTTAAT CC CAGA	
			CA_ _	
GAM768	LOC220538	3'	AGACCCACTAATTTGCACA 43625	CGC CAA
			TGTGCAAATTA GG GTTT	
			ACACGTTTAAT CC CAGA	
			CA_ _	
GAM768	LOC257286	3'	AGACCCACTAATTTGCACA 45372	CGC CAA
			TGTGCAAATTA GG GTTT	
			ACACGTTTAAT CC CAGA	
			CA_ _	
GAM769	ANK2	3'	ACCAGAAACCACACATTCA 6820	GTA
			TGAATG TGGTTTTTGGT	
			ACTTAC ACCAAAGACCA	
			AC_	
GAM769	ANK2	3'	ACCAGAAACCACACATTCA 21964	GTA
			TGAATG TGGTTTTTGGT	
			ACTTAC ACCAAAGACCA	
			AC_	
GAM769	BAZ2A	3'	AGGAAGAAACCACACCATCA 15116	A A GG
			TGA TGGT TGGTTTTT TCT	
			ACT ACCA ACCAAAGA GGA	
			_ C A_	
GAM769	TM4SF6	3'	ATAGACCAAAAACTACACCA 9283	A _
			TGGT TGGTTTTT GGTCTAT	
			ACCA ATCAAAAA CCAGATA	
			C A	
GAM769	FLJ12595	3'	ATAGACCACCACCACCCACTCA 24556	A TA TTT
			TGA TGG TGGT TGGTCTAT	
			ACT ACC ACCA ACCAGATA	
			C C_ CC_	
GAM769	KIAA1582	5'	TAGACCAAGGGCACATCCA 32591	T _
			TGG ATG GTTTTTGGTCTA	

ACC TAC CGGGAACCAGAT
 _ A
 GAM769 LOC196993 5' ATAGTCAGAAAACCATACCATT 43159 GGT
 AATGGTATGGTTTT CTAT
 ||||| ||||
 TTACCATACCAAAAG GATA
 ACT
 GAM770 GRM7 3' TTTGACTGATCAGTGTG 6518 T T
 CAC ACTG TCAGTCAAA
 ||| ||| |||||
 GTG TGAC AGTCAGTTT
 _ T
 GAM770 MGAT5 5' TCCTTTGACTGAAGCATGTATG 8240 C _ _ A
 T ACA TAC TGTT CAGTCAAA GA
 ||| ||| ||| ||||| ||
 TGT ATG ACGA GTCAGTTT CT
 _ T A C
 GAM770 XBP1 3' TCTTTTGACATCCAGCAGT 11533 CA__
 ACTGTT GTCAAAAGA
 ||||| |||||
 TGACGA CAGTTTTCT
 CCTA
 GAM770 DKFZP434B044 3' TCCTTTGACTGATGTTTCAGTGT 25553 ACTGT A
 C GACACT TCAGTCAAA GA
 ||||| ||||| ||
 CTGTGA AGTCAGTTT CT
 CTTGT C
 GAM770 FLJ12806 3' CTTTGGACTTAACGTCA 23112 ACTACT C
 TGAC GTT AGTCAAAAG
 ||| ||| |||||
 ACTG CAA TCAGTTTTC
 _ T
 GAM770 FLJ22635 3' CTCCTGAGAGCAGTGGTCA 24716 C AG AA
 A ACTACTGTTC TCA AG
 | ||||| ||| ||
 A TGGTGACGAG AGT TC
 C _ CC
 GAM770 FLJ23604 3' CTTTGGACTGGAAAGGTCA 24661 ACTACTG
 TGAC TTCAGTCAAAAG
 ||| |||||
 ACTG AGGTCAGTTTTC
 GAA__
 GAM770 KIAA0557 3' ACTGACATTATTTAGTGTCA 38202 C__ T
 TGACACTA TGT CAGT
 ||||| ||| |||
 ACTGTGAT ACA GTCA
 TTATT _
 GAM770 LOC144742 5' CTCTTGACCAGTAGTGTCA 37777 TTCA A
 TGACACTACTG GTCAA AG
 ||||| ||| ||

			ACTGTGATGAC CAGTT TC		
			_____ C		
GAM770	LOC145842	5'	CTTTGACTGGAAGAGTCA 37997	A ACTG	A
			TGAC CT TTCAGTCAAA G		
			ACTG GA AGGTCAGTTT C		
			A _____ C		
GAM770	LOC153711	3'	CTTCAGGTTGAACAGTAGCTTC 41668	CA	GT AA
	A		TGA CTACTGTTCA C AAG		
			ACT GATGACAAGT G TTC		
			TC TG AC		
GAM770	LOC51008	3'	CTCTTGACTATTGGGAGTAGTG 18064	G C__	A
			CACTACT TT AGTCAA AG		
			GTGATGA GG TCAGTT TC		
			G TTA C		
GAM771	DMD	3'	CAACAAAGAGGATTAGACAGTA 5569	GCCAAGGTA	
	A		T TACTG TTTTGTTG		
			AATGAC AGAAACAAC		
			AGATTAGG_		
GAM771	DMD	3'	CAACAAAGAGGATTAGACAGTA 10154	GCCAAGGTA	
	A		T TACTG TTTTGTTG		
			AATGAC AGAAACAAC		
			AGATTAGG_		
GAM771	DMD	3'	CAACAAAGAGGATTAGACAGTA 10159	GCCAAGGTA	
	A		T TACTG TTTTGTTG		
			AATGAC AGAAACAAC		
			AGATTAGG_		
GAM771	DMD	3'	CAACAAAGAGGATTAGACAGTA 10166	GCCAAGGTA	
	A		T TACTG TTTTGTTG		
			AATGAC AGAAACAAC		
			AGATTAGG_		
GAM771	DMD	3'	CAACAAAGAGGATTAGACAGTA 10172	GCCAAGGTA	
	A		T TACTG TTTTGTTG		
			AATGAC AGAAACAAC		
			AGATTAGG_		
GAM771	DMD	3'	CAACAAAGAGGATTAGACAGTA 10180	GCCAAGGTA	
	A		T TACTG TTTTGTTG		
			AATGAC AGAAACAAC		
			AGATTAGG_		
GAM771	DMD	3'	CAACAAAGAGGATTAGACAGTA 10185	GCCAAGGTA	
	A		T TACTG TTTTGTTG		

			AATGAC	AGAAACAAC	
			AGATTAGG_		
GAM771	DMD	3'	CAACAAAGAGGATTAGACAGTA	10191	GCCAAGGTA
	A		TTACTG	TTTTTGTTG	
			AATGAC	AGAAACAAC	
			AGATTAGG_		
GAM771	DMD	3'	CAACAAAGAGGATTAGACAGTA	10202	GCCAAGGTA
	A		TTACTG	TTTTTGTTG	
			AATGAC	AGAAACAAC	
			AGATTAGG_		
GAM771	DMD	3'	CAACAAAGAGGATTAGACAGTA	10207	GCCAAGGTA
	A		TTACTG	TTTTTGTTG	
			AATGAC	AGAAACAAC	
			AGATTAGG_		
GAM771	DMD	3'	CAACAAAGAGGATTAGACAGTA	10212	GCCAAGGTA
	A		TTACTG	TTTTTGTTG	
			AATGAC	AGAAACAAC	
			AGATTAGG_		
GAM771	DMD	3'	CAACAAAGAGGATTAGACAGTA	10218	GCCAAGGTA
	A		TTACTG	TTTTTGTTG	
			AATGAC	AGAAACAAC	
			AGATTAGG_		
GAM771	DMD	3'	CAACAAAGAGGATTAGACAGTA	10230	GCCAAGGTA
	A		TTACTG	TTTTTGTTG	
			AATGAC	AGAAACAAC	
			AGATTAGG_		
GAM771	BANK	3'	AACAAAAGACAGCCAG	19624	CAAG A
			CTGGC	GT TTTTGT	
			GACCG	CA GAAAACAA	
			A_ _		
GAM771	KIAA1219	3'	AAGTACCCACACCTTTGGCCAG	30755	_____
	TAA		TTACTGGCCAA	GGTATTT	
			AATGACCGTT	CCATGAA	
			TCCACAC		
GAM771	LOC92979	5'	CAAGGTTACTTAGCCAGTAA	28764	CA T
			TTACTGGC	AGGTA TTTTG	
			AATGACCG	TTCAT GGAAC	
			A_ T		
GAM772	FLJ10178	3'	TCAACCTGCACTTCTTACAACC	19755	A _ ATTTTA
	AA		TTG TTGTAAGA	GTG TGA	

			AAC AACATTCT CAC	ACT	
			C T GTCCA_		
GAM772	LOC158014	5'	TCATAAAATCTTATAGTCAA	39695	GTGA
			TTGATTGTAAGA TTTTATGA		
			AACTGATATTCT AAAATACT		
GAM772	LOC255231	3'	AAATCACCCCTTAAATCAA	45670	G A
			TTGATT TAAG GTGATTT		
			AACTAA ATTC CACTAAA		
GAM773	FANCF	3'	TGTATCTCACACTATGA	22926	TA
			TTATAGTGTGG GTACA		
			AGTATCACACT TATGT		
GAM773	NCKAP1	3'	TGGTTGTACTACAGTATAC	15097	—
			GTGTG GTAGTACAACCA		
			CATAT CATCATGTTGGT		
GAM773	SCA7	5'	TGTAGTTGTTTGGAGCACACTG	5887	GTAGT_ C
			TAGTGTG ACAAC ACA		
			GTCACAC TGTTG TGT		
			GAGGTT A		
GAM773	FLJ11259	3'	TGTGGCTGGATGTCCCACAACA	20388	_____ TAGTA A
			CTATAA TATAGTGT GG CA CCACA		
			ATATCACA CC GT GGTGT		
			ACAC TG TAG C		
GAM773	FLJ20139	3'	TGATTGCACCACTGCACTCTAA	19237	T TG A A C
			TTA AGTG GT GT CAA CA		
			AAT TCAC CA CA GTT GT		
			C GT C C A		
GAM773	KIAA0853	3'	TGATTGAGCCACCACACT	17439	A A C
			AGTGTGGT GT CAA CA		
			TCACACCA CG GTT GT		
			C A A		
GAM773	KIAA1189	3'	TGTACTAGTTACTATGA	35654	TGG
			TTATAGTG TAGTACA		
			AGTATCAT ATCATGT		
			TG_		
GAM773	KIAA1423	3'	TGTGATACCATACTATAA	30924	G
			TTATAGTGTGGTA TACA		

AATATCATACCAT GTGT
 A
 GAM773 LOC143879 3' TGTGATGATGTATACCAACTAT 37663 G G AC__
 AA TTATAGT TGGTA TACA CACA
 ||||| |||| ||| |||
 AATATCA ACCAT ATGT GTGT
 _ _ AGTA
 GAM773 LOC152905 3' TGGTTGTACTTTTCTTATTATA 30333 T T_
 A TTATAGTG GG AGTACAACCA
 ||||| || |||||
 AATATTAT CT TCATGTTGGT
 T TT
 GAM773 LOC170395 3' TGTGATTGCACCACTGCACT 37547 TG A A C
 AGTG GT GT CAA CACA
 ||| || || ||| |||
 TCAC CA CA GTT GTGT
 GT C C A
 GAM773 LOC200268 3' TGTGACTACAAGTACACACTA 42764 ____ _
 TAGTGTG GTAGT ACA
 ||||| |||| |||
 ATCACAC CATCA TGT
 ATGAA G
 GAM774 EIF1A 3' TACACTCTGATTCCTATAATA 42724 AT A
 TGTTATAGGAG TTA AGTGTA
 ||||| || |||||
 ATAATATCCTT AGT TCACAT
 _ C
 GAM775 TIMP3 3' CCAGAAGTGATGGAGAGAAACC 5926 GCC AA_
 GGT CTCTCCATTA TTGG
 || ||||| |||
 CCA GAGAGGTAGT GACC
 AA_ GAA
 GAM775 LOC90785 3' CCAATGCCAAAGAGGCACCGA 32006 C CCATTAA
 TCGGTGCC TCT ATTGG
 ||||| || |||||
 AGCCACGG AGA TAACC
 _ AACCG_
 GAM776 KIAA0826 5' GAATATTAGGAAACTGCCA 40216 CAG GGC
 TGGCGGTT TC AATATTC
 ||||| || |||||
 ACCGTCAA AG TTATAAG
 _ GA_
 GAM776 MGC2654 3' ATTGCCCTCAACAGCCA 23554 G C TC
 TGGC GTT AG GGCAAT
 ||| ||| || |||||
 ACCG CAA TC CCGTTA
 A C _
 GAM777 ANK1 3' TACCTGCAAGATGCTGCACA 30288 A _ ATACGAA
 TGT CA CA TTGCAGGTA
 ||| || || |||||

			ACA GT GT	AACGTCCAT		
			C C AG_____			
GAM777	GYG	3'	TACCTGCAGTGGCACCCTGTAC	10339	CAATACGA	
	A		TGTACA	ATTGCAGGTA		
			ACATGT	TGACGTCCAT		
			CCCACGG_			
GAM777	HNRPF	3'	ACCTGCAACTTATGTGCAC	11414	A ATAC A	
			GT CACA	GA TTGCAGGT		
			CA GTGT	TT AACGTCCA		
			C A__ C			
GAM777	IMPA2	5'	ACCTGCAATTTTGTGCACA	45631	A ATAC	
			TGT CACA	GAATTGCAGGT		
			ACA GTGT	TTTAACGTCCA		
			C _____			
GAM777	MADH4	3'	ACCTATGTTATTTTGTGTACA	11830	TACG TGC	
			TGTACACAA	AAT AGGT		
			ACATGTGTT	TTG TCCA		
			TTA_ TA_			
GAM777	RPS6KA5	3'	CTGTGCTTCATATTTGTACA	11143	C C TT	
			TGTACA AATA	GAA GCAG		
			ACATGT TTAT	CTT TGTC		
			_ A CG			
GAM777	FLJ20519	3'	ACCTGCAATGATTACTGTGCA	19536	CAATACGA	
			TGTACA	ATTGCAGGT		
			ACGTGT	TAACGTCCA		
			CATTAG_			
GAM777	HSPC072	5'	ACCCGTATTGTGGACA	15460	A AATTGCA	
			TGT CACAATACG	GGT		
			ACA GTGTTATGC	CCA		
			G _____			
GAM777	KIAA0678	3'	TACAGATCATTCATATGTGTAC	33196	A C TGCAG	
	A		TGTACACA TA	GAAT GTA		
			ACATGTGT AT	CTTA CAT		
			_ A CTAGA			
GAM777	ZDHC5	5'	ACCTGCAACCATTTGCATGTGT	44007	ATA _____	
	ACA		TGTACACA	CGAAT TGCAGGT		
			ACATGTGT	GTTTA ACGTCCA		
			AC_ CCA			
GAM777	LOC199990	3'	ACTCACATATTGTGTACA	42679	CGAAT CA	
			TGTACACAATA	TG GGT		

			ACATGTGTTAT AC TCA	
			_____ AC	
GAM778	NUP98	3'	CCAGGCACTTTGCATCACA 18440	C C _
			TGTGATGC AAA TGTC GG	
			ACACTACG TTT ACGG CC	
			_ C A	
GAM778	OXTR	5'	CCTCAGCTTAGCATCACA 6620	C A TC
			TGTGATGC AA CTG GG	
			ACACTACG TT GAC CC	
			A C T_	
GAM778	PRV1	3'	CTTCACCGCTGCTCACCACCAC 36399	A CCAAAC T
	A		TGTG TG G CGGTGAAG	
			ACAC AC C GCCACTTC	
			C CACTCGT_	
GAM778	TIMP3	5'	CTTCATAGCCCTAGCATCACA 5928	CAAAC CG
			TGTGATGC GT GTGAAG	
			ACACTACG CG TACTTC	
			ATCC_ A_	
GAM778	CLONE24945	3'	CATAGACAGTTCCAGCATCACA 17905	CA_ G
			TGTGATGC AACTGTC GTG	
			ACACTACG TTGACAG TAC	
			ACC A	
GAM778	HUMAGCGB	5'	CTTCATTGGTAACCTGGACCAC 14956	ATG AAC GT
	A		TGTG CCA T CGGTGAAG	
			ACAC GGT A GTTACTTC	
			CA_ CCA TG	
GAM778	KIAA0062	3'	TCACCACCGGCACACA 34794	A AAAC C
			TGTG TGCC GT GGTGA	
			ACAC ACGG CA CCACT	
			_ C_ _	
GAM778	MGC4737	5'	TCACCACCAATGGCATCA 25508	AAC TC
			TGATGCCA TG GGTGA	
			ACTACGGT AC CCACT	
			A_ CA	
GAM778	LOC118611	5'	CTTCACCAAGGAGACCCTGGCA 37188	AACT _____
	TCAC		TGATGCCA GTC GGTGAAG	
			ACTACGGT CAG CCACTTC	
			CC_ AGGAA	
GAM778	LOC146880	3'	CTTCATCCCAACCGGGCATCAC 38261	AAAC TC
	A		TGTGATGCC TG GGTGAAG	

ACACTACGG AC CTA^{CTTC}
 GCCA C_
 GAM778 LOC148811 3' TCACCACTGGCATCTACA 38600 _ AACT C
 TGT GATGCCA GT GGTGA
 ||| ||||| || |||||
 ACA CTACGGT CA CCACT
 T _ _
 GAM778 LOC150605 5' CACCAACGGGTGCATCACA 41229 CAAA C
 TGTGATGC CTGT GGTG
 ||||| ||| |||
 ACACTACG GGCA CCAC
 TG_ A
 GAM778 LOC152065 5' CTTCA^{GTCTGCCTGGCGTCACA} 41429 AACT C _
 TGTGATGCCA GT GG TGAAG
 ||||| || || |||||
 ACACTGCGGT CG CT ACTTC
 C_ T G
 GAM778 LOC221300 3' CTTCA^{CCAGACCACTGGCACAC} 44147 A AACT _
 A TGTG TGCCA GTC GGTGAAG
 ||| |||| || |||||
 ACAC ACGGT CAG CCACTTC
 _ CAC_ A
 GAM778 LOC221895 3' TCACCGACAGTACCATCA 44445 CCAA
 TGATG ACTGTCGGTGA
 |||| |||||
 ACTAC TGACAGCCACT
 CA_
 GAM778 LOC90170 5' CCAGGCAGTTTGGCACCA 30906 A _
 TG TGCCAAACTGTC GG
 || ||||| |||
 AC ACGGTTTGACGG CC
 C A
 GAM779 PTX3 3' CGTTTTTGAGAAGATAGTCATA 8746 GGATTT
 TATGACTATTTT AAAACG
 ||||| |||||
 ATACTGATAGAA TTTTGC
 GAGT_
 GAM779 SLC1A1 3' AAATCCAAAATAGTCATG 10376
 TATGACTATTTTGGATTT
 |||||
 GTACTGATAAAACCTAAA
 GAM779 KCNV1 3' TTTGAGTGTCCAAAATAGCCA 15714 A _
 TG CTATTTTGGAT TTAAA
 || ||||| |||||
 AC GATAAAACCTG AGTTT
 C TG
 GAM779 KIAA1028 3' AATCCTCAAAAATAGTCA 44153 _
 TGACTATTTT GGATT
 ||||| |||||

		ACTGATAAAA CCTAA		
		ACT		
GAM779	LOC201203 3'	AGATCCAAATAGTCATA	42536	T
		TATGACTATTTT GGATTT		
		ATACTGATAAAA CCTAGA		
		—		
GAM779	LOC221895 3'	TTTTGTACAAAATAGTC	44446	GATT
		GACTATTTTG TAAAA		
		CTGATAAAAC GTTTT		
		AT__		
GAM780	KIAA0471 3'	TGACCTGTTCTATGTTGAA	16915	_ AT
		TTCAACGTA AACA TCG		
		AAGTTGTAT TTGT AGT		
		C CC		
GAM781	DKFZp762L0311 3'	AAACAGAACCAGCCACCTCA	20798	C ACACT _
		TGAGGTGGC GG TTC GTTT		
		ACTCCACCG CC AAG CAAA		
		A ____ A		
GAM781	KIAA0182 3'	AAACGAAAGCACACCACCCA	35641	A CCGGACA
		TG GGTGG CTTTCGTTT		
		AC CCACC GAAAGCAAA		
		_ ACAC__		
GAM781	KIAA1671 3'	AAGTATCCAGTCACCTCA	32690	C C
		TGAGGTGGC GGA ACTT		
		ACTCCACTG CCT TGAA		
		A A		
GAM781	LOC148823 3'	AAACGGTGACCTGACCACCTCA	29790	C A_ TTT
		TGAGGTGG CGG CAC CGTTT		
		ACTCCACC GTC GTG GCAAA		
		A CA ____		
GAM782	ARHGDIA 3'	CCCCCTCCTCAGCCCTCCCCCA	10515	A _ TCAT
		TG GGGAGGGC GAG GGGGG		
		AC CCCTCCCG CTC CCCCC		
		C A CT__		
GAM782	ATRN 3'	CCACCCACCCTCCCTC	29298	CGAGTCA _
		GAGGGAGGG TGGG GG		
		CTCCCTCCC ACCC CC		
		_____ A		
GAM782	CBFA2T3 3'	CCCTGCCCACCCTCCCTC	11688	CGA CATG
		GAGGGAGGG GT GGGG		

CTCCCTCCC CG TCCC
ACC ____

GAM782 CENTD2 5' GCCCCTGTCCACCTCCCCA 29196 A CGAGTC
TG GGGAGGG ATGGGGGC
|| ||||| |||||
AC CCCTCCC TGTCCCCG
C ACC__

GAM782 DLG3 5' GCCCCACGGGTGCCCCCC 22094 A AG A
GGG GGGCG TC TGGGGGC
||| |||| || |||||
CCC CCCGT GG ACCCCCG
C G_ C

GAM782 F7 3' CCCCCAACTCTCCCC 21235 A C CA
GGG GGG GAGT TGGGGG
||| ||| |||| |||||
CCC CCT CTCA ACCCCC
_ _ A_

GAM782 F7 3' CCCCCAACTCTCCCC 5606 A C CA
GGG GGG GAGT TGGGGG
||| ||| |||| |||||
CCC CCT CTCA ACCCCC
_ _ A_

GAM782 GLRA1 5' GCCCCCATAACTCGTGGACTAC 5682 A GAGG C
A TG GG GCGAGT ATGGGGGC
|| || ||||| |||||
AC TC TGCTCA TACCCCG
A AGG_ A

GAM782 GPR56 3' GCCCCCTCCCTCCCTCA 12238 CGAGTCAT
TGAGGGAGGG GGGGGC
||||||| |||||
ACTCCCTCCC CCCCCG
T_____

GAM782 MPP2 3' GCCCCCTGCCACCCCTCCCCA 30084 A CGA T T
TG GGGAGGG G CA GGGGGC
|| ||||| | || |||||
AC CCCTCCC C GT CCCCCG
_ CAC _ _

GAM782 MSL3L1 5' GCCCCCGCCCGCCCTCCCCA 27814 A A CAT
TG GGGAGGGCG GT GGGGGC
|| ||||| || |||||
AC CCCTCCCGC CG CCCCCG
C C ____

GAM782 MSL3L1 5' GCCCCGGAGCCTCGCCCTCC 27815 TCATG
GGAGGGCGAG GGGGC
||||||| |||||
CCTCCCGCTC CCCCCG
CGAGG

GAM782 WDR1 3' CCCCCATGCCCCCACCCEA 18955 A A CGA T
TG GGG GGG G CATGGGGG
|| ||| ||| | |||||

AC CCC CCC C GTACCCCC
 _ A C _ _
 GAM782 ADAR3 5' GCCCTTCCCCGCCCTCCCT 20786 AGTCAT
 AGGGAGGGCG GGGGGC
 ||||| ||||
 TCCCTCCCGC TTCCCG
 CCC _
 GAM782 C6orf9 3' CCCTGCCCCACCCTCCCTC 22654 CGA CATG
 GAGGGAGGG GT GGGG
 ||||| || ||||
 CTCCCTCCC CG TCCC
 ACC _ _
 GAM782 CDH22 3' CCCCCTTTCTGCGCTCCCCCA 22214 A G TCAT
 TG GGGAGGGC AG GGGGG
 || ||||| || ||||
 AC CCCTCCCG TC CCCCC
 C _ CTTT
 GAM782 DKFZp547O146 3' CCCAGCCCCGCCCTCCCCA 21483 A AGTCA
 TG GGGAGGGCG TGGG
 || ||||| ||||
 AC CCCTCCCGC ACCC
 _ CCG _
 GAM782 FADS2 3' GCCCTCATGGGACCTGCCCTCC 10466 A _
 CTCAT TGAGGGAGGGCG GTC ATGGGGGC
 ||||| || |||||
 ACTCCCTCCCGT CAG TACTCCCG
 C GG
 GAM782 FLJ11320 3' GCCCCCATGACCCAATCAGCTC 20427 GGC _
 C GGAG GA GTCATGGGGGC
 ||| || |||||
 CCTC CT CAGTACCCCCG
 GA _ AACC
 GAM782 FLJ14351 5' CCCCCATGACCTTCTCCC 24071 CGA
 GGGAGGG GTCATGGGGG
 ||||| |||||
 CCCTCTT CAGTACCCCC
 C _
 GAM782 FLJ14816 3' CCCCCATGAGGCCTCCTCA 26637 GA GAG
 TGAGG GGGC TCATGGGGG
 |||| ||| |||||
 ACTCC TCCG AGTACCCCC
 _ G _
 GAM782 GGTLA4 5' GCCCCCTCCCCACCCTCCCTC 28141 CGAGTCAT
 GAGGGAGGG GGGGGC
 ||||| ||||
 CTCCCTCCC CCCCCG
 ACCCCT _
 GAM782 KIAA0153 3' GCCCCCATGTCCCTCCCCA 17497 A CGAGT
 TG GGGAGGG CATGGGGGC
 || ||||| |||||

			AC CCCTCCC	GTACCCCCG	
			— T_____		
GAM782	KIAA0285	3'	CCCCTCTTCACCTCCCTCA	16751	GC TCAT
			TGAGGGAGG GAG GGGGG		
			ACTCCCTCC TTC TCCCC		
			AC _____		
GAM782	KIAA0298	5'	GCCCCCCCACACCCTCCTTCA	37625	CGA CAT
			TGAGGGAGGG GT GGGGGC		
			ACTTCCTCCC CA CCCCCG		
			A_ CC_		
GAM782	KIAA0376	3'	GCCCCCTGTGCCACCCCTC	32674	A AGTCAT
			GAGGG GGGCG GGGGGC		
			CTCCC CCCGT CCCCCG		
			A GT_____		
GAM782	KIAA0563	5'	GCCCCCATCCCACCCTACCCCA	16842	A _ CGAGTC
			TG GGG AGGG ATGGGGGC		
			AC CCC TCCC TACCCCCG		
			_ A ACCC_		
GAM782	KIAA1076	3'	CCCCCGCGCCCGCCCCCA	32638	A A AGTCAT
			TG GGG GGGCG GGGGG		
			AC CCC CCCGC CCCCC		
			C G GC_____		
GAM782	KIAA1862	3'	CCCCAGGCCACCCTCTCCCA	34174	A CGA A
			TG GGGAGGG GTC TGGGG		
			AC CTCTCCC CGG ACCCC		
			C AC_ _		
GAM782	MARCKS	5'	CCCCACCCCCCTCCCTC	8167	CGAGTCA
			GAGGGAGGG TGGGGG		
			CTCCCTCCC ACCCCC		
			CCC_____		
GAM782	MGC4415	3'	CCCACTCACCCCTCCCTCA	25567	C CA
			TGAGGGAGGG GAGT TGG		
			ACTCCCTCCC CTCA ACC		
			A C_		
GAM782	SRF	3'	GCCTCCACCCGTCTCCCTCA	9098	A CAT
			TGAGGGAGGGCG GT GGGGGC		
			ACTCCCTCCTGC CA CCTCCG		
			C _____		
GAM782	STRAIT11499	3'	CCCATCTCACCCCTCTCTCA	22209	C TC
			TGAGGGAGGG GAG ATGGG		

ACTCTCTCCC CTC TACCC
 A _
 GAM782 STRAIT11499 5' CCCCGGCGCCCTCCCTCA 22210 AGTCATG
 TGAGGGAGGGCG GGGG
 ||||| |||
 ACTCCCTCCCGC CCCC
 GG____
 GAM782 LOC126823 5' CCCACCGCCCTCCCTC 36865 A CAT
 GAGGGAGGGCG GT GGGG
 ||||| || |||
 CTCCTCCCGC CA CCCC
 _ _
 GAM782 LOC146562 3' CCCCCAGGCCCTCTCCC 29179 CGA A
 GGGAGGG GTC TGGGGG
 ||||| || |||||
 CCCTCTC CGG ACCCCC
 C_ _
 GAM782 LOC158856 5' CCCCCACACCCTCCCCA 42033 A CGA CA
 TG GGGAGGG GT TGGGGG
 || ||||| || |||||
 AC CCCTCCC CA ACCCCC
 _ _ C_
 GAM782 LOC201220 5' GCCCCCATCCACCCTACCCCA 42225 A _ CGAGTC
 TG GGG AGGG ATGGGGGC
 || ||| ||| |||||
 AC CCC TCCC TACCCCG
 _ A ACCC_
 GAM782 LOC254057 5' CCCCCGTCACCCCTCCC 46342 CGA C
 GGGAGGG GT ATGGGGG
 ||||| || |||||
 CCCTCCC CA TGCCCCC
 C_ C
 GAM782 LOC254205 5' CCCCCGACGCCCTCCCCG 46217 A AGTCA
 TG GGGAGGGCG TGGGGG
 || ||||| |||||
 GC CCCTCCCGC GCCCCC
 _ A____
 GAM782 LOC92340 3' GCCCCACCCCTCTCTCCCTCA 34199 GC TCA
 TGAGGGAGG GAG TGGGGGC
 ||||| || |||||
 ACTCCCTCT CTC ACCCCCG
 _ CC_
 GAM783 MGC15429 3' TTGTTTCCAAATATGACC 26487 AT CTC
 GGTCATGTTT GA AACAA
 ||||| || |||||
 CCAGTATAAA CT TTGTT
 C_ ____
 GAM783 PLSCR4 3' TTTGTTGGCATAAAATAACC 21622 CATG A T
 GGT TTTATG C CAACAAA
 || ||||| |||||

			CCA AAATAC G GTTGTTT		
			ATA_ _ _		
GAM783	RGS18	3'	TGTTGGTCACAGAAACATGACC 28270	A_ _	T
			GGTCATGTTT TGAC CAACA		
			CCAGTACAAA ACTG GTTGT		
			GAC _		
GAM783	LOC122553	3'	TTTGCTAAGCAATGCATGACT 36692	TTA A CAA	
			GGTCATGT TG CT CAAA		
			TCAGTACG AC GA GTTT		
			TA_ _ ATC		
GAM783	LOC148195	5'	TTGAGTCATAAGTACC 40880	CATG	
			GGT TTTATGACTCAA		
			CCA GAATACTGAGTT		
			T_ _		
GAM783	LOC166341	3'	TGTTGAGAACATGGCC 40213	TATGA	
			GGTCATGTT CTCAACA		
			CCGGTACAA GAGTTGT		

GAM783	LOC254532	3'	TGTTGAGTACAGACC 46216	A TTATG	
			GGTC TGT ACTCAACA		
			CCAG ACA TGAGTTGT		

GAM783	LOC257319	3'	TTTGTTTATTTAAACATGA 45836	TGACTC	
			TCATGTTTA AACAAA		
			AGTACAAAT TTGTTT		
			TTAT_ _		
GAM783	LOC51289	5'	TTGTCCCCCAGAACATGACC 18640	A ACTCA	
			GGTCATGTTT TG ACAA		
			CCAGTACAAG AC TGTT		
			_ CCCC_		
GAM784	ARHU	3'	CTACCCAGGTATTACACAAGCC 22181	GCTC _ A	
	AAA		TTTGGCTTG ATGC TGG TAG		
			AAACCGAAC TATG ACC ATC		
			ACAT G C		
GAM784	C20orf42	3'	CCAACAAGGCAAGCCAAA 19213	G CA C	
			TTTGGCTTG CT TG TGG		
			AAACCGAAC GA AC ACC		
			G _ A		
GAM784	DKFZp761D0614	3'	CCACACAAGCAAGCCAAA 42309	G CA C	
			TTTGGCTTG CT TG TGG		

			AAACCGAAC GA AC ACC		
			_ AC _		
GAM784	KIAA1228	3'	CTACCTTGAGCCAAGCCAA 32442	TGC	
			TTGGCTTGGCTCA TGG		
			AACCGAACCGAGT ATC		
			TCC		
GAM784	LOC200473	5'	CTATCCAGCACGTGCACCAAG 43312	CT _	
			CTTGG CA TGCTGGATAG		
			GAACC GT ACGACCTATC		
			AC GC		
GAM784	LOC221296	3'	TACTTGTAAGCCAAGC 44170	CA T A	
			GCTTGGCT TGC GG TA		
			CGAACCGA ATG TC AT		
			_ T _		
GAM785	CALM3	3'	CCAATTGATTGACTGA 11682	CT	
			TCA GTTAATCAATTGG		
			AGT CAGTTAGTTAACC		
			_		
GAM785	LFG	3'	CCAATCCAGGCAGTGAGG 37691	G AATCA	
			CC TCACTGTT ATTGG		
			GG AGTGACGG TAACC		
			_ ACC_		
GAM785	FLJ22029	3'	CCAATGATTCACAGTGAC 24504	T A	
			GTCAGTGT AATCA TTGG		
			CAGTGACA TTAGT AACC		
			C _		
GAM785	SSH2	3'	CCAACTGAAAACAACAGTGAC 31178	AA_ A	
			GTCAGTGT TCA TTGG		
			CAGTGACAA AGT AACC		
			CAAA C		
GAM786	ALX3	3'	ACTGAGTCCCCTCACCTGA 13220	AA _	
			TCAGGTGAG GAC AGT		
			AGTCCACTC CTG TCA		
			CC AG		
GAM786	ASNS	5'	CTGCCCCCCTCCTCACCTGG 28515	A ACAGTA	
			TCAGGTGAG AG GCAG		
			GGTCCACTC TC CGTC		
			C CCCC_		
GAM786	EPB49	3'	GCTGCTTTCCTCACCTG 7708	AA C	
			CAGGTGAG GA AGTAGC		

			GTCCACTC CT TCGTCG		
			— T		
GAM786	FGFR2	3'	AGCCACCATGTAACCCCTCTCA 5638	AG____	GTAGCA
		CCTG	CAGGTGAGA ACA GCT		
			GTCCACTCT TGT CGA		
			CCCCAA ACCAC_		
GAM786	FGFR2	3'	AGCCACCATGTAACCCCTCTCA 23300	AG____	GTAGCA
		CCTG	CAGGTGAGA ACA GCT		
			GTCCACTCT TGT CGA		
			CCCCAA ACCAC_		
GAM786	FGFR2	3'	AGCCACCATGTAACCCCTCTCA 23234	AG____	GTAGCA
		CCTG	CAGGTGAGA ACA GCT		
			GTCCACTCT TGT CGA		
			CCCCAA ACCAC_		
GAM786	FGFR2	3'	AGCCACCATGTAACCCCTCTCA 23241	AG____	GTAGCA
		CCTG	CAGGTGAGA ACA GCT		
			GTCCACTCT TGT CGA		
			CCCCAA ACCAC_		
GAM786	FGFR2	3'	AGCCACCATGTAACCCCTCTCA 23288	AG____	GTAGCA
		CCTG	CAGGTGAGA ACA GCT		
			GTCCACTCT TGT CGA		
			CCCCAA ACCAC_		
GAM786	FGFR2	3'	AGCCACCATGTAACCCCTCTCA 23294	AG____	GTAGCA
		CCTG	CAGGTGAGA ACA GCT		
			GTCCACTCT TGT CGA		
			CCCCAA ACCAC_		
GAM786	GLO1	3'	GCTGTTCTTTTTCACCT 13530	ACAGT	
			AGGTGAGAAG AGCAGC		
			TCCACTTTTC TTGTCG		
			C_____		
GAM786	GRM1	3'	GCTGCTGATTTCTCAGCC 6496	— A	
			GG TGAGAAG CAGTAGC		
			CC ACTCTTT GTCGTCG		
			G A		
GAM786	KAL1	3'	CTGCTACCTTCTCATC 5717	ACA	
			GGTGAGAAG GTAGCAG		
			CTACTCTTC CATCGTC		

GAM786	MKI67	3'	CTAGGGTTGCTCTCACCTGA 8254	A_ AG	
			TCAGGTGAGA GAC TAG		

AGTCCACTCT TTG ATC
 CG GG
 GAM786 SERPINH2 3' AGCCAGGTACCTTCTCACCTG 6905 ACA GCA_
 CAGGTGAGAAG GTA GCT
 ||||| ||| |||
 GTCCACTCTTC CAT CGA
 ____ GGAC
 GAM786 DKFZP434O125 3' AGCCCTACCTGTCTTCCCACCT 32404 A _ CA
 G CAGGTG GAAGACAG TAG GCT
 ||||| ||||| ||| |||
 GTCCAC CTTCTGTC ATC CGA
 C C C_
 GAM786 DMWD 5' AGTTCGCCTTCTCGCCCGA 30527 A ACAGTA _
 TC GGTGAGAAG GC AGCT
 || ||||| || |||
 AG CCGCTCTTC CG TTGA
 C ____ C
 GAM786 FLJ14106 3' AGCCACTCTCCTGTCTTCTCTC 24664 T T CA_
 C GG GAGAAGACAG AG GCT
 || ||||| || |||
 CC CTCTTCTGTC TC CGA
 T C TCAC
 GAM786 FLJ20202 3' GCTACTTGTCTTCTCACTTGA 19288 _
 TCAGGTGAGAAGACA GTAGC
 ||||| |||||
 AGTTCACTCTTTTGT CATCG
 T
 GAM786 FLJ20255 3' AGCTCCTGGCTGTTCCCTCACCT 19317 AA _ C
 GA TCAGGTGAG GACAGT AG AGCT
 ||||| ||||| || |||
 AGTCCACTC TTGTCG TC TCGA
 C_ G C
 GAM786 KIAA0426 3' GCTGTCTCTTCTCACC 16311 CAGTA
 GGTGAGAAGA GCAGC
 ||||| |||||
 CCACTCTTCT TGTCTG
 C_
 GAM786 LEC3 3' CTATATCCCTTCTTACCTGA 17568 ACA_
 TCAGGTGAGAAG GTAG
 ||||| |||||
 AGTCCATTCTTC TATC
 CCTA
 GAM786 MGC16384 5' GCCACTGCCTCTTACCT 27594 A A A
 AGGTGAGA G CAGT GC
 ||||| ||||| |||
 TCCATTCT C GTCA CG
 _C C
 GAM786 NDP52 3' AGCTGTATCATCCTCTCACCTG 12441 A CA G
 CAGGTGAGA GA GTA CAGCT
 ||||| || ||| |||||

			GTCCACTCT CT TAT GTCGA		
			C AC _		
GAM786	SCMH1	3'	AGCTCGTACCTTCTCACC 14538	ACA	GC
			GGTGAGAAG GTA AGCT		
			CCACTCTTC CAT TCGA		
			_ GC		
GAM786	SERPINH1	3'	AGCCAGGTACCTTCTCACCTG 10559	ACA	GCA_
			CAGGTGAGAAG GTA GCT		
			GTCCACTCTTC CAT CGA		
			_ GGAC		
GAM786	ZNF317	3'	GCCATGGTCCCCTCACTTGA 35637	AA	A A
			TCAGGTGAG GAC GT GC		
			AGTTCACTC CTG TA CG		
			CC G C		
GAM786	LOC201229	3'	AGCTCGTGTGTCTTCTCAACTG 42538	G	GTA _
	A		TCAG TGAGAAGACA GC AGCT		
			AGTC ACTCTTCTGT TG TCGA		
			A G_ C		
GAM786	LOC201799	3'	CTAATGTTCTCCTCAGCTGA 42915	G	A _ G
			TCAG TGAG AGA CA TAG		
			AGTC ACTC TCT GT ATC		
			G C T A		
GAM786	LOC221272	3'	AGTTTGGCTGTGTCCCCACC 44962	A_	AG AGC
			GGTG GA ACAGT AGCT		
			CCAC CT TGTCG TTGA		
			CC G_ GT_		
GAM786	LOC91056	3'	GCTACAGAGTTCCTTCTCACC 45439	_	A_
			GGTGAGAAG AC GTAGC		
			CCACTCTTC TG CATCG		
			CT AGA		
GAM787	CLCN4	3'	CTATTGGAGCATACAGTA 7571	C	AA TG
			TACTGTA GC CA ATAG		
			ATGACAT CG GT TATC		
			A AG _		
GAM787	CXorf1	3'	CTATCATAGCACAGTA 11055	AC	AAC
			TACTGT GC ATGATAG		
			ATGACA CG TACTATC		
			_ A_		
GAM787	GTF2E1	3'	TGTCACTACAGTATTA 12038	CGCAACA	
			TAATACTGTA TGATA		

			ATTATGACAT	ACTGT	
			C_____		
GAM787	MADP-1	3'	CTATCATGTTAATACTATTA	26962	CT CGC
			TAATA GTA AACATGATAG		
			ATTAT CAT TTGTACTATC		
			__ AA_		
GAM787	LOC120856	3'	CTATCTCTGGGCTACAGTATTA	36637	C AACAT
			TAATACTGTA GC GATAG		
			ATTATGACAT CG CTATC		
			_ GGTCT		
GAM787	LOC152756	3'	CTATCAATAAAACAGTATTA	41548	ACGCAACA
			TAATACTGT TGATAG		
			ATTATGACA ACTATC		
			AAATA__		
GAM787	LOC157931	3'	TCATCGCAAACAGTATTA	41904	AC AAC
			TAATACTGT GC ATGA		
			ATTATGACA CG TACT		
			AA C__		
GAM788	FLJ10178	3'	CTCAGTATAAGGCATCCTA	19753	GTCAT A _
			TAGGATGC TTTG GC GAG		
			ATCCTACG GAAT TG CTC		
			_____ A A		
GAM788	FLJ12681	3'	CCCGCCACAGCCTACACGCATC	23036	CATT_ A_ A
			C GGATGCGT TTG GCG GG		
			CCTACGCA GAC CGC CC		
			CATCC AC _		
GAM788	FLJ32865	3'	GTTCAAAGGACACACCCTA	29430	A C A
			TAGG TG GTC TTTTGAGC		
			ATCC AC CAG GAAACTTG		
			C A _		
GAM789	VAT1	3'	ATTGTCTAAATGAGGCCT	13066	T C C
			AG GCCTCATTTA GC GT		
			TC CGGAGTAAAT TG TA		
			_ C T		
GAM789	BLCAP	3'	TTACAATGTGAATAATGGCACT	13523	TC_ CC
			GA TCAGTGCC ATTTACG GTAA		
			AGTCACGG TAAGTGT CATT		
			TAA AA		
GAM789	LOC152790	5'	GGTGGTAAATGACACACT	41554	CC _
			AGTG TCATTTAC GCC		

		TCAC AGTAAATG TGG		
		AC G		
GAM789	LOC162333 5'	ACAGGTGCTAACAGGGCACTGA 42121	CA TA _	
		TCAGTGCCT TT CGCC GT		
		AGTCACGGG AA GTGG CA		
		AC TC A		
GAM789	LOC202126 3'	TACAGCGTGCCTTGGCACTGG 43412	TCATT C	
		TCAGTGCC TACGC GTA		
		GGTCACGG GTGCG CAT		
		TTCC_ A		
GAM790	KIAA0635 3'	CCAAAATGCCATTTTAAACGCC 16056	A GTTTTC A	
	GA	TC GCG GTG CATTTTGG		
		AG CGC TAC GTAAAACC		
		C AATTTT C		
GAM790	LOC150142 5'	CCACCTCTCACGAAAACGGCT 38850	G CATT	
		AGC GTTTTCGTGA TGG		
		TCG CAAAAGCACT ACC		
		G CTCC_		
GAM790	LOC158187 3'	CAAAATGTCATCACCT 41922	C TTTC	
		AG GGT GTGACATTTTG		
		TC CCA TACTGTAAAAC		
		_ C_		
GAM791	AHCY 3'	TTGCCCAGGCCCCACCTCTCCT 6345	AT AT	
		AGGAGA GTGG CTTGGGCAA		
		TCCTCT CACC GGACCCGT		
		C_ CC		
GAM791	CBFA2T2 3'	TGCCTCCACATTCTTC 11554	ATCTT	
		GGAGAATGTGG GGGCA		
		CTTCTTACACC TCCGT		
		C_		
GAM791	CBS 3'	CCCTTGCCCACTTCTCCTT 5516	T ATCTT	
		AAGGAGAA GTGG GGG		
		TTCTCTT CACC CCC		
		_ CGTT_		
GAM791	ETV3 3'	GCTCCCCACATTCTCT 11751	ATCTT	
		GGAGAATGTGG GGGC		
		TCTCTTACACC CTCG		
		C_		
GAM791	FSTL1 3'	CCAAGAGCAAATCCACATTCCT 13950	GA _	
	CTT	AAG GAATGTGGA TCTTGG		

			TTC CTTACACCT	AGAACC		
			TC	AAACG		
GAM791	GA	5'	CCGGGCCCACATTCTCC	14935	AT	
			GGAGAATGTGG	CTTGG		
			CCTCTTACACC	GGGCC		
			C_			
GAM791	MGAM	3'	CCCGCTCCACATTTCCCT	35821	AG	TCT
			AGG AATGTGGA	TGGG		
			TCC TTACACCT	GCCC		
			CT	C_		
GAM791	SH3GL1	3'	CCACATTACATTCCCCT	8960	A	CT
			AGG GAATGTGGAT	TGG		
			TCC CTTACACTTA	ACC		
			C	C_		
GAM791	SORBS1	3'	TGCCCAAGACCAAATCCCT	17691	A	ATG A
			AGG GA	TGG TCTTGGGCA		
			TCC CT	ACC AGAACCCGT		
			_	AA_		
GAM791	TMOD2	3'	TGCCCAAGGCAACTCACCCCTC	15862	AAT	A_
			GAG GTGG	TCTTGGGCA		
			CTC CACT	GGAACCCGT		
			C_	CAAC		
GAM791	TNFRSF8	3'	TTGCCCAGGGACTTCCTCC	6912	AATGT	A
			GGAG	GG TCTTGGGCAA		
			CCTC	TC GGGACCCGTT		
			CT_	A		
GAM791	ABCA5	5'	TTGCTATTTCTACATTCTCC	20747		TCTTG
			GGAGAATGTGGA	GGCAA		
			CCTCTTACATCT	TCGTT		
			TTA_			
GAM791	CSEN	3'	CCACTGGGCCCCATTCTCC	15088	T	AT _
			GGAGAATG	GG CT TGG		
			CCTCTTAC	CC GG ACC		
			_	CG TC		
GAM791	DKFZP667O116	3'	CCAAAAATCCACATTCTCC	45264		C_
			GGAGAATGTGGAT	TTGG		
			CCTCTTACACCTA	AACC		
			AA			
GAM791	FLJ14326	3'	GCCGCCACATTTCCCTT	25905	A	ATCTTG
			AAGGAGA	TGTGG	GGC	

TTCCTTT ACACC CCG
 _ G_
 GAM791 FLJ20359 3' CAAGGCCACATTCTCCTT 19412 AT
 AAGGAGAATGTGG CTTG
 ||||| |||
 TTCCTCTTACACC GAAC
 CG
 GAM791 FLJ22471 3' CCGACCCATTCTCCTT 24778 T ATC
 AAGGAGAATG GG TTGG
 ||||| || |||
 TTCCTCTTAC CC AGCC
 _ _
 GAM791 KIAA0543 3' TGCTAGGTTACACCCTCCT 34178 AA TG
 AGGAG TGTGGATCT GGCA
 ||| ||||| |||
 TCCTC ACACTTGA TCGT
 CC _
 GAM791 KIAA0775 3' CCCACCTACATTTCTT 16320 A ATCT
 AGGAGA TGTGG TGGG
 |||| ||| |||
 TCCTTT ACATC ACCC
 _ C_
 GAM791 KIAA0939 3' TGCCCCATCCCATCCCCCT 31067 AGA T CTT
 AGG ATG GGAT GGGCA
 || ||| ||| |||
 TCC TAC CCTA CCCGT
 CCC _ C_
 GAM791 KIAA1054 3' TGCCCTGGGTCAATTCTCCTT 33958 GTG T
 AAGGAGAAT GATCT GGGCA
 ||||| ||| |||||
 TTCCTCTTA CTGGG CCCGT
 A_ T
 GAM791 KIAA1155 3' TGCCTCTGTCCACATTTCCC 31202 AG CTT
 GG AATGTGGAT GGGCA
 || ||||| |||
 CC TTACACCTG TCCGT
 CT TC_
 GAM791 PCDH19 3' CCACCCACCTTCTCCTT 31862 T ATCT
 AAGGAGAA GTGG TGG
 ||||| ||| |||
 TTCCTCTT CACC ACC
 C CC_
 GAM791 PFDN1 3' TGCCCAGGACACTCTTCCCT 8484 A T_ GA
 AGG GAA GTG TCTTGGGCA
 ||| ||| ||| |||||
 TCC CTT CAC AGGACCCGT
 _ CT _
 GAM791 RAI16 3' TGCCTCTCCACATTCCTCC 22971 _ ATCTT
 GGAG AATGTGG GGGCA
 ||| ||||| |||

		CCTC TTACACC TCCGT		
		C CTC__		
GAM791	LOC115509 3'	TTAAGTACCACATTCTCCT 36365	AT	
		AGGAGAATGTGG CTTGG		
		TCCTCTTACACC GAATT		
		AT		
GAM791	LOC127281 3'	TTGCCCAAGACCACTGCTACCT 36892	_ AAT A	
		AGG AG GTGG TCTTGGGCAA		
		TCC TC CACC AGAACCCGTT		
		A GT_ _		
GAM791	LOC130813 3'	TCAAACATCCGCATTCTCCT 37314	C_	
		AGGAGAATGTGGAT TTGG		
		TCCTCTTACGCCTA AACT		
		CA		
GAM791	LOC145468 3'	TGCCCAAGGCCAACCTCCT 36550	AATG A	
		AGGAG TGG TCTTGGGCA		
		TCCTC ACC GGAACCCGT		
		CA__ _		
GAM791	LOC150155 3'	TGCCCAAGGCCAACCTCCT 35092	AATG A	
		AGGAG TGG TCTTGGGCA		
		TCCTC ACC GGAACCCGT		
		CA__ _		
GAM791	LOC200982 3'	TGCCCTGAGCTCCACATTCTCC 43378	T _	
	T	AGGAGAATGTGGA CTT GGGCA		
		TCCTCTTACACCT GAG CCCGT		
		C T		
GAM791	LOC204301 3'	TTGCCCAAACTGTTCTCTTT 43096	GT ATC	
		AAGGAGAAT GG TTGGGCAA		
		TTTCTCTTG TC AACCCGTT		
		_ AA_		
GAM791	LOC221968 3'	TGAAGAGATCCACATTTTCCTT 44470	A GGG	
		AAGGAGA TGTGGATCTT CA		
		TTCTTTT ACACCTAGAG GT		
		_ AA_		
GAM791	LOC253128 3'	CTAAAATCCACATCACCT 45485	AGA C	
		AGG ATGTGGAT TTGG		
		TCC TACACCTA AATC		
		CAC A		
GAM791	LOC254358 3'	TTGCCCAAACTGTTCTCTTT 45534	GT ATC	
		AAGGAGAAT GG TTGGGCAA		


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          TTTCTCTTG TC AACCCGTT
            __ AA_
GAM791 LOC254413 5' TGCCCAAGATTATTCTCTCA 46404 A GTG
          A GGAGAAT GATCTTGGGCA
          | ||||| |||||
          A TCTCTTA TTAGAACCCGT
          C __
GAM791 LOC254428 3' CCCAAATCCACATTCTCC 45717 C
          GGAGAATGTGGAT TTGGG
          ||||| |||
          CCTCTTACACCTA AACCC
          A
GAM791 LOC254659 5' TGTCTCATGCCACATTCTCC 45601 ATCT _
          GGAGAATGTGG TG GGCA
          ||||| |||
          CCTCTTACACC AC CTGT
          GT__ T
GAM791 LOC254755 3' TGCCTCTCCCACATTCCTCC 46489 _ ATCTT
          GGAG AATGTGG GGGCA
          ||| ||||| |||
          CCTC TTACACC TCCGT
          C CTC__
GAM791 LOC254848 5' CCACTCCACATTCTCT 46379 TCT
          GGAGAATGTGGA TGG
          ||||| |||
          TCTCTTACACCT ACC
          C__
GAM791 LOC51107 3' TGCCCAAGACTCACCTCC 18098 AAT GA
          GGAG GTG TCTTGGGCA
          ||| ||| |||||
          CCTC CAC AGAACCCGT
          __ TC
GAM792 EFEMP1 3' CAGTAAGCAAAATTTTCCA 10317 C ATCGT
          TGGAAAATT TGT CTG
          ||||| ||| |||
          ACCTTTTAA ACG GAC
          A AAT__
GAM792 EFEMP1 3' CAGTAAGCAAAATTTTCCA 20837 C ATCGT
          TGGAAAATT TGT CTG
          ||||| ||| |||
          ACCTTTTAA ACG GAC
          A AAT__
GAM792 NEU3 3' TGGACAGAATTTCCACACA 13459 A A
          TGTGG AAATTCTGT TCG
          |||| ||||| |||
          ACACC TTTAAGACA GGT
          C _
GAM792 SLC6A6 3' GCAGACCGCAGAATTTTCACA 9005 G ATC
          TGTG AAAATTCTGT GTCTGC
          ||| ||||| |||||

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ACAC TTTTAAGACG CAGACG
 _ C_
 GAM792 ARHGAP10 3' CAGGTGGATACAGAACTTCC 21887 AA _GT
 GGAA TTCTGTAT C CTG
 ||| ||||| | |||
 CCTT AAGACATA G GAC
 C_ G TG
 GAM792 FLJ21126 3' ACGTACAGAATGTTCCACA 43417 A T
 TGTGGAA ATTCTGTA CGT
 ||||| ||||| |||
 ACACCTT TAAGACAT GCA
 G _
 GAM793 MYLK 3' ACAATTTTAAATAAAGGATAC 46357 CACTGAAGT
 CA TGGTATCTT AATTGT
 ||||| |||||
 ACCATAGGA TTAACA
 AATAAATTT
 GAM793 DEPC-1 5' GCTCAGAAAGATACCA 29192 CA A
 TGGTATCTT CTGA GT
 ||||| ||| ||
 ACCATAGAA GACT CG
 A_ _
 GAM793 LOC154007 3' ACATAATGCTCAGTGAAAATAG 39450 G C A AT_
 CA TG TAT TTCACTGA GTA TGT
 || ||| ||||| ||| |||
 AC ATA AAGTGA CT CGT ACA
 G A _ AAT
 GAM794 PDGFRA 3' ATCTATGTTTATAATACTACTA 12879 C CAAT A
 CT AG AGTAGTAT AACG AGAT
 || ||||| ||| |||||
 TC TCATCATA TTGT TCTA
 A ATAT A
 GAM794 KIAA0222 3' TCGAGTATTAATACTACTGC 16047 C A_
 GCAGTAGTAT AATA CGA
 ||||| ||| |||
 CGTCATCATA TTAT GCT
 A GA
 GAM794 PRO1600 5' GTCATTCATACTACTGCT 15315 C A
 AGCAGTAGTAT AAT AC
 ||||| ||| |||
 TCGTCATCATA TTA TG
 C C
 GAM794 TEB4 3' TCTTCTGACATTACTGCT 30429 A ATAAC
 AGCAGTAGT TCA GAAGA
 ||||| ||| |||||
 TCGTCATTA AGT CTTCT
 C _
 GAM794 LOC125268 3' CTTCTAGTGGACATTACTGCT 37452 A AATAAC
 AGCAGTAGT TC GAAG
 ||||| || |||

TCGTCATTA AG CTTC
 C GTGAT_
 GAM794 LOC220469 3' TTCCTATTGACATCTACTGCT 37556 TA_ AC
 AGCAGTAG TCAATA GAA
 ||||| ||||| ||
 TCGTCATC AGTTAT CTT
 TAC C_
 GAM795 APAF1 3' TCTTGTTTCTTACATATCA 6832 CAT G
 TGATATG GAAG AAGA
 ||||| ||||| |||||
 ACTATAC CTTT TTCT
 ATT G
 GAM795 APAF1 3' TCTTGTTTCTTACATATCA 14871 CAT G
 TGATATG GAAG AAGA
 ||||| ||||| |||||
 ACTATAC CTTT TTCT
 ATT G
 GAM795 CDH17 3' CTACCTGCCATGCATACA 10269 A A_ A
 TG TATGCATG AGG AG
 || ||||| ||||| ||
 AC ATACGTAC TCC TC
 _ CG A
 GAM795 DEK 3' TTTCTTTTGTGCAGATCA 9538 A TG
 TGAT TGCA AAGGAAG
 ||||| ||||| |||||
 ACTA ACGT TTTCTTT
 G GT
 GAM795 EGLN1 3' TCTCCCTTTTTTATATCA 22587 CAT A
 TGATATG GAAGG AGA
 ||||| ||||| |||||
 ACTATAT TTTCC TCT
 TT_ C
 GAM795 EGR3 3' TCGCTCCTTCTGGTATATGCAT 29958 _____ A_
 GTCA TGATATGCAT GAAGGA GA
 ||||| ||||| ||||| ||
 ACTGTACGTA CTTCT CT
 TATGGT CG
 GAM795 GABRP 3' TTCCCCCACTATGCATATC 15480 AA AA
 GATATGCATG GG GAA
 ||||| ||||| ||||| ||
 CTATACGTAT CC CTT
 CA CC
 GAM795 MTERF 3' TTTCTTCCTTTTATA 13842 CAT
 TATG GAAGGAAGAAA
 ||||| ||||| ||||| |||||
 ATAT TTTCTTCTTT

 GAM795 PRKACB 3' TTTCTTCCTTTTCAATTTCA 8604 T GCAT
 TGA AT GAAGGAAGAAA
 ||||| ||||| ||||| |||||

ACT TA TTTCTTCTTT
 T ACT_
 GAM795 PRKWNK3 3' TTGTTTCTCACATGCATA 30856 AAG A
 TATGCATG GA GAAACAA
 ||||| || |||||
 ATACGTAC CT CTTTGTT
 A__ _
 GAM795 RAB30 3' TGTAGGGATCCCTCCTGCACAT 15833 A T A AGAA_
 CA TGAT TGCA GA GGA ACA
 ||| ||| || ||| |||
 ACTA ACGT CT CCT TGT
 C C C AGGGA
 GAM795 RB1 3' TGTTTCTGCATGAATATCA 43706 G AAGGA
 TGATAT CATG AGAAACA
 ||||| ||| |||||
 ACTATA GTAC TCTTTGT
 A G____
 GAM795 TGFB3 3' TGTTTCTTCCCATACTGCATAC 9252 A _ AA
 A TG TATGCA TG GGAAGAAACA
 || ||||| || |||||
 AC ATACGT AT CCTTCTTTGT
 _ C AC
 GAM795 APCL 3' CTTCTCTGAATGCATGTCA 12499 GA _
 TGATATGCAT AG GAAG
 ||||| || |||
 ACTGTACGTA TC CTTC
 AG T
 GAM795 CECR7 5' TGTCTCTTCCTTCACTACCTTC 38882 TATGCA A
 GA TGAAGGAAGA ACA
 || ||||| |||
 CT ACTTCCTTCT TGT
 TCCATC C
 GAM795 FHX 3' CTGCTTTTCATGCATATTA 20459 A_
 TGATATGCATGAAGG AG
 ||||| ||| ||
 ATTATACGTACTTTT TC
 CG
 GAM795 FLJ10079 3' TTTTCCCCTTGCATATCA 30217 TGAA
 TGATATGCA GGAAGA
 ||||| |||
 ACTATACGT CCTTTT
 TCC_
 GAM795 FLJ20371 3' CTGGCCTCAGCATATCA 19425 A A A_
 TGATATGC TGA GG AG
 ||||| ||| || ||
 ACTATACG ACT CC TC
 _ _ GG
 GAM795 FLJ22408 5' TCTTCCTTCAGCGCGTC 24174 TA A
 GA TGC TGAAGGAAGA
 || ||| |||||

CT GCG ACTTCCTTCT
 GC _
 GAM795 FLJ22471 3' TGTTTAATCCCATGCATGCCA 24779 A AA AG
 TG TATGCATG GGA AAACA
 || ||||| || |||||
 AC GTACGTAC CCT TTTGT
 C _ AA
 GAM795 GRIN3A 3' CTTTCTCAGCATATCA 28534 A A
 TGATATGC TGA GGAAG
 ||||| || |||||
 ACTATACG ACT CTTTC

 GAM795 KIAA0286 3' TTGTTTCTTTTCTACATAGCA 33908 _ A _
 TGC ATG AGGA AGAAACAA
 || || || || |||||
 ACG TAC TCTT TCTTTGTT
 A A TT
 GAM795 KIAA0471 3' TTGTTGAAAACTCATGCATCC 16917 AT AGGAAGA
 CA TG ATGCATGA AACAA
 || ||||| |||||
 AC TACGTACT TTGTT
 CC CAAAAGG
 GAM795 KIAA0523 3' TTTCTTCCTAGTATCA 33649 GCATGA
 TGATAT AGGAAGAAA
 ||||| |||||
 ACTATG TCCTTCTTT
 A____
 GAM795 KIAA0560 3' TTGTTTCTTCTGTTATACTATC 30839 TGC A
 A TGATA ATGA GGAAGAAACAA
 |||| ||| |||||
 ACTAT TATT TCTTCTTTGTT
 CA_ G
 GAM795 KIAA1069 3' TTGTTTCTCATCTTCATAATAC 33727 A GC A_
 CA TG TAT ATGAAGG AGAAACAA
 || || ||||| |||||
 AC ATA TACTTCT TCTTTGTT
 C A_ AC
 GAM795 NXPH3 3' TTGTTTCTTCCTCTATGACATG 32724 _ A
 TATG CATG AGGAAGAAACAA
 |||| ||| |||||
 GTAC GTAT TCCTTCTTTGTT
 A C
 GAM795 PFTK1 3' TTCCTCTTTTCATACATTCCA 14755 AT C A
 TG ATG ATGAAGGA GAA
 || || ||||| |||||
 AC TAC TACTTTCT CTT
 CT A C
 GAM795 PRO2893 5' TCGTTCCTCTGCATATC 20705 T A _
 GATATGCA GA GGAA GA
 ||||| || ||||| ||

CTATACGT CT CCTT CT
 _ _ G
 GAM795 ZFP 3' TTTCTTAGTTATGCATCTCA 20721 T AGG
 TGA ATGCATGA AAGAAA
 ||| ||||| |||||
 ACT TACGTATT TTCTTT
 C GA_
 GAM795 LOC124599 3' GTTTCTTCCTGTTGATATTCA 37258 TATG TGA
 TGA CA AGGAAGAAAC
 ||| || |||||
 ACT GT TCCTTCTTTG
 TATA TG_
 GAM795 LOC145622 3' CTTCTTTTCATCACATCA 37909 A C
 TGAT TG ATGAAGGAAG
 ||| || |||||
 ACTA AC TACTTTCTTC
 C _
 GAM795 LOC148479 3' TTGTCTCTTCCTTTACCTCA 38544 TA CAT A
 TGA TG GAAGGAAGA ACAA
 ||| || ||||| |||||
 ACT AC TTTCCTTCT TGTT
 CC _ C
 GAM795 LOC151996 5' TTGCCTCTTCCTTTCTCCCATC 41418 ATGCAT AA
 A TGAT GAAGGAAGA CAA
 ||| ||||| |||||
 ACTA TTTCCTTCT GTT
 CCCTC_ CC
 GAM795 LOC152674 5' TTGTTTCTTCATGACATACA 41540 A _ G
 TG TATG CATGAAGGAA AA
 || ||||| ||||| ||
 AC ATAC GTACTTCTTT TT
 _ A G
 GAM795 LOC154743 3' TTTCTTCCTTATATTA 39482 CATGA
 TGATATG AGGAAGAAA
 ||||| |||||
 ATTATAT TCCTTCTTT
 _
 GAM795 LOC163231 5' TCTCCTTCATCATATCA 40102 C A
 TGATATG ATGAAGGA GA
 ||||| ||||| ||
 ACTATAC TACTTCCT CT
 _ _
 GAM795 LOC200845 3' TGTTTCTTTCTATGCATAT 42865 GA
 ATATGCAT AGGAAGAAACA
 ||||| |||||
 TATACGTA TCTTTCTTTGT
 _
 GAM795 LOC219700 5' TGTGCGACTTCAGGCATATCA 44703 A GAAGAA
 TGATATGC TGAAG ACA
 ||||| ||||| |||

		ACTATACG ACTTC TGT		
		G AGCG__		
GAM795	LOC221468 3'	TGCTTCCTCCTTTATTGTATC 29828	C	A A
		GATATG ATGAAGGA GAA CA		
		CTATGT TATTCCT CTT GT		
		_ C C		
GAM795	LOC254042 3'	GTTTCTCCCTTTTGTGTATT 45792	T	A
		GATATGCA GAAGG AGAAAC		
		TTATGTGT TTTCC TCTTTG		
		_ C		
GAM795	LOC90075 5'	CTTCCTTCATGCACATCA 30738	A	
		TGAT TGCATGAAGGAAG		
		ACTA ACGTACTTCCTTC		
		C		
GAM795	LOC90075 5'	GTTTCCTTCCTTCATGCACATCA 30740	A	A
		TGAT TGCATGAAGGAAG AAC		
		ACTA ACGTACTTCCTTC TTG		
		C C		
GAM795	LOC90736 3'	TTGTTTCTCCCTCTGGTAACAT 31960	A_	ATGA A
	C	GAT TGC AGG AGAAACAA		
		CTA ATG TCC TCTTTGTT		
		CA GTC_ C		
GAM795	LOC90982 5'	TGTTTCATATTCTTGCATATCA 32235	T	GAA A
		TGATATGCA GAAG GAA CA		
		ACTATACGT CTTT CTT GT		
		T ATA _		
GAM795	LOC92391 3'	TGTTTCTTCCACATATT 34274	CATGAA	
		GATATG GGAAGAAACA		
		TTATAC CCTTCTTTGT		
		A_____		
GAM796	FLJ10842 3'	AACATATCCAGTACAATTTA 20186	T	C__
		A AATTGTACT TATGTT		
		A TTAACATGA ATACAA		
		T CCT		
GAM796	LOC202309 5'	CAATACAGTACAATTATA 43421	CTA	
		TATAATTGTACT TGTTG		
		ATATTAACATGA ATAAC		
		C__		
GAM797	EDNRA 5'	TATTCCTCAAATTTGCCTCA 32058	G	TGCCT
		TGAGGCAAA TTTG ATA		

			ACTCCGTTT AAAC TAT		
			_ TCCTT		
GAM797	ESRRG	3'	AGTCACAGACCTTGCCTCA 32995	A	C
			TGAGGCAA GTTTGTG CT		
			ACTCCGTT CAGACAC GA		
			C T		
GAM797	GCH1	3'	GTACAGTAATTTGCCTCA 5668	GT_	
			TGAGGCAAA TTGTGC		
			ACTCCGTTT GACATG		
			AAT		
GAM797	NLGN1	5'	TATAAATACGTTTGCCTCA 17231	___	
			TGAGGCAAA GTTTGTG		
			ACTCCGTTT TAAATAT		
			GCA		
GAM797	RFXAP	5'	GGTATAGGCGCCTTTTACCCCA 6136	A C	TTT
			TG GG AAAG GTGCCTATACC		
			AC CC TTTT CGCGGATATGG		
			C A C_		
GAM797	SRR	3'	ATAGAAAATAAACTTTGCCCA 22473	A	GC_
			TG GGCAAAGTTTGT CTAT		
			AC CCGTTTCAAATA GATA		
			_ AAA		
GAM797	STAC	3'	GTACAAATGCTCTTTGCCTC 9120	___	
			GAGGCAAAG TTTGTGC		
			CTCCGTTTC AAACATG		
			TCGT		
GAM797	FLJ10922	3'	GCACAAGCAATACGCTTGCCTT 20256	A_	
	A		TGAGGCAA GTTTGTGC		
			ATTCCGTT CGAACACG		
			CGCATAA		
GAM797	KIAA1900	3'	GGTATCTAACTTGCCTCA 36261	A	___
			TGAGGCAA GTTT GTGCC		
			ACTCCGTT CAAA TATGG		
			_ TC		
GAM797	MEGF11	3'	TATAGGTAAGCAGCTTACCTCA 26206	CA	TG_
			TGAGG AAGTT TGCCTATA		
			ACTCC TTCGA ATGGATAT		
			A_ CGA		
GAM797	Rab11-FIP2	3'	TATAGGCATATACCTCA 17100	CAAAGTT	
			TGAGG TGTGCCTATA		

			ACTCC ATACGGATAT		
			AT_____		
GAM797	RNF8	3'	GGTACTTCGTAGACTCTGCCTC 10096	A	_____
	A		TGAGGCA AGTTT GTGCC		
			ACTCCGT TCAGA CATGG		
			C TGCTT		
GAM797	LOC146894	3'	GGCACGATCTGCAAACCTCCGCC 29782	AA	_____
	TC		GAGGC AGT TTGTGCC		
			CTCCG TCA AGCACGG		
			CC AACGTCT		
GAM797	LOC168391	5'	GGCACAGACCCCTGCCTC 40244	AA_	
			GAGGCA GTTTGTGCC		
			CTCCGT CAGACACGG		
			CCC		
GAM797	LOC255328	3'	GGCACAAGCTCTGGCCCA 46179	A AA_	
			TG GGC AGTTTGTGCC		
			AC CCG TCGAACACGG		
			_ GTC		
GAM798	CSRP1	3'	TGTTTGATCTTCTCAAACA 10280	A A	
			TGT TTGGGAA ATCAAACA		
			ACA AACTCTT TAGTTTGT		
			_ C		
GAM798	CUL5	3'	TTGCTTGTCCCAATACAA 9548	A T	
			TTGTATTGGGA AA CAA		
			AACATAACCCT TT GTT		
			G C		
GAM798	CYP4A11	3'	TTGTTTGATCACCAATAAATA 6420	G GAAA	
			TATT TATTGG ATCAAACAA		
			ATAA ATAACC TAGTTTGT		
			_ AC_		
GAM798	GLUD1	3'	TGTGGCTTTTCCCAACACAAT 11776	A TCAA	
			ATTGT TTGGGAAAA ACA		
			TAACA AACCCCTTTT TGT		
			C CGG_		
GAM798	ROBO1	3'	TTGTTTGATCCCTAACCCCTACA 28590	___ AAA	
	A		TTGTA TTGGG ATCAAACAA		
			AACAT AATCC TAGTTTGT		
			CCC C_		
GAM798	ROBO1	3'	TTGTTTGATCCCTAACCCCTACA 8853	___ AAA	
	A		TTGTA TTGGG ATCAAACAA		

			AACAT AATCC TAGTTTGTT		
			CCC C__		
GAM798	SLC16A1	3'	TTGTTTGACTCCTTACCAATA 9013	TATT	AAA
			TATTG GGGG TCAAACAA		
			ATAAC TCCT AGTTTGTT		
			CAT_ C__		
GAM798	SLC18A1	3'	TTGCCTGATTTTCTCTGGCA 9018	ATT	AA
			TGT GGGAAAATCA CAA		
			ACG CTCTTTTAGT GTT		
			GT_ CC		
GAM798	FLJ11539	3'	TTGTTTGACTTTTGTACAA 24090	TG	A
			TTGTAT GGAAA TCAAACAA		
			AACATG TTTT AGTTTGTT		
			_ C		
GAM798	FLJ14326	3'	TTGCCTGATCCTCCTAGTGC 25906	AA	AA
			GTATTGGGA ATCA CAA		
			CGTGATCCT TAGT GTT		
			CC CC		
GAM798	KIAA0057	3'	TGTCTGATTTTACAATG 14628	GG	A
			TATTG AAAATCA ACA		
			GTAAC TTTTAGT TGT		
			AT C		
GAM798	KIAA0961	3'	TGGTTTCCCAACCAATA 17073	TA	A
			TATTG TTGGGAAA TCA		
			ATAAC AACCCCTT GGT		
			C_ _		
GAM798	LHX6	3'	TGAGCTTCCCAATCAATA 15700	T	AA
			TATTG ATTGGGAA TCA		
			ATAAC TAACCCTT AGT		
			_ CG		
GAM798	MGC5139	5'	TTTGATTTCOAATACA 36680	AA	
			TGTATTGGGA ATCAAA		
			ACATAACCTT TAGTTT		
			_		
GAM798	PFTK1	3'	TTGTTTGATTTCCCTCTGCAG 14756	TT	A
			TTGTA GGGAAA TCAAACAA		
			GACGT CCCTT AGTTTGTT		
			CT _		
GAM798	LOC133418	3'	TGTTTGACTAAATACAAT 37043	G	AAAA
			ATTGTATT GG TCAAACA		

			TAACATAA TC AGTTTGT		
			A _____		
GAM798	LOC51696	3'	TGTTTGAAACAATACAG 18317	GGAAAA	
			TTGTATTG TCAAACA		
			GACATAAC AGTTTGT		
			AA_____		
GAM799	ANK1	3'	AACAATAAATACTATGCA 5474 G	CTA	
			TG ATAGTATTT GTTGTT		
			AC TATCATAAA TAACAA		
			G _____		
GAM799	ANK1	3'	AACAATAAATACTATGCA 21727 G	CTA	
			TG ATAGTATTT GTTGTT		
			AC TATCATAAA TAACAA		
			G _____		
GAM799	ANK1	3'	AACAATAAATACTATGCA 30277 G	CTA	
			TG ATAGTATTT GTTGTT		
			AC TATCATAAA TAACAA		
			G _____		
GAM799	FLJ14075	3'	AACCATCCAGAAATACCATCC 24371	A A_ T	
			GGAT GTATTTCT GT GTT		
			CCTA CATAAAGA TA CAA		
			C CC C		
GAM799	KIAA1796	3'	AACAGCTAATACTACCA 43962	A TTC	
			TGG TAGTAT TAGTTGTT		
			ACC ATCATA ATCGACAA		
			— —		
GAM800	EVI5	3'	TTGACCAAAACATACATTTGA 12216	C AAGC	
			TCAAA GTAT TTGGTCAA		
			AGTTT CATA AACCAGTT		
			A CAA_		
GAM800	KIAA1789	5'	TGACCAAGTCATTTGAC 33314	CGTATAA	
			GTCAAA GCTTGGTCA		
			CAGTTT TGAACCAGT		
			AC_____		
GAM800	LOC221773	3'	CCAATTATAGTTTGACA 43763	G GC	
			TGTCAAAC TATAA TTGG		
			ACAGTTTG ATATT AACC		
			— —		
GAM801	ATP10C	3'	AAACAGCTGCATGGCACAT 23685	CCTCT	
			ATGTGCCGT TTGTTT		

			TACACGGTA	GACAAA	
			CGTC_		
GAM801	MGEA5	3'	AACAAAGAAGACTATGT	14516	TGCC C
			GCATG GTC TCTTTGTT		
			TGTAT CAG AGAAACAA		
			_____ A		
GAM801	MSTP032	3'	AACAAAGAGAAATGCTG	24903	GTGCCGTC
			TAGCAT CTCTTTGTT		
			GTCGTA GAGAAACAA		
			AA_____		
GAM801	TED	3'	AAACAAAAGGCTGCAGCACATG	17910	C _ C
	TTA		TAGCATGTGC GT CCT TTTGTTT		
			ATTGTACACG CG GGA AAACAAA		
			A TC _		
GAM801	LOC151126	5'	AAACAAAGGCAGTACATGC	39055	C CCT
			GCATGTGC GT CTTTGTTT		
			CGTACATG CG GAAACAAA		
			A _____		
GAM802	CHRNA2	5'	GAAAAGCCTCCGCTGCTCAT	6402	AGTTGC
			GTGAGCAGG GCTTTTC		
			TACTCGTCC CGAAAAG		
			GCCTC_		
GAM802	MLLT2	3'	GAAGGCAACCCCGCTC	12569	A A G
			GAGC GG GTTGC CTTT		
			CTCG CC CAACG GAAG		
			C C _		
GAM802	THRB	5'	GAAAAGAGACCTCCTGCTC	6076	TTGCG
			GAGCAGGAG CTTTTC		
			CTCGTCCTC GAAAAG		
			CAGA_		
GAM802	FLJ11413	3'	GAGGCATTCTGCTCAT	23774	T G
			GTGAGCAGGAGT GC CTT		
			TACTCGTCCTTA CG GAG		

GAM802	IL14	5'	AAGCAAGCCCTGCTCAC	45702	A GC
			GTGAGCAGG GTT GCTT		
			CACTCGTCC CGA CGAA		
			_ A_		
GAM802	KIAA0916	3'	GAAGTTTAACTCTGCTCAC	17416	G GC_
			GTGAGCAG AGTT GCTTT		

CACTCGTC TCAA TGAAG
 _ ATT
 GAM802 KRT6IRS 3' GAAAAGCAGGCACTGTTTAC 27252 GA GC
 GTGAGCAG GTT GCTTTTC
 ||||| || |||||
 CACTTGTC CGG CGAAAAG
 A_ A_
 GAM802 LOC137991 5' GAAAAGCCCTGGCTCCCGC 37114 A GC_
 GC GGAGTT GCTTTTC
 || ||||| |||||
 CG CCTCGG CGAAAAG
 C TCC
 GAM802 LOC151234 3' AAAAACGCAAATCCTGTTTAC 39077 G C
 GTGAGCAGGA TTGCG TTTT
 ||||| ||||| |||||
 CACTTGTCCT AACGC AAAA
 A A
 GAM803 BACE 3' AGAGATTCCCCTGGACCACACC 14416 A _ ACTTT C
 TCC GGA GTG GGTCCA ATC CT
 ||| || ||||| ||| ||
 CCT CAC CCAGGT TAG GA
 C A CCCCT A
 GAM803 BACE 3' AGAGATTCCCCTGGACCACACC 29084 A _ ACTTT C
 TCC GGA GTG GGTCCA ATC CT
 ||| || ||||| ||| ||
 CCT CAC CCAGGT TAG GA
 C A CCCCT A
 GAM803 KCNK4 3' AGGGATCGGCAGGGACCACTTC 18713 GT AA TT
 C GGAAGTGG CC CT ATCCCT
 ||||| || || |||||
 CCTTCACC GG GG TAGGGA
 AG AC C_
 GAM803 NCOA4 3' GGGATAAAGTCATCCTCT 11924 T CCA
 AG GGGT ACTTTATCCC
 || |||| |||||
 TC CCTA TGAAATAGGG
 T C_
 GAM803 PIK3C2B 3' GGATAAAGCTGGCTGCTTCC 8507 TG GT A
 GGAAG G CCA CTTTATCC
 |||| | || |||||
 CCTTC C GGT GAAATAGG
 GT _ C
 GAM803 SFTPA2 3' AAAGACTGGATCCAAACCCATC 13807 _ A_
 TTCC GGAAG TGGGTCCA CTTT
 |||| ||||| |||||
 CCTTC ACCTAGGT GAAA
 TACCCAA CA
 GAM803 SNRP70 5' AGGGATTTCGCGCCGGGACCCA 38406 AA AA_ TT_
 CCCCC GG GTGGGTCC CT ATCCCT
 || ||||| || |||||

				CC CACCCAGG GG TAGGGA			
				CC GCC CGTT			
GAM803	TBXAS1	5'	AGGAATAAAGTTGCTGATTCAT 25246	G	___	C	
	TCC		GGAA TGGGTC CAACTTTAT CCT				
			CCTT ACTTAG GTTGAAATA GGA				
			___ TC A				
GAM803	TBXAS1	5'	AGGAATAAAGTTGCTGATTCAT 6732	G	___	C	
	TCC		GGAA TGGGTC CAACTTTAT CCT				
			CCTT ACTTAG GTTGAAATA GGA				
			___ TC A				
GAM803	VAT1	3'	AGGGCGGGAATCAGACCTACTC 13065	A	CAAC	AT_	
	C		GGA GTGGGTC TTT CCCT				
			CCT CATCCAG AAG GGGA				
			___ ACT_ GGC				
GAM803	CHRA1	3'	GGACAGCCCTGGACCCACTCC 18905	A	ACTTTA		
			GGA GTGGGTCCA TCC				
			CCT CACCCAGGT AGG				
			___ CCCGAC				
GAM803	DKFZP586B2420	3'	GGAAGTGTGATGGACCACTTCC 37011	G	___	TTTA	
			GGAAGTGG TCCA AC TCC				
			CCTTCACC AGGT TG AGG				
			___ AG TCA_				
GAM803	FLJ10044	3'	GGGACAGGACCCACCTCC 19711	A	AACTTTA		
			GGA GTGGGTCC TCCC				
			CCT CACCCAGG AGGG				
			C AC_____				
GAM803	FLJ11320	3'	AGAGTTGAACCCCTTCC 20424	T	C		
			GGAAG GGGT CAACTTT				
			CCTTC CCA GTTGAGA				
			___ A				
GAM803	FLJ21940	3'	ATAAAGTTGGATGTTCT 23107	GTGG			
			GGAA GTCCAACCTTTAT				
			TCTT TAGGTTGAAATA				
			G_____				
GAM803	FLJ23047	3'	GGATAAAGTTGAGGATCAC 23762	GT_			
			GTGG C CAACTTTATCC				
			CACT G GTTGAAATAGG				
			AG A				
GAM803	FLJ23185	5'	GGATTCGTGCTGGGCCCACTCC 24653	A	ACTTT_		
			GGA GTGGGTCCA ATCC				

			CCT CACCCGGGT	TAGG		
			CGTGCT			
GAM803	FLJ23309	3'	GGACAAAGCCAACAATCCACTT	24378	CCAA__	A
		C	GAAGTGGGT	CTTT TCC		
			CTTCACCTA	GAAA AGG		
			ACAACC	C		
GAM803	PIP5K1C	3'	AGGGAGGCTGCTGGACCCACCC	35015	AA	ACTTTA
		C	GG GTGGGTCCA	TCCCT		
			CC CACCCAGGT	AGGGA		
			C_	CGTCGG		
GAM803	LOC144558	3'	ATAAAGTTCCTCCCAGTTCC	40437	G	TCC
			GGAA TGGG	AACTTTAT		
			CCTT ACCC	TTGAAATA		
			G	TCC		
GAM803	LOC145371	3'	GGGATAAAAAGTCACCTCC	37848	A	GTCCAAC
			GGA GTGG	TTTATCCC		
			CCT CACT	AAATAGGG		
			C	GAA__		
GAM803	LOC145371	3'	GGATAAGAACCTCACTTCC	37847	_	CCAAC
			GGAAGTG GGT	TTTATCC		
			CCTTCAC CCA	GAATAGG		
			T	A__		
GAM803	LOC157278	3'	ATAAAGTTCCTCCCAGTTCC	41778	G	TCC
			GGAA TGGG	AACTTTAT		
			CCTT ACCC	TTGAAATA		
			G	TCC		
GAM803	LOC161742	3'	AGGGATAAAGTTGAGAAGTGTG	40026	AAGTGGG	_
		CC	GG	TC CAACTTTATCCCT		
			CC	AG GTTGAAATAGGGA		
			GTGTGA_	A		
GAM803	LOC201191	3'	AGGGACAGAGGACCACTTCC	43213	_	AAC A
			GGAAGTGG GTCC	TTT TCCCT		
			CCTTCACC CAGG	AGA AGGGA		
			A	_ C		
GAM803	LOC221486	3'	AGGGACAGCTGCTGGGACCCAC	43740	A	AACTTTA__
		CTCC	GGA GTGGGTCC	TCCCT		
			CCT CACCCAGG	AGGGA		
			C	GTCGTCGAC		
GAM804	CAV1	5'	TTTCCCCCATACAATAACAAG	7492	G TACA	A
			CT GT	TATGGGG GAAA		

			GA CA ATACCCC CTTT		
			A TAAC C		
GAM804	CD53	3'	CTGTCTTATACAACCAGAGA 6169 C ACA _		
			TC CTGGTT TATGGGG AG		
			AG GACCAA ATATTCT TC		
			A C_ G		
GAM804	CELSR1	3'	CTCCCCATGCCAGGG 15514 TTACA		
			CCCTGG TATGGGGAG		
			GGGACC GTACCCCTC		
			C_		
GAM804	DYRK2	5'	TCTCCAGCGGCCATGTTAACCA 9634 C _		
	GG		CCTGGTTA ATATGG GGAGA		
			GGACCAAT TGTACC CCTCT		
			_ GCGA		
GAM804	EVX1	5'	TTTCTCCCTCTTGCAACCA 7714 A TAT		
			TGGTT CA GGGGAGAAA		
			ACCAA GT TCCCTCTTT		
			C TC_		
GAM804	F2RL3	3'	TTTCTGTCAATGTCACCAGGGA 10086 T ATG G		
			TCCCTGGT ACAT GG AGAAA		
			AGGGACCA TGTA CT TCTTT		
			C A_ G		
GAM804	FLRT2	3'	TTTCTCTAACCTATAACAAGG 14888 G TACA _		
			CCT GT TATGGG GAGAAA		
			GGA CA ATATCC CTCTTT		
			A _ AAT		
GAM804	MS4A2	3'	TTTCTCCATCAGCAACCAGGGA 22478 ACAT		
			TCCCTGGTT ATGGGGAGA		
			AGGGACCAA TACCTCTTT		
			CGAC		
GAM804	MYEOV	3'	TTTCTCCCCATTTTCCAGGGA 29003 TTACAT		
			TCCCTGG ATGGGGAGAAA		
			AGGGACC TACCCCTCTTT		
			TTT_		
GAM804	NCOA6	5'	TTTCCCTATGTATAACCAGTGA 15296 C C		
			TC CTGGTTA ATATGGGGAGA		
			AG GACCAAT TGTATCCCTTT		
			T A		
GAM804	PRKACA	3'	TTCTCCCCATCCCAGG 8600 TTACAT		
			CCTGG ATGGGGAGAA		

GGACC TACCCCTCTT
C____
GAM804 RERE 3' TTTCTCCCATATCCCAAGGCG 14412 _ _ TTAC
A TC CCT GG ATATGGGGAGAAA
|| ||| || |||||
AG GGA CC TATACCCCTCTTT
C A C____
GAM804 SELPLG 3' CTCCCCATGTACCCAAGGA 30018 C T TA
TCC TGG TACA TGGGGAG
||| ||| ||| |||||
AGG ACC ATGT ACCCCTC
A C ____
GAM804 ZNF200 3' TTCCCCCACCACATGGGGA 9505 TGGTTA A A
TCCC CAT TGGGG GAA
||| ||| ||||| |||
AGGG GTA ACCCC CTT
____ C C
GAM804 ZNF36 3' CTCCCCATAACAAGAGA 45103 C G TACA
TC CT GT TATGGGGAG
|| ||| |||||
AG GA CA ATACCCCTC
A A ____
GAM804 AD034 3' TTTCTTTGTACACACCAGAGA 25560 C TACA GG
TC CTGGT TAT GGAGA
|| |||| ||| |||||
AG GACCA ATG TCTTT
A CAC_ TT
GAM804 APOL6 3' TCTAAACATATGTAAACAGAGA 24971 C G GGG
TC CTG TTACATATG AGA
|| ||| ||||| |||
AG GAC AATGTATAC TCT
A A AAA
GAM804 ARHGAP5 3' TTTCTTTTACACACATACCAAG 37823 C TACATATG
GA TCC TGGT GGGAGAAA
||| ||| |||||
AGG ACCA TTTTCTTT
A TACACACA
GAM804 BCAA 5' CTCCCCCACCAGGGA 18510 ACATAT
TCCCTGGTT GGGGAG
||||||| |||||
AGGGACCAA CCCCTC
CC____
GAM804 C20orf13 3' CTCCTCATTGTGTGACCAGG 19299 _
CCTGGTTACATA TGGGGAG
||||||| |||||
GGACCAGTGTGT ACTCCTC
T
GAM804 C3F 3' TCTCCCCATCTAGCCAGG 12333 CAT
CCTGGTTA ATGGGGAGA
||||||| |||||

GGACCGAT TACCCCTCT
 C__
 GAM804 CKAP4 3' TCTCTCCGGAGGTCACCAAGGA 13704 C T ATA
 TCC TGGT AC TGGGGAGA
 ||| ||| || |||||
 AGG ACCA TG GCCTCTCT
 A C GAG
 GAM804 CRIPT 3' TTTCTTTAATATGTGACCA 36540 GG
 TGGTTACATAT GGAGAAA
 ||||| |||||
 ACCAGTGTATA TTTCTTT
 A_
 GAM804 DIO2 3' TTCTCCCGTTAACCAGG 15176 CATATG
 CCTGGTTA GGGAGAA
 ||||| |||||
 GGACCAAT CCCTCTT
 TG____
 GAM804 DIO2 3' TTCTCCCGTTAACCAGG 6464 CATATG
 CCTGGTTA GGGAGAA
 ||||| |||||
 GGACCAAT CCCTCTT
 TG____
 GAM804 dJ309H15.1 3' TCTCCCCACAGCCTCAAGG 28890 ____ ACATA
 CCT GGTT TGGGGAGA
 ||| ||| |||||
 GGA CCGA ACCCCTCT
 ACT C____
 GAM804 DKFZP434D193 3' TTTCTCCCCAATACCACCAACG 42854 CC TACATA
 A TC TGGT TGGGGAGAAA
 || ||| |||||
 AG ACCA ACCCCTCTTT
 CA CCATA_
 GAM804 ESDN 3' CTCCTCAATGTGTAAACAGG 28153 G _
 CCTG TTACATAT GGGGAG
 ||| ||||| |||||
 GGAC AATGTGTA CTCCTC
 A A
 GAM804 FLJ10415 3' TTCCCCGTGAAACCAGAGA 19853 C ACA
 TC CTGGTT TATGGGGAG
 || ||||| |||||
 AG GACCAA GTGCCCCTT
 A A_
 GAM804 FLJ10743 3' TTCTCCCCATGCTTCTAGG 20083 TTACA
 CCTGG TATGGGGAGAA
 |||| |||||
 GGATC GTACCCCTCTT
 TTC____
 GAM804 GABBR1 5' CTCCCCACAAAATCAGGGA 22421 ACATA
 TCCCTGGTT TGGGGAG
 ||||| |||||

			AGGGACTAA ACCCCTC	
			AAC__	
GAM804	HRD1	3'	CTCTCTGTCTGCACCAGGGA 34471	TA T
			TCCCTGGT CA ATGGGGAG	
			AGGGACCA GT TGTCTCTC	
			C_ C	
GAM804	HSPC063	5'	TCTTCCCACAGCCAGG 15440	ACATA
			CCTGGTT TGGGGAGA	
			GGACCGA ACCCTTCT	
			C_____	
GAM804	ICB-1	3'	TCTCCCCATAGCCACAGTGGA 11260	_ GTTACA
			TCC CTG TATGGGGAGA	
			AGG GAC ATACCCCTCT	
			T ACCG__	
GAM804	KIAA0258	3'	TTTCCCTAATGTATCCA 16653	T A
			TGG TACAT TGGGGAGA	
			ACC ATGTA ATCCCTTT	
			T _	
GAM804	KIAA0326	3'	TTTCTCCCTGCCAGCCAGGGA 32162	ACATAT
			TCCCTGGTT GGGGAGAAA	
			AGGGACCGA TCCCTCTTT	
			CCCG__	
GAM804	KIAA0495	5'	TTCTCCTGTGGGACAACCAGGG 31368	ACATATG
	A		TCCCTGGTT GGGAGAA	
			AGGGACCAA TCCTCTT	
			CAGGGTG	
GAM804	KIAA1332	3'	TTTCCCATACTCAGGGA 35263	_ ACA
			TCCCTG GTT TATGGGGAG	
			AGGGAC CAA ATACCCCTTT	
			T C__	
GAM804	KIAA1962	3'	TCCCTCAAATGCTGTAAGTAGG 39835	- _
			CCTGGTTACA TAT GGGGA	
			GGATCAATGT GTA TCCCT	
			C AAC	
GAM804	LAP1B	3'	TCCCTAAATGTAACCAGGGA 32265	A
			TCCCTGGTTACAT TGGGGA	
			AGGGACCAATGTA ATCCCT	
			A	
GAM804	MGC15396	5'	CTCCCCATGGCCGGG 27437	TACA
			CCTGGT TATGGGGAG	

GGGCCG GTACCCCTC

GAM804 MGC29891 3' TTTCTCTGTGCAACTAG 29440 A T
CTGGTT CATA GGGGAG
||||| ||| |||||
GATCAA GTGT CTCTTT

C _

GAM804 MGC4549 3' CTCCCCATGGTAACCAGG 26169 A
CCTGGTTAC TATGGGGAG
||||||| |||||
GGACCAATG GTACCCCTC

GAM804 NEUROD4 5' CTCTCCGGGGAGCTAACCAGGG 22169 CATA__
A TCCCTGGTTA TGGGGAG
||||||| |||||
AGGGACCAAT GCCTCTC
CGAGGG

GAM804 PASK 5' TCTCTCATGTAACCA 17504 ATG
TGGTTACAT GGGAGA
||||||| |||||
ACCAATGTA CTCTCT

GAM804 PPP4R1L 5' TCTCCCTGACATAAGCAAGGA 38819 C G CATAT
TCC TG TTA GGGGAGA
||| ||| |||||
AGG AC AAT TCCCTCT
A G ACAG_

GAM804 PRO2214 5' TCTCCCTTGGGTGTATACCAGG 20590 _ AT_
GA TCCCTGGT TACAT GGGGAGA
||||||| ||||| |||||
AGGGACCA ATGTG TCCCTCT
T GGT

GAM804 SBB103 3' CTCCTCCAAAACCAGGGA 12365 ACATA _
TCCCTGGTT TGG GGAG
||||||| ||| |||||
AGGGACCAA ACC CCTC
A__ T

GAM804 SLC25A18 3' CTCCCTGTAACCAAGGA 25562 C TATG
TCC TGGTTACA GGGAG
||| ||||| |||||
AGG ACCAATGT CCCTC
A _

GAM804 SYNE-2 3' CTCCCCAGGAGCAGGGA 17533 G ACATA
TCCCTG TT TGGGGAG
||||| ||| |||||
AGGGAC AG ACCCCTC
G G__

GAM804 TIX1 3' TTCTCCCCTACCCAGGGA 30932 T CATAT
TCCCTGG TA GGGGAGAA
||||| ||| |||||

AGGGACC AT CCCCTCTT
 C _____
 GAM804 LOC112868 3' TCTCTCCTGCAATAACTAGG 36085 CATAT
 CCTGGTTA GGGGAGA
 ||||| |||||
 GGATCAAT CCTCTCT
 AACGT
 GAM804 LOC130951 3' TCTCCCCACATGTACCA 29028 T A
 TGGT ACAT TGGGGAGA
 ||| ||| |||||
 ACCA TGTA ACCCCTCT
 _ C
 GAM804 LOC144512 5' CCCCTTGGTCACATGAACCAGG 40429 A AT_____
 GA TCCCTGGTT CAT GGGG
 ||||| ||| |||
 AGGGACCAA GTA CCCC
 _ CACTGGTT
 GAM804 LOC145773 5' CTTCTCGTGTACCAAGGA 37982 C TAC
 TCC TGGT ATATGGGGAG
 ||| ||| |||||
 AGG ACCA TGTGCTCTTC
 A C_
 GAM804 LOC150848 5' TTCCTCATTTATAACAGGGA 41261 G CAT
 TCCCTG TTA ATGGGGAG
 ||||| ||| |||||
 AGGGAC AAT TACTCCTT
 _ ATT
 GAM804 LOC157860 3' TTCCCAGTCACACAACCAGGGA 41863 ACATA____
 TCCCTGGTT TGGGGA
 ||||| |||||
 AGGGACCAA ACCCTT
 CACACTG
 GAM804 LOC200609 5' TCTCCCCATCCCCAGGG 43337 TTACAT
 CCCTGG ATGGGGAGA
 ||||| |||||
 GGGACC TACCCCTCT
 CC____
 GAM804 LOC219988 3' CTTCCAAATGTAACCATGGA 44044 C ATG
 TCC TGGTTACAT GGGAG
 ||| ||||| |||||
 AGG ACCAATGTA CCTTC
 T AA_
 GAM804 LOC221399 5' CTCCCTAGTGACCAGGGA 45050 ATA
 TCCCTGGTTAC TGGGGAG
 ||||| |||||
 AGGGACCAGTG ATCCCTC

 GAM804 LOC253675 3' TCTCACCATATGTACCAAAGA 46267 CC T G
 TC TGGT ACATATGG GAGA
 || ||| ||||| |||||

AG ACCA TGTATACC CTCT
 AA _ A
 GAM804 LOC253805 3' TCTCCCCCAGGATCAGGGA 46137 ACATAT
 TCCCTGGTT GGGGAGA
 ||||| |||||
 AGGGACTAG CCCCTCT
 GACC_
 GAM804 LOC254042 5' TCTCTTCATATATCCAAAGA 45793 CC TTAC
 TC TGG ATATGGGGAGA
 || || |||||
 AG ACC TATACTTCTCT
 AA TA_
 GAM804 LOC254143 5' CCCCTTGGTCACATGAACCAGG 46158 A AT_____
 GA TCCCTGGTT CAT GGGG
 ||||| || |||||
 AGGGACCAA GTA CCCC
 _ CACTGGTT
 GAM804 LOC256942 3' CTCCTCCAAAACCAGGGA 45364 ACATA _
 TCCCTGGTT TGG GGAG
 ||||| || |||||
 AGGGACCAA ACC CCTC
 A_ T
 GAM804 LOC57109 3' TTCTCCCCATAGCACGAGG 21657 G TACA
 CCT GT TATGGGGAGAA
 || || |||||
 GGA CA ATACCCCTCTT
 G CG_
 GAM804 LOC91263 5' TTTCTCCCCACGTGCCA 32597 TTA TA
 TGG CA TGGGGAGAAA
 || || |||||
 ACC GT ACCCCTCTTT
 _ GC
 GAM805 BCL2L2 3' TTGTTCTTCATCATCCCCC 10265 A A TATCT
 GG GG ATGATGAAG CAG
 || ||||| |||||
 CC CC TACTACTTC GTT
 _ C CTT_
 GAM805 ITGA1 3' CTGAAAAAGATCATTTCTCC 31789 GAAGTATC
 GGAGGAATGAT TCAG
 ||||| |||||
 CCTCTTTACTA AGTC
 GAAAA_
 GAM805 AMOTL1 3' CTGAACTGTCATCATTCCT 36466 _ ATC
 AGGAATGATGA AGT TCAG
 ||||| || |||||
 TCCTTACTACT TCA AGTC
 G _
 GAM805 C20orf98 3' TCCAAGATACCAGCATTCCTC 35418 A AA CA
 GAGGAATG TG GTATCT GA
 ||||| || ||||| ||

CTCCTTAC AC CATAGA CT
G _ AC
GAM805 DKFZP762D096 3' TCTGACCACACTTCATCCTCCC 32667 A AT ATC_
CC GG GGA GATGAAGT TCAGA
|| ||| ||||| |||||
CC CCT CTACTTCA AGTCT
C C_ CACC
GAM805 DOK4 3' TCTGAAACCAAGACCTTCCCAT 19882 AT TA _____
TCCTCC GGAATG GAAG TC TCAGA
||||| ||| || |||||
CCTTAC CTTC AG AGTCT
C_ C_ AACCAA
GAM805 FLJ10043 3' CTGTCCATCCATTCTCC 19707 _ AAGTATCT
GGAGGAATG ATG CAG
||||||| ||| |||
CCTCCTTAC TAC GTC
C CT_____
GAM805 FLJ14743 3' TGAGATCCATTCTTCC 33763 ATGAAGT
GGAGGAATG ATCTCA
||||||| |||||
CCTTCTTAC TAGAGT
C_____
GAM805 KIAA0889 3' CTGATATCATATTCCTCC 17677 A AGTATC
GGAGGAATG TGA TCAG
||||||| ||| |||
CCTCCTTAT ACT AGTC
_ AT_____
GAM805 MGC15476 3' CTGATGAGCCCTCTCATTCTC 29688 T AGTA _
C GGAGGAATGA GA TC TCAG
||||||| || ||| |||||
CCTCCTTACT CT AG AGTC
_ CCCG T
GAM805 PIP5K2B 3' CTGAAATTTTCATTGCTCC 9611 AT ATC
GGA GATGAAGT TCAG
||| ||||| |||||
CCT TTA CTTTA AGTC
CG A_
GAM805 RAI16 3' TCTGCCTCTCCCACATTCTCC 22970 A A_ TATCT
GGAGGAATG TG AG CAGA
||||||| || || |||||
CCTCCTTAC AC TC GTCT
_ CC TCC____
GAM805 LOC115297 3' TCTGACTCCTTTTCATTCTCC 36072 _ TATC
TCC GGAGGAATGA TGAAG TCAGA
||||||| ||||| |||||
CCTCCTTACT ACTTT AGTCT
T CCTC
GAM805 LOC146988 3' CTGGTTCTCTCCATTCTCC 40779 AT A TAT T
GGAGGAATG GA G C CAG
||||||| || | |||||

			CCTCCTTAC CT C G GTC		
			CT _ TT _ _		
GAM805	LOC254755	3'	TCTGCCTCTCCCACATTCTCC 46488	A A_	TATCT
			GGAGGAATG TG AG CAGA		
			CCTCCTTAC AC TC GTCT		
			_ CC TCC _		
GAM805	LOC51075	3'	TCTGTGGTTTCATCATTCTTC 18069	GT T	
			GGAGGAATGATGAA ATC CAGA		
			CTTCCTTACTACTT TGG GTCT		
			_ T		
GAM805	LOC90072	3'	CTGATATCATATTCCTCC 30728	A	AGTATC
			GGAGGAATG TGA TCAG		
			CCTCCTTAT ACT AGTC		
			_ AT _ _		
GAM806	ADRBK2	3'	GCATTAGAACTACTGAAGA 11643	C AA	A
			TCT CAGTA TTTCTGGT GC		
			AGA GTCAT AAAGATTA CG		
			A C_ _		
GAM806	EXTL1	3'	GCACTACCAAGGCCGACCACTA 10754	C AAAT_ TC	C
			GAGG TCTC AGT T TGGTAG GC		
			GGAG TCA G ACCATC CG		
			A CCAGCC GA A		
GAM806	GPR65	5'	GCACCAATCTACTGTGAGA 30052	_ A TTC	A
			TCTC CAGTA AT TGGT GC		
			AGAG GTCAT TA ACCA CG		
			T C _ _		
GAM806	PODXL	3'	ACTGGAATTTACTGAGA 11869	C T TG	
			TCTC AGTAAATT C GT		
			AGAG TCATTTAA G CA		
			_ _ GT		
GAM806	TSLP	3'	ACTAAAAATTTACAAGAGA 26928	CA C	
			TCTC GTAAATTT TGGT		
			AGAG CATTTAAA ATCA		
			AA A		
GAM806	TSLP	3'	ACTAAAAATTTACAAGAGA 28848	CA C	
			TCTC GTAAATTT TGGT		
			AGAG CATTTAAA ATCA		
			AA A		
GAM806	ZNF266	3'	ATCAGAAATCTCACTGGAGA 42599	AA_	
			TCTCCAGT ATTTCTGGT		

			AGAGGTCA TAAAGACTA			
			CTC			
GAM806	C20orf121	3'	ATCAGGAACTTACTGGAGA	23628	A_	
			TCTCCAGTAA TTTCTGGT			
			AGAGGTCATT AAGGACTA			
			CA			
GAM806	C8orf14	5'	CTCCAGAAACCTACTGGATGA	27639	_ AA T	
			TC TCCAGTA TTTCTGG AG			
			AG AGGTCAT AAAGACC TC			
			T CC _			
GAM806	FLJ11274	5'	GCACCATTTAAAGCCACTGGA	20399	AAA C_ A	
			TCCAGT TTT TGGT GC			
			AGGTCA AAA ACCA CG			
			CCG TTT _			
GAM806	FLJ21657	3'	GCTTCAGAAATCCATGGA	22857	GTAA T	
			TCCA ATTTCTGG AGC			
			AGGT TAAAGACT TCG			
			ACC_ _			
GAM806	FLJ32334	3'	GCGCTGGGCCGAACATACTGGA	29368	AAT T _	
	GA		TCTCCAGTA TTC GGT AGCGC			
			AGAGGTCAT AAG CCG TCGCG			
			AC_ _ GG			
GAM806	PRKRIR	3'	ACAAGAAATTACCGGAGA	11051	A A G	
			TCTCC GTAA TTTCT GT			
			AGAGG CATT AAAGA CA			
			C _ A			
GAM806	SLC26A7	3'	GCACTTTCTAATTTATTAGAGA	27414	C TCT_ A	
			TCTC AGTAAATT GGT GC			
			AGAG TTATTTAA TCA CG			
			A TCTT _			
GAM806	UBXD2	3'	ACTAAAATTCTACTGGAGA	33911	_ C	
			TCTCCAGTA AATTT TGGT			
			AGAGGTCAT TTAAA ATCA			
			C _			
GAM806	LOC144473	5'	GCGCTACCAAGAACCACCACTG	40413	AAAT_ _	
	GGGA		TCTCCAGT TTCT GGTAGCGC			
			AGGGGTCA AAGA CCATCGCG			
			CCACC A			
GAM806	LOC152345	3'	ACCAGAAATCCTCTGAAGA	39265	C TAA	
			TCT CAG ATTTCTGGT			

			AGA GTC TAAAGACCA		
			A TCC		
GAM806	LOC222678	5'	ATCAAAAAAGCCACTGGAGA	44605	AAA_ C
			TCTCCAGT TTT TGGT		
			AGAGGTCA AAA ACTA		
			CCGA A		
GAM806	LOC91796	3'	CTACCAGACTTCAAAATTTACT	33372	_____
			AGTAAATT TCTGGTAG		
			TCATTTAA AGACCATC		
			AACTTC		
GAM807	ADCY7	3'	CAGGAGAAGACTCTCCGC	6781	C CGCG
			GCGG GAG TTTCTCCTG		
			CGCC CTC GAAGAGGAC		
			T A__		
GAM807	CALM3	3'	TCAAGAGAAACGCACCTGC	11685	CGAGC C
			GCGG GCGTTTCTC TGA		
			CGTC CGCAAAGAG ACT		
			CA__ A		
GAM807	CDK5R2	3'	CAGGAGAAACTGCAGCC	10041	GA C
			GGC GCG GTTTCTCCTG		
			CCG CGT CAAAGAGGAC		
			A_ _		
GAM807	MAP1A	3'	CAGGAGAGGACCTCGCC	8182	CGCG
			GGCGAG TTTCTCCTG		
			CCGCTC GGAGAGGAC		
			CA__		
GAM807	CHST3	5'	CAGGAATCCGCCGCCGCTA	10476	A C TTC
			TAGCGGCG GCG GT TCCTG		
			ATCGCCGC CGC TA AGGAC		
			_ C _		
GAM807	FLJ10350	3'	CAGGAGAAATGGCTTCTCC	45729	C C GT
			GG GAG GC TTCTCCTG		
			CC CTT CG AAGAGGAC		
			T _ GT		
GAM807	TBL1Y	5'	CAGGTACGCGCCGCCGC	27099	A TTCT
			GCGGCG GCGCGT CCTG		
			CGCCGC CGCGCA GGAC		
			_ T__		
GAM807	TBL1Y	5'	CAGGTACGCGCCGCCGC	28609	A TTCT
			GCGGCG GCGCGT CCTG		

CGCCGC CGCGCA GGAC
 _ T_

GAM807 TBL1Y 5' CAGGTACGCGCCGCGC 28610 A TTCT
 GCGGCG GCGCGT CCTG
 ||||| ||||| |||
 CGCCGC CGCGCA GGAC
 _ T_

GAM807 LOC122416 5' CAGGAACGCCCCGCGC 36684 AGC TTC
 GCGGCG GCGT TCCTG
 ||||| ||| |||||
 CGCCGC CGCA AGGAC
 CC_ _

GAM807 LOC125268 3' CAGGTGCCTGCACTCGCTGC 37449 C TTTCT
 GCGGCGAG GCG CCTG
 ||||| ||| |||
 CGTCGCTC CGT GGAC
 A CCGT_

GAM808 AIM1 5' CGCCAGGGTCGCCCACCCA 44114 A AGA TGT
 TG GGT CGA CCCTGGCG
 || ||| ||| |||||
 AC CCA GCT GGGACCGC
 _ CCC _

GAM808 EPHB4 3' CCAGGGACACCGCCTCCCCA 10738 A T A A
 TG GG AG CG TGTCCCTGG
 || ||| ||| |||||
 AC CC TC GC ACAGGGACC
 _ C C C

GAM808 HOXA3 3' GCGCCAGGAGAGTCTCCCCCA 24993 A TA C G _
 TG GG GA GAT TC CCTGGCGC
 || || ||| ||| |||||
 AC CC CT CTG AG GGACCGCG
 _ CC _ _ A

GAM808 TNC 3' GCACCAAAGACATCAGTCTCC 7935 T _ CC C
 GG AGAC GATGTC TGG GC
 || ||| ||||| ||| ||
 CC TCTG CTACAG ACC CG
 _ A AA A

GAM808 DKFZP434G1415 3' GCATGTTAACATTGCCTACCTC 25315 A CCCTG_
 A TGAGGTAG CGATGT GC
 ||||| ||||| ||
 ACTCCATC GTTACA CG
 C ATTGTA

GAM808 FLJ10508 3' GCACCAAGAAGTTACTGTTACC 19894 AC_ G CC C
 TCA TGAGGTAG GAT TC TGG GC
 ||||| ||| ||| ||| ||
 ACTCCATT TTG AG ACC CG
 GTCA A A_ A

GAM808 FLJ14708 3' CCAGGGACTTGCCCCA 26600 A ACGAT
 TG GG TAG GTCCCTGG
 || ||||| |||||

			AC CCGTT CAGGGACC		
			C _____		
GAM808	KIAA0930	3'	GCTGATACCACCTACCTCA 34917	ACGA	CCT
			TGAGGTAG TGTC GGC		
			ACTCCATC ATAG TCG		
			CACC _____		
GAM808	KIAA1655	3'	CCAGGCTCGTGTCTACCCA 33085	A	G TC
			TG GGTAGAC ATG CCTGG		
			AC CCATCTG TGC GGACC		
			_____ TC		
GAM808	KIAA1924	3'	GCGCCAGGGACACCAGGAATTC 36478	GTAGACGA	
			GAG TGTCCCTGGCGC		
			CTT ACAGGGACCGCG		
			AAGGACC_		
GAM808	LRBA	5'	CGCCAAGGACTTTCCACATCA 13556	G A	CGAT C
			TGA GT GA GTCC TGGCG		
			ACT CA CT CAGG ACCGC		
			A C TT_ A		
GAM808	MGC9753	5'	CCAGGGACACTGACCTCA 27240	AGA	A
			TGAGGT CG TGTCCCTGG		
			ACTCCA GT ACAGGGACC		
			_____ C		
GAM808	SEMA4C	3'	GCACAGGCACCAGCTACCTCA 19421	ACGAT C	_
			TGAGGTAG GT CCTG GC		
			ACTCCATC CA GGAC CG		
			GAC_ C A		
GAM808	LOC255631	5'	GCATCTACACCGTTACCTCA 46038	A A	CCCTG
			TGAGGT GACG TGT GC		
			ACTCCA TTGC ACA CG		
			_ C TCTA_		
GAM809	ADAMTS4	5'	GCCAGACCCCTGGGCACCTC 11566	CCGA	
			GAGGTGCCCCG GGGTCTGGC		
			CTCCACGGGT CCCAGACCG		
			C_____		
GAM809	ANK1	3'	CCTCGCGCGGGCACCCCA 30283	A	_
			TG GGTGCCCCG CGAGG		
			AC CCACGGGCG GCTCC		
			C C		
GAM809	MBD3	3'	GCCTGGGCCCCAGCGAGCCCCCA 10021	A T C	CGA _
			TG GG GC CGC GGGTCT GGC		

AC CC CG GCG CCCGGG CCG
 C _ A A__ T
 GAM809 SPI1 5' GCCCCTGACGGGCACCCCA 9091 A C A
 TG GGTGCCCG CG GGGT
 || ||||| || ||||
 AC CCACGGGC GT CCCG
 C A C
 GAM809 FLJ13841 5' CCAGACCCTCAGCACGCA 24016 CC C
 TGC GC GAGGGTCTGG
 ||| || |||||
 ACG CG CTCCCAGACC
 CA A
 GAM809 FLJ20200 5' CCAGACCCCGGGGACCCA 19287 A G CCGA
 TG GGT CCCG GGGTCTGG
 || ||| ||| |||||
 AC CCA GGGC CCCAGACC
 _ G C__
 GAM809 GMPPB 5' GCCAGGCGGGCTGCAGGCACCT 22499 C CGAGG
 CA TGAGGTGCC GC GTCTGGC
 ||||| || |||||
 ACTCCACGG CG CGGACCG
 A TCGGG
 GAM809 GMPPB 5' GCCAGGCGGGCTGCAGGCACCT 14981 C CGAGG
 CA TGAGGTGCC GC GTCTGGC
 ||||| || |||||
 ACTCCACGG CG CGGACCG
 A TCGGG
 GAM809 MGC4796 3' ACCCCGAGGGGCACCTCA 30825 GC A
 TGAGGTGCCC CG GGGT
 ||||| || ||||
 ACTCCACGGG GC CCA
 A _ _
 GAM809 PPP1R3B 3' GCCAAGGCGGGCAGCTCA 23859 G GAG
 TGAG TGCCCGCC GGT
 ||| ||||| |||
 ACTC ACGGGCGG CCG
 G AA_
 GAM809 RBT1 3' TCCTCGGCAGGACCCCA 15012 A G C
 TG GGT CC GCCGAGGG
 || ||| || |||||
 AC CCA GG CGGCTCCT
 C _ A
 GAM809 TREX1 5' CCACGACCAGCTGGCACCTCA 27335 C CGAG _
 TGAGGTGCC GC GGTC TGG
 ||||| || ||| |||
 ACTCCACGG CG CCAG ACC
 T A__ C
 GAM809 TREX1 5' CCACGACCAGCTGGCACCTCA 27344 C CGAG _
 TGAGGTGCC GC GGTC TGG
 ||||| || ||| |||

			ACTCCACGG CG CCAG ACC		
			T A__ C		
GAM809	USP24	3'	CATCCCAGCGGGCATCTCA 43815	CGA	TCTG
			TGAGGTGCCCCG GGG G		
			ACTCTACGGGCG CCC C		
			A__ TA__		
GAM809	LOC124446	5'	CCAGCGGCGGCGGACCCTCA 36749	TGC	AGG T
			TGAGG CCGCCG G CTGG		
			ACTCC GGCGGC C GACC		
			CA_ GG_		
GAM809	LOC165229	5'	GCCACAGCCACAAGCACCTCA 40123	CCGCCGAG	C_
			TGAGGTGC GGT TGGC		
			ACTCCACG CCG ACCG		
			AACA__ AC		
GAM809	LOC165288	5'	GCCCTCCGGCGGACCCTCA 40129	TGC	_
			TGAGG CCGCCG AGGGT		
			ACTCC GGCGGC TCCCG		
			CA_ C		
GAM809	LOC203871	5'	CCCCCTTCAGCAGGCACCTC 43079	C C	TCT
			GAGGTGCC GC GAGGG GG		
			CTCCACGG CG CTTCC CC		
			A A C__		
GAM809	LOC253128	5'	CTAGCTCGGCGGTCACCCCA 45486	A C	GGT
			TG GGTG CCGCCGAG CTGG		
			AC CCAC GGCGGCTC GATC		
			C T _		
GAM809	LOC255714	5'	CCAAACCCCAAGGCCCTCA 46140	T	CGCCGA C
			TGAGG GCC GGGT TGG		
			ACTCC CGG CCCA ACC		
			_ AAC_ A		
GAM809	LOC51308	3'	CCAAACTCTGGCACCTCA 18708	CGCCG	C
			TGAGGTGCC AGGGT TGG		
			ACTCCACGG TCTCA ACC		
			_ A		
GAM809	LOC90170	5'	GCCAGACCCCTGACACGCCC 30910	T	CCGC A
			GG GC CG GGGTCTGGC		
			CC CG GT CCCAGACCG		
			_ CACA C		
GAM810	AQP9	3'	TAATAGATGTTACTTTTGA 21969	T	
			TCAA AGTAACATCTGTTG		

			AGTT TCATTGTAGATAAT		
			T		
GAM810	CED-6	3'	CAACAAACATGTTACTATT 18430	C__	
			AATAGTAACAT TGTTG		
			TTATCATTGTA ACAAC		
			CAA		
GAM810	EPLIN	3'	TAATACAACAGAGCACTTTTTG 18496	T_ AACA	
	A		TCAA AGT TCTGTTGTATTA		
			AGTT TCA AGACAACATAAT		
			TT CG__		
GAM810	FLJ11827	3'	TAATATTGCAAGATGTTACCAT 24725	A _ T	
	TGG		TCAAT GTAACATCT GT GTATTA		
			GGTTA CATTGTAGA CG TATAAT		
			C A T		
GAM810	KIAA0820	3'	TAATACAACAGATAGCTTTGA 34220	T AAC	
			TCAA AGT ATCTGTTGTATTA		
			AGTT TCG TAGACAACATAAT		
			_ A__		
GAM810	LOC116228	3'	ACTGCAGAATTACTATT 36532	CA T	
			AATAGTAA TCTGT GT		
			TTATCATT AGACG CA		
			A_ T		
GAM810	LOC120856	3'	TAAGTATGTAACCATGA 36641	A A T	
			TCAAT GT ACATC GTTG		
			AGTTA CA TGTA CAAT		
			C A T		
GAM810	LOC149711	3'	AATATTGAATGATGTTACTTTG 41068	T TGTT_	
	A		TCAA AGTAACATC GTATT		
			AGTT TCATTGTAG TATAA		
			_ TAAGT		
GAM810	LOC163782	5'	CAACGGATGCCACTATTGG 39964	AA	
			TCAATAGT CATCTGTTG		
			GGTTATCA GTAGGCAAC		
			CC		
GAM810	LOC199675	3'	CAGCAGATGTCACTCTGA 42586	AT A	
			TCA AGT ACATCTGTTG		
			AGT TCA TGTAACGAC		
			C_ C		
GAM810	LOC253613	3'	CAGCAGAGTTACCACTGA 46012	ATA A	
			TCA GTAAC TCTGTTG		

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AGT CATTG AGACGAC
CAC _
GAM811 FOXD2 5' AGAATATGGCTACACTTATACA 10786 TAAT__ A
TCA TGATGTATA GC TGTGTTCT
||||||| || |||||||
ACTACATAT CG GTATAAGA
TCACAT _
GAM811 LUM 3' AGAACACACACATATACA 8144 TAA CA
TGTATA TG TGTGTTCT
||||| || |||||||
ACATAT AC ACACAAGA
__ AC
GAM811 UBE2H 3' AACACATGCAGAGTCACATC 9351 ATATAA
GATGT TGCATGTGTT
||||| |||||||||
CTACA ACGTACACAA
CTGAG_
GAM811 C6orf37 3' ACACACCAATATACATCA 33507 AA CA
TGATGTATAT TG TGTGT
||||||| || |||||
ACTACATATA AC ACACA
__ C_
GAM811 C6orf5 3' AGAACACATACACATATCCAT 17778 T AA C
ATG ATAT TG ATGTGTTCT
||| |||| || |||||||
TAC TATA AC TACACAAGA
C C_ A
GAM811 DREV1 3' AACACATACATTTATGCA 18105 T C
TGTATA AATG ATGTGTT
||||| |||| |||||||
ACGTAT TTAC TACACAA
_ A
GAM811 FLJ12716 3' AGAACACATACACAACAACAT 22457 ATATAA C
ATGT TG ATGTGTTCT
|||| || |||||||
TACA AC TACACAAGA
ACAAC_ A
GAM811 FLJ13920 3' GATATTCATATTATATACATCA 23780 CAT
TGATGTATATAATG GTGTT
||||||||| |||||
ACTACATATATTAT TATAG
ACT
GAM811 FLJ23071 3' GAACACATTTAAACATCA 24845 ATA TGC
TGATGT TAA ATGTGTTT
||||| ||| |||||||
ACTACA ATT TACACAAG
A__ __
GAM811 FLJ23119 3' ACATGCATTACACACATGCA 23948 _ ATA
TG ATGT TAATGCATGT
|| |||| |||||||

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			AC TACA ATTACGTACA		
			G CAC		
GAM811	KIAA1500	3'	GACACATCACATGCATCA 32067	ATAA C T	
			TGATGTAT TG ATGTGT C		
			ACTACGTA AC TACACA G		
			C___ _ C		
GAM811	KIAA1615	3'	ACACACACTATATACAT 34079	A CA	
			ATGTATATA TG TGTGT		
			TACATATAT AC ACACA		
			C _		
GAM811	SURB7	3'	AGAACATACTTCCACTACATCA 10464	TATAATGCA	
			TGATGTA TGTGTTCT		
			ACTACAT ATACAAGA		
			CACCTTC_		
GAM811	LOC122792	3'	AACACATGCGCGGCACACA 29761	A ATATAA	
			TG TGT TGCATGTGTT		
			AC ACA GCGTACACAA		
			_ CGCGC_		
GAM811	LOC127435	3'	GACACATGCACACACATCA 37462	ATATAA	
			TGATGT TGCATGTGTT		
			ACTACA ACGTACACAG		
			CAC_		
GAM812	DBY	3'	TGGTTATTTCTGTCAGTGA 11030	_ CTTC	
			TCACTGATA AAAT AACCA		
			AGTGA CTGT TTTA TTGGT		
			C _		
GAM812	LAMC1	3'	TGGCTGAAGATTTTCTAGT 8080	AT A	
			ACTG AAAATCTTCA CCA		
			TGAT TTTTAGAAGT GGT		
			CT C		
GAM812	KIAA1941	3'	TGGCTGAAGATTGACTTAGAGA 36953	A TAA A	
			TC CTGA AATCTTCA CCA		
			AG GATT TTAGAAGT GGT		
			A CAG C		
GAM812	RAB39	3'	TTGAAAAGATTTTATCAGGA 37648	A _	
			TC CTGATAAAATCT TCAA		
			AG GACTATTTTAGA AGTT		
			_ AA		
GAM812	SMARCF1	3'	TTGAGATTTTTCAGTGA 12627	T T	
			TCACTGA AAAATCT CAA		

			AGTGACT TTTTAGA GTT		
			T _		
GAM812	SMARCF1	3'	TTGAGATTTTTCAGTGA 20525	T	T
			TCACTGA AAAATCT CAA		
			AGTGACT TTTTAGA GTT		
			T _		
GAM812	SMARCF1	3'	TTGAGATTTTTCAGTGA 29165	T	T
			TCACTGA AAAATCT CAA		
			AGTGACT TTTTAGA GTT		
			T _		
GAM812	SNRPD1	3'	GTTGAAGATTTATGGACAG 13822	A_ _	
			CTG TA AAATCTTCAAC		
			GAC GT TTTAGAAGTTG		
			AG A		
GAM812	TUSP	5'	CGTGGCTCTGTTTTGTCAG 21526		CTTCAA
			CTGATAAAAT CCACG		
			GACTGTTTTG GGTGC		
			TCTC_		
GAM812	LOC149420	3'	TGGAAAGATTTTACCTGTGA 38749	TGA	CAA
			TCAC TAAAATCTT CCA		
			AGTG ATTTTAGAA GGT		
			TCC A_		
GAM812	LOC90786	3'	GGGAAGTTTATCAGT 32014	T	AA
			ACTGATAAAA CTTC CC		
			TGACTATTTT GAAG GG		
			_ _		
GAM812	LOC91661	3'	CGTGGTTGAGAAGCATCAG 28751	AAAA	T
			CTGAT TCT CAACCACG		
			GACTA AGA GTTGGTGC		
			CGA_ _		
GAM813	BAZ2B	5'	AATGGAAGTAATACATCA 15123		GTTCCCTT
			TGATGTA TTTCCATT		
			ACTACAT GAAGGTAA		
			AAT_		
GAM813	CREBL2	3'	GGGAAGAACTACATTA 6994		CCTT
			TGATGTAGTTC TTTCC		
			ATTACATCAAG AAGGG		
			_		
GAM813	FLRT2	3'	AAATGGAAAAAGATACTCACA 14873	A _ _	CC
	CA		TG TGT AGT TC TTTTCCATTT		

			AC ACA TCA AG AAAAAAGGTAAA		
			_ C T A _		
GAM813	CCR6	3'	AATGGAAGCCAACACATCA 10574	A	CCCTT
			TGATGT GTT TTTCCATT		
			ACTACA CAA GAAGGTAA		
			_ CC _		
GAM813	CCR6	3'	AATGGAAGCCAACACATCA 25366	A	CCCTT
			TGATGT GTT TTTCCATT		
			ACTACA CAA GAAGGTAA		
			_ CC _		
GAM813	FLJ22332	5'	GAAAAAGAAAACATCA 24062		CC
			TGATGTAGTT CTTTTTC		
			ACTACATCAA GAAAAAG		
			AA		
GAM813	HSPCAL3	3'	GAAAAAGAACAACATCA 37619	A	CC
			TGATGT GTTC TTTTTC		
			ACTACA CAAG AAAAAAG		
			A _		
GAM813	KIAA1529	5'	TGGAAAGCTACATCA 34950		TCCCTT
			TGATGTAGT TTTCCA		
			ACTACATCG AAAGGT		

GAM813	PMAIP1	3'	GGAAGATGGAATACATCA 22101	G	CT
			TGATGTA TTCC TTTTCC		
			ACTACAT AAGG AGAAGG		
			_ T _		
GAM813	LOC162333	5'	AAATGGAAAAAGATGAAGAATC 42118		GTAG CC
	A		TGAT TT CTTTTTCCATTT		
			ACTA AG GAAAAAGGTAAA		
			AGA_ TA		
GAM813	LOC169270	3'	AAATGGGAGAAATCACATCA 40273	A	CCCT
			TGATGT GTT TTTTCCATTT		
			ACTACA TAA AGAGGGTAAA		
			C _		
GAM813	LOC220763	5'	GAAAAAGAACAACATCA 36302	A	CC
			TGATGT GTTC TTTTTC		
			ACTACA CAAG AAAAAAG		
			A _		
GAM813	LOC51277	3'	AAATGGAAGCAAACAACATCA 39022	A	CC TTT
			TGATGT GTT CT TCCATTT		

ACTACA CAA GA AGGTAAA
 A AC ____
 GAM814 FKBP1A 3' CCACCATTCCCACCCACCCTC 6473 T TTA AAA
 GAGG GT GT AATGGTGG
 ||| || || |||||
 CTCC CA CA TTACCACC
 _ CC_ CCC
 GAM814 FSTL3 3' CCACCATTCCCTGCCAGCCCA 12467 A GTT TAAA
 TG GGT TAG AATGGTGG
 || ||| || |||||
 AC CCG GTC TTACCACC
 _ ACC CC_
 GAM814 CGI-142 3' CACCATCATCAAACACTCA 18146 G A AAAA
 TGAG TGTTT GT ATGGTG
 ||| |||| || |||||
 ACTC ACAA TA TACCAC
 _ C C_
 GAM814 FLJ21777 3' CCACCATTCTCACTACAGGCC 25922 T _ AAA
 C GG GTT TAGT AATGGTGG
 || ||| |||| |||||
 CC CGG ATCA TTACCACC
 C AC CTC
 GAM814 IMP13 5' CCACCACTCCCTGGGCACCCA 16074 A TAAAAA
 TG GGTGTTTAG TGGTGG
 || ||||| |||||
 AC CCACGGGTC ACCACC
 _ CCTC_
 GAM814 KIAA1671 3' CCACCACCCCTTTGCACATCA 32692 G TT TAAAAA
 TGA GTGT AG TGGTGG
 ||| |||| || |||||
 ACT CACG TC ACCACC
 A TT CCC_
 GAM814 PPI5PIV 3' CACCACCTTGAACACCT 21274 TAAAAA
 AGGTGTTTAG TGGTG
 ||||| |||||
 TCCACAAGTT ACCAC
 CC_
 GAM814 STAT2 5' CACCATTTCGGACACCCCG 9958 A AGTAA
 TG GGTGTTT AAATGGTG
 || ||||| |||||
 GC CCACAGG TTTACCAC
 C C_
 GAM814 STAT2 5' CACCATTTCGGACACCCCG 45369 A AGTAA
 TG GGTGTTT AAATGGTG
 || ||||| |||||
 GC CCACAGG TTTACCAC
 C C_
 GAM814 TBX19 3' CCACCATTCTTCTGCACTCC 11623 A T T TA_
 CA TG GG GT TAG AAAATGGTGG
 || ||| || |||||

AC CC CA GTC TTTTACCACC
 _ T C TTC
 GAM814 LOC201685 5' TACCCTACTAAACACCCA 43388 A AAAAT
 TG GGTGTTTAGTA GGTG
 || ||||| |||
 AC CCACAAATCAT CCAT
 _ C____
 GAM815 KIAA0089 3' CCATTAAACCCACTTTGCTTGTC 34663 T TT TA_
 TCA TG GACA CGGA GGTTAATGG
 || ||| ||| |||||
 AC CTGT GTTT CCAATTACC
 T TC CAC
 GAM815 LOC197196 3' ATTTGTCTGAACATCACA 43200 CA
 TGTGA TTCGGATAGGT
 |||| |||||
 ACACT AAGTCTGTTTA
 AC
 GAM815 LOC200982 3' CCATTGTTACAACCCAAATGTC 43374 C ATAG ____
 AC GTGACATT GG GT TAATGG
 ||||| || || |||||
 CACTGTAA CC CA GTTACC
 A CAA_ TT
 GAM816 ARF4L 3' TGTCTGTGAAAGTGCCAAGA 34605 CC TAA C_
 TCT GT ACT CACAGACA
 ||| || ||| |||||
 AGA CG TGA GTGTCTGT
 AC ____ AA
 GAM816 CACNA1C 3' GTCTGCAGAGGCGGGGA 6381 TAAA CA
 TCTCCGT CTC CAGAC
 ||||| ||| |||||
 AGGGGCG GAG GTCTG
 ____ AC
 GAM816 PTGFRN 5' TGTCTGTGGCTGAAGGA 33366 G AACT
 TCC TTA CCACAGACA
 ||| ||| |||||
 AGG AGT GGTGTCTGT
 A C____
 GAM816 RAD52 3' GTCTGTGGAGGAGGCAAGA 28646 CC AAA
 TCT GTT CTCCACAGAC
 ||| ||| |||||
 AGA CGG GAGGTGTCTG
 A_ AG_
 GAM816 RAD52 3' GTCTGTGGAGGAGGCAAGA 28654 CC AAA
 TCT GTT CTCCACAGAC
 ||| ||| |||||
 AGA CGG GAGGTGTCTG
 A_ AG_
 GAM816 RAD52 3' GTCTGTGGAGGAGGCAAGA 28663 CC AAA
 TCT GTT CTCCACAGAC
 ||| ||| |||||

			AGA CGG GAGGTGTCTG		
			A_ AG_		
GAM816	RBBP9	3'	TGTCTGTGAAGTCTGAGA 34746	CGTTAA C	
			TCTC ACT CACAGACA		
			AGAG TGA GTGTCTGT		
			TC___ A		
GAM816	SLC4A4	3'	TCTGTGGAGTACATTGAAGA 9839	C TTAA	
			TCT CG ACTCCACAGA		
			AGA GT TGAGGTGTCT		
			A TACA		
GAM816	SRRM1	3'	TGCCTGTGGAGTCTCTGCTGA 12452	C TAA_ A	
			TC GT ACTCCACAG CA		
			AG CG TGAGGTGTC GT		
			T TCTC C		
GAM816	TBL2	3'	GTCTGGCTGGCCAACGGGGA 26870	AAACT _	
			TCTCCGTT CCA CAGAC		
			AGGGGCAA GGT GTCTG		
			CC___ CG		
GAM816	TIMM17A	3'	TCTGTGGGAAATGGAGA 13035	AAAC	
			TCTCCGTT TCCACAGA		
			AGAGGTAA GGGTGTCT		
			A___		
GAM816	TNFRSF10B	3'	TGTCTGTGGAGTTTTAGGAG 9941	GTT	
			CTCC AAAC TCCACAGACA		
			GAGG TTTGAGGTGTCTGT		
			AT_		
GAM816	ZNF205	5'	TGTCTGCAGACGGCGGAGG 9514	AAAC CA	
			TCTCCGTT TC CAGACA		
			GGAGGCGG AG GTCTGT		
			C___ AC		
GAM816	ADG-90	5'	GTCTGTGGAAC TGAAGA 26935	C TAAAC	
			TCTC GT TCCACAGAC		
			AGAG CA AGGTGTCTG		
			T _		
GAM816	DKFZP434H132	3'	TGCCTGTGGAGTGCTGAG 17762	C TAA A	
			CTC GT ACTCCACAG CA		
			GAG CG TGAGGTGTC GT		
			T _ C		
GAM816	FLJ11155	3'	GTCTATCGGACAGCGGAGA 20349	AAAC AC_	
			TCTCCGTT TCC AGAC		

			AGAGGCGA AGG TCTG		
			C__ CTA		
GAM816	FLJ11259	3'	TGGAAGAGTTTGACAGAGA 20387	C	CA_
			TCTC GTTAAACTC CA		
			AGAG CAGTTTGAG GT		
			A AAG		
GAM816	FLJ20294	3'	TGCCTGCCGACCAGCGGAGA 19353	AAAC	CA A
			TCTCCGTT TC CAG CA		
			AGAGGCGA AG GTC GT		
			CC__ CC C		
GAM816	FLJ23604	3'	TGTCTGTGAAGTGCCTAAC 24662	A__	C
			GTTA ACT CACAGACA		
			CAAT TGA GTGTCTGT		
			CCG A		
GAM816	JAM1	3'	TGTCTGTGGAAAATGGGA 29323	T	AAAC
			TC CCGTT TCCACAGACA		
			AG GGTAAGGTTGTCTGT		
			_ A__		
GAM816	JAM1	3'	TGTCTGTGGAAAATGGGA 29332	T	AAAC
			TC CCGTT TCCACAGACA		
			AG GGTAAGGTTGTCTGT		
			_ A__		
GAM816	JAM1	3'	TGTCTGTGGAAAATGGGA 29353	T	AAAC
			TC CCGTT TCCACAGACA		
			AG GGTAAGGTTGTCTGT		
			_ A__		
GAM816	JAM1	3'	TGTCTGTGGAAAATGGGA 29343	T	AAAC
			TC CCGTT TCCACAGACA		
			AG GGTAAGGTTGTCTGT		
			_ A__		
GAM816	JAM1	3'	TGTCTGTGGAAAATGGGA 18865	T	AAAC
			TC CCGTT TCCACAGACA		
			AG GGTAAGGTTGTCTGT		
			_ A__		
GAM816	KIAA0319	3'	TCTGTGGAGGTACGGAG 16763	TAAA	
			CTCCGT CTCCACAGA		
			GAGGCA GAGGTGTCT		
			TG__		
GAM816	KIAA0339	3'	TGTCTGTGTGGCACAGAGA 35405	C	TAAA TC
			TCTC GT C CACAGACA		

AGAG CA G GTGTCTGT
 A C__ GT
 GAM816 KIAA0350 3' TGTCTGTGGGGCAGCAGA 30673 C AAA
 TC GTT CTCCACAGACA
 || ||| |||||
 AG CGA GGGGTGTCTGT
 A C__
 GAM816 KIAA1795 3' TGTCTGTGAAGCTTTTAAAC 35704 __ _ C
 GTT AAA CT CACAGACA
 ||| ||| || |||||
 CAA TTT GA GTGTCTGT
 AT C A
 GAM816 PEF 3' TCTGTGGAGAGTGGAG 14748 AAA
 CTCCGTT CTCCACAGA
 ||||| |||||
 GAGGTGA GAGGTGTCT

 GAM816 PRIC285 3' TGTCTGTGGAGTTCAGG 30806 GTTA
 CC AACTCCACAGACA
 || |||||
 GG TTGAGGTGTCTGT
 AC__
 GAM816 RGS20 3' TGTCTACATGGTTAATGGA 9803 ACT C__
 TCCGTAA CCA AGACA
 ||||| ||| ||||
 AGGTAATT GGT TCTGT
 __ ACA
 GAM816 LOC120114 3' TGTCTGTGGAATGAGAAGGGA 37216 G AAAC_
 TCC TT TCCACAGACA
 ||| || |||||
 AGG AA AGGTGTCTGT
 G GAGTA
 GAM816 LOC144817 5' TGTCTGTGAGGAGCAAGA 37789 CC AAA TC
 TCT GTT C CACAGACA
 ||| ||| | |||||
 AGA CGA G GTGTCTGT
 A_ __ GA
 GAM816 LOC151196 5' TCTGTGAAATCTGTAACAATGG 41318 AA_ TC____
 AGA TCTCCGTT AC CACAGA
 ||||| || |||||
 AGAGGTAA TG GTGTCT
 CAA TCTAAA
 GAM816 LOC196955 5' TGTCTGTGGAGCTAGCTGAG 37940 C AA
 CTC GTTA CTCCACAGACA
 ||| ||| |||||
 GAG CGAT GAGGTGTCTGT
 T C_
 GAM816 LOC200081 3' TGCCTGTGGAGGGACTGGAG 42706 TTAAA A
 CTCCG CTCCACAG CA
 |||| ||||| ||

			GAGGT GAGGTGTC GT		
			CAGG_ C		
GAM816	LOC200488	5'	TGTCTGCAGAAAGATGGAGA 43316	AAAC	CA
			TCTCCGTT TC CAGACA		
			AGAGGTAG AG GTCTGT		
			AA_ AC		
GAM816	LOC58489	3'	TGTCTGGTTGGTTTAACAAAGA 35909	CC	CCA
			TCT GTTAAACT CAGACA		
			AGA CAATTTGG GTCTGT		
			AA TTG		
GAM816	LOC92609	3'	TCTGTGGAGAAGGGAAGAGA 36062	CG	AAA
			TCTC TT CTCCACAGA		
			AGAG GG GAGGTGTCT		
			AA GAA		
GAM817	AMFR	3'	CCCAGGTTCCATACCA 29064	T	A
			TGGTATGGAA CCTG GG		
			ACCATACCTT GGAC CC		
			- -		
GAM817	CHGA	5'	TAGGTGCCCCGGCCCCACACC 6939	A	AATC A
			GGT TGG CTG GGCACCTA		
			CCA ACC GGC CCGTGGAT		
			C CC_ _		
GAM817	F3	3'	AGGTGCGCACTACCACACCA 33297	A	AATCC AG
			TGGT TGG TG GCACCT		
			ACCA ACC AC CGTGGA		
			C ATC_ G_		
GAM817	JPH3	3'	AGATGCCTCAGTGCTACACCA 21825	A	AATC C
			TGGT TGG CTGAGGCA CT		
			ACCA ATC GACTCCGT GA		
			C GT_ A		
GAM817	ZNF192	3'	GTACTATTATTCCATACTA 12988	CC	AG
			TGGTATGGAAT TG GC		
			ATCATACCTTA AT TG		
			TT CA		
GAM817	C1orf17	3'	CCCAGGCATCCCATACCA 33852	A _	A
			TGGTATGG AT CCTG GG		
			ACCATACC TA GGAC CC		
			C C _		
GAM817	ELOVL1	3'	GTGCCTCAGGACTGCACC 23099	AT	AA
			GGT GG TCCTGAGGCAC		

CCA TC AGGACTCCGTG
 CG ____
 GAM817 FLJ10842 3' AGGTGCCTCAGCCATCCCA 20187 T AATC
 TGG ATGG CTGAGGCACCT
 ||| ||| |||||
 ACC TACC GACTCCGTGGA
 C ____
 GAM817 FLJ22969 3' TAGGTGCCCTGCATTCCACCCA 34067 TA CCTGA
 TGG TGAAT GGCACCTA
 ||| ||||| |||||
 ACC ACCTTA CCGTGGAT
 C_ CGTC_
 GAM817 FLJ23519 3' AGGCGCCCGTCACCACACCA 25971 A AATCC A A
 TGGT TGG TG GGC CCT
 |||| ||| || ||| |||
 ACCA ACC GC CCG GGA
 C ACT__ _ C
 GAM817 KIAA0876 3' AGGTGCCTCTCCCTCACCA 32294 AT AATCCT
 TGGT GG GAGGCACCT
 |||| || |||||
 ACCA CC CTCCGTGGA
 CT CT____
 GAM817 KIAA0961 3' AGGCGCCCGCCACCACACCA 17071 A AATCC A A
 TGGT TGG TG GGC CCT
 |||| ||| || ||| |||
 ACCA ACC GC CCG GGA
 C ACC__ _ C
 GAM817 KIAA1265 3' TAGGTGCCCTGTTCTCCTACCA 35034 T ATCCTGA
 TGGTA GGA GGCACCTA
 |||| ||| |||||
 ACCAT CCT CCGTGGAT
 _ CTTGTC_
 GAM817 KIAA1678 3' GTGAACAGGTTCCCATACCA 35788 AAT AGG
 TGGTATGG CCTG CAC
 ||||| ||| |||
 ACCATACC GGAC GTG
 CTT AA_
 GAM817 RAB17 5' GTGCAACAAAGATTCCATAC 22787 C_ AG
 GTATGGAATC TG GCAC
 ||||| || |||
 CATACCTTAG AC CGTG
 AA AA
 GAM817 SLC6A14 3' AGGTGCCCCGCCACCACACCA 14100 A AATCC A
 TGGT TGG TG GGCACCT
 |||| ||| || |||||
 ACCA ACC GC CCGTGGA
 C ACC__ _
 GAM817 LOC146229 3' AGGCACCCACCATCCCATCCA 38104 T A CC A CA
 TGG ATGG AT TG GG CCT
 ||| |||| || || |||

		ACC TACC TA AC CC GGA		
		_ C CC _ AC		
GAM817	LOC146229 3'	AGGCGCCCACCTCCACACC	38105	A ATCC A A
		GGT TGA TG GGC CCT		
		CCA ACCT AC CCG GGA		
		C CC_ _ C		
GAM817	LOC147429 3'	CAGGAAAAATTTCATACCA	38337	_____
		TGGTATGGAA TCCTG		
		ACCATACTTT AGGAC		
		AAAA		
GAM817	LOC164395 5'	TAGGTGCCCCAAGAAATTAC	40145	TGGAA C A
		GTA TC TG GGCACCTA		
		CAT AG AC CCGTGGAT		
		TAA_ A C		
GAM817	LOC196337 5'	CCTGCAGGATTCCATCCA	42358	T _
		TGG ATGGAATCCTG AGG		
		ACC TACCTTAGGAC TCC		
		_ G		
GAM817	LOC200197 3'	AGGTGCCTTCTCCACCCA	42730	TA ATCCT
		TGG TGA GAGGCACCT		
		ACC ACCT TTCCGTGGA		
		C_ C_		
GAM817	LOC200681 5'	TGCCTCCATCTCCATACCA	43341	ATCCT
		TGGTATGGA GAGGCA		
		ACCATACCT CTCCGT		
		CTAC_		
GAM817	LOC51301 3'	AGGTGTCCAAAATTCCATAC	18670	CC A
		GTATGGAAT TG GGCACCT		
		CATACCTTA AC CTGTGGA		
		AA _		
GAM818	APXL 3'	AGAAAACAAACAGCCCAAGTGA	7353	CGT ATTC_
		TCAC TTGGGT GTTTTCT		
		AGTG AACCCG CAAAAGA		
		_ ACAA		
GAM818	LOC150142 5'	AGAAAACGAATACAGGCAAC	38849	TGG_
		GTT GTATTCGTTTTCT		
		CAA CATAAGCAAAAGA		
		CGGA		
GAM818	LOC202316 3'	AGAAAACGAAACAAAC	43424	GGTA
		GTTTG TTCGTTTTCT		

			CAAAC AAGCAAAAGA	
			A____	
GAM818	LOC90190	3'	AGAAAAATCTTTACCCAAAT 30945	TTCG_
			GTTTGGGTA TTTTCT	
			TAAACCCAT AAAAGA	
			TTCTA	
GAM819	DMD	3'	TTTGGAGAGTGGGCTGACAT 5575	C T G G
			ATG CA GC TA TCTCCAAA	
			TAC GT CG GT AGAGGTTT	
			A _ G G	
GAM819	DMD	3'	TTTGGAGAGTGGGCTGACAT 10158	C T G G
			ATG CA GC TA TCTCCAAA	
			TAC GT CG GT AGAGGTTT	
			A _ G G	
GAM819	DMD	3'	TTTGGAGAGTGGGCTGACAT 10165	C T G G
			ATG CA GC TA TCTCCAAA	
			TAC GT CG GT AGAGGTTT	
			A _ G G	
GAM819	DMD	3'	TTTGGAGAGTGGGCTGACAT 10189	C T G G
			ATG CA GC TA TCTCCAAA	
			TAC GT CG GT AGAGGTTT	
			A _ G G	
GAM819	DMD	3'	TTTGGAGAGTGGGCTGACAT 10206	C T G G
			ATG CA GC TA TCTCCAAA	
			TAC GT CG GT AGAGGTTT	
			A _ G G	
GAM819	DMD	3'	TTTGGAGAGTGGGCTGACAT 10179	C T G G
			ATG CA GC TA TCTCCAAA	
			TAC GT CG GT AGAGGTTT	
			A _ G G	
GAM819	DMD	3'	TTTGGAGAGTGGGCTGACAT 10216	C T G G
			ATG CA GC TA TCTCCAAA	
			TAC GT CG GT AGAGGTTT	
			A _ G G	
GAM819	DMD	3'	TTTGGAGAGTGGGCTGACAT 10240	C T G G
			ATG CA GC TA TCTCCAAA	
			TAC GT CG GT AGAGGTTT	
			A _ G G	
GAM819	DMD	3'	TTTGGAGAGTGGGCTGACAT 10228	C T G G
			ATG CA GC TA TCTCCAAA	

			TAC GT CG GT AGAGGTTT	
			A _ G G	
GAM819	DMD	3'	TTTGGAGAGTGGGCTGACAT 10171	C T G G
			ATG CA GC TA TCTCCAAA	
			TAC GT CG GT AGAGGTTT	
			A _ G G	
GAM819	DMD	3'	TTTGGAGAGTGGGCTGACAT 10184	C T G G
			ATG CA GC TA TCTCCAAA	
			TAC GT CG GT AGAGGTTT	
			A _ G G	
GAM819	DMD	3'	TTTGGAGAGTGGGCTGACAT 10211	C T G G
			ATG CA GC TA TCTCCAAA	
			TAC GT CG GT AGAGGTTT	
			A _ G G	
GAM819	DMD	3'	TTTGGAGAGTGGGCTGACAT 10201	C T G G
			ATG CA GC TA TCTCCAAA	
			TAC GT CG GT AGAGGTTT	
			A _ G G	
GAM819	IL16	3'	TTGGAAGTTGCATGGCAT 10842	TA TC
			ATGCCATGCG G TCCAA	
			TACGGTACGT T AGGTT	
			_ GA	
GAM819	SSH2	3'	TTTGGAGACACCCAGG 31189	A C A
			CC TG GT GTCTCCAAA	
			GG AC CA CAGAGGTTT	
			_ C _	
GAM819	LOC123036	3'	TTTGGAGAGGCAGATGACATTA 36719	C GC AG
			TAATG CAT GT TCTCCAAA	
			ATTAC GTA CG AGAGGTTT	
			A GA G_	
GAM820	KLHL3	3'	ACCAAAGCCAATCTGCTCTAG 42265	A A TCA
			TTA AGCA AT TGGCTTTGGT	
			GAT TCGT TA ACCGAAACCA	
			C C _	
GAM820	PCDH11X	3'	ACCAAAAAATTGCAATTTGTTT 26801	_ TGGC
			AAGCAAATT CA TTTGGT	
			TTTGTTTAA GT AAACCA	
			C TAAA	
GAM820	PCDH11X	3'	ACCAAAAAATTGCAATTTGTTT 26786	_ TGGC
			AAGCAAATT CA TTTGGT	

			TTTGTTTAA GT AAACCA		
			C TAAA		
GAM820	PCDH11Y	3'	ACCAAAAAATTGCAATTTGTTT 26820	_	TGGC
			AAGCAAATT CA TTTGGT		
			TTTGTTTAA GT AAACCA		
			C TAAA		
GAM820	FLJ12476	3'	ACCAAAACCATTATTGTTTTAA 23067	ATTC	C
			TTAAAGCAA ATGG TTTGGT		
			AATTTTGTT TACC AAACCA		
			AT__ A		
GAM821	DGUOK	3'	ACCAAAATTGGGCCTGCACT 28133	T A	A
			AGTGCA GT TCAATTTT GT		
			TCACGT CG GGTTAAAA CA		
			C _ C		
GAM821	DLEC1	3'	ACTAAGTAAATTCATGCACTTT 14263	TATCAAT	
	T		AAAAGTGCATG TTTAGT		
			TTTTCACGTAC GAATCA		
			TTAAAT_		
GAM821	DLEC1	3'	ACTAAGTAAATTCATGCACTTT 14269	TATCAAT	
	T		AAAAGTGCATG TTTAGT		
			TTTTCACGTAC GAATCA		
			TTAAAT_		
GAM821	MYO1B	3'	ACTTCTTAGGAGACATGCACTT 14522	A AATTTT	
	TT		AAAAGTGCATGT TC AGT		
			TTTTCACGTACA AG TCA		
			G GATTCT		
GAM821	NPTX1	3'	ACTGAATAATACATGCCT 8352	T CAAT	
			AG GCATGTAT TTTAGT		
			TC CGTACATA AAGTCA		
			_ AT__		
GAM821	SUFU	3'	ACTAAAATTGAAAAATCCAC 18249	C GTA	
			GTG AT TCAATTTTAGT		
			CAC TA AGTTAAAATCA		
			C AAA		
GAM821	CG012	3'	TTGATACCATGCACTTTT 40491	_	
			AAAAGTGCATG TATCAA		
			TTTTCACGTAC ATAGTT		
			C		
GAM821	FLJ20396	3'	ACTAAAATTAATACAGCTCT 19445	T A C	
			AG GC TGTAT AATTTTAGT		

			TC CG ACATA TTAAAATCA		
			T _ A		
GAM821	KIAA0276	3'	ACTGTAATGTTACATGCAC	35134	TCA T
			GTGCATGTA ATT TAGT		
			CACGTACAT TAA GTCA		
			TG_ T		
GAM822	MAF	5'	TAGCTGTAGCTCGGGCTGCTT	11838	G A _ _
			AAGCAGCC CGA CT C GTTA		
			TTCGTCGG GCT GA G CGAT		
			_ C T T		
GAM822	GRIN3A	5'	CGAGGAACTCCGGCTGCTT	28532	C A _ _
			AAGCAGCCG GA CTCG		
			TTCGTCGGC CT GAGC		
			_ CAAG		
GAM822	KIAA1879	5'	ACAGTGCTGCGGCTGCTT	36408	A_ C
			AAGCAGCCGCG ACT GT		
			TTCGTCGGCGT TGA CA		
			CG _		
GAM823	NFIA	3'	CATGGAAACAGCAAGCA	34839	A C A
			TG CT GCT TTTCCATG		
			AC GA CGA AAAGGTAC		
			_ A C		
GAM823	DKFZP434A043	3'	CATGGAACTTGTGCTCAAAC	17700	CT TA_
			GTTTGA CGC TTTCCATG		
			CAAAC GTG AAAGGTAC		
			C_ TTC		
GAM823	LOC201799	3'	CATGGAAAAGACACCAAAC	42912	ACTCG A
			GTTTG CT TTTCCATG		
			CAAAC GA AAAGGTAC		
			CACA_ _		
GAM824	COCH	3'	AATAAAAGAATCTGATA	10290	T
			TATCA GATTCTTTTGTT		
			ATAGT CTAAGAAAATAA		
			_		
GAM824	FRK	3'	TAGCAAAACAAATTCA	7786	TTCT
			TGA TTTGTTTTGCTA		
			ACT AAACAAAACGAT		
			T_ _		
GAM824	SQSTM1	3'	AGCAAAACAAGTGACATGA	9987	AT T
			TCATG TC TTTGTTTTGCT		

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AGTAC AG GAACAAAACGA
  _ T
GAM824 TTN 3' AGCAAAAAGTAAAGAACA 28501 A TG_
      TG TTCTTT TTTTGCT
      || ||||| |||||
      AC AAGAAA AAAACGA
      _ TGA
GAM824 TTN 3' AGCAAAAAGTAAAGAACA 28506 A TG_
      TG TTCTTT TTTTGCT
      || ||||| |||||
      AC AAGAAA AAAACGA
      _ TGA
GAM824 TTN 3' AGCAAAAAGTAAAGAACA 28516 A TG_
      TG TTCTTT TTTTGCT
      || ||||| |||||
      AC AAGAAA AAAACGA
      _ TGA
GAM824 ZNF202 3' AACAAATTACAGAATCATGAT 9506 T___
      ATCATGATTCT TTGTT
      ||||| |||||
      TAGTACTAAGA AACAA
      CATT
GAM824 DKFZP434O047 5' AGCAAACAAAATCATG 17861 CTT T
      CATGATT TTGTTT GCT
      ||||| ||||| |||
      GTACTAA AACAAA CGA
      _ _
GAM824 EVI5 3' GGTGTTAAAAGAATCATGGTA 12212 TTTT
      TATCATGATTCTTTTG GCT
      ||||| ||||| |||
      ATGGTACTAAGAAAAT TGG
      TG_
GAM824 FENS-1 3' TAGCGGGGACAAAAAATCA 21895 C _
      TGATT TTTTGTTTT GCTA
      |||| ||||| |||||
      ACTAA AAAACAGGG CGAT
      _ G
GAM824 KIAA1432 5' AGCAAAACAGTATCCTGA 33146 T TCTT
      TCA GAT TTGTTTTGCT
      ||| ||| ||||| |||||
      AGT CTA GACAAAACGA
      C T_
GAM824 STAG2 3' AGCTAAAAAGATCATGATA 34927 T GTTTT
      TATCATGAT CTTTT GCT
      ||||| ||||| |||
      ATAGTACTA GAAAA CGA
      _ AT_
GAM824 LOC255654 5' AGCAAACAAAATCATG 46301 CTT T
      CATGATT TTGTTT GCT
      ||||| ||||| |||

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GTACTAA AACAAA CGA

GAM825 ITGA6 3' CCATCACGTTAGCTGT 5702 TTTT
GCA CTAACGTGATGG
||| |||||
TGT GATTGCACTACC
C__

GAM825 MAPK3 3' CCAGACTGTTAGAAAATGGA 36322 G TGA
TC CATTCTTAACG TGG
|| ||||| |||
AG GTAAAAGATTGT ACC

GAM825 FLJ12903 3' GTTAAGTAAAGATGGA 22982 ACG
TCGCATTTTCTA TGAT
||||||| |||
AGTGTAAGAT ATTG

GAM825 UCH37 3' CCATATGAAGCTAGAAAATGC 18080 A__ A
GCATTTTCTA CGTG TGG
||||||| ||| |||
CGTAAAGAT GTAT ACC

GAM825 LOC132321 3' CCATCCATAGGAAAATGGATA 37026 G AACGT
TATC CATTCTTCT GATGG
||| ||||| |||||
ATAG GTAAAAGG CTACC

GAM825 LOC222066 3' CCAACATTTAAAAGATGCGA 44554 CTAAC A
TCGCATTTT GTG TGG
||||||| ||| |||
AGCGTAGAA TAC ACC
AAATT A

GAM826 DHFR 5' CAGTCCCAGACAGAACCTA 6447 T TAT A
TGGGTTCT G TCTG GACTG
||||||| | ||| |||||
ATCCAAGA C AGAC CTGAC
__ C

GAM826 HSPA1B 5' CAGTCTCAGAGCGGAGCCCA 11819 T AT
TGGGTTCT GT TCTGAGACTG
||||||| || |||||
ACCCGAGG CG AGACTCTGAC

GAM826 PIK3R1 3' TCAAAAAACAAAACCCA 34040 C A C
TGGGTT TTGT TT TGA
||||| ||| || |||
ACCCAA AACA AA ACT
A A A

GAM826 ZNF80 5' CAGTGAGACCAAGAACCCA 13986 TA TGAG
TGGGTTCTTG TTC ACTG
||||||| ||| |||||

			ACCCAAGAAC GAG TGAC		
			CA ____		
GAM826	KIAA0562	3'	TCAGCCCCAGGTAGCAGAACTC 16244	T AT	AGA
	A		TGGGTTCT GT TCTG CTGA		
			ACTCAAGA CG GGAC GACT		
			_ AT CCC		
GAM826	KIAA1219	3'	TCATTGATGAATACAAGTACCC 30761	T	TGA C
	A		TGGGT CTTGTATTC GA TGA		
			ACCCA GAACATAAG TT ACT		
			T TAG _		
GAM826	ORCTL3	3'	CAATCCCAGACTGGGAACC 10443	TAT	A C
			GGTTCTTG TCTG GA TG		
			CCAAGGGT AGAC CT AC		
			C__ C A		
GAM826	SDC3	5'	CAGCCTCAACTCTGAGAAGCCC 16079	_ GTATTC	A
	A		TGGGTT CTT TGAG CTG		
			ACCCGA GAG ACTC GAC		
			A TCTCA_ C		
GAM826	LOC115219	5'	CAGTCCCAGAACACCGCCTA 36276	TCTT A	A
			TGGGT GT TTCTG GACTG		
			ATCCG CA AAGAC CTGAC		
			C__ C C		
GAM826	LOC223073	5'	TCAATCTCAGGGATAATACCCA 45317	TC A	C
			TGGGT TTGT TTCTGAGA TGA		
			ACCCA AATA GGGACTCT ACT		
			T_ _ A		
GAM827	ATP6V1A1	3'	TTTCTGACCAATAGTG 7412	TGCTA	
			CACTGTTG TCAGAAA		
			GTGATAAC AGTCTTT		
			C__		
GAM827	DYRK1A	5'	TTTTCTTCACACAGTGTT 28192	T CTATC	
			AACACTGT GTG AGAAAA		
			TTGTGACA CAC TCTTTT		
			_ T__		
GAM827	ENTPD6	3'	TTTTCTGGACACCAACTGTGT 6920	T _ CTA	
			ACAC GTTG TG TCAGAAAA		
			TGTG CAAC AC GGTCTTTT		
			T C A__		
GAM827	FLRT1	3'	TTTTGTAGAACACAACAGTG 29992	_ T	
			CACTGTTGTG CTA CAGAA		

			GTGACAACAC GAT GTTTT	
			AA _	
GAM827	GPM6A	3'	TTTTTCTGATATATGCAGT 11782	TGTGC
			ACTGT TATCAGAAAAA	
			TGACG ATAGTCTTTT	
			TAT__	
GAM827	ITGA2	3'	TTTtaggAGGCACAACAGT 7963	A AG
			ACTGTTGTGCT TC AAAA	
			TGACAACACGG AG TTTT	
			_ GA	
GAM827	MEOX2	3'	CTGATTGACAACAGTGTT 12551	GCT
			AACACTGTTGT ATCAG	
			TTGTGACAACA TAGTC	
			GT_	
GAM827	NCALD	3'	TTTTCTGAGCAGATCAATA 25749	TG A_
			TGTTG CT TCAGAAAA	
			ATAAC GA AGTCTTTT	
			TA CG	
GAM827	NEURL	3'	CTTTTGCAAACAGTGT 10412	G TC
			ACACTGTT TGCTA AG	
			TGTGACAA ACGGT TC	
			_ TT	
GAM827	PIK3R3	3'	TTTCATCACAGAACAGTGTT 30610	G CTATCA
			AACACTGTT TG GAAA	
			TTGTGACAA AC CTTT	
			G ACTA__	
GAM827	RAB3B	3'	TTCTCAAAGCACAACGTG 8772	T ATC
			CAC GTTGTGCT AGAA	
			GTG CAACACGA TCTT	
			_ AAC	
GAM827	RNF14	3'	TTTCTTTGCAACAGCAGTGTT 10506	_ TATC
			AACACTGTTGT GC AGAAA	
			TTGTGACGACA CG TCTTT	
			A TT__	
GAM827	SLC22A5	3'	TTCTCTAAGTGCCAAAAACAGT 9029	____ TG ATC
	GT		ACACTGTT G CT AGAA	
			TGTGACAA C GA TCTT	
			AAAC GT ATC	
GAM827	STX7	3'	TTTTTCTGGTTCACAACAG 9625	CT
			CTGTTGTG ATCAGAAAAA	

GACAACAC TGGTCTTTTT
 T_
 GAM827 SURF6 3' CTGAGAGACAGACACAACAGT 13610 _____ A
 ACTGTTGTG CT TCAG
 ||||| ||||
 TGACAACAC GA AGTC
 AGACA G
 GAM827 ARHGEF9 5' CTGGAACACTACAGTGTT 17539 T CTA
 AACACTGT GTG TCAG
 ||||| || ||||
 TTGTGACA CAC GGTC
 T AA_
 GAM827 DOCK3 3' TTCTGATACCACCAGGTT 33042 A TT C
 AAC CTG GTG TATCAGAA
 || || || |||||
 TTG GAC CAC ATAGTCTT
 _ _ C
 GAM827 FLJ14153 3' TTTCTGATCACGAACAATAG 22942 GCT_
 CTGTTGT ATCAGAAA
 ||||| |||||
 GATAACA TAGTCTTT
 AGCAC
 GAM827 FLJ22127 3' TTTTCTGTCTCAGGAAAACAATG 23044 C GTG AT
 TT
 AACA TGTT CT CAGAAAAA
 || || || |||||
 TTGT ACAA GA GTCTTTTT
 A AAG CT
 GAM827 KIAA0276 3' TCTTTGCAAACAGTGTT 35140 G TATC
 AACACTGTT TGC AGA
 ||||| || ||
 TTGTGACAA ACG TCT
 _ TT_
 GAM827 KIAA0367 3' TCTCCCAGAACACAGTGTT 33427 T G ATC
 AACACTGT GT CT AGA
 ||||| || || ||
 TTGTGACA CA GA TCT
 _ A CCC
 GAM827 KIAA0494 5' TCTGCGGCCAAGCAGTGTT 16592 GT AT
 AACACTGTT GCT CAGA
 ||||| || ||||
 TTGTGACGA CGG GTCT
 AC C_
 GAM827 KIAA1000 3' TTTTCCTGAGATCACACACAG 32536 _ CTA _
 CTGT TGTG TCAG AAAA
 || || || ||||
 GACA ACAC AGTC TTTT
 C TAG C
 GAM827 KIAA1155 3' TTTCTGATTGCTACTGTG 31203 T TGT T
 CAC GT GC ATCAGAAA
 || || || |||||

			GTG CA CG TAGTCTTT		
			T T_ T		
GAM827	KIAA1437	3'	TCTCCACGCACAGTGTT	30386	_ CTATC
			AACACTGT TGTG AGA		
			TTGTGACA GCAC TCT		
			C C_		
GAM827	KIAA1884	3'	TTTCTAGTCTGCACAATA	36299	T_ C
			TGTTGTGC AT AGAAA		
			ATAACACG TG TCTTT		
			TC A		
GAM827	NX-17	3'	TTTTTCTGACAGTATAGTGT	21836	TGT A
			ACACTGT GCT TCAGAAAAA		
			TGTGATA TGA AGTCTTTTT		
			_ C		
GAM827	PAFAH2	3'	TGACAGAACAACAGTGTT	6022	G A
			AACACTGTTGT CT TCA		
			TTGTGACAACA GA AGT		
			A C		
GAM827	PLAC3	5'	TTCTCACAACAGTGT	34369	CTATC
			ACACTGTTGTG AGAA		
			TGTGACAACAC TCTT		
			_		
GAM827	PRO2405	5'	TTTCTGATAGGCAGT	20700	TGTG
			ACTGT CTATCAGAAA		
			TGACG GATAGTCTTT		
			_		
GAM827	ROBO2	3'	TTTCTAATACATGTACAGTG	31318	_ C C
			CACTGT TGTG TAT AGAAA		
			GTGACA GTAC ATA TCTTT		
			T _ A		
GAM827	SEMA5A	3'	TCTGATATACCCAATGTGT	10107	T TGC_
			ACAC GTTG TATCAGA		
			TGTG TAAC ATAGTCT		
			_ CCAT		
GAM827	LOC133688	3'	TCTGATAGCTGGTGTT	37051	TTGT
			AACACTG GCTATCAGA		
			TTGTGGT CGATAGTCT		
			_		
GAM827	LOC145815	5'	TTTCTGGTCAACATTGTT	40608	C TGCT
			AACA TGTTG ATCAGAAA		

		TTGT ACAAC TGGTCTTT	
		T _ _ _	
GAM827	LOC153338 3'	TTTTCTGACAGGGCAGCA 41612	G A
		TGTTGT CT TCAGAAAA	
		ACGACG GA AGTCTTTT	
		G C	
GAM827	LOC155032 3'	TCTTTAGACAACAGTGTT 41749	G TC
		AACACTGTTGT CTA AGA	
		TTGTGACAACA GAT TCT	
		_ T _	
GAM827	LOC155376 5'	TTCTGGATCCCAGCAGTGT 39564	TGCTA
		ACACTGTTG TCAGAA	
		TGTGACGAC GGTCTT	
		CCTA _	
GAM827	LOC158046 3'	TTTGATAGCACAACAGTGT 29801	
		ACACTGTTGTGCTATCAGA	
		TGTGACAACACGATAGTTT	
GAM827	LOC196527 3'	TTTCCCATGCCATCCACAGTG 42403	___ T TATCA
		TT AACACTGT TG GC GAAA	
		TTGTGACA AC CG CTTT	
		CCT _ TACCC	
GAM827	LOC245728 5'	TTCTGGCAAACAGTGTT 43803	G TAT
		AACACTGTT TGC CAGAA	
		TTGTGACAA ACG GTCTT	
		_ _	
GAM827	LOC253532 5'	TTCTGGATCCCAGCAGTGT 45950	TGCTA
		ACACTGTTG TCAGAA	
		TGTGACGAC GGTCTT	
		CCTA _	
GAM827	LOC253613 3'	TTTCCTGATAGCTGCAG 46014	TGT A
		CTGT GCTATCAG AAA	
		GACG CGATAGTC TTT	
		T _ C	
GAM827	LOC254337 5'	TCTGACCTGGAACAGCAGT 46066	G _
		ACTGTTGT CTA TCAGA	
		TGACGACA GGT AGTCT	
		A CC	
GAM827	LOC254875 5'	TTCTGGATCCCAGCAGTGT 45954	TGCTA
		ACACTGTTG TCAGAA	

			TGTGACGAC GGTCTT	
			CCTA_	
GAM827	LOC51141	3'	TTTTCTAATCACAGCAGT 34052	CT C
			ACTGTTGTG AT AGAAAA	
			TGACGACAC TA TCTTTT	
			_ A	
GAM827	LOC90321	3'	TTTTCCTGACAGGCACAGTG 31213	T G A _
			CACTGT GT CT TCAG AAAA	
			GTGACA CG GA AGTC TTTT	
			_ _ C C	
GAM827	LOC93349	3'	TCCGGGAAGCCAACAGTGTT 28770	T A_ A
			AACACTGTTG GCT TC GA	
			TTGTGACAAC CGA GG CT	
			_ AG C	
GAM828	D12S2489E	3'	TTTTGGAAGCACATAACTTG 14293	AAAT G
			TAAGTTAT TG TTCCAAAA	
			GTTCAATA AC AAGGTTTT	
			C_ G	
GAM828	NCOA6	5'	GTTTTGGATGACCTTCCAAACT 15291	ATAAATT _
	TA		TAAGTT GGT TCCAAAAC	
			ATTCAA CCA AGGTTTTG	
			ACCTT_ GT	
GAM828	PRPS2	3'	TTGGAAAATTTATAATT 8658	GG
			AGTTATAAATT TTCCAA	
			TTAATATTTAA AAGGTT	
			_	
GAM828	SCML1	3'	TTTTGTTATAAATTTATAACTT 13594	G TC
			AAGTTATAAATT GT CAAAA	
			TTCAATATTTAA TA GTTTT	
			A TT	
GAM828	SEL1L	3'	GTTTTGGAAGTGCATAACT 11504	AAAT
			AGTTAT TGGTTCCAAAAC	
			TCAATA GTCAAGGTTTTG	
			GC_	
GAM828	SIM1	3'	TTTTGGCCCTACCTGTAACCTTA 11514	AAT TT
			TAAGTTATA TGG CAAAA	
			ATTCAATGT ATC GGTTTT	
			CC_ CC	
GAM828	SPOCK	3'	GTTTTGGTCTTTTATAACTT 31459	TT TT
			AAGTTATAAA GG CCAAAAC	

			TTCAATATTT TC GGTTTGTG	
			T_ T_	
GAM828	B1	3'	TTGGATTTTATTTATAATT 15801	TGGT
			AGTTATAAAT TCCAA	
			TTAATATTTA AGGTT	
			TTTT	
GAM828	FLJ14281	3'	TTGGACTGTTTATGAC 24453	T T
			GTTATAAAT GGT CCAA	
			CAGTATTTG TCA GGTT	
			- -	
GAM828	HSPC019	3'	TTTGGCAATTTATAATTTA 15254	GTT
			TAAGTTATAAATTG CCAAA	
			ATTTAATATTTAAC GGTTT	
			-	
GAM828	KIAA0296	3'	TTTTGCTACAATTTGTAACCTTA 16224	GTTC
			TAAGTTATAAATTG CAAAA	
			ATTCAATGTTTAAC GTTTT	
			ATC_	
GAM828	KIAA0453	3'	TTTTGGTGTTTATAACT 34231	TGGTT
			AGTTATAAAT CCAAAA	
			TCAATATTTG GGTTTT	
			T_	
GAM828	KR18	3'	GTTTTGGAAACCTATAAC 27120	AATT _
			GTTATA GGTT CCAAAAC	
			CAATAT CCAA GGTTTTG	
			_ A	
GAM828	LAT1-3TM	3'	GTTTTGGAGACTGCCTATAAGT 25253	G AATTGG
	TA		TAA TTATA TTCCAAAAC	
			ATT AATAT GAGGTTTTG	
			G CCGTCA	
GAM828	MEGF10	3'	TTTTGGACCCTATAACT 26214	AATT T
			AGTTATA GG TCCAAAA	
			TCAATAT CC AGGTTTT	
			_ C	
GAM828	MGC2488	3'	GTTTTGGAATCTGCCTTATACC 23474	T ATT_
	T		AG TATAA GGTTCCAAAAC	
			TC ATATT CTAAGGTTTTG	
			C CCGT	
GAM828	STIM2	3'	TGGACTATATAACTTA 21917	AAT T
			TAAGTTATA TGGT CCA	

ATTCAATAT ATCA GGT

GAM828 LOC120103 3' TTTTGGAAAGTAATCATAACT 36619 AA G
AGTTAT ATTG TTCCAAAA
||||| ||| |||||
TCAATA TAAT AAGGTTTT
C_ G

GAM828 LOC138639 3' TTTTGGAAATAATCATAACTTG 37140 AA G
TAAGTTAT ATTG TTCCAAAA
||||| ||| |||||
GTTCAATA TAAT AAGGTTTT
C_ A

GAM828 LOC145945 5' GTTTCAGAACCAATTTAAAAT 40635 A CA
GTT TAAATTGGTTC AAAC
||| ||||| |||
TAA ATTTAACCAAG TTTG
A AC

GAM828 LOC197423 5' GTTTTGGAGACTGCCTATAAGT 38144 G AATTGG
TA TAA TTATA TTCCAAAAC
||| ||| |||||
ATT AATAT GAGGTTTTG
G CCGTCA

GAM828 LOC220672 3' TGGAAGTTGAAGTATAATTTA 30310 AATT_
TAAGTTATA GGTTCCA
||||| |||||
ATTTAATAT TCAAGGT
GAAGT

GAM829 TCF12 3' ATTCAGTGTTAATCAGCTA 9201 A TCT G
TAG TGATT AC ACTGAAAT
||| ||| |||||
ATC ACTAA TG TGA CTTTA
G T_ _

GAM829 B3GNT7 3' TCAGCGGGAGTCACCTA 35239 A TA A
TAG TGATTTC CG CTGA
||| ||||| |||
ATC ACTGAGG GC GACT
C _ _

GAM829 KIAA1344 3' TATTCAGACTTCAGAAACCAT 35872 A ACGA_
T GATG TTTCT CTGAAATA
||||| |||||
TTAC AAAGA GACTTTAT
C CTTCA

GAM829 KIAA1894 3' TTTGGCTGGCAGAAATTATCTA 36562 A_ A TG
TAGATGATTTCT CG C AA
||||||| |||
ATCTATTAAAGA GT G TT
CG C GT

GAM829 PIP3-E 3' ATTCAGTCGTAACGCATC 33175 ATTTC
GATG TACGACTGAAAT
||| |||||

			CTAC	ATGCTGACTTTA		
			GCA__			
GAM829	UBE2V2	3'	TATTTTCAGAAAAGAAATTATCT	9377	ACGA	
	A		TAGATGATTTCT	CTGAAATA		
			ATCTATTAAAGA	GACTTTAT		
			AAA_			
GAM829	LOC253143	5'	TTTCATGTGAAATCATC	46316	T AC	
			GATGATTTT	ACG TGAAA		
			CTACTAAAG	TGT ACTTT		
			— —			
GAM829	LOC254170	3'	TATTTTCAGAGTAAAATCTCCTA	45505	AT C GA	
			TAG GATTT	TAC CTGAAATA		
			ATC CTAAG	ATG GACTTTAT		
			CT _ A_			
GAM830	MSN	3'	ATATTGATTTCTGCCTT	30225	TACATAT	
			AAGGCA	GATCAATAT		
			TTCCGT	TTAGTTATA		
			CT_____			
GAM830	PLAG1	3'	GATATATATGTAGGCCTTT	8523	A _	
			AAAGGC	TACATATG ATC		
			TTTCCG	ATGTATAT TAG		
			G A			
GAM830	UTY	3'	ATATTAATCATATGTTTTGT	13982	T_ C	
			GCA ACATATGAT	AATAT		
			TGT TGTATACTA	TTATA		
			TT A			
GAM830	ABLIM	3'	ATCAAATGTATATGCTTTT	8113	_ A	
			AAAGGCA	TACAT TGAT		
			TTTTCGT	ATGTA ACTA		
			AT A			
GAM830	ABLIM	3'	ATCAAATGTATATGCTTTT	13546	_ A	
			AAAGGCA	TACAT TGAT		
			TTTTCGT	ATGTA ACTA		
			AT A			
GAM830	DKFZp761H079	3'	GATATTGATTATACACCTTT	29599	CATACA	
			AAAGG	TATGATCAATATC		
			TTTCC	ATATTAGTTATAG		
			AC_____			
GAM830	KIAA0650	3'	ATGTATGTCATATATATGTCTT	42570	C CA	
	T		AAAGGCATA	ATATGAT ATAT		

			TTTCTGTAT TATACTG TGTA		
			A TA		
GAM830	KIAA1560	3'	GATAAATATGCATGCTTTT 32103	A	G_
			AAAGGCAT CATAT ATC		
			TTTTCGTA GTATA TAG		
			C AA		
GAM830	TUSP	3'	GATACCATGTTCTATGCCTT 21529	C_	__
			AAGGCATA ATATG ATC		
			TTCCGTAT TGTAC TAG		
			CT CA		
GAM830	LOC126731	3'	GATACTGACACCAAATGCCTTT 29772	ACATA	A A
			AAAGGCAT TG TCA TATC		
			TTTCCGTA AC AGT ATAG		
			AACC_ _ C		
GAM830	LOC129831	3'	GTTGAACATATGTATACC 36979	C	A
			GG ATACATATG TCAAT		
			CC TATGTATAC AGTTG		
			A A		
GAM830	LOC157858	5'	GACATATTATATGCCTTT 41868	C_	A
			AAAGGCATA ATATG TC		
			TTTCCGTAT TATAC AG		
			AT _		
GAM830	LOC199718	5'	GATCATATGCTGCCTTT 42606	TA	
			AAAGGCA CATATGATC		
			TTTCCGT GTATACTAG		
			C_		
GAM830	LOC221288	3'	TGGGCCATAACATGCCTTT 44972	ACA	A_
			AAAGGCAT TATG TCA		
			TTTCCGTA ATAC GGT		
			CA_ CG		
GAM831	DAZ	3'	TGCTTTTAACATTCCGACATAC 10285	C C	C__
	ATCA		TGA GTG GTCGGAAT GGAAGCA		
			ACT CAT CAGCCTTA TTTTCGT		
			A A CAA		
GAM831	DKFZp434N074	5'	GCCCTTGATGCAACGCACGTCA 31390	CGGA	AA
			TGACGTGCGT ATCGG GC		
			ACTGCACGCA TAGTT CG		
			ACG_ CC		
GAM831	FLJ10140	3'	CTTCCGATTCCGCCAC 19738	C T	
			GTG G CGGAATCGGAAG		

CAC C GCCTTAGCCTTC

GAM831 LOC201780 5' GCCCCCGACGCCGCCGAGCACG 42910 GT__ AA AA
TCA TGACGTGC CGG TCGG GC

||||||| ||| ||| ||
ACTGCACG GCC AGCC CG
AGCC GC CC

GAM831 LOC256160 5' GCCCCCGACGCCGCCGAGCACG 45886 GT__ AA AA
TCA TGACGTGC CGG TCGG GC

||||||| ||| ||| ||
ACTGCACG GCC AGCC CG
AGCC GC CC

GAM832 SEPN1 3' TGA CTTGCCCAGGGTCACTCA 32992 GATTCGA A
TGAGTGATCT CAA TCA

||||||| ||| |||
ACTCACTGGG GTT AGT
ACCC__ C

GAM832 KIAA1055 3' GACTTGTGGA AATCATTCA 32852 CTGA G A
TGAGTGAT TTC ACAA TC

||||||| ||| ||| ||
ACTTACTA AAG TGTT AG
__ G C

GAM832 KIAA1951 3' TGATCTGTACCAGGTCACCCA 36513 A ATTCG A
TG GTGATCTG ACA ATCA

|| ||||| ||| |||
AC CACTGGAC TGT TAGT
C CA__ C

GAM832 NYD-SP27 5' ATTTATCGAATTATCACGCA 26968 A CT C
TG GTGAT GATTCGA AAAT

|| |||| ||||| ||||
AC CACTA TTAAGCT TTTA
G _ A

GAM832 LOC92223 5' TGATTCA GTGTCAGATCATCC 33995 AG T ACA
A TG TGATCTGAT CG AATCA

|| ||||| || ||||
AC ACTAGACTG GT TTAGT
CT _ GAC

GAM833 CBFA2T2 3' ATTAGGGTTGGATGCCCATTTTC 11546 A GA
T GGAAATGG TAT CAACCCTAAT

||||||| ||| ||||| ||||
TCTTTACC GTA GTTGGGATTA
C G_

GAM833 TAL1 3' TTAGGGTTGGTTCCTTTCC 9173 T TATGA
GGAAA GGA CAACCCTAA

||||| ||| ||||| ||||
CCTTT CCT GTTGGGATT
_ TG__

GAM833 KIAA0798 3' AGGGTTTGTGTATCCATTC 16067 A G _
GAA TGGATAT ACAA CCCT

||| ||||| |||| ||||

CTT ACCTATG TGTT GGG
 _ _ T
 GAM833 KIAA1155 3' TAGGGTTGATCTGCCACCTC 31198 AA ATAT _
 GA TGG GA CAACCCTA
 || ||| || |||||
 CT ACC CT GTTGGGAT
 CC GT_ A
 GAM833 MYH10 3' GGTTACCATGTCCATCCCC 34265 AA AC
 GG ATGGATATG AACC
 || ||||| |||
 CC TACCTGTAC TTGG
 CC CA
 GAM833 LOC154739 5' AGGATAATTTGCATATCCATCA 41713 AA A C____
 CC GG ATGGATATG CAA CCT
 || ||||| ||| |||
 CC TACCTATAC GTT GGA
 AC _ TAATA
 GAM833 LOC203276 3' AGGATAATTTGCATATCCATCA 43480 AA A C____
 CC GG ATGGATATG CAA CCT
 || ||||| ||| |||
 CC TACCTATAC GTT GGA
 AC _ TAATA
 GAM833 LOC203305 3' AGGATAATTTGCATATCCATCA 43504 AA A C____
 CC GG ATGGATATG CAA CCT
 || ||||| ||| |||
 CC TACCTATAC GTT GGA
 AC _ TAATA
 GAM833 LOC254243 3' AGGATAATTTGCATATCCATCA 46506 AA A C____
 CC GG ATGGATATG CAA CCT
 || ||||| ||| |||
 CC TACCTATAC GTT GGA
 AC _ TAATA
 GAM833 LOC51131 3' TTAGGGATTACCATTTCC 18201 A TGACAA
 GGAAATGG TA CCCTAA
 ||||| || |||||
 CCTTTACC AT GGGATT
 _ TA____
 GAM833 LOC90038 3' AGGATAATTTGCATATCCATCA 30643 AA A C____
 CC GG ATGGATATG CAA CCT
 || ||||| ||| |||
 CC TACCTATAC GTT GGA
 AC _ TAATA
 GAM833 LOC91115 3' ATTAGGGTAAAGTATCCATCAC 32392 AA GACA
 C GG ATGGATAT ACCCTAAT
 || ||||| |||||
 CC TACCTATG TGGGATTA
 AC AAA_
 GAM834 ALG6 5' GAATCGATAACATTTCAAGAA 14987 _ C
 TTCTT AGATGTTATCGA TC
 ||||| ||||| ||||| ||

			AAGAA TTTACAATAGCT AG	
			C A	
GAM834	BAZ2A	3'	GAGCTGAGGCATCCAAGAAA 15119	A A A
			TTTCTT GATGTT TCG CTC	
			AAAGAA CTACGG AGT GAG	
			C _ C	
GAM834	BCL2	3'	GAGTCTCAGCTACCTAAGAAA 6259	AT_ ATC
			TTTCTTAG GTT GACTC	
			AAAGAATC CGA CTGAG	
			CAT CT_	
GAM834	NDRG1	3'	AGTTGGTGCATCTAGAAA 29964	T T
			TTTCT AGATGT ATCGACT	
			AAAGA TCTACG TGGTTGA	
			— —	
GAM834	EPN2	3'	GTTTTAACTCTAAGAAA 17349	T TC
			TTTCTTAGA GTTA GAC	
			AAAGAATCT CAAT TTG	
			— T_	
GAM834	FLJ31952	5'	AGTCTGGTTACATTAAGAAA 29497	A T _
			TTTCTT GATGT ATC GACT	
			AAAGAA TTACA TGG CTGA	
			— T T	
GAM834	H326	3'	AGTCATTAATCTAAGGAA 17937	GTT C
			TTTCTTAGAT AT GACT	
			AAGGAATCTA TA CTGA	
			AT_ _	
GAM834	HABP4	3'	GAGTCAGACTCTAAGAA 34925	T ATC
			TTCTTAGA GTT GACTC	
			AAGAATCT CAG CTGAG	
			— A_	
GAM834	KIAA0894	3'	AGTATAACACTAAGAAA 17054	A CG
			TTTCTTAG TGTTAT ACT	
			AAAGAATC ACAATA TGA	
			— —	
GAM834	KIAA1157	3'	AGTGATCCAATCTAAGAAA 35748	GTT G
			TTTCTTAGAT ATC ACT	
			AAAGAATCTA TAG TGA	
			ACC _	
GAM834	KIAA1594	3'	GAGTCCATTACCTGAGAAA 35675	A TT C
			TTTCTTAG TG AT GACTC	

		AAAGAGTC AC TA CTGAG	
		C T_ C	
GAM834	MGC12928 5'	GAGTTGATCCATCTGAGAAA 26714	TT
		TTTCTTAGATG ATCGACTC	
		AAAGAGTCTAC TAGTTGAG	
		C_	
GAM834	LOC142955 5'	GAGTACAGCAGCTAAGAAA 37574	A ATCG
		TTTCTTAG TGTT ACTC	
		AAAGAATC ACGA TGAG	
		G CA__	
GAM834	LOC144519 3'	AGTCGATGATATGAGAAA 37757	AG
		TTTCTT ATGTTATCGACT	
		AAAGAG TATAGTAGCTGA	
		—	
GAM834	LOC146056 3'	AGTGGCCACATTTAAGAAA 38051	TA G
		TTTCTTAGATGT TC ACT	
		AAAGAATTTACA GG TGA	
		CC _	
GAM834	LOC149153 3'	GAGTCACAGATCTGAGAAA 40965	GTTATC
		TTTCTTAGAT GACTC	
		AAAGAGTCTA CTGAG	
		GACA__	
GAM834	LOC149420 3'	AGTCATCAGCACTTAAGAAA 38747	A ATC
		TTTCTTAG TGTT GACT	
		AAAGAATT ACGA CTGA	
		C CTA	
GAM834	LOC92106 5'	TCGTGGACTTCTAAGAAA 28756	T AT
		TTTCTTAGA GTT CGA	
		AAAGAATCT CAG GCT	
		T GT	
GAM835	GAS7 3'	AGTTTTCTGTCACTGGTGGG 9714	TGC
		CCCATCAGTGATA AACT	
		GGGTGGTCACTGT TTGA	
		CTT	
GAM835	HS2ST1 3'	GTAGCCTTGACACTGATGG 14577	A T_ A
		CCATCAGTG TA GC AC	
		GGTAGTCAC GT CG TG	
		A TC A	
GAM835	LUZP1 3'	AGCTGCAGCTGATGGG 27351	GATA A
		CCCATCAGT TGCA CT	

			GGGTAGTCG	ACGT GA		
			_____ C			
GAM835	SSX3	3'	GTAGCAGTCACTGACAGTA	22003	CCA	A A
			TAC TCAGTGAT TGC AC			
			ATG AGTCACTG ACG TG			
			AC_ _ A			
GAM835	C1orf24	3'	TGCATATCACCATGAGT	27536	C CA	
			AC CAT GTGATATGCA			
			TG GTA CACTATACGT			
			A C_			
GAM835	DKFZP586C1619	3'	GTTCAATCACTGATGGG	31021		A C
			CCCATCAGTGAT TG AAC			
			GGGTAGTCACTA AC TTG			
			— —			
GAM835	DKK2	3'	AGTGGAATTA	15773	C	ATGCA
			TAC CATCAGTGAT ACT			
			ATG GTAGTCATTA TGA			
			A AAGG_			
GAM835	FLJ14213	3'	GTAGTTGTCGGTCTCACTGAT	24255		T _
			ATCAGTGA AT GCAACTAC			
			TAGTCACT TG TGTTGATG			
			C GC			
GAM835	FLJ23548	5'	GCACATCACTGACTGGTA	23825	CA	A
			TACC TCAGTGAT TGC			
			ATGG AGTCACTA ACG			
			TC C			
GAM835	KIAA0831	3'	GTATATCACCATTGGGTA	17209		TCA
			TACCCA GTGATATGC			
			ATGGGT CACTATATG			
			TAC			
GAM835	MGC13061	3'	GTAGCCACACATCATTGCTGGG	26129	T	A CAA
			CCCA CAGTGAT TG CTAC			
			GGGT GTTACTA AC GATG			
			C C ACC			
GAM835	LOC154739	5'	GCCATATCACTGAGGGTA	41719	A	_
			TACCC TCAGTGATATG C			
			ATGGG AGTCACTATAC G			
			_ C			
GAM835	LOC203276	3'	GCCATATCACTGAGGGTA	43487	A	_
			TACCC TCAGTGATATG C			

			ATGGG AGTCACTATAC G		
			— C		
GAM835	LOC203305	3'	GCCATATCACTGAGGGTA 43511	A	—
			TACCC TCAGTGATATG C		
			I		
			ATGGG AGTCACTATAC G		
			— C		
GAM835	LOC219686	3'	GTAGCCATGTCACTGTG 43675	T	CAA
			CA CAGTGATATG CTAC		
			GT GTCAGTGTAC GATG		
			— C—		
GAM835	LOC254243	3'	GCCATATCACTGAGGGTA 46514	A	—
			TACCC TCAGTGATATG C		
			I		
			ATGGG AGTCACTATAC G		
			— C		
GAM835	LOC63923	3'	TAGTTGCACAGTATGTGTA 33324	C	CAG ATA
			TAC CAT TG TGCAACTA		
			ATG GTA AC ACGTTGAT		
			T TG_ _		
GAM835	LOC90038	3'	GCCATATCACTGAGGGTA 30651	A	—
			TACCC TCAGTGATATG C		
			I		
			ATGGG AGTCACTATAC G		
			— C		
GAM836	RPL15	3'	CTTAGACGTCAACCCTAA 8860	ATC	
			TTAG TGACGTCTAAG		
			AATC ACTGCAGATTC		
			CCA		
GAM836	BCCIP	3'	TACTGGAGAGAGACACAGAT 27786	AC_	AAGGA_
	CTAA		TTAGATCTG GTCT AGTA		
			AATCTAGAC CAGA TCAT		
			ACA GAGAGG		
GAM836	KIAA1110	3'	ACCCCTCTGCAGATCTGA 30981	A	TCTA AA
			TTAGATCTG CG AGG GT		
			AGTCTAGAC GT TCC CA		
			— C— CC		
GAM836	KIAA1877	3'	TACCTCCTCACCTGCAGATCTA 32885	A	TCTA A
			TAGATCTG CG AGGA GTA		
			ATCTAGAC GT TCCT CAT		
			— CCAC C		
GAM836	PRRG1	3'	TACTTCCTTAAAGTAAATGTAA 6656	G	CTG GTC
			TTA AT AC TAAGGAAGTA		

AAT TA TG ATTCCTTCAT
 G AA_ AA_
 GAM836 LOC149910 3' TACTTCCTCACTGTCAGCCTAA 38828 AT TCTA
 TTAG CTGACG AGGAAGTA
 |||| ||||| |||||
 AATC GACTGT TCCTTCAT
 C_ CAC_
 GAM836 LOC151405 5' ACTTCTTCATGACACCAAATC 41338 C AC TA_
 GAT TG GTC AGGAAGT
 ||| || ||| |||||
 CTA AC CAG TTCTTCA
 A CA TAC
 GAM836 LOC153196 5' ACTCCCCAGCATCTAGATCTAA 41587 _ C T AA A
 TTAGATCT GA G CT GGA GT
 ||||| || || ||| ||
 AATCTAGA CT C GA CCT CA
 T A_ CC _
 GAM837 UBL3 3' GACATTACATTCTGTACTTA 13966 CTGGCT
 TAAGTACG TAATGTC
 ||||| |||||
 ATTCATGT ATTACAG
 CTTAC_
 GAM837 FLJ13611 3' ACACGAGTCAGCACACTTTTTTA 24485 T AC AA
 TAA AAGT GCTGGCTT TGT
 ||| ||| ||||| |||
 ATT TTCA CGACTGAG ACA
 T CA C_
 GAM838 AXUD1 3' ACCCACAGCTTGCTCTTCT 26917 C A
 AGAAGAGCAAGCT TGG GT
 ||||| ||||| ||| ||
 TCTTCTCGTTCTGA ACC CA
 C _
 GAM838 CDH13 3' ATGACATATGACTTGATCTTCT 6926 G C TGGA
 AGAAGA CAAG TC GTCAT
 ||||| ||||| || |||||
 TCTTCT GTTC AG CAGTA
 A _ TATA
 GAM838 CYP27B1 3' ACTCTCCTTTGCTCTCT 6431 A CTCT
 AGA GAGCAAG GGAGT
 ||| ||||| |||||
 TCT CTCGTTT TCTCA
 _ CC_
 GAM838 DAAM2 3' TGTTCCAGAGCTCAGCCTTCT 44335 A A_ T
 AGAAG GC AGCTCTGGAG CA
 ||||| || ||||| ||||| ||
 TCTTC CG TCGAGACCTT GT
 _ AC _
 GAM838 GAB2 3' CTCCAGAGCTGGCCCTTC 14650 A A
 GAAG GC AGCTCTGGAG
 |||| || ||||| |||||

			CTTC CG TCGAGACCTC		
			C G		
GAM838	GAB2	3'	CTCCAGAGCTGGCCCTTC 27845	A A	
			GAAG GC AGCTCTGGAG		
			CTTC CG TCGAGACCTC		
			C G		
GAM838	LOXL2	3'	ACAGTGGAGCCGCGCTCTTCT 8131	AA_ GA	
			AGAAGAGC GCTCTG GT		
			TCTTCTCG CGAGGT CA		
			CGC GA		
GAM838	MSL3L1	3'	TATGACCTGTGCCCTGTTCTTC 27811	A_ TCT A	
			GAAGAGCA GC GG GTCATA		
			CTTCTTGT CG TC CAGTAT		
			CC TG_ _		
GAM838	MTP	3'	ATGACTAAGTACTTGCTCTCT 5794	A CT GG	
			AGA GAGCAAG CT AGTCAT		
			TCT CTCGTTT GA TCAGTA		
			_ AT A_		
GAM838	NOS1	3'	TATGACTCACCTTGCTCT 6233	CTCTG	
			AGAGCAAG GAGTCATA		
			TCTCGTTT CTCAGTAT		
			CA__		
GAM838	PATE	3'	ACACTTGAGCTTGCCACTCT 28708	AGA T A	
			AGA GCAAGCTC GG GT		
			TCT CGTTTCGAG TC CA		
			CAC T A		
GAM838	PPP1R12A	3'	GAAAAGAACACTTGCTCTTCT 8305	C__ GGAG	
			AGAAGAGCAAG TCT TC		
			TCTTCTCGTTT AGA AG		
			ACA AA__		
GAM838	ABLIM	3'	TATGCCCCAAAGCTTGCTCTTT 13552	C A T	
	T		AGAAGAGCAAGCT TGG G CATA		
			TTTTCTCGTTTCGA ACC C GTAT		
			A C_		
GAM838	ABLIM	3'	TATGCCCCAAAGCTTGCTCTTT 8119	C A T	
	T		AGAAGAGCAAGCT TGG G CATA		
			TTTTCTCGTTTCGA ACC C GTAT		
			A C_		
GAM838	CRA	3'	ATTGGGGAGCTTGCCCTTT 13516	A GG	
			GAAG GCAAGCTCT AGT		

TTTC CGTTCGAGG TTA
 C GG
 GAM838 FLJ12768 3' ATGACTCCCACTGCTGCCTCT 24801 CA TCT_
 AGAG AGC GGAGTCAT
 ||| ||| |||||
 TCTC TCG CCTCAGTA
 CG TCAC
 GAM838 FLJ14547 3' ACTTAGAGCTTATCTTC 26558 GC G
 GAAGA AAGCTCTG AGT
 |||| ||||| |||
 CTTCT TTCGAGAT TCA
 A _ _
 GAM838 FLJ22477 3' GTGTCCAGAGCTGGCCCTTC 24076 A A GT
 GAAG GC AGCTCTGGA CAT
 ||| || ||||| |||
 CTTC CG TCGAGACCT GTG
 C G _
 GAM838 KIAA0227 3' ACCTAGAGCTCACTCTCT 30447 A CA A
 AGA GAG AGCTCTGG GT
 ||| ||| ||||| ||
 TCT CTC TCGAGATC CA
 _ AC _
 GAM838 KIAA0265 3' ACTGCCAGGCTTGCTCCTC 34619 A T _
 GA GAGCAAGC CTGG AGT
 || ||||| ||| |||
 CT CTCGTTTCG GACC TCA
 C _ G
 GAM838 KIAA0298 3' ACTTCAGAGCCCGCCCTCT 37623 A A AA
 AGA G GC GCTCTGGAGT
 ||| || |||||
 TCT C CG CGAGACTTCA
 _ C CC
 GAM838 MGC4415 3' ATTCCAGAGCTCACTGCCCT 25565 A _
 AG GCA AGCTCTGGAGT
 || ||| |||||
 TC CGT TCGAGACCTTA
 C CAC
 GAM838 MLZE 5' TCCAGACTTACTCTTCT 25395 C C
 AGAAGAG AAG TCTGGA
 ||||| ||| |||||
 TCTTCTC TTC AGACCT
 A _
 GAM838 NCE2 3' TGAGGCCAGAGCTTGCTTT 27972 AG
 AGAGCAAGCTCTGG TCA
 ||||| ||||| |||
 TTTCGTTTCGAGACC AGT
 GG
 GAM838 p25 3' ATGACTCCAGAGGACCTC 13889 CAAG
 GAG CTCTGGAGTCAT
 ||| |||||

			CTC	GAGACCTCAGTA		
			CAG_			
GAM838	LOC149706	5'	GCCCAGAGCTCACTCTTTT	41061	CA	A
			AGAAGAG AGCTCTGG GT			
			TTTTCTC TCGAGACC CG			
			AC _			
GAM838	LOC150208	3'	ACTGCTACTTGCTCTGCT	41156	A	CTC _
			AG AGAGCAAG TGG AGT			
			TC TCTCGTTC ATC TCA			
			G _ G			
GAM838	LOC157653	5'	ACTCCAAACTTGCTCTTC	39630	CTC	
			GAAGAGCAAG TGGAGT			
			CTTCTCGTTC ACCTCA			
			AA_			
GAM838	LOC221495	3'	GATCAGAGCTCACCTTTCT	45057	AGCA	GA
			AGAAG AGCTCTG GTC			
			TCTTT TCGAGAC TAG			
			CCAC _			
GAM838	LOC221747	3'	GATGTGACTTGCTCCTCT	44365	A	C TGGA
			AGA GAGCAAG TC GTC			
			TCT CTCGTTC AG TAG			
			C _ TG_			
GAM839	ABCC1	3'	AGAGCTGGCATATCTGGTCA	21281	G	TC
			TGACTAGATATG TAG CT			
			ACTGGTCTATAC GTC GA			
			G GA			
GAM839	ABCC1	3'	AGAGCTGGCATATCTGGTCA	21285	G	TC
			TGACTAGATATG TAG CT			
			ACTGGTCTATAC GTC GA			
			G GA			
GAM839	ABCC1	3'	AGAGCTGGCATATCTGGTCA	11437	G	TC
			TGACTAGATATG TAG CT			
			ACTGGTCTATAC GTC GA			
			G GA			
GAM839	C7orf2	3'	TAGGAAGTATCATGTAATCA	22796	CTAG	G_
			TGA ATATGGTA TCCTA			
			ACT TGTACTAT AGGAT			
			AA_ GA			
GAM839	CRHR2	3'	AGAACCACCATGTCTTCA	7610	CT	A C
			TGA AGATATGGT GT CT			

			ACT TCTGTACCA CA GA		
			— C A		
GAM839	TCP10	3'	TAGGACTACCCAAGTCA 10950	AGATAT	
			TGACT GGTAGTCCTA		
			ACTGA CCATCAGGAT		
			AC—		
GAM839	ARPP-19	3'	TAGAATTTCTATATCTAGTC 13422	T C	
			GACTAGATATGG AGT CTA		
			CTGATCTATATC TTA GAT		
			T A		
GAM839	DKFZP586C1619	3'	AGGACTACCAGCTTGCTCA 31016	C ATA	
			TGA TAG TGGTAGTCCT		
			ACT GTT ACCATCAGGA		
			C CG_		
GAM839	DOC2B	3'	GGGAGTTCCCATCTAGTCA 9637	AT TAG	
			TGACTAGAT GG TCCT		
			ACTGATCTA CC AGGG		
			C_ TTG		
GAM839	HSA243666	3'	TAGGACTACTTTTCTAGTCA 19021	TAT	
			TGACTAGA GGTAGTCCTA		
			ACTGATCT TCATCAGGAT		
			TT_		
GAM839	KIAA0172	5'	AGGACCACATCTGGTCA 32408	A TAG	
			TGACTAGAT TGG TCCT		
			ACTGGTCTA ACC AGGA		
			C —		
GAM839	MGC15563	3'	AGGATTTATATCTATTCA 26698	C GT	
			TGA TAGATATG AGTCCT		
			ACT ATCTATAT TTAGGA		
			T —		
GAM839	SLC39A3	3'	TAGGACTACAGACGTTTATCA 29361	C ATG_	
			TGA TAGAT GTAGTCCTA		
			ACT ATTTG CATCAGGAT		
			_ CAGA		
GAM839	LOC145508	3'	AGGACTTTTATATCTATCA 37886	C T	
			TGA TAGATATGG AGTCCT		
			ACT ATCTATATT TCAGGA		
			_ T		
GAM839	LOC220753	5'	AGGGCTACATCCAGCA 44659	A A ATG	
			TG CT GAT GTAGTCCT		

			AC GA CTA CATCGGGA		
			_ C _		
GAM839	LOC92078	3'	TAGGACTTGAAGTCTAGTTA 33746		ATGGT
			TGACTAGAT AGTCCTA		
			ATTGATCTG TCAGGAT		
			AAGT_		
GAM840	RAG1	3'	GTGGATTCAGAATTGTGTA 6039	C C	
			TACACAA TTC GAATCCAC		
			ATGTGTT AAG CTTAGGTG		
			_ A		
GAM840	TMEM1	3'	CCGTGGATGTGCAAGTTGTG 9289	C A	
			CACAACTT CG ATCCACGG		
			GTGTTGAA GT TAGGTGCC		
			C G		
GAM840	TRIM8	3'	CCGGGCTCGGGAGTTATG 25180	C AT A	
			CA AACTTCCGA CC CGG		
			GT TTGAGGGCT GG GCC		
			A C_ _		
GAM840	DDX33	3'	TCTGTCCGGAGTTGTGTA 21378	T AATCC	
			TACACA ACT CCG ACGGA		
			ATGTGTTGA GGC TGTCT		
			_ C _		
GAM840	DKFZP586M1120	5'	TCCGTTGACAGTTGTGTA 25324	TCCGAA C	
			TACACA ACT TC ACGGA		
			ATGTGTTGA AG TGCCT		
			C _ T		
GAM840	KIAA0237	3'	CCATGAGGGTAAAGTTGTGTG 16442	CCGA AC_	
			TACACA ACTT ATCC GG		
			GTGTGTTGAA TGGG CC		
			A _ AGTA		
GAM840	KIAA0711	5'	CCGTGACCTTGCAGTTGTGTA 16956	TC ATC	
			TACACA ACT CGA CACGG		
			ATGTGTTGA GTT GTGCC		
			C_ CCA		
GAM840	VLCS-H1	5'	TCCGTGGAGAGCTGTG 15261	A CCGAA	
			CACA CTT TCCACGGA		
			GTGT GAG AGGTGCCT		
			C _		
GAM840	LOC147138	5'	CTCCGTGGGGGAGGAGCTGTA 38308	CAA GAA	
			TACA CTTCC TCCACGGAG		

			ATGT GGAGG GGGTGCCTC		
			CGA ____		
GAM841	GAN	3'	CCACCCTAGTGTGAAA 22562	GTAA A	
			TTTCACACT AG GTGG		
			AAAGTGTGA TC CACC		
			____ C		
GAM841	GOLGA4	5'	ATGTGAATTTAAGTGTGAAA 30164	G GAGTG	
			TTTCACACT TAAA GCAT		
			AAAGTGTGA ATTT TGTA		
			_ AAG_		
GAM841	COQ7	3'	TCCTCTCCACAGTGTGAGA 18223	AA T	
			TTTCACACTGT AGAG GG		
			AGAGTGTGACA TCTC CT		
			CC _		
GAM841	FLJ20136	3'	CATTGTTTACAGGTGTGAAA 19229	_ G	
			TTTCACAC TGTAAGT		
			AAAGTGTG ACATTT TTAC		
			G G		
GAM841	GPR64	3'	ATGCTTGACAGTGTGAAA 12315	AAAGAGT	
			TTTCACACTGT GGCAT		
			AAAGTGTGACA TCGTA		
			GT_____		
GAM842	ADM	3'	GCGAGGTGTAAAGTTGT 6795	ACA	
			ACAACCTTTACATT GC		
			TGTTGAAATGTGG CG		
			AG_		
GAM842	CDH12	5'	ATGCAAAGCAGTGTGTTG 10267	AA A	
			CAACACAC CTTT CAT		
			GTTGTGTG GAAA GTA		
			AC C		
GAM842	CLN5	3'	GCTGTAAAGATGTAAGTTGTGT 13229	T ____	
			ACACAACCTT ACATT ACAGC		
			TGTGTTGAA TGTAAG TGTCG		
			_ AAA		
GAM842	CX3CR1	3'	GCTGTGCCCAAGTTGTGGT 34978	A TACAT	
			AC CACAACCTT TACAGC		
			TG GTGTTGAA GTGTCTG		
			_ CCC_		
GAM842	MAN1A1	3'	GCTGTAATGTTTTGCCATGTTG 44134	CA_ CTTT	
			CAACA CAA ACATTACAGC		

			GTTGT GTT TGTAATGTCG		
			ACC T__		
GAM842	PTPRN	3'	TGTGAATAAAGTTAGTGTGTTG 8735	_	CA
			CAACACAC AACTTTA TTACA		
			GTTGTGTG TTGAAAT AGTGT		
			A A_		
GAM842	SCG3	3'	CTGAAAGTAAAGTTGTATGT 14900	C	A A
			ACA ACAACTTTAC TT CAG		
			TGT TGTGAAATG AA GTC		
			A A_		
GAM842	SOCS5	3'	GCTGCAATGTAGTCTTGTGTGT 15227	CT	A
			ACACACAA TTACATT CAGC		
			TGTGTGTT GATGTAA GTCG		
			CT C		
GAM842	ABLIM	3'	GTGAATAAAGTTGTGTG 8118	CA	
			CACACAACCTTTA TTAC		
			GTGTGTTGAAAT AGTG		
			A_		
GAM842	ABLIM	3'	GTGAATAAAGTTGTGTG 13551	CA	
			CACACAACCTTTA TTAC		
			GTGTGTTGAAAT AGTG		
			A_		
GAM842	ARHGEF9	3'	AGTGTCAAAGTTGTGTGTT 17536	_	
			AACACACAACCTTT ACATT		
			TTGTGTGTTGAAA TGTGA		
			C		
GAM842	DKFZp434O0320	3'	CTGTAAACTAATAAATGTGTGT 40705	ACT_	CA
	TG		CAACACACA TTA TTACAG		
			GTTGTGTGT AAT AATGTC		
			AAAT CA		
GAM842	FLJ11040	3'	CTGTAATTCTGTTGTGTGT 20295	TTTAC	
			ACACACAAC ATTACAG		
			TGTGTGTTG TAATGTC		
			TCT__		
GAM842	HYPH	3'	CTGTGATGAAAATCATGTG 45482	CAAC	A
			CACA TTT CATTACAG		
			GTGT AAA GTAGTGTC		
			ACTA _		
GAM842	KIAA0261	3'	GCTGTAATGTTTTTAAATGCAG 33832	A_	ACTTT__
	TG		CAC CA ACATTACAGC		

			GTG GT	TGTAATGTCG		
			AC	AAATTTT		
GAM842	KIAA0937	3'	GCTGCAATATAGTGTGTGTT	44016	A TTAC	A
			AACACACA CT	ATT CAGC		
			TTGTGTGT GA	TAA GTCG		
			_ TA_	C		
GAM842	KIAA1091	3'	GCTGTAATGCAAATGGCTGGTG	34541	A A TTA_	
			CAC CA CT	CATTACAGC		
			GTG GT GG	GTAATGTCG		
			_ C	TAAAC		
GAM842	KIAA1576	3'	GCTGTAGTCCAGTGCGTGT	32773	A A TTAC	
			ACAC CA CT	ATTACAGC		
			TGTG GT GA	TGATGTCG		
			C _ CC_			
GAM842	MGEA6	3'	CTGTAGTGAATGATGTGTCA	12561	C ACT A	
			A ACACA	TT CATTACAG		
			A TGTGT	AA GTGATGTC		
			C	AGT _		
GAM842	NYD-SP20	5'	CTGAGGGCGAAAGTTGTGTGT	26329	ACA TA	
			ACACACAAC TTT	T CAG		
			TGTGTGTTGAAA	G GTC		
			GCG GA			
GAM842	SEMA5A	3'	GCTGTGGAATAAGTTGTGTTTG	10105	C TACA	
			CAA ACACAAC TTT	TTACAGC		
			GTT TGTGTTGAA	GGTGTCG		
			_ TAA_			
GAM842	LOC151473	3'	GTTTGTACAGTTGTGTGTTG	39122	T TT	
			CAACACACAAC T	TACA AC		
			GTTGTGTGTTGA	ATGT TG		
			C	T_		
GAM842	LOC219594	3'	CTGTAATGATTAGTCTGTATGT	43640	C _ TTA	
			ACA ACA ACT	CATTACAG		
			TGT TGT TGA	GTAATGTC		
			A C	TTA		
GAM842	LOC219673	5'	GCTGTAATTAGAGTCATG	44693	CA C	
			CA ACTTTA	ATTACAGC		
			GT TGAGAT	TAATGTCG		
			AC	_		
GAM842	LOC221466	5'	CTGTAAATGTCTAGGCATGTGC	44993	A CAA TT	_
			TG	CA CACA CT	ACATT ACAG	

			GT GTGT GA TGTAATGTC		
			C ACG TC A		
GAM842	LOC221477	3'	TAATATAAAGCTGTGTGTT 44258	A C	
			AACACACA CTTTA ATTA		
			TTGTGTGT GAAAT TAAT		
			C A		
GAM842	LOC253820	5'	GCTGTAATACAGTTGGCAGTT 45808	ACA TTAC	
			AAC CAACT ATTACAGC		
			TTG GTTGA TAATGTCG		
			ACG CA__		
GAM842	LOC257282	5'	GCTGCATTGGAATTGTGTGTTG 46121	C A TTA	
			CAACACACAA TTT CA CAGC		
			GTTGTGTGTT AAG GT GTCG		
			_ _ TAC		
GAM842	LOC90333	3'	GCTGACACTACAGTTGTGTG 31225	T CATTA	
			CACACA ACT TA CAGC		
			GTGTGTTGA AT GTCG		
			C CACA_		
GAM842	LOC91547	3'	GCTGTGATCACAGTTGTATG 33003	C TTAC	
			CA ACAACT ATTACAGC		
			GT TGTTGA TAGTGTCG		
			A CAC_		
GAM843	BCHE	5'	AACTTTACCATCTTTGTTGC 5512	_ A A	
			GCA TAGA AT GTAAAGTTT		
			CGT GTTT TA CATTTCAAA		
			T C C		
GAM843	ANKRD6	3'	AACTTCAGTTCTATTTCTATA 17250	GC TA__	
	GA		TC ATAGAAATAG AAGTTT		
			AG TATCTTTATC TTCAAA		
			A_ TTGAC		
GAM843	CSE-C	3'	AACTTTACTACTATCAGATA 43979	GC AAA	
			TATC ATAG TAGTAAAGTTT		
			ATAG TATC ATCATTTCAAA		
			AC _		
GAM843	LOC145009	5'	AACTTTACTAGATGC 30262	AGAAA	
			GCAT TAGTAAAGTTT		
			CGTA ATCATTTCAAA		
			G__		
GAM844	LATS1	3'	TAACCCATTAGGAAATAGAGC 30237	ACGGA A	
			GTT TCCTAATG GTTA		

			CGA AGGATTAC CAAT		
			GATAA C		
GAM844	SCDGF-B	3'	ATTTGATAGGATCCATATCTAA 24877	T C	A
			TTAG TA GGATCCTA TGAGT		
			AATC AT CCTAGGAT GTTTA		
			T A A		
GAM844	SCDGF-B	3'	ATTTGATAGGATCCATATCTAA 26979	T C	A
			TTAG TA GGATCCTA TGAGT		
			AATC AT CCTAGGAT GTTTA		
			T A A		
GAM845	IL12B	3'	TCAGTCCCTATTATGCAA 7943	ACGG	TT
			TTGCATAAT AGGG CTGA		
			AACGTATTA TCCC GACT		
			_____ T_		
GAM845	SDCCAG1	3'	ATCAGGATTTCCGCATTAT 11069	A	G
			ATAAT CGGAGG TTCTGAT		
			TATTA GCCTTT AGGACTA		
			C _		
GAM846	ACO1	3'	ACATAAAAAGAAATGTGAA 7953	AAGTTG	
			TTCACATTTTT TATGT		
			AAGTGTAAGA ATACA		
			AAA_____		
GAM846	ANXA7	3'	CTACATACAATCAATGT 10253	TTTAA	
			ACATT GTTGTATGTAG		
			TGTAA TAACATACATC		
			C_____		
GAM846	ANXA7	3'	CTACATACAATCAATGT 6824	TTTAA	
			ACATT GTTGTATGTAG		
			TGTAA TAACATACATC		
			C_____		
GAM846	FLJ14440	5'	CTACATATATTTTAAAAA 26532	T	
			TTTTTAAG TGTATGTAG		
			AAAAATTT ATATACATC		
			T		
GAM846	KIAA1729	5'	ACAGCTTAAAAATGTGAA 42946		
			TTCACATTTTTTAAGTTGT		
			AAGTGTAATAATTGACA		
GAM846	PRO1575	5'	CTAAATATAACTTAAAAAGTGA 15311	A	G
	A		TTCAC TTTTTAAGTTGTAT TAG		

AAGTG AAAAATTCAATATA ATC

A

GAM846 LOC51339 3' ACATACAATAGTGTGAA 18767 TTAA
TTCACATT GTTGTATGT
||||| |||||
AAGTGTGA TAACATACA

GAM847 ABCC3 3' CCCCAGGCTATGCCATCA 21291 CA A TTCTG
TGA GCATG CCT GGGG
|| ||||| || ||||
ACT CGTAT GGA CCCC
AC C

GAM847 ACVR1B 3' TCCCCCAGAGCCCCTCATGC 10512 CCT_
GCATGA TTCTGGGGGA
||||| |||||
CGTACT GAGACCCCCT
CCCC

GAM847 BLTR2 5' TCCCCCAGCTCTATCCATCTGC 21246 A C ACCTTT_
CA TG CAG ATG CTGGGGGA
|| ||| |||||
AC GTC TAC GACCCCCT
C _ CTATCTC

GAM847 IGSF8 5' CCCCCAGAACCCGCGCCATC 27449 CA A ACCT
GA GC TG TTCTGGGGG
|| || |||||
CT CG GC AAGACCCCC
AC C CC_

GAM847 LPIN1 3' TCCAGAAAGTCACACTCTCA 33469 C CA C
TGA AG TGAC TTTCTGGG
||| || |||||
ACT TC ACTG AAAGACCT
C AC _

GAM847 SH3BP4 3' TCCCAGAGACCATCTATCA 15854 C C ACC
TGA AG ATG TTTCTGGGG
||| || |||||
ACT TC TAC AGAGACCCT
A _ C_

GAM847 TIMP3 3' AGAAAGGTCTATGCTGTCA 5925 _
TGACAGCAT GACCTTTCT
||||| |||||
ACTGTCGTA CTGGAAAGA
T

GAM847 AFAP 3' CCCCCAGACATACTTTCA 22292 C C ACCTT
TGA AG ATG TCTGGGGG
||| || |||||
ACT TC TAC AGACCCCC
T A _

GAM847 ARFD1 3' TCAGGTAAAAGGTCATGCTGTT 7373 _
A TGACAGCATGACCTT TCTGG
||||||| |||||

ATTGTCGTA CTGGAA GGACT

AAT

GAM847 ARNTL2 3' TCCAGTTTCAGATCATGCTGCC 21417 A C TT__
A TG CAGCATGA CT CTGGG

|| ||||| || ||||

AC GTCGTA CT GA GACCT

C A CTTT

GAM847 CYP2S1 3' CCCCCTCCGGGGTCATGC 24964 TCT
GCATGACCTT GGGGG

||||||| ||||

CGTACTGGGG CCCCC

CCT

GAM847 FBXO26 5' CCCCCTGGGCCACGCCGATCA 24404 CA_ A A TTCT
TGA GC TG CCT GGGGG

|| |||| ||||

ACT CG AC GGG CCCCC

AGC C C T__

GAM847 FLJ12587 3' TCCCCAGGAGACCACGCTG 22853 A ACC
CAGC TG TTTCTGGGGG

|||| || |||||

GTCG AC GAGGACCCCT

C CA_

GAM847 FLJ20174 3' TCCCCCAGGTTTCTGATGCCAT 19272 CA GACCTT
CA TGA GCAT TCTGGGGGA

|| |||| |||||

ACT CGTA GGACCCCT

AC GTCTTT

GAM847 KIAA1396 3' TCCCCCTTGGGTGCCTATGC 31548 __ TTCT
GCATG ACCT GGGGGA

|||| |||| |||||

CGTAT TGGG CCCCCT

CCG TT__

GAM847 MGC2752 5' TCCCAGGAGGCCACACTGCA 38369 A CA A T
TG CAG TG CCTT CTGGGG

|| |||| |||||

AC GTC AC GGAG GACCCT

_ AC C _

GAM847 NXPH3 3' CCCCCACATCATGCTTC 32716 C CCTTTC
GA AGCATGA TGGGGG

|| ||||| ||||

CT TCGTA CT ACCCCC

_ AC__

GAM847 LOC145501 3' TCCCATGTCATGCTGCCA 37885 A CTTTC
TG CAGCATGAC TGGGG

|| ||||| ||||

AC GTCGTA CT ACCCT

C T__

GAM848 CEACAM1 3' CAGAAACAACCTTTCTCC 7439 A A
A AGAAAGTTGT TTCTG

| ||||| ||||

C TCTTTCAACA AAGAC
 C _
 GAM848 EPB49 3' ACCGGGCAGAAGCTGGGCCTTC 7707 A GTA_
 GAA GTT TTCTGCCCCGT
 ||| ||| |||||
 CTT CGG AAGACGGGCCA
 C GTCG
 GAM848 MGAT2 3' ACCTTCATAGAACACACTTTTCT 8230 T A CCC_
 TT AAAGAAAGT GT TTCTG GGT
 ||||| || ||| |||
 TTTCTTTCA CA AAGAT CCA
 _ C ACTT
 GAM848 PHLDA3 3' ACCGGGCGCACCATCTTTC 14758 T TATTC
 GAAAG TG TGCCCCGT
 |||| || |||||
 CTTTC AC GCGGGCCA
 T CAC_
 GAM848 DRCTNNB1A 3' ACCTGGAAATACAACCTTTGCTT 26315 _ CTG C
 AAG AAAGTTGTATT CC GGT
 ||| ||||| || |||
 TTC TTTCAACATAA GG CCA
 G A_ T
 GAM848 KIAA0876 3' ACCTTTGCAGAATAAACTCTCT 32292 A A G CC_
 CC A AGA AGTT TATTCTGC GGT
 | ||| ||| ||||| |||
 C TCT TCAA ATAAGACG CCA
 C C _ TTT
 GAM848 L3MBTL2 3' CCAAGCAGAATGCCTCTC 42786 A TT CC
 GA AG GTATTCTGC GG
 || || ||||| ||
 CT TC CGTAAGACG CC
 C _ AA
 GAM848 OAZIN 3' ACCAGACAAAATCAGCTTTC 18019 T C CCC
 GAAAGTTG ATT TG GGT
 ||||| ||| || |||
 CTTTCGAC TAA AC CCA
 _ A AGA
 GAM848 LOC146336 3' ACCTCAGAATGCAACCTTC 38132 A CCC
 GAA GTTGTATTCTG GGT
 ||| ||||| ||| |||
 CTT CAACGTAAGAC CCA
 C T_
 GAM849 HNRPD L 3' AAAAGGTATCTTGGTTATGA 11946 _ C
 TCATA CCA AGGTACCTTTT
 |||| ||| |||||
 AGTAT GGT TCTATGGAAAA
 T _
 GAM849 IDH3A 3' AAAAGAGTGAATGTGGTAT 12050 GG _
 ATACCACA TAC CTTTT
 ||||| ||| |||||

			TATGGTGT GTG GAAAA	
			AA A	
GAM849	IRS1	3'	AAAAGAGTAGAATAGGGTATGA 12067	ACAGG_ _
	T		ATCATACC TAC CTTTT	
			TAGTATGG ATG GAAAA	
			GATAAG A	
GAM849	PAG	3'	AAAAGGCAGGAAAGTAGGTATG 20507	_ AGGTA__
	AT		ATCATACC AC CCTTTT	
			TAGTATGG TG GGAAAA	
			A AAAGGAC	
GAM849	TP63	3'	AAAAGGTATTATACATGTGAT 9813	CCACA
			ATCATA GGTACCTTTT	
			TAGTGT TTATGGAAAA	
			ACATA	
GAM849	ARHE	3'	AAAAGGTGTCTTGTTTGAT 11665	T C GT
			ATCA ACCA AG ACCTTTT	
			TAGT TGGT TC TGGAAAA	
			T _ TG	
GAM849	CCR8	3'	AAAAAGTGCCTGTAGATGA 11700	ACC C
			TCAT ACAGGTAC TTTT	
			AGTA TGTCCGTG AAAA	
			GA_ A	
GAM849	FLJ10110	3'	AAAAGTTTATTTGTGGTAT 19726	C_
			ATACCACAGGTA CTTTT	
			TATGGTGTAT GAAAA	
			TT	
GAM849	FLJ10895	3'	AAAATGTATCTGTGTTACGA 21156	A C C
			TC TA CACAGGTAC TTTT	
			AG AT GTGTCTATG AAAA	
			C T T	
GAM849	KIAA0419	5'	AAAAGGTACCTGTACTTATG 16257	CC_
			CATA ACAGGTACCTTTT	
			GTAT TGTCCATGGAAAA	
			TCA	
GAM849	KIAA0445	5'	AAAAGGTAGAACTTGGATGAT 16144	A C G_
			ATCAT CCA AG TACCTTTT	
			TAGTA GGT TC ATGGAAAA	
			_ _ AAG	
GAM849	KIAA1627	3'	AAAAGATCCAGTCTGTGGTAT 39343	TAC__
			ATACCACAGG CTTTT	

			TATGGTGTCT	GAAAA	
			GACCTA		
GAM849	MAP2K6	3'	AAAAGGTGCTACGGTAGTGAT	25699	_ ACA
			ATCAT ACC GGTACCTTTT		
			TAGTG TGG TCGTGGA AAA		
			A CA_		
GAM849	MAP2K6	3'	AAAAGGTGCTACGGTAGTGAT	8639	_ ACA
			ATCAT ACC GGTACCTTTT		
			TAGTG TGG TCGTGGA AAA		
			A CA_		
GAM849	NID2	3'	AAAAGGTGCTAAAATGAT	35875	ACCACA
			ATCAT GGTACCTTTT		
			TAGTA TCGTGGA AAA		
			AAA_		
GAM849	LOC128338	5'	AAAAGGTGCAGGTATGA	36924	ACAG
			TCATACC GTACCTTTT		
			AGTATGG CGTGGA AAA		
			A_		
GAM849	LOC130507	3'	AAAATGTACTGGTGTGAT	36994	CAG C
			ATCATACCA GTAC TTTT		
			TAGTGTGGT CATG AAAA		
			_ T		
GAM849	LOC137090	5'	AAGAGGTACCCATAAATGAT	37392	ACCACA
			ATCAT GGTACCTTTT		
			TAGTA CCATGGAGAA		
			AATAC_		
GAM849	LOC144262	5'	AAAAGGTACCTGAGGATG	37702	A A
			CAT CC CAGGTACCTTTT		
			GTA GG GTCCATGGA AAA		
			_ A		
GAM849	LOC145482	3'	AAAAGAGACTTAATGGTATGAT	37876	C_ AC
			ATCATACCA AGGT CTTT		
			TAGTATGGT TTCA GAAAA		
			AA GA		
GAM849	LOC149579	5'	AAAAGGTAGAACTTGGATGAT	35240	A C G_
			ATCAT CCA AG TACCTTTT		
			TAGTA GGT TC ATGGA AAA		
			_ _ AAG		
GAM849	LOC154792	3'	AAAAGGGGGTGGTATGA	41727	_ AGGTA
			TCAT ACCAC CCTTTT		

			AGTA TGGTG GGAAAA		
			G GG__		
GAM850	ACTN2	3'	GCTTCTGTAATCACTCATCC 6758	A __ C	
			A ATG G GAT ACAGAAGC		
			C TAC C CTA TGTCTTCG		
			C T A A		
GAM850	B4GALT1	3'	CTTCTGTGTTATTTTA 7247	GAT	
			TAAAATGG CACAGAAG		
			ATTTTATT GTGTCTTC		

GAM850	BRPF1	3'	GGCCTCTGCACTGACTCATTT 36174	A __ A	
			AAATGGG TCA CAGA GCC		
			TTTACTC AGT GTCT CGG		
			_ CAC C		
GAM850	CEACAM6	3'	GCTCCTCCAATCCCATTTTA 8310	CAC A	
			TAAAATGGGAT AG AGC		
			ATTTTACCCTA TC TCG		
			ACC C		
GAM850	CRTAP	3'	GGCTTTTGCCCCACTTTG 13062	A ATCA	
			TAAA TGGG CAGAAGCC		
			GTTT ACCC GTTTTCGG		
			C C__		
GAM850	DPP4	3'	CTTCCTTGGA CTCA TTTTA 7648	A CA	
			TAAAATGGG TCA GAAG		
			ATTTTACTC GGT CTTC		
			A TC		
GAM850	FSTL1	3'	GGCTTCTATATTGCATTT 13952	G CAC	
			AAATG GAT AGAAGCC		
			TTTAC TTA TCTTCGG		
			G TA_		
GAM850	FUT9	3'	CTTTTATATCCCATTTTG 33701	CAC	
			TAAAATGGGAT AGAAG		
			GTTTTACCCTA TTTTC		
			TA_		
GAM850	GM2A	3'	CTTCTGTGACTAATTTTTA 33660	TG_ A	
			TAAAA GG TCACAGAAG		
			ATTTT TC AGTGTCTTC		
			TAA _		
GAM850	NUP62	3'	GGCTTCTGTGGCTTTTCATTT 18629	GG _	
			AAATG A TCACAGAAGCC		

		TTTAC T GGTGTCTTCGG	
		TT C	
GAM850	PLAG1	3' CTTTACAAATCCCATTTT 8522	CAC_
		AAAATGGGAT AGAAG	
		TTTTACCCTA TTTTC	
		AACA	
GAM850	PLXNA2	3' GGCCTCCACGAGGTTCCATTT 24815	ACA__ A
		AAATGGGATC GA GCC	
		TTTACCTTGG CT CGG	
		AGCAC C	
GAM850	PPP2R5B	3' GGCTTCTGAGGACTCCCA 12914	_ A_
		TGGGA TC CAGAAGCC	
		ACCCT AG GTCTTCGG	
		C GA	
GAM850	TRRAP	3' GGCTCCTGTGCTTTTTTAT 9590	T_ A
		ATGGGA CACAG AGCC	
		TATTTT GTGTC TCGG	
		TC C	
GAM850	VTN	5' GGCTTTGTTAATCCTATTTTA 6273	CACA
		TAAAATGGGAT GAAGCC	
		ATTTTATCCTA TTTCGG	
		ATTG	
GAM850	C22orf5	3' GGCTTCTCCCTCCCGTTT 14584	TCAC
		AAATGGGA AGAAGCC	
		TTTGCCCT TCTTCGG	
		CCC_	
GAM850	CARD14	3' GGCTTCTGTGTGCCTGTT 23557	AT
		AATGGG CACAGAAGCC	
		TTGTCC GTGTCTTCGG	
		GT	
GAM850	CEACAM7	3' GCTCCTTCAATCCCATTTT 13757	CAC A
		AAAATGGGAT AG AGC	
		TTTTACCCTA TC TCG	
		ACT C	
GAM850	CENTG2	3' GGCTTCTGTGTTATGTATTT 17159	GGAT_
		AAATG CACAGAAGCC	
		TTTAT GTGTCTTCGG	
		GTATT	
GAM850	CUGBP2	3' GGCTCCCTGCTCTCATTTTA 13331	TCA A_
		TAAAATGGGA CAG AGCC	

ATTTTACTCT GTC TCGG
 C__ CC
 GAM850 CXYorf1 5' GCCTCTGTGATCTTCTCCAT 39909 ____ A
 ATGG GATCACAGA GC
 ||| ||||| ||
 TACC CTAGTGTCT CG
 TCTT C
 GAM850 FLJ10716 3' GGCTTTTCTTGAGCCCATTTTA 20047 A C_
 TAAAATGGG TCA AGAAGCC
 ||||| || |||||
 ATTTTACCC AGT TTTTCGG
 G TC
 GAM850 FLJ10719 3' GGCTTCTGCTTCATTTT 31340 ATCA
 AAAATGGG CAGAAGCC
 ||||| |||||
 TTTTACTT GTCTTCGG
 C__
 GAM850 FLJ20296 3' GGCTTCTGCTCTCATTCA 19355 A TCA
 A AATGGGA CAGAAGCC
 | ||||| |||||
 A TTA CTCT GTCTTCGG
 C C_
 GAM850 FLJ20772 3' GGCTTCTGTGGTTGTCCA 19666 ____
 TGG GATCACAGAAGCC
 ||| |||||
 ACC TTGGTGTCTTCGG
 TG
 GAM850 FLJ22215 3' GGCTTCTGTGGACGACTCA 46282 A__
 TGGG TCACAGAAGCC
 ||| |||||
 ACTC GGTGTCTTCGG
 AGCA
 GAM850 FLJ32752 5' GGCTTCTGTCTGTATCTCA 29482 ____
 TGGGAT C ACAGAAGCC
 ||||| | |||||
 ACTCTA G TGTCTTCGG
 T TC
 GAM850 GAB3 3' GGCCTCTGGAGACCATCTTG 27928 A GA A A
 TAA ATGG TC CAGA GCC
 ||| ||| || ||| |||
 GTT TACC AG GTCT CGG
 C AG _ C
 GAM850 GR6 3' CTTCTGTCCCATTTT 14284 TCA
 AAAATGGGA CAGAAG
 ||||| |||||
 TTTTACCCT GTCTTC

 GAM850 HSPC213 3' GCAATGTGTTCCCATTTTA 18576 T GAA
 TAAAATGGGA CACA GC
 ||||| ||| ||

		ATTTTACCCT GTGT CG	
		T AA_	
GAM850	IL17D	3' GGCTTCTGTTTCTGCATT 28700	_ TC
		AATG GGA ACAGAAGCC	
		TTAC TCT TGTCTTCGG	
		G T_	
GAM850	KHDRBS1	3' GGCTTCTGTATGTAGTATTTT 13328	GG C_
		AAAATG AT ACAGAAGCC	
		TTTTAT TG TGTCTTCGG	
		GA TA	
GAM850	KIAA0298	3' GGCTTCCGTGATCCCGTTTT 37627	A
		AAAATGGGATCAC GAAGCC	
		TTTTGCCCTAGTG CTTCGG	
		C	
GAM850	KIAA0461	3' GCTTTTGCCTGATGCCATTTT 35075	G C__
	A	TAAAATGG ATCA AGAAGC	
		ATTTTACC TAGT TTTTCG	
		G CCGT	
GAM850	KIAA0493	3' GGCTCTTTAATCTCATTTTA 32142	CAC A
		TAAAATGGGAT AGA GCC	
		ATTTTACTCTA TCT CGG	
		ATT _	
GAM850	KIAA0766	3' GGCTTCTGTTGGCATT 16743	GGA _
		AAATG TCA CAGAAGCC	
		TTTAC GGT GTCTTCGG	
		_ T	
GAM850	KIAA0853	3' CTCCTGTGAGCCTCAATTTTA 17437	_ A_ A
		TAAAAT GGG TCACAG AG	
		ATTTTA CTC AGTGTC TC	
		A CG C	
GAM850	KIAA0978	3' CTTCAAGTCTCATTTTA 34887	CACA
		TAAAATGGGAT GAAG	
		ATTTTACTCTG CTTC	
		AA_	
GAM850	KIAA1530	3' GGCTTCTGCGAGTCCTCG 33735	T _ A
		A GGGG TC CAGAAGCC	
		G TCCT AG GTCTTCGG	
		C G C	
GAM850	KIAA1559	3' GCTTCTGTGCCTCATTTTG 36164	AT
		TAAAATGGG CACAGAAGC	

GTTTTACTC GTGTCTTCG
 C_
 GAM850 MGC2835 3' GGCCTGGTCTGATCTCATTTTA 23506 ____ AA
 TAAAATGGGATCA CAG GCC
 ||||| ||| |||
 ATTTTACTCTAGT GTC CGG
 CTG _
 GAM850 MGC2865 5' GCCCCTGTGGCCGCCATCTTG 26168 A GA_ AA
 TAA ATGG TCACAG GC
 ||| ||| ||||| ||
 GTT TACC GGTGTC CG
 C GCC CC
 GAM850 MGC3130 3' GGCTTCTGTGGTTGCTCCCA 23461 ____
 TGGGA TCACAGAAGCC
 |||| |
 ACCCT GGTGTCTTCGG
 CGTT
 GAM850 moblak 3' GGCTTCTGACTCATTT 28309 ATCA
 AAATGGG CAGAAGCC
 |||| |
 TTTACTC GTCTTCGG
 A_
 GAM850 MYOZ2 3' CTTCTGTGATAGATGTTT 18692 GG_
 AAATG ATCACAGAAG
 |||| |
 TTTGT TAGTGTCTTC
 AGA
 GAM850 NDP52 3' GGCTTCTGCTGCCATCCT 12444 _ _
 GGGAT CA CAGAAGCC
 |||| ||
 TCCTA GT GTCTTCGG
 CC C
 GAM850 NEIL2 3' GCTCCTGTGTTTTGTTTT 29675 GG T A
 AAAAT GA CACAG AGC
 |||| ||
 TTTTG TT GTGTC TCG
 TT _ C
 GAM850 NRF 5' GGCTTCTGAGTCCATTT 18988 ATCA
 AAATGGG CAGAAGCC
 |||| |
 TTTACCT GTCTTCGG
 GA_
 GAM850 NUDT11 3' GCTTGGACTCCATTTTA 30144 GA A GA
 TAAAATGG TC CA AGC
 ||||| || |||
 ATTTTACC AG GT TCG
 TC _ _
 GAM850 PACSIN2 3' GCTTACATCCCATTTTG 14097 CACAG
 TAAAATGGGAT AAGC
 ||||| |||

			GTTTTACCCTA	TTCG	
			CA__		
GAM850	PPP1R10	3'	GGCTTCTGTGAGGCCCATTTT	8577	A_
			AAAATGGG TCACAGAAGCC		
			TTTTACCC AGTGTCTTCGG		
			GG		
GAM850	RBT1	3'	GGCCTCCTTTGTTCCCATTT	15011	T CA_ A
			AAATGGGA CA GA GCC		
			TTTACCCT GT CT CGG		
			T TTC C		
GAM850	SLC39A3	3'	GGCTTCTGGGGCCATCTTG	29359	A GA A
			TAA ATGG TC CAGAAGCC		
			GTT TACC GG GTCTTCGG		
			C G_ _		
GAM850	SV2	3'	GCCTCAGTTTCCCCATTTTA	16885	ATC A A
			TAAAATGGG AC GA GC		
			ATTTTACCC TG CT CG		
			CTT A C		
GAM850	TAF9L	3'	TTTCTAGATCCCATTCA	18075	A AC
			A AATGGGATC AGAAG		
			A TTACCCTAG TCTTT		
			C A_		
GAM850	TUBB5	3'	TCTATGAGTCCCATTTTA	12730	_ C
			TAAAATGGGA TCA AGA		
			ATTTTACCCT AGT TCT		
			G A		
GAM850	UBP1	3'	CTTCTATTCCATTTTA	15847	CAC
			TAAAATGGGAT AGAAG		
			ATTTTACCTTA TCTTC		

GAM850	LOC125456	5'	GCTGCTTGTTCCCATTTTA	37266	T C A
			TAAAATGGGA CA AG AGC		
			ATTTTACCCT GT TC TCG		
			T _ G		
GAM850	LOC125929	3'	CTTCTGTGAAGCTCCCAT	37269	_____
			ATGGGA TCACAGAAG		
			TACCCT AGTGTCTTC		
			CGA		
GAM850	LOC144438	3'	GCTTCTGTAAATCTCATT	37738	C_
			AATGGGAT ACAGAAGC		

		TTACTCTA TGTCTTCG	
		AA	
GAM850	LOC146733 3'	GCTTCATGATCTCATTTTA 40730	CA
		TAAAATGGGATCA GAAGC	
		ATTTTACTCTAGT CTTCG	
		A_	
GAM850	LOC149668 3'	GGCTTCTGTAGGTGCTCCCA 41030	___ _
		TGGGA TC ACAGAAGCC	
		ACCCT GG TGTCTTCGG	
		CGT A	
GAM850	LOC149911 5'	GCTTCTGTGGATTTCTAT 41083	___
		ATGGGA TCACAGAAGC	
		TATCTT GGTGTCTTCG	
		TA	
GAM850	LOC150271 5'	GCCTGTCCCCATTTTG 41172	ATC AA
		TAAAATGGG ACAG GC	
		GTTTTACCC TGTC CG	
		C_ _	
GAM850	LOC151647 3'	CTTCTGTGTTAGCCATCTTA 39155	A GAT_
		TAA ATGG CACAGAAG	
		ATT TACC GTGTCTTC	
		C GATT	
GAM850	LOC152220 3'	CTTCTTCCCATTTTG 41444	TCAC
		TAAAATGGGA AGAAG	
		GTTTTACCCT TCTTC	

GAM850	LOC155054 3'	GGCTCCCGCCTGTAATCCCAT 39540	C A_____
		ATGGGAT ACAG AGCC	
		TACCCTA TGTC TCGG	
		A CGCCC	
GAM850	LOC158055 3'	GGCTTCTGTTGGCTCCTA 39706	_ _
		TGGGA TCA CAGAAGCC	
		ATCCT GGT GTCTTCGG	
		C T	
GAM850	LOC200093 5'	GCCTCTGTGATCTTCTCCAT 31601	___ A
		ATGG GATCACAGA GC	
		TACC CTAGTGTCT CG	
		TCTT C	
GAM850	LOC200310 3'	GCATTGTCCCATTTTA 32709	CACA A
		TAAAATGGGAT GA GC	

		ATTTTACCCTG TT CG	
		_____ A	
GAM850	LOC202024 5'	GCTTCTGTGGGATATTTTG 42959	GGA
		TAAAATG TCACAGAAGC	
		GTTTTAT GGTGTCTTCG	
		AG_	
GAM850	LOC202347 5'	GCTTCTGAGCCATTTTG 43431	GATCA
		TAAAATGG CAGAAGC	
		GTTTTACC GTCTTCG	
		GA_	
GAM850	LOC202934 5'	GCCTCTAATGATCCTTTTTA 43461	T C_ A
		TAAAA GGGATCA AGA GC	
		ATTTT TCCTAGT TCT CG	
		_ AA C	
GAM850	LOC220514 3'	GCTTACATCCCATTTTG 30321	CACAG
		TAAAATGGGAT AAGC	
		GTTTTACCCTA TTCG	
		CA_	
GAM850	LOC220776 3'	GGCCTGCAAATCCCATTT 33935	CA_ AA
		AAATGGGAT CAG GCC	
		TTTACCCTA GTC CGG	
		AAC _	
GAM850	LOC221931 3'	GGCTTCTGCAGGAGGCCATT 45119	GA A_
		AATGG TC CAGAAGCC	
		TTACC AG GTCTTCGG	
		GG GAC	
GAM850	LOC253675 3'	GGCTTCTGCAGTCATGTTT 46265	GG CA
		AAAT GAT CAGAAGCC	
		TTTG CTG GTCTTCGG	
		TA AC	
GAM850	LOC253782 3'	GGCCTGAATCTTCCATTTTA 45798	TCA_ AA
		TAAAATGGGA CAG GCC	
		ATTTTACCTT GTC CGG	
		CTAA _	
GAM850	LOC254428 3'	CGGCCCTGTGATCCCA 45718	AA
		TGGGATCACAG GCC G	
		ACCCTAGTGTC CGG C	
		CC	
GAM850	LOC254848 5'	GGCCTCAATGTTCTCATTTTA 46381	T CA A
		TAAAATGGGA CA GA GCC	

		ATTTTACTCT GT CT CGG		
		T AA C		
GAM850	LOC56267	3' GCTTCTGTGAGGACCTTTTG 21228	T GA_	
		TAAAA GG TCACAGAAGC		
		GTTTT CC AGTGTCTTCG		
		_ AGG		
GAM850	LOC57105	3' GCTCTGAGTTCCATTTTA 21641	CA A	
		TAAAATGGGAT CAGA GC		
		ATTTTACCTTG GTCT CG		
		A_ _		
GAM850	LOC83693	3' GCCTCTGACCCATTTTA 25496	ATCA A	
		TAAAATGGG CAGA GC		
		ATTTTACCC GTCT CG		
		A_ _ C		
GAM850	LOC90670	3' GGCCTGTAGCCCCATTTT 31882	ATC AA	
		AAAATGGG ACAG GCC		
		TTTTACCC TGTC CGG		
		CGA _		
GAM850	LOC91040	5' GCCTCTGTGATCTTCTCCAT 32318	_ A	
		ATGG GATCACAGA GC		
		TACC CTAGTGTCT CG		
		TCTT C		
GAM850	LOC96597	3' GGCCTTGAAAAATCCCATTCA 33232	A CA_ AA	
		A AATGGGAT CAG GCC		
		A TTACCCTA GTT CGG		
		C AAAG C_		
GAM851	CLCA2	3' TGTATTA AAAATGCATTG 13290	TGTA	
		TAATGC TTTAATACA		
		GTTACG AAATTATGT		
		TA_		
GAM851	PTTG1IP	3' TTGTATTA AATAGCATTG 10540	AT	
		TAATGCTGT TTAATACAA		
		GTTACGATA AATTATGTT		
		_		
GAM851	XK	3' TTGTCAAATACAGCATT 22063	AAT	
		AATGCTGTATTT ACAA		
		TTACGACATAAA TGTT		
		C_		
GAM851	DKFZp564K142	3' GTATCTCTAAATACAGGATTA 25807	G _	
		TAAT CTGTATTTA ATAC		

		ATTA GACATAAAT TATG		
		G CTC		
GAM851	FLJ13197 3'	TGTTTAAAAACAGCATT 23876	A	T
		TAATGCTGT TTAA ACA		
		ATTACGACA AAATT TGT		
		A _		
GAM851	KIAA0186 3'	TGTATCTGTAATCACAGCATT 22040	AT	___
		AATGCTGT TTA ATACA		
		TTACGACA AAT TATGT		
		CT GTC		
GAM851	MGC4562 3'	AGTTGCATTAAATAAAGTAT 28497	G	A
		ATGCT TATTTAAT CAACT		
		TATGA ATAAATTA GTTGA		
		A C		
GAM851	LOC151258 5'	GTAAAAATACAGCATTG 39091	AA	
		TAATGCTGTATTT TAC		
		GTTACGACATAAA ATG		
		A_		
GAM851	LOC157798 5'	AGTTGTATTGAGTACAGC 41845		
		GCTGTATTTAATACAACT		
		CGACATGAGTTATGTTGA		
GAM851	LOC200803 3'	AGTTGTATTGGATTACATTA 42855	CTGT	
		TAATG ATTTAATACAACT		
		ATTAC TAGGTTATGTTGA		
		AT_		
GAM851	LOC256642 3'	TTGTACTTTACTACTACAGCAT 46080	TT_	__
	TA	TAATGCTGTA TAA TACAA		
		ATTACGACAT ATT ATGTT		
		CATC TC		
GAM851	LOC89932 3'	GTCATTAAAAACAGCATT 30493	A	_
		TAATGCTGT TTAAAT AC		
		ATTACGACA AAATTA TG		
		A C		
GAM852	KCNAB2 3'	CCAAGTCGCTGCCAGACACCA 9705	AG	C_ GTAG
		TG GTC GC AGCGACTTGG		
		AC CAG CG TCGCTGAACC		
		CA AC _		
GAM852	LTF 5'	CCAAGTCGCCTCCAGACCGCA 8142	A	CGCGT A
		TG GGTC AG GCGACTTGG		

			AC CCAG TC CGCTGAACC	
			G ACC__ _	
GAM852	FLJ20294	3'	CCAAGCAGAAACCGGACCTCA 19344	C AGAGCGA
			TGAGGTCCG GT CTTGG	
			ACTCCAGGC CA GAACC	
			_ AAGAC__	
GAM853	LOC168512	5'	ATATACGAGGTGAAACATTA 40251	C
			TAATGT TTATCTCGTATAT	
			ATTACA AGTGGAGCATATA	
			A	
GAM853	LOC200059	3'	ATATATTTTGTATAAGACAT 42699	CT T_
			ATGTCTTAT CG ATATAT	
			TACAGAATA GT TATATA	
			TT TT	
GAM853	LOC81537	3'	ATGTAAAAATAAGACATTA 25087	CTCG
			TAATGTCTTAT TATAT	
			ATTACAGAATA ATGTA	
			AAA_	
GAM854	EGLN1	5'	ATCCTGCTTTTGAAATACATAT 22581	C TTGACC
	T		AATA GT AAAGCAGGAT	
			TTAT CA TTTCGTCCTA	
			A TAAAGT	
GAM854	KIP2	3'	ATCCTGCCCTGCAGTCACATG 13087	T __ AA
			CGT TGAC CA GCAGGAT	
			GTA ACTG GT CGTCCTA	
			C AC CC	
GAM854	MTMR8	3'	CCTGCTTTAGAGCTGTGTGTTG 17743	TTTGACC
			CAATACG AAAGCAGG	
			GTTGTGT TTTCGTCC	
			GTCGAGA	
GAM854	UBE2A	3'	CCTCTATGAAATCAAATGTACT 9340	A C__ A C
	G		CA TACGTTTGA CA AG AGG	
			GT ATGTAAACT GT TC TCC	
			C AAA A _	
GAM854	BLZF1	5'	ATCCTGCTCTTTTGAAACGTA 9749	GA ____
	TT		AATACGTTT CCAA AGCAGGAT	
			TTATGCAAA GGTT TCGTCCTA	
			_ TTC	
GAM854	FLJ20069	3'	TTGTTGGTCAAAGTATTG 19160	G AA
			CAATAC TTTGACCA GCAG	

GTTATG AAAC TGGT TGTT

GAM854 LCE 3' ATCCTGCTTCAAGTCAGC 23533 T CA_
GTT GAC AAGCAGGAT
||| ||| |||||
CGA CTG TTCGTCCTA
_ AAC

GAM854 LOC147219 5' CCGTGTTTTGGTCAAACGTA 40821 _
TACGTTTGACCAAAGCA GG
||||||| ||
ATGCAAAC TGGTTTTGT CC
G

GAM855 EHF 3' GAAACAAAGAACTCCTGGA 14451 G AC GGTG
TC CAGGA TC TTGTTTC
|| ||| || |||||
AG GTCCT AG AACAAAG
_ CA A__

GAM855 ESR1 3' AGAAACAACATACTTGTCCCAT 5598 CA ACTCG
GA TCG GGA GTGTTGTTTCT
||| ||| |||||
AGT CCT TACAACAAAGA
AC GTTCA

GAM855 FLJ11053 3' AGAAACTCTAAGTTCCTGGGA 42776 G CG TGTT
TC CAGGAACT G GTTTCT
|| ||||| | |||||
AG GTCCTTGA C CAAAGA
G ATT__

GAM855 FLJ11827 3' AGAAACAAATCATTCGTGC 24720 G CTC G
GCA GAA GGT TTGTTTCT
||| ||| ||| |||||
CGT CTT CTA AACAAAGA
G A__ _

GAM855 LOC253664 3' AGAAACAACACCACAGAACCC 45447 AA_ C_
GG CT GGTGTTGTTTCT
|| || |||||
CC GA CCACAACAAAGA
CAA CA

GAM856 SPOCK 5' CAGGACTACCAGACCGCC 31455 AAT ACA
GGC GTTT TAGTCCTG
||| ||| |||||
CCG CAGA ATCAGGAC
C__ CC_

GAM856 BOP 5' AGGACTACCATTGACCTC 41207 _ TTTACA
GAGG CAATG TAGTCCT
||| ||| |||||
CTCC GTTAC ATCAGGA
A C__

GAM856 CHR FAM7A 3' CAGAACTCCTACATTGCCTGG 45552 G TTACAT C
C AGGCAATGT AGT CTG
| ||||| ||| |||

G TCCGTTACA TCA GAC
 G TCC__ A
 GAM856 KIAA1416 3' CAGAACTACAGTTCCATTGTCT 41799 TTT A_ C
 CG CGAGGCAATG AC TAGT CTG
 ||||| || |||||
 GCTCTGTTAC TG ATCA GAC
 CT_ AC A
 GAM856 LBP-9 3' GGATGTAGACATTGCC 15878 TAG
 GGCAATGTTTACA TCC
 ||||| |||
 CCGTTACAGATGT AGG

 GAM856 LOC132625 3' AGTGACAAACATGCCTC 37371 A ACATA _
 GAGGCA TGTTT GTC CT
 ||||| ||| |||
 CTCCGT ACAA CAG GA
 _ _ T
 GAM856 LOC148811 3' ACATTGTAAACATTGCC 38597 _ TA
 GGCAATGTTT ACA GT
 ||||| ||| |||
 CCGTTACAAA TGT CA
 A TA
 GAM856 LOC256733 5' CAGGATGTGAAAAGATTGCCTC 46367 G A G
 GAGGCAAT TTT CATA TCCTG
 ||||| ||| ||| |||||
 CTCCGTTA AAA GTGT AGGAC
 G A _
 GAM856 LOC90936 5' CAGGACTACGTAAATTGGACT 32188 GCAAT A
 AG GTTTAC TAGTCCTG
 || ||||| |||||
 TC TAAATG ATCAGGAC
 AGGT_ C
 GAM857 EDN3 3' TATACCGTCTGACAGTTCAAA 5583 A AATGT
 TTT AACTGTTA TGGTATA
 ||| ||||| |||||
 AAA TTGACAGT GCCATAT
 C CT__
 GAM857 DKFZP564F013 3' TATACCTCTCAACAGTTTA 45203 AAATGTT
 TAAACTGTT GGTATA
 ||||| |||||
 ATTTGACAA CCATAT
 CTCT__
 GAM857 EPN2 3' TATACCAACATCCTGAAAGTT 17350 G A_
 AACT TTA ATGTTGGTATA
 ||| ||| |||||
 TTGA AGT TACAACCATAT
 A CC
 GAM857 KIAA1486 3' TACCAACATTTAAAGCTTAAA 33463 A G
 TTAA CT TTAAATGTTGGTA
 ||||| ||| |||||

			AAATT GA AATTTACAACCAT	
			C _	
GAM857	USP15	3'	TAGCATTTAAAAGTTTAAA 13005	G
			TTTAAACT TTAAATGTTG	
			AAATTTGA AATTTACGAT	
			A	
GAM857	LOC152317	5'	TATACCAGCACATTAACA 41468	A_
			TGTTAA TGTTGGTATA	
			ACAATT ACGACCATAT	
			AC	
GAM858	KIAA0143	3'	TACTACTACACTTTACCA 32351	ATTAAA
			TGGTAAA TAGTAGTA	
			ACCATTT ATCATCAT	
			CAC__	
GAM858	SLC26A7	3'	TTATTTTATTTTACCATA 27417	T
			TATGGTAAAAT AAATAG	
			ATACCATTTTA TTTATT	
			T	
GAM858	LOC158292	5'	GTACTACTGTTTACTACCATA 41934	AAAT
			TATGGTA TAAATAGTAGTAC	
			ATACCAT ATTTGTCATCATG	
			C__	
GAM858	LOC158292	5'	TACTACCACCAAATTTTACCAT 41935	AAATA
			ATGGTAAAATT GTAGTA	
			TACCATTTTAA CATCAT	
			ACCAC	
GAM858	LOC92689	3'	ACTACTTATAGATTTTACC 34781	AAAT
			GGTAAAATT AGTAGT	
			CCATTTTAG TCATCA	
			ATAT	
GAM859	ADAM22	3'	ACTGTTTACATGTGATA 22323	CGCC
			TATCACATG GGCAGT	
			ATAGTGTAC TTGTCA	
			AT__	
GAM859	ADAM22	3'	ACTGTTTACATGTGATA 22325	CGCC
			TATCACATG GGCAGT	
			ATAGTGTAC TTGTCA	
			AT__	
GAM859	GBAS	3'	TGACTGTTACCATGTGA 7228	CGCC
			TCACATG GGCAGTCA	

			AGTGTAC TTGTCAGT		
			CA__		
GAM859	KPNA1	3'	TGACTCCTAAATGTGATA 39150	GCGCC	C
			TATCACAT GG AGTCA		
			ATAGTGTA CC TCAGT		
			AAT__ _		
GAM859	P4HA1	3'	ACTGGGTTCCATGTGAT 6624	C_	GG
			ATCACATG GCC CAGT		
			TAGTGTAC TGG GTCA		
			CT _		
GAM859	SLC1A4	3'	TGACTGTTTTGTACATGTGA 8999	CG	C_
			TCACATG C GGCAGTCA		
			AGTGTAC G TTGTCAGT		
			AT TT		
GAM859	C20orf13	3'	ACTGTCGCTGATGTGATA 19298	G	C
			TATCACAT CG CGGCAGT		
			ATAGTGTA GT GCTGTCA		
			_ C		
GAM859	DIS3	3'	TGACTGCCAGCAGTGGA 17305	A	GC C
			TC CAT GC GGCAGTCA		
			AG GTG CG CCGTCAGT		
			_ A_ A		
GAM859	DKFZp547A023	3'	TGACTGCCATATGAATGTGAT 35945	G	CC_
			ATCACAT CG GGCAGTCA		
			TAGTGTA GT CCGTCAGT		
			A ATA		
GAM859	FLJ13072	5'	TGACTGCCAATGTGTGAT 43237	CGCC	
			ATCACATG GGCAGTCA		
			TAGTGTGT CCGTCAGT		
			AA_		
GAM859	FLJ22794	5'	TTGTCGGCATGTAATA 44038	C	GC
			TAT ACAT GCCGGCAG		
			ATA TGTA CGGCTGTT		
			A _		
GAM859	ZNF197	3'	ACTGTTGGACAAATGATA 13855	CA	CG
			TATCA TG CCGGCAGT		
			ATAGT AC GGTGTGCA		
			AA A_		
GAM859	LOC115297	3'	TGACTGTGTCCATGTGATG 36073	C	CG
			TATCACATG GC GCAGTCA		

		GTAGTGTAC TG TGTCAGT	
		C _	
GAM859	LOC145790 3'	TGACTACTGCATGCATGTG 37980	C_ C
		CACATGCG CGG AGTCA	
		GTGTACGT GTC TCAGT	
		AC A	
GAM859	LOC145951 5'	TGGGGTCAACACATGTGATG 38017	CGCC AG
		TATCACATG GGC TCA	
		GTAGTGTAC CTG GGT	
		ACAA G_	
GAM859	LOC152220 3'	TGACTGCCTGGCACATAGT 41446	_ C _
		AC ATG GCC GGCAGTCA	
		TG TAC CGG CCGTCAGT	
		A A T	
GAM859	LOC199678 3'	TGACCATGACCATGTGATG 43228	CGC GCA
		TATCACATG CG GTCA	
		GTAGTGTAC GT CAGT	
		CA_ AC_	
GAM859	LOC254896 5'	TGACTGCTGCAAGTGA 45989	A GCC
		TCAC TGC GGCAGTCA	
		AGTG ACG TCGTCAGT	
		A _	
GAM859	LOC257478 5'	TGACTGCCAGCGTGCGGA 36184	ACA C
		TC TGCGC GGCAGTCA	
		AG GTGCG CCGTCAGT	
		GC_ A	
GAM859	LOC57147 3'	TGACTGTTCCACATGTAGTA 21681	C CGCC
		TAT ACATG GGCAGTCA	
		ATG TGTAC TTGTCAGT	
		A ACC_	
GAM860	KIAA0143 3'	TACTACTACACTTTACCA 32351	ATTAAA
		TGGTAAA TAGTAGTA	
		ACCATT TATCATCAT	
		CAC_	
GAM860	SLC26A7 3'	TTATTTTATTTTACCATA 27417	T
		TATGGTAAAAT AAATAG	
		ATACCATT TTA TTTATT	
		T	
GAM860	LOC158292 5'	GTACTACTGTTTACTACCATA 41934	AAAT
		TATGGTA TAAATAGTAGTAC	

			ATACCAT ATTTGTCATCATG	
			C__	
GAM860	LOC158292	5'	TACTACCACCAAATTTTACCAT 41935	AAATA
			ATGGTAAATT GTAGTA	
			TACCATTTTAA CATCAT	
			ACCAC	
GAM860	LOC92689	3'	ACTACTTATAGATTTTACC 34781	AAAT
			GGTAAATT AGTAGT	
			CCATTTTAG TCATCA	
			ATAT	
GAM861	ESRRG	3'	TGTTTTTCAAGTCTTCCAGGT 33001	C CCGTTATC
	A		TGCC GG GAAAAACA	
			ATGG CC CTTTTTGT	
			A TTCTGAA_	
GAM861	GPC4	3'	TGTTTTTTTTTAAACCAGGCA 7179	C CCG TC
			TGCC GG TTA GAAAAACA	
			ACGG CC AAT TTTTTTGT	
			A AA_ T_	
GAM861	KDR	5'	GTTTCCTCTGCCTGCGCCGGGC 8055	C TATC_ AA
	A		TGCCCGGC GT GA AAAC	
			ACGGGCCG CG CT TTTG	
			_ TCCGT CC	
GAM861	MSL3L1	3'	TTTTTTTGATGAAGCCGAGCA 13673	C CG
			TGC CGGC TTATCGAAAAAA	
			ACG GCCG AGTAGTTTTTTT	
			A A_	
GAM861	MSL3L1	3'	TTTTTTTGATGAAGCCGAGCA 27813	C CG
			TGC CGGC TTATCGAAAAAA	
			ACG GCCG AGTAGTTTTTTT	
			A A_	
GAM861	MSL3L1	3'	TTTTTTTGATGAAGCCGAGCA 27816	C CG
			TGC CGGC TTATCGAAAAAA	
			ACG GCCG AGTAGTTTTTTT	
			A A_	
GAM861	RGL	3'	TGTTTCCTGGTGGACAGCCGGG 17510	C _ AAA
	TA		TGCCCGGC GTT ATCG AAACA	
			ATGGGCCG CAG TGGT TTTGT	
			A G CC_	
GAM861	SP3	3'	TTTCAATAACGAAGTTGGGCA 40136	_ C
			TGCCCGGC CGTTAT GAAA	

ACGGGTTG GCAATA CTTT
 AA A
 GAM861 C21orf25 3' GTTCTCTCAGTTAGCAGCTGGG 31802 C TC_ AAA
 CA TGCCCGGC GTTA GA AAC
 ||||| ||| || |||
 ACGGGTCG CGAT CT TTG
 A TGA CTC
 GAM861 FLJ21106 3' TGTTTTTTCAGAATGGCC 24736 ATC
 GGCCGTT GAAAAACA
 ||||| |||||
 CCGGTAA CTTTTTTGT
 GA_
 GAM861 KIAA0427 3' TTTTATTGAGGCCGGGCA 16582 G TC
 TGCCCGGCC TTA GAAA
 ||||| ||| |||
 ACGGGCCGG AGT TTTT
 _ TA
 GAM861 PIP5K1C 3' GTTTTCTCCATGGCAGGACA 35019 C G TATC A
 TG CC GCCGT GA AAAAC
 || ||||| || |||||
 AC GG CGGTA CT TTTTG
 A A C__ C
 GAM861 TOM1 3' GTTCCTTCTGGCCGGGCA 11988 TTATC AA
 TGCCCGGCCG GAA AAC
 ||||| ||| |||
 ACGGGCCGGT CTT TTG
 ____ CC
 GAM861 LOC116028 3' TTTCCTAACGGCAGGCA 36494 CG TC
 TGCC GCCGTTA GAAA
 ||| ||||| |||
 ACGG CGGCAAT CTTT
 A_ C_
 GAM861 LOC150848 3' TGTTTTTCTTCTGCCAGGCA 41260 C_ CGTTATC
 TGCC GGC GAAAAACA
 ||| ||| |||||
 ACGG CCG CTTTTTTGT
 AC TCTT__
 GAM861 LOC257471 3' TTTCAATAACGAAGTTGGGCA 45788 _ C
 TGCCCGGC CGTTAT GAAA
 ||||| ||||| |||
 ACGGGTTG GCAATA CTTT
 AA A
 GAM861 LOC51696 5' TTCGCTGACGCCGGGCA 18318 C T
 TGCCCGGC GTTA CGAA
 ||||| ||| |||
 ACGGGCCG CAGT GCTT
 _ C
 GAM862 BLTR2 5' CACCCACCATCCAGTTTTGCC 21242 C_ G AAC AA
 GGCA AC TG GGTG GTG
 ||| ||| ||| |||

			CCGT TG AC CCAC CAC		
			TT _ CTA CC		
GAM862	DVL3	3'	CACCCCATCAGGCACGTGTGC 10691	AAC	AA
			GCACACGTG GGTG GTG		
			CGTGTGCAC CTAC CAC		
			GGA CC		
GAM862	FGF5	3'	CACATGCACACATGTGCCA 10772	C	AA _
			TGGCACA GTG CG GTG		
			ACCGTGT CAC GT CAC		
			A AC A		
GAM862	FGF5	3'	CACATGCACACATGTGCCA 26999	C	AA _
			TGGCACA GTG CG GTG		
			ACCGTGT CAC GT CAC		
			A AC A		
GAM862	PCLO	3'	ATTTACCCACACTGCCA 45214	CAC	AAC
			TGGCA GTG GGTGAAGT		
			ACCGT CAC CCACTTTA		
			_ AC _		
GAM862	SLC8A2	3'	ACTTCACCCCATGTCCCA 32966	CAC	AAC
			TGG ACGTG GGTGAAGT		
			ACC TGTAC CCACTTCA		
			C_ C_		
GAM862	SOLH	5'	CACTGGGTGATTCACGTGTGCC 12163		
			GGCACACGTGAA CGGTG		
			CCGTGTGCACTT GTCAC		
			AGTGG		
GAM862	FLJ12816	3'	CACTTCACCCCATCCCATACCA 22602	CACAC_	AAC
			TGG GTG GGTGAAGTG		
			ACC TAC CCACTTCAC		
			ATACCC C_		
GAM862	FLJ22471	3'	CACTACTGATGTTACGATGCC 24777	CA	GTGA_
	A		TGGCA CGTGAACG AGTG		
			ACCGT GCACTTGT TCAC		
			A_ AGTCA		
GAM862	KIAA1322	3'	ACTCCACTTCACATGCC 36020	CAC	AC A
			GGCA GTGA GGTG AGT		
			CCGT CACT TCAC TCA		
			A_ _ C		
GAM862	PRO0097	5'	CACTTTCAAGTCAGGTGTGCCA 15364	G	A GGT
			TGGCACAC TGA C GAAGTG		

ACCGTGTG ACT G TTTCAC
 G _ AC_
 GAM862 ZFP106 5' CACTAATTTTTCTACTGTGCCA 22829 C CG GA
 TGGCACA GTGAA GT AGTG
 ||||| |||| || ||||
 ACCGTGT CACTT TA TCAC
 _ TT A_
 GAM862 LOC150397 3' CATCTCACTCACGTGTATCA 38959 GC ACG AG
 TG ACACGTGA GTGA TG
 || ||||| |||| ||
 AC TGTGCACT CACT AC
 TA _ CT
 GAM862 LOC163682 5' CACTGCAGTGACGTGTGCCA 42086 AA G A
 TGGCACACGTG CG TG AGTG
 ||||| || || ||||
 ACCGTGTGCAC GT AC TCAC
 _ G G
 GAM862 LOC222171 5' CACCCCGCAGCCACGTGTGGC 44558 G AACG AA
 A TG CACACGTG GTG GTG
 || ||||| || ||||
 AC GTGTGCAC CGC CAC
 G CCGA CC
 GAM863 AXIN1 3' AGAAATGCCAAGAAGGCTGAGT 30513 CTA_ C
 C GAC TTCT GGCATTTCT
 || |||| |||||
 CTG AAGA CCGTAAAGA
 AGTCGG A
 GAM863 LAMP2 3' AGGAGAAAGCAAAATACATCA 15182 CC CTCG A
 TGA TATT GC TTTCTCCT
 || |||| || |||||
 ACT ATAA CG AAAGAGGA
 AC AA_ _
 GAM863 LTA 3' AGGAGAAACAGAGACAGG 6193 AT GGCA
 CCT TCTC TTTCTCCT
 || |||| |||||
 GGA AGAG AAAGAGGA
 C_ AC_
 GAM863 ABCA9 3' AGGAGAAATACCTGATGTAG 27826 TC _ C
 CTAT TC GG ATTTCTCCT
 |||| || || |||||
 GATG AG CC TAAAGAGGA
 T_ T A
 GAM863 FASTK 3' AGGAGAAATACCGCCAGG 24726 ATTCT C
 CCT CGG ATTTCTCCT
 || |||| |||||
 GGA GCC TAAAGAGGA
 CC_ A
 GAM863 FLJ14437 3' AGGAGAAAGGCGGACAGGTCA 26306 ATTC G A
 TGACCT TC GC TTTCTCCT
 |||| || || |||||

ACTGGA AG CG AAAGAGGA
 C__ G G
 GAM863 KIAA0125 3' AGAAGAAATGCCTCCCCAGGTC 30344 ATTCTC C
 GACCT GGCATTTCT CT
 |||| ||||| ||
 CTGGA CCGTAAAGA GA
 CCCCT_ A
 GAM863 KIAA1505 5' AGAAAGCAAGAATAGGT 45191 CG A
 ACCTATTCT GC TTTCT
 ||||| || ||||
 TGGATAAGA CG AAAGA
 A_ _
 GAM863 MGC39436 5' AGGAGAGAGAAGAAACAGGCCA 29495 A A_ CGGCA
 TG CCT TTCT TTTCTCCT
 || ||| |||||
 AC GGA AAGA AGAGAGGA
 C CA AG__
 GAM863 NYD-SP27 5' AGGAGAAACGGCTCTACAGGTC 26967 ATTCTC A_
 A TGACCT GGC TTTCTCCT
 |||| ||| |||||
 ACTGGA TCG AAAGAGGA
 CATC__ GC
 GAM863 ST7L 3' AGGAGAAACAATTTATAGGCA 29203 A TCTCGGCA
 TG CCTAT TTTCTCCT
 || |||| |||||
 AC GGATA AAAGAGGA
 _ TTTAAC__
 GAM863 LOC158434 3' AGGAGAGAACCCAGAATA 41981 C CA
 TATTCT GG TTTCTCCT
 |||| || |||||
 ATAAGA CC AGAGAGGA
 C A_
 GAM864 FGF9 3' CGCTGTGTCATCACATCA 7751 ATC T
 TGAT GATGACAT GTG
 ||| ||||| |||
 ACTA CTA CTACTGTG CGC
 CA_ T
 GAM864 GBP1 3' CTACAATGTCCCAATATCA 7809 CGAT
 TGATAT GACATTGTGG
 |||| |||||
 ACTATA CTGTAACATC
 ACC_
 GAM864 GEMIN5 5' TCCATCAGCATACGATATCA 42974 _ ACATT
 TGATATCG ATG GTGGA
 ||||| || ||||
 ACTATAGC TAC TACCT
 A GAC__
 GAM864 DKFZp434D177 3' TCAGCATTATCATGATATCA 26009 G CAT G
 TGATATC ATGA TGT GA
 ||||| ||| ||| ||

			ACTATAG TACT ACG CT		
			_ ATT A		
GAM864	LOC123745	5'	TCTACCTCACCATCAATGTCA 37255	C	ACATT
			TGATAT GATG GTGGA		
			ACTGTA CTAC CATCT		
			A CACTC		
GAM864	LOC149010	3'	TCAGCATTATCATGATATCA 38629	G	CAT G
			TGATATC ATGA TGT GA		
			ACTATAG TACT ACG CT		
			_ ATT A		
GAM864	LOC162333	5'	TTGTCAATGTCATCGACTTCA 42143	TA	TG
			TGA TCGATGACATTG GA		
			ACT AGCTACTGTAAC TT		
			TC TG		
GAM865	LNK	3'	ACTGATCCAGATTTGCAGT 11968	G	AAT TA
			AC GCAAATCT GG TAGT		
			TG CGTTTAGA CC GTCA		
			A _ TA		
GAM865	RCN1	3'	TACCAGATTTTTATATTTGCC 8803	C	_
			GGCAAAT TAA TGGTA		
			CCGTTTA ATT ACCAT		
			T TTTAG		
GAM865	FLJ22795	3'	ACTGTGCTCAGATTCCC 24688	CA	AAT
			GG AATCT GGTATAGT		
			CC TTAGA TCGTGTCA		
			C_ C_		
GAM865	TRAF6	5'	ACTGGATCCAGAGTTTGCCGT 10969	CTAA	TA_
			ACGGCAAAT TGG TAGT		
			TGCCGTTTG ACC GTCA		
			AG_ TAG		
GAM865	LOC121599	5'	TACCGTTGAATTTACCGTT 36672	C	C
			AACGG AAAT TAATGGTA		
			TTGCC TTTA GTTGCCAT		
			A A		
GAM865	LOC145717	3'	ACTGTGCTCAGATTCCC 33189	CA	AAT
			GG AATCT GGTATAGT		
			CC TTAGA TCGTGTCA		
			C_ C_		
GAM865	LOC220537	3'	ACTGTGCTCAGATTCCC 43621	CA	AAT
			GG AATCT GGTATAGT		

CC TTAGA TCGTGTCA
 C_ C_
 GAM865 LOC51580 3' ACTATCTAAATTTGCTG 18010 CTAA T
 CGGCAAAT TGG ATAGT
 ||||| |||||
 GTCGTTTA ATC TATCA
 A_ _
 GAM865 LOC54103 3' TACTAAATCAGATTTGCC 45209 AAT A
 GGCAAATCT GGT TAGTA
 ||||| |||||
 CCGTTTAGA CTA ATCAT
 _ A
 GAM866 KIF5C 3' TATCAGTGCCAGCCCAATA 10856 AT C
 TATTGGGCT GCATT GATA
 ||||| |||||
 ATAACCCGA CGTGA CTAT
 C_ _
 GAM867 CAP350 3' AAGACTACCAAGTATGGAGTTCA 16768 AATGA
 TGA ACTCCGTACT AGTTTT
 ||||| |||||
 ACTTGAGGTATGA TCAGAA
 CCA_
 GAM867 LOC219942 3' TCATTAGTGCAGAACTCA 44827 AC C
 TGA TC GTACTAATGA
 || |||||
 ACT AG CGTGATTACT
 CA A
 GAM868 MATN3 3' TAATAAAAGTTATTACCTTTAC 8197 A TTTC
 A TGTGAA GTA ACTTTTATTA
 ||||| |||||
 ACATTT CAT TGAAAATAAT
 C TAT_
 GAM868 AAK1 3' TAATAAAAGTGAAATTAC 17144 _
 GTA TTTCAC TTTTATTA
 || |||||
 CAT AAAGTGAAAATAAT
 T
 GAM868 DKFZP434A043 3' TGAAATAACACTTTTCA 17703 _
 TGTGAAAGT ATTTCA
 ||||| |||||
 ACACTTTCA TAAAGT
 CAA
 GAM868 LOC221074 5' TAACTGTGAAATACTCTCCA 44748 T A TT
 TG GA AGTATTTTCA TTA
 || ||||| |||||
 AC CT TCATAAAGTG AAT
 _ C TC
 GAM869 MSF 3' ACAGATGACCAAAGTCCCTT 42518 C_ TACTAC
 AAGGGATTT GTT CTGT
 ||||| |||||

TTCCCTGAA CAG GACA
 AC TA____
 GAM869 SIM2 3' ACAGGTAAACAGAAATCCTTT 11515 _ TAC
 AAGGGATTTC GTT TACCTGT
 ||||| ||| |||||
 TTTCCTAAAG CAA ATGGACA
 A ____
 GAM870 CNTNAP2 3' TCTCTGGTAGTTTTTTC 15421 TATA A
 GAAAA GCTACCA AGA
 |||| ||||| |||
 CTTTT TGATGGT TCT
 ____ C
 GAM870 FGF5 3' TCTGCATTGAGCATATTTTCTT 10777 A ACCAA_
 A TAAGAAAATAT GCT AGA
 ||||| ||| |||
 ATTCTTTTATA CGA TCT
 _ GTTACG
 GAM870 FGF5 3' TCTGCATTGAGCATATTTTCTT 27004 A ACCAA_
 A TAAGAAAATAT GCT AGA
 ||||| ||| |||
 ATTCTTTTATA CGA TCT
 _ GTTACG
 GAM870 FMOD 3' TCTCTGAGCTATATCCTC 7772 AA AC A
 GA ATATAGCT CA AGA
 || ||||| |||||
 CT TATATCGA GT TCT
 CC _ C
 GAM870 MYBL1 3' ATCTTGTAAGGCTATATTTTTT 32042 ACCA
 AGAAAATATAGCT AAGAT
 ||||| |||||
 TTTTTTATATCGG TTCTA
 AATG
 GAM870 CRNKL1 3' ATCTTTGATGGCTACTTTTT 18772 TA C
 AAAA TAGCTA CAAAGAT
 ||| |||| |||||
 TTTT ATCGGT GTTTCTA
 TC A
 GAM870 FLJ11142 3' CTTTGAGTTTGCTATTTTCT 20344 AT T_ _
 AGAAA ATAGC AC CAAAG
 |||| |||| |||||
 TCTTT TATCG TG GTTTC
 _ TT A
 GAM870 FLJ12770 3' ATCTTTGGTCCCAGCATTTTC 25883 ATA ____
 GAAAAT GCT ACCAAAGAT
 |||| ||| |||||
 CTTTTA CGA TGGTTTCTA
 _ CCC
 GAM870 KIAA0275 3' CTTTGGTGGAGAATTTCTTA 16552 ATATAG
 TAAGAAA CTACCAAAG
 ||||| |||||

			ATTCTTT	GGTGGTTTC	
			AAGA__		
GAM870	NIR3	3'	ATCCTTGGCTGCTTCCTTTTCT	32924	TAT TA A
	TA		TAAGAAAA AGC CCAA GAT		
			ATTCTTTT TCG GGTT CTA		
			CCT TC C		
GAM870	PRMT6	3'	ATCTCTCCAGAGCCATATTTTC	19933	A ACCAA_
	T		AGAAAATAT GCT AGAT		
			TCTTTTATA CGA TCTA		
			C GACCTC		
GAM870	STX6	3'	ATCTTTGGCAGCTCTTTTCTT	12420	TAT A
			AAGAAAA AGCT CCAAAGAT		
			TTCTTTT TCGA GGTTTCTA		
			C_ C		
GAM870	LOC146059	3'	ATCTTGGGAGTCTACATTTTCT	38052	A _ A A
	TA		TAAGAAAAT TAG CT CC AAGAT		
			ATTCTTTTA ATC GA GG TTCTA		
			C T _ G		
GAM870	LOC51107	3'	TCCTTGGGCTATATTTTCT	18097	TA A
			AGAAAATATAGC CCAA GA		
			TCTTTTATATCG GGTT CT		
			_ C		
GAM870	LOC91408	3'	ATCTTTGGTATGGTTGCCTTA	32789	AA ATAGC
			TAAG AAT TACCAAAGAT		
			ATTC TTG ATGGTTTCTA		
			CG GT__		
GAM871	KIAA0677	3'	TACGTATGAACACTATAAAC	16111	C GA A
			GTTTATAGT GT TA ACGTA		
			CAAATATCA CA GT TGCAT		
			_ A_ A		
GAM871	LOC90777	3'	TACGTTTATTTTCTTCATAAAT	31994	AGTCGT
	TA		TAGTTTAT GATAAACGTA		
			ATTAAATA TTATTTGCAT		
			CTTCTT		
GAM872	ITM2B	3'	AAATCTTAAGAGAATCCACATA	22537	TCCGCGATG
	A		TTATGTGG AAGATTT		
			AATACACC TTCTAAA		
			TAAGAGAA_		
GAM872	DKFZP434G1411	3'	AAATCTCCATCTGACCCTACAT	44228	_ CGC A
	AA		TTATGT GGTC GATG AGATTT		

			AATACA CCAG CTAC TCTAAA	
			TC T__ C	
GAM872	LOC151103	3'	AAATCTTCCTCAACCAAATAA 41298	G CCGC T
			TTAT TGGT GA GAAGATTT	
			AATA ACCA CT CTTCTAAA	
			A A__ C	
GAM873	APPBP2	3'	CTAAGATGGTAACTGTGTGATT 13081	A__ AG
			AATCACACA ACCAT TTAG	
			TTAGTGTGT TGGTA AATC	
			CAA G_	
GAM873	CNR1	3'	TCTAACTGTATATTTGTATGAT 18166	C CC_
			ATCA ACAAA ATAGTTAGA	
			TAGT TGTTT TGTCAATCT	
			A ATA	
GAM873	CXorf6	3'	CTATTGCCTTGTGTGATT 11990	AC _
			AATCACACAA CA TAG	
			TTAGTGTGTT GT ATC	
			CC T	
GAM873	IVD	3'	GGCTAGTGTGTGTGATT 8002	ACCA
			AATCACACAA TAGTT	
			TTAGTGTGTT ATCGG	
			GTG_	
GAM873	MS4A3	3'	CTAACTATAAATCCTATTTGTG 12778	CC_____
	TG		CACACAAA ATAGTTAG	
			GTGTGTTT TATCAATC	
			ATCCTAAA	
GAM873	MYEOV	5'	CTGCTGAGCTCTGTGTGATT 29000	AACCA T
			AATCACACA TAGT AG	
			TTAGTGTGT GTCG TC	
			CTCGA _	
GAM873	PPP1CB	3'	AACTAGTTGGTAATGTGATT 8554	CAA _
			AATCACA ACCA TAGTT	
			TTAGTGT TGGT ATCAA	
			AA_ TG	
GAM873	TEAD3	3'	CTTGCATGGCTTGTGTGGT 9212	A A T
			ATCACACAA CCAT GT AG	
			TGGTGTGTT GGTA CG TC	
			C _ T	
GAM873	USP6	3'	TCTACTAATGTTGTGTGATT 43812	ACCA T
			AATCACACAA TAGT AGA	

			TTAGTGTGTT ATCA TCT		
			GTA_ _		
GAM873	VANGL2	3'	CTAATGTTTTTGGTTTGTATGG 35479	C	TA__
		T	ATCA ACAAACCA GTTAG		
			TGGT TGTTTGGT TAATC		
			A TTTTG		
GAM873	AKAP11	3'	TCTAACTATCAAATTGTGT 18374	ACC_	
			ACACAA ATAGTTAGA		
			TGTGTT TATCAATCT		
			AAAC		
GAM873	DJ667H12.2	3'	CTAACAGTCTTGTGTGA 21216	ACC A	
			TCACACAA AT GTTAG		
			AGTGTGTT TG CAATC		
			C_ A		
GAM873	FLJ00001	3'	CTAACGTGTCTGTGTGAT 39778	A CATA	
			ATCACACA AC GTTAG		
			TAGTGTGT TG CAATC		
			C TG__		
GAM873	FLJ14007	3'	TCTTTTTTGTGTGTGA 24009	CAT TT	
			TCACACAAAC AG AGA		
			AGTGTGTTTG TT TCT		
			T_ TT		
GAM873	FLJ23017	3'	TCTATGGATGTGTTTGTGTGA 23132	C GT__	
			TCACACAAA CATA TAGA		
			AGTGTGTTT GTGT ATCT		
			T AGGT		
GAM873	KIAA0229	3'	TCTAATCAGCCTGTGTGATT 44404	AACCATA	
			AATCACACA GTTAGA		
			TTAGTGTGT TAATCT		
			CCGAC__		
GAM873	KIAA0285	3'	TCTAATTACTTGTGTGA 16754	ACCA	
			TCACACAA TAGTTAGA		
			AGTGTGTT ATTAATCT		
			C__		
GAM873	KIAA0513	3'	TCCAGCTAGGCCCGTGTGGTT 16362	AAA A A	
			AATCACAC CC TAGTT GA		
			TTGGTGTG GG ATCGA CT		
			CCC _ C		
GAM873	KIAA1041	3'	CTAACTGTTGTGTGATT 17263	AACC	
			AATCACACA ATAGTTAG		

TTAGTGTGT TGTCAATC

GAM873 KIAA1171 3' CTAGAAGGTATGTGTGATT 42481 A ATAG
AATCACACA ACC TTAG
||||||| ||| ||||
TTAGTGTGT TGG GATC
A AA__

GAM873 KIAA1348 3' CTAACTTTTTTTTTTGTGATT 34027 C CCAT
AATCACA AAA AGTTAG
||||||| ||| |||||
TTAGTGT TTT TCAATC
T TTTT

GAM873 PLU-1 5' TCTCATAGGGTTGTGTGATT 13403 A ATA T
AATCACACAA CC GT AGA
||||||| || |||||
TTAGTGTGTT GG TA TCT
_ GA_ C

GAM873 SETBP1 3' TCTCGATGGAATTGTGTGAT 17828 A_ AGTT
ATCACACAA CCAT AGA
||||||| ||| |||
TAGTGTGTT GGTA TCT
AA GC__

GAM873 TCF6L1 3' AACTATGGCCTGTGGAT 9188 A AA
ATC CACA CCATAGTT
||| ||| |||||
TAG GTGT GGTATCAA
_ CC

GAM873 UBE2D3 3' TCTAACTTG GTTATGAGA 9346 A CA T
TC CA AACCA AGTTAGA
|| || ||||| |||||
AG GT TTGGT TCAATCT
A A_ _

GAM873 LOC153778 5' CTACGGTCACCTGTGTGGTT 39408 A__ A
AATCACACA ACC TAG
||||||| ||| |||
TTGGTGTGT TGG ATC
CCAC C

GAM873 LOC196955 5' CTATTGTGGGACCTTGTGATT 37934 CAAA_ T
AATCACA CCATAGT AG
||||||| ||||| ||
TTAGTGT GGTGTTA TC
TCCAG _

GAM873 LOC199858 3' CTATTGTGGGACCCTGTGATT 42637 CAAA_ T
AATCACA CCATAGT AG
||||||| ||||| ||
TTAGTGT GGTGTTA TC
CCCAG _

GAM873 LOC199870 3' CTGATTGTTTTATGTGATT 42647 C CC
AATCACACA AAA ATAGTTAG
||||||| ||| |||||

TTAGTGT TTT TGTTAGTC
 A _
 GAM873 LOC200488 5' TCCAACATATGGTTAACTGT 43315 CA_ A
 ACA AACCATAGTT GA
 ||| ||||| ||
 TGT TTGGTATCAA CT
 CAA C
 GAM873 LOC200942 3' TCTACACTGCTGGTTGTATGA 42872 C A _ _
 TCA ACAA CCA TAGT TAGA
 ||| ||| ||| ||| |||
 AGT TGTT GGT GTCA ATCT
 A _ C C
 GAM873 LOC202181 5' GCAGTGGACTGTGTGATT 42968 AA A
 AATCACACA CCAT GT
 ||||| ||| ||
 TTAGTGTGT GGTG CG
 CA A
 GAM873 LOC93259 5' TCTGGGGTGGACCCTGTGTGAT 35563 AA__ AG
 T AATCACACA CCAT TTAGA
 ||||| ||| ||| |||
 TTAGTGTGT GGTG GGTCT
 CCCA G_
 GAM874 GABRA5 3' ATCATATGTTAGATA 30213 CCG
 TATCTGACA TATGGT
 ||||| ||| ||
 ATAGATTGT ATACTA
 _
 GAM874 HAS2 3' AGTATTGTGGCATCAGATA 11800 CA GT TG
 TATCTGA CC A GTACT
 ||||| || | ||| |||
 ATAGACT GG T TATGA
 AC _ GT
 GAM874 RALBP1 3' AGTATGGTCGGGTGTCAGATA 13656 GT G
 TATCTGACACC AT GTACT
 ||||| ||| ||| ||| |||
 ATAGACTGTGG TG TATGA
 GC G
 GAM874 WTAP 3' AGTTTCAGTGTTAGATA 11344 CGTA T
 TATCTGACAC TGG ACT
 ||||| ||| ||| |||
 ATAGATTGTG ACT TGA
 _ T
 GAM874 CYR1 3' TACTTTTTGGGGTCAGATA 27515 A TAT
 TATCTGAC CCG GGTA
 ||||| ||| ||| |||
 ATAGACTG GGT TCAT
 G TTT
 GAM874 FLJ21945 3' AGTACCAGCTTAGTCAGGTA 24867 ACC A
 TATCTGAC GT TGGTACT
 ||||| || |||||

			ATGGACTG CG ACCATGA	
			ATT _	
GAM874	HTEX4	5'	ACCGTACGTTGCCAAATA 44214	C A C
			TAT TG CA CGTATGGT	
			ATA AC GT GCATGCCA	
			A C T	
GAM874	HTEX4	5'	ACCGTACGTTGCCAAATA 46650	C A C
			TAT TG CA CGTATGGT	
			ATA AC GT GCATGCCA	
			A C T	
GAM874	HTEX4	5'	ACCGTACGTTGCCAAATA 46719	C A C
			TAT TG CA CGTATGGT	
			ATA AC GT GCATGCCA	
			A C T	
GAM874	LOC146229	5'	AGTAAGTGGGTGTCAG 38107	G GG
			CTGACACC TAT TACT	
			GA CTGTGG GTG ATGA	
			_ A _	
GAM874	LOC147353	3'	TACCAGTGTCAGATA 40837	CGTA
			TATCTGACAC TGGTA	
			ATAGACTGTG ACCAT	

GAM874	LOC148530	5'	TACCAGCTACTGTGCCAGA 40887	A C _
			TCTG CAC GTA TGGTA	
			AGAC GTG CAT ACCAT	
			C T CG	
GAM874	LOC149827	5'	AGTAGTCAAGGTGTCAGA 41111	GTA _
			TCTGACACC TGG TACT	
			AGACTGTGG ACT ATGA	
			A _ G	
GAM874	LOC158490	3'	AGTACCATGGTTCTGA 39847	T C GT
			TC GA ACC ATGGTACT	
			AG CT TGG TACCATGA	
			T _ _	
GAM874	LOC196484	5'	AGTACCATGGTTCTGA 31484	T C GT
			TC GA ACC ATGGTACT	
			AG CT TGG TACCATGA	
			T _ _	
GAM874	LOC220073	5'	AGTACCATGGTTCTGA 44872	T C GT
			TC GA ACC ATGGTACT	

AG CT TGG TACCATGA
 T _ _
 GAM874 LOC222160 5' AGTACCATACAGTCTTGATG 45164 T_ ACC
 TATC GAC GTATGGTACT
 ||| ||| |||||
 GTAG CTG CATACCATGA
 TT A_
 GAM874 LOC91069 3' AGTACCATGGTTCTGA 32344 T C GT
 TC GA ACC ATGGTACT
 || ||| |||||
 AG CT TGG TACCATGA
 T _ _
 GAM875 MGC10818 3' GGTGCACAGCCCCTGACCA 24942 C AC
 TGG CAG GCTGTGCATC
 ||| ||| |||||
 ACC GTC CGACACGTGG
 A CC
 GAM875 SV2B 3' GACAATGTACAGCATTCTGGCC 16881 C_ CCC
 A TGGCCAGA GCTGTGCAT GTC
 ||||| ||||| |||
 ACCGGTCT CGACATGTA CAG
 TA A_
 GAM876 EHD2 3' ACTGGCACACGCAGGC 15960 T A G C
 GCCTGCGT G TGC CA GT
 ||||| | ||| ||
 CGGACGCA C ACG GT CA
 -- -- --
 GAM876 LOC51289 5' GCACGTCCCGCAGGCTA 18639 TT C
 TGGCCTGCG GATG GC
 ||||| ||| ||
 ATCGGACGC CTGC CG
 C_ A
 GAM877 CTNNA2 3' CTCTACAAAAGCAAACCTCT 10618 A_ AG
 AGA TGCT TTTGTAGAG
 ||| ||| |||||
 TCT ACGA AAACATCTC
 CAA _
 GAM877 KAL1 3' CTCTACTGAATATTCTAGTGA 5716 C CTAGTTT
 TCAC AGAATG GTAGAG
 ||| ||||| |||||
 AGTG TCTTAT CATCTC
 A AAGT_
 GAM877 NBS1 3' CTCTTACCTAAACTCTGGTGA 34436 ATGC TTTGT
 TCACCAGA TAG AGAG
 ||||| ||| |||
 AGTGGTCT ATC TCTC
 CAA_ CAT_
 GAM877 OPHN1 3' CTCTACAAATTTTCTGTGGTG 8403 GAATGCT
 A TCACCA AGTTTGTAGAG
 ||||| |||||

			AGTGGT	TTAAACATCTC		
			GTCTTT_			
GAM877	AKAP7	3'	CAAACCAACATTTGGTGA	11253	A CTA	
			TCACCAGA TG GTTTG			
			AGTGGTTT AC CAAAC			
			_ AAC			
GAM877	AKAP7	3'	CAAACCAACATTTGGTGA	18516	A CTA	
			TCACCAGA TG GTTTG			
			AGTGGTTT AC CAAAC			
			_ AAC			
GAM877	AKAP7	3'	CAAACCAACATTTGGTGA	28906	A CTA	
			TCACCAGA TG GTTTG			
			AGTGGTTT AC CAAAC			
			_ AAC			
GAM877	DKFZP434D193	3'	CTCTACAATGCTAATTCTGG	42851	GC _	
			CCAGAAT TAGT TTGTAGAG			
			GGTCTTA ATCG AACATCTC			
			_ T			
GAM877	HARSL	3'	CTACGGAACCAGATTCTGGTGA	14509	G A _	
			TCACCAGAAT CT GTTT GTAG			
			AGTGGTCTTA GA CAAG CATC			
			_ C G			
GAM877	KIAA1939	5'	CTCTACAAACCAGGACAGCTG	24243	AATG_ A	
			CAG CT GTTTGTAGAG			
			GTC GA CAAACATCTC			
			GACAG C			
GAM877	LOC144699	3'	CTCTGCGCCTCCGGCACTCTGG	37769	A AGTT_	
		TGA	TCACCAGA TGCT TG TAGAG			
			AGTGGTCT ACGG GCGTCTC			
			C CCTCC			
GAM878	PCDHB8	5'	TATCTGTAGAAAACCACAGCCT	21207	ATC ATGATG	
		CA	TGAG GT CTACAGATA			
			ACTC CA GATGTCTAT			
			CGA CCAAAA			
GAM878	LOC145871	5'	TATCTGTGTAGAAATACA ACTC	40622	ATC GA_ T	
			GAG GTAT TGC ACAGATA			
			CTC CATA ATG TGTCTAT			
			AA_ AAG _			
GAM879	KIAA0256	3'	ATATGTTCCGGTAAATGCTC	32184	T AAA T	
			GAGCATTT CC GAAT TAT			

CTCGTAAA GG CTTG ATA
T _ T

GAM879 TOLLIP 3' GTTCTGGAAAATGCTC 21094 AA
GAGCATTTTCCA GAAT
||||||| |||
CTCGTAAAAGGT CTTG

—
GAM879 LOC133744 5' ATATAAGAAATATTGGAAAGAT 37059 _ AGAA_
GCTC GAGCATTTT CCAA TTTATAT
||||||| ||| |||||
CTCGTAGAA GGTT GAATATA
A ATAAA

GAM879 LOC203369 3' AAATTCTTTGGATTGC 43031 TTT
GCA TCCAAAGAATTT
||| |||||
CGT AGGTTTCTTAAA
T_

GAM880 CLCA3 3' TCAGAGGTTTCAAACATTG 11355 C T AA
CAATGTTT GA GC CTGA
||||||| || |||
GTTACAAA CT TG GACT
_ T GA

GAM880 ELMO2 3' CAGTTGTGAGCCAAGATTGTA 28394 G TCGAT
TACAAT TT GCAACTG
||||| || |||||
ATGTTA AA TGTTGAC
G CCGAG

GAM880 LFG 3' CAGCTTTCAAGAAACATTG 37690 GA C _
CAATGTTTC TG AA CTG
||||||| || |||
GTTACAAAG AC TT GAC
A_ T C

GAM880 SRD5A1 3' TTTCAGTTGTCTTTAACAACAT 6717 TC_ T
ATGTT GA GCAACTGAAA
||||| || |||||
TACAA TT TGTTGACTTT
CAAT C

GAM880 Di-Ras2 3' TTTCAGTTGGCAGAACATTTA 19047 C CGA _
A AATGTTT TGC AACTGAAA
| ||||| ||| |||||
A TTACAAG ACG TTGACTTT
T _ G

GAM880 FLJ12700 3' TTCAGTTGCACCCCTCACTTGT 24417 _ TTTCGA
ACAA TG TGCAACTGAA
||||| || |||||
TGTT AC ACGTTGACTT
C TCCCC_

GAM880 KIAA0427 3' TCAGCTGCAGGGCACTGTG 16581 A CGA A
TACA TGTTT TGCA CTGA
||||| ||| |||

		GTGT ACGGG ACGT GACT		
		C _ C		
GAM880	KIAA1223 3'	TTTCAGTCACATTGCATTGTA 35250	TTC CA	
		TACAATGT GATG ACTGAAA		
		ATGTTACG TTAC TGACTTT		
		_ AC		
GAM880	KIAA1383 3'	TTTCACAAAATCAAAATATTGT 34586	C GCAAC	
	A	TACAATGTTT GAT TGAAA		
		ATGTTATAAA CTA ACTTT		
		A AAAC_		
GAM880	KIAA1872 3'	TTTCAGCTGCTTGAAAACATTG 31524	_ T A	
	TA	TACAATGTTT CGA GCA CTGAAA		
		ATGTTACAAA GTT CGT GACTTT		
		A _ C		
GAM880	TAF2 3'	CAGTGAAATATTGTA 9159	GATGCA	
		TACAATGTTTC ACTG		
		ATGTTATAAAG TGAC		
GAM880	LOC144262 5'	TCAGTTGCACACGTGTACGT 37706	TT_ A_	
		ATGT CG TGCAACTGA		
		TGCA GC ACGTTGACT		
		TGT AC		
GAM880	LOC149103 3'	CAACTGCACGGGACATTGT 38650	TT A AC	
		ACAATGT CG TGCA TG		
		TGTTACA GC ACGT AC		
		GG _ CA		
GAM880	LOC199733 3'	TCAGCAAGAAACATTG 43247	GA AAC	
		CAATGTTTC TGC TGA		
		GTTACAAAG ACG ACT		
		A_ _		
GAM880	LOC253805 3'	CAATTGCAGAAACATT 46132	GA C	
		AATGTTTC TGCAA TG		
		TTACAAAG ACGTT AC		
		_ A		
GAM880	LOC90321 3'	TAGACATCGAAACATTCA 31211	C CAA	
		A AATGTTTCGATG CTG		
		A TTACAAAGCTAC GAT		
		C A_		
GAM880	LOC92249 5'	CAGTCTGGCAAGCATTGTA 34021	TCGA A_	
		TACAATGTT TGC ACTG		

			ATGTTACGA	ACG	TGAC	
			_____	GTC		
GAM881	CROT	3'	ACTTACCAAAACATATCA	22121	CCCA	
			TGATATGTT	GTAGGT		
			ACTATACAA	CATTCA		
			AAC_			
GAM881	DUSP1	3'	ACATACCTACCAGTATTA	10680	GTTCCCA	
			TGATAT	GTAGGTATGT		
			ATTATG	CATCCATACA		
			AC_____			
GAM881	HUS1	3'	ACACACAGTTGGATAAACATAT	43788	C__ TAG A	
	CA		TGATATGTT	CCAG GT TGT		
			ACTATACAA	GGTT CA ACA		
			ATA	GA_ C		
GAM881	MBNL	3'	ACTATACTAAGAACATAT	22024	CC _	
			ATATGTTT	AGTA GGT		
			TATACAAG	TCAT TCA		
			AA	A		
GAM881	FIBL-6	3'	ATCTAACAGGACATATCA	36099	CCAG	
			TGATATGTTT	TAGGT		
			ACTATACAGG	ATCTA		
			ACA_			
GAM881	FLJ30046	3'	GATATATCAGCAAAAACACATC	29410	A CCCA A	
	A		TGAT TGTT	GT GGTATGTC		
			ACTA ACAA	CG CTATATAG		
			C	AAA_ A		
GAM881	GPR105	3'	GACACACCCACACCGTAGAACA	17022	CCA__ A A	
	TAT		ATATGTTT	GT GGT TGTC		
			TATACAAG	CA CCA ACAG		
			ATGCCA	C C		
GAM881	KIAA0261	3'	ATATACCAAGAACATTCA	33829	T CCAGTA	
			TGA ATGTTT	GGTATGT		
			ACT TACAAG	CCATATA		
			_	AA_____		
GAM881	KIAA1143	3'	ACATATATTAAGACATATCA	34069	CCCAGTAG	
			TGATATGTT	GTATGT		
			ACTATACAG	TATACA		
			AATTA_____			
GAM881	TP53INP1	3'	TATTTCTGGAAACATATCA	27109	C T	
			TGATATGTT	CCAG AGGTA		

		ACTATACAA GGTC TTTAT		
		A _		
GAM881	TP53INP1	3' TATTTCTGGAACATATCA 36118	C	T
		TGATATGTT CCAG AGGTA		
		ACTATACAA GGTC TTTAT		
		A _		
GAM881	LOC203276	3' GACAAGCCTGAGCAACATATCA 43485	CCCAG	A
		TGATATGTT TAGGT TGTC		
		ACTATACAA GTCCG ACAG		
		CGA_ A		
GAM881	LOC203305	3' GACAAGCCTGAGCAACATATCA 43509	CCCAG	A
		TGATATGTT TAGGT TGTC		
		ACTATACAA GTCCG ACAG		
		CGA_ A		
GAM881	LOC254243	3' GACAAGCCTGAGCAACATATCA 46511	CCCAG	A
		TGATATGTT TAGGT TGTC		
		ACTATACAA GTCCG ACAG		
		CGA_ A		
GAM881	LOC90038	3' GACAAGCCTGAGCAACATATCA 30648	CCCAG	A
		TGATATGTT TAGGT TGTC		
		ACTATACAA GTCCG ACAG		
		CGA_ A		
GAM882	AVPR1A	3' ATCAATCACCTTGCATTTC 6373	_	CG
		TGAAATGCA TGA GAT		
		ACTTTACGT ACT CTA		
		TCC AA		
GAM882	EGFL5	3' TAGGCTTCATCATGCATTTTC 41885	C	TCA
		GAAATGCATGA GGA CTA		
		CTTTACGTACT CTT GAT		
		A CG_		
GAM882	EIF3S10	3' TGGAGAATTCATGCCTTTCA 35501	T	CGGA A
		TGAAA GCATGA TC CTA		
		ACTTT CGTACT AG GGT		
		C TA_ A		
GAM882	NCOA6	5' AGTGATCCCAGCATCATTT 15287	C	AC_
		AAATG ATG GGATCACT		
		TTTAC TAC CCTAGTGA		
		_ GAC		
GAM882	PAH	3' AGTAATCTGTGCGCATTTTC 5822	AT	C
		TGAAATGC GACGGAT ACT		

ACTTTACG CTGTCTA TGA
 — A
 GAM882 TMOD 3' ATTAGTGATTTTCAGCAAATC 9292 AA A CG
 GA TGC TGA GATCACTAAT
 || ||| ||| |||||
 CT ACG ACT TTAGTGATTA
 AA _ _
 GAM882 PCDH20 3' AGTGATTTATCACTTTCA 23134 TGCA CG
 TGAAA TGA GATCACT
 |||| | |||||
 ACTTT ACT TTAGTGA
 C _ AT
 GAM882 PPP1R3B 3' ATCACGTCACCTGCATTTCA 23856 _ _
 TGAAATGCA TGACG GAT
 ||||| ||| |||
 ACTTTACGT ACTGC CTA
 C A
 GAM882 LOC151446 3' ATTAGTGATGTGTACACCTGCA 41351 _ _ G
 TGCA TG ACG ATCACTAAT
 ||| || ||| |||||
 ACGT AC TGT TAGTGATTA
 CC A G
 GAM882 LOC161823 3' ATTAGTGATCATAAAATTTCA 40031 GCATGACG
 TGAAAT GATCACTAAT
 |||| | |||||
 ACTTTA CTAGTGATTA
 AAATA _
 GAM882 LOC221490 5' TAGTCCCATCTGCATTTCA 44988 T C ATC
 TGAAATGCA GA GG ACTA
 ||||| || || |||
 ACTTTACGT CT CC TGAT
 _ A C _
 GAM883 ADCY9 3' CGCCTCTCACCCCGACCCCTCC 6792 T AG C
 A TGGAG GGTGCGGG GG AGGCG
 |||| ||||| || |||||
 ACCTC CCAGCCCC CT TCCGC
 _ CA C
 GAM883 DLG4 3' CCTGCCCTCCCCCATCCT 7046 T C
 AG GGT GGGGAGGGCAGG
 || ||| |||||
 TC CTA CCCCTCCCGTCC
 _ C
 GAM883 ELAVL3 3' GCCTGCCCTCCCACCCCC 7120 AGT CG
 GG GGT GGGAGGGCAGGC
 || ||| |||||
 CC CCA CCCTCCCGTCCG
 C _ _
 GAM883 IL1R1 3' GCCTGCCCCCAGCACTCC 6566 GTCGG A
 GGAGTG GG GGGCAGGC
 |||| | |||||

CCTCAC CC CCCGTCCG
 GA__ _
 GAM883 LHX5 5' CCCGCCCCCCACCACCCCACTC 22750 TC_ _ A A
 C GGAGTGG GG GG GGGC GG
 ||||| || || ||||| ||
 CCTCAC CC CC CCCG CC
 CCA A C C
 GAM883 MAPRE3 3' CCTGCCCTCCCCACCCCC 14712 AGT C
 GG GGT GGGGAGGGCAGG
 || || ||||| |||||
 CC CCA CCCCTCCCGTCC
 C__ _
 GAM883 RELA 3' GCCTGCCCTCCCCAGAGCA 22500 G _
 TG TC GGGGAGGGCAGGC
 || || ||||| |||||
 AC AG CCCCTCCCGTCCG
 G A
 GAM883 SLC5A5 5' CCCGCCCTCCCGTCCTGCCTC 6068 T__ T A
 C GGAG GG CGGGGAGGGC GG
 |||| || ||||| |||||
 CCTC CC GCCCTCCCG CC
 CGT T C
 GAM883 SLC6A8 3' CGCCACCCCTGCCACCTCT 12148 T C G CA__
 CCA TGGAG GGT GGG AGGG GGCG
 |||| || || ||||| |||||
 ACCTC CCA CCC TCCC CCGC
 T _ G CCAC
 GAM883 CNNM3 3' CGCCTGCCCCCATCCCCTCCA 19123 T TCGG A
 TGGAG GG GG GGGCAGGCG
 |||| || || ||||| |||||
 ACCTC CC CC CCCGTCCGC
 C TA__ _
 GAM883 DKFZp761F2014 3' CCCACCCTGGCCCACTCCA 21459 _ A
 TGGAGTGG TCGGGG GGG
 ||||| ||||| |||||
 ACCTCACG GGTCCC CCC
 C A
 GAM883 ELL2 3' CTGGTCCTCCCCACCACCCA 14367 A C _
 TGG GTGGT GGGGAGGGC AG
 || |||| ||||| |||||
 ACC CACCA CCCCTCCTG TC
 C _ G
 GAM883 FLJ10315 5' CCCACCCTCCCACACCTCC 19818 TG CG CA
 GGAG GT GGGAGGGG GG
 |||| || ||||| |||||
 CCTC CA CCCTCCC CC
 CA _ AC
 GAM883 FLJ32865 3' CCTGCCCTCCCCAGCCAGCTCC 29427 _ C
 GGAG TGGT GGGGAGGGCAGG
 |||| |||| ||||| |||||

CCTC ACCG CCCCTCCCGTCC
 G A
 GAM883 ITGA10 3' CCCTCCCCAACCCACTCCA 29860 TC_
 TGGAGTGG GGGGAGGG
 ||||| |||||
 ACCTCACC CCCCTCCC
 CAA
 GAM883 KIAA0211 5' CGCCTGCCCCCCCCGCCAATCC 15992 G T A
 GGA TGG CGGGG GGGCAGGCG
 ||| ||| ||||| |||||
 CCT ACC GCCCC CCCGTCCGC
 A _ C
 GAM883 KIAA0552 3' CCTGCCCTCCTAGCTCCA 16344 GGTCG
 TGGAGT GGGAGGGCAGG
 ||||| |||||
 ACCTCG TCCTCCCGTCC
 A____
 GAM883 KIAA1111 3' CCTGTACCACCCACTCCA 46020 TC GGAGG
 TGGAGTGG GG GCAGG
 ||||| || |||||
 ACCTCACC CC TGTCC
 CA A____
 GAM883 KIAA1196 3' CCCACCCTCCCCATTCC 30817 TCG CA
 GGAGTGG GGGAGGG GG
 ||||| ||||| ||
 CCTTACC CCCTCCC CC
 ____ AC
 GAM883 KIAA1750 3' CCTACCCTCCCCAGCTTTCCA 33874 T C C
 TGGAG GGT GGGGAGGG AGG
 ||||| ||| ||||| |||
 ACCTT TCG CCCCTCCC TCC
 _ A A
 GAM883 KIAA1755 3' CGCCACCCCCCCCCGACCCAC 30750 AGT A CA
 CA TGG GGTGCGGG GGG GGCG
 ||| ||||| ||| |||
 ACC CCAGCCCC CCC CCGC
 ACC C AC
 GAM883 KIAA1910 3' CCCACCCTCCCCGCCCA 36287 AGT T CA
 TGG GG CGGGGAGGG GG
 ||| || ||||| ||
 ACC CC GCCCCTCCC CC
 ____ AC
 GAM883 LRRFIP1 3' CGCCTGTAATCCCAGCCACTCC 11119 CG GG
 A TGGAGTGGT GGGA GCAGGCG
 ||||| ||| |||||
 ACCTACCG CCCT TGTCCGC
 A_ AA
 GAM883 MFN2 3' CCTGCCCTCCTTGCAGCCA 17010 A G T
 TGG GT G CGGGGAGGGCAGG
 ||| || | |||||

ACC CG C GTTCCTCCCGTCC
 _ A _
 GAM883 MGC20255 3' CGCCTGCCCCATCCCCATCCCC 27428 AGT TC _
 A TGG GG GGGGA GGGCAGGCG
 ||| || |||| |||||
 ACC CC CCCCT CCCGTCCGC
 _ TA AC
 GAM883 NRN1 3' GCCCACCCACACTCACTCCA 18663 _ CG A
 TGGAGTG GT GGG GGGC
 ||||| || ||| |||
 ACCTCAC CA CCC CCG
 T CA A
 GAM883 PPP1R1A 3' GCCTGCCCTCCAAGCCCCA 13591 AGT CGG
 TGG GGT GGAGGGCAGGC
 ||| ||| |||||
 ACC CCG CCTCCCGTCCG
 _ AA_
 GAM883 RAB10 3' CCCTCCCCAACCACCTCA 41279 GA C
 TG GTGGT GGGGAGGG
 || |||| |||||
 AC CACCA CCCCTCCC
 TC A
 GAM883 LOC116113 3' CCTGCCCTCCAGTCTCCCACC 44285 A TCG_
 CC GG GTGG GGGAGGGCAGG
 || |||| |||||
 CC CACC CCCTCCCGTCC
 C CTCTGA
 GAM883 LOC146488 3' CGCCCACCCCCTGCCACCTCT 35044 T C G CA_
 CCA TGGAG GGT GGG AGGG GGCG
 ||||| ||| ||| ||| |||
 ACCTC CCA CCC TCCC CCGC
 T _ G CCAC
 GAM883 LOC149577 3' CCTGCCCTCCCAGCCACACC 41022 A CG
 GG GTGGT GGGAGGGCAGG
 || |||| |||||
 CC CACCG CCCTCCCGTCC
 A A_
 GAM883 LOC158310 5' TCCTCCCCGCCACCCCA 41949 A T
 TGG GTGG CGGGGAGGG
 ||| ||| |||||
 ACC CACC GCCCCTCCT
 C _
 GAM883 LOC196500 5' CGCCCGCCCCCACCAGCTCCA 42389 TCG A A
 TGGAGTG GGG GGGC GGCG
 ||||| ||| ||| |||
 ACCTCGCC CCC CCG CCGC
 CA_ _ C
 GAM883 LOC201475 5' GCCTGCCCCCAGCACTCTA 42578 GTCGG A
 TGGAGTG GG GGGCAGGC
 ||||| || |||||

ATCTCAC CC CCCGTCCG
 GA__ _
 GAM883 LOC253216 3' CCTGCCCCGAGACCCAGCCCC 45519 A __ GG A
 A TGG GT GGTC GG GGGCAGG
 ||| || ||| || |||||
 ACC CG CCAG CC CCCGTCC
 C AC AG _
 GAM883 LOC253868 3' CCCACCCCTGACCACCTCA 45747 GA _ A
 TG GTGGTC GGGG GGG
 || ||||| ||| |||
 AC CACCAG CCCC CCC
 TC T A
 GAM883 LOC90019 3' CGCCTGCCCTTGCCCCACTCC 28871 TC G
 GGAGTGG GG GAGGGCAGGCG
 ||||| || |||||
 CCTCACC CC TTCCCGTCCGC
 _ G
 GAM883 LOC91397 5' GCCCACCCCCACACCCTCCA 32782 T C__ A
 TGGAG GGT GGGG GGGC
 ||||| ||| |||||
 ACCTC CCA CCCC CCCG
 _ CAC A
 GAM883 LOC95702 5' CCTGCCCCCGAGACCCAGCCCC 31382 A __ GG A
 A TGG GT GGTC GG GGGCAGG
 ||| || ||| || |||||
 ACC CG CCAG CC CCCGTCC
 C AC AG _
 GAM884 MAPK1 3' CGCCCTTGAGCTACTTCA 8617 TTGTAC
 TGAAGTAGTTC AGGGCG
 ||||| ||| |||||
 ACTTCATCGAG TCCCGC
 T____
 GAM884 LOC126302 3' TGACAAGAACTACTTCA 36825 A
 TGAAGTAGTTCTTGT CA
 ||||| ||||| ||
 ACTTCATCAAGAACA GT
 _
 GAM884 LOC51277 3' CCCCTGTACTTCATTTCA 39023 AGTTCTT C
 TGAAGT GTACAGGG G
 ||||| ||||| |
 ACTTTA CATGTCCC C
 CTT__ A
 GAM884 LOC56965 3' CCCAAGAACTACTCCA 21450 A TACA
 TG AGTAGTTCTTG GG
 || ||||| ||
 AC TCATCAAGAAC CC
 C ____
 GAM885 ALPI 3' GCTCTGGGTACAGGGCAGC 7344 CC CT
 GC CCCTG CCCAGAGC
 || ||||| |||||

			CG GGGAC GGGTCTCG		
			AC AT		
GAM885	ARHC	5'	TCCCAGAGCGCCCCGGGGGGCT 11664	TG_____	CCA
			GCGA GCAGCCCCC CTC GA		
			CGTCGGGGGG GAG CT		
			CCCCGIIIC ACC		
GAM885	BLTR2	5'	GCTCTGGAAGGAGGC 21244 CC GC		
			GCC CCT TCCCAGAGC		
			CGG GGA AGGGTCTCG		
			A_ _		
GAM885	CAPN10	3'	CCTGCCAGGGGGCTGCGG 23347 C CTCC A		
			TCGCAGCCCCC TG CAG G		
			GGCGTCGGGGG AC GTC C		
			_ C_ C		
GAM885	CAPN10	3'	CCTGCCAGGGGGCTGCGG 23349 C CTCC A		
			TCGCAGCCCCC TG CAG G		
			GGCGTCGGGGG AC GTC C		
			_ C_ C		
GAM885	CAPN10	3'	CCTGCCAGGGGGCTGCGG 23351 C CTCC A		
			TCGCAGCCCCC TG CAG G		
			GGCGTCGGGGG AC GTC C		
			_ C_ C		
GAM885	CAPN10	3'	CCTGCCAGGGGGCTGCGG 23353 C CTCC A		
			TCGCAGCCCCC TG CAG G		
			GGCGTCGGGGG AC GTC C		
			_ C_ C		
GAM885	CCND2	3'	GCCCTGGGAGCTCTGGGACTG 7518 C CCT A		
			CAG CCC GCTCCCAG GC		
			GTC GGG CGAGGGTC CG		
			A TCT C		
GAM885	CDC2L2	5'	GGGAGCAGAAGGAGCGCGA 27301 A _ CC		
			TCGC GC CC CTGCTCCC		
			AGCG CG GG GACGAGGG		
			_ A AA		
GAM885	DNASE1L1	3'	GCCCTGGGGCTGGGGGGCT 13567 T T A		
			AGCCCCC GC CCCAG GC		
			TCGGGGGG CG GGGTC CG		
			T _ C		
GAM885	DNASE2	3'	CTTTGGGAGGCTGAGA 7049 G CCCCTGC		
			TC CAGCC TCCCAGAG		

			AG GTCGG	AGGGTTTC	
			A	_____	
GAM885	HHIP	5'	CTGGGCGGGGGCGCGCGA	22842	A C TC
			TCGC GC CCCCTGC CCAG		
			AGCG CG GGGGGCG GGTC		
			_ C _		
GAM885	HPS1	3'	CTGAGAGCCCTGGGACTGGGA	5694	G C CCT C
			TC CAG CCC GCTC CAG		
			AG GTC GGG CGAG GTC		
			G A TCC A		
GAM885	IFNGR2	5'	GCTCTGGGAGGCCGGCTGCG	12054	CC TGC
			CGCAGCC CC TCCCAGAGC		
			GCGTCGG GG AGGGTCTCG		
			CC _		
GAM885	LRP1	5'	CTCCGAGATGGGGCTGTGA	8137	CCTG CCA
			TCGCAGCCCC CTC GAG		
			AGTGTCGGGG GAG CTC		
			TA_ C_		
GAM885	NFYC	3'	CTCTGGGAACAGCTGC	15494	CCCCC C
			GCAGC TG TCCCAGAG		
			CGTCG AC AGGGTCTC		
			_ A		
GAM885	PACE	3'	GCCCTGAGGTGTGGGGGCTGC	8427	CT T _ A
			GCAGCCCC GC CC CAG GC		
			CGTCGGGGG TG GG GTC CG		
			_ T A C		
GAM885	PACSIN1	3'	CTCCAGGGCAGGGACTCGA	44316	C CCC T CA
			TCG AG CCCTGC CC GAG		
			AGC TC GGGACG GG CTC		
			_ A_ _ AC		
GAM885	PAX8	5'	GAGCCCTCGGCGGGCTGCGA	15136	_ CT_
			TCGCAGCCC CC GCTC		
			AGCGTCGGG GG CGAG		
			C CTCC		
GAM885	PAX8	5'	GAGCCCTCGGCGGGCTGCGA	15177	_ CT_
			TCGCAGCCC CC GCTC		
			AGCGTCGGG GG CGAG		
			C CTCC		
GAM885	PAX8	5'	GAGCCCTCGGCGGGCTGCGA	15135	_ CT_
			TCGCAGCCC CC GCTC		

AGCGTCGGG GG CGAG
 C CTCC
 GAM885 PLCB4 5' GCTCTGGGAACAGAGGACACTG 6639 CCC _ C
 CAG CC CTG TCCCAGAGC
 ||| || ||| |||||
 GTC GG GAC AGGGTCTCG
 ACA A A
 GAM885 RAD52 3' CTCTGAAAAGTGGGCTGTGA 28644 CCCT CC_
 TCGCAGCCC GCT CAGAG
 ||||| ||| ||||
 AGTGTCGGG TGA GTCTC
 ____ AAA
 GAM885 RAD52 3' CTCTGAAAAGTGGGCTGTGA 28653 CCCT CC_
 TCGCAGCCC GCT CAGAG
 ||||| ||| ||||
 AGTGTCGGG TGA GTCTC
 ____ AAA
 GAM885 RAD52 3' CTCTGAAAAGTGGGCTGTGA 28662 CCCT CC_
 TCGCAGCCC GCT CAGAG
 ||||| ||| ||||
 AGTGTCGGG TGA GTCTC
 ____ AAA
 GAM885 TMEM4 5' GCCCTGGGAGCAGAGGTGGAGC 15530 AG _ C A
 GA TCGC CC CC CTGCTCCCAG GC
 ||| || ||| ||||| ||
 AGCG GG GG GACGAGGGTC CG
 A_ T A C
 GAM885 BIRC8 5' CTCTGGGAAGTGGCTGC 27196 CCCCT _
 GCAGCC GCT CCCAGAG
 |||| ||| |||||
 CGTCGG TGA GGGTCTC
 ____ A
 GAM885 C5orf6 5' GCCCTGGGAGCTGGAGGAACCG 18705 AGCC _ T A
 CG CGC CC CC GCTCCCAG GC
 || ||| ||| ||||| ||
 GCG GG GG CGAGGGTC CG
 CCAA A T C
 GAM885 CUL2 5' CTGTGAGCAGGGGAACGCGA 9647 AGCC C
 TCGC CCCCTGCTC CAG
 ||| ||||| |||
 AGCG GGGGACGAG GTC
 CAA_ T
 GAM885 DKFZP434J037 3' CTGAGCAGGGCTGGA 25219 G CCC CC
 TC CAGCCC TGCTC AG
 || |||| |||| ||
 AG GTCGGG ACGAG TC
 _ _ _
 GAM885 DKFZP564C1940 5' GCTCTGGCCTGGGAGCTGGCGA 15273 _ C CTGCTC
 TCGC AGC CCC CCAGAGC
 ||| ||| ||| |||||

AGCG TCG GGG GGTCTCG
 G A TCC___
 GAM885 DKFZp762A227 5' GCTCTGGGAGTGTGAAACTGGG 19107 G CCCCCCT
 A TC CAG GCTCCCAGAGC
 || ||| |||||
 AG GTC TGAGGGTCTCG
 G AAAGTG_
 GAM885 EFS2 3' GCTCTGGGGCAGTGAGGAACTA 12478 GCAG_ CCC T
 GA TC CC CTGC CCCAGAGC
 || || ||| |||||
 AG GG GACG GGGTCTCG
 ATCAA AGT _
 GAM885 FJX1 3' GGAGCAGGGCTGTGA 15663 CCC
 TCGCAGCCC TGCTCC
 ||||| |||||
 AGTGTCTGGG ACGAGG

 GAM885 FLJ10898 5' CTGGAAGCAGGGGAGGTACGA 29891 CA _ C
 TCG GCC CCCCTGCT CCAG
 ||| ||| ||||| |||||
 AGC TGG GGGGACGA GGTC
 A_ A A
 GAM885 FLJ21709 3' CTCTGGGAGGAAGCTGC 38170 CC CTGC
 GCAGC CC TCCCAGAG
 |||| || |||||
 CGTCG GG AGGGTCTC
 AA ____
 GAM885 FLJ23476 3' CTCTGGGAAGCAGGAAGGC 23921 CC _
 GCC CCTGCT CCCAGAG
 ||| ||||| |||||
 CGG GGACGA GGGTCTC
 AA A
 GAM885 IGF2AS 3' GCCCTGGGGCTGGGGGCTGGA 18540 G CT T A
 TC CAGCCCCC GC CCCAG GC
 || ||||| || |||||
 AG GTCGGGGG CG GGGTC CG
 _ T_ _ C
 GAM885 ITGB8 5' GCTCCGCAGACGGGGCTGC 7978 C_ TCCCA
 GCAGCCCC CTGC GAGC
 ||||| ||| |||||
 CGTCGGGG GACG CTCG
 CA C____
 GAM885 KIAA0255 5' CTCCGGGAGCGGGAGCTGGA 16416 G CCC A
 TC CAGC CCTGCTCCC GAG
 || ||| ||||| |||
 AG GTCG GGGCGAGGG CTC
 _ A_ C
 GAM885 KIAA0275 3' GCTCCACCTGGGGGGACTGGGA 16553 G _ TGCTCCCA
 TC CAG CCCCCC GAGC
 || ||| ||||| |||||

		AG GTC GGGGGG	CTCG		
		G A TCCAC__			
GAM885	KIAA0514	3'	GCCCTGGGGTAGGGGCTGTGA	16209	CC T A
			TCGCAGCCCC TGC CCCAG GC		
			AGTGTCTGGGG ATG GGGTC CG		
			__ _ C		
GAM885	KIAA0601	3'	GCTCTGCTGAGTGGGCTGCGA	31327	CCCT C_
			TCGCAGCCC GCTC CAGAGC		
			AGCGTCGGG TGAG GTCTCG		
			_____ TC		
GAM885	KIAA0769	3'	CTAGGAGCAAAGAGGGGGGCAG	16802	A _____ C
	C		GC GCCCCCCCT GCTCC AG		
			CG CGGGGGGA CGAGG TC		
			A GAAA A		
GAM885	KIAA0945	3'	CTCTGTGAGGGGGCTGGA	17296	G CTGC C
			TC CAGCCCCC TC CAGAG		
			AG GTCGGGGG AG GTCTC		
			_ _____ T		
GAM885	KIAA1161	5'	CTCTGTGTGGGGCTACGA	39752	C CCT TCC
			TCG AGCCCC GC CAGAG		
			AGC TCGGGG TG GTCTC		
			A _____ T__		
GAM885	KIAA1908	5'	CTCTGGGAGCAAAGTGGCCTG	36335	_ CCCC
			CAG CC TGCTCCCAGAG		
			GTC GG ACGAGGGTCTC		
			C TGAA		
GAM885	MAPK8IP3	3'	CTCCGGGAGGCGGGCTGCG	27220	C TGC A
			CGCAGCCC CC TCCC GAG		
			GCGTCGGG GG AGGG CTC		
			C _____ C		
GAM885	MGC4172	5'	GCCCTGGTCCAGCAGGGACTG	23599	CCC C__ A
			CAG CCCTGCT CCAG GC		
			GTC GGGACGA GGTC CG		
			A__ CCT C		
GAM885	P2RX1	5'	CTGAGAGCAGAGGCCGTGC	33355	_ CCC C
			GCA GCC CTGCTC CAG		
			CGT CGG GACGAG GTC		
			GC A__ A		
GAM885	SEMA4B	3'	GCCCTGGCTTCAGGGGCTGTGA	34225	CC CTC A
			TCGCAGCCCC TG CCAG GC		

AGTGTCTGGGG AC GGTC CG
 _ TTC C
 GAM885 SULT4A1 3' CTCTGGAAGCAGCGTGTGA 33975 _ CCCCC C
 TCGCA GC TGCT CCAGAG
 ||||| || ||| |||||
 AGTGT CG ACGA GGTCTC
 G _ _ A
 GAM885 U5-116KD 3' GCCCTGGAGTAGGGGGCCAGA 10440 GCA C C A
 TC GCCCCC TGCTCC AG GC
 || ||||| ||||| || ||
 AG CGGGGG ATGAGG TC CG
 AC _ _ _ C
 GAM885 LOC115708 3' CTGGGCAGGGAGGCCAGA 36406 GCA C TC
 TC GCC CCCTGC CCAG
 || ||| ||||| |||
 AG CGG GGGACG GGTC
 AC _ A _
 GAM885 LOC126432 5' CTCCGAGCACCGGAGCTGCGG 36840 C CC CCA
 TCGCAGC CC TGCTC GAG
 ||||| || |||| |||
 GGCGTCG GG ACGAG CTC
 A CC C_
 GAM885 LOC129011 3' GCCCTGGGAGCAGATGGCCCTG 36965 CA CCC A
 A TCG GCC CTGCTCCCAG GC
 ||| ||| ||||| ||
 AGT CGG GACGAGGGTC CG
 CC TA _ C
 GAM885 LOC145468 3' TCCCAGAGCGCCCCGAGGGGGC 36549 A CT _ CCA
 AGCGA C GCCCCC GCTC GA
 | ||||| |||| ||
 G CGGGGG CGAG CT
 A AGCCCCG ||| ACC
 GAM885 LOC147072 5' CTGTGCAGGGGGGCTGCGG 30298 TCC
 TCGCAGCCCCCTGC CAG
 ||||| ||||| |||
 GGCGTCGGGGGGACG GTC
 T _
 GAM885 LOC148304 5' CTGGAGCAGAGCGGGCTGCGA 38520 CC _ C
 TCGCAGCCC CTGCTCC AG
 ||||| ||||| ||
 AGCGTCGGG GACGAGG TC
 CGA _
 GAM885 LOC148479 3' CTGGCGAGGAGGCTGCGA 38540 CCCC G _
 TCGCAGCC T CTC CCAG
 ||||| | ||| |||
 AGCGTCGG A GAG GGTC
 _ G C
 GAM885 LOC150155 3' TCCCAGAGCGCCCCGAGGGGGC 35091 A CT _ CCA
 AGCGA C GCCCCC GCTC GA
 | ||||| |||| ||

G CGGGGG CGAG CT
 A AGCCCCGIII ACC
 GAM885 LOC151429 5' CTGGGAGCAGAGAGGCTGGA 41342 G CCC
 TC CAGCC CTGCTCCCAG
 || |||| |||||
 AG GTCGG GACGAGGGTC
 _ AGA
 GAM885 LOC152274 5' GGGAGGGCAGGGCTGGA 39231 G CC G
 TC CAGCCC CT CTCCC
 || |||| || ||||
 AG GTCGGG GG GAGGG
 _ AC _
 GAM885 LOC152283 3' CTCTGGGAAGGTGGCCAGA 41485 GCA CC GC
 TC GCC CCT TCCCAGAG
 || ||| || |||||
 AG CGG GGA AGGGTCTC
 AC_ T_ _
 GAM885 LOC158056 5' GCTCCGAGACAGGGCAGGGGCC 39717 A _ _ CCA
 GC GC GCCCC CCTG CTC GAGC
 || |||| ||| || ||||
 CG CGGGG GGAC GAG CTCG
 C ACG A C_
 GAM885 LOC161190 5' GCTCTGGGAGCAAGAGAAGCCG 40014 CA CCCCC_
 A TCG GC TGCTCCCAGAGC
 ||| || |||||
 AGC CG ACGAGGGTCTCG
 _ AAGAGA
 GAM885 LOC200853 3' GCTCTGAAGTTGCAGGGCTGCG 42868 CCCT CC
 A TCGCAGCCC GCT CAGAGC
 ||||| || |||||
 AGCGTCGGG TGA GTCTCG
 ACGT A_
 GAM885 LOC204965 5' GCTCTGGGGAGGAGAGGCTGGG 43575 G CC_ GT
 A TC CAGCC CCT C CCCAGAGC
 || |||| ||| |||||
 AG GTCGG GGA G GGGTCTCG
 G AGA _ _
 GAM885 LOC219397 3' GCTCTGGGCTCAGGGAAGCTGC 44900 CC CT
 G CGCAGC CCCTG CCCAGAGC
 |||| |||| |||||
 GCGTCG GGGAC GGGTCTCG
 AA TC
 GAM885 LOC219654 5' CTGCGGAGGGGGGCGCGA 43874 A TGC _
 TCGC GCCCCCC TCC CAG
 ||| |||| ||| |||
 AGCG CGGGGGG AGG GTC
 C _ C
 GAM885 LOC219920 5' GCTCCGGAACAGAGTGGGG 44808 C_ C A
 CCCC CTG TCCC GAGC
 ||| ||| ||| |||

GGGG GAC AGGG CTCG
TGA A C
GAM885 LOC256239 5' CTCCGGGCAGGGCTGGGA 45344 G CCC CCA
TC CAGCCC TGCTC GAG
|| ||||| |||| |||
AG GTCGGG ACGGG CTC
G _ C_
GAM885 LOC91960 3' GCTCTGGGACTAAGCCTGCGA 33614 CCCCC GC_
TCGCAG CT TCCCAGAGC
||||| || |||||
AGCGTC GA AGGGTCTCG
C _ ATC
GAM886 SOX9 3' ATGATCCTAAAAATAACCG 5899 TG C_
CG TGTTT AGGATCAT
|| |||| |||||
GC ATAAA TCCTAGTA
CA AA
GAM886 KIAA0982 3' ATGACCCTGAAATGACTG 15247 C G A
CA GT TGTTTCAGG TCAT
|| || ||||| |||
GT CA GTAAAGTCC AGTA
_ _ C
GAM886 KIAA1028 3' ATGATCCTGAAGAAAAAGGTGA 44155 ACGTGTG
TCACC TTTTCAGGATCAT
||||| |||||
AGTGG GAAGTCCTAGTA
AAAAA_
GAM886 PCQAP 3' CCTTAAACACACATGGGA 18032 A C C_
TC CCA GTGTGTTT AGG
|| || ||||| |||
AG GGT CACACAAA TCC
_ A AT
GAM886 PRKWINK2 3' GATCCTGAAATCAAGG 43523 ACG T
CC TG GTTTCAGGATC
|| || |||||
GG AC TAAAGTCCTAG
A _ _
GAM886 RCD-8 3' ATGACCCTGAGATCGTG 15641 TGT A
CACG GTTTCAGG TCAT
|||| ||||| |||
GTGC TAGAGTCC AGTA
_ C
GAM886 SMOC2 3' ATGATCCTAAACTTTTTGG 35832 CGTGT C
CCA GTTT AGGATCAT
|| || |||||
GGT CAAA TCCTAGTA
TTTT_ _
GAM886 SYNJ2 3' ATCCTGAGCCATGGTG 30942 CG T T
CACCA TG GTT CAGGAT
|||| || || |||||

GTGGT AC CGA GTCCTA

GAM886 TSGA14 3' CTGTGGACACACAAGGTGA 20793 AC _
TCACC GTGTGTTT CAG
||||| ||||| |||
AGTGG CACACAGG GTC
AA T

GAM886 LOC197201 3' TCTGGAAAACAACACACGGTGA 42465 AC ____
TCACC GTGTGT TTCAGG
||||| ||||| |||||
AGTGG CACACA AGGTCT

ACAAA
GAM886 LOC219401 3' ATGAAGCAAACACACGTAGG 44587 _ CAGGA
CC ACGTGTGTTT TCAT
|| ||||| |||
GG TGCACACAAA AGTA
A CGA_

GAM887 M11S1 3' ATTATGTTTAATCGCCA 12516 GC AATG
TGGCG TAG GCATAAT
||||| ||| |||||
ACCGC ATT TGTATTA
TA _

GAM887 PLAC1 5' ATTATCCCCAGCTGCCAGA 22352 AGAAT C
TCTGGCGGCT GG ATAAT
||||||| || |||||
AGACCGTCGA CC TATTA
C_ C

GAM887 UBE3A 3' ATTACTGCTGTTCTAGCCCCCA 28360 C _
TGG GGCTAGAATGGCA TAAT
||| ||||| ||||| |||
ACC CCGATCTTGTTCGT ATTA
C C

GAM887 UBE3A 3' ATTACTGCTGTTCTAGCCCCCA 28364 C _
TGG GGCTAGAATGGCA TAAT
||| ||||| ||||| |||
ACC CCGATCTTGTTCGT ATTA
C C

GAM887 UBE3A 3' ATTACTGCTGTTCTAGCCCCCA 6079 C _
TGG GGCTAGAATGGCA TAAT
||| ||||| ||||| |||
ACC CCGATCTTGTTCGT ATTA
C C

GAM887 SIAT4B 5' ATTATTTCAAGCCGCCA 13812 A TGGC
TGGCGGCT GAA ATAAT
||||| ||| |||||
ACCGCCGA CTT TATTA
A _

GAM887 LOC91250 5' GATTACAGGCATCAGCCACCA 32548 C A ATG A_
TGG GGCT GA GC TAATC
||| ||||| || ||| |||||

ACC CCGA CT CG ATTAG
 A _ A_ GAC
 GAM888 TNFSF4 3' CTATATCAGCCTATGC 9331 T ACCCA
 GCATA GCT GATATAG
 ||||| ||| |||||
 CGTAT CGA CTATATC
 C _____
 GAM888 FLJ20038 3' CTATATCTACATATGC 19141 CTACCC
 GCATATG AGATATAG
 ||||| |||||
 CGTATAC TCTATATC
 A _____
 GAM888 KIAA1805 3' TATTTTGTGGCATATGC 39000 CC
 GCATATGCTAC AGATA
 ||||| |||||
 CGTATACGGTG TTTAT
 T_
 GAM888 MSTP032 3' TCCATATCTGGCTTGCATGTGC 24908 TAC A
 GCATATGC CCAGATAT GA
 ||||| ||||| ||
 CGTGTACG GGTCTATA CT
 TTC C
 GAM888 NCK1 3' CTATATATGACATATGCTA 12810 CTACC G
 TAGCATATG CA ATATAG
 ||||| || |||||
 ATCGTATAC GT TATATC
 A_____ A
 GAM888 LOC120114 3' TCTAAATCGGTAGCAT 37214 CA A
 ATGCTACC GAT TAGA
 ||||| ||| ||||
 TACGATGG CTA ATCT
 _____ A
 GAM888 LOC146669 5' CTAAGTGGTAGCATTTGC 38223 T C ATA
 GCA ATGCTACC AG TAG
 ||| ||||| || |||
 CGT TACGATGG TC ATC
 T _ A_
 GAM889 MFAP4 3' CCAGGAGCCACTCTCCAGCT 34328 TAAAAAT AC_ _
 AGCTG AGA GC CCTGG
 |||| ||| || |||||
 TCGAC TCT CG GGACC
 CC_____ CAC A
 GAM889 TRPM6 3' AGGGCACTTTGCAGCT 19197 AAAT AAC
 AGCTGTAA AG GCCCT
 ||||| || |||||
 TCGACGTT TC CGGGA
 _____ A_
 GAM889 C20orf30 3' GCTCTATTTTTCAGC 15431 T AC
 GCTG AAAAATAGA GC
 |||| ||||| ||

CGAC TTTTATCT CG

GAM889 DKFZP434P211 5' CCAGGGCGTCCTCCAGCTCAGC 15866 TAAAAAT A
GCTG AG ACGCCCTGG
|||| || |||||
CGAC TC TGCGGGACC
TCGACC_ C

GAM889 GRIN3A 3' CCAAGCACTTTCCTCTTTTACA 28531 ATA C_ CC
GCT AGCTGTAAAA GAA GC TGG
||||||| ||| || |||
TCGACATTTT CTT CG ACC
CTC TCA A_

GAM889 IMP-2 3' CCAGGGCGTTAAATTCACAG 13303 AAA AG
CTGT AAT AACGCCCTGG
|||| ||| |||||
GACA TTA TTGCGGGACC
C_ AA

GAM889 KIAA0164 5' CAGGAAGAATTTTACAGT 16405 AGAACGC
GCTGTAAAAAT CCTG
||||||| |||
TGACATTTTTA GGAC
AGAA_

GAM889 KIAA1389 3' CAGTAGTTTTATTTCACAGC 34569 AA GCC
GCTGT AAATAGAAC CTG
|||| ||||| |||
CGACA TTTATTTTG GAC
CC AT_

GAM889 KIAA1416 5' CCAAGGCTTTGCCTCTTTACAG 41801 AATA_ C C
C GCTGTAAA GAA GCC TGG
|||||| ||| ||| |||
CGACATTT TTT CGG ACC
CTCCG _ A

GAM889 TCL6 3' CCAGGCAGGCATTTTACAGC 21769 AGAAC C
GCTGTAAAAAT GCC TGG
||||||| ||| |||
CGACATTTTTA CGG ACC
CGGA_ _

GAM889 TCL6 3' CCAGGCAGGCATTTTACAGC 21775 AGAAC C
GCTGTAAAAAT GCC TGG
||||||| ||| |||
CGACATTTTTA CGG ACC
CGGA_ _

GAM889 LOC150213 5' CCAGGGCGTCCTCCAGCTCAGC 36957 TAAAAAT A
GCTG AG ACGCCCTGG
|||| || |||||
CGAC TC TGCGGGACC
TCGACC_ C

GAM889 LOC199858 5' CCAAGGCACTCACTTTACAGCT 42633 AATA AC C
AGCTGTAAA GA GCC TGG
|||||| || ||| |||

TCGACATTT CT CGG ACC
 CA__ CA A
 GAM889 LOC256176 5' GCCCTATTTTACAGCT 46170 A AAC
 AGCTGTAAAA TAG GC
 ||||| || ||
 TCGACATTTT ATC CG
 _ C_
 GAM889 LOC57105 3' CCAAAGCTCTGAGTTCCATTTT 21637 ATA ____ CC
 ACAGCT CTGTAAAA GAAC GC TGG
 ||||| || || ||
 GACATTTT CTTG CG ACC
 AC_ AGTCT AA
 GAM889 LOC81558 3' CCAAAGACACTATTTTTGCAGC 25109 AACGCCC
 T AGCTGTAAAAATAG TGG
 ||||| || ||
 TCGACGTTTTTATC ACC
 ACAGAA_
 GAM890 GAC1 5' CAGGGTTGCTGACCCTTA 13036 AC A
 TGAGG CA CAACCCTG
 |||| || |||||
 ATTCC GT GTTGGGAC
 CA C
 GAM890 LZTS1 3' CAAGCACAGAGCCTGGCCCCA 22004 A A ACAACC
 TG GG CCA CTGTGCTTG
 || || || |||||
 AC CC GGT GACACGAAC
 C _ CCGA_
 GAM890 SUOX 5' GCACAGAGCTGTGGTCCTCA 6071 A ACC
 TGAGGACCA CA CTGTGC
 ||||| || |||||
 ACTCCTGGT GT GACACG
 _ CGA
 GAM890 FLJ20297 3' AGATGGGTGCTGGTCCTCA 19357 ACA TGTG
 TGAGGACCA ACCC CT
 ||||| || ||
 ACTCCTGGT TGGG GA
 CG_ TA_
 GAM890 FLJ20297 3' AGATGGGTGCTGGTCCTCA 19646 ACA TGTG
 TGAGGACCA ACCC CT
 ||||| || ||
 ACTCCTGGT TGGG GA
 CG_ TA_
 GAM890 FLJ22160 3' CAAGCACAAGGCCATGCAGGT 23818 AA A__ C
 ACC CA CC TGTGCTTG
 || || || |||||
 TGG GT GG ACACGAAC
 AC ACC A
 GAM890 KIAA1867 3' CAAGCACAAATCTGGGTCCCCA 45453 A AACAAACC
 TG GGACC TGTGCTTG
 || || || |||||

			AC CCTGG	ACACGAAC	
			C	GTCTAA__	
GAM890	KIAA1940	5'	GTAGAGCTGCTGGCCTCA	39009	A A ACC G
			TGAGG CCA CA	CT TGC	
			ACTCC GGT GT	GA ATG	
			_ C C_	G	
GAM890	PPIL2	3'	CAAGCACAAAGGCCTGCCCTACA	15649	_ AC ACAA C
			TG AGG CA	CC TGTGCTTG	
			AC TCC GT	GG ACACGAAC	
			A C_ CC_	A	
GAM890	PRDM10	3'	CACAGATGCTGGTCCTCA	21496	A ACC
			TGAGGACCA CA	CTGTG	
			ACTCCTGGT GT	GACAC	
			C A_		
GAM890	TOPBP1	5'	CAGAATTGTTGGTCCTCA	13886	CC
			TGAGGACCAACAA	CTG	
			ACTCCTGGTTGTT	GAC	
			AA		
GAM890	LOC150776	3'	AGATGGGTGCTGGTCCTCA	31673	ACA TGTG
			TGAGGACCA	ACCC CT	
			ACTCCTGGT	TGGG GA	
			CG_ TA_		
GAM890	LOC152274	3'	CAAGCACAGGGCCCTCCTCA	39230	CCAACAA
			TGAGGA	CCCTGTGCTTG	
			ACTCCT	GGGACACGAAC	
			CCC_		
GAM890	LOC199837	5'	CAAGCACAGAAAGCACAGTCAT	42626	G CAACAACC
	CA		TGA GAC	CTGTGCTTG	
			ACT CTG	GACACGAAC	
			A	ACACGAAA	
GAM890	LOC255104	3'	CAAGCACAGGTTAGAGTCCCA	45682	A CAACAAC
			TG GGAC	CCTGTGCTTG	
			AC CCTG	GGACACGAAC	
			_ AGATT_		
GAM891	TNFSF4	3'	CTATATCAGCCTATGC	9331	T ACCCA
			GCATA GCT	GATATAG	
			CGTAT CGA	CTATATC	
			C		
GAM891	FLJ20038	3'	CTATATCTACATATGC	19141	CTACCC
			GCATATG	AGATATAG	

			CGTATAC	TCTATATC		
			A_____			
GAM891	KIAA1805	3'	TATTTTGTGGCATATGC	39000	CC	
			GCATATGCTAC AGATA			
			CGTATACGGTG TTTAT			
			T_			
GAM891	MSTP032	3'	TCCATATCTGGCTTGCATGTGC	24908	TAC	A
			GCATATGC CCAGATAT GA			
			CGTGTACG GGTCTATA CT			
			TTC C			
GAM891	NCK1	3'	CTATATATGACATATGCTA	12810	CTACC	G
			TAGCATATG CA ATATAG			
			ATCGTATAC GT TATATC			
			A_____ A			
GAM891	LOC120114	3'	TCTAAATCGGTAGCAT	37214	CA	A
			ATGCTACC GAT TAGA			
			TACGATGG CTA ATCT			
			_____ A			
GAM891	LOC146669	5'	CTAACTGGTAGCATTTGC	38223	T	C ATA
			GCA ATGCTACC AG TAG			
			CGT TACGATGG TC ATC			
			T _ A__			
GAM892	TNFRSF10B	3'	TCAGACCTTCCCTGGTTTACCT	9939	_____	C AA C
			AAGGT ACCGG GA AGGTC GA			
			TTCCA TGGTC CT TCCAG CT			
			TT C _ A			
GAM892	LOC146880	5'	CGGGCGCTCTCCGCCGGTGCCT	38258	AAA	_____
			AGGTACCGGCG AG GTCCG			
			TCCGTGGCCGC TC CGGGC			
			CTC G			
GAM893	CELSR3	5'	TGTGGTGGGGGCGGAAAAAGC	7104	CG_	ATA
			GCTT CT CCCCACCACA			
			CGAA GG GGGGTGGTGT			
			AAA CG_			
GAM893	DXS1283E	3'	TTGTGGTGGGAAGGTGAAAGGC	35069	_____	ATACC
			GCT TCGCT CCACCACAA			
			CGG AGTGG GGTGGTGTT			
			AA AA_____			
GAM893	KCNA6	5'	TGCGGCGGCGGCAGCGAAGC	8018	ATA	_ A A
			GCTTCGCT CC CC CC CA			

			CGAAGCGA GG GG GG GT	
			C__ C C C	
GAM893	SCA1	5'	TGGTGAAGTATAGGCTGAGGCT 5881	_ _ CC
	A		TAGCTTC GC TATAC CACCA	
			ATCGGAG CG ATATG GTGGT	
			T G AA	
GAM893	GDAP2	3'	TTGTGGTGGGGTATCTTCAGTT 19240	TCGCT
	A		TAGCT ATACCCCAACCACAA	
			ATTGA TATGGGGTGGTGTT	
			CTTC_	
GAM893	KIAA1708	3'	TGTGGTGGGAAAAGCTA 33273	CGCTATAC
			TAGCTT CCCACCACA	
			ATCGAA GGGTGGTGT	
			AA_____	
GAM893	MRF2	3'	TTGTGGTGGGGAGAAAAAGCTA 37602	CG_ ATA
			TAGCTT CT CCCCACCACAA	
			ATCGAA GA GGGGTGGTGTT	
			AAA _____	
GAM893	PHF5A	3'	GTGGGGTACAGTAGCTG 26502	TC A
			TAGCT GCT TACCCAC	
			GTCGA TGA ATGGGGTG	
			_ C	
GAM893	SERP1	3'	GTGGTGGAGTGAAGT 15796	ATACC
			GCTTCGCT CCACCAC	
			TGAAGTGA GGTGGTG	

GAM893	LOC153196	5'	TGTGGTGGAGCATCCTGCTG 41595	TTC__ ATACC
			TAGC GCT CCACCACA	
			GTCG CGA GGTGGTGT	
			TCCTA _____	
GAM894	ADAMTS3	3'	TGTGTTGGTCGCTCTCTGAA 15510	AATATCT
			TTCAGA GCCAACACA	
			AAGTCT TGGTTGTGT	
			CTCGC_	
GAM894	C8orf1	3'	TGTACTGGCTTGAATTTTCTGG 10533	TA T_ AC
	A		TTCAGAAA TC GCCA ACA	
			AGGTCTTT AG CGGT TGT	
			TA TT CA	
GAM894	CDKN2A	3'	TGTGTTGGAGTTTTCTGGA 27760	TAT G
			TTCAGAAA CT CCAACACA	

AGGTCTTT GA GGTGTGT
 T__ _
 GAM894 CRYZ 3' ATGTATTGGACTTTGAACATTT 7617 TA__ TG__ C III
 TCTGAA GAAA TC CCAA ACA T
 |||| || |||| || |
 CTTT AG GGT TGT A
 TACA TTTCA A III
 GAM894 CYP1B1 3' TTGGTTATTTCTGAA 5568 TCT
 TTCAGAAATA GCCAA
 ||||| ||||
 AAGTCTTTAT TGGTT

 GAM894 FOXP2 5' GTGCTGGCTTTTTTGAA 15835 TATCT A
 TTCAGAAA GCCA CAC
 ||||| |||||
 AAGTTTTT CGGT GTG
 T__ C
 GAM894 IL18R1 3' TGTAGTAGATATTACTGAA 9952 A CA
 TTCAG AATATCTGC ACA
 |||| ||||| ||
 AAGTC TTATAGATG TGT
 A A_
 GAM894 MEIS1 3' TGTGACTTTATTTCTGAG 8219 TCTGC
 TTCAGAAATA CAACA
 ||||| ||||
 GAGTCTTTAT GTTGT
 TTCA_
 GAM894 NAGA 5' GTTGTTTCGTATTTCTGAA 5803 CTGC
 TTCAGAAATAT CAAC
 ||||| ||||
 AAGTCTTTATG GTTG
 CTTT
 GAM894 PAICS 3' TGTGCGTGAATTTCTGA 13166 ATC
 TCAGAAAT TGCCAACA
 ||||| |||||
 AGTCTTTA GTGGTTGT
 ATT
 GAM894 PPP2R5D 3' TGTGCTGGCAGATAGGGTTG 12919 AAA A
 CAG TATCTGCCA CACA
 || ||||| ||||
 GTT ATAGACGGT GTGT
 GGG C
 GAM894 SH2D1A 3' TGTACTGGCAAGACCTGATTTC 8156 A__ _ AC
 TGAG TTCAGAAAT TCT GCCA ACA
 ||||| ||||| ||||
 GAGTCTTTA AGA CGGT TGT
 GTCC A CA
 GAM894 SLC21A9 3' TGTGTTGGCCATTTCTGGA 14127 ATCT
 TTCAGAAAT GCCAACACA
 ||||| |||||

			AGGTCTTTA CGGTTGTGT		
			C__		
GAM894	TADA2L	5'	TGTGTTGGCCGTTCTGAA 7229	AAT T	
			TTCAGA ATC GCCAACACA		
			AAGTCT TGG CGGTTGTGT		
			__ C		
GAM894	TADA2L	5'	TGTGTTGGCCGTTCTGAA 28520	AAT T	
			TTCAGA ATC GCCAACACA		
			AAGTCT TGG CGGTTGTGT		
			__ C		
GAM894	TNFSF10	3'	TGTGTTGGCACATGCCTG 9901	AAA C	
			CAG TAT TGCCAACACA		
			GTC GTA ACGGTTGTGT		
			C__ C		
GAM894	TRIP15	3'	TGTGTCCGTATATTTCTG 10432	CT CA	
			CAGAAATAT GC ACACA		
			GTCTTTATA TG TGTGT		
			__ CC		
GAM894	USP9Y	5'	TGTATCAGCAGCATTTCTGA 32019	AT CAAC	
			TCAGAAAT CTGC ACA		
			AGTCTTTA GACG TGT		
			C_ ACTA		
GAM894	ZHX1	3'	TGATGGAGACATTCTGAA 14092	ATA G A	
			TTCAGAA TCT CCA CA		
			AAGTCTT AGA GGT GT		
			AC_ _ A		
GAM894	AP3M2	3'	TGTGTTGGTTTCTTTCTGA 13678	TATCT	
			TCAGAAA GCCAACACA		
			AGTCTTT TGGTTGTGT		
			CTT__		
GAM894	C8orf17	3'	TGTGTTGGCACATGCCTG 21506	AAA C	
			CAG TAT TGCCAACACA		
			GTC GTA ACGGTTGTGT		
			C__ C		
GAM894	DKFZP434J1813	3'	TGTGTTTCATGTATTTTCTGAA 30950	_ C CC	
			TTCAGAAA TAT TG AACACA		
			AAGTCTTT ATG AC TTGTGT		
			T T __		
GAM894	FLJ10520	3'	TGTGTCCGTTTATTTCTGA 19908	TCT A_	
			TCAGAAATA GCC ACACA		

			AGTCTTTAT TGG TGTGT	
			T__ CC	
GAM894	FLJ13449	5'	GTGTTGGCGGGATTCTGAA 23760	ATA
			TTCAGAA TCTGCCAACAC	
			AAGTCTT GGGCGGTTGTG	
			A__	
GAM894	FLJ13842	3'	TGTGTCAGCAATTTCTGGA 23930	ATC CA
			TTCAGAAAT TGC ACACA	
			AGGTCTTTA ACG TGTGT	
			__ AC	
GAM894	GMFB	3'	TGTGTTTCAAACATTTCTGGA 10331	ATC CC
			TTCAGAAAT TG AACACA	
			AGGTCTTTA AC TTGTGT	
			CAA T_	
GAM894	HCA127	3'	TGTGTTGGCTTTTGTTCAGAA 20761	A ATATCT
			TTC GAA GCCAACACA	
			AAG CTT CGGTTGTGT	
			A GTTTT_	
GAM894	HMP19	3'	TGTGCTGGAGTTGTCTGAA 42274	AATAT G A
			TTCAGA CT CCA CACA	
			AAGTCT GA GGT GTGT	
			GTT__ _ C	
GAM894	ICK	3'	TGTGCAGATATTTATGAA 17198	G _
			TTCA AAATATCTGC CA	
			AAGT TTTATAGACG GT	
			A T	
GAM894	KIAA0057	3'	GTGCTGGCTTTTCTGGA 14623	TATCT A
			TTCAGAAA GCCA CAC	
			AGGTCTTT CGGT GTG	
			T__ C	
GAM894	KIAA0319	3'	TGTGTTGACAAGGTATTTCT 16765	GC_
			AGAAATATCT CAACACA	
			TCTTTATGGA GTTGTGT	
			ACA	
GAM894	KIAA0354	3'	TGTGCTGCTGCATTTCTGAG 17000	ATCT CAA
			TTCAGAAAT GC CACA	
			GAGTCTTTA CG GTGT	
			CGT_ TC_	
GAM894	KIAA0703	5'	TGTGTTTCTGCATTTCTGGA 16930	TATC C__
			TTCAGAAA TGC AACACA	

			AGGTCTTT ACG TTGTGT		
			_____ TCT		
GAM894	KIAA0961	3'	TGTTAGAGATAATTTCTGAA 17074	_	GCC
			TTCAGAAAT ATCT AACA		
			AAGTCTTTA TAGA TTGT		
			A GA_		
GAM894	KIAA1257	3'	TGCGTTGGTCTTTTCTGAG 31442	TATCT	A
			TTCAGAAA GCCAAC CA		
			GAGTCTTT TGGTTG GT		
			TC_____ C		
GAM894	KIAA1500	3'	TGTGTTATGAATTTCTGA 32072	A	TGCC
			TCAGAAAT TC AACACA		
			AGTCTTTA AG TTGTGT		
			_ TA_		
GAM894	MIC2L1	3'	TGTGTCAGAAAGCACTTCTGAA 25493	ATA_____	CCA
			TTCAGAA TCTG ACACA		
			AAGTCTT AGAC TGTGT		
			CACGAA _____		
GAM894	MR	5'	TGTGTTGGAGGCCCTCTGGA 25257	AATA	G
			TTCAGA TCT CCAACACA		
			AGGTCT GGA GGTGTGT		
			CCC_ _		
GAM894	NUDT11	3'	TGTATCAGGTGTTTCAGAA 30146	A	CCA
			TTC GAAATATCTG ACA		
			AAG CTTTGTGGAC TGT		
			A TA_		
GAM894	PPP2R3A	3'	TGTGTTGGCTGGCATCCCTGAG 8587	AA	AT T
			TTCAG AT C GCCAACACA		
			GAGTC TA G CGGTTGTGT		
			CC CG T		
GAM894	SEN7	3'	TGTGTTGGGGGGTACTTTT 21823	A	G
			AGAA TATCT CCAACACA		
			TTTT ATGGG GGTGTGT		
			C G		
GAM894	SFRS11	3'	TGTTGATGTACAGTTTCTGAA 11160	ATC	_
			TTCAGAAAT TGC CAACA		
			AAGTCTTTG ATG GTTGT		
			AC_ TA		
GAM894	TAF2	3'	GTGTTTTTATTTCTGAA 9160	TCTGCC	
			TTCAGAAATA AACAC		

			AAGTCTTTAT	TTGTG	
			TT_____		
GAM894	ZMPSTE24	3'	TGTGACTGAAGACATTTCTGA	12463	A GCCAA
			TCAGAAAT TCT	CACA	
			AGTCTTTA AGA	GTGT	
			C AGTCA		
GAM894	ZNF262	3'	TGTGTTTGTCAATTTCTGA	11558	ATCT C
			TCAGAAAT GC AACACA		
			AGTCTTTA TG TTGTGT		
			C___ T		
GAM894	LOC147991	5'	TGTACCAGATATTCCTGGA	38438	A CCA
			TTCAG AATATCTG	ACA	
			AGGTC TTATAGAC	TGT	
			C CA_		
GAM894	LOC149271	5'	GTAGATGTAACATTTCTGGA	38682	_____
			TTCAGAA ATATCTGC		
			AGGTCTT TG TAGATG		
			TACAA		
GAM894	LOC150170	5'	TGTGTTCCGGATATTTT	38864	CC
			GAAATATCTG AACACA		
			TTTTATAGGC TTGTGT		
			C_		
GAM894	LOC150175	5'	TGTGTTCCGGATATTTT	38886	CC
			GAAATATCTG AACACA		
			TTTTATAGGC TTGTGT		
			C_		
GAM894	LOC150215	5'	TGTGTTCCGGATATTTT	38890	CC
			GAAATATCTG AACACA		
			TTTTATAGGC TTGTGT		
			C_		
GAM894	LOC150218	5'	TGTGTTCCGGATATTTT	38917	CC
			GAAATATCTG AACACA		
			TTTTATAGGC TTGTGT		
			C_		
GAM894	LOC151201	3'	TGTGTCCTTAAACTATTTCTGA	41325	TCTGCCA_
	A		TTCAGAAATA ACACA		
			AAGTCTTTAT TGTGT		
			CAAATTCC		
GAM894	LOC206338	5'	GTGTTGGTTGGGCCTTGAA	43112	AAATA T
			TTCAG TC GCCAACAC		

			AAGTT GG TGGTTGTG		
			CCG__ T		
GAM894	LOC221576	3'	TGTGTTGGCTTAATTTCTGGA 45001	ATCT	
			TTCAGAAAT GCCAACACA		
			AGGTCTTTA CGGTTGTGT		
			ATT_		
GAM894	LOC257282	5'	TGTTGGTGTATCTGAA 46123	A ATCT	
			TTCAGA AT GCCAACA		
			AAGTCT TG TGGTTGT		
			A ____		
GAM894	LOC257515	3'	TGTGTTGGCTTAATTTCTGGA 46685	ATCT	
			TTCAGAAAT GCCAACACA		
			AGGTCTTTA CGGTTGTGT		
			ATT_		
GAM894	LOC257572	3'	TGTGTTGGCTTAATTTCTGGA 46746	ATCT	
			TTCAGAAAT GCCAACACA		
			AGGTCTTTA CGGTTGTGT		
			ATT_		
GAM894	LOC91445	3'	GCACCAAATGGTATTTCTGGA 30369	_____	
			TTCAGAAATATC TGC		
			AGGTCTTTATGG ACG		
			TAAACC		
GAM895	KOC1	5'	TAAAACACATCTAGACAA 43781	CA	
			TTG TAGATGTGTTTTA		
			AAC ATCTACACAAAAT		
			AG		
GAM895	SE57-1	3'	GTGGTGAAACCACCTATGCAA 24890	A T	
			TTGCATAG TG GTTTTATTAT		
			AACGTATC AC CAAAGTGGTG		
			C _		
GAM896	BCL9	3'	ACCAAACCTACGACCTCA 10521	T C	
			TGAGGTTGTA TTTG GT		
			ACTCCAGCAT AAAC CA		
			C _		
GAM896	FLNB	3'	ACCAGCAATACAACGTCA 31137	G _ C	
			TGA GTTGTATT TTG GT		
			ACT CAACATAA GAC CA		
			G C _		
GAM896	C20orf103	3'	ACACAGAATACAACCTCA 14567	C	
			TGAGGTTGTATTTTG GT		

			ACTCCAACATAAGAC CA		
			A		
GAM896	SLC5A7	3'	GCATCAAAATACAACCTCA 22392	C_	
			TGAGGTTGTATTTTGT GT		
			ACTTCAACATAAAAC CG		
			TA		
GAM896	LOC197201	3'	GATCTGATGAAAATACAACCTC 42462	G TA	
			GAGGTTGTATTTT CGTC ATC		
			CTCCAACATAAAA GTAG TAG		
			_ TC		
GAM896	LOC254122	3'	AGATGGGACACAACCTCA 45434	ATT G	
			TGAGGTTGT TT CGTCT		
			ACTCCAACA AG GTAGA		
			C_ G		
GAM897	CLASP2	3'	GTTTGCCATTGTTGCAGA 32269	GA A T	
			TC CAACAATG GTG AC		
			AG GTTGTTAC CGT TG		
			AC _ T		
GAM897	FUT1	3'	GGCAGGTACCGTGCTCATTG 5645	___ A	
			CAATGAGT GTACCT CC		
			GTTACTCG CATGGA GG		
			TGC C		
GAM897	NR4A1	5'	AGGTGCAAGCCACATTGTTG 7911	AG___	
			CAACAATG TGTACCT		
			GTTGTTAC ACGTGGA		
			ACCGA		
GAM897	TNFRSF17	5'	AGGCGAAGTTCATTGTTCTC 6862	C GTA_	
			GA AACAATGAGT CCT		
			CT TTGTTACTTG GGA		
			C AAGC		
GAM897	CCR6	5'	GGTACAAACTCATTGCTG 25371	A _	
			CA CAATGAGT GTACC		
			GT GTTACTCA CATGG		
			C AA		
GAM897	DSCR1L1	3'	GGTATACTCACTATTGTGA 12430	G CAA	
			TC ACAA TGAGTGTACC		
			AG TGTT ACTCATATGG		
			_ ATC		
GAM897	FLJ10826	3'	GTACATTCTCATTGTTGTC 20174	___	
			GACAACAATGAG TGTAC		

			CTGTTGTTACTC ACATG		
			TT		
GAM897	FLJ12888	3'	GGTGACCCACTATTGTTG 24497	G	___
			CAACAAT AGTG TACC		
			GTTGTTA TCAC GTGG		
			_ CCA		
GAM897	GOLPH2	3'	ACAAAGTTCATTGATGTCGA 18623	A	___
			TCGACA CAATGAG TGT		
			AGCTGT GTTACTT ACA		
			A GAA		
GAM897	LOC168667	3'	GGTAGTCAGGTCATTGTTTC 44568	C	GTGTAC
			GA AACAATGA CTACC		
			CT TTGTTACT GATGG		
			_ GGA CT_		
GAM897	LOC204010	5'	GGCAGGTCATGCCATTGTTGTC 43082	A_ T	A
			GACAACAATG GTG ACCT CC		
			CTGTTGTTAC TAC TGGA GG		
			CG _ C		
GAM898	DKFZP564O0423	3'	GTGAGAACGAGCACTGCAC 44069		TG G
			GTGCAGTGCTCGTT CT GC		
			CACGTCACGAGCAA GA TG		
			_ G		
GAM898	FLJ14251	3'	AGGAGCGAACACTGCAC 24322	C	G
			GTGCAGTG TCGTTT CT		
			CACGTCAC AGCGAG GA		
			A _		
GAM898	FLJ32743	5'	GCCAGCGGTTTGGCACCGTAC 29628	A	CGT
			GTGC GTGCT TTGCTGGC		
			CATG CACGG GGCGACCG		
			C TTT		
GAM898	MGC20486	5'	GGCCAGCATTGCCACTGC 27423	_	TCGTT
			GCAGTG C TGCTGGCC		
			CGTCAC G ACGACCGG		
			C TT_		
GAM898	ZNF226	5'	CTTCTCAAAAAGCACTGCAC 18564	CG	CT_
			GTGCAGTGCT TTTG GG		
			CACGTCACGA AAAC TC		
			A_ TCT		
GAM898	LOC151614	3'	ATGGTGCAAAACAAGCACTGCA 39141	CG_	TG
			TGCAGTGCT TTTGC GCCAT		

			ACGTCACGA AAACG TGGTA	
			ACA ____	
GAM899	AQP6	5'	CCCAGAGACAGCCCCACATCC 7358	AAAGCA CCC__
	CA		TGGGATGT GCTG GGG	
			ACCCTACA CGAC CCC	
			CCCC__ AGAGA	
GAM899	AQP6	5'	CCCAGAGACAGCCCCACATCC 27612	AAAGCA CCC__
	CA		TGGGATGT GCTG GGG	
			ACCCTACA CGAC CCC	
			CCCC__ AGAGA	
GAM899	CACNA1A	5'	CCCGGGCAGCCGCCTTCTGAGC 23319	ATGTAAA_ A
	CC		GGG GC GCTGCCCGGG	
			CCC CG CGACGGGCCC	
			GAGTCTTC C	
GAM899	CACNA1A	5'	CCCGGGCAGCCGCCTTCTGAGC 5515	ATGTAAA_ A
	CC		GGG GC GCTGCCCGGG	
			CCC CG CGACGGGCCC	
			GAGTCTTC C	
GAM899	FLG	3'	CCCATCACAGCCACACCACATC 35106	AAAGCA CCC__
	CCA		TGGGATGT GCTG GGG	
			ACCCTACA CGAC CCC	
			CCACAC ACTA	
GAM899	FLG	5'	CCCATCACAGCCACACCACATC 35107	AAAGCA CCC__
	CCA		TGGGATGT GCTG GGG	
			ACCCTACA CGAC CCC	
			CCACAC ACTA	
GAM899	GPR62	5'	CCATTCTGCCATCTACATCCCA 43109	AA__ CTGCCC
			TGGGATGTA GCAG GG	
			ACCCTACAT CGTC CC	
			CTAC TTA__	
GAM899	SLC17A5	3'	CCCAGGCAGCTGCCAAGCACTC 14812	_ AAA C
	CC		GGGA TGT GCAGCTGCC GGG	
			CCCT ACG CGTCGACGG CCC	
			C AAC A	
GAM899	TGM2	3'	CCCAAGGTCCCCTCCACATCCC 10953	AA CAGCT C_
	A		TGGGATGT AG GCC GGG	
			ACCCTACA TC TGG CCC	
			CC CCC__ AA	
GAM899	ZFP36L1	3'	CCCTACCCTGCACCCACATCCC 11363	AAA_ CTGCCC
	A		TGGGATGT GCAG GGG	

			ACCCTACA CGTC CCC		
			CCCA CCAT__		
GAM899	ACTR1A	3'	CCCAGGCAGCTGCTGCCTCC 31532	T AA	C
			GGA GT AGCAGCTGCC GGG		
			CCT CG TCGTCGACGG CCC		
			C _ A		
GAM899	C20orf28	3'	CCGCTAAGCTGCTTCTCACCCC 17719	A TA	GCC
	A		TGGG TG AAGCAGCT CGG		
			ACCC AC TTCGTCGA GCC		
			C TC ATC		
GAM899	KIAA1322	3'	CCCGGACTCTGCCCTACATCT 36022	AA_	CTGC
	CA		TGGGATGTA GCAG CCGGG		
			ACTCTACAT CGTC GGCCC		
			CCC TCA_		
GAM899	KIAA1372	5'	CCTGGGCTGCCCTCACCCCA 44057	A TAAA	GCT
			TGGG TG GCA GCCCGGG		
			ACCC AC CGT CGGGTCC		
			C TCC_ _		
GAM899	KIAA1453	5'	CCAAGTCTGCACATCCCA 24712	AAA _	GCCC
			TGGGATGT GCAG CT GG		
			ACCCTACA CGTC GA CC		
			_ T A_		
GAM899	MGC4342	3'	CCCGGGCAGGCCCCAGCACCC 23622	A AAA_	AG
	CA		TGGG TGT GC CTGCCCGGG		
			ACCC ACG CG GACGGGCCC		
			C ACCCC _		
GAM899	MICAL	5'	CCCGGGCCGCCCCGCATCCCA 23010	AAAGCA	T
			TGGGATGT GC GCCCGGG		
			ACCCTACG CG CGGGCCC		
			CCC_ C		
GAM899	MSTP032	3'	CCCAGCATCACTTACACATCCC 24907	A_	CAGC CC
	A		TGGGATGT AAG TGC GGG		
			ACCCTACA TTC ACG CCC		
			CA ACT_ A_		
GAM899	PIP5K1C	3'	CCCAAACACTGGTTTGCATCCC 35017	G C	CCC
	A		TGGGATGTAAA CAG TG GGG		
			ACCCTACGTTT GTC AC CCC		
			G _ AAA		
GAM899	SDC3	3'	CCTGGCTCCTCACATCCCA 16082	AAAGC	CT C
			TGGGATGT AG GCC GG		

		ACCCTACA TC CGG CC		
		C____ CT T		
GAM899	TOR2A 3'	CCGGGCGGCTTCACCCA 28219	A TAAAGC	
		TGGG TG AGCTGCCCGG		
		ACCC AC TCGGCGGGCC		
		C T____		
GAM899	LOC125268 3'	CCAGGCCGCCCACGTCCA 37450	AAAGCA T C	
		TGGGATGT GC GCC GG		
		ACCCTGCA CG CGG CC		
		CC____ C A		
GAM899	LOC145757 5'	CCCAGGTGCAAAACCCACATC 37972	AAAGCAGC _ _	
	CCA	TGGGATGT TGC CC GGG		
		ACCCTACA ACG GG CCC		
		CCCCAAA_ T A		
GAM899	LOC148397 5'	CCCAGGCAGCTGGACAGCACCC 38527	A AAAG C	
	A	TGGG TGT CAGCTGCC GGG		
		ACCC ACG GTCGACGG CCC		
		_ ACAG A		
GAM899	LOC148479 5'	CCCGGGCGGGCCCGCTCCAGCA 38539	AA_ A__	
	TCCA	TGGGATGT AGC GCTGCCCGGG		
		ACCCTACG TCG CGGCGGGCCC		
		ACC CCC		
GAM899	LOC151568 5'	CCCAGGTGAGGATTACATCCC 28835	A GCAG _ C	
	A	TGGGATGT AA CT GCC GGG		
		ACCCTACA TT GA TGG CCC		
		C AG__ G A		
GAM899	LOC152633 5'	CCCAGGCAGCTGCCACTGCCCA 41532	AT AAA C	
		TGGG GT GCAGCTGCC GGG		
		ACCC CA CGTCGACGG CCC		
		GT C__ A		
GAM899	LOC222057 3'	CCCAGGCAGCTGCTGCCTCA 44572	ATGTAA C	
		TGGG AGCAGCTGCC GGG		
		ACTC TCGTCGACGG CCC		
		CG____ A		
GAM899	LOC51112 5'	CCAGGCAGCTGCGCCCCC 18112	AT AAA C	
		GGG GT GCAGCTGCC GG		
		CCC CG CGTCGACGG CC		
		C_ ____ A		
GAM900	AXIN1 3'	ACAGTGTTGGGTGTACCACCC 30511	AGCT_ C	
		GGG CACCCAACAC GT		

			CCC GTGGGTTGTG CA		
			ACCAT A		
GAM900	CDS2	5'	GACGGCACTGGGTGGGGCC 9909	AG	ACA
			GG CTCACCCA CCGTC		
			CC GGGTGGGT GGCAG		
			G_ CAC		
GAM900	KIF3C	3'	GACAGTGTGGGCATCTGCTCC 8057	TCA__	C
	C		GGGAGC CCCAACAC GTC		
			CCCTCG GGGTTGTG CAG		
			TCTAC A		
GAM900	LYL1	5'	ACAGTGCTGGGGTGAGTACCCC 12109	A A	AA_ C
	CA		TG GGG GCTCACCC CAC GT		
			AC CCC TGAGTGGG GTG CA		
			C A GTC A		
GAM900	RP2	3'	GACGGCATTAGTTTTTCCCTTA 13793	CTC	CCAACA
			TGAGGGAG AC CCGTC		
			ATTCCCTT TG GGCAG		
			TT_ ATTAC_		
GAM900	ATP6V1EL2	5'	ACGGTGACGAGCTCCCTC 27940		ACCCA
			GAGGGAGCTC ACACCGT		
			CTCCCTCGAG TGTGGCA		
			CA__		
GAM900	C20orf162	5'	GACAATGCTGAATGGGCTCCT 27916	CC A	CC
			GGGAGCTCA CA CA GTC		
			TCCTCGGGT GT GT CAG		
			AA C AA		
GAM900	GAPCENA	3'	GCTGTGGACAGAGCTCCCTCA 14494	ACCCAA	C
			TGAGGGAGCTC CAC GT		
			ACTCCCTCGAG GTG CG		
			ACAG_ T		
GAM900	KIAA1126	3'	GACGGCACCCCTGGCTTCCTCA 35609	T	CCCAACA
			TGAGGGAGC CA CCGTC		
			ACTCCTTCG GT GGCAG		
			_ CCCAC_		
GAM900	MGC2574	3'	GACTGGCAGGTGACTCCCTCA 23538	C	CAACA _
			TGAGGGAG TCACC CC GTC		
			ACTCCCTC AGTGG GG CAG		
			_ AC_ T		
GAM900	RNF24	5'	GACTGGAGGGTGAGTCCCTCA 14086	G	AA CC
			TGAGGGA CTCACCC CA GTC		

ACTCCCT GAGTGGG GT CAG
 _ AG _
 GAM900 Rpo1-2 3' ACGGTGTTAGAACTCTC 25931 C ACCC
 GGGAG TC AACACCGT
 ||||| || |||||
 CTCTC AG TTGTGGCA
 A A__
 GAM900 Rpo1-2 3' ACGGTGTTAGAACTCTC 21096 C ACCC
 GGGAG TC AACACCGT
 ||||| || |||||
 CTCTC AG TTGTGGCA
 A A__
 GAM900 LOC200169 5' GACATGTCACTGAGCTCCCCCA 43285 A CCCA CC
 TG GGGAGCTCA ACA GTC
 || ||||| || |||
 AC CCCTCGAGT TGT CAG
 C CAC_ A_
 GAM900 LOC221416 3' GACAGCGTTGTGTCTCCCCTCA 45025 _ CTC C ACC
 TGAGGG AG AC CAAC GTC
 ||||| || || ||| |||
 ACTCCC TC TG GTTG CAG
 C _ T CGA
 GAM900 LOC253502 3' GACGGCGTCCTGCGCTCCCCA 45382 A T CCCA A
 TG GGGAGC CA AC CCGTC
 || ||||| || || |||
 AC CCCTCG GT TG GGCAG
 _ C CC_ C
 GAM901 CENTD1 3' GGAGTTAAATGTCCTGCA 29200
 TGCAGGATATTTAACTTT
 ||||| |||||
 ACGTCCTGTAAATTGAGG
 GAM901 CENTD1 3' GGAGTTAAATGTCCTGCA 17562
 TGCAGGATATTTAACTTT
 ||||| |||||
 ACGTCCTGTAAATTGAGG
 GAM901 DDX6 3' TTGGAGATCAAAATCCTGCAGA 10650 ATTTAA
 TCTGCAGGAT CTTTAA
 ||||| |||||
 AGACGTCCTA GAGGTT
 AAATA
 GAM901 TEM5 3' TAAAGCTAGTCCTGTA 26521 ATT A
 TGCAGGAT TA CTTTA
 ||||| || |||||
 ATGTCCTG AT GAAAT
 _ C
 GAM901 EFA6R 3' TAAAGTTAAAATCTCCGCA 17627 A TA_
 TGC GGA TTAACTTTA
 || ||| |||||

ACG CCT AAATTGAAAT
 _ CTA
 GAM901 FLJ13910 3' TTAAAGTTAGAAGCTAGCA 23059 A ATA
 TGC GG TTAACTTTAA
 ||| || |||||
 ACG TC AGATTGAAATT
 A GA_
 GAM901 KIAA1077 5' CTTCAAAGGACCCTATCTGCAG 36094 G TTAA A
 A TCTGCAG ATA CTTT AAG
 ||||| || ||| |||
 AGACGTC TAT GAAA TTC
 _ CCCAG C
 GAM902 HDAC4 3' ATGCATCATCTCACTTTT 12659 T A
 AAAAGTGA AT ATGCAT
 ||||| || |||||
 TTTTCACT TA TACGTA
 C C
 GAM902 UBE2A 3' ATGCATTTATCACTTCC 9339 A T
 A AAGTGATA AATGCAT
 | ||||| |||||
 C TTCACTAT TTACGTA
 C _
 GAM902 C20orf54 5' AAAGGTGCATATACCACT 27226 A A
 AGTG TATA TGCATTTT
 ||| ||| |||||
 TCAC ATAT ACGTGGAAA
 C _
 GAM902 CAP350 3' ATGCATCACATCACTTTT 16770 ATA
 AAAAGTGAT ATGCAT
 ||||| |||||
 TTTTCACTA TACGTA
 CAC
 GAM902 PHCA 3' AAATTGCATCACTTTT 20374 TATAA TT
 AAAAGTGA TGCA TTT
 ||||| ||| |||
 TTTTCACT ACGT AAA
 _ T_
 GAM903 FLJ20707 3' AAGGATTA AAACTGAGATTTGA 19628 AAATT
 TCAAAT TTTTAATCCTT
 ||||| |||||
 AGTTTA AAAATTAGGAA
 GAGTC
 GAM903 FLJ21934 3' TTATAAAATTTATTTGATA 24080 T
 TATCAAATAAATTTT TAA
 ||||| ||||| |||
 ATAGTTTATTTAAAA ATT
 T
 GAM904 CARPX 3' ACATTGTATATATATCAC 21394 TCC
 GTGATATATAT CAATGT
 ||||| |||||

			CACTATATATA GTTACA		
			T__		
GAM904	IFNAR1	3'	ACATTGGCTTCCACATCACAGT 6245		ATATATTC
	A		TATTGTGAT CCAATGT		
			ATGACACTA GGTTACA		
			CACCTTC_		
GAM904	KIAA0318	3'	ACATTGGGAACATATTTT 34183	T A	
			GA ATAT TTCCCAATGT		
			CT TATA AAGGGTTACA		
			T C		
GAM904	LOC160414	5'	ACATTGGGAATGGCCACAA 42102		ATATA
			TTGTG TATTCCCAATGT		
			AACAC GTAAGGGTTACA		
			CG__		
GAM904	LOC57086	3'	ACATTGGGAATATAAGACAAT 21615		GATA
			ATTGT TATATTCCCAATGT		
			TAACA ATATAAGGGTTACA		
			GA__		
GAM905	ABH	3'	TGTTATTGTGTATTGCC 30056	A G AAG	
			GGCAATG CA A GTAACA		
			CCGTTAT GT T TATTGT		
			_ G _		
GAM905	BAALC	3'	GCCTCTCTGTACACTGCC 24195	A _ A	
			GGCA TG ACAGA AGGT		
			CCGT AC TGTCT TCCG		
			C A C		
GAM905	CD34	3'	TGCTTTTCTGTCTCTGCC 7537		AT
			GGCA GACAGAAAGGTA		
			CCGT CTGTCTTTTCGT		
			CT		
GAM905	DCK	3'	GCTTCCTTCTGTCATTCC 6443	C _	
			GG AATGACAGAA AGGT		
			CC TTA CTGTCTT TTCG		
			_ CC		
GAM905	FACL4	5'	TGCTGCTTCTATTATTGCC 23255		C A_
			GGCAATGA AGAA GGTA		
			CCGTTATT TCTT TCGT		
			A CG		
GAM905	FREB	3'	ACCGACTCTGTCGTTGCC 26466		AA_
			GGCAATGACAGA GGT		

			CCGTTGCTGTCT CCA		
			CAG		
GAM905	IL1R1	3'	ATGCCGCTCTTCTGTCATCC 6563	CA	AG AA
			GG ATGACAGAA GT CAT		
			CC TACTGTCTT CG GTA		
			___ CT CC		
GAM905	JAM3	3'	GTTCCCTCCATCATTGCC 26555	CA AA T	
			GGCAATGA GA GG AAC		
			CCGTTACT CT CC TTG		
			AC ___ C		
GAM905	NCOA3	3'	ATGTTACCTTTTCATCCCC 13283	CA	CAG
			GG ATGA AAAGGTAACAT		
			CC TACT TTTCCATTGTA		
			CC ___		
GAM905	NRIP1	5'	TTATCTTGTCATTGCC 30122	GAA	
			GGCAATGACA AGGTAA		
			CCGTTACTGT TCTATT		

GAM905	PROML1	3'	ATGTTGGATCTGTCATTATC 12634	GC	AAGG
			G AATGACAGA TAACAT		
			C TTA CTGTCT GTTGTA		
			TA AG___		
GAM905	RGL	3'	ATGTCACTGCTTCATTGCC 17505	C AAA A	
			GGCAATGA AG GGT ACAT		
			CCGTTACT TC TCA TGTA		
			___ G___ C		
GAM905	AMOT	3'	TGAATTTCTGTCTTGCC 28420	T	GG
			GGCAA GACAGAAA TA		
			CCGTT CTGTCTTT GT		
			___ AA		
GAM905	ARSDR1	3'	TTGCTTCTGTTACTGCC 18111	A	AA
			GGCA TGACAGA GGTA		
			CCGT ATTGTCT TCGTT		
			C ___		
GAM905	FLJ12171	3'	TTGCTTCTGTTATTACC 23880	C	AA
			GG AATGACAGA GGTA		
			CC TTATTGTCT TCGTT		
			A ___		
GAM905	GRID1	3'	ACCAACTCTGTTTCCTCATTGC 33977	___	AA_
	C		GGCAATGA CAGA GGT		

CCGTTACT GTCT CCA
 CCTTT CAA
 GAM905 KIAA0332 3' ATGTTTTTCTCCCCTGCTCATT 31417 _ AA_ T_
 GCC GGCAATGA CAG AGG AACAT
 ||||| ||| ||| |||||
 CCGTTACT GTC TCT TTGTA
 C CCC TT
 GAM905 KIAA0556 3' ATGTGGCTGCTTTCTGTCTCTG 34248 AT _ A
 CC GGCA GACAGAAAG GT ACAT
 ||| ||||| || |||||
 CCGT CTGTCTTTC CG TGTA
 CT GT G
 GAM905 KIAA0826 3' ATGTTACCTTCTTGAATTGCC 40214 GA GA
 GGCAAT CA AAGGTAACAT
 ||||| || |||||
 CCGTTA GT TTCCATTGTA
 A_ TC
 GAM905 KIAA0977 3' ATGTTACCCTGCCACACC 17080 CAA A AAA
 GG TG CAG GGTAACAT
 || ||| |||||
 CC AC GTC CCATTGTA
 AC_ C _
 GAM905 KIAA1041 3' GTTACCTTTCTGTGC 17265 AATG
 GC ACAGAAAGGTAAC
 || |||||
 CG TGTCTTTCATTG

 GAM905 KIAA1238 3' ATGCTACCTTTTTTGTTA 35215 _ A
 TGACAGAAA GGTA CAT
 ||||| ||| |||
 ATTGTTTTT CCAT GTA
 T C
 GAM905 METAP1 3' GTTGCTTTTATCACTGCC 35958 A CAG
 GGCA TGA AAAGGTAAC
 ||| ||| |||||
 CCGT ACT TTTTCGTTG
 C A_
 GAM905 NIN283 3' TATCTTGA CTTCATTGCC 26015 C A_
 GGCAATGA AG AAGGTA
 ||||| || |||||
 CCGTTACT TC TTCTAT
 _ AG
 GAM905 PRO1331 5' ATGTTACAGAGCATGTCATTGT 25067 GAAAG_
 C GGCAATGACA GTAACAT
 ||||| |||||
 CTGTTACTGT CATTGTA
 ACGAGA
 GAM905 STK39 3' ATGTCACCCTGATCTGTGCATGC 14891 A AA_ A
 C GGCA TGACAGA GGT ACAT
 ||| ||||| ||| |||||

		CCGT ACTGTCT CCA TGTA	
		— AGTC C	
GAM905	TRIP-Br2 3'	GTTACCTTCCTGTAAGTACC 16493	ATG A
		GGCA ACAG AAGGTAAC	
		CCGT TGTC TTCCATTG	
		CAA C	
GAM905	LOC120856 3'	ATGTTACTTGCTATCATTCC 36633	C C AA
		GG AATGA AG AGGTAACAT	
		CC TTACT TC TTCATTGTA	
		— A G_	
GAM905	LOC120939 3'	ATGTTACTGTTGTCACACC 37510	CAA GAAA
		GG TGACA GGTAACAT	
		CC ACTGT TCATTGTA	
		AC_ TG_	
GAM905	LOC130612 3'	ATGTCTGGTGTCTGTCATGCC 36997	A AAGGTA
		GGCA TGACAGA ACAT	
		CCGT ACTGTCT TGTA	
		— GTGGTC	
GAM905	LOC148936 5'	GTGACTTGCTCCTCATTGCC 40931	CA A_ A
		GGCAATGA GA AGGT AC	
		CCGTTACT CT TTCA TG	
		C_ CG G	
GAM905	LOC148938 5'	GTGACTTGCTCCTCATTGCC 40924	CA A_ A
		GGCAATGA GA AGGT AC	
		CCGTTACT CT TTCA TG	
		C_ CG G	
GAM905	LOC221504 3'	TACTTTTCCCTCACTGCC 44396	A CA
		GGCA TGA GAAAGGTA	
		CCGT ACT CTTTTCAT	
		C CC	
GAM905	LOC91151 5'	TTACTCTGTCATTGCC 27056	AAG
		GGCAATGACAGA GTAA	
		CCGTTACTGTCT CATT	
		—	
GAM905	LOC92391 3'	GTGTTGCCTCCTACCTTGCC 34273	TGAC AA
		GGCAA AG AGGTAACAT	
		CCGTT TC TCCGTTGTG	
		CCA_ C_	
GAM906	UGDH 3'	ACAGATGAAAATTACATA 9387	A
		TATG AATTTTCATTTGT	

			ATAC TTAAAAGTAGACA	
			A	
GAM906	XPR1	3'	ACCCAAATGAAAATTTCA 11122	T
			TGAAATTTTCATTTG GT	
			ACTTTAAAAGTAAAC CA	
			C	
GAM906	AP1GBP1	3'	CAGAGACTATAAAGATTTCA 14115	C TT G
			TGAAATTTT AT GT TCTG	
			ACTTTAGAA TA CA AGAC	
			A T_ G	
GAM906	AP1GBP1	3'	CAGAGACTATAAAGATTTCA 27877	C TT G
			TGAAATTTT AT GT TCTG	
			ACTTTAGAA TA CA AGAC	
			A T_ G	
GAM906	AP1GBP1	3'	CAGAGACTATAAAGATTTCA 27870	C TT G
			TGAAATTTT AT GT TCTG	
			ACTTTAGAA TA CA AGAC	
			A T_ G	
GAM906	FLJ11827	3'	CAGATGGGATGAAATTTCA 24722	T G
			TGAAATTT CATTT TGTCTG	
			ACTTTAAA GTAGG GTAGAC	
			- -	
GAM906	FLJ12598	5'	GCAGAGAACAAAAATTTCA 24097	CATT G_
			TGAAATTTT TGT TCTGC	
			ACTTTAAAA ACA AGACG	
			AG	
GAM906	FLJ21140	3'	GCAGGTAAAAATGAAAATCCAT 24141	AA G GT
	A		TATG ATTTTCATTT T CTGC	
			ATAC TAAAAGTAAA A GACG	
			C_ A TG	
GAM906	HMG17L1	3'	GCATCAAATGAAAAC TTCATA 22014	A _
			TATGAA TTTTCATTTG TGT	
			ATACTT AAAAGTAAAC ACG	
			C T	
GAM906	MYNN	3'	GCATAAAAATAAAATTTTCATA 20725	CA_
			TATGAAATTTT TTTGTGT	
			ATACTTTAAAA AAATACG	
			TAA	
GAM906	NAP1L1	3'	GCAGCTAAAATAAAATTTCA 29224	C GT T
			TGAAATTTT ATTT G CTGC	

		ACTTTAAAA TAAA C GACG		
		A AT_		
GAM906	LOC146050 3'	GCAGAAACAATGAAAACCTTAT 38055	AA	T G
	A	TATGA TTTTCATT GT TCTGC		
		ATATT AAAAGTAA CA AGACG		
		CC _ A		
GAM906	LOC158549 5'	GCATCTAATGAAAATTTC A 42009	T_	
		TGAAATTTTCATT GTGT		
		ACTTTAAAAGTAA TACG		
		TC		
GAM906	LOC169166 3'	ACATAAATGAAAGTCTCATA 40271	A	
		TATGA ATTTTCATTTGTGT		
		ATACT TGAAAGTAAATACA		
		C		
GAM906	LOC199957 3'	CAAACACAAATAGAGATTTTCAT 42671	TC	C
	A	TATGAAATTT ATTTGTGT TG		
		ATACTTTAGA TAAACACA AC		
		GA A		
GAM907	HCA4 3'	CTTATACCTGTTGCTTACTA 38022	T TGC_	
		TGGTAAGCA AC ATAAG		
		ATCATTCGT TG TATTC		
		_ TCCA		
GAM907	KIAA1600 3'	AGCTCTAGAATGCTTACCA 35391	A CATA	
		TGGTAAGCAT CTG AGCT		
		ACCATTCGTA GAT TCGA		
		A C_		
GAM907	P2RXL1 3'	TAGCAGAGGTATGCTTACCA 11933	GCATAA	
		TGGTAAGCATACT GCTA		
		ACCATTCGTATGG CGAT		
		AGA_		
GAM907	LOC133418 3'	AGCTTATGCAACATGCTCAGC 37038	A_ AC	
		GT AGCAT TGCATAAGCT		
		CG TCGTA ACGTATTCGA		
		AC CA		
GAM907	LOC153222 3'	TTAGCTTATTGTAGTATACTTC 39369	T C _	
	CA	TGG AAG ATACTGCA TAAGCTAA		
		ACC TTC TATGATGT ATTCGATT		
		_ A T		
GAM907	LOC255098 3'	AGCTTATGCAACATGCTCAGC 45687	A_ AC	
		GT AGCAT TGCATAAGCT		

			CG TCGTA ACGTATTCGA		
			AC CA		
GAM908	EYA1	5'	ACAGAACGGTGGGAGCTG 6115	T AC_	
			CAGCTTC CGC TCTGT		
			GTCGAGG GTG AGACA		
			_ GCA		
GAM908	GGT1	5'	CAGACAGAGCCCTCTAGCTGCT 15081	TCTCGCA	
			AGCAGCT CTCTGTCTG		
			TCGTCGA GAGACAGAC		
			TCTCCC_		
GAM908	GGT2	5'	CAGACAGAGCCCTCTAGCTGCT 36487	TCTCGCA	
			AGCAGCT CTCTGTCTG		
			TCGTCGA GAGACAGAC		
			TCTCCC_		
GAM908	MHC2TA	3'	CAGATACAGGAAAAGCTGCTG 5777	C GCA C	
			CAGCAGCTT TC CT TGTCTG		
			GTCGTCGAA AG GA ATAGAC		
			A _ C		
GAM908	NEU3	3'	CAGACAGGTTAACAGAAGCTAC 13454	C CGC_ T	
	TG		CAG AGCTTCT AC CTGTCTG		
			GTC TCGAAGA TG GACAGAC		
			A CAAT _		
GAM908	ASPN	3'	CAGACAGAAACCGAAAGCTCT 19223	C C CAC	
			AG AGCTT TCG TCTGTCTG		
			TC TCGAA AGC AGACAGAC		
			_ _ CAA		
GAM908	C20orf110	3'	CAGACACGTTGAGAAGCTGC 38834	C TC	
			GCAGCTTCTCG AC TGTCTG		
			CGTCGAAGAGT TG ACAGAC		
			_ C_		
GAM908	DKFZP566K023	3'	CAGACAGAACACAAAAGGTTTC 17756	C CTCGCAC	
	TG		CAG AGCTT TCTGTCTG		
			GTC TTGGA AGACAGAC		
			T AAACACA		
GAM908	FBXO24	3'	CAGAGTTCAGCAAGGAGCTGCT 14463	C _	
	G		CAGCAGCTTCT GC ACTCTG		
			GTCGTCGAGGA CG TGAGAC		
			A ACT		
GAM908	FLJ10956	3'	ACAGAGTATGGCTGTTG 20275	TCTCGC	
			CAGCAGCT ACTCTGT		

			GTTGTCGG	TGAGACA		
			TA_____			
GAM908	FLJ20281	5'	CAGAGCTCAGCGAGAAGCTGT	43724	A_____	
			GCAGCTTCTCGC	CTCTG		
			TGTCGAAGAGCG	GAGAC		
			ACTC			
GAM908	ITGA10	3'	CAGATGGGACAAGAAGCCGC	29859	A	CGCAC
			GC GCTTCT	TCTGTCTG		
			CG CGAAGA	GGGTAGAC		
			C	ACA_____		
GAM908	KIAA0601	3'	GGCAGGAGAAGCTGCTG	31328		GCACT
			CAGCAGCTTCTC	CTGTC		
			GTCGTCGAAGAG	GACGG		

GAM908	KIAA0700	5'	AGGCCACGAGAAGCTGC	35657		CACTCT
			GCAGCTTCTCG	GTCT		
			CGTCGAAGAGC	CGGA		
			AC_____			
GAM908	KIAA1373	5'	CAGAATGCGGGAAGCCGC	35124	A	C
			GC GCTTCTCGCA	TCTG		
			CG CGAAGGGCGT	AGAC		
			C	A		
GAM908	KIAA1981	3'	CAGACAGAACCAGGAACTG	42607	C	CGCAC
			CAG TTCT	TCTGTCTG		
			GTC AAGG	AGACAGAC		
			_	ACCA_		
GAM908	RNAC	3'	CAGACAAAGCAGAAGCTGC	12344	C	ACTC
			GCAGCTTCT GC	TGTCTG		
			CGTCGAAGA CG	ACAGAC		
			_	AA_		
GAM908	LOC129676	5'	CAGACAGGTCAGAGACCACTG	37281	CT_	GC T
			CAG TCTC AC	CTGTCTG		
			GTC AGAG TG	GACAGAC		
			ACC AC	_		
GAM908	LOC145678	3'	CAGATGGCTGAGAAGCCACT	40554	CA	_ AC
			AG GCTTCTC GC	TCTG		
			TC CGAAGAG CG	AGAC		
			AC	T GT		
GAM908	LOC152762	3'	AGTCGCTGAGAAGCTGCTG	39304	_	_
			CAGCAGCTTCTC GC	ACT		

			GTCGTCGAAGAG CG TGA	
			T C	
GAM908	LOC199957	3'	CAGACAGGCTGTGAAGAAGCTC 42673	C _ CT
		T	AG AGCTTCT CGCA CTGTCTG	
			TC TCGAAGA GTGT GACAGAC	
			_ A CG	
GAM908	LOC253024	5'	CAGACAGAAAAAGAAGAAGCT 46604	_ GCAC
			AGCTTCT C TCTGTCTG	
			TCGAAGA G AGACAGAC	
			A AAAA	
GAM909	DFFB	3'	GAATTCTTCTGTTCTCTGG 42245	A CCAAA
			CCAGAGAA CA AATTC	
			GGTCTCTT GT TTAAG	
			_ CTTC_	
GAM909	DSC2	3'	GAATTTTGGATAATTTGGA 11392	GAAACA
			TCCAGA CCAAAAATTC	
			AGGTTT GGTTTTTAAG	
			AATA_	
GAM909	EPHB2	3'	GAATTTTCTGTCTTTGGA 10735	AACACC
			TCCAGAGA AAAAATTC	
			AGGTTTCT TTTTAAAG	
			GTC_	
GAM909	EPHB2	3'	GAATTTTCTGTCTTTGGA 18910	AACACC
			TCCAGAGA AAAAATTC	
			AGGTTTCT TTTTAAAG	
			GTC_	
GAM909	EYA1	3'	GAATTTTGGTGTAATTTG 6116	GAA
			CAGA ACACCAAAAATTC	
			GTTT TGTGGTTTTTAAG	
			AAA	
GAM909	JJAZ1	3'	GATTTTGCCTCTGGA 17657	AAACAC
			TCCAGAG CAAAATT	
			AGGTCTC GTTTTAG	
			C_	
GAM909	MAP2K1	3'	AATTTTGGTGAATGTGGG 8634	GAGAAA
			TCCA CACCAAAAATT	
			GGGT GTGGTTTTTAA	
			GTAA_	
GAM909	NAPB	3'	GAATTTTCTCTTTTCTGGA 34767	CACC
			TCCAGAGAAA AAAAATTC	

			AGGTCTTTTT TTTTAAAG	
			CTC_	
GAM909	RBBP9	3'	GAATTTTGGTGCTGTCCGGA 34742	A GAAA
			TCC GA CACCAAAAATTC	
			AGG CT GTGGTTTTTAAG	
			C GTC_	
GAM909	STAT1	3'	GAATTTTTTTCATCTTCTCTGG 14231	ACACC_
			CCAGAGAA AAAAATTC	
			GGTCTCTT TTTTAAAG	
			CTACTT	
GAM909	TIM3	3'	GAATTCTTGACGTGGGGTCTCT 26524	AA_ _ A
			GGA TCCAGAGA CAC CAA AATTC	
			AGGTCTCT GTG GTT TTAAG	
			GGG CA C	
GAM909	BFAR	5'	AATTTTTTATGTCTCTGGA 30478	AA CC
			TCCAGAGA CA AAAAATT	
			AGGTCTCT GT TTTTAA	
			_ AT	
GAM909	CMRF-35H	3'	TGGTGGCAAGTTTCTCTGGA 34862	_____
			TCCAGAGAAAC ACCA	
			AGGTCTCTTTG TGGT	
			AACGG	
GAM909	CPSF2	5'	GAATTCCTGGTGTTTCATC 30863	_ AA
			GA GAAACACCA AATTC	
			CT CTTTGTGGT TTAAG	
			A CC	
GAM909	DKFZP564D0764	3'	GAATTTTTTTTTCCCTGGA 42574	A CACC
			TCCAG GAAA AAAAATTC	
			AGGTC CTTT TTTTAAAG	
			C T__	
GAM909	FLJ10697	3'	GAATATCAAGTATTTCTCTGG 20016	C CAAAA
			CCAGAGAAA AC ATTC	
			GGTCTCTTT TG TAAG	
			A AACTA	
GAM909	FLJ10704	3'	AATTTTtagatCTCTGGA 20030	AACACC
			TCCAGAGA AAAAATT	
			AGGTCTCT TTTTAA	
			AGA__	
GAM909	FLJ11722	3'	GAATTTCATTGGTGTTTCT 24521	_____
			AGAAACACCAA AAATTC	

		TCTTTGTGGTT TTTAAG	
		ACC	
GAM909	KIAA0335	3' TTTTGCTGGTTCTTTGGA 16734	A C
		TCCAGAGAA CA CAAAA	
		AGGTTTCTT GT GTTTT	
		G C	
GAM909	KIAA0976	3' AATTTGTGATCAGTAGTCTCTC 17162	A _ _ _ _ A
		TGGA TCCAGAGA AC AC CA AAATT	
		AGGTCTCT TG TG GT TTTAA	
		C A ACTA G	
GAM909	KIAA1727	3' GAATGCTGGATTCTCTGGA 32031	CA AAA
		TCCAGAGAAA CCA ATTC	
		AGGTCTCTTT GGT TAAG	
		A_ CG_	
GAM909	KIAA1938	3' GATTTTTCGGTGTCTCTCTG 44279	_
		CAGAGAAACACC AAAAATT	
		GTCTCTTTGTGG TTTTAG	
		C	
GAM909	SEC15L	3' GAATTATATGTACATCTCTGGA 35765	AAC CAAA
		TCCAGAGA AC AATTC	
		AGGTCTCT TG TTAAG	
		ACA TATA	
GAM909	TSPAN-2	3' AATTTTCAATGTTTTTTTGG 12278	CCA
		CCAGAGAAACA AAAATT	
		GGTTTTTTTGT TTTTAA	
		AAC	
GAM909	ZNF297B	3' GAATTTTGTAACTCTGG 15220	AAACAC
		CCAGAG CAAAAATTC	
		GGTCTC GTTTTAAAG	
		AAAT_	
GAM909	LOC143879	3' AATTTTGGATTCTGGG 37659	AAACA
		TCCAGAG CCAAAAATT	
		GGGTCTT GGTTTTTAA	
		A_	
GAM909	LOC151057	3' GAATTTTAAATGTGAACTGGA 41294	AGAA CC
		TCCAG ACA AAAAATTC	
		AGGTC TGT TTTTAAAG	
		AAG_ AA	
GAM909	LOC199957	3' GAATTTTGCAATGCTCTCTGGA 42674	AACACCA
		TCCAGAGA AAAATTC	

			AGGTCTCT	TTTTAAG		
			CGTAACG			
GAM909	LOC202934	3'	GAATTATTGTGCTTCTTTGGA	43460	A C A	
			TCCAGAGAA CAC AA AATTC			
			AGGTTTCTT GTG TT TTAAG			
			C _ A			
GAM909	LOC253612	3'	GAATTTTGAATTCTGGA	46255	AAACAC	
			TCCAGAG CAAAAATTC			
			AGGTCTT GTTTTAAAG			
			AA_____			
GAM909	LOC257017	5'	AATTTTGGTGCTTGG	46491	G AAA	
			CCA AG CACCAAAAATT			
			GGT TC GTGGTTTTTAA			
			— —			
GAM909	LOC92573	5'	GAAGGTTGGTCATTTCTCTG	34599	C_ AAA	
			CAGAGAAA ACCAA TTC			
			GTCTCTTT TGGTT AAG			
			AC GG_			
GAM910	BMP4	5'	GCAGCTTCCCTGAGCCTTTCCA	6867	A T AAGTCCT	
			TG AAAGGCT CA CTGC			
			AC TTTCCGA GT GACG			
			C _ CCCTTC_			
GAM910	BMP4	5'	GCAGCTTCCCTGAGCCTTTCCA	28388	A T AAGTCCT	
			TG AAAGGCT CA CTGC			
			AC TTTCCGA GT GACG			
			C _ CCCTTC_			
GAM910	BMP4	5'	GCAGCTTCCCTGAGCCTTTCCA	28389	A T AAGTCCT	
			TG AAAGGCT CA CTGC			
			AC TTTCCGA GT GACG			
			C _ CCCTTC_			
GAM910	CSNK1G3	3'	GCAGAAAACCTTTGGATGTGCC	10611	___ CC	
			GGC TTCAAAGT TCTGC			
			CCG AGGTTTCA AGACG			
			TGT AA			
GAM910	F8	3'	GCAGACACTGCCTTGAAGCCT	5616	A CC_	
			AGGCTTCAA GT TCTGC			
			TCCGAAGTT CG AGACG			
			C TCAC			
GAM910	IL2RB	3'	GCAGAGGACCTTGGGTCCC	6573	C_ A	
			GG TTCAA GTCCTCTGC			

CC GGGTT CAGGAGACG
 CTT C
 GAM910 KRTHA8 3' CAAAGGACCAGGCTTGCCTTTT 13644 TTCAAA_ C
 C GAAAAGGC GTCCT TG
 ||||| |||||
 CTTTCCG CAGGA AC
 TTCGGAC A
 GAM910 MEOX2 3' CAGAGGACCAGCTCCATTC 12548 AA_ TCAAA
 GAA GGCT GTCCTCTG
 || ||| |||||
 CTT TCGA CAGGAGAC
 ACC C____
 GAM910 NOS1 5' AGAGGGCTGAAGCCTTGTCA 6228 A AA
 TGA AAGGCTTCA GTCCTCT
 || ||||| |||||
 ACT TTCCGAAGT CGGGAGA
 G ____
 GAM910 PACSIN1 3' GCAGAGGACCTGTCCCCTCTCA 44318 AA CTT AA
 TGA AGG CA GTCCTCTGC
 || || || |||||
 ACT TCC GT CAGGAGACG
 C_ CCT C_
 GAM910 SOST 3' GCAGAAATGGAAGCATTTTCA 24918 G AAAGTCC
 TGAAAA GCTTC TCTGC
 ||||| |||||
 ACTTTT CGAAG AGACG
 A GTAA____
 GAM910 AMOT 3' GCAGAAGATAGATACAGCCTTT 28414 TCAAA_ C
 TCA TGAAAAGGCT GTC TCTGC
 ||||| || |||||
 ACTTTTCCGA TAG AGACG
 CATAGA A
 GAM910 AP4S1 3' CAGAAAACCTCCACGGCCTTTT 13942 TCAAA_ CC
 CA TGAAAAGGCT GT TCTG
 ||||| || |||||
 ACTTTTCCGG CA AGAC
 CACCTC AA
 GAM910 DKFZP434N161 3' CAGAAAACCTCAGTCTTTTCA 38396 TCAA CC
 TGAAAAGGCT AGT TCTG
 ||||| || |||||
 ACTTTTCTGA TCA AGAC
 C__ AA
 GAM910 FLJ11004 5' CAAAGGACTTTTTATTCCCTTC 20285 A CTTC__ C
 C A AAGG AAAGTCCT TG
 || ||||| |||||
 C TTCC TTTCAGGA AC
 C CTTATT A
 GAM910 FLJ11560 5' CAGCTAGGCTTGAGGCCTCTTC 24819 A A CT_
 A TGAA AGGCTTCAA GTC CTG
 |||| ||||| || |||||

ACTT TCCGGAGTT CGG GAC
 C _ ATC
 GAM910 FLJ13263 3' GCAGAGGACTTCAGCTACCTTC 24768 AA_ TCA
 GAA GGCT AAGTCCTCTGC
 ||| ||| |||||
 CTT TCGA TTCAGGAGACG
 CCA C_
 GAM910 IMPACT 3' GCAGAGAGAAGGAGCAAACCTT 20503 C___ AAAG _
 TTCA GAAAAGG TTC TC CTCTGC
 ||||| ||| |||||
 CTTTTCC GAG AG GAGACG
 AAAC GA_ A
 GAM910 KIAA1157 3' GCAGAGGACTCTTCAGCCTGTC 35750 AA TCAA
 A TGA AGGCT AGTCCTCTGC
 ||| ||| |||||
 ACT TCCGA TCAGGAGACG
 G_ CTTC
 GAM910 KIAA1170 3' CAGAAAATTATCCTTTTCA 34610 CTTCAA CC
 TGAAAAGG AGT TCTG
 ||||| ||| |||
 ACTTTTCC TTA AGAC
 TA___ AA
 GAM910 KIAA1276 5' GCAGAGGAGGAAGCCCTTC 33018 AA AAAG
 GAA GGCTTC TCCTCTGC
 ||| ||||| |||||
 CTT CCGAAG AGGAGACG
 C_ G_
 GAM910 KIAA1937 3' GCAGAGGACCGTTTCCTTTT 36484 CTTCAAA
 AAAAGG GTCCTCTGC
 ||||| |||||
 TTTTCC CAGGAGACG
 TTTGC_
 GAM910 LCE 3' GCAGAAACTAAAGCCTTTTCA 23534 CAA CC
 TGAAAAGGCTT AGT TCTGC
 ||||| ||| |||
 ATTTTCCGAA TCA AGACG
 A_ A_
 GAM910 MAD4 3' CAGAGGACCCTGACCCTCG 13168 A CT AA
 A AGG TCA GTCCTCTG
 ||| ||| |||||
 G TCC AGT CAGGAGAC
 C C_ CC
 GAM910 RASGRP4 3' GCAAAGAACTTTGAGGGTC 27503 _ C C
 GGCT TCAAAGT CT TGC
 ||| ||||| ||| |||
 CTGG AGTTTCA GA ACG
 G A A
 GAM910 LOC127262 3' CAGAGGACTTTGTCCAAGTCTC 37458 A _
 A A AGGCTT CAAAGTCCTCTG
 ||||| |||||

A TCTGAA GTTTCAGGAGAC
 C CCT
 GAM910 LOC137075 3' CAGAGGACTCTAGGTTT 37103 CAA
 AGGCTT AGTCCTCTG
 ||||| |||||
 TTTGGA TCAGGAGAC
 TC_
 GAM910 LOC153688 3' CAGAGGACACACCTTGTC 41655 A CTTCAA
 TGA AAGG GTCCTCTG
 ||| ||| |||||
 ACT TTCC CAGGAGAC
 G ACA____
 GAM910 LOC158972 3' CAGAGGACTCCAGGTTGCTCA 42042 AAA CAA
 TGA GGCTT AGTCCTCTG
 ||| ||||| |||||
 ACT TTGGA TCAGGAGAC
 CG_ CC_
 GAM910 LOC196540 3' GCAGAGGACTCCAGAGGCTCA 43151 A AA_
 A GGCTTC AGTCCTCTGC
 | ||||| |||||
 A TCGGAG TCAGGAGACG
 C ACC
 GAM910 LOC221832 5' GCAGTCCCTCACTTTGAAACCT 44426 AA C CCT____
 TCGCA TG AAGG TTCAAAGT CTGC
 || ||| ||||| |||
 AC TTCC AAGTTTCA GACG
 GC A CTCCCT
 GAM910 LOC255465 5' GCAATGATTTTGAAGCCT 46453 CTC
 AGGCTTCAAAGTC TGC
 ||||| |||
 TCCGAAGTTT TAG ACG
 TA_
 GAM910 LOC57109 3' GCAACTCTGGTGAAACCTTTTC 21655 C A_ TCCTC
 A TGAAAAGG TTCA AG TGC
 ||||| ||| |||
 ACTTTTCC AAGT TC ACG
 A GG TCA____
 GAM910 LOC90538 3' GCAGAGGATTTAACCTTTGCA 31656 A CTTCA
 TG AAAGG AAGTCCTCTGC
 || ||||| |||||
 AC TTTCC TTAGGAGACG
 G AA____
 GAM911 CDH1 3' CGGGGTCTCCCTGTGTTACC 10562 T A GGA
 GGTAACAC GG AGA CG
 ||||| || ||| ||
 CCATTGTG CC TCT GC
 T C GGG
 GAM911 NDRG1 3' GCATCCTCTTCCATTAACC 29967 AACAC C
 GGT TGGAAGAGGA GC
 ||| ||||| |||

CCA ACCTTCTCCT CG
 ATT__ A
 GAM911 SNTB1 5' GCGTCCTCCCCCGGCCACC 22012 AACAA AA_
 GGT CTGG GAGGACGC
 ||| ||| |||||
 CCA GGCC CTCCTGCG
 CC__ CCC
 GAM911 ZNF138 5' CGTCCTCTTACTCCTA 39508 TAACACT _
 TAGG GG AAGAGGACG
 ||| || |||||
 ATCC TC TTCTCCTGC
 _____ A
 GAM911 AOP2 3' CGTCCTCTCCTGTCACC 11341 A CT A
 GGT ACA GGA GAGGACG
 ||| ||| ||| |||||
 CCA TGT CCT CTCCTGC
 C _ _
 GAM911 BCL2L12 5' CTCTTCCGCGTTACCTA 28915 AC
 TAGGTAAC TGGAAGAG
 ||||| |||||
 ATCCATTG GCCTTCTC
 C_
 GAM911 FLJ14129 3' GCGTCCTCCCCCGTACCT 25164 ACAC AA
 AGGTA TGG GAGGACGC
 |||| ||| |||||
 TCCAT GCC CTCCTGCG
 _____ CC
 GAM911 HSPC043 3' TCCTCTTATTTAGTGTTACC 33637 _
 GGTAACACTGGA AGAGGA
 ||||| |||||
 CCATTGTGATTT TCTCCT
 AT
 GAM911 LOC199796 5' GCATCCTCTTCCAGGAGTTCC 36810 T A_ C
 GG AAC CTGGAAGAGGA GC
 || ||| ||||| |||
 CC TTG GACCTTCTCCT CG
 _ AG A
 GAM912 MMP8 3' CTATCTGACTTCATACATCCCT 8258 C T C A
 CA TGAGGGA GT TG AG TAGATAG
 ||||| || || |||||
 ACTCCCT CA AC TC GTCTATC
 A T T A
 GAM912 KIAA1024 3' CTATCTATCTCCCCTATTCCCT 34235 CGTTTGC
 CA TGAGGGA AGATAGATAG
 ||||| |||||
 ACTCCCT TCTATCTATC
 TATCCCC
 GAM912 LOC145820 3' TATCTATCTATCCCATCA 37992 _ CGTTTGC
 TGA GGGA AGATAGATA
 ||| ||| |||||

ACT CCCT TCTATCTAT
 A A____
 GAM912 LOC151248 5' CTATCTATCTATATCTTCATCC 39087 _ CGTT__ C
 CATCA TGA GGA TG AGATAGATAG
 ||| ||| || |||||
 ACT CCCT AT TCTATCTATC
 A ACTTCT A
 GAM912 LOC54550 5' CTGTCTGCAACATCCCTCA 38076 C T
 TGAGGGA GTT GCAGATAG
 ||||| ||| |||||
 ACTCCCT CAA CGTCTGTC
 A _
 GAM912 LOC92539 5' CTATCTATCTACAAATCTATC 34502 G CG C
 GA GGA TTTG AGATAGATAG
 || ||| |||| |||||
 CT TCT AAAC TCTATCTATC
 A _ A
 GAM913 CTNNBIP1 3' GTGTTTGATTGGCTTTTCG 21547 T C A
 CGAA GCCAA CAAA AC
 ||| |||| ||| ||
 GCTT CGGTT GTTT TG
 T A G
 GAM913 HARS2 3' ATAGTTTTTAGTTATTATTC 28078 CC C
 GAATG AAC AAAAACTAT
 |||| ||| |||||
 CTTAT TTG TTTTGTATA
 TA A
 GAM913 LOC118738 3' TGTGTCTTAGGTTGGCATTTC 37196 A A T
 GAATGCCAACC AA AC ATA
 ||||| || || |||
 CTTACGGTTGG TT TG TGT
 A C _
 GAM913 LOC164684 3' AGTAATTTGGTTGACATTGGG 40159 G C A_
 CC AATG CAACCAAA ACT
 || |||| ||||| |||
 GG TTAC GTTGGTTT TGA
 G A AA
 GAM913 LOC170425 3' TATAGTTACTGGCATTAGG 37552 G ACCAAA
 CC AATGCCA AACTATA
 || ||||| |||||
 GG TTACGGT TTGATAT
 A CA____
 GAM914 PRPSAP1 3' GATGTTGAACCTGGTTAGGG 8660 GGTCTG
 CCC CAGGTTCAACATC
 ||| |||||
 GGG GTCCAAGTTGTAG
 ATTG_
 GAM914 RAP1B 3' GATGTAAATGGTGGACGAGTA 17897 C G TG AG C
 TAC CG TC C GTT AACATC
 ||| || | ||| |||||

ATG GC AG G TAA TTGTAG
 A _ GT G_ A
 GAM914 KIAA0316 3' ATGTCAAAAATCTGCAAACC 34529 C CA__
 GGT TGCAGGTT ACAT
 ||| ||||| |||
 CCA ACGTCTAA TGTA
 A AAAC
 GAM914 LOC149271 3' GATGCTCAGCACTGCAGACC 38681 _ CAA
 GGTCTGCAG GTT CATC
 ||||| ||| |||
 CCAGACGTC CGA GTAG
 A CTC
 GAM914 LOC149372 3' GATGCGGGCACTGCAGACCAGG 38730 C _ AA
 CC GGTCTGCAG GTTC CATC
 || ||||| ||| |||
 GG CCAGACGTC CGGG GTAG
 A A C_
 GAM914 LOC150245 5' ATGCCCAGCATGCAGACCAGG 41160 C G CAA
 CC GGTCTGCA GTT CAT
 || ||||| ||| |||
 GG CCAGACGT CGA GTA
 A A CCC
 GAM914 LOC153416 3' GATGTTAAATGGTGGACGAGTA 30362 C G TG AG C
 TAC CG TC C GTT AACATC
 ||| || | ||| |||||
 ATG GC AG G TAA TTGTAG
 A _ GT G_ A
 GAM914 LOC196500 3' ATGTTGGGGTGCAGCC 42385 T GG
 GG CTGCA TTCAACAT
 || |||| |||||
 CC GACGT GGGTTGTA
 _ G_
 GAM914 LOC200317 3' GATATGTGCAGCCGGGTA 42804 T G _
 TACCCGG CTGCA GT TC
 ||||| |||| |||
 ATGGGCC GACGT TA AG
 _ G T
 GAM915 CARD15 3' ACTTTGTTTACTGTCTTA 22714 C T_
 TAAGACAG AGAAT AGT
 ||||| |||| |||
 ATTCTGTC TTTTG TCA
 A TT
 GAM915 CD2AP 3' ACTAAGCTTCTGTCTTA 14432 C AA
 TAAGACAG AG TTAGT
 ||||| || |||||
 ATTCTGTC TC AATCA
 T G_
 GAM915 GALT 3' TCATTGAACTAATTCTACTATT 5663 C C _
 T AGA AG AGAATTAGT TAATGA
 ||| || ||||| |||||

		TTT TC TCTTAATCA GTTACT		
		A A A		
GAM915	C17orf31 5'	TCATTTATTTCCACTGTCTTA 19008	CA	TTAGTT
		TAAGACAG GAA AATGA		
		ATTCTGTC CTT T TACT		
		AC TAT__		
GAM915	FLJ11362 5'	CATCTGGCTCCTGCTGTC 22469	AATT	_
		GACAGCAG AGTTA ATG		
		CTGTCGTC TCGGT TAC		
		C__ C		
GAM915	KIAA0449 3'	TCATTAGGCTCCTGCTGTC 19055	AATT	_
		GACAGCAG AGT TAATGA		
		CTGTCGTC TCG ATTACT		
		C__ G		
GAM915	SETBP1 3'	TCATTAACCTTACTTGCTGCCTT 17827	A	AATT
		AAG CAGCAG AGTTAATGA		
		TTC GTCGTT TCAATTACT		
		C CAT_		
GAM915	LOC149302 5'	CATCTAGGTACTCTGCTGTTCA 38703	A	AT G _
		A GACAGCAGA TA TTA ATG		
		A TTGTCGTCT AT GAT TAC		
		C C_ G C		
GAM915	LOC203378 3'	AGCAATTCTCCTGTCTTA 43546	C	A
		TAAGACAG AGAATT GTT		
		ATTCTGTC TCTTAA CGA		
		C _		
GAM915	LOC256267 5'	TCATCCTCCTAAATTTCACTGT 46277	CA	_ TTA_
	CTTA	TAAGACAG GAATT AG ATGA		
		ATTCTGTC TTTAA TC TACT		
		AC A CTCC		
GAM915	LOC92466 5'	TCATCCTCCTAAATTTCACTGT 34396	CA	_ TTA_
	CTTA	TAAGACAG GAATT AG ATGA		
		ATTCTGTC TTTAA TC TACT		
		AC A CTCC		
GAM916	STAU 3'	AAATCCCAACATATATACT 10938	TT	AA
		AGTATATA TGTTG GATTT		
		TCATATAT ACAAC CTAAA		
		_ C_		
GAM916	STAU 3'	AAATCCCAACATATATACT 18911	TT	AA
		AGTATATA TGTTG GATTT		

			TCATATAT ACAAC CTAAA		
			— C_		
GAM916	STAU	3'	AAATCCCAACATATATACT 18917	TT	AA
			AGTATATA TGTTG GATTT		
			TCATATAT ACAAC CTAAA		
			— C_		
GAM916	STAU	3'	AAATCCCAACATATATACT 18923	TT	AA
			AGTATATA TGTTG GATTT		
			TCATATAT ACAAC CTAAA		
			— C_		
GAM916	FLJ10246	3'	AATCTTCAACAGACATTCA 19782	ATATA	
			TGAGT TTTGTTGAAGATT		
			ACTTA AGACAACTTCTAA		
			C_		
GAM916	FLJ13187	3'	AAATCTTCAAATCTGAATATAC 23868	ATTTG_	
			GTATAT TTGAAGATTT		
			CATATA AACTTCTAAA		
			AGTCTA		
GAM916	SFRS12	3'	AAATTGGTGCAAATATATAC 29173	TGAA	
			GTATATATTTGT GATTT		
			CATATATAAACG TTAAC		
			TGG_		
GAM917	ATP10B	3'	CCAGGCAATATCTCAGGATA 31735	A	CT AA
			TATCC GAGATAT TGT TGG		
			ATAGG CTCTATA ACG ACC		
			A _ G_		
GAM917	BDG-29	3'	CCATTACAGTGGCCTGGATA 35815	AGA	CT
			TATCCAG TAT TGTAATGG		
			ATAGGTC GTG ACATTACC		
			CG_ _		
GAM917	GW112	3'	CCACTTACTTAGATATCTGCAG 13131	CAG	T_ _
	ATA		TATC AGATATCT GTAA TGG		
			ATAG TCTATAGA CATT ACC		
			ACG TT C		
GAM917	HSPB7	3'	CCATTACAACAGCTCCAGGA 15780	A_	ATATC
			TCC GAG TTGTAATGG		
			AGG CTC AACATTACC		
			AC GAC_		
GAM917	KIAA1464	3'	CCAGTATTTATCTCTGGA 33882	TCTT	A
			TCCAGAGATA GTA TGG		

		AGGTCTCTAT TAT ACC		
		T__ G		
GAM917	KIAA1634	3' CCACCAACTATTTCTGGATA 31752	TC	TAA
		TATCCAGAGATA TTG TGG		
		ATAGGTCTTTAT AAC ACC		
		C_ C__		
GAM917	NETO1	3' CCATCATCTCATCTCTGGATG 29097	ATCT	TA
		TATCCAGAGAT TG ATGG		
		GTAGGTCTCTA AC TACC		
		CTCT __		
GAM917	PRO2533	3' CCATTACAAAATGTAATGG 20703	GAG	C
		CCA ATAT TTGTAATGG		
		GGT TGTA AACATTACC		
		AA_ A		
GAM917	LOC151201	3' TGTAATAACCTCTGGATA 41324	A	C
		TATCCAGAG TAT TTGTA		
		ATAGGTCTC ATA AATGT		
		C A		
GAM918	MYO1E	5' ATGGAGTCCCCTCTAGGGTT 11441	ATC	A A
		GACC GA GG GACTCCAT		
		TTGG CT CC CTGAGGTA		
		GAT C _		
GAM918	ROCK2	3' ATGAAGTCTTTTAACAGTCTC 32836	CATCGA	C
		GAGAC AGGAGACT CAT		
		CTCTG TTTTCTGA GTA		
		ACAA__ A		
GAM918	MGC15937	5' GAGTTTCTTCTTCAAGGTCTCA 27949	ATC	_
		TGAGACC GAAGGAGA CTC		
		ACTCTGG CTTCTTCT GAG		
		AA_ TT		
GAM918	LOC148029	5' GGAGTCTCCATCCTCA 38447	ACCATC	A
		TGAG GA GGAGACTCC		
		ACTC CT CCTCTGAGG		
		_____ A		
GAM918	LOC169436	5' TGGAGTTCAATGAGCTCA 40279	AC	C AGGAG
		TGAG CAT GA ACTCCA		
		ACTC GTA CT TGAGGT		
		GA A _____		
GAM918	LOC256267	3' ATGGAGTCTCCCTCTGTC 46276	CATC	A
		GAC GA GGAGACTCCAT		

			CTG CT CCTCTGAGGTA		
			T__ C		
GAM918	LOC257426	3'	GAGTCCTTCGGTGGCCTCA 33098	A	GA
			TGAG CCATCGAAGGA CTC		
			ACTC GGTGGCTTCCT GAG		
			C _		
GAM918	LOC92466	3'	ATGGAGTCTCCCTCTGTC 34395	CATC	A
			GAC GA GGAGACTCCAT		
			CTG CT CCTCTGAGGTA		
			T__ C		
GAM919	LOC152078	3'	GGCCTCAAAAAATATTA 39213	G	A
			TAATATTTTT TGAG CC		
			ATTATAAAAA ACTC GG		
			_ C		
GAM920	LOC152078	3'	GGCCTCAAAAAATATTA 39213	G	A
			TAATATTTTT TGAG CC		
			ATTATAAAAA ACTC GG		
			_ C		
GAM921	ADSS	3'	TGGATGCCTACTGTGGA 35541	G	
			TCCACAGTAGGC ATCCA		
			AGGTGTCATCCG TAGGT		
			_		
GAM921	LMO7	3'	GTCTGGATGTGTTTACTG 17971	_	
			CAGTAGGCG ATCCAGAC		
			GTCATTTGT TAGGTCTG		
			G		
GAM921	LMO7	3'	GTCTGGATGTGTTTACTG 11828	_	
			CAGTAGGCG ATCCAGAC		
			GTCATTTGT TAGGTCTG		
			G		
GAM921	PLAG1	3'	TCTAGAGCCATTGTGGA 8526	A	GA C
			TCCACAGT GGC TC AGA		
			AGGTGTTA CCG AG TCT		
			_ _ A		
GAM921	RNGTT	3'	ATGGTCTGAATTGTATATGT 9895	GTAG	C
			ACA GCGAT CAGACCAT		
			TGT TGTTA GTCTGGTA		
			ATA_ A		
GAM921	FLJ14906	3'	GTCTGGATCATGGCATGTAGA 26662	C _	AGGC
			TC ACA GT GATCCAGAC		

AG TGT CG CTAGGTCTG
 A A GTA_
 GAM921 KIAA1727 3' GTCCAGGAGGCCTGTGGA 32036 GTA GA A_
 TCCACA GGC TCC GAC
 ||||| ||| ||| |||
 AGGTGT CCG AGG CTG
 ____ G_ AC
 GAM921 KIAA1854 3' ATGGTCTGAATGTAACTG 35524 AG ATC
 CAGT GCG CAGACCAT
 |||| ||| |||||
 GTCA TGT GTCTGGTA
 AA AA_
 GAM921 LOC153114 5' ATGGTCTGGAGTGCTCTGTAGA 41573 C TA A
 TC ACAG GGCG TCCAGACCAT
 || |||| |||| |||||
 AG TGTC TCGT AGGTCTGGTA
 A ____ G
 GAM922 NOTCH2 3' TTTGGTATGGTTCTCAG 23651 ACAA
 CTGA AACCATACCAAA
 |||| |||||
 GACT TTGGTATGGTTT
 C____
 GAM922 POLQ 3' TTGGTATGGTTGGAGTGTAGG 13368 A AAA
 CCTG AC AACCATACCAA
 |||| || |||||
 GGAT TG TTGGTATGGTT
 G AGG
 GAM922 RAD1 5' ATGCTTTTATTCAGGGA 28436 C AC
 TCCCTGAA AAAA CAT
 ||||| |||| |||
 AGGGACTT TTTT GTA
 A C_
 GAM922 RNMT 3' GTGGCTTGTGTTTCAGGGA 9890 A A
 TCCCTGAACA AA CCAT
 ||||| || |||||
 AGGGACTTGT TT GGTG
 G C
 GAM922 SIP 3' TGGTCATTTTGTTCAGGA 15759 C ____
 TCC TGAACAAAA ACCA
 ||| ||||| |||||
 AGG ACTTGTTTT TGGT
 A AC
 GAM922 SLC38A3 3' TGGAAGGTTTTTGTTC A 13714 ATA
 TGAACAAAAACC CCA
 ||||| ||||| |||
 ACTTGTTTTTGG GGT
 AA_
 GAM922 ARHGEF9 3' TGGAGTGGACTTCTGTTCAGGG 17544 AAAA_ A
 A TCCCTGAACA CCAT CCA
 ||||| ||||| |||

			AGGGACTTGT	GGTG GGT		
			CTTCA	A		
GAM922	CG018	5'	GGATGATTTTTTCTTCAGGGA	27401	C_	C A
			TCCCTGAA	AAAAA CAT CC		
			AGGGACTT	TTTTT GTA GG		
			CT	A _		
GAM922	DKFZP434J214	3'	TTTGGTATAGTATAAGTTCA	30550	AAAA	C
			TGAAC	AC ATACCAAA		
			ACTTG	TG TATGGTTT		
			AATA	A		
GAM922	HCA127	3'	TGTGTTGGCTTTTGTTCAG	20760	A T	_
			CTGAACAAAA	CCA AC CA		
			GACTTGTTTT	GGT TG GT		
			C	_ T		
GAM922	KIAA0931	3'	TTTGGGAAGATTTTTGTTC	33488	CCATA	
			TGAACAAAAA	CCAAA		
			ACTTGTTTTT	GGTTT		
			AGAAG			
GAM922	KIAA1795	3'	GTAGAGTTTATTGTTTCAGAGA	35702	C	_ CA
			TC CTGAACAA	AAAC TAC		
			AG GACTTGTT	TTTG ATG		
			A	A AG		
GAM922	MGC5457	3'	TTTGGTATGGGAGGTGTTAG	26348	A	AAAA
			CTGA CA	CCATACCAAA		
			GATT GT	GGTATGGTTT		
			_	GGAG		
GAM922	NYD-SP27	5'	TGAGATGGTTTTTGTCAAAGA	26969	CC A	AC
			TC TGA	CAAAAACCAT CA		
			AG ACT	GTTTTTGGTA GT		
			AA	_ GA		
GAM922	PRO0132	5'	TTGGTGTGCGTTCAGAGA	15369	C	AAAAAC
			TC CTGAAC	CATACCAA		
			AG GACTTG	GTGTGGTT		
			A	C_____		
GAM922	SHAPY	3'	TATGTTCTTTTGTTCAGTGA	29016	C	AC_
			TC CTGAACAAAA	CATA		
			AG GACTTGTTTT	GTAT		
			T	CTT		
GAM922	UCK1	3'	GGCATGTGTGTTTCAGGGA	25428	AAAAC	A
			TCCCTGAACA	CAT CC		

			AGGGACTTGT	GTA GG		
			GT__ C			
GAM922	WDR9	3'	TTGATATGACTAATTCAGGGA	21034	CAAAAAC	C
			TCCCTGAA	CATA CAA		
			AGGGACTT	GTAT GTT		
			AATCA__	A		
GAM922	LOC143465	5'	TTTGGTGGCATTGTTCA	40367	ACCA	
			TGAACAAAA	TACCAA		
			ACTTGTTTT	GTGGTTT		
			ACG_			
GAM922	LOC159963	5'	TGGTAATCATTTTCTTCAGGGA	39988	C	ACCA
			TCCCTGAA	AAAA TACCA		
			AGGGACTT	TTTT ATGGT		
			C	ACTA		
GAM922	LOC200609	5'	TTGGTATGAGAGTCTTAGGGA	43340	_	AAAAAC
			TCCCTGA	AC CATACCAA		
			AGGGATT	TG GTATGGTT		
			C	AGA__		
GAM922	LOC222237	3'	GGTATAGAATTTTGTGTTAG	45270	CC__	
			CTGAACAAAAA	ATACC		
			GATTTGTTTTT	TATGG		
			AAGA			
GAM923	ADAMTS4	3'	AGCAATTCTCCTGCCTCA	11565	A	A A
			TGA	GTA GAGAATTG CT		
			ACT	CGT CTCTTAAC GA		
			C	C _		
GAM923	ADCY6	5'	AAGCAATTCTCCTGCCTCA	17584	A	A A
			TGA	GTA GAGAATTG CTT		
			ACT	CGT CTCTTAAC GAA		
			C	C _		
GAM923	APAF1	3'	AAGCAATTCTCCTGCCTCA	14866	A	A A
			TGA	GTA GAGAATTG CTT		
			ACT	CGT CTCTTAAC GAA		
			C	C _		
GAM923	APAF1	3'	AAGCAATTCTCCTGCCTCA	6827	A	A A
			TGA	GTA GAGAATTG CTT		
			ACT	CGT CTCTTAAC GAA		
			C	C _		
GAM923	CLECSF12	3'	AAGCAATTCTCCTGCCTCA	37683	A	A A
			TGA	GTA GAGAATTG CTT		

			ACT CGT CTCTTAAC GAA			
			C C _			
GAM923	CORO2B	5'	AAGCAATTCTCCTGCTTCA 32252	A	A	
			TGAAGTA GAGAATTG CTT			
			ACTTCGT CTCTTAAC GAA			
			C _			
GAM923	CYP8B1	3'	AAGCAATTCTCCTGCCTCA 10619	A	A	A
			TGA GTA GAGAATTG CTT			
			ACT CGT CTCTTAAC GAA			
			C C _			
GAM923	FCAR	3'	AAGCAATTCTCCTGCCTCA 28432	A	A	A
			TGA GTA GAGAATTG CTT			
			ACT CGT CTCTTAAC GAA			
			C C _			
GAM923	GM2A	3'	AAGCAATTCTCCTGCCTCA 33656	A	A	A
			TGA GTA GAGAATTG CTT			
			ACT CGT CTCTTAAC GAA			
			C C _			
GAM923	GPR81	3'	AAGCAATTCTCCTGCCTCA 26278	A	A	A
			TGA GTA GAGAATTG CTT			
			ACT CGT CTCTTAAC GAA			
			C C _			
GAM923	HCS	3'	AAGCGATTCTCTCACTTCA 21013	A	A	
			TGAAGT AGAGAATTG CTT			
			ACTTCA TCTCTTAGC GAA			
			C _			
GAM923	IL11	3'	AAGCAATTCTCCTGCCTCA 6277	A	A	A
			TGA GTA GAGAATTG CTT			
			ACT CGT CTCTTAAC GAA			
			C C _			
GAM923	NQO1	3'	AGCAATTCTCCTGCCTCA 6605	A	A	A
			TGA GTA GAGAATTG CT			
			ACT CGT CTCTTAAC GA			
			C C _			
GAM923	PAICS	3'	AAGCAGTTCTCCACCTCA 13161	A	AA	A
			TGA GT GAGAATTG CTT			
			ACT CA CTCTTGAC GAA			
			C CC _			
GAM923	PCDHA9	3'	AAGCAATTCTCCTGCCTCA 15206	A	A	A
			TGA GTA GAGAATTG CTT			

			ACT CGT CTCTTAAC GAA			
			C C _			
GAM923	PIK3C2B	3'	AAGCGATTCTCCTACCTCA 8503	A	A	A
			TGA GTA GAGAATTG CTT			
			ACT CAT CTCTTAGC GAA			
			C C _			
GAM923	RHD	3'	AAGCAATTCTCCTGCCTCA 18213	A	A	A
			TGA GTA GAGAATTG CTT			
			ACT CGT CTCTTAAC GAA			
			C C _			
GAM923	RHD	3'	AAGCAATTCTCCTGCCTCA 18333	A	A	A
			TGA GTA GAGAATTG CTT			
			ACT CGT CTCTTAAC GAA			
			C C _			
GAM923	RPH3AL	3'	AAGCGATTCTCTCACCTCA 13846	A	A	A
			TGA GT AGAGAATTG CTT			
			ACT CA TCTCTTAGC GAA			
			C C _			
GAM923	SCML2	3'	AAGCAATTCTCCTGCCTCA 12734	A	A	A
			TGA GTA GAGAATTG CTT			
			ACT CGT CTCTTAAC GAA			
			C C _			
GAM923	SEDL	3'	AAGCAATTCTCCTTCTTCA 15900	TAA		A
			TGAAG GAGAATTG CTT			
			ACTTC CTCTTAAC GAA			
			TTC _			
GAM923	SEDL	3'	AAGCAATTCTCCTTCTTCA 15901	TAA		A
			TGAAG GAGAATTG CTT			
			ACTTC CTCTTAAC GAA			
			TTC _			
GAM923	SEDL	3'	AAGCAATTCTCCTGCCTCA 15899	A	A	A
			TGA GTA GAGAATTG CTT			
			ACT CGT CTCTTAAC GAA			
			C C _			
GAM923	SEPN1	3'	AAGCAATTCTCTTGCTCA 32986	A		A
			TGA GTAAGAGAATTG CTT			
			ACT CGTTCTCTTAAC GAA			
			C _			
GAM923	SERPINB9	3'	AAGCAATTCTCTTGCTCA 10357			A
			TGAAGTAAGAGAATTG CTT			

ACTTCGTTCTCTTAAC GAA

GAM923 SLC24A1 3' AAGCAATTCTCCTGCCTCA 11099 A A A
TGA GTA GAGAATTG CTT
||| ||| ||||| |||
ACT CGT CTCTTAAC GAA
C C _

GAM923 TNFRSF10B 3' AAGCGATTCTCCCACCTCA 9933 A AA A
TGA GT GAGAATTG CTT
||| || ||||| |||
ACT CA CTCTTAGC GAA
C CC _

GAM923 AAK1 3' AGGCAATTCTCCTGCCTCA 17143 A A A
TGA GTA GAGAATTG CTT
||| ||| ||||| |||
ACT CGT CTCTTAAC GGA
C C _

GAM923 ADMP 3' TACTGGAAATTCTTTTACTTCA 29658 GA TC
TGAAGTAAGAGAATT CT GTA
||||||| || |||
ACTTCATTTTCTTAA GG CAT
A_ T_

GAM923 ASB16 5' AAGCAATTCTCCTGCCTCA 34652 A A A
TGA GTA GAGAATTG CTT
||| ||| ||||| |||
ACT CGT CTCTTAAC GAA
C C _

GAM923 C1orf34 3' AGATCAATTCCCTTACTTC 30433 A _
GAAGTAAG GAATTGA CT
||||| ||||| ||
CTTCATTC CTTAACT GA
C A

GAM923 CIP29 3' AAGCAATTCTCCCATCTCA 26147 AG AA A
TGA T GAGAATTG CTT
||| | ||||| |||
ACT A CTCTTAAC GAA
CT CC _

GAM923 DKFZp434C0923 3' AAGCAATTCTCCCACCTCA 19061 A AA A
TGA GT GAGAATTG CTT
||| || ||||| |||
ACT CA CTCTTAAC GAA
C CC _

GAM923 DKFZP566I1024 3' AAGCAATTCTCCCACCTCA 34733 A AA A
TGA GT GAGAATTG CTT
||| || ||||| |||
ACT CA CTCTTAAC GAA
C CC _

GAM923 FLJ10535 3' AAGCAATTCTCCTGCCTCA 19915 A A A
TGA GTA GAGAATTG CTT
||| ||| ||||| |||

			ACT CGT CTCTTAAC GAA			
			C C _			
GAM923	FLJ10956	3'	AAGCAATTCTCCTACCTCA 20274	A	A	A
			TGA GTA GAGAATTG CTT			
			ACT CAT CTCTTAAC GAA			
			C C _			
GAM923	FLJ13072	5'	AAGCAATTCTCCTGCCTCA 43231	A	A	A
			TGA GTA GAGAATTG CTT			
			ACT CGT CTCTTAAC GAA			
			C C _			
GAM923	FLJ13952	3'	AAGCAATTCTCCTGCCTCA 24175	A	A	A
			TGA GTA GAGAATTG CTT			
			ACT CGT CTCTTAAC GAA			
			C C _			
GAM923	FLJ14803	3'	AAGCAATTCTCCTGCCTCA 26624	A	A	A
			TGA GTA GAGAATTG CTT			
			ACT CGT CTCTTAAC GAA			
			C C _			
GAM923	FLJ20045	3'	AGGCAATTCTCCCACCTCA 19143	A	AA	A
			TGA GT GAGAATTG CTT			
			ACT CA CTCTTAAC GGA			
			C CC _			
GAM923	FLJ20671	3'	AAGCAATTCTCCTGCCTCA 19590	A	A	A
			TGA GTA GAGAATTG CTT			
			ACT CGT CTCTTAAC GAA			
			C C _			
GAM923	FLJ22969	3'	AAGCAATTCTCCCACCTCA 34063	A	AA	A
			TGA GT GAGAATTG CTT			
			ACT CA CTCTTAAC GAA			
			C CC _			
GAM923	FLJ23356	3'	AAGCAATTCTCCCACCTCA 25956	A	AA	A
			TGA GT GAGAATTG CTT			
			ACT CA CTCTTAAC GAA			
			C CC _			
GAM923	GR6	5'	AAGCAATTCTCCTGCCTCA 14279	A	A	A
			TGA GTA GAGAATTG CTT			
			ACT CGT CTCTTAAC GAA			
			C C _			
GAM923	HSPC065	3'	AAGCAATTCTCCCACCTCA 15447	A	AA	A
			TGA GT GAGAATTG CTT			

			ACT CA CTCTTAAC GAA			
			C CC _			
GAM923	HSPC065	3'	AAGCGATTCTCCTACCTCA 15448	A	A	A
			TGA GTA GAGAATTG CTT			
			ACT CAT CTCTTAGC GAA			
			C C _			
GAM923	KIAA0022	3'	AAGCAATTCTCCTGCCTCA 17023	A	A	A
			TGA GTA GAGAATTG CTT			
			ACT CGT CTCTTAAC GAA			
			C C _			
GAM923	KIAA0513	3'	AAGCAATTCTCCTGCCTCA 16350	A	A	A
			TGA GTA GAGAATTG CTT			
			ACT CGT CTCTTAAC GAA			
			C C _			
GAM923	KIAA0527	3'	AAGCAATTCTCCTGCCTCA 45839	A	A	A
			TGA GTA GAGAATTG CTT			
			ACT CGT CTCTTAAC GAA			
			C C _			
GAM923	KIAA1041	3'	AAGCAATTCTCCTGCCTCA 17262	A	A	A
			TGA GTA GAGAATTG CTT			
			ACT CGT CTCTTAAC GAA			
			C C _			
GAM923	KIAA1198	3'	AAGCAATTCTCCTGCCTCA 31700	A	A	A
			TGA GTA GAGAATTG CTT			
			ACT CGT CTCTTAAC GAA			
			C C _			
GAM923	KIAA1200	3'	AAGCAATTCTCCTGCCTCA 31261	A	A	A
			TGA GTA GAGAATTG CTT			
			ACT CGT CTCTTAAC GAA			
			C C _			
GAM923	KIAA1257	3'	AAGCAATTCTCCTGCTTCA 31427	A		A
			TGAAGTA GAGAATTG CTT			
			ACTTCGT CTCTTAAC GAA			
			C _			
GAM923	KIAA1655	3'	AAGCAATTCTCCTGCCTCA 33079	A	A	A
			TGA GTA GAGAATTG CTT			
			ACT CGT CTCTTAAC GAA			
			C C _			
GAM923	KIAA1655	3'	AAGCAATTCTCCTGCCTCA 33080	A	A	A
			TGA GTA GAGAATTG CTT			

			ACT CGT CTCTTAAC GAA			
			C C _			
GAM923	KIAA1784	3'	AAGCAATTCTCCTGCCTCA 32482	A	A	A
			TGA GTA GAGAATTG CTT			
			ACT CGT CTCTTAAC GAA			
			C C _			
GAM923	KIAA1878	3'	ACGAACTCTCTCTTACTCCG 44073	A		ATT C
			TG AGTAAGAGA GA TTCGT			
			GC TCATTCTCT CT AAGCA			
			C _ C			
GAM923	MGC13138	3'	AAGCAATTCTCCTTC 27231	TAA		A
			GAAG GAGAATTG CTT			
			CTTC CTCTTAAC GAA			
			_ _			
GAM923	MGC15606	5'	AAGCAATTCTCCTACCTCA 29660	A	A	A
			TGA GTA GAGAATTG CTT			
			ACT CAT CTCTTAAC GAA			
			C C _			
GAM923	NDUFC2	3'	AAGCAATTCTCCTGCCTCA 10893	A	A	A
			TGA GTA GAGAATTG CTT			
			ACT CGT CTCTTAAC GAA			
			C C _			
GAM923	PP1201	3'	ACGAGGTTCCCCTCCCACCTC 22710	A	AA	AATT
			GA GT GAG GACTTCGT			
			CT CA CTC TTGGAGCA			
			C CC CCC_			
GAM923	SLC11A2	3'	ACAAAGCTGCTGCTTTTACTTC 6220			AATTGA C
	A		TGAAGTAAGAG CTT GT			
			ACTTCATTTTC GAA CA			
			GTCGTC A			
GAM923	SLC12A8	3'	AAGCAATTCTCCTGCCTCA 23892	A	A	A
			TGA GTA GAGAATTG CTT			
			ACT CGT CTCTTAAC GAA			
			C C _			
GAM923	TRIM16	3'	AAGCAATTCTCCTGCCTCA 13194	A	A	A
			TGA GTA GAGAATTG CTT			
			ACT CGT CTCTTAAC GAA			
			C C _			
GAM923	TRIM5	3'	AAGCAATTCTCCTGCCTCA 26926	A	A	A
			TGA GTA GAGAATTG CTT			

			ACT CGT CTCTTAAC GAA			
			C C _			
GAM923	VPS33A	3'	AAGCAATTCTCCTGCCTCA	23230	A A	A
			TGA GTA GAGAATTG CTT			
			ACT CGT CTCTTAAC GAA			
			C C _			
GAM923	LOC119392	3'	AGCAATTCTCCTGCCTCA	29758	A A	A
			TGA GTA GAGAATTG CT			
			ACT CGT CTCTTAAC GA			
			C C _			
GAM923	LOC128989	3'	AAGCAATTCTCCTGCCCA	36938	AA A	A
			TG GTA GAGAATTG CTT			
			AC CGT CTCTTAAC GAA			
			CC C _			
GAM923	LOC135154	3'	AAGCAATTCTCCTGCCTCA	37090	A A	A
			TGA GTA GAGAATTG CTT			
			ACT CGT CTCTTAAC GAA			
			C C _			
GAM923	LOC147166	3'	AAGCAATTCTCCTGCCTCA	38312	A A	A
			TGA GTA GAGAATTG CTT			
			ACT CGT CTCTTAAC GAA			
			C C _			
GAM923	LOC148195	3'	AAGCAATTCTCCTGCCTCA	40870	A A	A
			TGA GTA GAGAATTG CTT			
			ACT CGT CTCTTAAC GAA			
			C C _			
GAM923	LOC149577	3'	AAGCAATTCTCCTGCCCA	41020	AA A	A
			TG GTA GAGAATTG CTT			
			AC CGT CTCTTAAC GAA			
			CC C _			
GAM923	LOC152343	3'	AAGCAATTCTCCTGCCTCA	39259	A A	A
			TGA GTA GAGAATTG CTT			
			ACT CGT CTCTTAAC GAA			
			C C _			
GAM923	LOC152620	3'	AAGCAATTCTCCTGCCTCA	30170	A A	A
			TGA GTA GAGAATTG CTT			
			ACT CGT CTCTTAAC GAA			
			C C _			
GAM923	LOC152719	5'	AAGCAATTCTCCTGCCTCA	41542	A A	A
			TGA GTA GAGAATTG CTT			

			ACT CGT CTCCTTAAC GAA			
			C C _			
GAM923	LOC158476 3'	AAGCAATTCTCCTGCCTCA	41993	A	A	A
		TGA GTA GAGAATTG CTT				
		ACT CGT CTCCTTAAC GAA				
		C C _				
GAM923	LOC158549 5'	AAGCAATTCTCCTTC	42003	TAA		A
		GAAG GAGAATTG CTT				
		CTTC CTCCTTAAC GAA				
		— —				
GAM923	LOC161829 3'	AAGCAATTCTCCTGCCTCA	40035	A	A	A
		TGA GTA GAGAATTG CTT				
		ACT CGT CTCCTTAAC GAA				
		C C _				
GAM923	LOC163590 5'	AAGCGATTCTCCACCTCA	29651	A	AA	A
		TGA GT GAGAATTG CTT				
		ACT CA CTCTTAGC GAA				
		C CC _				
GAM923	LOC202025 3'	AAGCAATTCTCCTGCCTCA	43398	A	A	A
		TGA GTA GAGAATTG CTT				
		ACT CGT CTCCTTAAC GAA				
		C C _				
GAM923	LOC202908 5'	AAGCAATTCTCCTGCCTCA	42993	A	A	A
		TGA GTA GAGAATTG CTT				
		ACT CGT CTCCTTAAC GAA				
		C C _				
GAM923	LOC202934 3'	AAGCAATTCTCCTGCCTCA	43451	A	A	A
		TGA GTA GAGAATTG CTT				
		ACT CGT CTCCTTAAC GAA				
		C C _				
GAM923	LOC220662 3'	AAGCAATTCTCCTGCCTCA	43820	A	A	A
		TGA GTA GAGAATTG CTT				
		ACT CGT CTCCTTAAC GAA				
		C C _				
GAM923	LOC222070 5'	AAGCAATTCTCCTGCCTCA	45175	A	A	A
		TGA GTA GAGAATTG CTT				
		ACT CGT CTCCTTAAC GAA				
		C C _				
GAM923	LOC256306 3'	AAGCAATTCTCCTGCCTCA	46233	A	A	A
		TGA GTA GAGAATTG CTT				

			ACT CGT CTCTTAAC GAA			
			C C _			
GAM923	LOC51200	3'	AAGCAATTCTCCTGCCTCA	18478	A A	A
			TGA GTA GAGAATTG CTT			
			ACT CGT CTCTTAAC GAA			
			C C _			
GAM923	LOC51219	5'	AAGCAATTCTCCCGCCTCA	18543	A AA	A
			TGA GT GAGAATTG CTT			
			ACT CG CTCTTAAC GAA			
			C CC _			
GAM923	LOC90333	5'	AAGCAATTCTCCTGCCTCA	31215	A A	A
			TGA GTA GAGAATTG CTT			
			ACT CGT CTCTTAAC GAA			
			C C _			
GAM923	LOC90333	3'	AAGCAATTCTCCTGCCTCA	31216	A A	A
			TGA GTA GAGAATTG CTT			
			ACT CGT CTCTTAAC GAA			
			C C _			
GAM923	LOC90591	3'	AAGCAATTCTCCTGCCTCA	31755	A A	A
			TGA GTA GAGAATTG CTT			
			ACT CGT CTCTTAAC GAA			
			C C _			
GAM923	LOC93408	5'	AAGCAATTCTCCTGCCTCA	28772	A A	A
			TGA GTA GAGAATTG CTT			
			ACT CGT CTCTTAAC GAA			
			C C _			
GAM924	SFRS11	3'	TGATGGATCTACTTATGG	11159	TCGAA	C
			TCATA TAGATCCA CA			
			GGTAT ATCTAGGT GT			
			TC__ A			
GAM924	LOC205251	5'	TGTGGTGGACAGATATAGA	43592	_	GAATAGA
			TC ATATC TCCACCACA			
			AG TATAG AGGTGGTGT			
			A AC__			
GAM925	APBA2	3'	CACCCCAGCCTGGCCACGCAGC	12016	A	__ CATA
		C	G GCTGCGTG GGC GGGTG			
			C CGACGCACC CCG CCCAC			
			_ GGT AC__			
GAM925	DNMT3A	5'	CCCAGCCCCGCGCAGC	22881		CATA
			GCTGCGTG GGG			

			CGACGCGCCCCG	CCC			
			A				
GAM925	DNMT3L	5'	CACCCCAAGTGACCCCCGCAG	15016	T	C	A
	CTC		GAGCTGCG GGGG CAT	GGGTG			
			CTCGACGC CCCC GTG	CCCAC			
			C	A AAC			
GAM925	FGF18	5'	CCTGGCCCCACGCAGCTC	27382			TA
			GAGCTGCGTGGGGCCA	GG			
			CTCGACGCACCCCGGT	CC			
GAM925	FGF18	5'	CCTGGCCCCACGCAGCTC	9954			TA
			GAGCTGCGTGGGGCCA	GG			
			CTCGACGCACCCCGGT	CC			
GAM925	GDI1	3'	CACCTCCCCCCCCACCAACTC	30130	C	C	CCATA
			GAG TG GTGGGG	GGGTG			
			CTC AC CACCCC	TCCAC			
			A	CCC			
GAM925	LFNG	3'	CCAGTGGCCCCACGAAGC	44508	G		A
			GCT CGTGGGGCCAT	GG			
			CGA GCACCCCGGTG	CC			
			A	A			
GAM925	LILRA1	5'	CACTGCCACACGCAGCTC	13736	G		CATAG
			GAGCTGCGTG GGC	GGTG			
			CTCGACGCAC CCG	TCAC			
			A				
GAM925	LILRB2	5'	CACTGCCACACGCAGCTC	12492	G		CATAG
			GAGCTGCGTG GGC	GGTG			
			CTCGACGCAC CCG	TCAC			
			A				
GAM925	SYN3	3'	CACCCTCGCCTCACAGC	28591	GC		CAT
			GCT GTGGGGC	AGGGTG			
			CGA CACTCCG	TCCCAC			
				C			
GAM925	CLIPR-59	3'	CACCCCACATGGCCACAGCTC	17785	CGTG		A
			GAGCTG	GGGCCAT GGGTG			
			CTCGAC	CCCGGTA CCCAC			
			A	CAC			
GAM925	FLJ22160	3'	CACCCCATGGCCCCGGC	23819	G		A
			GC TGGGGCCAT	GGGTG			

				CG GCCCCGGTA CCCAC		
				— C		
GAM925	HGC6.1.1	5'	GCAGCCCCCGCAGCTC	15686	T	CATAGG
			GAGCTGCG GGGGC	GT		
			CTCGACGC CCCCCG	CG		
			— A			
GAM925	KIAA0514	3'	TCCGGCCCCACACAGCT	16211	C	ATA
			AGCTG GTGGGGCC	GGG		
			TCGAC CACCCCGG	CCT		
			A			
GAM925	KIAA1089	3'	TCACCCACACACGCAGACTC	34141	—	— GCCATA
			GAG CTGCGTG GG	GGGTGA		
			CTC GACGCAC CC	CCCACT		
			A A AC			
GAM925	KIAA1110	3'	CCTTAGGTGGCCCCACGAGC	30983	G	—
			GCT CGTGGGGCCAT	AGGG		
			CGA GCACCCCGGTG	TTCC		
			— GA			
GAM925	KIAA1274	3'	CACAGGGCCCCACGCAG	43908		ATAGG
			CTGCGTGGGGCC	GTG		
			GACGCACCCCGG	CAC		
			GA			
GAM925	KIAA1388	3'	CCAAGGGCCCCACCCAGCTC	44949	C	ATA
			GAGCTG GTGGGGCC	GG		
			CTCGAC CACCCCGG	CC		
			C GAA			
GAM925	KIAA1533	5'	CCCAGCCCCGCGCAGC	36510		CATA
			GCTGCGTGGGGC	GGG		
			CGACGCGCCCCG	CCC		
			A			
GAM925	PTK6	5'	CACCTGTGCCCCCGCAGCTC	12598	T	CATA
			GAGCTGCG GGGGC	GGGTG		
			CTCGACGC CCCCCG	TCCAC		
			— TG			
GAM925	SDC3	3'	CCTGGCCCCACCAGC	16081	C	TA
			GCTG GTGGGGCCA	GG		
			CGAC CACCCCGGT	CC		
			—			
GAM925	SPIN	5'	CACCCTAGTCCAGCAGCTC	29979	GTG	CA
			GAGCTGC GGGC	TAGGGTG		

CTCGACG CCTG ATCCAC
A__ __
GAM925 SPINT1 5' CCCGGCCCCACCCAATC 31391 C C ATA
GAG TG GTGGGGCC GGG
||| || ||||| |||
CTC AC CACCCCGG CCC
A C ____
GAM925 UBP1 5' CCAGTGGGGCCCCCGCAGCTC 15845 T ATAG_
GAGCTGCG GGGGCC GG
||||| ||||| ||
CTCGACGC CCCC GG CC
_ GGTGA
GAM925 ZFP106 3' TATGGCCCCACAAGCTC 22834 GC
GAGCT GTGGGGCCATA
||||| |||||
CTCGA CACCCCGGTAT
A_
GAM925 LOC147180 5' TCACCCCATGGCTTCCCA 40817 _ A
TGGG GCCAT GGGTGA
||||| ||||| |||||
ACCC CGGTA CCCACT
TT C
GAM925 LOC167040 5' CCTGGCCCCACCCAGCTC 42200 C TA
GAGCTG GTGGGGCCA GG
||||| ||||| ||
CTCGAC CACCCCGGT CC
C ____
GAM925 LOC200213 5' CACCCTGCTGCCCAACAGC 42739 CGTG CA
GCTG GGGC TAGGGTG
||||| ||||| |||||
CGAC CCCG GTCCAC
AA__ TC
GAM925 LOC90170 5' CCCAACCTCACGCAGCTC 30907 CCATA
GAGCTGCGTGGGG GGG
||||| ||||| |||
CTCGACGCACTCC CCC
AA____
GAM925 LOC93624 5' CACAGCTGACCCAGCGCAGC 36014 _ C TAGG
GCTGCG TGGGG CA GTG
||||| ||||| || |||
CGACGC ACCCC GT CAC
G A CGA_
GAM926 KERA 5' AATCCATTACCATGTACA 13907 CC CTGCC
TGTACA GG AGTGGATT
||||| || |||||
ACATGT CC TTACCTAA
A_ A____
GAM926 HT008 3' TTCAGGCAGCCGGTGCACA 30073 A AG
TGT CACCGGCTGCC TGGA
||| ||||| ||||| |||

ACA GTGGCCGACGG ACTT
 C _
 GAM926 LOC151827 5' CCCGGCAGGCCGGTGCACA 39168 A _ AGT
 TGT CACCGGC TGCC GG
 ||| ||||| ||| ||
 ACA GTGGCCG ACGG CC
 C G C_
 GAM927 ADRB3 3' GGACTTGGACAGAGGGCCCACA 5461 AAT AAA _
 TGT GCC TG CCAAGTCC
 ||| ||| || |||||
 ACA CGG AC GGTTCAAG
 CC_ GAG A
 GAM927 ANKTM1 3' CTTGTGTAGCATTGCA 14259 CAAA _
 TGTAATGC TGC CAAG
 ||||| ||| |||
 ACGTTACG ATG GTTC
 _ T
 GAM927 ARHGAP6 3' ACTTGGCATTCAACATTA 6840 CCA
 TAATG AATGCCAAGT
 ||||| |||||
 ATTAC TTACGGTTCA
 AAC
 GAM927 ATRN 3' ACCTGGGATCTCTGGCATTAC 29296 A_ G A
 GTAATGCCA AT CCA GT
 ||||| || ||| ||
 CATTACGGT TA GGT CA
 CTC G C
 GAM927 BCL11B 3' ACCTGCCACTTGGCATTCA 23158 A C A
 TAATGCCAA TG CA GT
 ||||| || ||| ||
 ATTACGGTT AC GT CA
 C C C
 GAM927 FAP 5' ACTTGGCACGGTATTCA 10766 T AAA
 TG AATGCC TGCCAAGT
 || ||||| |||||
 AC TTATGG ACGGTTCA
 _ C_
 GAM927 LIF 3' GGAGGTCACTTGGCATTCA 8097 T A _ AAG
 TG AATGCCAA TG CC TCC
 || ||||| || ||| |||
 AC TTACGGTT AC GG AGG
 _ C T _
 GAM927 PRPS2 3' GGACCTGGCATTATCTGGC 8655 _ A
 GCCA AATGCCA GTCC
 ||| ||||| |||
 CGGT TTACGGT CAGG
 CTAT C
 GAM927 SLC10A2 3' GACTTGGCTTTCTTACA 6064 TGCC T
 TGTA A AAGCCAAGTC
 |||| ||| |||||

ACATT TTT CGGTTTCAG
 C___ _
 GAM927 STAM 3' ACTTTTACATTTTGGCATGACA 9539 A _ CC_
 TGT ATGCCAAA TG AAGT
 ||| ||||| || ||||
 ACA TACGGTTT AC TTCA
 G T ATT
 GAM927 TCN2 5' GACTTAGCCGTGCATTGCA 5916 CAAAT C
 TGTAATGC GC AAGTC
 ||||| || ||||
 ACGTTACG CG TTCAG
 TGC__ A
 GAM927 TEC 3' GACTGCTCTTAGTATTACA 9216 C AT CA
 TGTAATGC AA GC AGTC
 ||||| || || ||||
 ACATTATG TT CG TCAG
 A CT __
 GAM927 AIG-1 3' ACTTGGTGGCATCAGCA 18190 A_ AAAT
 TGT ATGCC GCCAAGT
 ||| |||| |||||
 ACG TACGG TGGTTCA
 AC ____
 GAM927 BTN2A1 3' GGA CTTGGAATGAGGCCTACA 27804 AT AA G
 TGTA GCC AT CCAAGTCC
 |||| ||| || |||||
 ACAT CGG TA GGTTCAGG
 C_ AG A
 GAM927 FLJ10120 3' ACTCATCTTGGCATTA 19728 _ CCA
 TAATGCCAA ATG AGT
 ||||| ||| |||
 ATTACGGTT TAC TCA
 C ____
 GAM927 FLJ10540 5' GGA CTTGCGCACCATTTC A 19929 T CCAAA
 TG AATG TGCCAAGTCC
 || |||| |||||
 AC TTAC GCGGTTTCAGG
 T CA__
 GAM927 FLJ23045 3' GGA CTTAATGTAGCATTGCA 24020 CAAA C__
 TGTAATGC TGC AAGTCC
 ||||| ||| |||||
 ACGTTACG ATG TTCAGG
 ____ TAA
 GAM927 KIAA1361 3' GACTTAGTGACCATTGTCAT 31169 ____ C
 ATGCCAAATG C AAGTC
 ||||| || ||||
 TACGGTTTAC G TTCAG
 CAGT A
 GAM927 KIAA1750 3' ACTTGGCACTGCGCACACA 33870 AA _ AA
 TGT TGC CA TGCCAAGT
 ||| ||| || |||||

ACA ACG GT ACGGTTCA
C_ C C_
GAM927 PTPRU 3' GGACTTGGCATTTAGGATTCCA 28402 T G _
TG AAT CC AAATGCCAAGTCC
|| ||| || |||||
AC TTA GG TTTACGGTTCAGG
C _ A
GAM927 PTPRU 3' GGACTTGGCATTTAGGATTCCA 28407 T G _
TG AAT CC AAATGCCAAGTCC
|| ||| || |||||
AC TTA GG TTTACGGTTCAGG
C _ A
GAM927 PTPRU 3' GGACTTGGCATTTAGGATTCCA 12257 T G _
TG AAT CC AAATGCCAAGTCC
|| ||| || |||||
AC TTA GG TTTACGGTTCAGG
C _ A
GAM927 PV1 3' ACTTGGCATGACGTCACA 25348 A CCAA
TGT ATG ATGCCAAGT
||| ||| |||||
ACA TGC TACGGTTCA
C AG_
GAM927 LOC144962 5' GGACTTCAACGAGCATTACA 37792 CAAA CC
TGTAATGC TG AAGTCC
||||| || |||||
ACATTACG AC TTCAGG
AGCA _
GAM927 LOC151248 5' TTTGGCATCTACATTACA 39090 CCAA
TGTAATG ATGCCAAG
||||| |||||
ACATTAC TACGGTTT
ATC_
GAM927 LOC157421 5' GGACTTGGCACCTGGAATACA 41795 ATG AA
TGTA CCA TGCCAAGTCC
||| ||| |||||
ACAT GGT ACGGTTTCAGG
AA_ CC
GAM927 LOC158014 5' GAGTAACTGGCATTACA 39693 AA CAAG
TGTAATGCCA TGC TC
||||| ||| ||
ACATTACGGT ATG AG
CA _
GAM927 LOC220846 3' GGACTTGGACAGAGGGCCCACA 43663 AAT AAA _
TGT GCC TG CCAAGTCC
||| ||| || |||||
ACA CGG AC GGTTTCAGG
CC_ GAG A
GAM927 LOC220930 3' ACTTAGGAGGTATTACA 44731 AAATG _
TGTAATGCC CC AAGT
||||| || |||

ACATTATGG GG TTCA
 A___ A
 GAM927 LOC51320 3' GGAGGGTACTTGGCATTACA 18741 A AAG
 TGTAATGCCAA TGCC TCC
 ||||| ||| ||
 ACATTACGGTT ATGG AGG
 C G__
 GAM927 LOC84549 3' GACTTGGTCAGGCACATACA 26261 A_ AAAT
 TGTA TGCC GCCAAGTC
 ||| ||| |||||
 ACAT ACGG TGGTTCAG
 AC AC__
 GAM928 SFRP4 3' CATGTATTTTATAAGGCATTCA 8938 GCCACC AC
 TGAATGCC GGG CATG
 ||||| ||| |||
 ACTTACGG TTT GTAC
 AATAT_ AT
 GAM928 ATPAF2 5' CATGCGGAAGATGGCGGCGTCC 36790 A ____ GGAC
 AA TG ATGCCGCCA CCG CATG
 || ||||| ||| |||
 AC TGCGGCGGT GGC GTAC
 C AGAA ____
 GAM929 DTR 3' CTCACTTCCCTTGTGTCA 7661 CCGC A
 TGACACGG AAA TGAG
 ||||| ||| |||
 ACTGTGTT TTT ACTC
 CCC_ C
 GAM929 LYZ 3' AGCTCATTTTGTCTCTCTCA 5756 CAC CC
 TGA GG GCAAAATGAGCT
 ||| || |||||
 ACT TC TGTTTACTCGA
 C__ TC
 GAM929 RNMT 3' CTCATTTTGATTGTTATA 9886 CGGCCG
 TATGACA CAAAATGAG
 ||||| |||||
 ATATTGT GTTTTACTC
 TA____
 GAM929 FLJ14166 3' AGACTCTGCCACCGTGTCA 23790 CC AAAT _
 TGACACGG GCA GAG CT
 ||||| ||| ||| ||
 ACTGTGCC CGT CTC GA
 AC ____ A
 GAM929 GAB3 3' AGCTCATTCCTCTACCTCATA 27927 CAC CCGCAA
 TATGA GG AATGAGCT
 |||| || |||||
 ATACT CC TTTACTCGA
 ____ ATCTCC
 GAM929 KIAA1223 3' CTCATTTTGTCTGTCAT 35246 C GCC
 ATGACA G GCAAAATGAG
 ||||| | |||||

TACTGT C TGTTTTACTC

GAM929 LMOD1 5' AGCCCATTTTGCCTAAGATGTC 14444 CGGCC A
GACA GCAAAATG GCT
||||| ||||| |||
CTGT CGTTTTAC CGA
AGAAC C

GAM929 STAG2 3' CTCATTTTGCGAGGCTTA 34929 C _
A GGCC GCAAAATGAG
| ||| |||||
A TCGG CGTTTTACTC
T AG

GAM929 LOC115129 5' AGCTAGGGGTGGCCGTGTCA 36250 AAAATG
TGACACGGCCGC AGCT
||||||| |||
ACTGTGCCGGTG TCGA
GGGA_

GAM930 FLJ13391 3' AATAAATGCAATTTCTT 25895 TT
AGGA ATTGCATTTATT
||| |||||
TCCT TAACGTAAATAA
T_

GAM930 KIAA0783 3' ACTTAATAAATACAATATGCT 16104 AT C
GG TATTG ATTTATTAAGT
|| ||| |||||
TC ATAAC TAAATAATTCA
GT A

GAM930 KIAA1209 3' CTTAAGAAATGCAATAATCCTT 30470 A
T AAAGGATTATTGCATTT TTAAG
||||||| |||
TTTCCTAATAACGTAAA AATTC
G

GAM930 NX-17 3' ACTTAATAAAGTAATAATC 21834 A
GATTATTGC TTTATTAAGT
||||| |||||
CTAATAATG AAATAATTCA

GAM930 PV1 3' ACTTAATAAATATTAGTAAATC 25347 _ C_
CTT AAGGATT ATTG ATTTATTAAGT
||||| ||| |||||
TTCCTAA TGAT TAAATAATTCA
A TA

GAM930 LOC153277 3' ACTTAATAAATGACGTCC 41603 TATTG
GGAT CATTTATTAAGT
||| |||||
CCTG GTAAATAATTCA
CA_

GAM931 FCRH1 3' AAATTTTGGAAATCGTGGT 27497 GA TG
ACCA ATTTCAA GTTT
||| ||||| |||

		TGGT TAAAGTT TAAA			
		GC TT			
GAM931	ID4	3' AGACCAAAATTCTGATGA 7271 C CAA			
		TCA CAGAATTT TGGTTT			
		AGT GTCTTAAA ACCAGA			
		A A__			
GAM931	PCDHA1	3' CAGAATGCTTTGAAATTCTAAT 20863 CC	T _		
	GG	TCA AGAATTTCAA GGT TTCTG			
		GGT TCTTAAAGTT TCG AAGAC			
		AA _ T			
GAM931	PCDHA1	3' CAGAATGCTTTGAAATTCTAAT 25382 CC	T _		
	GG	TCA AGAATTTCAA GGT TTCTG			
		GGT TCTTAAAGTT TCG AAGAC			
		AA _ T			
GAM931	PCDHA10	3' CAGAATGCTTTGAAATTCTAAT 20873 CC	T _		
	GG	TCA AGAATTTCAA GGT TTCTG			
		GGT TCTTAAAGTT TCG AAGAC			
		AA _ T			
GAM931	PCDHA10	3' CAGAATGCTTTGAAATTCTAAT 25614 CC	T _		
	GG	TCA AGAATTTCAA GGT TTCTG			
		GGT TCTTAAAGTT TCG AAGAC			
		AA _ T			
GAM931	PCDHA11	3' CAGAATGCTTTGAAATTCTAAT 20883 CC	T _		
	GG	TCA AGAATTTCAA GGT TTCTG			
		GGT TCTTAAAGTT TCG AAGAC			
		AA _ T			
GAM931	PCDHA12	3' CAGAATGCTTTGAAATTCTAAT 20894 CC	T _		
	GG	TCA AGAATTTCAA GGT TTCTG			
		GGT TCTTAAAGTT TCG AAGAC			
		AA _ T			
GAM931	PCDHA13	3' CAGAATGCTTTGAAATTCTAAT 20904 CC	T _		
	GG	TCA AGAATTTCAA GGT TTCTG			
		GGT TCTTAAAGTT TCG AAGAC			
		AA _ T			
GAM931	PCDHA2	3' CAGAATGCTTTGAAATTCTAAT 20914 CC	T _		
	GG	TCA AGAATTTCAA GGT TTCTG			
		GGT TCTTAAAGTT TCG AAGAC			
		AA _ T			
GAM931	PCDHA3	3' CAGAATGCTTTGAAATTCTAAT 20924 CC	T _		
	GG	TCA AGAATTTCAA GGT TTCTG			

			GGT TCTTAAAGTT TCG AAGAC		
			AA _ T		
GAM931	PCDHA4	3'	CAGAATGCTTTGAAATTCTAAT 20934	CC	T _
	GG		TCA AGAATTTCAA GGT TTCTG		
			GGT TCTTAAAGTT TCG AAGAC		
			AA _ T		
GAM931	PCDHA5	3'	CAGAATGCTTTGAAATTCTAAT 20944	CC	T _
	GG		TCA AGAATTTCAA GGT TTCTG		
			GGT TCTTAAAGTT TCG AAGAC		
			AA _ T		
GAM931	PCDHA6	3'	CAGAATGCTTTGAAATTCTAAT 25586	CC	T _
	GG		TCA AGAATTTCAA GGT TTCTG		
			GGT TCTTAAAGTT TCG AAGAC		
			AA _ T		
GAM931	PCDHA6	3'	CAGAATGCTTTGAAATTCTAAT 20954	CC	T _
	GG		TCA AGAATTTCAA GGT TTCTG		
			GGT TCTTAAAGTT TCG AAGAC		
			AA _ T		
GAM931	PCDHA7	3'	CAGAATGCTTTGAAATTCTAAT 20964	CC	T _
	GG		TCA AGAATTTCAA GGT TTCTG		
			GGT TCTTAAAGTT TCG AAGAC		
			AA _ T		
GAM931	PCDHA8	3'	CAGAATGCTTTGAAATTCTAAT 20974	CC	T _
	GG		TCA AGAATTTCAA GGT TTCTG		
			GGT TCTTAAAGTT TCG AAGAC		
			AA _ T		
GAM931	PCDHA9	3'	CAGAATGCTTTGAAATTCTAAT 25599	CC	T _
	GG		TCA AGAATTTCAA GGT TTCTG		
			GGT TCTTAAAGTT TCG AAGAC		
			AA _ T		
GAM931	PCDHAC1	3'	CAGAATGCTTTGAAATTCTAAT 20843	CC	T _
	GG		TCA AGAATTTCAA GGT TTCTG		
			GGT TCTTAAAGTT TCG AAGAC		
			AA _ T		
GAM931	PCDHAC2	3'	CAGAATGCTTTGAAATTCTAAT 20853	CC	T _
	GG		TCA AGAATTTCAA GGT TTCTG		
			GGT TCTTAAAGTT TCG AAGAC		
			AA _ T		
GAM931	PCDHB16	3'	AGCCTCCCAAATTCTGGGA 21944	A	CAAT_
			TC CCAGAATTT GGTT		

			AG GGTCTTAAA CCGA	
			ACCCT	
GAM931	ZNF268	3'	CAGAAACCATATGTGTGTAATG 31499	GA TT_ _
			CA AT CA ATGGTTTCTG	
			GT TG GT TACCAAAGAC	
			AA TGT A	
GAM931	C2orf6	3'	CAGAGGCCTTAAAATTCTGG 20141	C T
			CCAGAATTT AA GGTTTCTG	
			GGTCTTAAA TT CCGGAGAC	
			A _	
GAM931	FLJ20086	3'	CAGAAACATCAAATTCTG 19191	CAATG
			CAGAATTT GTTTCTG	
			GTCTTAAA CAAAGAC	
			CTA_	
GAM931	FLJ20220	3'	CCATGAAATTCCAGTGA 19302	CA A
			TCAC GAATTTCA TGG	
			AGTG CTAAAGT ACC	
			AC _	
GAM931	FLJ20436	3'	CAGGGATCTCGAAATTCTG 19473	AAT TT
			CAGAATTC GGT CTG	
			GTCTTAAAG CTA GAC	
			CT_ GG	
GAM931	IL18BP	3'	CAGAAACCACCAAGACTGTTGA 12250	C AA TCAA
			TCA CAG TT TGGTTTCTG	
			AGT GTC AA ACCAAAGAC	
			T AG CC_	
GAM931	KIAA1219	3'	CAGTTAGCTCTAAATTCTGG 30757	CAAT T_
			CCAGAATTT GGTT CTG	
			GGTCTTAAA TCGA GAC	
			TC_ TT	
GAM931	KIAA1884	3'	CAGAAACCAGCTGTCTGCTGA 36293	C ATTTCAA
			TCA CAGA TGGTTTCTG	
			AGT GTCT ACCAAAGAC	
			C GTCG_	
GAM931	PDP	3'	TCAGTGAAGATTCCAGTGA 20514	CA A
			TCAC GAATTTCA TGG	
			AGTG CTTAGAGT ACT	
			AC C	
GAM931	SETBP1	3'	CAGAAGGTGGAATTCTAGTGA 17824	C ATGGT
			TCAC AGAATTTCA TTCTG	

		AGTG TCTTAAGGT AAGAC	
		A GG__	
GAM931	LOC150358 3'	CAGAAACCAGCCCCCTCGGTGA 41158	A ATTTCAA
		TCACC GA TGGTTTCTG	
		AGTGG CT ACCAAAGAC	
		_ CCCCCG_	
GAM931	LOC155081 3'	CAGAAAAAACATAATTCTGGT 39543	TCAATGG
	GA	TCACCAGAATT TTTCTG	
		AGTGGTCTTAA AAAGAC	
		TACAAAA	
GAM931	LOC157280 3'	TCATTGAATTCTGGTGA 36594	T
		TCACCAGAATT CAATGG	
		AGTGGTCTTAA GTTACT	
		-	
GAM931	LOC202802 3'	CAGAAAAAACATAATTCTGGT 42988	TCAATGG
	GA	TCACCAGAATT TTTCTG	
		AGTGGTCTTAA AAAGAC	
		TACAAAA	
GAM931	LOC219401 3'	CAGAAGGCAGAAATCCTGTGA 44589	C A AA G
		TCAC AG ATTTG TG TTTCTG	
		AGTG TC TAAAG AC GAAGAC	
		_ C _ G	
GAM931	LOC221543 3'	AAACCTTAAAATTTGGTGA 45011	A CAAT
		TCACCAGA TTT GGTTT	
		AGTGGTTT AAA CCAAA	
		A TT__	
GAM931	LOC222228 3'	CAGAAAAATACATAATTCTGGT 45274	TCAATGG
	GA	TCACCAGAATT TTTCTG	
		AGTGGTCTTAA AAAGAC	
		TACATAA	
GAM931	LOC222233 3'	CAGAAAAAACATAATTCTGGT 45243	TCAATGG
	GA	TCACCAGAATT TTTCTG	
		AGTGGTCTTAA AAAGAC	
		TACAAAA	
GAM931	LOC254018 3'	CAGAAAACTGCTGAATTCTGG 46318	T AT _
		CCAGAATT CA GGTT TCTG	
		GGTCTTAA GT TCAA AGAC	
		_ CG AA	
GAM931	LOC255448 3'	TCATTGAATTCTGGTGA 45404	T
		TCACCAGAATT CAATGG	

AGTGGTCTTAA GTTACT

GAM931 LOC257596 3' AAACCTTAAATTTGGTGA 46752 A CAAT
TCACCAGA TTT GGT
||||| ||| ||||
AGTGGTTT AAA CCAAA
A TT__

GAM931 LOC91308 3' CAGAAACCATTTGAGCCAGG 32655 AGAAT _
CC TTCAA TGGTTTCTG
|| |||| |||||
GG GAGTT ACCAAAGAC
ACC__ T

GAM932 PIF1 3' CCTCACCCACAAAGAGAAGACA 30585 A GGAATAAC
TGTC TTCTCTT GAGG
||| ||||| |||
ACAG AAGAGAA CTCC
_ ACACCCA_

GAM932 SE57-1 3' CCTCACACACATCAGAGAATG 24888 __ GACTAAC
AC GTCATTCTCT TG GAGG
||||||| || |||
CAGTAAGAGA AC CTCC
CT ACACCA_

GAM933 ENTPD6 3' AGCCACAGTCCCAGAACCA 6917 C GA C CGCA
TGG TC GGG CTGT GCT
||| || ||| ||| |||
ACC AG CCC GACA CGA
A A_ T C__

GAM933 C17orf26 3' GAGCTGCAACAGGCCTTGCCA 29185 TCG C
TGGC AGGGCCTGT GCAGCTC
||| ||||| |||||
ACCG TTCCGGACA CGTCGAG
_ A

GAM933 FLJ13265 3' GAACTGGGCACCCTCGAGCC 24311 CC G C
GGCTCGAGGG TGTC CAG TC
||||||| ||| ||| |||
CCGAGCTCCC ACGG GTC AG
_ _ A

GAM933 KCNT1 3' GAGCCGCAAGGCGCCCAAGC 30973 CGA _ GTC A
GCT GGGC CT GC GCTC
||| ||| || ||| |||
CGA CCCG GG CG CGAG
A_ C AA_ C

GAM933 KIAA1493 3' GGCAGCAGGGCCCTCAAGCCA 32092 C GTC A
TGGCT GAGGGCCT GC GCT
||||| ||||| || |||
ACCGA CTCCCGGG CG CGG
A A_ A

GAM933 LOC113230 5' GCGAAGTCCTCGAGCCA 36131 CTG
TGGCTCGAGGGC TCGC
||||||| |||

ACCGAGCTCCTG AGCG
 A__
 GAM933 LOC115399 3' GAGCCCTCCGGGACCTCGAGCC 36347 G TCGCA
 A TGGCTCGAGG CCTG GCTC
 ||||| ||| |||
 ACCGAGCTCC GGGC CGAG
 A CTCC_
 GAM933 LOC147817 5' GAGCTGCGCACACCCCAAGGCC 38387 CGA CC T
 A TGGCT GGG TG CGCAGCTC
 |||| ||| || |||||
 ACCGG CCC AC GCGTCGAG
 AAC AC _
 GAM933 LOC148147 3' AGCTACAAGTACTCAAGGCCA 38474 C_ GG C CGC
 TGGCT GAG C TGT AGCT
 |||| ||| | ||| |||
 ACCGG CTC G ACA TCGA
 AA AT A ____
 GAM933 LOC163412 5' GAGGCCAGGCCCTCGAGCCA 39953 TC AG
 TGGCTCGAGGGCCTG GC CTC
 ||||| ||| |||
 ACCGAGCTCCCGGAC CG GAG
 C_ _
 GAM933 LOC58525 5' GCAAGGGCCTCTCGAGCCA 38457 _ GTC
 TGGCTCGAG GGCCT GC
 ||||| ||| ||
 ACCGAGCTC CCGGG CG
 T AA_
 GAM934 SF1 5' GTGCGCGCTGCGACACCTCC 11003 A A T
 GGAGGTG TC CAGCGCG CAT
 ||||| || ||||| |||
 CCTCCAC AG GTCGCGC GTG
 _ C _
 GAM934 FLJ22002 3' ACATGAGAACTCCATGTCACCT 24244 CACAGCGCG
 CC GGAGGTGAT TCATGT
 ||||| |||||
 CCTCCACTG AGTACA
 TACCTCAAG
 GAM934 P2RX1 3' ACATGGTCCGTGCCATGTCACC 33349 T CA _
 TCC GGAGGTGA CA GCGCG TCATGT
 ||||| || ||||| |||||
 CCTCCACT GT CGTGC GGTACA
 _ AC CT
 GAM934 LOC255598 5' ACAGCTCATGACTCACCTCC 46558 _ C_ GC
 GGAGGTGA TCA AGC GT
 ||||| ||| ||| ||
 CCTCCACT AGT TCG CA
 C AC A_
 GAM934 LOC257103 5' ACATGACGCAGGCTTCACCTCT 45753 TCAC _
 GGAGGTGA AGC GCGTCATGT
 ||||| ||| |||||

			TCTCCACT TCG CGCAGTACA		
			____ GA		
GAM935	TIMM8A	3'	TAGAGGCCTTTAGTTATAA 10289	AAAT	A
			TTATAACTAAA CCT CTA		
			AATATTGATTT GGA GAT		
			CC__ _		
GAM935	BDG-29	3'	ATTTAGTAGAATTTTTAGTTT 35813	T	C III
			TA TA AACTAAAAAAT CTAATAA	T	
			AT TTGATTTTTTA GATGATTT	A	
			T A III		
GAM935	C1orf26	3'	TTTAGTTGACTTTTTAGTTATA 19217	A	CT
			G TTATAACTAAAAA TC ACTAAA		
			GATATTGATTTTT AG TGATTT		
			C T_		
GAM936	DKFZp547A023	3'	CTGAAATATGACTGCCATATGA 35943		AATTTTA
			A TTCATAT ATATTCAG		
			AAGTATA TATAAAGTC		
			CCGTCAG		
GAM936	DKFZP564O123	3'	TGAGAATTATAATTATATGAA 29906	T	A
			TTCATATAATT TAAT TTTCA		
			AAGTATATTAA ATTA AGAGT		
			T _		
GAM936	ZDHC2	3'	GTATTAAGAATTATATGAA 18490		_
			TTCATATAATTTT AATAT		
			AAGTATATTAAGA TTATG		
			A		
GAM936	LOC129446	3'	TCTGAAATAAGATTTTATGAA 37468	T	TAA
			TTCATA AATTT TATTCAGA		
			AAGTAT TTAGA ATAAAGTCT		
			T _		
GAM936	LOC149722	5'	TCTGAATATACATTATATGAA 41044	TTTA	T
			TTCATATAAT ATATT CAGA		
			AAGTATATTA TATAA GTCT		
			CA__ _		
GAM936	LOC151414	3'	TCTGAAGATAAATTATGTGAA 39113		TAATA
			TTCATATAATTT TTTCAGA		
			AAGTGTATTAAA GAAGTCT		
			TA__		
GAM937	BTN3A3	3'	CTAAAAGAATTACAGGGATGTT 13856	AA	C
			AACA TTTTGTAATTC TTTAG		

TTGT GGGACATTAAG AAATC
 A_ A
 GAM937 FENS-1 3' TAAAGGACTAAATTTGTT 21893 TGTAAT
 AACAAATTT TCCTTTA
 ||||| |||||
 TTGTTTAAA AGGAAAT
 TC____
 GAM937 KIAA1164 3' CTATTTCTGTTACACAATTTGT 34440 T TCCTT
 TA TAACAAATT TGTAAT TAG
 ||||| ||||| ||
 ATTGTTTAA ACATTG ATC
 C TCTTT
 GAM938 PRKAR2B 3' TTGGCAATTAAACATGCT 8612 GCA
 AGCA TTTAATTGCTAA
 ||| |||||
 TCGT AAATTAACGGTT
 AC_
 GAM938 LOC154789 3' ACCAACTAGCTTTAGTAGTGCT 39486 TAATT_ A
 GCT AGCAGCATT GCTA TTGGT
 ||||| ||| |||||
 TCGTCGTGA CGAT AACCA
 TGATTT C
 GAM939 ADAM28 3' GAGGAACATATGCCTGAGAA 15540 C CGCTCAA
 TTC CGGGCATA CCTC
 ||| ||||| |||
 AAG GTCCGTAT GGAG
 A ACAA____
 GAM939 ICOS 3' GAGGCTGAAGTCACCCTGGGAA 14390 CAT GC A
 TTCCCGGG AC TCA CCTC
 ||||| || ||| |||||
 AAGGGTCC TG AGT GGAG
 CAC A_ C
 GAM939 TNFRSF1B 3' GAAATCGTTTGAACCCGGGAA 6734 _ T C_
 TTCCCGGG CA ACG TC
 ||||| || ||| ||
 AAGGGCCC GT TGC AG
 AA T TAA
 GAM939 A4GALT 3' AGATTGAGGGCCCCGGGAG 18894 ATACG C
 TTCCCGGGC CTCAA CT
 ||||| ||||| ||
 GAGGGCCCCG GAGTT GA
 G____ A
 GAM939 Apg4B 3' GAGGCTGCGCTGCCCCGGGAG 14974 TAC T A
 TTCCCGGGCA GC CA CCTC
 ||||| || ||| |||||
 GAGGGCCCCG CG GT GGAG
 _ C C
 GAM939 FLJ22405 5' AGGTTGAGCGCATTGAGAA 22863 C GCATA
 TTC CGG CGCTCAACCT
 ||| ||| |||||

			AAG GTT GCGAGTTGGA		
			A AC__		
GAM939	HGC6.2	3'	AGGTGGCCTGCCCGGGAA 15687	TAC CA	
			TTCCCGGGCA GCT ACCT		
			AAGGGCCCGT CGG TGGA		
			C__ _		
GAM939	HRD1	3'	GAAGTTGAATGCTTAATCCCGG 34472	CA C __ C	
	GAA		TTCCCGGG TA GC TCAAC TC		
			AAGGGCCC AT CG AGTTG AG		
			TA T TA A		
GAM939	OS4	3'	GAGGTTTTCTCCCTGCCCGGGA 12289	TACGCTC	
	A		TTCCCGGGCA AACCTC		
			AAGGGCCCGT TTGGAG		
			CCCTCTT		
GAM939	LOC115557	5'	GAGGCTGAGCATCATGAAGAGA 28556	CCGGG AC_ A	
	A		TTC CAT GCTCA CCTC		
			AAG GTA CGAGT GGAG		
			AGAA_ CTA C		
GAM939	LOC124976	3'	AGGCTGAGGCCCGGGAG 36781	CATACG A	
			TTCCCGGG CTCA CCT		
			GAGGGCCC GAGT GGA		
			CG__ C		
GAM939	LOC148343	5'	AGGCTGAGACCTGGGAA 38521	CATACG A	
			TTCCCGGG CTCA CCT		
			AAGGGTCC GAGT GGA		
			A__ C		
GAM939	LOC150175	5'	AGGTTGAGCACTTCAGGA 38883	C CATAC	
			TCC GGG GCTCAACCT		
			AGG CTT CGAGTTGGA		
			A CA__		
GAM939	LOC150215	5'	AGGTTGAGCACTTCAGGA 38887	C CATAC	
			TCC GGG GCTCAACCT		
			AGG CTT CGAGTTGGA		
			A CA__		
GAM939	LOC150218	5'	AGGTTGAGCACTTCAGGA 38914	C CATAC	
			TCC GGG GCTCAACCT		
			AGG CTT CGAGTTGGA		
			A CA__		
GAM939	LOC152002	3'	GAGGTCGAGATCAGCCTGGGAA 39195	ATACG A	
			TTCCCGGGC CTC ACCTC		

			AAGGGTCCG	GAG TGGAG		
			ACTA_	C		
GAM939	LOC152765	3'	AGGTTAAGAACATGCCCAGGA	39312	C	ACG C
			TCC GGGCAT	CT AACCT		
			AGG CCCGTA	GA TTGGA		
			A	CAA A		
GAM939	LOC166979	5'	AGACTGACTTAGACCTGGGAA	40225		CA CGC AC
			TTCCCGGG	TA TCA CT		
			AAGGGTCC	AT AGT GA		
			AG	TC_ CA		
GAM939	LOC196746	3'	GAGGTGGTCATGCCCGGG	42289		AC CA
			CCCGGGCAT	GCT ACCTC		
			GGGCCCGTA	TGG TGGAG		
			C_	_		
GAM939	LOC253962	5'	AGCTGTGGGTACCCGGGAG	46224		_ C
			TTCCCGGG	CATA GCT		
			GAGGGCCC	GTGT CGA		
			ATGG	_		
GAM940	BCL2	3'	GAACACTGGTGGAGGATGG	6257		A
			CCATCCTCCACCA	TGTTT		
			GGTAGGAGGTGGT	ACAAG		
			C			
GAM940	CREBL2	3'	AGAGCAGTAGAGGATG	6992		C CAA
			CATCCTC	AC TGTTTT		
			GTAGGAG	TG ACGAGA		
			A	_		
GAM940	DMD	5'	GAAAACATTCACAAAATGGGTA	10162		CCTCCACC
			TACCCAT	AATGTTTTC		
			ATGGGTA	TTACAAAAG		
			AAACAC_			
GAM940	DMD	5'	GAAAACATTCACAAAATGGGTA	10176		CCTCCACC
			TACCCAT	AATGTTTTC		
			ATGGGTA	TTACAAAAG		
			AAACAC_			
GAM940	KDR	3'	GCTCTGGTGGAGGTGGG	8054	T	AT
			CCCA	CCTCCACCA GT		
			GGGT	GGAGGTGGT CG		
			_	CT		
GAM940	MTMR8	3'	AAAACATTATAGGCTGGG	17740	T	CCACC
			CCCA	CCT AATGTTTT		

GGGT GGA TTACAAAA
C TA__

GAM940 TEC 3' AAGCACAAGGAAGGATGGG 9215 _ ACCAA
CCCATCCT CC TGTTT
||||||| || |||||
GGGTAGGA GG ACGAA
A AAC__

GAM940 TNFRSF8 3' AAACAGATGGCAGGATGGG 6907 _ CCAA
CCCATCCT CCA TGTTT
||||||| ||| |||||
GGGTAGGA GGT ACAA
C AG__

GAM940 ZNF277 5' GAAAACATTACGTCGACGGGG 22534 ATCC C C_
CCC TC AC AATGTTTTTC
||| ||| |||||
GGG AG TG TTACAAAAG
GC__ C CA

GAM940 FHX 3' ATTGGTGGAGGAGAGTA 20456 CCA
TAC TCCTCCACCAAT
||| |||||
ATG AGGAGGTGGTTA
AG__

GAM940 FLJ10035 3' AAGATATAATGGAGGATG 19705 CCA
CATCCTCCA ATGTTTT
||||||| |||||
GTAGGAGGT TATAGAA
AA__

GAM940 FLJ10283 3' AAAATGTTGCGAAAACATGGGT 19794 CCTCCAC
A TACCCAT CAATGTTTT
||||||| |||||
ATGGGTA GTTGTA AAA
CAAAAGC

GAM940 FLJ20127 3' GAAAACATCAGGGAGATG 19219 C ACCA
CATC TCC ATGTTTTTC
||| ||| |||||
GTAG AGG TACAAAAG
_ GAC__

GAM940 KIAA0828 3' GAAAGCCACAGAGGATGGG 39514 CACCAAT
CCCATCCTC GTTTTC
||||||| |||||
GGGTAGGAG CGAAAG
ACAC__

GAM940 KIAA1163 3' GAGCTTTGGCGGGGGATG 38560 A T
CATCCTCC CCAA GTTT
||||||| ||| |||||
GTAGGGGGG GGTT CGAG
C T

GAM940 KIAA1434 3' GAACATGGTGGAATG 34487 CC A
CAT TCCACCA TGTTT
||| ||||| |||||

			GTA AGGTGGT ACAAG			
			AA _			
GAM940	KIAA1821	3'	GAGGCAGTGGAAGAAGG	35553	A C	CAA
			CC TC TCCAC TGTTTT			
			GG AG AGGTG ACGGAG			
			A A _			
GAM940	MAEA	3'	AAAACATTTGGATTGGTA	12494	C	TCCACC
			TACC ATCC AATGTTTT			
			ATGG TAGG TTACAAAA			
			T T _			
GAM940	ZNF31	5'	GCCTTGGTGGAGGATTGG	32422	C	T
			CC ATCCTCCACCAA GT			
			GG TAGGAGGTGGTT CG			
			T C			
GAM940	LOC118709	5'	GAAGTGTGGTGAAGGTGG	36599	T C	ATGT
			CCA CCT CACCA TTTC			
			GGT GGA GTGGT GAAG			
			_ A GT_			
GAM940	LOC158310	5'	GAAACATTGGCGGCAGCAGGT	41946	CATC _	A
			ACC CT CC CCAATGTTTTC			
			TGG GA GG GGTTACAAAAG			
			AC_ C C			
GAM940	LOC256519	5'	GAATTTATTAGTGGAGGATG	45852	C	TT
			CATCCTCCAC AATG TTC			
			GTAGGAGGTG TTAT AAG			
			A TT			
GAM941	ATM	5'	AGAAAAATTACCAGGTCA	28704	G CTC	
			TGACC GG ATTTTCT			
			ACTGG CC TAAAAAGA			
			A AT_			
GAM941	ATM	5'	AGAAAAATTACCAGGTCA	28706	G CTC	
			TGACC GG ATTTTCT			
			ACTGG CC TAAAAAGA			
			A AT_			
GAM941	DXYS155E	3'	AGAAAGGACACCCGGTCA	11539		CTCA
			TGACCGGG TTTTCT			
			ACTGGCCC GGAAAGA			
			ACA_			
GAM941	FCGR2A	3'	CAGAAGAACAAAGAGCCC	38698	A T	
			GGGCTC TT TTCTTCTG			

CCGGAG AA AAGAAGAC
 A C
 GAM941 LAMC1 3' CAGAAGAAAAACAAGCCTCCTC 8074 CC CA
 GA GGGCT TTTTCTTCTG
 || |||| |||||
 CT TCCGA AAAAAGAAGAC
 CC AC
 GAM941 MYO10 3' CAGAAGAAAAATAATCTGGTC 14731 CTC
 GACCGGG ATTTTCTTCTG
 ||||| |||||
 CTGGTCT TAAAAAGAAGAC
 AA_
 GAM941 NDUFV3 5' CAGAAGGAGCGTGGCCC 22043 T T
 GGGC CAT TTTCTTCTG
 ||| || |||||
 CCGG GTG GAGGAAGAC
 _ C
 GAM941 PDGFRA 3' CAGAAGAAAATTTGCCAATC 12881 CCG TCAT
 GA GGC TTTTCTTCTG
 || ||| |||||
 CT CCG AAAAGAAGAC
 AA_ TTT_
 GAM941 SLC20A2 5' AAGAAAAGTACCCGGCA 13599 A CTC
 TG CCGGG ATTTTCTT
 || |||| |||||
 AC GGCCC TGAAAAGAA
 _ A_
 GAM941 TCF2 3' CAGAAGAAAAAGTTGCAGTC 6074 CGG TCA
 GAC GC TTTTCTTCTG
 ||| || |||||
 CTG CG AAAAAGAAGAC
 A_ TTG
 GAM941 BLZF1 3' AAGACAAACCTGGTCA 9747 CTCA T
 TGACCGGG TTT TCTT
 ||||| ||| |||
 ACTGGTCC AAA AGAA
 _ C
 GAM941 DGKD 3' CAGAGGGAGAAATAAGCC 29877 CA_
 GGCT TTTTCTTCTG
 |||| |||||
 CCGA AAGAGGGAGAC
 ATA
 GAM941 FLJ21195 3' CAGAAAAAAAATGCCTGGTCA 22824 TCA C
 TGACCGGGC TTTT TTCTG
 ||||| |||| |||||
 ACTGGTCCG AAAAA AAGAC
 TA_ A
 GAM941 KIAA0164 3' CAGAAGAAAACTGTAATCC 16404 CT_ _
 GGG CA TTTTCTTCTG
 ||| || |||||

CCT GT AAAAAGAAGAC
 AAT C
 GAM941 KIAA0350 3' CAGAAGAATTGGACCAGGTCA 30661 G CT TTT
 TGACC GG CA TTCTTCTG
 ||||| || || |||||
 ACTGG CC GT AAGAAGAC
 A AG T__
 GAM941 KIAA1396 3' CAGAAGAAAAACCTTCAGCC 31546 CA__
 GGCT TTTTCTTCTG
 ||| |||||
 CCGA AAAAAGAAGAC
 CTTCC
 GAM941 KIAA1853 3' AAAATTGAGCCCTGGCCA 34382 A _ T
 TG CC GGGCTCA TTTT
 || || ||||| |||
 AC GG CCCGAGT AAAA
 C T T
 GAM941 KIAA1884 3' AGAGTGCAGAAACCCGGTCA 36291 __ _
 TGACCGGG CT CATTTT
 ||||| || |||||
 ACTGGCCC GA GTGAGA
 AAA C
 GAM941 SH3BGRL2 3' CAGAAGAATTACAGCCCTGTCA 25526 C CATT
 TGAC GGGCT TTCTTCTG
 ||| |||| |||||
 ACTG CCCGA AAGAAGAC
 T CATT_
 GAM941 LOC127255 3' CAGAAGAAAAATAAAGCTT 29773 C_
 GGGCT ATTTTCTTCTG
 |||| |||||
 TTCGA TAAAAAGAAGAC
 AA
 GAM941 LOC158563 3' CAGAAAGGAGGTGGCCCAGTCA 39868 C T TC
 TGAC GGGC CATTTT TTCTG
 ||| |||| ||||| |||||
 ACTG CCCG GTGGAG AAGAC
 A _ GA
 GAM941 LOC163081 5' AGAAGAAAAACCCTATCA 40085 CC CTCA
 TGA GGG TTTTCTTCT
 ||| ||| |||||
 ACT CCC AAAAAGAAGA
 AT ____
 GAM941 LOC51279 3' CAGAAGCCAGGTGAGCCC 18616 TT
 GGGCTCATTT CTTCTG
 ||||| |||||
 CCCGAGTGGA GAAGAC
 CC
 GAM942 EPHB2 3' CAGACTCCCTCCTGTGA 10732 TA A C
 TTACAGGA GGGA G CTG
 ||||| ||||| |||

AGTGTCTCT CCCT C GAC
 — _ A
 GAM942 GATA2 5' GCTCCTACCCTGTAAGC 7804 A GA
 GCTTACAGG TAGG AGC
 ||||| ||| ||
 CGAATGTCC ATCC TCG
 C _
 GAM942 GRAF 3' CAGGCTCCCCTCCTTCCTATTA 17441 TAC T_ A
 GCTA TAGCT AGGA AGGG AGCCTG
 |||| ||| ||| |||||
 ATCGA TCCT TCCC TCGGAC
 TTA TCC C
 GAM942 IRAK1 3' CAGGCTTCGGAGGCCACAAGCT 7298 ACA ATAGG
 AGCTT GG GAAGCCTG
 |||| || |||||
 TCGAA CC CTCGGAC
 CA_ GGAGG
 GAM942 KIAA0450 3' CAGACCCCCCTGACCAAGCT 16027 ACA A AAGC
 AGCTT GG TAGGG CTG
 |||| || |||| |||
 TCGAA CC GTCCC GAC
 _ A CCCA
 GAM942 KIAA0789 5' CAGGCTCCCCTTTCTTAAAGC 31845 AC T A
 GCTT AGGA AGGG AGCCTG
 ||| ||| ||| |||||
 CGAA TCCT TCCC TCGGAC
 AT T C
 GAM942 LIG-1 3' CAGGCTTCCCTGTCTGTAGAGC 31950 _ G
 GCTT ACAG ATAGGGAAGCCTG
 ||| ||| ||||| |||||
 CGAG TGTC TGTCCCTTCGGAC
 A _
 GAM942 PPP1R3B 3' AGGCCTTTTCTGCAAGCTG 23855 A T GGAA
 TAGCTT CAGGA AG GCCT
 ||||| ||||| || |||
 GTCGAA GTCCT TC CGGA
 C T _
 GAM942 STI2 3' CAGGCTTCCTGTTTGTA 42876 GATA
 TTACAG GGGAAGCCTG
 ||||| |||||
 AATGTT TCCTTCGGAC
 TG_
 GAM942 LOC51285 3' CAGGCTTCCCGACCCACAGGC 18637 ACA ATA
 GCTT GG GGGAAGCCTG
 ||| || |||||
 CGGA CC CCCTTCGGAC
 CA_ CAG
 GAM943 APC 3' TGAACAAGCTTTACCCAGC 5482 C_
 GCTG TGAAGCTTGTCA
 ||| ||||| |||||

			CGAC ATTTCTGAACAAGT		
			CC		
GAM943	CDH17	3'	AGGAACCAAGTCAGCTGGCCA 10268		_ AAG
			TGGCCAGCTG CTG CTT		
			ACCGGTCGAC GAC GGA		
			T CAA		
GAM943	DIAPH2	3'	AACCTCTTCAGCACTAGCCA 13558	C C	CTT
			TGGC AG TGCTGAAG GTT		
			ACCG TC ACGACTTC CAA		
			A _ TC_		
GAM943	GCNT2	5'	TGGGCTTCAGCAACCTGCCA 7240	C C_	
			TGGC AG TGCTGAAGCTTG		
			ACCG TC ACGACTTCGGGT		
			_ CA		
GAM943	HAL	5'	AAGGGACAGCAGCTGACCA 7887	C	AAG
			TGG CAGCTGCTG CTT		
			ACC GTCGACGAC GAA		
			A AGG		
GAM943	SCP2	3'	CAATGCCAACAGCTGGCCA 8881	C AA _	
			TGGCCAGCTG TG GC TTG		
			ACCGGTCGAC AC CG AAC		
			A _ T		
GAM943	FLJ10759	3'	TGAACAAGAGTCCAGCCAACC 20103	CCA	CT AG
			GG GCTG GA CTTGTTCA		
			CC CGAC CT GAACAAGT		
			AAC _ GA		
GAM943	FLJ20151	3'	TGAGTCTCAGCAGCCGCC 19246	CA	AG
			GGC GCTGCTGA CTTG		
			CCG CGACGACT GAGT		
			C_ CT		
GAM943	FLJ21617	5'	CGACCTTCCAGCAGCTGACC 25166	C	_ C
			GG CAGCTGCTG AAG TTG		
			CC GTCGACGAC TTC AGC		
			A C C		
GAM943	KIAA0673	5'	GGATCTTCAGCAACCAGCC 31214	CAGC	CTT
			GGC TGCTGAAG GTTC		
			CCG ACGACTTC TAGG		
			ACCA _		
GAM943	KLK15	3'	AAGCCCCACAGCTGGCCA 28861	C AA_	
			TGGCCAGCTG TG GCTT		

			ACCGGTCGAC AC CGAA		
			_ CCC		
GAM943	KLK15	3'	AAGCCCCACAGCTGGCCA 23263	C AA_	
			TGGCCAGCTG TG GCTT		
			ACCGGTCGAC AC CGAA		
			_ CCC		
GAM943	MGC20470	3'	CAGGCCCTCCAGCTGCTGGCCA 29684	T AA_	
			TGGCCAGC GCTG GCTTG		
			ACCGGTCG CGAC CGGAC		
			T CTCC		
GAM943	SDC3	5'	GAACATCAGCAACTGACCA 16084	C C AGCT	
			TGG CAG TGCTGA TGTTC		
			ACC GTC ACGACT ACAAG		
			A A _		
GAM943	TGOLN2	3'	AAGACTTCAGCAGCAAACCA 32021	CCA _	
			TGG GCTGCTGAAG CTT		
			ACC CGACGACTTC GAA		
			AAA A		
GAM943	LOC125268	3'	TGAAGGAGCTTCAGCGCCAGCC 37453	CA T G	
	A		TGGC GC GCTGAAGCTT TTCA		
			ACCG CG CGACTTCGAG AAGT		
			AC _ G		
GAM943	LOC144017	5'	CGAGAACTCAGCAGCTGCCA 40388	C AG_	
			TGGC AGCTGCTGA CTTG		
			ACCG TCGACGACT GAGC		
			_ CAA		
GAM943	LOC148137	3'	CAAGTCCCTGCAGCTGGCCA 29513	TGAA	
			TGGCCAGCTGC GCTTG		
			ACCGGTCGACG TGAAC		
			TCCC		
GAM943	LOC204970	3'	TAGGTTCTTCAGCAGCAGCCA 43073	CA _	
			TGGC GCTGCTGAAG CTTG		
			ACCG CGACGACTTC GGAT		
			A_ TT		
GAM943	LOC219654	3'	TGAGCTGTTTCAGCAGGTAGCCA 43878	CAG G TT	
			TGGC CTGCTGAA C GTTCA		
			ACCG GACGACTT G CGAGT		
			ATG _ T_		
GAM943	LOC253539	5'	GACCCTCCAGCAGCTGGGCA 45938	G A CTT	
			TG CCAGCTGCTG AG GTT		

AC GGTGACGAC TC CAG
 G C C__
 GAM943 LOC254559 5' GAACTCGCCAGCAGCTAGC 46197 C AA TT
 GC AGCTGCTG GC GTTC
 || ||||| || ||||
 CG TCGACGAC CG CAAG
 A _ CT
 GAM944 PRO1386 3' CAGAAGGAAAAAATACTCTCT 25289 _ G AGG
 AGAG GTATTTTTTT TT TCTG
 ||| ||||| || ||||
 TCTC CATAAAAAAA GA AGAC
 T G ____
 GAM945 KCNJ1 5' GCCTGCTGCCAGAGACCTTAG 5727 AA_ _ A A
 CTGA TCAGCTAA CTTT GCA CA GC
 ||||| ||| ||| ||
 AGTCGATT GAGA CGT GT CG
 CCA CC C C
 GAM945 TFDP1 3' TGCCCCTGAAAAGTTTTGCTG 13977 T G ACAA
 A TCAGC AAAACTTT CA GCA
 |||| ||||| || |||
 AGTCG TTTTGAAA GT CGT
 T A CCC_
 GAM945 VBP1 3' TGCCTGTCATAAGAAAACCTTT 9400 AAC____ CA A
 AGCTGA CAGCTAA TTTG ACA GCA
 ||||| ||| ||| |||
 GTCGATT GAAT TGT CGT
 CTCAAAA AC C
 GAM945 FBXO30 3' TGCCTTTTAAAGTTTTGCTGA 25839 T C CAA
 TCAGC AAAACTTTG AA GCA
 |||| ||||| || |||
 AGTCG TTTTGAAAT TT CGT
 _ T C_
 GAM945 FLJ23112 5' CTTGTCAAGGGCTCTTTGGCTG 24467 A____ CA
 A TCAGCTAAA CTTTG ACAAG
 ||||| |||| |||||
 AGTCGGTTT GGAAC TGTTT
 CTCG _
 GAM945 MGC13114 3' TGCCCACCAGGCTGGCCTTGGC 26154 AA TT AACAA_
 TGA TCAGCTAA CT GC GCA
 ||||| || || |||
 AGTCGGTT GG CG CGT
 CC T_ GACCACC
 GAM945 SPRY2 3' TGCTTGTTAGAACTCAGCT 12456 AAAAC GC
 AGCT TTT AACAAGCA
 ||| || |||||
 TCGA AAG TTGTTCGT
 CTC_ A_
 GAM945 LOC144871 3' GCGTTGCAAAGTTTTCACTGA 40470 CT AA
 TCAG AAAACTTTGCAAC GC
 ||| ||||| ||| ||

AGTC TTTTGAAACGTTG CG
 AC _
 GAM945 LOC145988 5' GCTCGCTGGGATTTGGCTGA 38040 A TT AACA
 TCAGCTAAA CT GC AGC
 ||||| || || ||
 AGTCGGTTT GG CG TCG
 A GT C_
 GAM945 LOC219940 3' TGGGGGCAAGTTTTAGATGA 44834 G T AA_
 TCA CTAAACTT GC CA
 || ||||| || ||
 AGT GATTTTGAA CG GT
 A _ GGG
 GAM946 CKAP2 3' GAACATATCATACTGAACA 20088 GC G TC
 TG TC AGT GATATGTTC
 || || || |||||
 AC AG TCA CTATACAAG
 A_ _ TA
 GAM946 KIAA0427 5' GACGCTCCGAACTCGAGGCA 16574 G ATA
 TG CTCGAGTTTCG TGTT
 || ||||| ||||
 AC GAGCTCAAGC GCAG
 G CTC
 GAM946 MGC15705 3' AACACATCTTGGGCCA 26498 GTTC A
 TGGCTCGA GAT TGTT
 ||||| || ||||
 ACCGGGTT CTA ACAA
 _ C
 GAM946 MRPL10 3' GAACAGGGACTTGAACCA 29769 C GATA
 TGG TCGAGTTC TGTTTC
 || ||||| ||||
 ACC AGTTCAGG ACAAG
 A G_
 GAM946 LOC220021 5' GAACATATCTGCAGAGCC 44851 GA TC
 GGCTC GT GATATGTTC
 |||| || |||||
 CCGAG CG CTATACAAG
 A_ T_
 GAM946 LOC91012 5' AACATCACTTGAGCCA 32278 TCGAT
 TGGCTCGAGT ATGTT
 ||||| ||||
 ACCGAGTTCA TACAA
 C_
 GAM947 PCOLN3 3' ACCCTCTACCATCTGTAA 8661 T A C
 TTAC AGATGGTA AG GT
 || ||||| || ||
 AATG TCTACCAT TC CA
 _ C C
 GAM948 CD1A 5' CAATTTTCTGAGAGAAG 35271 C_
 CTTCTC C GAAAAATTG
 |||| | |||||

			GAAGAG G CTTTTTAAC		
			A T		
GAM948	DLEU2	5'	CAATCTAGCGGGAGAGACAGGA 12638	CAC	AAAA
	TA		TATCC TTCTCCCG ATTG		
			ATAGG GAGAGGGC TAAC		
			ACA GATC		
GAM948	EEF1B2	5'	CAATTCGTACGTGGAGAAGTGG 7682	_ AAA_	
	GA		TCCCACTTCTCC CG AATTG		
			AGGGTGAAGAGG GC TTAAC		
			T ATGC		
GAM948	GLUL	3'	CAACTTTTCTATTAAAAGTG 7834	CTCCC_ A	
	A		TCCCACTT GAAAA TTG		
			AGGGTGAA CTTTT AAC		
			AATTAT C		
GAM948	LOC220753	5'	CAATTTTTTAAGATGAAGAAGT 44660	_____ CC	
	GGGA		TCCCACTTC TC GAAAAATTG		
			AGGGTGAAG AG TTTTTTAAC		
			AAGT AA		
GAM949	APM1	3'	CAAACCTCTTAATGCTGTGTT 11206	T CCCCAC	
			AACACAG CAT AGTTTG		
			TTGTGTC GTA TCAAAC		
			_ ATTC_		
GAM949	APM1	3'	GCAACTGCCCAGGAAGGACTGT 11212	A_ CCA_ T	
	G		CACAGTC TCC CAGTT GC		
			GTGTCAG AGG GTCAA CG		
			GA ACCC _		
GAM949	B4GALT5	3'	CAAACCTGTGGGAGTGATTG 11167	TC	
			CAGTCA CCCACAGTTTG		
			GTTAGT GGGTGTCAAAC		
			GA		
GAM949	CASP8	3'	ACTGTGAATAACTGTGTT 27205	C CCC	
			AACACAGT AT CACAGT		
			TTGTGTCA TA GTGTCA		
			A A_		
GAM949	CORO1C	3'	CAAACCTAATTCTGATTGTGT 15628	TCCCCAC	
			ACACAGTCA AGTTTG		
			TGTGTTAGT TCAAAC		
			CTTAA_		
GAM949	DNMT3B	3'	CAAATATGGGGAAAAAACTGTG 13759	CA_ CA	
			CACAGT TCCCCA GTTTG		

			GTGTCA AGGGGT TAAAC		
			AAAA A_		
GAM949	EIF3S10	3'	TTGTAGTAATGACTGTGTT 35502	CCCC	
			AACACAGTCAT ACAG		
			TTGTGTCAGTA TGTT		
			ATGA		
GAM949	FAT2	3'	GCAAAGCCTGATTGACTGTG 7174	TCCCCA _	
			CACAGTCA CAG TTTGC		
			GTGTCAGT GTC AAACG		
			TA__ CG		
GAM949	NAP1L4	3'	GCAGCCGGGGATGGCCGTGT 12589	A ACA T	
			ACAC GTCATCCCC GTT GC		
			TGTG CGGTAGGGG CGA CG		
			C C_ _		
GAM949	PEA15	3'	ACTCTGGAGAGACTGTG 9845	A C C	
			CACAGTC TC CCA AGT		
			GTGTCAG AG GGT TCA		
			_ A C		
GAM949	PNUTL2	3'	CAAAGTGTGGAGATCACT 27836	C C	
			AGT ATC CCACAGTTTG		
			TCA TAG GGTGTCAAAC		
			C A		
GAM949	SCN1A	3'	CAAAGTGTGACTCTGTGT 42832	TCATCCC	
			ACACAG CACAGTTTG		
			TGTGTC GTGTCAAAC		
			TCA__		
GAM949	SIAT4C	5'	ACTTGGGAGCTGACTGTG 12957	TC_ C	
			CACAGTCA CCCA AGT		
			GTGTCAGT GGGT TCA		
			CGA _		
GAM949	SLC26A4	3'	GCAAAGTGC GGGAATACTGT 6028	C C A	
			ACAGT AT CCC CAGTTTGC		
			TGTCA TA GGG GTCAAACG		
			_ A C		
GAM949	CDK5RAP3	5'	GCAAGTACAGGACTAACTGTGT 24852	CA_ CCAC T	
	T		AACACAGT TCC AGTT GC		
			TTGTGTCA AGG TCAA CG		
			ATC ACA_ _		
GAM949	DIS3	3'	CAAATCAACATGACTGTGTT 17298	CCCCACA	
			AACACAGTCAT GTTTG		

		TTGTGTCAGTA	TAAAC		
		CAAC__			
GAM949	FLJ11113	5'	CAGTCTGGGAAAACTGTG	29875	CA_ CAC T
			CACAGT TCCC AG TTG		
			GTGTCA AGGG TC GAC		
			AAA __ T		
GAM949	FLJ21324	5'	GCAGGAAGGAGGATGGCTGTGT	43828	_ ACAG
			ACACAGTCATCC CC TTTGC		
			TGTGTCGGTAGG GG GGACG		
			A AA__		
GAM949	FLJ21918	3'	CAAAC TATTTT GATGGACTGTG	24482	_ CCCAC
			CACAGTC ATC AGTTTG		
			GTGTCAG TAG TCAAAC		
			G TTTTA		
GAM949	KIAA0254	3'	AGGCAGGGATGCTGTGTT	16504	T CACA
			AACACAG CATCCC GTTT		
			TTGTGTC GTAGGG CGGA		
			_ A__		
GAM949	KIAA0258	3'	ACTGTTCAGAAATGACTGTGT	16641	CCCC__
			ACACAGTCAT ACAGT		
			TGTGTCAGTA TGTC A		
			AAGACT		
GAM949	KIAA0828	3'	CTGTAGGGACACTGTGTT	39513	CA C
			AACACAGT TCCC ACAG		
			TTGTGTCA AGGG TGTC		
			C_ A		
GAM949	MAP2K4	3'	CAAAC TGTGAAAATAGTGT	8916	A CATCCC
			ACAC GT CACAGTTTG		
			TGTG TA GTGTCAAAC		
			A AAA__		
GAM949	TNRC6	5'	CAAAC TGTAGAATGCTGTTGT	34899	_ T CCCC
			ACA CAG CAT ACAGTTTG		
			TGT GTC GTA TGTC AAAC		
			T _ AGAA		
GAM949	TU12B1-TY	3'	ACTGTGGGAATGACCATG	18642	CA C
			CA GTCAT CCCACAGT		
			GT CAGTA GGGTGTCA		
			AC A		
GAM949	LOC115297	3'	ACTGTGAAATTGACTGTGT	36068	TCCC
			ACACAGTCA CACAGT		

		TGTGTCAGT GTGTCA	
		TAAA	
GAM949	LOC147165 3'	ACTGAGGATGAACTGTGTT 40812	_ CCA
		AACACAGT CATCC CAGT	
		TTGTGTCA GTAGG GTCA	
		A A__	
GAM949	LOC150605 5'	CGAGCAGGGAAACTGTGT 41230	CA CACA
		ACACAGT TCCC GTTTG	
		TGTGTCA AGGG CGAGC	
		A_ A__	
GAM949	LOC169436 5'	GCAAACCTGCAGGACCTGAGTT 40278	A TCA CCA
		AAC CAG TCC CAGTTTGC	
		TTG GTC AGG GTCAAACG	
		A C__ AC_	
GAM949	LOC170425 3'	GCACTTTAAGGGATGATTATGT 37550	C CAC TT
		ACA AGTCATCCC AG TGC	
		TGT TTAGTAGGG TT ACG	
		A AA_ TC	
GAM949	LOC220729 3'	TGAACGAGGCTGACTGTG 35449	T CCACA
		CACAGTCA CC GTTTG	
		GTGTCAGT GG CAAGT	
		C AG__	
GAM949	LOC255031 5'	GCAAACCTGTGAAGTGCAGTG 46431	A T CCC
		CAC G CAT CACAGTTTGC	
		GTG C GTG GTGTCAAACG	
		A_ AA_	
GAM949	LOC257422 5'	GTGCAGGTATGACTGTGTT 46191	_ C_
		AACACAGTCAT CC CAC	
		TTGTGTCA GTA GG GTG	
		T AC	
GAM949	LOC91272 3'	GTGGGAGAGTTGACTGTGT 32613	_ _
		ACACAGTCA TC CCCAC	
		TGTGTCAGT AG GGGTG	
		TG A	
GAM949	LOC93512 3'	ACTGAGGATGAACTGTGTT 35876	_ CCA
		AACACAGT CATCC CAGT	
		TTGTGTCA GTAGG GTCA	
		A A__	
GAM950	RIG 3'	CGACAGGCAAAAGAGATTTTG 13106	AAT A
		CAAAATCTCTT CTT TCG	

GTTTTAGAGAA GGA AGC
 AAC C
 GAM950 GOLPH3 3' AGGATTAAGAATTTTGT 22684 C
 AAAAAAT TCTTAATCTT
 ||||| |||||
 TGTTTTA AGAATTAGGA

 —
 GAM951 FABP2 3' CAATTTTCCAGGGCTCAAA 5623 — —
 TTT AGCCC GGAAAATTG
 || ||| |||||
 AAA TCGGG CCTTTTAAC
 C A
 GAM951 LOC114971 3' CAATCTTCCAGAGGGATGGGGC 36208 AGCCC A
 A TGTCCCATTT GGAA ATTG
 ||||| ||| |||
 ACGGGGTAGG CCTT TAAC
 GAGA_ C
 GAM952 B4GALT4 3' TGTTACAGCTCATTGTTGAG 9862 GTTA
 TTCAACGG AGCTGTAACA
 ||||| |||||
 GAGTTGTT TCGACATTGT
 AC__
 GAM952 CCNT2 3' TTTGTTACAAAGCCACTGA 27771 ACG AAGC
 TCA GGTT TGTAACAAA
 || ||| |||||
 AGT CCGA ACATTGTTT
 CA_ A__
 GAM952 FLRT2 3' TTTGTTACAGCCTCACCTG 14890 TAA
 CGGGT GCTGTAACAAA
 |||| |||||
 GTCCA CGACATTGTTT
 CTC
 GAM952 NEO1 3' TTGGAACCTTAACCCTTGAA 8321 C CTGTAA
 TTCAA GGGTTAAG CAA
 |||| ||||| |||
 AAGTT CCAATTC GTT
 — AAG__
 GAM952 PPARGC1 3' TTTGTTACAGCTATGCACTGT 14934 _ TA
 ACGG GT AGCTGTAACAAA
 |||| || |||||
 TGTC CG TCGACATTGTTT
 A TA
 GAM952 C21orf100 3' TTTGTTACAGCAGCACTG 29650 _ AA
 CGG GTT GCTGTAACAAA
 ||| || |||||
 GTC CGA CGACATTGTTT
 A _
 GAM952 DKFZP434N178 3' TTGCTACAGCTTTTATTTGTGA 35600 A T_ A
 A TTCA CGGGT AAGCTGTA CAA
 |||| |||| ||||| |||

AAGT GTTTA TTCGACAT GTT
 _ TT C
 GAM952 DSCR6 3' TACCCTTAACCCATGAA 21031 AC CT
 TTCA GGGTTAAG GTA
 ||| ||||| |||
 AAGT CCCAATTC CAT
 A_ C_
 GAM952 FACTP140 3' ACAGTTTCTGTTGAA 14046 TTA
 TTCAACGGG AGCTGT
 ||||| |||||
 AAGTTGTCT TTGACA

 GAM952 FLJ23360 3' TTTGTTTTCTCCCTTAACCCTC 23338 AC CTGT_
 TGAA TTCA GGGTTAAG AACAAA
 ||| ||||| |||||
 AAGT CCCAATTC TTGTTT
 CT CCTCTT
 GAM952 HSA250839 3' TTGTTACATCCTGCTGAA 20440 A TTAAGC
 TTCA CGGG TGTAACAA
 ||| ||| |||||
 AAGT GTCC ACATTGTT
 C T____
 GAM952 LOC143943 5' TTGTGCCAGACCCGTTGAA 40385 TAAG TA
 TTCAACGGGT CTG ACAA
 ||||| ||| |||
 AAGTTGCCCA GAC TGTT
 ____ CG
 GAM952 LOC151610 3' TTGTTACAGCTATGTG 39139 G TA
 CG GT AGCTGTAACAA
 || || |||||
 GT TA TCGACATTGTT
 G _
 GAM952 LOC200609 5' TGTTACAGCTAGTTGA 43339 GGGTTA
 TCAAC AGCTGTAACA
 |||| |||||
 AGTTG TCGACATTGT
 A____
 GAM953 EHD4 3' GGGGGCTTACCAGCAAAGC 29256 ATC TT
 GCTTTGTTG TA TCCCT
 ||||| || |||||
 CGAAACGAC AT GGGGG
 C_ TC
 GAM953 EXTL2 5' AGGGAAATAAATCGGCTGGC 7160 TT C
 GCT GTTGAT TATTTCCCT
 || ||||| |||||
 CGG CGGCTA ATAAAGGGA
 T_ A
 GAM953 IL1F5 3' GGAAACAGATCTCAGCAAAGC 14603 _ A
 GCTTTGTTGA TCT TTTCC
 ||||| ||| |||||

			CGAAACGACT AGA AAAGG	
			CT C	
GAM953	S100A5	5'	AGGGAAATAAAGGCAGAAGGC 8876	G ATC_
			GCTTT TTG TATTTCCCT	
			CGGAA GAC ATAAAGGGA	
			_ GGAA	
GAM953	C12orf2	3'	AGGGAAATGCAAATCAAAGC 40290	TTGATC
			GCTTTG TATTTCCCT	
			CGAAAC GTAAAGGGA	
			TAAAC_	
GAM953	C20orf38	3'	GGAAATAGATGGCTTAAAGT 20323	TTG_
			GCTTTG ATCTATTTC	
			TGAAAT TAGATAAAGG	
			TCGG	
GAM953	C6orf5	3'	AGGGACATCAACAAAGCTG 17779	CTATT
			TAGCTTTGTTGAT TCCCT	
			GTCGAAACAATA AGGGA	
			C_	
GAM953	CRTAC1	3'	GGAAGTCACAAAGCTA 19827	T TCTAT
			TAGCTTTGT GA TTCC	
			ATCGAAACA CT AAGG	
			_ C_	
GAM953	DKFZp547A023	3'	AAATAAATAGGCAGAGCTA 35940	TG C
			TAGCTTTGT AT TATTT	
			ATCGAGACG TA ATAAA	
			GA A	
GAM953	FLJ10314	5'	AGGGAAACAATGTGTTCAAGGC 19815	TTGATCTA_
	TA		TAGCTTTG TTTCCCT	
			ATCGGAAC AAAGGGA	
			TTGTGTAAC	
GAM953	GIT2	3'	GGAACATGGGGACCAACAAAGC 16604	A AT_
			GCTTTGTTG TCT TTCC	
			CGAAACAAC AGG AAGG	
			C GGTAC	
GAM953	GIT2	3'	GGAACATGGGGACCAACAAAGC 27686	A AT_
			GCTTTGTTG TCT TTCC	
			CGAAACAAC AGG AAGG	
			C GGTAC	
GAM953	GIT2	3'	GGAACATGGGGACCAACAAAGC 27699	A AT_
			GCTTTGTTG TCT TTCC	

			CGAAACAAC AGG AAGG		
			C GGTAC		
GAM953	KIAA1128	3'	AGGGAAAATAATAAAGC 33964	ATCTA	
			GCTTTGTTG TTTCCCT		
			CGAAATAAT AAAGGGA		
			CA__		
GAM953	LASP1	3'	GGAAAGAGGCATCAAAGCTA 12801	T A A	
			TAGCTTTG TG TCT TTTCC		
			ATCGAAAC AC GGA AAAGG		
			T _ G		
GAM953	MGC30052	3'	GAAAATTTTCACAGAGCTA 29543	T TCTA	
			TAGCTTTGT GA TTTC		
			ATCGAGACA CT AAAG		
			_ TTA_		
GAM953	LOC149386	3'	AGGGAAATGCAAATCAAACTA 40985	C TTGATC	
			TAG TTTG TATTTCCCT		
			ATC AAAC GTAAAGGGA		
			A TAAAC_		
GAM953	LOC154789	5'	AGAGAAACCCTGAACAAAGCTG 39487	GATCTA C	
			TAGCTTTGTT TTTC CT		
			GTCGAAACAA AAAG GA		
			GTCCC_ A		
GAM953	LOC158563	3'	AAGTAGCTTCAACCAAAGCTA 39866	_ T_	
			TAGCTTTG TTGA CTATTT		
			ATCGAAAC AACT GATGAA		
			C TC		
GAM953	LOC255270	5'	AGGGAAATAAAGGCAGAAGGC 45389	G ATC_	
			GCTTT TTG TATTTCCCT		
			CGGAA GAC ATAAAGGGA		
			_ GGAA		
GAM953	LOC51026	3'	TAGGGAAACATTTCAACAGC 18142	TT TCTA	
			GCT GTTGA TTTCCCTA		
			CGA CAACT AAAGGGAT		
			_ TTAC		
GAM954	GATM	3'	GTTTTTAATATTCTCATCT 7225	TCT_	
			AGATGAGAAT AAAAC		
			TCTACTCTTA TTTTG		
			TAAT		
GAM954	HIF1A	3'	AGTAATTTTAGAAGCATTATTT 7264	GAA C	
	TA		TAAGATGA TTCTAAAA TACT		

			ATTTTATT AAGATTTT ATGA		
			ACG A		
GAM954	AUTL1	3'	TAGTTTCAAAATTCTCAGTTTG 26650	A	CTA
			TAAG TGAGAATT AAATA		
			GTTT ACTCTTAA TTTGAT		
			G AAC		
GAM954	PMAIP1	3'	AGTTAGTTCTCATCT 22099	CTAA	
			AGATGAGAATT AACT		
			TCTACTCTTGA TTGA		

GAM954	PRO2037	3'	TTTAAATTCTCATCTTA 20688	C	
			TAAGATGAGAATT TAAA		
			ATTCTACTCTTAA ATTT		

GAM954	LOC149711	3'	AGTAATTTTTTAAATATTTTCATC 41069	_ CT	C
			TTA TAAGATGAGA ATT AAAA TACT		
			ATTCTACTTT TAA TTTT ATGA		
			A AT A		
GAM954	LOC158156	3'	AGTAAGAAGGGATTCTCATC 39737	AAAAC	
			GATGAGAATTCT TACT		
			CTACTCTTAGGG ATGA		
			AAGA_		
GAM954	LOC162137	3'	TTTLAGAACTCTTCATCTTA 42116	_ A	
			TAAGATGA GA TTCTAAAA		
			ATTCTACT CT AAGATTTT		
			T C		
GAM955	ATP11A	3'	CTGGGATGAAGAGTCCCCCTCC 37806	AAA	TT
			GGAGG ATTCTTCAT CAG		
			CCTCC TGAGAAGTA GTC		
			CCC GG		
GAM955	BAALC	3'	TCTGGAAGTATTTTCCTCC 24199	T	ATTT
			GGAGGAAAAT CTTC CAGA		
			CCTCCTTTTA GAAG GTCT		
			T _____		
GAM955	CYP3A4	3'	TCTGAAATGAAGATGGGCTTC 18932	AAAAT	
			GAGG TCTTCATTTT CAGA		
			CTTC AGAAGTAAAGTCT		
			GGGT_		
GAM955	DYRK2	5'	CTGAAATGCATTTTCCTCT 9631	TCTT	
			GGAGGAAAAT CATTTT CAG		

TCTCCTTTTA GTAAAGTC
 C___
 GAM955 DYRK2 5' CTGAAATGCATTTTCCTCT 13207 TCTT
 GGAGGAAAAT CATTTTCAG
 ||||| |||||
 TCTCCTTTTA GTAAAGTC
 C___
 GAM955 MAPRE2 3' TTCTAGAATAAAGAATTTTCCC 15549 GA C TC
 TC G GGAAAATTCTT ATT AGAA
 | ||||| || ||||
 C CCTTTTAAGAA TAA TCTT
 TC A GA
 GAM955 C5orf4 5' TTCTGAAATTGGGTCTCCTCC 18477 AA TTC
 GGAGGA ATTC ATTTTCAGAA
 |||| || |||||
 CCTCCT TGGG TAAAGTCTT
 CC T___
 GAM955 C5orf4 3' TTCTGAAATTGGGTCTCCTCC 26186 AA TTC
 GGAGGA ATTC ATTTTCAGAA
 |||| || |||||
 CCTCCT TGGG TAAAGTCTT
 CC T___
 GAM955 CAS1 3' CTGAAATGATTTTCTTCC 23180 TTCT
 GGAGGAAAA TCATTTTCAG
 ||||| |||||
 CCTTCTTTT AGTAAAGTC
 T___
 GAM955 DKFZp434F142 3' TCTGAAGACCCAAATCGTCCTC 25996 AA CTCA
 C GGAGGA ATT TTTCAGA
 |||| || |||||
 CCTCCT TAA GAAGTCT
 GC ACCCA
 GAM955 DKFZP434K1772 3' CTGAAATGGTTCCCAACC 33632 A_ AATTCT
 GG GGAA TCATTTTCAG
 || || |||||
 CC CCTT GGTAAGTC
 AC _____
 GAM955 FHOD2 5' AGGTGAAGAATCCTCC 36551 AAA
 GGAGGA TTCTTCATTT
 |||| |||||
 CCTCCT AAGAAGTGGA

 GAM955 FLJ14437 5' GGCGTGAAGAATTTCCCTCT 26309 A T
 GGAGG AAATTCTTCAT TC
 |||| ||||| ||
 TCTCC TTTAAGAAGTG GG
 C C
 GAM955 KIAA0084 5' TCTGTATGGCACAACTTTTCCT 33807 ATTCT__ TT
 CC GGAGGAAA TCAT CAGA
 ||||| || ||||

			CCTCCTTT	GGTA GTCT		
			CAAACAC	T_		
GAM955	MGC3130	3'	TTCTGAAATAAAGCATCTCC	23462	AAAATT	C
			GGAGG	CTT ATTTTCAGAA		
			CCTCT	GAA TAAAGTCTT		
			AC__	A		
GAM955	PKNOX2	3'	CTGAAATGAATGTATTTCTCC	43694	A	TC
			GGAGGAA	AT TTCATTTTCAG		
			CCTCTTT	TG AAGTAAAGTC		
			A	T_		
GAM955	SBB103	3'	TCTGGAAAAATTTCTCC	12368	A	CTTCA
			GGAGGAAA	TT TTTCAGA		
			CCTCCTTT	AA AAGGTCT		
			A	_____		
GAM955	SCOP	3'	CTGAACCCATTTTCTCC	44103	TCTTCAT	
			GGAGGAAAAT	TTCAG		
			CCTCCTTTTA	AAGTC		
			CCC	_____		
GAM955	TIP120A	3'	TTCTGAAATAAAAGACATCTCC	20517	AAAAT	C_
			GGAGG	TCTT ATTTTCAGAA		
			CCTCT	AGAA TAAAGTCTT		
			AC__	AA		
GAM955	TRIAD3	3'	GGATGGAGAACCCTCC	45349	AAAA	
			GGAGG	TTCTTCATTT		
			CCTCC	AAGAGGTAGG		
			C	_____		
GAM955	VAV3	3'	CTGATGGAAATATTTCTCC	12759	ATTC	ATT
			GGAGGAAA	TTC TCAG		
			CCTCCTTT	AAG AGTC		
			ATA_	GT_		
GAM955	ZNF361	5'	CTAAAATGAAGAAGCTTC	20635	AA	C
			GAA	TTCTTCATTT AG		
			CTT	AAGAAGTAAA TC		
			CG	A		
GAM955	LOC144161	3'	TTCTGAAAGAAAGAATTTTGCC	40389	A	_ CA
	CC		GG GG	AAAATTCTT TTTCAGAA		
			CC CC	TTTAAAGAA AAAGTCTT		
			_ G	AG		
GAM955	LOC150035	5'	GAAGGAAGAATTCCCCC	41121	A	AA A
			GG GG	AATTCTTC TTTC		

CC CC TTAAGAAG GAAG
 _ CC _
 GAM955 LOC151098 5' TCTGAAATGAAGACTCCTC 39049 AAAT
 GAGGA TCTTCATTTCAGA
 |||| |||||
 CTCCT AGAAGTAAAGTCT
 C__
 GAM955 LOC219540 5' CTGAAATGCCTCTTCTTCC 44957 AATTCTT
 GGAGGAA CATTTCAG
 ||||| |||||
 CCTTCTT GTAAAGTC
 CTCC__
 GAM955 LOC257475 5' TCTAATCAAGAGAATTTTGCTC 35860 G CATTTC
 C GGAG AAAATTCTT AGA
 ||| ||||| ||
 CCTC TTTTAAGAG TCT
 G AACTAA
 GAM956 JAZ1 3' CACCATCAGATGCAGTTCC 17656 GGTT C A A
 GGAAT CATCT AT GTG
 |||| |||| ||
 CCTTG GTAGA TA CAC
 AC__ C C
 GAM956 NEBL 3' CACTTTGGAATCACCCCA 13099 AA TCTAAT
 TGG TGGTTCCA AGTG
 || ||||| ||
 ACC ACTAAGGT TCAC
 CC T____
 GAM956 TEM7 3' CACTAAAGCTAACCATT C 21671 CCAT AA
 GAATGGTT CT TAGTG
 ||||| || ||||
 CTTACCAA GA ATCAC
 TC__ A_
 GAM956 FLJ11274 5' CACTCTCTTGGAACCA 20397 AA TCTAAT
 TGG TGGTTCCA AGTG
 || ||||| ||
 ACC ACCAAGGT TCAC
 _ TCTC__
 GAM956 MGC12981 3' CACTACTTTGAAACCATTCTA 26142 C TCTAA
 TGGAATGGTT CA TAGTG
 ||||| || ||||
 ATCTTACCAA GT ATCAC
 A TTC__
 GAM956 LOC143310 5' TCACTATTAAATAACAGTCC 37610 ATG CC C
 GGA GTT AT TAATAGTGA
 || || || |||||
 CCT CAA TA ATTATCACT
 GA_ A_ A
 GAM957 GOLGA4 3' TTGGCAGTGTCTCTGAGA 30165 CA ATAC A
 TC AGA ATGACACT CCAA
 || || ||||| ||||

AG TCT TACTGTGA GGTT
 AG C___ C
 GAM957 ODF2 3' TGGAATGCATTTATTCTTG 8389 C A CTA
 CAAGAATA ATG CA CCA
 ||||| ||| || |||
 GTTCTTAT TAC GT GGT
 T _ AA_
 GAM957 PAFAH1B1 3' TTGACAGTGTCAATTTATGTTG 6015 GA C_ AC
 GA TCCAA ATA ATGACACT CAA
 |||| ||| ||||| |||
 AGGTT TAT TACTGTGA GTT
 G_ TT CA
 GAM957 SRD5A2 5' TGGTATGGCTATTCTTG 29888 CATGA C
 CAAGAATA CA TACCA
 ||||| || |||||
 GTTCTTAT GT ATGGT
 CG___ _
 GAM957 TRPS1 5' TAGTGTGGGTGTCTTG 15358 A A
 CAAGA TAC TGACACTA
 |||| ||| |||||
 GTTCT GTG GTTGTGAT
 _ _
 GAM957 C20orf21 3' TTGGCAGAAATTGTGTTCTT 19443 TGACA A
 AAGAATACA CT CCAA
 ||||| || |||||
 TTCTTGTGT GA GGTT
 TAAA_ C
 GAM957 DKFZP564O0423 3' TGGCAGGATCATTCTTGGA 44071 ATAC CA A
 TCCAAGA ATGA CT CCA
 ||||| ||| || |||
 AGGTTCT TACT GA GGT
 _ AG C
 GAM957 FLJ13072 5' TTGATAGTGTTAGCATTCTTG 43238 ACA C
 A TCCAAGAAT TGACACTA CAA
 ||||| ||||| |||
 AGGTTCTTA ATTGTGAT GTT
 CG_ A
 GAM957 FLJ20055 3' TGGAGTCACAGTATTCTTGGA 19147 A_ A
 TCCAAGAATAC TGAC CTA
 ||||| ||| |||
 AGGTTCTTATG ACTG GGT
 AC A
 GAM957 MGC14798 3' TAGTGCCAACTTTCTTGGA 27939 TACA A
 TCCAAGAA TG CACTA
 ||||| || |||||
 AGGTTCTT AC GTGAT
 TCA_ C
 GAM957 PPFIA4 3' TGGCATGTGTTTCTTGGA 34823 _ A
 TCCAAGAA TACATG CA
 ||||| ||||| ||

AGGTTCTT GTGTAC GT
 T G
 GAM957 PRDM8 5' TTGGTAGTGTGGCGCTCCTG 21492 A ATACA
 CA GA TGACACTACCAA
 || || |||||
 GT CT GTTGTGATGGTT
 C CGCG_

GAM957 LOC129607 3' TGGCATAGTAAACATTTTCTTG 36977 TAC AC_ _
 GA TCCAAGAA ATG ACTA CCA
 ||||| || ||| |||
 AGGTTCTT TAC TGAT GGT
 T_ AAA AC

GAM957 LOC196424 3' AGTTAATGTGCTTTCTTGGA 42370 _ GAC
 TCCAAGAA TACAT ACT
 ||||| |||| |||
 AGGTTCTT GTGTA TGA
 TC AT_

GAM957 LOC199692 3' GTAGTGA CTGTATTCTTG 29812 TGA
 CAAGAATACA CACTAC
 ||||| |||||
 GTTCTTATGT GTGATG
 CA_

GAM957 LOC199848 5' AGTAGTTATTATTTTGGGA 43250 C _
 TCCAAGAATA ATGAC ACT
 ||||| ||||| |||
 AGGTTTTTAT TATTG TGA
 _ A

GAM957 LOC90841 3' TAGTGTCA TTTTCAGGA 32113 AA TAC
 TCC GAA ATGACACTA
 || || |||||
 AGG CTT TACTGTGAT
 A_ _

GAM958 B4GALT5 3' TTGCATTGCAAAGCTCTT 11172 A GG TT
 AAGA GCTT TGT TGCAA
 |||| |||| || |||||
 TTCT CGAA ACG ACGTT
 _ _ TT

GAM958 BSG 3' TTGCAAGATTCCAAGTTCT 7458 G T
 AGAA CTTGG GTTTTGCAA
 |||| |||| |||||
 TCTT GAACC TAGAACGTT
 _ T

GAM958 BSG 3' TTGCAAGATTCCAAGTTCT 33669 G T
 AGAA CTTGG GTTTTGCAA
 |||| |||| |||||
 TCTT GAACC TAGAACGTT
 _ T

GAM958 CYP8B1 3' TTGCAAACATCAGCCTC 10629 A T T
 GA GCT GGTGTTT GCAA
 || |||| ||||| |||

			CT CGA CTACAAA CGTT		
			C _ _		
GAM958	DMPK	3'	GCAAAGTGCAAAGCTTTCTT 10665	_	G TG
			AAGAA GCTT G TTTTGC		
			TTCTT CGAA C GAAACG		
			T A GT		
GAM958	DXYS155E	3'	TGCAAAGCCAAGACCCTT 11544	AAG	GT
			AAG CTTGGT TTTGCA		
			TTC GAACCG AAACGT		
			CCA _		
GAM958	EPO	5'	TGCACCGCCGAGCTTC 6468	TTT	
			GAAGCTTGGTG TGCA		
			CTTCGAGCCGC ACGT		
			C _		
GAM958	GABPB1	3'	TGCAAAATCTGTGCTTTTT 11761	T T	
			AAGAAGC TGG GTTTTGCA		
			TTTTTCG GTC TAAAACGT		
			T _		
GAM958	HNRPDL	3'	CAAAACTGGTAAGTTTCTT 11949	G _	
			AAGAAGCTTG T GTTTTG		
			TTCTTTGAAT G CAAAAC		
			G T		
GAM958	LDHB	5'	TGCTCAACCCAAGCTTCT 8090	T TT	
			AGAAGCTTGG GTT GCA		
			TCTTCGAACC CAA CGT		
			_ CT		
GAM958	MAN2C1	5'	TTGCAGGGGCCAGAACTTCTT 36103	C_	GT
			AAGAAG TTGGT TTTGCAA		
			TTCTTC GACCG GGACGTT		
			AA _		
GAM958	MAT1A	3'	TTGCAGGTGGCCAAGTTCCT 43670	A	GT
			AG AGCTTGGT TTTGCAA		
			TC TTGAACCG GGACGTT		
			C GT		
GAM958	MTL5	3'	TGCAGCAACAACCAGGCT 11360	_ _	
			AGCTTGGT GTT TTGCA		
			TCGGACCA CAA GACGT		
			A C		
GAM958	MYH11	3'	TGCAAACCTTTCCAACCTTCT 8302	C	TGT_
			AGAAG TTGG TTTGCA		

			TCTTC AACC AAACGT		
			_ TTTCC		
GAM958	MYH11	3'	TGCAAACCTTTCCAAGCTTCT 23144	C	TGT__
			AGAAG TTGG TTTGCA		
			TCTTC AACC AAACGT		
			_ TTTCC		
GAM958	NTRK2	3'	TGGAGGCCACCAAGCTGCT 12848	A	TT G
			AG AGCTTGGTG TT CA		
			TC TCGAACCAC GA GT		
			G CG G		
GAM958	PPIF	3'	TGCAACACTAAGCTTC 12283	C	TT
			GAAG TTGGTGT TGCA		
			CTTC AATCACA ACGT		
			- -		
GAM958	PROS1	3'	TGCAAAGATGGAAAAGCTTCTT 42257		GGTG__
			AAGAAGCTT TTTTGCA		
			TTCTTCGAA GAAACGT		
			AAGGTA		
GAM958	RTN3	3'	TGCATTCCAAGCTTTTT 36587		TGTTT
			AAGAAGCTTGG TGCA		
			TTTTTCGAACC ACGT		
			TT__		
GAM958	SECTM1	3'	GCACCTGCCGAGCCTCTT 8911	A	TTT
			AAGA GCTTGGTG TGC		
			TTCT CGAGCCGT ACG		
			C CC_		
GAM958	SPTBN4	3'	TTGCAAAACGTCGATCTCCT 24885	A C	GT
			AG AG TTG GTTTTGCAA		
			TC TC AGC CAAAACGTT		
			C T TG		
GAM958	TRIP15	3'	TTGCAAAATGTCAATTCT 10433	GC	TG
			AGAA TTGG TTTTGCAA		
			TCTT AACT AAAACGTT		
			_ GT		
GAM958	ZFP36L1	3'	TGCAAATTGAGTTTCTT 11366	TG	GTT
			AAGAAGCT GT TTGCA		
			TTCTTTGA TA AACGT		
			GT _		
GAM958	ADAR3	5'	TTGCAACCTCAAGCTTC 20787	T	TT
			GAAGCTTGG GT TGCAA		

CTTCGAACT CA ACGTT
C _

GAM958 APOL3 5' TTGCAGAGATCCAGCCCCT 15676 AA T TG
AG GCT GG TTTTGCAA
|| ||| || |||||
TC CGA CC GAGACGTT
CC _ TA

GAM958 C17orf26 3' TGGGACAACAAGCTTCTT 29189 G TT
AAGAAGCTTG TGTT G
||||||| ||| |
TTCTTCGAAC ACAG T
A GG

GAM958 C19orf7 3' TGCAGGCCAAGCTCTT 30637 A GTT
AAGA GCTTGGT TTGCA
||| ||||| ||||
TTCT CGAACCG GACGT

GAM958 C1orf34 3' TTGCAAAACCTCCGAGCCTTC 30441 _ T_
GAAG CTTGG GTTTTGCAA
||| |||| |||||
CTTC GAGCC CAAAACGTT
C TC

GAM958 C20orf150 3' GCCACCAAGCTTTTT 32598 TTTT
AAGAAGCTTGGTG GC
||||||| ||
TTTTTCGAACCAC CG

GAM958 C22orf5 3' CAGGACCACCAAGCCCCT 14583 AA _
AG GCTTGGTG TTTTG
|| ||||| ||||
TC CGAACCAC AGGAC
CC C

GAM958 CLSTN2 3' TTGCAATCATTGCAGCTTCTT 22694 _ TT
AAGAAGCT TGGTG TTGCAA
||||| |||| |||||
TTCTTCGA GTTAC AACGTT
C T_

GAM958 CNNM4 3' TGCAAAACTCCAGGCTTC 21428 T
GAAGCTTGG GTTTTGCA
||||| |||||
CTTCGGACC CAAAACGT
T

GAM958 EPB41L1 3' TGCAAAACCTACCTTC 34945 CT T
GAAG TGG GTTTTGCA
||| || |||||
CTTC ATC CAAAACGT
C_ _

GAM958 EVI5 3' TTGCAAAATGACTGCTTT 12217 TT _
GAAGC GGT GTTTTGCAA
|||| ||| |||||

			TTTCG TCA TAAAACGTT		
			___ G		
GAM958	FLJ10619	3'	TGCAAAACATTGGTTTTCT	19969	C TG
			AGAAG T GTGTTTTGCA		
			TCTTT G TACAAAACGT		
			T GT		
GAM958	FLJ10751	3'	TGCATGCCAAGCTGCCT	20096	A_ TTT
			AG AGCTTGGTG TGCA		
			TC TCGAACCGT ACGT		
			CG		
GAM958	FLJ10751	3'	TGCATGCCAAGCTGCCT	20195	A_ TTT
			AG AGCTTGGTG TGCA		
			TC TCGAACCGT ACGT		
			CG		
GAM958	FLJ12934	3'	CAAAAACAAGCTTCTT	23176	GTG
			AAGAAGCTTG TTTTG		
			TTCTTCGAAC AAAAC		
			A_		
GAM958	FLJ14642	3'	TTGCCTGGACCAAGCTACT	26596	A G TT
			AG AGCTTGGT TT GCAA		
			TC TCGAACCA GG CGTT		
			A _ TC		
GAM958	FLJ20054	3'	TTGCATCCAAGCTTCT	21131	TGTTT
			AGAAGCTTGG TGCAA		
			TCTTCGAACC ACGTT		
			T_		
GAM958	FLJ20772	3'	TTGCAAAATGAGAGTTTCTT	19667	GG
			AAGAAGCTT TGTTTTGCAA		
			TTCTTTGAG GTAAAACGTT		
			A_		
GAM958	FLJ21657	5'	TGCAGGTCCAGCTTCTT	22858	T TGT
			AAGAAGCT GG TTTGCA		
			TTCTTCGA CC GGACGT		
			_ T_		
GAM958	FLJ21657	3'	TTGCAAAACCTTTTCT	22859	CTT T
			AGAAG GG GTTTTGCAA		
			TCTTT TC CAAAACGTT		

GAM958	FLJ32334	3'	CAAGACACCAAACCCTTC	29365	C_
			GAAG TTGGTGTTTTG		

CTTC AACCACAGAAC
 CCA
 GAM958 H11 5' TTGCAAACCCGCCTC 15695 A TT T
 GA GC GG GTTTTGCAA
 || || || |||||
 CT CG CC CAAAACGTT
 C _ _
 GAM958 HABP2 3' TTGCACAATATCACCAGGCTTC 10345 TTT__
 TT AAGAAGCTTGGTG TGCAA
 ||||| ||||
 TTCTTCGGACCAC ACGTT
 TATAAC
 GAM958 ITGB5 3' TTGCAAATGTCAGTTTC 29924 T TG T
 GAAGCT GG TTT GCAA
 |||| || || ||||
 CTTTGA CT AAA CGTT
 _ GT _
 GAM958 KIAA0040 5' TGCTCAACCCAAGCTTCT 16100 T TT
 AGAAGCTTGG GTT GCA
 ||||| || ||
 TCTTCGAACC CAA CGT
 _ CT
 GAM958 KIAA0205 3' TTGCAAATGCACTTTTT 17009 CTG
 AAGAAG GTGTTTTGCAA
 |||| |||||
 TTTTC CGTAAAACGTT
 A__
 GAM958 KIAA0319 3' TTGCATGTAGCAAGCTTT 16767 G TTT
 GAAGCTTG TG TGCAA
 ||||| || ||||
 TTTTGAAC AT ACGTT
 G GT_
 GAM958 KIAA0481 5' TGCAGGCTCAGGCTTCT 35572 T T
 AGAAGCTTGG GTTT GCA
 ||||| || ||
 TCTTCGGACT CGGA CGT
 _ _
 GAM958 KIAA1084 3' TGTAGCACCAAAATTCT 17140 GC TT
 AGAA TTGGTGT TGCA
 ||| ||||| |||
 TCTT AACCACG ATGT
 AA _
 GAM958 KIAA1253 3' TGCAAAACACTAGGCTTT 44133
 GAAGCTTGGTGTTTTGCA
 |||||
 TTTTCGGATCACAAAACGT
 GAM958 KIAA1500 3' TGTGAGACTCCAAGCTCCTT 32071 A T TG
 AAG AGCTTGG GTTT CA
 || ||||| ||| ||

			TTC TCGAACC CAGA GT		
			C T GT		
GAM958	KIAA1673	3'	TTGCAAAGAGTAGCTTTTT 35027		TGGTG
			AAGAAGCT TTTTGCAA		
			TTTTTCGA GAAACGTT		
			TGA__		
GAM958	KIAA1719	5'	TTGAGGCCACCAAGCTCCT 33827	A	TT G
			AG AGCTTGGTG TT CAA		
			TC TCGAACCAC GA GTT		
			C CG _		
GAM958	KIAA1817	3'	TGCAGAATCCAGCCCCT 33864	AA	T T
			AG GCT GG GTTTTGCA		
			TC CGA CC TAAGACGT		
			CC _ _		
GAM958	MGC3265	3'	GCCCACCAGGCTTCTT 23458		TTTT
			AAGAAGCTTGGTG GC		
			TTCTTCGGACCAC CG		
			C__		
GAM958	MKNK1	5'	TGGAAGACACCAACTTC 9795	C	G
			GAAG TTGGTGTTTT CA		
			CTTC AACACAGAA GT		
			_ G		
GAM958	PRO2955	3'	TTGCAAAGGGCCAAATTC 20623	C	G
			GAAG TTGGT TTTTGCAA		
			CTTT AACCG GAAACGTT		
			A G		
GAM958	PSTPIP2	3'	TTGCAAAGGGCCAAATTC 23684	C	G
			GAAG TTGGT TTTTGCAA		
			CTTT AACCG GAAACGTT		
			A G		
GAM958	SIMRP7	3'	TTGCACGTGTACCAAGCTT 44375		TTT_
			AAGCTTGGTG TGCAA		
			TTCGAACCAT ACGTT		
			GTGC		
GAM958	SS-56	5'	TGCGGAACCAGGCTTCTT 29991		GT
			AAGAAGCTTGGT TTTGCA		
			TTCTTCGGACCA AGGCGT		
			_		
GAM958	WAC	3'	TGCAAAATTAGCTTTTT 28157		TGGT
			AAGAAGCT GTTTTGCA		

			TTTTTCGA	TAAAACGT		
			T__			
GAM958	WAC	3'	TGCAAAATTAGCTTTTT	28158	TGGT	
			AAGAAGCT	GTTTTGCA		
			TTTTTCGA	TAAAACGT		
			T__			
GAM958	WAC	3'	TGCAAAATTAGCTTTTT	18743	TGGT	
			AAGAAGCT	GTTTTGCA		
			TTTTTCGA	TAAAACGT		
			T__			
GAM958	LOC112476	3'	TGCATCTTGCCAGGCTCCT	29753	A	TTT
			AG AGCTTGGTG	TGCA		
			TC TCGGACCGT	ACGT		
			C	TCT		
GAM958	LOC115073	5'	GCAGGACAAGGCTCT	36240	A	GG
			AGA GCTT	TGTTTTGC		
			TCT CGGA	ACAGGACG		
			- -			
GAM958	LOC124460	3'	TGCAAAAGGAGGTAAGTTTCT	37447		GTG__
			AGAAGCTTG	TTTTGCA		
			TCTTTGAAT	AAAACGT		
			GGAGG			
GAM958	LOC125929	3'	AAACATCCTCAGGCTTCT	37268		__
			AGAAGCTTG	GTGTTT		
			TCTTCGGAC	TACAAA		
			TCC			
GAM958	LOC129011	3'	TGCAAAATACAAGCTC	36967	A	G
			GA GCTTG	TGTTTTGCA		
			CT CGAAC	ATAAAACGT		
			- -			
GAM958	LOC129138	3'	CACAGCTCCCAGCTTCTT	29019		T T T
			AAGAAGCT	GG GTT TG		
			TTCTTCGA	CC CGA AC		
			C T C			
GAM958	LOC144308	3'	TTGCAAAAACCAACCTTC	40408	C	G
			GAAG TTGGT	TTTTGCAA		
			CTTC AACCA	AAAACGTT		
			C	-		
GAM958	LOC144699	3'	TTGCAATTTGCAAGCTTCTT	37771		G TT
			AAGAAGCTTG	TG TTGCAA		

TTCTTCGAAC GT AACGTT
 _ TT
 GAM958 LOC145508 3' CATAGCACCAAACCTCCTT 37887 A C T
 AAG AG TTGGTGTGTT TG
 ||| || ||||| ||
 TTC TC AACCACGA AC
 C A T
 GAM958 LOC146243 3' TGCAAAATCACTGCACCTT 40680 AA TT _
 AAG GC GGTG TTTTGCA
 ||| || ||| |||||
 TTC CG TCAC AAAACGT
 CA _ T
 GAM958 LOC146243 3' TGCAGGACCAGAGCCCCTT 40681 AA GGT
 AAG GCTT GTTTTGCA
 ||| ||| |||||
 TTC CGAG CAGGACGT
 CC AC_
 GAM958 LOC146332 5' TGCACTCATGCAAGCTTCT 38131 _ TTT
 AGAAGCTTG GTG TGCA
 ||||| ||| |||
 TCTTCGAAC TAC ACGT
 G TC_
 GAM958 LOC147077 3' TTGCAAAACATTGCTGCCT 38296 A_ TT
 AG AGC GGTGTTTTGCAA
 || ||| |||||
 TC TCG TTACAAAACGTT
 CG _
 GAM958 LOC149127 3' TTGCATGCTTCCAAGCCTTC 40952 _ T_ TT
 GAAG CTTGG GT TGCAA
 ||| |||| || ||||
 CTTT GAACC CG ACGTT
 C TT T_
 GAM958 LOC149271 5' TTGCAAAGCAAAGCCTC 38685 A GG
 GA GCTT TGTTTTGCAA
 || ||| |||||
 CT CGAA ACGAAACGTT
 C _
 GAM958 LOC152343 3' GCAAAACATGTTTTT 39262 TTG
 AGAAGC GTGTTTTGC
 |||| |||||
 TTTTGT TACAAAACG
 _
 GAM958 LOC152905 3' TGCATTCCAAGCTTTTT 30332 TGTTT
 AAGAAGCTTGG TGCA
 ||||| |||
 TTTTTCGAACC ACGT
 TT_
 GAM958 LOC153232 5' TGCTCCACCAGCTTCTT 41599 T TTTT
 AAGAAGCT GGTG GCA
 ||||| ||| |||

		TTCTTCGA CCAC CGT		
		CT__		
GAM958	LOC157657 3'	TTGCAAAAACACTGCCTC 39628	A TT	
		GA GC GGTGTTTT GCAA		
		CT CG TCACAAAA CGTT		
		C _ A		
GAM958	LOC157737 5'	TGTATGCAACAAGCTTC 41844	G TT	
		GAAGCTTG TGT TGCA		
		CTTCGAAC ACG ATGT		
		A T_		
GAM958	LOC158230 3'	TTGCAGGAGGGCAAGCCCCTT 39768	AA GTG	
		AAG GCTTG TTTTGCAA		
		TTC CGAAC AGGACGTT		
		CC GGG		
GAM958	LOC165693 5'	TGCAATACCAGCTCCTT 40189	A T TT	
		AAG AGCT GGTGT TGCA		
		TTC TCGA CCATA ACGT		
		C _ _		
GAM958	LOC169026 3'	TTGCAAAGAGACAAGCCTC 40270	A GTG	
		GA GCTTG TTTTGCAA		
		CT CGAAC GAAACGTT		
		C AGA		
GAM958	LOC196074 5'	TTGAGATCACCAGGCCTC 42323	A T G	
		GA GCTTGGTG TTT CAA		
		CT CGGACCAC AGA GTT		
		C T _		
GAM958	LOC200058 3'	TGCAAAGCAAAGGCTCCTT 42703	A GG	
		AAG AGCTT TGTTTTGCA		
		TTC TCGGA ACGAAACGT		
		C A_		
GAM958	LOC202152 5'	TGCGGGGCCCAAGTCCTT 42966	AA T	
		AAG GCTTGG GTTTTGCA		
		TTC TGAACC CGGGGCGT		
		C_ _		
GAM958	LOC220522 3'	TGCACAACAAGCTTCT 30355	G TTT	
		AGAAGCTTG TGT GCA		
		TCTTCGAAC ACA CGT		
		A _		
GAM958	LOC220753 3'	TTGCAGTATACAAGCTTTT 44664	G T	
		AGAAGCTTG TGT TTGCAA		

		TTTTCGAAC ATA GACGTT		
		_ T		
GAM958	LOC253258 3'	TGTGAACACCAACTTCT	46149	C TTG
		AGAAG TTGGTGT T CA		
		TCTTC AACACA A GT		
		_ _ GT		
GAM958	LOC253612 5'	TTGCAGGAGGCCAAGCTC	46258	A G
		GA GCTTGGT TTTTGCAA		
		CT CGAACCG AGGACGTT		
		_ G		
GAM958	LOC255057 3'	TGCAAAACACACTGGCTC	45663	A TG_
		GA GCT GTGTTTTGCA		
		CT CGG CACAAAACGT		
		_ TCA		
GAM958	LOC257482 3'	TGCAAAACAGCCTCCTTC	45237	CTT _
		GAAG GG TGTTTTGCA		
		CTTC CC ACAAAACGT		
		CT_ G		
GAM958	LOC90494 5'	TTGCAAAGAGCACGCCTCTT	31578	A TTG G
		AAGA GC GT TTTTGCAA		
		TTCT CG CG GAAACGTT		
		C CA_ A		
GAM958	LOC92405 3'	TGCACGGGACCCAGCTCCTT	34305	A T G TT
		AAG AGCT GGT T TGCA		
		TTC TCGA CCA G ACGT		
		C C G GC		
GAM958	LOC92578 5'	TGCAAAGCCAGAACTTCT	34608	C__ GT
		AGAAG TTGGT TTTGCA		
		TCTTC GACCG AAACGT		
		AAA _		
GAM959	HMG1 3'	ACAAAGCATATTAAATGGCAAT	11411	AAC_ A
	A	TGTTGT TAATAT CTTTGT		
		ATAACG ATTATA GAAACA		
		GTAA C		
GAM959	PIG8 3'	ACAAAGTGCCACTACAACA	11314	ACTAATA
		TGTTGTA TACTTTGT		
		ACAACAT GTGAAACA		
		CACC__		
GAM959	KIAA1095 3'	ACAAAATCATGATTAGTTACAA	33504	ATAC__
		TTGTAATAAT TTTGT		

		AACATTGATTA	AAACA		
		GTACTA			
GAM959	LOC145854 3'	ACAAAGCATATTAAATGGCAAT	38004	AAC_	A
	A	TGTTGT TAATAT CTTTGT			
		ATAACG ATTATA GAAACA			
		GTAA C			
GAM959	LOC158956 3'	ACAAAGCATATTAAATGGCAAT	33095	AAC_	A
	A	TGTTGT TAATAT CTTTGT			
		ATAACG ATTATA GAAACA			
		GTAA C			
GAM960	NARS 3'	TATCGTATAAAAATCTGCT	10890	TT C	
		GGC GTTT TATACGATA			
		TCG TAAA ATATGCTAT			
		TC A			
GAM960	SLC16A2 3'	TATCATATAGGGAAGAAACCTT	13272	C G_ TT	C
		AAGG TT T CTATA GATA			
		TTCC AA A GATAT CTAT			
		A GA GG A			
GAM960	KIAA0391 3'	CGTTTAGAAACAAAACCCCT	16137	C__	T
		AGG TTGTTTCTA ACG			
		TCC AACAAAGAT TGC			
		CAA T			
GAM961	COL19A1 3'	GCCACTCATATTAATTTA	7596	AT C	
		TAAATTAATAT GTG GC			
		ATTTAATTATA CAC CG			
		CT _			
GAM962	ADCY7 3'	AGACAACCTTGGACAACCTGTGA	6778	CGC T CC	
		TCACGGGT TTCG AG GTCT			
		AGTGTCCA AGGT TC CAGA			
		AC_ _ AA			
GAM962	CHRA1 3'	AGACAGCCAGAGGGAAAGCGAC	18901	_____	GTA C
	CC	GGGTCGCT TC GC GTCT			
		CCCAGCGA AG CG CAGA			
		AAGGG AC_ A			
GAM962	KIAA1538 5'	ACGGCTGCAGACCCATGA	35421	C GCTTC	
		TCA GGGTC GTAGCCGT			
		AGT CCCAG CGTCGGCA			
		A A_____			
GAM962	MGC2752 5'	AGACGGCTCGCACTGCGACCCG	38366	TT__	T
		CGGGTCGC CG AGCCGTCT			

GCCCAGCG GC TCGGCAGA
 TCAC _
 GAM962 LOC146445 3' AGAGCAAGCAAAGCGACCCTGA 40697 C C A_ CG
 TCA GGGTCGCTT GT GC TCT
 ||| ||||| || || |||
 AGT CCCAGCGAA CG CG AGA
 _ A AA _
 GAM963 EZFIT 3' GTAACAAAAGACCTTAGACTGG 22197 TTAGCG CA
 TCAGTCTA CTTT TTAC
 ||||| ||| ||||
 GGTCAGAT GAAA AATG
 TCCA_ AC
 GAM963 KIAA0009 3' TAATGAAAGCACTAAGTTTGG 16024 TCTA C
 TCAG TTAG GCTTTCATTA
 ||| ||| |||||
 GGTT AATC CGAAAGTAAT
 TG_ A
 GAM963 UBN1 3' GTAATGAAAGAGCGAATGACTG 18853 T A G
 A TCAGTC ATT GC CTTTCATTAC
 ||||| ||| || |||||
 AGTCAG TAA CG GAAAGTAATG
 _ G A
 GAM964 ANKTM1 3' ATTGCACAATATAGATCT 14257 C_
 GGATCTATA TGCAAT
 ||||| ||||
 TCTAGATAT ACGTTA
 AAC
 GAM964 CHES1 3' AATAATGGTACAGATCTTT 11696 A GCA
 AAGGATCT TACT ATTATT
 ||||| ||| |||||
 TTTCTAGA ATGG TAATAA
 C _
 GAM964 DGUOK 3' GAAGCCAGTACAGATCTTT 28136 A CAATTA
 AAGGATCT TACTG TTC
 ||||| |||| |||
 TTTCTAGA ATGAC AAG
 C CG_
 GAM964 DGUOK 3' GAAGCCAGTACAGATCTTT 28139 A CAATTA
 AAGGATCT TACTG TTC
 ||||| |||| |||
 TTTCTAGA ATGAC AAG
 C CG_
 GAM964 MARK3 5' GGAATAATTGCAATCCCCGATC 8192 TATAC_
 C GGATC TGCAATTATTCC
 |||| |||||
 CCTAG ACGTTAATAAGG
 CCCCTA
 GAM964 ZNF202 3' GGATAACTGCATAGATCC 9508 TAC A
 GGATCTA TGCA TTATTC
 ||||| ||| |||||

CCTAGAT ACGT AATAGG
 ____ C
 GAM964 C20orf121 3' GGAACCCTAAGTATAGACCT 23632 A GCAATTA
 AGG TCTATACT TTCC
 ||| ||||| |||
 TCC AGATATGA AAGG
 _ ATCCC_
 GAM964 FLJ14213 3' GGAAGTGTGTCAGTATAGACCC 24254 A _ ATTA
 GG TCTATACTG CA TTCC
 || ||||| || |||
 CC AGATATGAC GT AAGG
 C T G_
 GAM964 FLJ22794 5' GAATAATTGCAGTACTTCTCT 44030 TCTA
 GGA TACTGCAATTATTC
 ||| |||||
 TCT ATGACGTTAATAAG
 CTTC
 GAM964 FUSIP1 3' GAATAATTGAAGTCCCTT 13409 ATCTAT G
 AAGG ACT CAATTATTC
 ||| ||| |||||
 TTCC TGA GTTAATAAG
 C____ A
 GAM964 HCA4 3' AATAATTGCCTATATCCTT 38018 TC CT
 AAGGA TATA GCAATTATT
 |||| ||| |||||
 TTCCT ATAT CGTTAATAA
 _ C_
 GAM964 KIAA0157 3' GGAATAATTGCAGTATGTGT 25899 C
 AT TATACTGCAATTATTC
 || |||||
 TG GTATGACGTTAATAAG
 T
 GAM964 KIAA0310 3' GAATTAGCACAGATCCTT 39710 ATAC AATT
 AAGGATCT TGC ATTC
 ||||| ||| |||
 TTCCTAGA ACG TAAG
 C__ AT_
 GAM964 KIAA0884 3' AATTGCAAATATCAGATCCTT 34772 _ C_
 AAGGATCT ATA TGCAATT
 ||||| ||| |||||
 TTCCTAGA TAT ACGTTAA
 C AA
 GAM964 KIAA1077 5' GAATAATTGCAGAAAATCTT 36095 CTATA
 AGGAT CTGCAATTATTC
 |||| |||||
 TTCTA GACGTTAATAAG
 AAA_
 GAM964 KIAA1948 5' AATTTAAGTATAGATTCT 40076 GC
 AGGATCTATACT AATT
 ||||| |||

TCTTAGATATGA TTAA

AT

GAM964 LOC151556 5' GGAATAATCGCAAGTTCC 39133 T ATAC A
GGA CT TGC ATTATTCC
||| || ||| |||||
CCT GA ACG TAATAAGG
T ____ C

GAM964 LOC256946 3' GAATAATTGAAGTCCCTT 45359 ATCTAT G
AAGG ACT CAATTATTC
|||| ||| |||||
TTCC TGA GTTAATAAG
C ____ A

GAM965 HLCS 3' ATACAAGTCCACACCATCC 5990 AT GT TAA
GGAT TGTGG T TGTAT
|||| |||| | ||||
CCTA ACACC A ACATA
CC TG ____

GAM965 C13orf1 3' ATACACTAAATTCACATCACC 21688 ATAT A
GG TGTGGGTTTA TGTAT
|| ||||| ||||
CC ACACTTAAAT ACATA
ACT_ C

GAM965 DKFZp761B1514 3' ATACATTAACTTTTATTCTT 26045 TTGT
AAGGATA GGGTTTAATGTAT
||||| |||||
TTCTTAT TTCAAATTACATA
T ____

GAM966 EPB41L2 3' CATGCCCTTCGGCAGCATTCCA 7154 ATTA CA_
TGGAATGC TCGGA CATG
||||| |||| ||||
ACCTTACG GGCTT GTAC
AC_ CCC

GAM966 RDS 3' CTGAGAAATAGTGCACCTCCA 5863 A ____
TGGA TGCATTA TCGG
|||| ||||| ||||
ACCT ACGTGAT AGTC
C AAAG

GAM966 KIAA1946 3' GCATGTGTATTGTATCATCC 40118 ____ TTATCGG
GGA ATGCA ACACATGC
||| |||| |||||
CCT TATGT TGTGTACG
AC TA ____

GAM966 MGC3130 3' GCACGTGTCTGGTCACATCCA 23460 A CATT A
TGGA TG ATCGGACAC TGC
|||| ||| ||||| ||||
ACCT AC TGGTCTGTG ACG
_ AC_ C

GAM966 MGC4415 3' CACGTGCCTGTAGCATTCCA 25566 AT C A A
TGGAATGC TAT GG CAC TG
||||| ||| || ||| ||

			ACCTTACG ATG CC GTG AC		
			___ T _ C		
GAM966	PRO0611	3'	GCACGTGTCCAGGGACACTGCA 15304	TTA__ _	A
			TGCA TC GGACAC TGC		
			ACGT GG CCTGTG ACG		
			CACAG A C		
GAM966	LOC63929	3'	CACATGTCCATGCATTCCA 22639	TATC	CA
			TGGAATGCAT GGACA TG		
			ACCTTACGTA CCTGT AC		
			_____ AC		
GAM967	LOC161589	5'	ATTGACAAAAGAACCATTGA 40023	A G	
			TCAAT GTTC TTTTGTGCGAT		
			AGTTA CAAG AAAACAGTTA		
			C _		
GAM967	LOC202108	5'	ATCGACAAAAGAACCATTGA 42965	A G	
			TCAAT GTTC TTTTGTGCGAT		
			AGTTA CAAG AAAACAGCTA		
			C _		
GAM967	LOC202333	3'	AAAATCGACAAGAAAACCTTGA 42970	TA CG	
			TCAA GTT TTTTGTGCGATTTT		
			AGTT CAA AGAACAGCTAAAA		
			C_ A_		
GAM967	LOC221838	5'	ATCGACAAAAGAACCATTGA 44459	A G	
			TCAAT GTTC TTTTGTGCGAT		
			AGTTA CAAG AAAACAGCTA		
			C _		
GAM967	LOC221839	5'	ATCGACAAAAGAACCATTGA 44430	A G	
			TCAAT GTTC TTTTGTGCGAT		
			AGTTA CAAG AAAACAGCTA		
			C _		
GAM968	MAML1	3'	ATCATGGTGATTTTATC 16496	T AG	
			GATAAAATC AC GTGAT		
			CTATTTTAG TG TACTA		
			_ G_		
GAM968	KIAA0628	3'	CAAATGTAGATTTTACCAGA 16673	GA_	GG
			TC TAAAATCTACA TG		
			AG ATTTTAGATGT AC		
			ACC AA		
GAM968	KIAA1281	3'	ATTACAGATTTTATC 42963	ACAG	
			GATAAAATCT GTGAT		

CTATTTTAGA CATT

GAM968 MIG 3' CACCGAGATCCTTATCGAA 8245 A_ ACA
TTCGATAA ATCT GGTG
||||| ||| |||
AAGCTATT TAGA CCAC
CC G_

GAM968 LOC222865 3' TATCACCTTATTTTATCGAA 44623 CTAC
TTCGATAAAAT AGGTGATA
||||||| |||||
AAGCTATTTTA TCCACTAT
T_

GAM968 LOC92303 3' ATCAGAACTTGGATTTTATC 34134 C G_
GATAAAATCTA AG TGAT
||||||| || |||
CTATTTTAGGT TC ACTA
_ AAG

GAM969 KIAA0534 3' ACAATTGATGTTTAGTACTAT 35375 A ATTT
ATA TAC ATATCAATTGT
||| ||| |||||
TAT ATG TGTAGTTAACA
C ATT_

GAM969 KIAA1708 3' ACAATTGATATATTGCTTTATT 33271 TA TT
AATAA CA TATATCAATTGT
|||| || |||||
TTATT GT ATATAGTTAACA
TC T_

GAM969 LOC157464 5' TTGATATAAATGTATTTTTA 41796 T
TAA AATACATTTATATCAA
||| |||||
ATT TTATGTAAATATAGTT
T

GAM970 B29 3' TAAGTATACATTTTATTAATT 25684 T_ C
TA TAAATTAATA ATGTG ACTTA
||||||| ||| |||
ATTTAATTAT TACAT TGAAT
TTT A

GAM970 CD2AP 3' AAGTGCAATGACTTGATTTA 14431 TATATG
TAAATTAA TGCACCT
||||| |||||
ATTTAGTT ACGTGAA
CAGTA_

GAM970 MDM4 3' ATTAAGTGCCATGGATTACTTT 8208 T A T
A TAAA TAAT TATG GCACTTAAT
||| ||| ||| |||||
ATTT ATTA GTAC CGTGAATTA
C G _

GAM970 SERP1 3' ATTAAGTGCAGTTTATATT 15795 TG_
AATATA TGCACCTTAAT
||||| |||||

			TTATAT ACGTGAATTA	
			TTG	
GAM970	SKIL	5'	TAAGTCGCAAAATTTATTAATT 11885	TATG_ _
	TA		TAAATTAATA TGC ACTTA	
			ATTTAATTAT ACG TGAAT	
			TTAAA C	
GAM970	LOC149271	3'	ATTAAGTGCTCAATAAATTTA 38676	AA A T
			TAAATT TAT TG GCACTTAAT	
			ATTTAA ATA AC CGTGAATTA	
			_ _ T	
GAM971	PTPRC	3'	CATGTTATTAAATTTGTAT 28149	TTT
			ATACAAATTTAATA TG	
			TATGTTTAAATTAT AC	
			TGT	
GAM971	SERPINB9	3'	GCCAAATAAAATTGTATTA 10366	A ATAT
			TAATACAA TTTA TTTGGC	
			ATTATGTT AAAT AAACCG	
			A _	
GAM971	TCF3	3'	CCAGATGATTAAACGTTGTATT 35006	A_ AT
	A		TAATACAA TTTAAT TTTGG	
			ATTATGTT AAATTA AGACC	
			GC GT	
GAM971	VAPB	3'	CCAAGCTAAATTTGTATTG 11132	ATAT
			TAATACAAATTTA TTTGG	
			GTTATGTTTAAAT GAACC	
			C _	
GAM971	DEPP	3'	GGCCAAGATAGAATCTGTA 13877	A AA
			TACA ATTT TATTTTGGCC	
			ATGT TAAG ATAGAACCGG	
			C _	
GAM971	DORFIN	3'	GGCCAAAATACTGCCTGTA 17729	AATT A
			TACA TA TATTTTGGCC	
			ATGT GT ATAAAACCGG	
			CC_ C	
GAM971	KIAA1423	3'	GGCCAAAGGGAAGTTGTATTA 30923	A AATA
			TAATACAA TTT TTTTGGCC	
			ATTATGTT GAA GAAACCGG	
			_ GG_	
GAM971	PLCL2	3'	GGCCAAAATATGCTATATTTGT 33795	TTA_
	AT		ATACAAAT ATATTTTGGCC	

			TATGTTTA	TATAAAACCGG		
			TATCG			
GAM971	SFRS11	3'	CCAATAAATTTGTGTTA	11158	ATATT	
			TAATACAAATTTA	TTGG		
			ATTGTGTTTAAAT	AACC		
GAM971	UBE3B	3'	GGCTTTATTAATTTGTA	37775	TTTT	
			TACAAATTTAATA	GGCC		
			ATGTTTAAATTAT	TCGG		
			T			
GAM971	LOC155054	3'	GGCCATTTTACTTAAATCTGTA	39539	A	TTT
			TTA	TAATACA ATTTAA TA	TGGCC	
			ATTATGT TAAATT AT	ACCGG		
			C	C TTT		
GAM972	EPM2A	3'	CACAACTTGTTTTCCCA	12225	A	TTAA
			TGG AAAACAAGTT	GTG		
			ACC TTTTGTTC	CAC		
			C			
GAM972	KNSL1	3'	ATTTAAACTTGTTGCCCA	10863	AAA	
			TGG AACAAAGTTTAAAGT			
			ACC TTGTTCAAAATTTA			
			CCG			
GAM972	BANP	5'	AAACATCACCTTGTTTTTCCA	32910	TTTTAA	
			TGGAAAAACAAG	GTGTTT		
			ACCTTTTGTTC	TACAAA		
			CAC			
GAM972	GFR	3'	TTTAAACTGCTTTTCCA	14645	ACA	
			TGGAAAA	AGTTTAAAG		
			ACCTTTT	TCAAAATTT		
			CG			
GAM972	PHCA	3'	AAACACTGTTGTCATTTTTTCC	20373	CAAGTTT	TA
	A		TGGAAAAA	AGTGTTT		
			ACCTTTT	TCACAAA		
			TACTGTTG			
GAM972	PSMD10	3'	AAACATCCTAACTTGTTTTTC	8678	TTAA	
			GAAAAACAAGTT	GTGTTT		
			CTTTTGTTC	TACAAA		
			TCC			
GAM973	MX1	5'	CCAGTGTCACGGTGGA	8291	T	CGCA C
			TC CATCGTG	ACAC GG		

AG GTGGCAC TGTG CC
 _ _ _ A
 GAM973 DGKD 3' CCCAGTGTGCGACGGTGAAGAT 29878 _ CA C
 ATCT CATCGTGCG ACAC GGG
 ||| ||||| ||| |||
 TAGA GTGGCACGC TGTG CCC
 A _ A
 GAM973 LOC201696 3' CCCAGTGATAACAATGGGATA 31623 C GCGCAA C
 TATCTCAT GT CAC GGG
 ||||| || ||| |||
 ATAGGGTA CA GTG CCC
 A ATA _ A
 GAM974 ARNT2 3' ACCAAGGATTTTCAAGACA 16932 G TAAT
 TG CTTG AGATCCTTGGT
 || ||| ||||| |||
 AC GAAC TTTAGGAACCA
 A T _
 GAM974 IL1F5 3' ACCAAGGATTGTGGCAACCA 14594 C AATA
 TGG TTGT GATCCTTGGT
 ||| ||| ||||| |||
 ACC AACG TTAGGAACCA
 _ GTG _
 GAM974 PTPN1 3' CCAAATCCACAAGCCA 8702 AATA CC
 TGGCTTGT GAT TTGG
 ||||| ||| |||
 ACCGAACA CTA AACC
 C _ _
 GAM974 TCF19 3' CCACTATTACAAGCCA 46656 ATCCT
 TGGCTTGTAATAG TGG
 ||||| ||| |||
 ACCGAACATTATC ACC
 _ _ _
 GAM974 TCF19 3' CCACTATTACAAGCCA 46705 ATCCT
 TGGCTTGTAATAG TGG
 ||||| ||| |||
 ACCGAACATTATC ACC
 _ _ _
 GAM974 KIAA0418 3' ACCAATGGATTACATGCCA 15994 T ATAG _
 TGGC TGTA ATCC TTGGT
 ||| ||| ||| |||
 ACCG ACAT TAGG AACCA
 T _ T
 GAM974 KIAA0461 3' ACCAAGGATCCATCTGGGCT 35071 GTA A
 GGCTT AT GATCCTTGGT
 ||| ||| ||||| |||
 TCGGG TA CTAGGAACCA
 TC _ C
 GAM974 LOC200597 3' ACCAAGGACCTGCTCACCA 42823 CT TAA A
 TGG TG TAG TCCTTGGT
 ||| ||| ||| |||||

ACC AC GTC AGGAACCA
 __ TC_ C
 GAM974 LOC220522 3' CCGATCTCCTACTACAAGCC 30354 A ATCC
 GGCTTGTA TAG TTGG
 ||||| || |||
 CCGAACAT ATC AGCC
 C CTCT
 GAM974 LOC257319 3' ACCAGCAGCCTATTACAAGC 45829 ATCC
 GCTTGTAATAG TTGGT
 ||||| |||
 CGAACATTATC GACCA
 CGAC
 GAM975 IHPK3 3' ATCTCTTAAATGAGGAA 27654 A CGAA
 TTC TCAT TTTAAGAGAT
 || ||| |||||
 AAG AGTA AAATTCTCTA
 G ____
 GAM975 DKFZP434D193 3' GATCTGGTTTTAATGATGAA 42852 CG TTAAAG
 TTCATCAT AA AGATC
 ||||| || |||
 AAGTAGTA TT TCTAG
 AT TGG____
 GAM975 FPGT 3' GACCTCTGAAATTGATGAT 9929 A A A
 ATCATCGA TTTA GAG TC
 ||||| ||| ||| ||
 TAGTAGTT AAGT CTC AG
 A _ C
 GAM975 KIAA0252 3' GGACCTCTCCTATCATGATGAA 31449 C ATTTA A
 TTCATCAT GA AGAG TCC
 ||||| || ||| |||
 AAGTAGTA CT TCTC AGG
 _ ATCC_ C
 GAM975 MAL2 3' ATCTGGTAACTCCATGATGAA 27467 C AT AG
 TTCATCAT GA TTA AGAT
 ||||| || ||| |||
 AAGTAGTA CT AAT TCTA
 C C_ GG
 GAM975 LOC122553 3' ATCTCCTAATGATGATG 36687 AAT A
 CATCATCG TTA GAGAT
 ||||| ||| |||
 GTAGTAGT AAT CTCTA
 ____ C
 GAM975 LOC170425 5' ATCTCTTAAATGAAATGAA 37548 CA AA
 TTCAT TCG TTTAAGAGAT
 |||| ||| |||||
 AAGTA AGT AAATTCTCTA
 A_ A_
 GAM976 FLRT2 3' ACCTATAACAAGGAGACATTAC 14877 CA A
 A
 TGTAATGTCTTT TGTTATA GT
 ||||| ||||| ||

ACATTACAGAGG ACAATAT CA
 A_ C
 GAM976 KIAA1468 3' ACTTACCTGAGGAAAGACAGCA 44097 AA ATGTTA
 CA TGT TGTCTTTC TAAGT
 ||| ||||| ||||
 ACA ACAGAAAG ATTCA
 CG GAGTCC
 GAM976 KIAA1979 3' ACTCATACTGGAGAGAAACATT 42588 _ ATGT A
 ACA TGTAATG TCTTTC TAT AGT
 ||||| ||||| ||| |||
 ACATTAC AGAGAG ATA TCA
 AA GTC_ C
 GAM977 HIS1 3' GCTACAATATACAGTTCAGGC 13179 G CACCA
 GTC GAGCTGTA TAGC
 ||| ||||| |||
 CGG CTTGACAT ATCG
 A ATAAC
 GAM977 ITPR2 3' GCTATAGGGTTTGCTCTGAC 7992 TGT A _
 GTCGGAGC AC CC ATAGC
 ||||| || || |||||
 CAGTCTCG TG GG TATCG
 TT_ _ A
 GAM977 KIAA0342 3' GCTATGGTGCAGACATTCC 34960 C A_
 GGAG TGT CACCATAGC
 ||| ||| |||||
 CCTT ACA GTGGTATCG
 _ GAC
 GAM977 KIAA1948 5' GCTATGGTGTAGAGACAAAGA 40083 GGAG_ G
 TC CT TACACCATAGC
 || || |||||
 AG GA ATGTGGTATCG
 AAACA G
 GAM977 MAC30 5' CTATGGGGGCTCCGGC 31404 GTACA
 GTCGGAGCT CCATAG
 ||||| |||||
 CGGCCTCGG GGTATC
 G_
 GAM977 MY014 5' ATGGTGTGTCCGACG 25189 GCTG
 CGTCGGA TACACCAT
 ||||| |||||
 GCAGCCT GTGTGGTA
 _
 GAM977 LOC158056 5' CTACAGCTGGCTCCGAGA 39713 G _ ACACCA
 TC TCGGAGCT GT TAG
 || ||||| || |||
 AG AGCCTCGG CG ATC
 _ T AC_
 GAM978 FLJ12806 3' CATCTCAAAATAATTA 23110 TA
 TAATTATTTTG AGATG
 ||||| |||||

ATTAATAAAAC TCTAC

GAM978 LOC157621 3' CGTTTTACAAATAATTA 41824 T
TAATTATTT GTAAGATG
||||||| |||||||
ATTAATAAA CATTTTGC

GAM979 ACF 5' ACAAAAATTATTGAGCAACCCT 15937 ATATA AA
A TAGG CTCAATAG TTTGT
||| ||||||| ||||
ATCC GAGTTATT AAACA
CAAC_ AA

GAM979 ACF 5' ACAAAAATTATTGAGCAACCCT 29058 ATATA AA
A TAGG CTCAATAG TTTGT
||| ||||||| ||||
ATCC GAGTTATT AAACA
CAAC_ AA

GAM979 DIS3 3' ACAAACCTAGATGGTATACCCT 17297 A CAA AA
A TAGG TATACT TAG TTTGT
||| |||||| | |||||
ATCC ATATGG ATC AAACA
C TAG C_

GAM979 PAK7 3' ACAAACCTCCGTTATGATATATC 34507 C _ TA A
CTA TAGGATATA TCA A GA TTTGT
||||||| ||| | |||||||
ATCCTATAT AGT T CT AAACA
_ AT GC C

GAM980 FLRT2 3' ACCTATAACAAGGAGACATTAC 14877 CA A
A TGTAATGTCTTT TGTTATA GT
||||||| ||||||| ||
ACATTACAGAGG ACAATAT CA
A_ C

GAM980 KIAA1468 3' ACTTACCTGAGGAAAGACAGCA 44097 AA ATGTTA
CA TGT TGTCTTTC TAAGT
||| ||||||| ||||
ACA ACAGAAAG ATTCA
CG GAGTCC

GAM980 KIAA1979 3' ACTCATACTGGAGAGAAACATT 42588 _ ATGT A
ACA TGTAATG TCTTTC TAT AGT
||||| |||||| | |||
ACATTAC AGAGAG ATA TCA
AA GTC_ C

GAM981 DKFZp761O0113 5' CCTAATGAGCACCTGGTGGGAA 20446 AA AA_ A
TA TATT TA GT CTCATTAGG
||| || || |||||||
ATAA GT CA GAGTAATCC
GG GGTC C

GAM981 KIAA1084 3' CCTGGATGGGTACTTTATTAA 17136 _
TTAATAAAGTACTCATT AGG
||||||| ||||| |||

AATTATTTTCATGGGTAG TCC
 G
 GAM981 LOC158629 5' CTAATGCATTATTAATATA 42021 A TACT
 TATATTAATAA G CATTAG
 ||||| ||| |||||
 ATATAATTATT C GTAATC
 A ____
 GAM982 LETM1 3' AGGGAAGAGAATGAGGACCAC 14696 A AG AC
 GTGG TT TAT TCTCTTCCCT
 ||| || ||| |||||
 CACC AG GTA AGAGAAGGGA
 _ GA _
 GAM982 PTPRO 3' AGGGAAGAGAGGGGTTCTACCC 8737 AT T A_
 AC GTGG TAG AT CTCTCTTCCCT
 ||| ||| ||| |||||
 CACC ATC TG GAGAGAAGGGA
 C_ T GG
 GAM982 PTPRO 3' AGGGAAGAGAGGGGTTCTACCC 25002 AT T A_
 AC GTGG TAG AT CTCTCTTCCCT
 ||| ||| ||| |||||
 CACC ATC TG GAGAGAAGGGA
 C_ T GG
 GAM982 PTPRO 3' AGGGAAGAGAGGGGTTCTACCC 25008 AT T A_
 AC GTGG TAG AT CTCTCTTCCCT
 ||| ||| ||| |||||
 CACC ATC TG GAGAGAAGGGA
 C_ T GG
 GAM982 PTPRO 3' AGGGAAGAGAGGGGTTCTACCC 25017 AT T A_
 AC GTGG TAG AT CTCTCTTCCCT
 ||| ||| ||| |||||
 CACC ATC TG GAGAGAAGGGA
 C_ T GG
 GAM982 PTPRO 3' AGGGAAGAGAGGGGTTCTACCC 25026 AT T A_
 AC GTGG TAG AT CTCTCTTCCCT
 ||| ||| ||| |||||
 CACC ATC TG GAGAGAAGGGA
 C_ T GG
 GAM982 SH3GL2 3' GGAAGAAAACACTAGTAACCA 8966 _ ATACTC
 TGG ATTAGT TCTTCC
 ||| ||||| |||||
 ACC TGATCA AGAAGG
 AA CAAA_
 GAM982 TRPS1 3' GGAAAAGAGTATGCCCA 15355 ATTA C
 TGG GTATACTCT TTCC
 ||| ||||| |||||
 ACC CGTATGAGA AAGG
 ____ A
 GAM982 ABCC13 3' GGAAAGAGAGCTAATTCAC 28973 TATA C
 GTGGATTAG CTCTCTT CC
 ||||| ||||| ||

		CACTTAATC	GAGAGAA GG		
		_____ A			
GAM982	C22orf20	3'	AGGGAAGAGAATAGCATGATCC 24901	GTA C	
			GGATTA TA TCTCTTCCCT		
			CCTAGT AT AGAGAAGGGA		
			ACG A		
GAM982	FLJ12056	3'	AGGGAAGAAAAGTGAAGGTAACC 24469	A GTA_ C	
		C	GG TTA TACT TCTTCCCT		
			CC AAT GTGA AGAAGGGA		
			C GGAA A		
GAM982	FLJ30681	3'	GGAAGAGAAAAGATCAACTCAC 44105	GA A ATAC	
			GTG TT GT TCTCTTCC		
			CAC AA TA AGAGAAGG		
			TC C GAA_		
GAM982	HSA249128	3'	GGAAAAGAGCCCCCTTTGATCCA 19028	TATA_ C	
		C	GTGGATTAG CTCT TTCC		
			CACCTAGTT GAGA AAGG		
			TCCCC A		
GAM982	KIAA0774	5'	AGAGAAGAGAGGAGTCAACCCA 44087	A AG ATA C	
			TGG TT T CTCTCTTC CT		
			ACC AA G GAGAGAAG GA		
			C CT AG_ A		
GAM982	KIAA1867	5'	GGAAGAGAAACTAACCAC 45456	A ATAC	
			GTGG TTAGT TCTCTTCC		
			CACC AATCA AGAGAAGG		
			_ A_		
GAM982	LAP1B	3'	GGAAATGTTACAGTAATCCAC 32264	_ T TCTC	
			GTGGATTA GTA AC TTCC		
			CACCTAAT CAT TG AAGG		
			GA _ TA_		
GAM982	MGC4796	3'	AGGAAAGAGAGTTCCAATCC 30827	AGTAT C	
			GGATT ACTCTCTT CCT		
			CCTAA TGAGAGAA GGA		
			CCT_ A		
GAM983	SULT1C1	3'	AACAATGTCAGTGTTAAA 6718	A C	
			TTTAACAT TGATATT GTT		
			AAATTGTG ACTGTAA CAA		
			_ _		
GAM983	CXorf1	3'	AACGAATTGCATGCATGTTGAA 11052	_ AT	
			TTTAACAT ATG ATTCGTT		

		AAGTTGTA TAC TAAGCAA		
		CG GT		
GAM983	KIAA1211 3'	GAATGATCACTATGTTAAA 34164	—	—
		TTTAACATA TGAT ATTC		
		AAATTGTAT ACTA TAAG		
		C G		
GAM983	SH3BGRL 3'	AATGTTTATGATATGTTAAA 31022	G	TT
		TTTAACATAT ATA CGTT		
		AAATTGTATA TAT GTAA		
		G TT		
GAM983	LOC221143 3'	AACGATGTTTATATGTTAAG 44940		TAT
		TTTAACATATGA TCGTT		
		GAATTGTATATT AGCAA		
		TGT		
GAM984	KIAA0442 3'	ATGTTATTAAAAAATGTG 17842		TT
		CACGTTTTTTAAT TGT		
		GTGTAAAAAATTA GTA		
		TT		
GAM984	KIAA0711 3'	AACAAAATGCACTAAGAAACGT 16953	—	
		ACGTTTTTTA ATTTTGT		
		TGCAAAGAAT TAAACAA		
		CACG		
GAM984	KIAA1240 3'	TGAAATTAAAAAAGTGGA 33143	G	
		TCCAC TTTTTTAATTTTG		
		AGGTG AAAAAATTAAAGT		
		—		
GAM984	PRO0245 5'	CATCATTGAAAAACATGGA 15376	C	TT
		TCCA GTTTTTTAAT TG		
		AGGT CAAAAAGTTA AC		
		A CT		
GAM984	ZFD25 3'	ACAAATGTAAAAAACGTGG 18319		AT
		CCACGTTTTTTA TTTGT		
		GGTGCAAAAAAT AAACA		
		GT		
GAM984	LOC157381 3'	TATAACAAGGGGAAAAAAC 41792		AA
		GTTTTTT TTTTGTATA		
		CAAAAAA GGAACAATAT		
		GG		
GAM985	MYO15A 5'	AGAGGAGATGAATTATGG 18353	CAAC	C
		CCG GATTCATC CCTCT		

			GGT TTAAGTAG GGAGA		
			A__ A		
GAM985	KIAA0514	3'	AGAGAGAACAAATGGCTGTGGG 16202	A_	ATTCA CC
		TA	TACCCGCA CG TC CTCT		
			ATGGGTGT GT AG GAGA		
			CG AAACA A_		
GAM985	MAP2K3	3'	AGAGGGGATGAGTTGTGTG 29713	A	
			CGCA CGATTCATCCCCTCT		
			GTGT GTTGAGTAGGGGAGA		
			—		
GAM985	MAP2K3	3'	AGAGGGGATGAGTTGTGTG 8636	A	
			CGCA CGATTCATCCCCTCT		
			GTGT GTTGAGTAGGGGAGA		
			—		
GAM985	LOC139065	5'	AGATCTCTGGAATCGTTGCAGG 37326	C	ATCCCC
			CC GCAACGATTC TCT		
			GG CGTTGCTAAG AGA		
			A GTCTCT		
GAM985	LOC148824	3'	AGAAGGGATGAATGTTAAGC 40906	__ G	C
			GC AAC ATTCATCCC TCT		
			CG TTG TAAGTAGGG AGA		
			AA _ A		
GAM985	LOC219690	5'	AGAGGGGATGAATCATTTCAGG 44705	GCAAC_	
			CC GATTCATCCCCTCT		
			GG CTAAGTAGGGGAGA		
			ACTTTA		
GAM985	LOC221431	3'	AGGGAATGAATCGATTTGC 44221	__	C
			GCAA CGATTCAT CCCT		
			CGTT GCTAAGTA GGGA		
			TA A		
GAM985	LOC255533	5'	AGAGGAGATGAATCATGTTGC 46329	__	C
			GCAAC GATTCATC CCTCT		
			CGTTG CTAAGTAG GGAGA		
			TA A		
GAM986	SUDD	3'	AATTTGGTTTCAGAATGGCTGA 9922		CTCAA
			TCAGCCATTTTG GAATT		
			AGTCGGTAAGAC TTAA		
			TTTGG		
GAM986	VBP1	3'	TCTTAGCTGAAATGGCCGA 9399	A _	C
			TC GCCATTTT GCT AAGA		

AG CGGTAAAG CGA TTCT
 C T _
 GAM986 VIP 3' AATTCTTGAAGGAAAATG 9411 G _
 CATTTT CT CAAGAATT
 ||||| || |||||
 GTAAAA GA GTTCTTAA
 G A
 GAM986 LOC144467 5' CTTGAAGCCCAGGCTGATG 28820 ATTTT _
 TATCAGCC GCT CAAG
 ||||| || ||||
 GTAGTCGG CGA GTTC
 ACC_ A
 GAM986 LOC50999 3' AATTCTTGATGAGCAATAATGA 18115 GCCATT _
 TA TATCA TTGCTCA AGAATT
 |||| ||||| ||||
 ATAGT AACGAGT TCTTAA
 AAT_ AGT
 GAM987 MGC2835 3' CCAAGACTTGAGTTGGCAACTC 23503 A_ CGACGA
 A TGAGTT CAACTC CTTGG
 ||||| ||||| ||||
 ACTCAA GTTGAG GAACC
 CG TTCA_
 GAM987 LOC143888 3' CCAAATCTATCTGAGTTGTATA 37667 A _ C C_ C
 CCCA TG GT TACAACTC GA GA TTGG
 || || ||||| || || ||||
 AC CA ATGTTGAG CT CT AACC
 C T T AT A
 GAM987 LOC148709 5' CCTGTATCAGAAATGTA ACTCA 38582 AC C CG TT
 TGAGTTACA TC GA AC GG
 ||||| || || || ||
 ACTCAATGT AG CT TG CC
 AA A A_ T_
 GAM987 LOC257017 5' CCAAGCAAAGAATTGTA ACT 46492 C CGACGA
 AGTTACAA TC CTTGG
 ||||| || ||||
 TCAATGTT AG GAACC
 A AAAC_
 GAM988 BRF1 3' TCGGGCTGCCGGCAGG 7259 GG TA
 CC GCCG GCAGCCGCA
 || |||| |||||
 GG CGGC CGTCGGCGT
 A_ _
 GAM988 LAD1 5' GCGGCCGGGCCGGCCTGGG 12088 TA A_
 CCCGGGCCG GC GCCGC
 ||||| || ||||
 GGGTCCGGC CG CGGCG
 _ GGC
 GAM988 LAD1 5' CTTGCGGCCTCGCGGCCGGG 12087 G AGCA
 CCCGG CCGT GCCGCAAG
 |||| |||| |||||

			GGGCC GGCG CGGCGTTC		
			— CTC—		
GAM988	NFRKB	5'	GCGGGCCGGCCTGGG 12820	TA	AG
			CCCGGGCCG GC CCGC		
			GGGTCCGGC CG GGCG		
			— —		
GAM988	RAB7	5'	GCGACGCGCCCGGCCCGG 11012	TA	A —
			CCGGGCCG GC GC CGC		
			GGCCCGGC CG CG GCG		
			C_ _ CA		
GAM988	RPS6KA2	5'	TGCGGCTGCTCCGGGCTG 22107	G	T
			CGG CCG AGCAGCCGCA		
			GTC GGC TCGTCGGCGT		
			G C		
GAM988	SFRP1	5'	CTTGC GGCCGCGGAGCCGGG 8930	G_	AGCA
			CCCGG CCGT GCCGCAAG		
			GGGCC GGCG CGGCGTTC		
			GA C_ _		
GAM988	VENTX2	3'	TGCGGCTGTGCCTGG 15818	CGTA	
			CCGGGC GCAGCCGCA		
			GGTCCG TGTCGGCGT		
			—		
GAM988	DKFZP564O0423	5'	TTGCGGCTGCTGCTGGCC 44072	_	
			GGCC GTAGCAGCCGCAA		
			CCGG CGTCGTCGGCGTT		
			T		
GAM988	FKBP4	3'	TGCGGCTGCCTGCCCCC 7755	CC	_
			GGG GTAG CAGCCGCA		
			CCC CGTC GTCGGCGT		
			CC C		
GAM988	FLJ10932	3'	TTGCACTCCAGCCCGGTT 20266	C_ _	A
			AACCCGGGC GT GCAG		
			TTGGGCCCG CA CGTT		
			ACCT _		
GAM988	FLJ13397	5'	GCAGCTGCTGTTTCCGGAGTT 24501	_	CCG C
			AAC CCGGG TAGCAGC GC		
			TTG GGCCT GTCGTCG CG		
			A TT_ A		
GAM988	FLJ22393	5'	TGCGGCGGGCGCGGCCCGGG 24757	A	A_
			CCCGGGCCGT GC GCCGA		

GGGCCCGGCG CG CGGCGT
_ GG
GAM988 GOLPH3 5' TGCGACCCTCTCGGCCCGG 22687 T C C__
CCGGGCCG AG AG CGCA
||||||| || || ||||
GGCCCGGC TC TC GCGT
_ _ CCA
GAM988 MGC15482 5' GCCGCAGCGCCCGGCCCGGG 26697 TA_ A C
CCCGGGCCG GC GC GC
||||||| || || ||
GGGCCCGGC CG CG CG
CCG A C
GAM988 OAZIN 5' GCAGCCTATGGCCCAGG 18021 C CA C
CC GGGCCGTAG GC GC
|| ||||| || ||
GG CCCGGTATC CG CG
A _ A
GAM988 PPM1A 5' TCGCGCTGCTCCGGACCT 21999 _ T
GGG CCG AGCAGCCGCA
||| ||| |||||
TCC GGC TCGTCGGCGT
A C
GAM988 Rab11-FIP2 5' GCAGCCCTCCGCCCGGGT 17099 C T CA C
ACCCGGGC G AG GC GC
||||||| | || ||
TGGGCCCG C TC CG CG
_ C C_ A
GAM988 RCD-8 3' TGCAGCTGCTGCAGCAGGG 15643 GG C C
CCC GC GTAGCAGC GCA
||| || ||||| |||
GGG CG CGTCGTCG CGT
A_ A A
GAM988 REC8 5' TGCAGTAGGCGGCCCGGG 11609 AGCA C
CCCGGGCCGT GC GCA
||||||| || |||
GGGCCCGGCG TG CGT
GA_ A
GAM988 TGIF2 3' CTGTACTCCAGCCCGGGT 22367 C__ G
AACCCGGGC GTA CAG
||||||| ||| |||
TTGGGCCCG CAT GTC
ACCT _
GAM988 TP53INP1 5' GCGCACCCCGCACGGCCCGGG 27108 A AGC__
CCCGGGCCGT GC CGC
||||||| || |||
GGGCCCGGCA CG GCG
_ CCCAC
GAM988 LOC139411 5' GGCGCTACGGCCGGGT 37342 G A
ACCCGG CCGTAGC GCC
||||| ||||| |||

TGGGCC GGCATCG CGG

GAM988 LOC146433 5' CTTGCGGCCACCGCCCCCGG 38147 CC AGCA
CCGGG GT GCCGCAAG
|||| || |||||
GGCCC CG CGGCGTTC
CC CCAC

GAM988 LOC51104 5' CGGCGCTTCGGCCCGGG 18091 T A
CCCGGGCCG AGC GCCG
||||||| ||| |||
GGGCCCGGC TCG CGGC
T _

GAM989 C7orf2 3' ACAGCGCATTCTTCTGTAGACA 22795 _ ATC GT
TGTC ACAGA GG TCGCTGT
||| |||| || |||||
ACAG TGTCT TC ACGCGACA
A _ TT

GAM989 FLJ14054 3' CAGACCAATTCTGTGAC 23783 CG TGCG
GTCACAGAAT GGT CTG
||||||| ||| |||
CAGTGTCTTA CCA GAC
A_ _

GAM989 FLJ20297 3' CAGCTACGCTCTGTGACA 19358 AT GGTTGC
TGTCACAGA CG GCTG
||||||| || |||
ACAGTGTCT GC CGAC
C_ AT_

GAM989 FLJ20297 3' CAGCTACGCTCTGTGACA 19648 AT GGTTGC
TGTCACAGA CG GCTG
||||||| || |||
ACAGTGTCT GC CGAC
C_ AT_

GAM989 PP3501 3' ACAGCAGCACGATTTGTGACA 22328 A GGT _
TGTCACAGA TCG TGC GCTGT
||||||| ||| ||| |||
ACAGTGTTT AGC ACG CGACA
_ _ A

GAM989 LOC150776 3' CAGCCACGCTCTGTGACA 31675 AT _
TGTCACAGA CG GGTTG
||||||| || |||
ACAGTGTCT GC CCGAC
C_ A

GAM990 DSCR1 3' TCCTGATGGAATTGTTATA 10676 C CCACA
TATAACAA TCCA AGGA
||||||| ||| |||
ATATTGTT AGGT TCCT
A AG_

GAM990 EMP1 3' TCCTTTTTGGGGAGTTGTTATG 7136 A C_
TATAACA ACTCC CCA AAGGA
||||||| ||| |||

GTATTGTTGAGG GGT TTCCT
 _ TT
 GAM990 SEDL 3' TCCTTGTGAACAGTGTAT 15914 A CCAC
 ATAACA CT CACAAGGA
 ||||| || |||||
 TATTGT GA GTGTTCT
 _ CAA_
 GAM990 ZNF22 3' TCCTTGTGGACAGTTGTTA 43970 CCA
 TAACAAC CT CACAAGGA
 ||||| |||||
 ATTGTTGA GGTGTTCT
 CA_
 GAM990 ABCC13 3' CCTTGTGTTTGTATATA 28972 CTCCAC
 TATAACAA CACAAGG
 ||||| |||||
 ATATTGTT GTGTTCC
 T_____
 GAM990 FLJ20308 3' TCCTGCGGCAGAGTTGTTCA 33199 T CA A A
 A AACAACTC CC CA GGA
 | ||||| || |||
 A TTGTTGAG GG GT CCT
 C AC C _
 GAM990 KIAA1511 3' CCCTGTGCTCAGCCTGGAATTG 34756 C C_____ A
 TTATA TATAACAA TCCA CACA GG
 ||||| || ||| ||
 ATATTGTT AGGT GTGT CC
 A CCGACTC C
 GAM990 MGC23980 3' CCTAATGTGTAGGGTTGTTATA 29606 T AC _
 TATAACAAC CC CACA AGG
 ||||| || ||| |||
 ATATTGTTG GG GTGT TCC
 _ AT AA
 GAM990 WSB1 3' CCTTGTGGTATAAAGTATTATA 28616 CA CC__
 TATAA ACT ACCACAAGG
 |||| ||| |||||
 ATATT TGA TGGTGTTC
 A_ AATA
 GAM990 WSB1 3' CCTTGTGGTATAAAGTATTATA 28622 CA CC__
 TATAA ACT ACCACAAGG
 |||| ||| |||||
 ATATT TGA TGGTGTTC
 A_ AATA
 GAM990 LOC129676 5' TCCTTGTGAAGGCTGTTA 37288 ACT AC
 TAACA CC CACAAGGA
 |||| || |||||
 ATTGT GG GTGTTCT
 C__ AA
 GAM990 LOC154043 3' TGGGGTGGTGTGTTATA 39460 T A
 TATAACAAC CCACC CA
 ||||| |||| ||

ATATTGTTG GGTGG GT
 T G
 GAM991 AGR2 3' ACCCTGAAGAAATCCTGGGA 13113 A A GTATAC
 TCC AG ATT TCAGGGT
 ||| ||| |||||
 AGG TC TAA AGTCCCA
 G C AGA____
 GAM991 SLC12A7 3' TACCCCATCCAGAACATTCTTG 13374 T ATACTCA_
 GA TCCAAGAAT GT GGGTA
 ||||| || |||||
 AGGTTCTTA CA CCCAT
 _ AGACCTAC
 GAM991 CLIPR-59 3' ACCCTGAGATAGAGATTC 17784 G_ A
 GAATT TAT CTCAGGGT
 |||| ||| |||||
 CTTAG ATA GAGTCCCA
 AG _
 GAM991 DCNP1 3' TACCCAGAGCACTACAATTCT 28386 CA TA_ A_
 CTGA TC AGAATTGTA CTC GGGTA
 || ||||| || |||||
 AG TCTTAACAT GAG CCCAT
 TC CAC AC
 GAM991 FLJ12875 3' ACCCTGAGCATATGCCCTCTTG 23753 ATT _
 G CCAAGA GTATA CTCAGGGT
 |||| |||| |||||
 GGTTC CGTAT GAGTCCCA
 CC_ AC
 GAM991 KIAA0323 3' ACCCTGAGTTGGTGCTTTGGA 31686 AATT _
 TCCAAG GTAT ACTCAGGGT
 |||| ||| |||||
 AGGTTT CGTG TGAGTCCCA
 ____ GT
 GAM991 LOC144308 3' ACCCTGAGTACACCCCTCT 40404 ATT A
 AGA GT TACTCAGGGT
 || ||| |||||
 TCT CA ATGAGTCCCA
 CCC C
 GAM991 LOC153480 5' ACCCTAAAAAGTCATTTCTTG 36088 T TATACTC
 A TCCAAGAA TG AGGGT
 ||||| || |||||
 AGGTTCTT AC TCCCA
 T TGAAAAA
 GAM991 LOC154739 5' TACCCTGAATCCTGCACTTT 41722 T TAC_
 GAA TGTA TCAGGGTA
 ||| ||| |||||
 TTT ACGT AGTCCCAT
 C CCTA
 GAM992 EGFL5 3' AGGCTATACAATGTGTGTGA 41879 A_ AC
 TCACACGCG GTA AGCCT
 ||||| ||| |||||

AGTGTGTGT CAT TCGGA
 AA A_
 GAM992 LRRC2 3' CGAGGCTGCAGTGTGCTGTGA 23703 C AGTAA
 TCACA GCG CAGCCTCG
 ||||| ||| |||||
 AGTGT CGT GTCGGAGC
 _ GTGAC
 GAM992 ZNFN2A1 3' CGAGGCTGCTGCTGGCTGTGA 30468 C G A
 TCACA GC AGTA CAGCCTCG
 ||||| || ||||| |||||
 AGTGT CG TCGT GTCGGAGC
 _ G C
 GAM992 CSEN 3' CGAGGCTGCCTCTGGGTG 15091 G _ TAA
 CAC C GAG CAGCCTCG
 ||| ||| |||||
 GTG G CTC GTCGGAGC
 G T C_
 GAM992 DOK4 3' AGGCTGTTTTTGAGTATGA 19879 C G T
 TCA AC CGAG AACAGCCT
 ||| || ||||| |||||
 AGT TG GTTT TTGTCGGA
 A A _
 GAM992 FLJ11800 3' CGAGGCTGCAGTGAGCTGTGA 24531 C GAGTAA
 TCACA GC CAGCCTCG
 ||||| || |||||
 AGTGT CG GTCGGAGC
 _ AGTGAC
 GAM992 FLJ22341 3' CGAGGCTGACTCCGCGTGAGA 23847 A _ AA
 TC CACGCG AGT CAGCCTCG
 || ||||| ||| |||||
 AG GTGCGC TCA GTCGGAGC
 A C _
 GAM992 KIAA1950 3' CGAGGCTGCAGTGGGATGTGA 44487 _ GAGTAA
 TCACA CGC CAGCCTCG
 ||||| ||| |||||
 AGTGT GTG GTCGGAGC
 AGG AC_
 GAM992 MGC15631 3' CGAGGCTGCAGGGAGCTGTGA 26494 C GAGTAA
 TCACA GC CAGCCTCG
 ||||| || |||||
 AGTGT CG GTCGGAGC
 _ AGGGAC
 GAM992 PRO2133 3' CGAGGCTGCTGTGAGCCGTG 20693 _ GA A
 CACG C GTA CAGCCTCG
 ||||| | ||| |||||
 GTGC G TGT GTCGGAGC
 C AG C
 GAM992 SIAT4A 3' CGAGGCTGCAGTGGGCTGTGA 8979 C GAGTAA
 TCACA GC CAGCCTCG
 ||||| || |||||

AGTGT CG GTCGGAGC
 _ GGTGAC
 GAM992 STAG3 5' CGAGGCTGTGGAGCGGCGTGA 14819 A_ GAGTA
 TCAC CGC ACAGCCTCG
 |||| || |||||
 AGTG GCG TGTCGGAGC
 CG AGG_
 GAM992 TOMM70A 3' CGAGGCTGTAATGTGCCATGA 16789 CAC A A
 TCA GCG GT ACAGCCTCG
 || || |||||
 AGT CGT TA TGTCGGAGC
 AC_ G A
 GAM992 LOC138241 5' CGAGGCTGCGCCGCGTGGA 37120 A A AA
 TC CACGCG GT CAGCCTCG
 || |||| |||||
 AG GTGCGC CG GTCGGAGC
 _ _ C_
 GAM992 LOC144848 3' AGGCCGCTGTGTGTGG 36420 G AACA
 TCACACGC AGT GCCT
 ||||| || |||
 GGTGTGTG TCG CGGA
 _ C_
 GAM992 LOC170395 3' CGAGGCTGCAGTGAGCTGTGA 37544 C GAGTAA
 TCACA GC CAGCCTCG
 |||| || |||||
 AGTGT CG GTCGGAGC
 _ AGTGAC
 GAM992 LOC220575 3' CGAGGCTGCAGTGAGCTGTGA 37529 C GAGTAA
 TCACA GC CAGCCTCG
 |||| || |||||
 AGTGT CG GTCGGAGC
 _ AGTGAC
 GAM992 LOC254181 5' CGAGGGCGGCCAGCGTGTGA 46597 GA AACAG
 TCACACGC GT CCTCG
 ||||| || |||
 AGTGTGCG CG GGAGC
 AC GCG_
 GAM993 EXTL1 3' ATCTGAAGAACAGCCCC 10751 A A TTC
 GG GGT GT TCTTCAGAT
 || || |||||
 CC CCG CA AGAAGTCTA
 _ A _
 GAM993 PKIA 5' ATCTGAAGGTCATCTCC 13699 AGTTT T
 GGAGGT C CTTTCAGAT
 |||| | |||||
 CCTCTA G GAAGTCTA
 CT__
 GAM993 PRDM2 3' GAGATCCAAAGAGAAGGGC 18005 AG CA
 GT TTTCTCTT GATCTC
 || ||||| |||||

			CG GAAGAGAA CTAGAG		
			G_ AC		
GAM993	RAP1A	3'	ATCTGAAGAGGCTTCTCC 8794	T TT	
			GGAGG AGT CTCTTCAGAT		
			CCTCT TCG GAGAAGTCTA		
			— —		
GAM993	DDX28	5'	CTGAAGACCTTATCTCC 20408	TTTC	
			GGAGGTAG TCTTCAG		
			CCTCTATT AGAAGTC		
			CC_		
GAM993	KCND1	3'	GAAATGAGAACTTCCTCC 11424	T _	
			GGAGG AGTTTCTC TTC		
			CCTCC TCAAAGAG AAG		
			T TA		
GAM993	MGC13251	3'	GAGAGTTGAAAACTACCT 26436	CTC A	
			AGGTAGTTT TTCAG TCTC		
			TCCATCAAA AAGTT AGAG		
			_ G		
GAM993	SS18L1	3'	AGATCTGAAAAGAAACCTT 32558	AGT C	
			GAGGT TTCT TTCAGATCT		
			TTCCA AAGA AAGTCTAGA		
			_ A		
GAM993	LOC124460	3'	GAGGCAGGAAACTACCCC 37445	A _	
			GG GGTAGTTTCT CTTC		
			CC CCATCAAAGG GGAG		
			_ AC		
GAM993	LOC138130	5'	AGACCTGAAACTGCCCC 37394	A TCTCT A	
			GG GGTAGTT TCAG TCT		
			CC CCGTCAA AGTC AGA		
			_ _ C		
GAM993	LOC152620	3'	AGAGCTGAAAACTACCT 30173	CTC A	
			AGGTAGTTT TTCAG TCT		
			TCCATCAAA AAGTC AGA		
			_ G		
GAM993	LOC158668	3'	AGACCTGAAAACTACCT 34377	CTC A	
			AGGTAGTTT TTCAG TCT		
			TCCATCAAA AAGTC AGA		
			_ C		
GAM993	LOC254312	5'	AGATCTGAAGATACGCCCC 46113	A A TTC	
			GG GGT GT TCTTCAGATCT		

			CC CCG CA AGAAGTCTAGA		
			— — T—		
GAM994	FZD4	3'	TGAGGACAGCTAATCCA 14489 A	ATCAA A	
			TG GATTAGCT GTT TCA		
			AC CTAATCGA CAG AGT		
			— ——— G		
GAM994	SLC7A6	3'	GATAACCAGCTAATCCCA 10131 A	ATCAA	
			TG GATTAGCT GTTATC		
			AC CTAATCGA CAATAG		
			C C—		
GAM994	FLJ10932	3'	CTGACATGTGTATAGTAATCTC 20264	G _ AGTTA	
	A		TGAGATTA CTAT CA TCAG		
			ACTCTAAT GATA GT AGTC		
			— T GTAC—		
GAM994	KIAA1906	3'	CTGATAACTGAGCTAATCCA 36230 A	ATCA	
			TG GATTAGCT AGTTATCAG		
			AC CTAATCGA TCAATAGTC		
			— G—		
GAM994	LOC126917	3'	CTGATAACTTGATGTTCTTC 36870	TT T	
			GA AGC ATCAAGTTATCAG		
			CT TTG TAGTTCAATAGTC		
			TC —		
GAM995	AHR	3'	TCACATGGAGGCATTGATG 7335	_ C	
			CATCAATGCCTCC TG TGA		
			GTAGTTACGGAGG AC ACT		
			T —		
GAM995	ATP8B2	5'	CAGCAGGAGCAGTGGATGAA 32509	AA_ C	
			TTCATC TGC TCCTGCTG		
			AAGTAG ACG AGGACGAC		
			GTG —		
GAM995	BCL2	3'	TCAGCCTTGAAACATTGATGGA 6262	CC CT_	
			TTCATCAATG TC GCTGA		
			AGGTAGTTAC AG CGACT		
			AA TTC		
GAM995	CALCRL	3'	CAGCACACCATTGATGAA 12376	CCTCC	
			TTCATCAATG TGCTG		
			AAGTAGTTAC ACGAC		
			CAC—		
GAM995	CAPN10	3'	TCAGCAGGAGGCTGCCGGAA 23355	ATCAAT	
			TTC GCCTCCTGCTGA		

			AAG CGGAGGACGACT		
			GCCGT_		
GAM995	CRACC	3'	TCAGAAAGGCATTGTGAA	22156	T CCTG
			TTCA CAATGCCT CTGA		
			AAGT GTTACGGA GACT		
			_ AA_		
GAM995	FADD	3'	CAGCAGGAAGCCAGGCTGAG	9918	_ AAT C
			TTCA TC GC TCCTGCTG		
			GAGT GG CG AGGACGAC		
			C AC_ A		
GAM995	IGF2R	3'	CAGCAGGGGTGTGATG	6558	A T
			CATCA TGCC CCTGCTG		
			GTAGT GTGG GGACGAC		
			_ -		
GAM995	LOH11CR2A	5'	CAGCATGGCATTGAGAA	15986	A TCC
			TTC TCAATGCC TGCTG		
			AAG AGTTACGG ACGAC		
			_ T_		
GAM995	SNAI1	3'	CACAGGACTTTGATGAA	12606	TGCC C
			TTCATCAA TCCTG TG		
			AAGTAGTT AGGAC AC		
			TC_ _		
GAM995	SULT1A2	5'	CAGCAGGAAATGGTGAG	35734	ATGCC
			TTCATCA TCCTGCTG		
			GAGTGGT AGGACGAC		
			AA_		
GAM995	ASB13	3'	CAGCCTGGCCAACTTGATGAA	24012	T_ TCCT
			TTCATCAA GCC GCTG		
			AAGTAGTT CGG CGAC		
			CAAC TC_		
GAM995	DKFZP434C1715	5'	TCAGCAGGTCACTGATGAA	41676	A CCT
			TTCATCA TG CCTGCTGA		
			AAGTAGT AC GGACGACT		
			C T_		
GAM995	FLJ10604	3'	TCAGCAGGATGCTGAGGAA	19964	A AT C
			TTC TCA GC TCCTGCTGA		
			AAG AGT CG AGGACGACT		
			G _ T		
GAM995	FLJ10898	3'	CAGTTTGGATTGATGAA	29889	G TCCT
			TTCATCAAT CC GCTG		

AAGTAGTTA GG TGAC
 _ TT_
 GAM995 KIAA0721 3' CAGAGTTGGGGCATTGAGGAA 45925 A CTG_
 TTC TCAATGCCTC CTG
 ||| ||||| |||
 AAG AGTTACGGGG GAC
 G TTGA
 GAM995 KIAA0721 3' CAGAGTTGGGGCATTGAGGAA 22318 A CTG_
 TTC TCAATGCCTC CTG
 ||| ||||| |||
 AAG AGTTACGGGG GAC
 G TTGA
 GAM995 KIAA0993 3' CAGCTTGGAAGGCATTGA 32078 _ T_
 TCAATGCCT CC GCTG
 ||||| || |||
 AGTTACGGA GG CGAC
 A TT
 GAM995 KIAA1091 3' CAGCAGCAGGACTGAGAA 34539 A ATG C
 TTC TCA CCT CTGCTG
 ||| ||| ||| |||||
 AAG AGT GGA GACGAC
 _ CA_ C
 GAM995 MGC4266 5' TCAGCAGGAGTGCCAGGAGAA 26401 A AAT _
 TTC TC GC CTCCTGCTGA
 ||| || ||| |||||
 AAG AG CG GAGGACGACT
 _ GAC T
 GAM995 PSMD12 3' CAGCAGGAGAGGTGATGAG 8681 ATGC
 TTCATCA CTCCTGCTG
 ||||| |||||
 GAGTAGT GAGGACGAC
 GGA_
 GAM995 RFX4 3' TCAGCAAAAGGCAGGAGAG 26242 A AA CC
 TTC TC TGCCT TGCTGA
 ||| || |||| |||||
 GAG AG ACGGA ACGACT
 _ G_ AA
 GAM995 LOC118709 5' CAGCAGGACTGTACGAGGAA 36598 A AA C_
 TTC TC TGC TCCTGCTG
 ||| || ||| |||||
 AAG AG ATG AGGACGAC
 G C_ TC
 GAM995 LOC126669 3' TCAGCAGGATTGCACTGA 37159 A C_
 TCA TGC TCCTGCTGA
 ||| ||| |||||
 AGT ACG AGGACGACT
 C TT
 GAM995 LOC138241 5' TCAGCAGGAGGCGGGGAT 37121 AA
 ATC TGCCTCCTGCTGA
 ||| |||||

		TAG GCGGAGGACGACT			
		GG			
GAM995	LOC145900 5'	CAGCAGGAGCCAAGAGGAA	38012	A AA C	
		TTC TC TG CTCCTGCTG			
		AAG AG AC GAGGACGAC			
		G A_ C			
GAM995	LOC149844 3'	TCAGCAAGAGGCGTTCTGA	38823	_ C	
		TC AATGCCTC TGCTGA			
		AG TTGCGGAG ACGACT			
		C A			
GAM995	LOC151438 5'	CAACAGGAGGCCGGGGAA	41346	A AAT	C
		TTC TC GCCTCCTG TG			
		AAG GG CGGAGGAC AC			
		_ GC_ A			
GAM995	LOC151438 5'	TCAGCAGGAGGAGTTTGG	41350	TG_	
		TCAA CCTCCTGCTGA			
		GGTT GGAGGACGACT			
		TGA			
GAM995	LOC153442 5'	CAGCAGGATTTTTATGAA	41635	C TGCC	
		TTCAT AA TCCTGCTG			
		AAGTA TT AGGACGAC			
		T TT_			
GAM995	LOC157376 3'	TCAGCAGGAAGCAAGATGGG	39601	AA C	
		TTCATC TGC TCCTGCTGA			
		GGGTAG ACG AGGACGACT			
		A_ A			
GAM995	LOC197342 3'	TCAGCAGGGTGGCTGATGA	42489	AT _	
		TCATCA GCC TCCTGCTGA			
		AGTAGT CGG GGGACGACT			
		_ T			
GAM995	LOC203286 3'	TCAGCAGGAGGCACTGTGAA	43497	T A	
		TTCA CA TGCCTCCTGCTGA			
		AAGT GT ACGGAGGACGACT			
		_ C			
GAM995	LOC222614 5'	CAATGGAGATATTGATGAA	45306	C TGC	
		TTCATCAATG CTCC TG			
		AAGTAGTTAT GAGG AC			
		A TA_			
GAM995	LOC253613 3'	TCAGCAGGAAATCAATGTGGA	46013	T A CC_	
		TTCA CA TG TCCTGCTGA			

			AGGT GT AC AGGACGACT		
			_ A TAA		
GAM995	LOC254936	5'	CAGCAGGAGCCAAGAGGAA 45527	A AA C	
			TTC TC TG CTCCTGCTG		
			AAG AG AC GAGGACGAC		
			G A_ C		
GAM995	LOC255870	3'	TCAGTGGGGCACTGAAGAA 45406	A A T T	
			TTC TCA TGCC CC GCTGA		
			AAG AGT ACGG GG TGA CT		
			A C _ _		
GAM995	LOC51336	3'	AGCAGGCAGCATTGATGAA 18753	CT	
			TTCATCAATGC CCTGCT		
			AAGTAGTTACG GGACGA		
			AC		
GAM995	LOC58486	5'	TCTGCGCATTGATGAA 22187	CTCCT T	
			TTCATCAATGC GC GA		
			AAGTAGTTACG CG CT		
			_ _ _ T		
GAM995	LOC89135	3'	TCAGCAAGAGGCGTTTGA 30250	_ C	
			TC AATGCCTC TGCTGA		
			AG TTGCGGAG ACGACT		
			C A		
GAM995	LOC90538	3'	TCAGCAGGCTGGTGATGGA 31658	AAT T_	
			TTCATC GCC CCTGCTGA		
			AGGTAG TGG GGACGACT		
			_ _ TC		
GAM995	LOC91974	5'	CAGAAGGCCATTGATGAA 33651	_ C	
			TTCATCAATG CCT CTG		
			AAGTAGTTAC GGA GAC		
			C A		
GAM996	ARAF1	5'	AGAGTGAGACAAGCAACA 31980	A CTT	
			TGT TGCTTGTC CTTT		
			ACA ACGAACAG GAGA		
			_ AGT		
GAM996	CARPX	3'	AAGAAAAAAGGACAGACA 21393	CT C C	
			TG TGTCCTT TTT CTT		
			AC ACAGGAA AAA GAA		
			AG A A		
GAM996	RP42	3'	AAAGATTTTCAAACAAGCATAC 21799	CCT_	
	A		TGTATGCTTGT TCTTT		

			ACATACGAACA	AGAAA	
			AACTTTT		
GAM996	SSPN	3'	AAGGAAAGAATGGCATAG	11535	_ C
			CT TGTC TTCTTTCCTT		
			GA ACGG AAGAAAGGAA		
			T T		
GAM996	WNT5A	3'	CAAGGAAAAAAGGTATATCA	9428	CT _ C
			TG TGT CCTT TTTCCTTG		
			AC ATA GGAA AAAGGAAC		
			T_ T A		
GAM996	CDT6	5'	CAAGGAAAGAGAGAAAACAACA	22118	A CTTG C
			TGT TG TC TTCTTTCCTTG		
			ACA AC AG GAGAAAGGAAC		
			_ AAA_ A		
GAM996	FLJ23251	3'	CAGGGAGAAGGACAAGGCATAC	24209	_ TT
	A		TGTATGC TTGTCCTTC TCCTTG		
			ACATACG AACAGGAAG AGGGAC		
			G _		
GAM996	KIAA0461	3'	CAAGGAAAGAAAAATTTTTTCTA	35073	TGCTTGTCC
	CA		TGTA TTCTTTCCTTG		
			ACAT AAGAAAGGAAC		
			CTTTTTTAA		
GAM996	KIAA1819	5'	CAAGGAAAGCTGGCAAACACAC	34532	A C T TT
			GT TG TTG CC CTTTCCTTG		
			CA AC AAC GG GAAAGGAAC		
			C A _ TC		
GAM996	MAC30	3'	CAAGGAAAAAAGAGAAAACATA	31402	CTTG _ C
	C		GTATG TC CTT TTTCCTTG		
			CATAC AG GAA AAAGGAAC		
			AAA_ A A		
GAM996	SEMA6A	5'	AAAGAGACAAGCACACA	21879	A CT
			TGT TGCTTGTC TCTTT		
			ACA ACGAACAG AGAAA		
			C _		
GAM996	TPD52	3'	CAAGGAAAGAACTACTAGCTAC	11530	T T CC
	A		TGTA GCT GT TTCTTTCCTTG		
			ACAT CGA CA AAGAAAGGAAC		
			_ T TC		
GAM996	LOC124460	3'	AAAGAATCACAGAGCATACA	37441	_ CC
			TGTATGCT TGT TTCTTT		

ACATACGA ACA AAGAAA
 G CT
 GAM996 LOC130814 3' CAAGGATACCAAGGCAAGCATA 37007 T CTT_
 CA TGTATGCTTG CCTT TCCTTG
 ||||| ||| |||||
 ACATACGAAC GGAA AGGAAC
 _ CCAT
 GAM996 LOC131827 3' CAAAGAAAGAAGGAAGAACA 37013 C G C
 TG TT TCCTTCTTTC TTG
 || || ||||| |||
 AC AG AGGAAGAAAG AAC
 A A A
 GAM996 LOC136319 3' AGGGAGAGCAAAGACAAAATAC 37101 GC C _
 A TGTAT TTGTC TT CTTTCCTT
 |||| |||| || |||||
 ACATA AACAG AA GAGAGGGA
 A_ A C
 GAM996 LOC148267 5' CAAGGAAATGGACAAACTACA 38516 TGC TTC
 TGTA TTGTCC TTTCCTTG
 ||| |||| |||||
 ACAT AACAGG AAAGGAAC
 CA_ T__
 GAM996 LOC221806 5' GAGAGATAAACAAGCATACA 44453 CCT
 TGTATGCTTGT TCTTTC
 ||||| |||||
 ACATACGAACA AGAGAG
 AAT
 GAM996 LOC91445 3' CAAGGAAAGGGGAAACCCA 30366 CTTG T
 TG TCCT CTTTCCTTG
 || ||| |||||
 AC AGGG GAAAGGAAC
 CCAA _
 GAM997 GRM1 3' CACACATTATTAACA 6494 TATG
 TGTTAATAAT GTGTG
 ||||| |||||
 ACAATTATTA CACAC

 GAM997 SLC13A1 3' CACTATAAACTATTAACATA 22774 A__
 TATGTTAATA TTATGGTG
 ||||| |||||
 ATACAATTAT AATATCAC
 CAA
 GAM997 GFR 3' CACCACAATCAACTATTGACA 14636 ATTA _
 TGTTAATA TGGT GTGGTG
 ||||| ||| |||||
 ACAGTTAT ACTA CACCAC
 CA__ A
 GAM997 KIAA1878 3' CATGAGCCATAATTATTAACA 44074 _
 TGTTAATAATTATGGT GTG
 ||||| ||||| |||

			ACAATTATTAATACCG TAC		
			AG		
GAM997	LOC222681	3'	CACCACACCATCCCCAGCA 44614	AATAATT	
			TGTT ATGGTGTGGTG		
			ACGA TACCACACCAC		
			CCCC__		
GAM997	LOC257507	3'	CACCACACCATCCCCAGCA 46680	AATAATT	
			TGTT ATGGTGTGGTG		
			ACGA TACCACACCAC		
			CCCC__		
GAM997	LOC257625	3'	CACCACACCATCCCCAGCA 46736	AATAATT	
			TGTT ATGGTGTGGTG		
			ACGA TACCACACCAC		
			CCCC__		
GAM997	LOC93297	3'	CACCACAAGACCTATTAACA 35615	ATTATGG	
			TGTTAATA TGTGGTG		
			ACAATTAT ACACCAC		
			CCAGA__		
GAM998	CPSF4	3'	ACACCAGTTCTTGGTGACGCCA 13511	A A	__
			TG CGT ACCAAGAA GTGT		
			AC GCA TGGTTCTT CACA		
			C G GAC		
GAM998	VHL	3'	TAGATACACTTCTTAAATAC 6163	ACC	
			GTA AAGAAGTGTATCTA		
			CAT TTCTTCACATAGAT		
			AAA		
GAM998	IMPACT	3'	TAGCTTTTCTTCTTGGTTATAT 20505	CG	TGTAT
	CA		TGA TAACCAAGAAG CTA		
			ACT ATTGGTTCTTC GAT		
			AT TTTTC		
GAM998	MGC20496	3'	TACCTTCTTAGTCACGTGCA 27425	_ A C	T
			TG ACGT AC AAGAAG GTA		
			AC TGCA TG TTCTTC CAT		
			G C A _		
GAM998	TIX1	3'	GTGCATTGTCAGTTACGTCA 30930	CAAGA	
			TGACGTAAC AGTGTAT		
			ACTGCATTG TTACGTG		
			ACTG_		
GAM999	FLRT2	3'	ACCTATAACAAGGAGACATTAC 14877	CA	A
	A		TGTAATGTCTTT TGTTATA GT		

ACATTACAGAGG ACAATAT CA
 A_ C
 GAM999 KIAA1468 3' ACTTACCTGAGGAAAGACAGCA 44097 AA ATGTTA
 CA TGT TGTCTTTC TAAGT
 ||| ||||| ||||
 ACA ACAGAAAG ATTCA
 CG GAGTCC
 GAM999 KIAA1979 3' ACTCATACTGGAGAGAAACATT 42588 _ ATGT A
 ACA TGTAATG TCTTTC TAT AGT
 ||||| ||||| ||| |||
 ACATTAC AGAGAG ATA TCA
 AA GTC_ C
 GAM1000 EPHB1 3' AACCCAGCTCCCACTCTC 10727 T AAC A
 GAGA GT GGGG CTGGGTT
 ||| || ||| |||||
 CTCT CA CCCT GACCCAA
 _ _ C
 GAM1000 EPHB1 3' AAACCCAGCTCCTGAGTCTC 10726 GTAA A
 GAGAT CGGGA CTGGGTTT
 |||| |||| |||||
 CTCTG GTCCT GACCCAAA
 A_ C
 GAM1000 KCNJ5 3' AAACCCAGCCCTCACAGCTC 6585 A AAC AA
 GAG TGT GGG CTGGGTTT
 ||| || ||| |||||
 CTC ACA CCC GACCCAAA
 G CT_ _
 GAM1000 MYCL2 3' ACCCAGCTCTCTCTCT 11854 TGTAAC A
 AGAGA GGGG CTGGGT
 |||| ||| |||||
 TCTCT CTCT GACCCA
 _ C
 GAM1000 PROK1 3' AAACCCAGCTCCCATGACTCTC 26195 T AAC A
 GAGA GT GGGG CTGGGTTT
 ||| || ||| |||||
 CTCT CA CCCT GACCCAAA
 _ GTA C
 GAM1000 TTID 5' AACCCAGCTGGCACCCTCT 13668 AT AA GAA
 AGAG GT CGG CTGGGTT
 ||| || ||| |||||
 TCTC CA GTC GACCCAA
 C_ CG _
 GAM1000 CAMKK1 3' AAACCCGGATCCCGCTGCATCT 26062 A A
 C GAGATGTA CGGGA CTGGGTTT
 ||||| ||||| |||||
 CTCTACGT GCCCT GGCCCAA
 C A
 GAM1000 DKFZp547I094 5' AAACCCAGCGCACTTTACCTC 25854 A TAAC GAA_
 GAG TG GG CTGGGTTT
 ||| || || |||||

		CTC AC TC GACCCAAA	
		C TT__ ACGC	
GAM1000	DKFZp761O17121	3' AACCCAGCTCCTCACTTC	26043 T AAC A
		GA GT GGG A CTGGGTT	
		CT CA TCCT GACCCAA	
		T C__ C	
GAM1000	FLJ21438	5' AAACCCAGCCCCACAGCCACCTC	30842 A TAAC_ AA
	T	AGAG TG GGG CTGGGTTT	
		TCTC AC CCC GACCCAAA	
		C CGACA _	
GAM1000	MAB21L2	5' AAACCCAGTCCAAACAACGCCT	13147 A AACG_ A
	C	GAG TGT GGA CTGGGTTT	
		CTC GCA CCT GACCCAAA	
		C ACAA _	
GAM1000	MDN1	5' AACCCAGCTCTCCTCTC	31408 TGTAAC A
		GAGA GGG A CTGGGTT	
		CTCT CTCT GACCCAA	
		C_____ C	
GAM1000	LOC220766	5' AAACCCAGCCCAAACAT	43645 AAC AA
		ATGT GGG CTGGGTTT	
		TACA CCC GACCCAAA	
		AA_ _	
GAM1000	LOC255565	3' AAACCCGAAACCGTTACATCT	45586 GAAC
		AGATGTAACGG TGGGTTT	
		TCTACATTGCC GCCCAA	
		AAA_	
GAM1000	LOC92230	5' AAACCCAGCCCCTTGC	34005 C AA
		GTAA GGG CTGGGTTT	
		CGTT CCC GACCCAAA	
		C _	
GAM1001	LETM1	3' AGGGAAGAGAATGAGGACCAC	14696 A AGTG C
		GTGG TT TA TCTCTTCCCT	
		CACC AG GT AGAGAAGGGA	
		_ GA_ A	
GAM1001	PTPRO	3' AGGGAAGAGAGGGGTTCTACCC	25002 AT TGTA_
	AC	GTGG TAG CTCTCTTCCCT	
		CACC ATC GAGAGAAGGGA	
		C_ TTGGG	
GAM1001	PTPRO	3' AGGGAAGAGAGGGGTTCTACCC	25008 AT TGTA_
	AC	GTGG TAG CTCTCTTCCCT	

			CACC ATC GAGAGAAGGGA		
			C_ TTGGG		
GAM1001	PTPRO	3'	AGGGAAGAGAGGGGTTCTACCC 25017	AT	TGTA_
	AC		GTGG TAG CTCTCTTCCCT		
			CACC ATC GAGAGAAGGGA		
			C_ TTGGG		
GAM1001	PTPRO	3'	AGGGAAGAGAGGGGTTCTACCC 25026	AT	TGTA_
	AC		GTGG TAG CTCTCTTCCCT		
			CACC ATC GAGAGAAGGGA		
			C_ TTGGG		
GAM1001	PTPRO	3'	AGGGAAGAGAGGGGTTCTACCC 8737	AT	TGTA_
	AC		GTGG TAG CTCTCTTCCCT		
			CACC ATC GAGAGAAGGGA		
			C_ TTGGG		
GAM1001	SH3GL2	3'	GGAAGAAAACACTAGTAACCA 8966	___	ACTC
			TGG ATTAGTGT TCTTCC		
			ACC TGATCACA AGAAGG		
			AA AA_		
GAM1001	TRPS1	3'	GGAAAAGAGTATGCCCA 15355	ATTA	C
			TGG GTGTACTCT TTCC		
			ACC CGTATGAGA AAGG		
			_____ A		
GAM1001	ABCC13	3'	GGAAAGAGAGCTAATTAC 28973	TGTA	C
			GTGGATTAG CTCTCTT CC		
			CACTTAATC GAGAGAA GG		
			_____ A		
GAM1001	C22orf20	3'	AGGGAAGAGAATAGCATGATCC 24901	G	AC_
			GGATTA TGT TCTCTTCCCT		
			CCTAGT ACG AGAGAAGGGA		
			_ ATA		
GAM1001	FLJ12056	3'	AGGGAAGAAAGTGAAGGTAACC 24469	A	GTG_ C
	C		GG TTA TACT TCTTCCCT		
			CC AAT GTGA AGAAGGGA		
			C GGAA A		
GAM1001	FLJ20232	3'	GGAAGAGAGCACACAGAT 21085	A	A
			ATT GTGT CTCTCTTCC		
			TAG CACA GAGAGAAGG		
			A C		
GAM1001	FLJ30681	3'	GGAAGAGAAAAGATCAACTCAC 44105	GA	A GTAC
			GTG TT GT TCTCTTCC		

		CAC AA TA AGAGAAGG		
		TC C GAA_		
GAM1001	HSA249128 3'	GGAAAAGAGCCCCCTTTGATCCA	19028	TGTA_ C
	C	GTGGATTAG CTCT TTCC		
		CACCTAGTT GAGA AAGG		
		TCCCC A		
GAM1001	KIAA0774 5'	AGAGAAGAGAGGAGTCAACCCA	44087	A AG GTA C
		TGG TT T CTCTCTTC CT		
		ACC AA G GAGAGAAG GA		
		C CT AG_ A		
GAM1001	KIAA1164 5'	GGAAGAGAACACACCCATC	34441	TA AC
		GAT GTGT TCTCTTCC		
		CTA CACA AGAGAAGG		
		CC CA		
GAM1001	KIAA1867 5'	GGAAGAGAACTAACCAC	45456	A GTAC
		GTGG TTAGT TCTCTTCC		
		CACC AATCA AGAGAAGG		
		_ A_		
GAM1001	LAP1B 3'	GGAAATGTTACAGTAATCCAC	32264	G CTCTC
		GTGGATTA TGTA TTCC		
		CACCTAAT ACAT AAGG		
		G TGTA_		
GAM1001	MGC4796 3'	AGGAAAGAGAGTTCCAATCC	30827	AGTGT C
		GGATT ACTCTCTT CCT		
		CCTAA TGAGAGAA GGA		
		CCT_ A		
GAM1001	LOC134285 5'	AGGGAAGAAAACACATCCAC	37490	ATTA ACTC
		GTGG GTGT TCTTCCCT		
		CACC CACA AGAAGGGA		
		CTA_ AA_		
GAM1002	EGFL4 5'	GGCATCTCACACTGCAACCGC	30967	_ _ AC A
		GCG TG AGT GAGAT CC		
		CGC AC TCA CTCTA GG		
		CA G CA C		
GAM1003	DDX3 3'	CCCGCCTACCCCCATCCCAA	7033	AAATC TC
		TTTGGGATG TAGG CGGG		
		AAACCCTAC ATCC GCCC		
		CCCC_ _		
GAM1003	GRM1 3'	CCAGGCCAGACCCATCCCAA	6495	AAA A C
		TTTGGGATG TCT GGTC GG		

		AAACCCTAC AGA CCGG CC		
		CC_ _ A		
GAM1003	TRPV3	3' CCGTGATCCCATCCCAGA 45597	AAATCTA	_
		TTTGGGATG GGTC CGG		
		AGACCCTAC CTAG GCC		
		C_____ T		
GAM1003	FLJ10936	3' CCATCTAGACTCCATCTCAAA 20268	AAA	CC
		TTTGGGATG TCTAGGT GG		
		AAACTCTAC AGATCTA CC		
		CTC _		
GAM1003	phorbolin-1	3' ACCAGACTCCATCTCAAA 42798	AAA	A
		TTTGGGATG TCT GGT		
		AAACTCTAC AGA CCA		
		CTC _		
GAM1003	LOC151568	5' CCCAGGTGAGGATTCACATCCC 28836	A_	AGGT _
		AAA TTTGGGATG AATCT CC GGG		
		AAACCCTAC TTAGG GG CCC		
		AC AGT_ A		
GAM1003	LOC151996	5' CCCAGACCCAGAGCGTCACAAA 41413	G	AAA A C
		TTTG GATG TCT GGTC GGG		
		AAAC CTGC AGA CCAG CCC		
		A G_ C A		
GAM1003	LOC196759	3' CCCAGACCTAGGAGCTCCCCAA 42294	ATGAAA	C
		TTGGG TCTAGGTC GGG		
		AACCC GGATCCAG CCC		
		CTCGA_ A		
GAM1003	LOC201617	5' CTTAGACTTTATCCCCAA 43382	A	
		TTTGGGATGAA TCTAGG		
		AAACCCTATTT AGATTC		
		C		
GAM1003	LOC220045	3' CCCAGACCTAGGGGCTCCCCAA 44859	ATGAAA	C
		TTGGG TCTAGGTC GGG		
		AACCC GGATCCAG CCC		
		CTCGG_ A		
GAM1003	LOC93070	3' CCATCTAGACTCCATCTCAAA 35323	AAA	CC
		TTTGGGATG TCTAGGT GG		
		AAACTCTAC AGATCTA CC		
		CTC _		
GAM1004	FLJ20330	3' AGTATGGGTTTGGCCATA 21059	CCCAATT	
		TATGGCCAA CCCATACT		

		ATACCGGTT	GGGTATGA		
		T_____			
GAM1004	PRO0529	3'	ATGGGACCAGGTGGCCATA	15298	A CAAT
			TATGGCCA CC TCCCAT		
			ATACCGGT GG AGGGTA		
			_ ACC_		
GAM1004	LOC93206	3'	TATGATGGACCAGGTTGGCCA	35517	CAAT _
			TGGCCAACC TCC CATA		
			ACCGGTTGG AGG GTAT		
			ACC_ TA		
GAM1005	BAT4	5'	CGCATGCGTCTTCGTGCCGT	27040	A _ GC
			GC GCACGAA ATGCG GCG		
			TG CGTGCTT TCGGT CGC		
			C C A_		
GAM1005	CCND2	3'	CGCAGAACACCCCATGCGTGCT	7514	AA C CGC_
	G		CAGCACG ATG GG GCG		
			GTCGTGC TAC CC CGC		
			G_ C ACAAGA		
GAM1005	CDC34	5'	CGCGCGGCCCGCGCTGCT	10561	A AAAT G
			AGCAGC CG GC GCGCG		
			TCGTGC GC CG CGCGC		
			C CC_ G		
GAM1005	DVL3	5'	GCGCGCCGCGCCGTCTG	10698	C AAAT
			CAG ACG GCGGCGCGC		
			GTC TGC CGCCGCGCG		
			_ CGC_		
GAM1005	FGFR1	5'	CGCACGGTACCCGTGCTGC	17977	AAA GG C
			GCAGCACG TGC CG GCG		
			CGTCGTGC ATG GC CGC		
			CC_ _ A		
GAM1005	FGFR1	5'	CGCACGGTACCCGTGCTGC	23361	AAA GG C
			GCAGCACG TGC CG GCG		
			CGTCGTGC ATG GC CGC		
			CC_ _ A		
GAM1005	FGFR1	5'	CGCACGGTACCCGTGCTGC	23371	AAA GG C
			GCAGCACG TGC CG GCG		
			CGTCGTGC ATG GC CGC		
			CC_ _ A		
GAM1005	FGFR1	5'	CGCACGGTACCCGTGCTGC	23376	AAA GG C
			GCAGCACG TGC CG GCG		

		CGTCGTGC ATG GC CGC	
		CC_ _ A	
GAM1005 FGFR1	5'	CGCACGGTACCCGTGCTGC 6206	AAA GG C
		GCAGCACG TGC CG GCG	
		CGTCGTGC ATG GC CGC	
		CC_ _ A	
GAM1005 FOXG1B	5'	CGCGCCGCCGCGCGCCGCTG 11758	A A AAAT
		CAGC GC CG GCGGCGCG	
		GTCG CG GC CGCCGCGC	
		C C GCC_	
GAM1005 FUT8	5'	CGCGCCGCCTCGCGCTCTG 10795	C A AAT
		CAG AGC CGA GCGGCGCG	
		GTC TCG GCT CGCCGCGC	
		_ C C_	
GAM1005 GARS	5'	CGCGCGCCGCTTCCGTCGC 7796	_ A T
		GC ACG AA GCGGCGCGCG	
		CG TGC TT CGCCGCGCGC	
		C C _	
GAM1005 GNL1	5'	CGCGCGCCTCCTTCCTCGCCGC 44187	A AC_ ATGC
		GC GC GAA GCGCGCGC	
		CG CG CTT CCGCGCGC	
		C CTC CCT_	
GAM1005 GNL1	5'	CGCGCGCCTCCTTCCTCGCCGC 46716	A AC_ ATGC
		GC GC GAA GCGCGCGC	
		CG CG CTT CCGCGCGC	
		C CTC CCT_	
GAM1005 HDAC4	5'	CGCGCACCCGCCGCGCCGC 12663	A A AAAT C_
		GC GC CG GCGG GCGCG	
		CG CG GC CGCC CGCGC	
		C C C_ CA	
GAM1005 HPCAL1	5'	CGCACGGAGGCCCGCGCTGCT 7928	A AAAT GG_ C
		AGCAGC CG GC CG GCG	
		TCGTGC GC CG GC CGC	
		C C_ GAG A	
GAM1005 IDS	5'	CGCACGGACGCACTCGCGCTGC 5697	A AA G_ C
		GCAGC CGA TGCG CG GCG	
		CGTCG GCT ACGC GC CGC	
		C C_ AG A	
GAM1005 JAG2	5'	GCGCGCCGCGGCGCTGC 8005	ACGAAA
		GCAGC TGCGGCGCGC	

		CGTCG	GCGCCGCGCG		
		CG_____			
GAM1005	MET	5'	CGCGTGTGGTCCTTGC	35304	A A AAT G
	G		CAGC GC CGA GC		
			GTCG CG GTT TG		
			C C CC_ G		
GAM1005	NRXN1	5'	CGCGCCGCTGCTCCGCGCGCTG	28995	A A AAAT_
			CAGC GC CG GCGGCGCG		
			GTCG CG GC CGCCGCGC		
			_ C CTCGT		
GAM1005	SCN1A	3'	TGTTTGCATTTCAACTGC	42837	CAC C
			GCAG GAAATGCGG GCG		
			CGTC CTTTACGTT TGT		
			AA_ _		
GAM1005	SLC30A3	5'	CGCGCGCCACAGTCGCTGC	9524	ACGAAA C
			GCAGC TG GGCGCGCG		
			CGTCG AC CCGCGCGC		
			CTG_ A		
GAM1005	AP1S2	5'	CGCGCTGCCTCCGGTGCCGCTG	10002	A GAAAT
			CAGC GCAC GCGGCGCG		
			GTCG CGTG CGTCGCGC		
			C GCCTC		
GAM1005	C22orf4	3'	GCTGTATTTCACTGCTGCTG	30424	C_
			CAGCAGCA GAAATGCGGC		
			GTCGTCGT CTTTATGTCG		
			CA		
GAM1005	CHFR	3'	CGCGCCGCTCCCTCATGCTGC	20148	C AAT_
			GCAGCA GA GCGGCGCG		
			CGTCGT CT CGCCGCGC		
			A CCCT		
GAM1005	DKFZp547C176	5'	GCGCGCCGGGAGCTGCTG	33380	ACGAAATG
			CAGCAGC CGGCGCGC		
			GTCGTCG GCCGCGCG		
			AGG_____		
GAM1005	DKFZP564I1171	5'	CGCGCGCCGCGCCCGCGCTG	35443	A AAAT_
	CTG		CAGCAGC CG GCGGCGCGC		
			GTCGTCG GC CGCCGCGCGC		
			C CCGC		
GAM1005	DKFZp761A052	5'	CGCGCGCCGCCACCGCCGCGC	36141	A A_ AAAT
			GC GC CG GCGGCGCGC		

CG CG GC CGCCGCGCGC
 C CC CAC_
 GAM1005 FLJ13262 3' CGCGCGCCGCGCGCGCTGC 24433 A_ AAAT
 GCAGC CG GCGGCGCGCG
 |||| || |||||
 CGTCG GC CGCCGCGCGC
 CC ____
 GAM1005 FLJ20979 5' CGCGCGCCACACCCAGCGCGC 23574 A AAA__ C
 T AGC CG TG GCGCGCGC
 ||| || |||||
 TCG GC AC CCGCGCGC
 C GACCCC A
 GAM1005 GABARAPL3 3' CGCTCCCATGCTGCTG 26298 CGAAA C C
 CAGCAGCA TG GG GCG
 ||||| || |||
 GTCGTCGT AC CC CGC
 ____ _ T
 GAM1005 KIAA0668 5' CGCGCGCCCCGGGCCCCGGCCGC 33048 A A AAA_ C
 TG CAGC GC CG TG GCGCGCGC
 |||| || |||||
 GTCG CG GC GC CCGCGCGC
 C _ CCGG C
 GAM1005 KIAA0997 5' CGCGCGCCGCGCGCACTGC 17281 CA_ AAAT
 GCAG CG GCGGCGCGCG
 |||| || |||||
 CGTC GC CGCCGCGCGC
 ACC ____
 GAM1005 KIAA1228 5' CGCGCTGGCGCTGCTG 32440 ACGAAAT _
 CAGCAGC GC GCGCGC
 ||||| || |||||
 GTCGTCG CG TCGCGC
 ____ G
 GAM1005 KIAA1228 5' CGCGGAGCTTCGCGCTGCTG 32441 A AT GG
 CAGCAGC CGAA GC CGCG
 ||||| |||| || |||
 GTCGTCG GCTT CG GCGC
 C _ AG
 GAM1005 MOST2 5' CGGCGCGCGCACACCCAGTGC 21550 GAAA_____ GCG
 TGCTG CAGCAC TGCG CG
 |||| |||| ||| ||
 GTCGTG GCGC GC
 ACCCCACAC||| GCG
 GAM1005 PSIP2 5' CGCCCGCATCCCCGCGCCGC 27067 A A AA_ C
 GC GC CG ATGCGG GCG
 || ||| ||||| |||
 CG CG GC TACGCC CGC
 C C CCC _
 GAM1005 PTGES2 5' CGCGCGCCCGCCCGCGGCGC 24669 A A AAAT _
 GC GC CG GCGG CGCGC
 || ||| |||| |||||

CG CG GC CGCC GCGCGC
 _ _ GCC_ C
 GAM1005 Rab11-FIP3 5' CGCGCGCCCGCCGCGCCGC 16227 A A AAAT _
 GC GC CG GCGG CGCGCG
 || || | ||| |||||
 CG CG GC CGCC GCGCGC
 C C C__ C
 GAM1005 RAP2B 3' GCGCGCCGCGCGCTCTG 45861 C A AAATG
 CAG AGC CG CGGCGCGC
 ||| ||| | |||||
 GTC TCG GC GCCGCGCG
 _ C CG__
 GAM1005 RHOBTB1 5' CGCGCGCAGCCGTGGCTGCTG 43951 _ AAAT G
 CAGCAGC ACG GC GCGCGCG
 ||||| ||| || |||||
 GTCGTCG TGC CG CGCGCGC
 G _ _ A
 GAM1005 RNPC1 5' CGCCCCCATGCTGCTG 18957 CGAAA C C
 CAGCAGCA TG GG GCG
 ||||| || |||
 GTCGTCGT AC CC CGC
 _ _ C C
 GAM1005 SEMA3C 5' GCGCGCCGCGGCGCTGT 13073 ACGAAA
 GCAGC TGCGGCGCGC
 |||| | |||||
 TGTGCG GCGCCGCGCG
 CG__
 GAM1005 WBSCR23 3' CGGTTACCTTGTGCTGC 24638 AA C G
 GCAGCACGA TG GGC CG
 ||||| || |||
 CGTCGTGTT AC TTG GC
 CC _ _
 GAM1005 LOC133308 5' CGCGGCTCTGCACCCGCGCCGC 37035 A A AAA C _
 GC GC CG TGCGG GC GCG
 || || | ||| |||
 CG CG GC ACGTC CG CGC
 C C CC_ T G
 GAM1005 LOC134145 5' TTTCATTCACTGCTGCTG 37062 C_ CG
 CAGCAGCA GAAATG G
 ||||| ||||| |
 GTCGTCGT CTTTAC T
 CA TT
 GAM1005 LOC143915 3' CGGAATTCATCTCGCTGCTGCT 40377 _ A CGGCG
 G CAGCAGCA CGA ATG CG
 ||||| ||| ||| ||
 GTCGTCGT GCT TAC GC
 C C TTAAG
 GAM1005 LOC145481 5' GCGCGCCGCGCCGCGCTG 37890 A A AAATG
 CAGC GC CG CGGCGCGC
 ||| || | |||||

		GTCG CG GC GCCGCGCG	
		C _ CG__	
GAM1005	LOC146894 3'	CGGCGCGCGCAGAATCTCGTGC 29781	AA_____ GCG
		TGCTG CAGCACGA TGCG CG	
		GTCGTGCT GCGC GC	
		CTAAGAC GCG	
GAM1005	LOC148709 5'	GCACCCAGTGCTGCTG 38583	GAAA C C
		CAGCAGCAC TG GG GC	
		GTCGTGCTG AC CC CG	
		_____ A	
GAM1005	LOC149297 5'	CGCGCGGGCCCCCGCGCTGC 40979	A AAAT GG
		GCAGC CG GC CGCGCG	
		CGTCG GC CG GCGCGC	
		C CCC_ G_	
GAM1005	LOC151127 5'	CGCGCCCGCGGCCCGCGCGC 39061	A A AAA C
		GC GC CG TGCGG GCGCG	
		CG CG GC GCGCC CGCGC	
		_ C CCG _	
GAM1005	LOC153474 5'	CGCGCGCCGCGCCCGCGCTG 39379	A AAAT_
		CTG CAGCAGC CG GCGGCGCGCG	
		GTCGTGCG GC CGCCGCGCGC	
		C CCGC	
GAM1005	LOC153505 3'	CGCGCGCCGCTGTGTGCTGCT 39382	AAAT
		G CAGCAGCACG GCGGCGCGCG	
		GTCGTGCTGT CGCCGCGCGC	
		GTC_	
GAM1005	LOC164537 5'	CGCGGCCCTCGTGCTGC 42172	AATGC G
		GCAGCACGA GGC CGCG	
		CGTCGTGCT CCG GCGC	
		CC_____	
GAM1005	LOC219513 3'	CGCTGCATTTGTACCGCTG 45294	AGC G
		CAGC AC AAATGCGGCG	
		GTCG TG TTTACGTCGC	
		CCA _	
GAM1005	LOC221938 5'	CGCGCGCCCTCCAACCTGCTGC 44513	CGAAATGC
		TG CAGCAGCA GCGCGCGC	
		GTCGTGCT CCGCGCGC	
		CCAACCTC	
GAM1005	LOC255104 5'	CGGCCTACAGCCCGTGCTGCTG 45684	AAA C_ G
		CAGCAGCACG TG GGC CG	

GTCGTCGTGC AC CCG GC
 CCG AT _
 GAM1005 LOC257541 5' CGCGCGCCTCCTTCCTCGCCGC 46671 A AC_ ATGC
 GC GC GAA GGC GCGC
 || || || |||||
 CG CG CTT CCGCGCGC
 C CTC CCT_
 GAM1006 ACADM 5' CCGCCTCTTCCCGCCCCGCCCC 5451 A C A____
 A TG GGC GGGGCGG AGGCGG
 || || ||||| |||||
 AC CCG CCCC GCC TCCGCC
 C _ CTTC
 GAM1006 AF5Q31 5' ACCCGCCCCCGCCTGCCTCA 15777 CG AA
 TGAGGC GGGCGG GGC GGGT
 ||||| ||||| |||||
 ACTCCG TCCGCC CCGCCCA
 _ C_
 GAM1006 ASGR2 5' CCTCTGCCCCAGCCCCA 28130 A C A
 TG GGC GGGGCGGA GG
 || || ||||| ||
 AC CCG CCCC GTCT CC
 C A _
 GAM1006 BARHL1 3' ACCCCAGCCCCCAGCCTCA 21300 C_ GGAAGGC
 TGAGGC GGGGC GGGT
 ||||| |||| ||||
 ACTCCG CCCC G CCA
 AC AC____
 GAM1006 CGTHBA 5' GCCCCCGGCCCGGCCCA 14362 A GGAA C
 TG GGCCGGGGC GG GGGT
 || ||||| || ||||
 AC CCGGCCCG CC CCG
 C G____
 GAM1006 CKTSF1B1 3' ACCCACCTCACCCCGGCTCA 15021 G C GA C
 TGAG CCGGGG G AGG GGGT
 |||| ||||| | |||||
 ACTC GGCCCC C TCC CCA
 _ A _ A
 GAM1006 ESPN 3' GCCCTCCGCCCCAGCCCCA 25549 A C A
 TG GGC GGGGCGGA GGC
 || || ||||| ||||
 AC CCG CCCC GCCT CCG
 C A C
 GAM1006 GPC1 3' GACCCGCCTGCTCCCATCCTCA 7872 CC _ GGA
 TGAGG GGG GC AGGCGGGT
 |||| || || |||||
 ACTCC CCC CG TCCGCCAG
 TA T ____
 GAM1006 HTRA3 5' GACCGCGCGTCCGCCCCAGTCC 42941 A C AG _
 CA TG GGC GGGGCGGA GCG GGTC
 || || ||||| || |||||

			AC CTG CCCCCGCT CGC CCAG			
			C A G_ G			
GAM1006	IGF2	5'	CTGGCCCCGCCAGCCCG	6215	A C	AAG G
			TG GGC GGGGCGG GC GG			
			GC CCG CCCCCGCC CG TC			
			_ A _ _ G			
GAM1006	KIFC3	5'	GCCCCGCCAGCCCCA	12082	A C	AA
			TG GGC GGGGCGG GGC			
			AC CCG CCCCCGCC CCG			
			C A _			
GAM1006	NOTCH3	3'	ACTCCCTCTGCCAGCCCCA	6016	A C	A C
			TG GGC GGGGCGGA GG GGGT			
			AC CCG CCCCCTCT CC CTCA			
			C A _ _			
GAM1006	PACE	3'	GCCCCGGCCCCGGCCCCA	8426	A	_ AA
			TG GGCCGGGGC GG GGC			
			AC CCGGCCCG CC CCG			
			C G _			
GAM1006	PACSIN1	3'	ACCCTTCCACCCGCCTCA	44310	C C	GGC
			TGAGGC GGGG GGAA GGGT			
			ACTCCG CCCC CCTT CCCA			
			_ A _			
GAM1006	RARA	3'	GCCCCACCCCGGCCTCA	6688		CGGAA C
			TGAGGCCGGGG GG GGGT			
			ACTCCGGCCCC CC CCG			
			CA _ _			
GAM1006	RNMT	3'	CCCCTCCCCCGGCCCA	9885	A	C A C
			TG GGCCGGGG GGA GG GG			
			AC CCGGCCCC CCT CC CC			
			C _ _ _			
GAM1006	ROR2	5'	CCCGCGCCCCGGCCCG	10898	A	GGAAG
			TG GGCCGGGGC GCGGG			
			GC CCGGCCCG CGCC			
			_ _ _ _			
GAM1006	CECR2	5'	GCCCCTCCGCCCTAGCCCCA	25393	A C_	A_
			TG GGC GGGGCGGA GGC			
			AC CCG CCCCCGCT CCG			
			C AT CC			
GAM1006	CEP3	5'	GCCCTCCGCCCGGCCCA	13158	A C	A
			TG GGC GGGGCGGA GGC			

AC CCG CCCCCGCT CCG
 C _ C
 GAM1006 DKFZP434H132 5' GACCCACCTGCTCTCTGGCCC 36449 A _ AA C
 CA TG GGCCGG G GCGG GG GGGTC
 || ||||| | ||| || |||||
 AC CCGGTC C CGTC CC CCCAG
 C T T _ A
 GAM1006 DKFZp547M072 3' GCCCTCCGCCCCGCCCA 30616 A C A
 TG GGC GGGGCGGA GGC
 || ||| ||||| |||
 AC CCG CCCCCGCT CCG
 C _ C
 GAM1006 DKFZp586I021 5' GACCCGCCTTTTCAGCCGTC 26026 CGG _
 GGC GGC GGAAGGCGGGTC
 ||| ||| ||||| |||||
 CTG CCG TTTCCGCCCAG
 _ AC
 GAM1006 FLJ10743 3' GCTCTGCCGCCCCAGCCTCA 20079 C A _
 TGAGGC GGGGCGG AG GC
 ||||| ||||| || ||
 ACTCCG CCCCCGCC TC CG
 A G T
 GAM1006 FLJ14810 5' GACCCGCGCTGCCCCGACCTCA 26635 C AAG
 TGAGG CGGGGCGG GCGGGTC
 ||||| ||||| |||||
 ACTCC GCCCCGTC CGCCCAG
 A G _
 GAM1006 FLJ21438 5' TCGACCCGCCCCCTTCTGTCCAC 30848 _ _ |||
 TCCCGGCCCA G GCGGAA GGCGGGTC GA
 | ||||| ||||| ||
 C TGTCTT CCGCCCAG CT
 TCACC CC |||
 GAM1006 FLJ22215 3' CCCGCAGCAGCCCCGGCCCCA 23117 A GGAAG
 TG GGCCGGGGC GCGGG
 || ||||| |||||
 AC CCGGCCCCG CGCCC
 C ACGA_
 GAM1006 KIAA0258 3' GCCCCCCCACCCCAACCCCG 16647 A CC C AA C
 TG GG GGGG GG GG GGGT
 || || ||| || || |||||
 GC CC CCCC CC CC CCGG
 C AA A _ _
 GAM1006 KIAA0552 5' GTCCCCTGCCCCGGCCTCA 16348 AA
 TGAGGCCGGGGCGG GGC
 ||||| ||||| |||
 ACTCCGGCCCCGTC CTG
 CC
 GAM1006 KIAA0618 5' GACAGCAGCCCCGCCCGGCCTC 16834 AAG GG
 GAGGCCGGGGCGG GC GTC
 ||||| ||||| || |||

CTCCGGCCCCGCC CG CAG
 CGA A_
 GAM1006 KIAA1530 5' GCCTCCGCCCCGGCCTC 33734 A
 GAGGCCGGGGCGGA GGC
 |||||
 CTCCGGCCCCGCCT CCG

 -
 GAM1006 MCLC 3' GACCCGCCCTTGTTCGGCCTC 17492 GG AA
 GAGGCCG GCGG GGCGGGTC
 ||||| ||| |||||
 CTCCGGC TGTT CCGCCCAG

 C_
 GAM1006 QKI 5' CGACCCGCCTCCCGCCCGCCCG 32617 A III
 CCGGCCTC GG GCGG AGGCGGGTC G
 || ||||| |||
 CC CCGCC TCCGCCAG C
 GCCGC C III
 GAM1006 RBAK 5' GACAGCAGCCCCGCCCGGCCT 22141 AA GG_
 C GAGGCCGGGGCGG GGC GTC
 ||||| ||| |||
 CTCCGGCCCCGCC CCG CAG
 ACGA
 GAM1006 LOC116113 3' GTCTCCACCCCGGCCCA 44287 A C A
 TG GGCCGGGG GG AGGC
 || ||||| || |||
 AC CCGGCCCC CC TCTG
 C A C
 GAM1006 LOC145547 3' GACCCAGGGGCCCGGCCTC 37893 GGAAGGC
 GAGGCCGGGGC GGGTC
 ||||| |||||
 CTCCGGCCCCG CCCAG
 GGGA_
 GAM1006 LOC221424 5' GCCTCCACCCCGGCCCA 44979 A C_ A
 TG GGCCGGGG GGA GGC
 || ||||| ||| |||
 AC CCGGCCCC CCT CCG
 C CA _
 GAM1006 LOC221486 3' GACCCACCTCCCCCTCCCGGC 43743 C A_ C
 C GGCCGGGG GG AGG GGGTC
 ||||| || ||| |||||
 CCGGCCCC CC TCC CCCAG
 T CCC A
 GAM1007 EP300 5' GCGAAGGAGGGGAGCGCCGGC 7150 ATA_ C C
 GT GC CCCCTCCT CGC
 || || ||||| |||
 CG CG GGGGAGGA GCG
 GCCG A A
 GAM1007 GAB2 3' GGAGGAGGGCAGGGCTTG 14653 T _
 A AGCCC CCCTCCTCC
 | |||| |||||

G TCGGG GGGAGGAGG
 T AC
 GAM1007 GAB2 3' GGAGGAGGGCAGGGCTTG 27848 T ____
 A AGCCC CCCTCCTCC
 | |||| |||||
 G TCGGG GGGAGGAGG
 T AC
 GAM1007 MLLT3 5' GCGGAGGAGGGGGGGTAC 10868 AG
 GTAT CCCCCCTCCTCCGC
 ||| |||||
 CATG GGGGGGAGGAGGCG
 G_
 GAM1007 TBL2 3' GCGGGAGGATGGGGGCTACACC 26869 A A C _
 TTC GAA GT TAGCCCC TCCTCC GC
 ||| || ||||| ||||| ||
 CTT CA ATCGGGGG AGGAGG CG
 C C T G
 GAM1007 CALN1 3' GCAGATCTTGAAGGGATATACT 25516 G CCCTCC_ C
 TTC GAAAGTATA CCC TC GC
 ||||| || |||
 CTTTCATAT GGG AG CG
 A AAGTTCT A
 GAM1007 CDC14B 3' CGGAGGAGTCTATACTATC 27168 A CCCCC
 GA AGTATAG CTCCTCCG
 || ||||| |||||
 CT TCATATC GAGGAGGC
 A T____
 GAM1007 DGS-A 3' AGGCTGGGAGGGACATACTTTC 41149 AG _ T_
 GAAAGTAT CCC CCC CCT
 ||||| ||| ||| |||
 CTTTCATA GGG GGG GGA
 CA A TC
 GAM1007 DKFZP761E2110 5' GCGGAGGAGGAAGCTGTGGCT 25226 _ CCC
 AGT ATAGC CCTCCTCCGC
 ||| ||||| |||||
 TCG TGTCTG GGAGGAGGCG
 G AA_
 GAM1007 HCCA2 5' GCGGAGGAGAGGAAGGCCTAC 33205 TA C_ _
 GTA GCC CC CTCCTCCGC
 ||| ||| || |||||
 CAT CGG GG GAGGAGGCG
 C_ AA A
 GAM1007 KIAA0449 5' GCAGAGGAGGGAAGTCTCCTT 19053 A TAT CC_ C
 C GAA G AGC CCCTCCTC GC
 ||| | ||| ||||| ||
 CTT C TCG GGGAGGAG CG
 _ C_ TCAA A
 GAM1007 KIAA0596 3' GAGGAGGGAGCTACCCTT 31462 TA CC
 AAG TAGC CCCTCCTC
 ||| ||||| |||||

TTC ATCG GGGAGGAG
 CC A_
 GAM1007 KIAA0599 3' GCGGAGGAGAGGCTGAGCCTTC 37858 A A CCC
 GAA GT TAGCC CTCCTCCGC
 ||| || |||| |||||
 CTT CG GTCGG GAGGAGGCG
 C A A_
 GAM1007 KIAA1283 5' GCGGAGGAGGGGCCCTCTTTC 35663 TATAGCC
 GAAAG CCCCTCCTCCGC
 |||| |||||
 CTTTC GGGGAGGAGGCG
 TCCCC_
 GAM1007 MGC2217 5' CAAGGAGGGGACTTTC 23589 ATAGCC CC
 GAAAGT CCCCTCCT G
 |||| ||||| |
 CTTTCA GGGGAGGA C
 AA
 GAM1007 LOC114932 3' GAGGAGAGCTATGTTTT 36006 CCCC
 AAAGTATAGC CTCCTC
 ||||| ||||
 TTTTGTATCG GAGGAG
 A_
 GAM1007 LOC159036 3' CGAAGGAGGAGGACACACTTTT 42053 ATAG CC C
 GAAAGT CC CCTCCT CG
 |||| || ||||| ||
 TTTTCA GG GGAGGA GC
 CACA A_ A
 GAM1007 LOC201595 5' GCGGAGGAGGAGAGCTAGAC 42886 A CCC
 GT TAGC CCTCCTCCGC
 || |||| |||||
 CA ATCG GGAGGAGGCG
 G AGA
 GAM1007 LOC222662 5' CGGAGGAGGGGGCGGGGCTCTC 44603 A ATA C
 GA AGT GCCCCC TCCTCCG
 || |||| |||||
 CT TCG CGGGGG AGGAGGC
 C GGG _
 GAM1007 LOC256586 5' GCGGAGGAGGAGGAGGCGCCGC 45515 ATA _ _
 GT GCC CC CTCCTCCGC
 || |||| |||||
 CG CGG GG GGAGGAGGCG
 CCG A A
 GAM1008 NGFR 3' TTGCAACACACAGACACACGCA 8336 A AGACG_ AT
 TG CGT GTGT GTTGCAA
 || |||| |||||
 AC GCA CACA CAACGTT
 _ CACAGA _
 GAM1008 OPA3 3' TTGCAACATAGCCCCCTCCATC 24775 CGT AC G
 A
 TGA AG GGT TATGTTGCAA
 || |||| |||||

ACT TC CCG ATACAACGTT
 ACC CC _
 GAM1008 KIAA0447 3' ACATCAACAGTCTACGTCA 35492 GG_ T
 TGACGTAGAC TG ATGT
 ||||| || ||||
 ACTGCATCTG AC TACA
 ACA _
 GAM1008 P2RX1 3' CAGTGTACACACCACCTACGTG 33353 _ ACG_ TG
 CA TG ACGTAG GTGTA TTG
 || |||| |||| ||
 AC TGCATC CACAT GAC
 G CACCA GT
 GAM1008 USP22 3' GGCATGCACCACCACGCCA 33752 A AGAC
 TG CGT GGTGTATGTT
 || || |||||
 AC GCA CCACGTACGG
 C CCA_
 GAM1008 LOC146229 3' TGCAATGCCATCCTCGCCA 38118 A TA C GTAT
 TG CG GA GGT GTTGCA
 || || || ||||
 AC GC CT CCG TAACGT
 C TC A _
 GAM1009 IL1F5 3' CGTCTGACTTAGTGGGCACCTG 14599 TATA_
 A TCAGGTGCCCACTGA ACG
 ||||| |||| ||
 AGTCCACGGGTGATT TGC
 CAGTC
 GAM1009 NBR2 3' GCGGCCAGCAGGCACCTGG 12424 CA ATATAA
 TCAGGTGCC CTG CGC
 ||||| || ||
 GGTCCACGG GAC GCG
 AC CG_
 GAM1009 LOC149134 5' CGTCTGTGATGTGGGCACCT 40957 TGA _
 AGGTGCCAC TATA ACG
 ||||| |||| ||
 TCCACGGGTG GTGT TGC
 TA_ C
 GAM1009 LOC168283 5' CGTTATATCAATGAAAACCT 40239 GCC C
 AGGT CA TGATATAACG
 || || |||||
 TCCA GT ACTATATTGC
 AAA A
 GAM1010 CISH 5' CCCAGCACGCGCTCCGCGCC 14971 T CT CA
 GGCGCGGA GT GCGTGC GG
 ||||| || |||| ||
 CCGCGCCT CG CGCACG CC
 _ _ AC
 GAM1010 MAPRE3 3' CCTGGCACCAGGCTCACCCACC 14713 CGC AT_ C
 CA TGG GG GTCTG GTGCCAGG
 || || |||| |||||

ACC CC CGGAC CACGGTCC
 CAC ACT _
 GAM1010 DKFZp434O0320 3' CCTGGCACACAGTAGGAGC 40704 GGA T C
 GC TG CTG GTGCCAGG
 || |||||
 CG AT GAC CACGGTCC
 AGG _ A
 GAM1010 EPSIN 5' CCTGGCACACAGCAGGGACCCA 14980 CGCGGA T C
 TGG TG CTG GTGCCAGG
 ||| |||||
 ACC AC GAC CACGGTCC
 CAGGG _ A
 GAM1010 FASTK 5' CCGACTTCGCCGACTCCGCGCC 24728 T T TGCCA
 A TGGCGCGGA GTC GCG GG
 ||||| |||||
 ACCGCGCCT CAG CGC CC
 _ C TTCAG
 GAM1010 HSPC065 3' CCTGGCACACAGCAAACACTC 15451 GA _ C
 G TGT CTG GTGCCAGG
 | ||| |||||
 C ACA GAC CACGGTCC
 TC AAC A
 GAM1010 MGC16025 3' CCTGGCACACAGCAGGAGCCA 26748 GCGGA T C
 TGGC TG CTG GTGCCAGG
 |||| |||||
 ACCG AC GAC CACGGTCC
 AGG _ A
 GAM1010 SEC8 3' CCTGGCACACTGGACCTCACCA 22360 CGCG T GC_
 TGG GA GTCT GTGCCAGG
 ||| |||||
 ACC CT CAGG CACGGTCC
 A _ C TCA
 GAM1010 SYNE-2 3' CCCAGCACGTGGCCCCAGACCA 17532 CGC AT T CA
 TGG GG GTC GCGTGC GG
 ||| |||||
 ACC CC CGG TGCACG CC
 AGA C _ AC
 GAM1010 TOB2 3' CCTGGCACCCCACTCC 45767 _ TC C_
 GGA TG TG GTGCCAGG
 ||| |||||
 CCT AC AC CACGGTCC
 C CC CC
 GAM1010 LOC127435 3' CCTGGCACACAGGCACCC 37461 A C_
 GG TGTCTG GTGCCAGG
 || |||||
 CC ACGGAC CACGGTCC
 C ACA
 GAM1010 LOC157556 5' CCTGGCATCGTACACCAGCACC 41822 C _ A CT _
 A TGG GC GG TGT GCG TGCCAGG
 ||| |||||

ACC CG CC ACA TGC ACGGTCC
 A A _ _ T
 GAM1010 LOC220143 5' CCTGGCACACAGACATAAAGC 44952 GG_ C
 GC ATGTCTG GTGCCAGG
 || ||||| |||||
 CG TACAGAC CACGGTCC
 AAA A
 GAM1011 MID1 3' AATAGCAGCACCCTTTG 5954 AG C
 CAAAGTGGT TGC TGTT
 ||||| || |||
 GTTTCACCA ACG ATAA
 CG _
 GAM1011 MUC3B 5' CGTCTGTGGGCACCAGCACTTC 45253 A GTA TG TGC
 A C AAGTG GTGCC T ACG
 | |||| |||| | |||
 A TTCAC CACGG G TGC
 C GAC GT TC_
 GAM1011 MYCL1 3' CGTGCCTCCCCACCACCTT 11852 A CCTGTT
 AAGTGGT GTG GCACG
 ||||| || ||||
 TTCACCA CAC CGTGC
 C CCCTC_
 GAM1011 TCL1A 3' GCCTTAGCACTACCACT 22498 C TT
 AGTGGTAGTGC TG GC
 ||||| || ||
 TCACCATCACG AT CG
 _ TC
 GAM1011 CAPN6 3' GCGCACGAACCTACCATTCA 15569 A GCC T
 A AGTGGTAGT TGT GC
 | ||||| || ||
 A TTACCATCA ACG CG
 C AGC _
 GAM1011 FLJ11127 3' ACAGAGAACCACTACTTTG 21108 A GC_
 CAAAGTGGT GT CTGT
 ||||| || |||
 GTTTCATCA CA GACA
 C AGA
 GAM1011 KIAA1971 3' ACAGGCGCCACCACCTTG 36726 A A
 CAA GTGGT GTGCCTGT
 || |||| |||||
 GTT CACCA CGCGGACA
 C C
 GAM1011 LOC146756 3' CAACAGGAGAGCCACTTT 40733 AGTG
 AAAGTGGT CCTGTTG
 ||||| |||||
 TTTCACCG GGACAAC
 AGA_
 GAM1011 LOC254015 3' CAACAGGAGAGCCACTTT 46241 AGTG
 AAAGTGGT CCTGTTG
 ||||| |||||

			TTTCACCG GGACAAC		
			AGA_		
GAM1012	COL18A1	3'	AAATAAAAGTGACCTTTTACA 24955	ATG	
			TGTAAAGGGT TTTTATTT		
			ACATTTTCCA GAAAATAAA		
			GT_		
GAM1012	COL18A1	3'	AAATAAAAGTGACCTTTTACA 28206	ATG	
			TGTAAAGGGT TTTTATTT		
			ACATTTTCCA GAAAATAAA		
			GT_		
GAM1012	COL18A1	3'	AAATAAAAGTGACCTTTTACA 28207	ATG	
			TGTAAAGGGT TTTTATTT		
			ACATTTTCCA GAAAATAAA		
			GT_		
GAM1012	UBE2A	3'	GTAATAAAAAATAACCTT 9341	A	
			AGGGT TGTTTTTATTTAC		
			TTCCA ATAAAAATAAATG		
			—		
GAM1012	EFS2	3'	TAAATAAAAACATAAACC 12479	G_	
			GG TATGTTTTTATTTA		
			CC ATACAAAAATAAAT		
			AA		
GAM1012	FLJ21032	3'	TAAATAAAAACATAAGTATA 24402	AAGGG	
			TGTA TATGTTTTTATTTA		
			ATAT ATACAAAAATAAAT		
			GA_		
GAM1012	FLJ23120	3'	TAAACAAAAATGTACCTTCACA 41266	AA	A
			TGT AGGGTATGTTTTT TTTA		
			ACA TTCCATGTAAAAA AAAT		
			C_ C		
GAM1012	KIAA0379	5'	AAATGGTTGACACCTTTACA 33810	GTA	T_
			TGTAAAGG TGTT TTATTT		
			ACATTTCC ACAG GGTAAG		
			— TT		
GAM1012	LAP1B	3'	ATAAATGTATACCCCTTAC 32263	A	TT
			GTAA GGGTATG TTTAT		
			CATT CCCATAT AAATA		
			C GT		
GAM1012	PBEF	3'	AAATAAACATGGCCTTAACA 12307	A	G T
			TGT AAGG TATGTTTT ATTT		

ACA TTCC GTACAAAA TAAA
 A G _
 GAM1013 DKFZP434O047 5' AACATGGGGGGGCCAGA 17859 GAT G
 TCTG GCC CCCATGTT
 ||| ||| |||||
 AGAC CGG GGGTACAA
 _ G
 GAM1013 FLJ32894 3' AACATGGGCAAAGTAATCA 29484 A C_
 TGG TGC GCCCATGTT
 ||| ||| |||||
 ACT ATG CGGGTACAA
 A AAA
 GAM1013 LOC151248 5' ACATCATCCAGATTCCA 39084 A CCGCCC
 TG AATCTGGATG ATGT
 || ||||| |||
 AC TTAGACCTAC TACA
 C _
 GAM1014 C6orf37 3' CATCTTGGCTCAGTCTCCCTCA 33510 A ACATC
 TGAG GAGATT TTAAGATG
 ||| ||||| |||||
 ACTC CTCTGA GGTTCTAC
 C CTC_
 GAM1014 LOC196761 5' ATCTTAAAATGTAGGCTC 43127 A C
 GAG TTACAT TTAAGAT
 ||| ||||| |||||
 CTC GATGTA AATTCTA
 G A
 GAM1014 LOC200609 3' CATCTTAACCTGAGTCCCTCTC 43326 A A TC
 A TGAGAG GATT CA TTAAGATG
 ||||| ||| || |||||
 ACTCTC CTGA GT AATTCTAC
 C _ CC
 GAM1015 EDN2 3' ACTTATTTGCCCTAAGAA 7680 G A C
 TTC TAG GGC AAGTAAGT
 ||| ||| ||| |||||
 AAG ATC CCG TTTATTCA
 A _ _
 GAM1015 SLC20A2 5' GAACTCTTGGCCTTACGAA 13602 A TAAG
 TTCGT GAGGCCAAG TC
 ||||| ||||| ||
 AAGCA TTCCGGTTC AG
 _ TCA_
 GAM1015 FLJ13231 3' GACTCCGGCCTCTAGAA 23329 G AAGTA
 TTC TAGAGGCC AGTC
 ||| ||||| |||
 AAG ATCTCCGG TCAG
 _ CC_
 GAM1015 KIAA0981 3' ACTTACTTTGTGTCTAGGAA 30795 G G C
 TTC TAGA GC AAGTAAGT
 ||| ||| || |||||

AAG ATCT TG TTCATTCA
 G G T
 GAM1015 LOC148014 3' TGACGGGAGCCTCTGCGAA 38441 CAAGTAA
 TTCGTAGAGGC GTCA
 ||||| ||||
 AAGCGTCTCCG CAGT
 AGGG__
 GAM1015 LOC152627 5' ACTCACTTCAATTCTATGAA 39292 GCC A
 TTCGTAGAG AAGT AGT
 ||||| ||||
 AAGTATCTT TTCA TCA
 AAC C
 GAM1016 AMD1 3' TAGTAATATAGGCTTTCA 7348 G TCA
 TGAGAG CT ATATTACTA
 ||||| |||||
 ACTTTC GA TATAATGAT
 G _
 GAM1016 PITPNB 3' ATTATATTGTTGAAGCCTTCA 14764 G T C
 TGA AGGCTTCAATA TA TAAT
 || ||||| || ||||
 ACT TCCGAAGTTGT AT ATTA
 _ T _
 GAM1016 RP2 3' ATTAGTAATATTGAGCGCTC 13791 _ T
 GAG GCT CAATATTACTAAT
 || || |||||
 CTC CGA GTTATAATGATTA
 G _
 GAM1016 ARHGEF2 3' ATTAGAGATCGAAGCCTC 11089 AAT A
 GAGGCTTC ATT CTAAT
 ||||| || ||||
 CTCCGAAG TAG GATTA
 C_ A
 GAM1016 CNOT7 3' AGTAATATTAGCAAATCTC 14999 G_ TC
 GAGA GCT AATATTACT
 ||| || |||||
 CTCT CGA TTATAATGA
 AAA _
 GAM1016 LOC163341 3' GATCAGTAATATCAAAGAGCAC 39948 AG CA_ A
 CT AG GCTT ATATTACT ATC
 || ||| ||||| ||||
 TC CGAG TATAATGA TAG
 CA AAAC C
 GAM1016 LOC219920 5' TAGTGCTTGAAGCCTCTCA 44811 TAT
 TGAGAGGCTTCAA TACTA
 ||||| ||||
 ACTCTCCGAAGTT GTGAT
 C_
 GAM1017 KIF3B 3' ATGGAGATCTGTTGTC 11215 GT A
 GACAA CA ATCTCCAT
 |||| || |||||

CTGTT GT TAGAGGTA
 — C
 GAM1017 LDHB 5' AGATGGAGAAGAGACCATCA 8086 CAA AAA
 TGA GTC TCTCCATCT
 ||| ||| |||||
 ACT CAG AGAGGTAGA
 AC_ AGA
 GAM1017 NEDD4L 3' AGACAGAGACTTGACTTGATC 17605 _ A CA
 GA CAAGTCAA TCTC TCT
 || ||||| ||| |||
 CT GTTCAGTT AGAG AGA
 A C AC
 GAM1017 PPP1R3C 3' TGGTCTTGACTTGTCATA 11877 ATCT
 TATGACAAGTCAA CCA
 ||||| |||
 ATACTGTT CAGTT GGT
 CT_
 GAM1017 RFXAP 3' GGTCAATTTGATTGTCATA 6137 G CT_
 TATGACAA TCAAAT CC
 ||||| ||| ||
 ATACTGTT AGTTTA GG
 _ ACT
 GAM1017 XK 3' ATGCAATTTGACTTGGCATA 22054 A CTC
 TATG CAAGTCAAAT CAT
 ||| ||||| |||
 ATAC GTTCAGTTTA GTA
 G AC_
 GAM1017 EVI5 3' AGACAGAGATT CAGTTTGTCA 12206 CA CA
 TGACAAGT AATCTC TCT
 ||||| ||||| |||
 ACTGTTTG TTAGAG AGA
 AC AC
 GAM1017 IMAGE145052 3' AGATGGAGTTATAACTGTCATA 15542 A CAAAT
 TATGACA GT CTCCATCT
 ||||| || |||||
 ATACTGT CA GAGGTAGA
 _ ATATT
 GAM1017 KIAA0040 5' AGATGGAGAAGAGACCATCA 16093 CAA AAA
 TGA GTC TCTCCATCT
 ||| ||| |||||
 ACT CAG AGAGGTAGA
 AC_ AGA
 GAM1017 KIAA0410 3' AGATGACAGAATTGACTTGCCA 16613 A A C_
 TA TATG CAAGTCAA TCT CATCT
 ||| ||||| ||| |||||
 ATAC GTTCAGTT AGA GTAGA
 C A CA
 GAM1017 KIAA1579 3' AGATGGAGAAAGATGATCATA 20117 CAA AAA
 TATGA GTC TCTCCATCT
 |||| ||| |||||

ATACT TAG AGAGGTAGA
 AG_ AA_
 GAM1017 MGC10999 3' AGATGGAGACCTTGTC 26088 TCAA
 GACAAG TCTCCATCT
 ||||| |||||
 CTGTTC AGAGGTAGA
 C____
 GAM1017 NEIL2 3' GATGGGGTCTTGCCATA 29674 A TCAAAT
 TATG CAAG CTCCATC
 ||| ||| |||||
 ATAC GTTC GGGGTAG
 C T____
 GAM1017 SSH2 3' AGACAGGTTTTTTGGCTTATCA 31174 C TCT A_
 TGA AAGTCAAA CC TCT
 || ||||| || |||
 ACT TTCGGTTT GG AGA
 A TT_ AC
 GAM1017 LOC126302 3' ATGGGCTACTTGTCATA 36818 CAAATC
 TATGACAAGT TCCAT
 ||||| |||||
 ATACTGTTCA GGGTA
 TC____
 GAM1017 LOC145463 3' AGATGGAGTTATAACTGTCATA 35121 A CAAAT
 TATGACA GT CTCCATCT
 ||||| || |||||
 ATACTGT CA GAGGTAGA
 _ ATATT
 GAM1017 LOC255082 5' AGATGGAGATTCAGAAACATA 46117 ACAAG A_
 TATG TC AATCTCCATCT
 ||| || |||||
 ATAC AG TTAGAGGTAGA
 AA__ AC
 GAM1018 KIAA0556 3' AACACGACACAAGCTCACTCCC 34247 CGC GC_
 GGG TGAGC GTCGTGTT
 || ||||| |||||
 CCC ACTCG CAGCACAA
 TC_ AACA
 GAM1018 LOC256052 5' ACACGTTCAAGTGCCCTCA 46603 C
 TGAGGGCGCTGAGCG GT
 ||||| ||||| ||
 ACTCCCGTGACTTGC CA
 A
 GAM1018 LOC90139 3' AACACCAGGCCCGAGCGCCCTC 28272 A GCGTC
 GAGGGCGCTG GC GTGTT
 ||||| || |||||
 CTCCCGCGAC CG CACAA
 C GAC_
 GAM1019 ANK1 3' TGAGTTTCAGAATATTCCA 30290 _C GG
 TGGAATAT C GG TTCA
 ||||| || |||

			ACCTTATA G CT GAGT		
			A A TT		
GAM1019	EPHB6	5'	GTCCACCCCGGAATCCCA 10740	A A	TC
			TGG AT TCCGGGGT AC		
			ACC TA AGGCCCCA TG		
			C _ CC		
GAM1019	ERBB2IP	3'	ATGTGAACTCAAATATTGCA 20771	G	CCG
			TG AATAT GGGTTCACAT		
			AC TTATA CTCAAGTGTA		
			G AA_		
GAM1019	ERBB2IP	3'	ATGTGAACTCAACACTTCCA 20772		TATCCG
			TGGAA GGGTTCACAT		
			ACCTT CTCAAGTGTA		
			CACAA_		
GAM1019	GGA3	3'	ATGGCTGTACTGGATATCCCA 28901	A	GG TCA
			TGG ATATCCGG T CAT		
			ACC TATAGGTC G GTA		
			C AT TCG		
GAM1019	GGA3	3'	ATGGCTGTACTGGATATCCCA 15198	A	GG TCA
			TGG ATATCCGG T CAT		
			ACC TATAGGTC G GTA		
			C AT TCG		
GAM1019	GYPA	3'	ATGTGGACTGGACACTCCA 42262	ATA	GG
			TGGA TCC GGTTCACAT		
			ACCT AGG TCAGGTGTA		
			CAC _		
GAM1019	SHOX	3'	ATGTGGACTTCGGAATCCCA 6054	A A	
			TGG AT TCCGGGGTTACAT		
			ACC TA AGGCTTCAGGTGTA		
			C _		
GAM1019	BART1	3'	GATGTGATCTTGGA ACTTCCA 14424	TA	T
			TGGAA TCCGGGGT CACATC		
			ACCTT AGGTTCTA GTGTAG		
			CA _		
GAM1019	CLIC4	3'	GATGTAGATGCAGATATTCTA 15130		CGGG TC
			TGGAATATC GT ACATC		
			ATCTTATAG TA TG TAG		
			ACG_ GA		
GAM1019	CMG2	3'	GATGCGAAATGGATATTC 27721	GGGG	A
			GAATATCC TTC CATC		

CTTATAGG AAG GTAG
 TA__ C
 GAM1019 DKFZp761K1423 5' GATGCAAAGAGCCAGAATATTC 20472 CCGG A__
 TA TGAATAT GTTC CATC
 ||||| ||| |||
 ATCTTATA CCGAG GTAG
 AGA_ AAAC
 GAM1019 GAPCENA 5' GATGTACTGATGGATCCTCCA 14493 AT G_ TC
 TGGA ATCCG GGT ACATC
 ||| |||| | ||||
 ACCT TAGGT TCA TGTAG
 CC AG _
 GAM1019 GPS2 5' ATGTGAACCTGAGCTCC 42145 ATA CG
 GGA TC GGGTTCACAT
 || | |||||
 CCT AG TCCAAGTGTA
 CG_ _
 GAM1019 HTEX4 5' ATGTGAATACAGATATCACA 44216 GA CGGG
 TG ATATC GTTCACAT
 || |||| |||||
 AC TATAG TAAGTGTA
 AC ACA_
 GAM1019 HTEX4 5' ATGTGAATACAGATATCACA 46652 GA CGGG
 TG ATATC GTTCACAT
 || |||| |||||
 AC TATAG TAAGTGTA
 AC ACA_
 GAM1019 HTEX4 5' ATGTGAATACAGATATCACA 46721 GA CGGG
 TG ATATC GTTCACAT
 || |||| |||||
 AC TATAG TAAGTGTA
 AC ACA_
 GAM1019 KIAA1145 3' ATGTGACAGAATGTTCCA 32679 CCGGG T
 TGGAATAT GT CACAT
 ||||| || ||||
 ACCTTGTA CA GTGTA
 AGA_ _
 GAM1019 KIAA1887 5' GAGCCCCCAAATGTTCCA 37716 CC_
 TGGAATAT GGGGTTC
 ||||| |||||
 ACCTTGTA CCCCAG
 AAC
 GAM1019 MGC13061 3' GATGTTTGAACCCTGGACATTC 26128 A _
 CA TGGAAT TCCGGGGTTC ACATC
 |||| ||||| ||||
 ACCTTA AGGTCCCAAG TGTAG
 C TT
 GAM1019 PLSCR2 5' ATGTGAAACCACAGATATTTCA 21630 CG_ G
 TGGAATATC GG TTCACAT
 ||||| || |||||

		ACTTTATAG CC AAGTGTA		
		ACA A		
GAM1019 ST7L	3'	ATGTGACTTTGTAGATATTCC 28975	___	T
		GGAATATC CGGGGT CACAT		
		CCTTATAG GTTTCA GTGTA		
		AT _		
GAM1019 ST7L	3'	ATGTGACTTTGTAGATATTCC 29205	___	T
		GGAATATC CGGGGT CACAT		
		CCTTATAG GTTTCA GTGTA		
		AT _		
GAM1019 ST7L	3'	ATGTGACTTTGTAGATATTCC 19333	___	T
		GGAATATC CGGGGT CACAT		
		CCTTATAG GTTTCA GTGTA		
		AT _		
GAM1019 STAG2	3'	ATGTAATGTTGTGATATTCC 34928	_ G C	
		GGAATATC CGG GTT ACAT		
		CCTTATAG GTT TAA TGTA		
		T G _		
GAM1019 TNRC9	3'	ATGTGAATACTATATTCC 35320	CC GG	
		GGAATAT GG TTCACAT		
		CCTTATA TC AAGTGTA		
		_ AT		
GAM1019 LOC120534	3'	ATGTGAATATAGAAATATTTCA 36625	CCGGG_	
		TGGAATAT GTTCACAT		
		ACTTTATA TAAGTGTA		
		AAGATA		
GAM1019 LOC147991	5'	ATGTACCAGATATTCC 38434	CGG TC	
		GGAATATC GGT ACAT		
		CCTTATAG CCA TGTA		
		A_ _		
GAM1019 LOC149386	5'	GTGTGTTGGACTTTCCA 40986	TA GGTT	
		TGGAA TCCGG CACAT		
		ACCTT AGGTT GTGTG		
		TC _		
GAM1019 LOC150378	5'	GATGTGAGGTGGCTATTCCA 38923	T GGG	
		TGGAATA CCG TTCACATC		
		ACCTTAT GGT GAGTGTA		
		C G_		
GAM1019 LOC151194	3'	ATGCAAAGTGGGATATTCTA 29797	GG_ CA	
		TGGAATATCC GGTT CAT		

		ATCTTATAGG TCAA GTA		
		GAG AC		
GAM1019	LOC152402 5'	ATGCAGACCCTGATATTCCA 41495	C	CA
		TGGAATATC GGGGTT CAT		
		ACCTTATAG TCCCAG GTA		
		_ AC		
GAM1019	LOC152633 5'	GATGGCGAGCCGGACATACCA 41533	A A	GG A_
		TGG AT TCC GGTTC CATC		
		ACC TA AGG CCGAG GTAG		
		A C _ CG		
GAM1019	LOC201116 5'	TGAGGTCCGGGTATTCCA 42525	G	
		TGGAATATCCGGG TTCA		
		ACCTTATGGGCCT GAGT		
		G		
GAM1019	LOC253142 5'	GATGTGAGAGTGTCAATTCCA 46501	ATC	GGG
		TGGAAT CG TTCACATC		
		ACCTTA GT GAGTGTAG		
		CT_ GA_		
GAM1019	LOC254065 5'	ATGTGAACGGGTATTTC 46520	T	GGG
		GAATA CC GTTCACAT		
		CTTAT GG CAAGTGTA		
		T G_		
GAM1020	ACHE 3'	GGAGGAGGGGGCCGTGC 17942	C	
		GC ACGGCCCCCTCCTCC		
		CG TGCCGGGGGAGGAGG		
		_		
GAM1020	ADD1 3'	GGAGGAGGAAGCCCATAGAC 15472	CGCCAC	CC
		GTCT GGC CTCCTCC		
		CAGA CCG GGAGGAGG		
		TAC_ AA		
GAM1020	B3GALT5 3'	AGAGGGGGCGGGACA 12697	GCCACG	C
		TGTCTC GCCCCCTC T		
		ACAGGG CGGGGGAG A		
		_ A		
GAM1020	B3GALT5 3'	AGAGGGGGCGGGACA 27021	GCCACG	C
		TGTCTC GCCCCCTC T		
		ACAGGG CGGGGGAG A		
		_ A		
GAM1020	B3GALT5 3'	AGAGGGGGCGGGACA 27025	GCCACG	C
		TGTCTC GCCCCCTC T		

			ACAGGG	CGGGGGAG A		
			_____	A		
GAM1020	B3GALT5	3'	AGAGGGGGCGGGACA	27030	GCCACG	C
			TGTCTC	GCCCCCTC T		
			ACAGGG	CGGGGGAG A		
			_____	A		
GAM1020	B3GALT5	3'	AGAGGGGGCGGGACA	27035	GCCACG	C
			TGTCTC	GCCCCCTC T		
			ACAGGG	CGGGGGAG A		
			_____	A		
GAM1020	CREBL2	5'	GAGGAGGAGGCAGCCAGA	6993	C CACG	C
			TCT GC	GCC CTCCTC		
			AGA CG	CGG GGAGGAG		
			C A__	A		
GAM1020	CRIM1	3'	GAGGAGGGAGAGGGTGACGA	18560	_	ACGGCC
			TC TCGCC	CCCTCCTC		
			AG AGTGG	GGGAGGAG		
			C	GAGA__		
GAM1020	EMP1	3'	GAGGAGGAAGCCGTTGA	7133	CC	CC
			TCG ACGGC	CCTCCTC		
			AGT TGCCG	GGAGGAG		
			__	AA		
GAM1020	F2RL3	3'	GAGAAGAAAGCCATGTGGCGG	10081	__	CCC C
			TCGCCAC	GGC CT CTC		
			GGCGGTG	CCG GA GAG		
			TA	AAA A		
GAM1020	GABRE	3'	GAGGGGGGGGCAGCAAGAGA	11408	GCCACG	
			TCTC	GCCCCCTCCTC		
			AGAG	CGGGGGGGGAG		
			AACGA_			
GAM1020	GABRE	3'	GAGGGGGGGGCAGCAAGAGA	22510	GCCACG	
			TCTC	GCCCCCTCCTC		
			AGAG	CGGGGGGGGAG		
			AACGA_			
GAM1020	GABRE	3'	GAGGGGGGGGCAGCAAGAGA	22514	GCCACG	
			TCTC	GCCCCCTCCTC		
			AGAG	CGGGGGGGGAG		
			AACGA_			
GAM1020	GABRE	3'	GAGGGGGGGGCAGCAAGAGA	22531	GCCACG	
			TCTC	GCCCCCTCCTC		

		AGAG CGGGGGGGGAG		
		AACGA_		
GAM1020 GFRA1	5'	AGGAGGGGGCGGGGACA 11771	T G	ACG
		TGTC C CC GCCCCTCCT		
		ACAG G GG CGGGGGAGGA		
		— — —		
GAM1020 GLUL	3'	GAGGAGGGTGGGGAGACA 7835	G	CGGCC
		TGTCTC CCA CCCTCCTC		
		ACAGAG GGT GGGAGGAG		
		G ———		
GAM1020 HR	5'	GGAGGAGGAAACCGGCGGAGCA 11617	CT	AC CCC
		TGT CGCC GG CCTCCTCC		
		ACG GCGG CC GGAGGAGG		
		AG — AAA		
GAM1020 ITGA3	3'	GAGGAGGGGACCAATTCTGGAC 12009	CGCCAC	C
A		TGTCT GG CCCCTCCTC		
		ACAGG CC GGGGAGGAG		
		TCTTAA A		
GAM1020 ITGA3	3'	GAGGAGGGGACCAATTCTGGAC 7966	CGCCAC	C
A		TGTCT GG CCCCTCCTC		
		ACAGG CC GGGGAGGAG		
		TCTTAA A		
GAM1020 LAMA4	5'	GAGGAGGGGAAAATAAGCGAGGC 8069	CACGGCC	
A		TGTCTCGC CCCTCCTC		
		ACGGAGCG GGGAGGAG		
		AATAAAA		
GAM1020 MAP1B	5'	GAGGAGCGGCCGGAGCGAGACA 12534	CA	CC
		TGTCTCGC CGGCC CTCCTC		
		ACAGAGCG GCCGG GAGGAG		
		AG C_		
GAM1020 RAD51L1	3'	GAGTCTTGTGGTCAAACA 8786	C	CCCC
		TGT TCGCCACGG CTC		
		ACA AGTGGTGTT GAG		
		A CT_		
GAM1020 RAD51L1	3'	GAGTCTTGTGGTCAAACA 28575	C	CCCC
		TGT TCGCCACGG CTC		
		ACA AGTGGTGTT GAG		
		A CT_		
GAM1020 WHSC1	3'	GAGGAGTGCATGGCGAGA 17181	CG	CCC
		TCTCGCCA GC CTCCTC		

			AGAGCGGT CG GAGGAG		
			A_ T__		
GAM1020 WHSC1	3'	GAGGAGTGCATGGCGAGA	28445	CG CCC	
		TCTCGCCA GC CTCCTC			
		AGAGCGGT CG GAGGAG			
		A_ T__			
GAM1020 WHSC1	3'	GAGGAGTGCATGGCGAGA	28462	CG CCC	
		TCTCGCCA GC CTCCTC			
		AGAGCGGT CG GAGGAG			
		A_ T__			
GAM1020 C16orf7	3'	GGAAGAGGGGGCCATGAGCCGG	11347	TC _ C	C
C		GTC GC CA GGCCCCCTC TCC			
		CGG CG GT CCGGGGGAG AGG			
		C_ A A A			
GAM1020 C1orf21	5'	GGAGGAGGGGGAGCCCCGGACA	25121	T CCACGG	
		TGTC CG CCCCCTCCTCC			
		ACAG GC GGGGGAGGAGG			
		_ CCCGA_			
GAM1020 C20orf12	5'	AGGAGGAGGCAAGAGGCGAGA	19956	ACG_ C	
		TCTCGCC GCC CCTCCT			
		AGAGCGG CGG GGAGGA			
		AGAA A			
GAM1020 CREB-H	3'	GGAGGAGGAAGCCGCCGAGAC	26330	CCA CC	
		GTCTCG CGGC CCTCCTCC			
		CAGAGC GCCG GGAGGAGG			
		C_ AA			
GAM1020 DDX12	3'	GAGAAAGGGGCCGTGGTCAGC	30023	T C	CTC
		G CT GCCACGGCCCC CTC			
		C GA TGGTGCCGGGG GAG			
		_ C AAA			
GAM1020 DKFZp566H0824	5'	AGGAGGGAGCTCGTGGCGAGGC	18973	_ C	
A		TGTCTCGCCACG GC CCCTCCT			
		ACGGAGCGGTGC CG GGGAGGA			
		T A			
GAM1020 FLJ11259	3'	GAAGAAAGGCCCAAGAGCGAGA	20384	CAC_ CCC C	
CA		TGTCTCGC GGCC TC TC			
		ACAGAGCG CCGG AG AG			
		AGAAC AA_ A			
GAM1020 FLJ14327	3'	GGAGGAGGACCCGGCATGACA	24428	TC AC CCC	
		TGTC GCC GG CCTCCTCC			

ACAG CGG CC GGAGGAGG
 TA C_ A_
 GAM1020 FOXD4 5' GGAGGAGGCGGCGAGCCA 40282 T ACG C
 TG CTCGCC GCC CCTCC
 || ||||| || |||||
 AC GAGCGG CGG GGAGG
 C _ A
 GAM1020 ITGA10 3' GGAGGAGGAAAAGCCACAAGAG 29865 GCCAC CC_
 A TCTC GGC CCTCCTCC
 ||| || |||||
 AGAG CCG GGAGGAGG
 AACA_ AAAA
 GAM1020 KIAA0544 3' GGAGGAGGAAGCCAGCAGCACA 35113 _ C CAC CC
 TGT CT GC GGC CCTCCTCC
 ||| || |||||
 ACA GA CG CCG GGAGGAGG
 C _ A_ AA
 GAM1020 KIAA0668 3' GGAGGAGGGGACTTTTAGAGCC 33052 T GCCAC C
 A TG CTC GG CCCCTCCTCC
 || || |||||
 AC GAG TC GGGGAGGAGG
 C ATTT_ A
 GAM1020 KIAA0774 5' GGAGGGGCCACAGAAGACA 44091 _ GCCAC C
 TGTCT C GGCCCC TCC
 ||||| |||||
 ACAGA G CCGGGG AGG
 A ACA_ _
 GAM1020 KIAA0789 5' GGAGGAGCCTTGGTGGCGAGA 31848 _ CC
 TCTCGCCAC GGC CCTCC
 ||||| || |||||
 AGAGCGGTG CCG GGAGG
 GTT A_
 GAM1020 KIAA1855 3' AGAAGGGGGCCTGAGAGA 44352 GC C C
 TCTC CA GGCCCCCT CT
 ||| ||||| ||
 AGAG GT CCGGGGGA GA
 A_ _ A
 GAM1020 MGC12538 3' GAGAAGTAGTTGTGAGACA 26482 C G CCC
 TGTCTCGC AC GC CTC
 ||||| || || |||
 ACAGAGTG TG TG GAG
 T A AA_
 GAM1020 MIC2L1 3' GGAGGAGAGGGGAAAGAGACA 25491 GCCACGG _
 TGTCTC CCCC CTCCTCC
 |||| |||||
 ACAGAG GGGG GAGGAGG
 AAA_ A
 GAM1020 NFASC 3' GGAGGAGGGGAGAAGGGGAGAC 34832 G ACGGC
 A TGTCTC CC CCCCTCCTCC
 ||||| || |||||

ACAGAG GG GGGGAGGAGG
 G AAGA_
 GAM1020 PEPP3 3' AGGAGGGGGAAGCAGCAGGACA 17234 TC CACGG
 TGTC GC CCCCTCCT
 |||| || |||||
 ACAG CG GGGGGAGGA
 GA ACGAA
 GAM1020 SIAT4A 5' GAGGAGGACGGCAGAGACA 8981 _ ACGGCCC
 TGTCTC GCC CCTCCTC
 ||||| || |||||
 ACAGAG CGG GGAGGAG
 A CA____
 GAM1020 SIRPB1 3' GAGAAGGAGCTGGCGAGA 12708 CG CC C
 TCTCGCCA GC CCT CTC
 ||||| || |||||
 AGAGCGGT CG GGA GAG
 _ A_ A
 GAM1020 STRAIT11499 3' GGAGGAGGGGGCCACGTGTGAG 22212 G C _
 AGA T TCTCGC AC GGCCCCCTCCTCC
 | ||||| || |||||
 A AGAGTG TG CCGGGGGAGGAGG
 G _ CA
 GAM1020 ZNF339 5' GGAGGAGGGGGCCGCGAGTCGGG 22199 _ CA
 A TCTCG C CGGCCCCCTCCTCC
 ||||| | |||||
 AGGGC G GCCGGGGGAGGAGG
 T AC
 GAM1020 LOC129676 5' GGAGGAGGAGGCCAGGGACA 37286 GCCAC C
 TGTCTC GGCC CCTCCTCC
 ||||| ||| |||||
 ACAGGG CCGG GGAGGAGG
 A____ A
 GAM1020 LOC132299 5' AGGAAGCCGGGGAGACA 37023 G A CC
 TGTCTC CC CGGC CCT
 ||||| || ||||| |||
 ACAGAG GG GCCG GGA
 _ _ AA
 GAM1020 LOC143287 3' GAGGAAGGGGCCGCGGTGGA 40345 C A C
 TCT GCC CGGCCCC TCCTC
 ||| ||| ||||| |||||
 AGG CGG GCCGGGG AGGAG
 T C A
 GAM1020 LOC144110 3' GAGGAGGGGGCTCCAATGACA 37681 TCGCCAC
 TGTC GGCCCCCTCCTC
 ||||| |||||
 ACAG TCGGGGGAGGAG
 TAACC_
 GAM1020 LOC144373 3' GAGAAAGGGGGCCGTGGTCAGC 37728 T C CTC
 G CT GCCACGGCCCC CTC
 | || ||||| |||

		C GA TGGTGCCGGGG GAG		
		_ C AAA		
GAM1020	LOC145622 3'	GAGGAGGGGGCATAAAGAC	37911	CGCCACG
		GTCT GCCCCCTCCTC		
		CAGA CGGGGGAGGAG		
		AATA__		
GAM1020	LOC146520 5'	GGAGGAGGGATGCCACACAGAC	38187	CGCCAC C_
	A	TGTCT GGC CCCTCCTCC		
		ACAGA CCG GGGAGGAGG		
		CACA__ TA		
GAM1020	LOC146953 5'	AGGAGGGGACGGGGAGA	38286	G A GC
		TCTC CC CG CCCCTCCT		
		AGAG GG GC GGGGAGGA		
		_ _ A_		
GAM1020	LOC152283 3'	GGAGGAGGAAGCCATGGATGAC	41486	TCG C CC
	A	TGTC CCA GGC CCTCCTCC		
		ACAG GGT CCG GGAGGAGG		
		TA_ A AA		
GAM1020	LOC152283 3'	GGAGGAGGAGGCTGTGGATGAC	41487	TCG C
	A	TGTC CCACGGCC CCTCCTCC		
		ACAG GGTGTCGG GGAGGAGG		
		TA_ A		
GAM1020	LOC154881 3'	AGGAAGGGCTGGGTGAGACA	39493	A CC
		TGTCTCGCC CGGCCC TCCT		
		ACAGAGTGG GTCGGG AGGA		
		_ A_		
GAM1020	LOC155389 5'	AGGAGGGCGAGTGGCGAGCA	39562	T GGCC
		TG CTCGCCAC CCCTCCT		
		AC GAGCGGTG GGGAGGA		
		_ AGC_		
GAM1020	LOC221218 5'	GGAGGAGGAAGCTGAAGACG	44092	CGCCA CC
		TGTCT CGGC CCTCCTCC		
		GCAGA GTCG GGAGGAGG		
		A__ AA		
GAM1020	LOC253451 5'	AGGAGGGCGAGTGGCGAGCA	45948	T GGCC
		TG CTCGCCAC CCCTCCT		
		AC GAGCGGTG GGGAGGA		
		_ AGC_		
GAM1020	LOC256974 5'	GGAGGAGGCAGTATGGCAAGA	46436	C CG CC
		TCT GCCA GC CCTCCTCC		

AGA CGGT TG GGAGGAGG
 A A_ AC
 GAM1020 LOC90495 3' GAAAAGGAGGTTTGGTGAGACA 31579 C C CC
 TGTCTCGCCA GGCC CCT TC
 ||||| ||| ||
 ACAGAGTGGT TTGG GGA AG
 _ A AA
 GAM1021 CEP2 5' GGCACCTGCAAACCACC 13652 TA C GT C
 GGT GTT TGCG GG GCC
 ||| ||| ||| ||
 CCA CAA ACGT CC CGG
 C_ _ _ A
 GAM1021 DTNA 3' CACTCAGAAGCTAACCTC 7080 _ C
 GAGGTTAGTT CTG GGTG
 ||||| ||| |||
 CTCCAATCGA GAC TCAC
 A _
 GAM1021 DTNA 3' CACTCAGAAGCTAACCTC 26838 _ C
 GAGGTTAGTT CTG GGTG
 ||||| ||| |||
 CTCCAATCGA GAC TCAC
 A _
 GAM1021 DTNA 3' CACTCAGAAGCTAACCTC 26843 _ C
 GAGGTTAGTT CTG GGTG
 ||||| ||| |||
 CTCCAATCGA GAC TCAC
 A _
 GAM1021 DTNA 3' CACTCAGAAGCTAACCTC 26848 _ C
 GAGGTTAGTT CTG GGTG
 ||||| ||| |||
 CTCCAATCGA GAC TCAC
 A _
 GAM1021 LPIN2 3' GGAGCCCAGAACCAACC 16062 A CGGT G
 GGTT GTTCTG GGC CC
 ||| ||||| ||| ||
 CCAA CAAGAC CCG GG
 C _ _ A
 GAM1021 C6orf33 3' GGACCCACAAACTAACCT 28493 CTGCG CG
 AGGTTAGTT GTGG CC
 ||||| ||| ||
 TCCAATCAA CACC GG
 AA_ CA
 GAM1021 KIAA0089 3' GCGCCACCATTAAACC 34667 A TCTGC
 G GGTTAGT GGTGGCGC
 | ||||| |||||
 C CCAATTA CCACCGCG
 _ _ _
 GAM1021 PISD 5' GGCGCCACCAACCAGCCTC 15657 A CTGC
 GAGGTT GTT GGTGGCGC
 ||||| ||| |||||

CTCCGA CAA CCACCGCGG
 C ____
 GAM1021 PNAS-127 5' CATTGATAACAGAACTAACTTC 26241 ____
 GAGGTTAGTTCTG CGGTG
 ||||| ||||
 CTTCAATCAAGAC GTTAC
 AATA
 GAM1021 WBSCR21 5' CGGCAGCAAACTAACTTC 25326 C GG G
 GAGGTTAGTT TGC TG CG
 ||||| || ||
 CTTCAATCAA ACG AC GC
 A _ G
 GAM1021 LOC149721 5' CACAGGTCAAGAACTAACTC 38809 G _ G_
 GAG TTAGTTCT GC GTG
 || ||||| || ||
 CTC AATCAAGA TG CAC
 A AC GA
 GAM1022 CASQ2 3' AACTGGGATGGGAGGTTGA 6902 T GAAAG
 TCAA CC TCATCCCAGTT
 ||| || |||||
 AGTT GG GGTAGGGTCAA
 _ AG_
 GAM1022 RAP1A 3' AACTGGGATAACTGATTC 8792 _ C
 GAA AGT ATCCCAGTT
 || || |||||
 CTT TCA TAGGGTCAA
 TAG A
 GAM1022 DKFZp547I094 3' AACTGGGATTCAGAT 25855 C AGTC
 ATC GAA ATCCCAGTT
 ||| || |||||
 TAG CTT TAGGGTCAA
 A ____
 GAM1022 MGC11082 5' AACTAGAGCTAGTCTTCGGATT 26411 AG CA__ CC
 GA TCAATCCGAA T TC AGTT
 ||||| | || ||
 AGTTAGGCTT G AG TCAA
 CT ATCG A_
 GAM1023 AKAP13 3' AAGGCTTGATGTGTATAA 29558 T GG
 TTATAC CAT TAGGCCTT
 |||| || |||||
 AATATG GTA GTTCGGAA
 T _
 GAM1023 AKAP13 3' AAGGCTTGATGTGTATAA 13589 T GG
 TTATAC CAT TAGGCCTT
 |||| || |||||
 AATATG GTA GTTCGGAA
 T _
 GAM1023 AKAP13 3' AAGGCTTGATGTGTATAA 14054 T GG
 TTATAC CAT TAGGCCTT
 |||| || |||||

AATATG GTA GTTCGGAA
 T _
 GAM1023 COL4A3 3' AAGGCCTGATGGAACACAGA 25351 TATAC GG
 TCT TCAT TAGGCCTT
 ||| ||| |||||
 AGA GGTA GTCCGGAA
 CACAA _
 GAM1023 COL4A3 3' AAGGCCTGATGGAACACAGA 25357 TATAC GG
 TCT TCAT TAGGCCTT
 ||| ||| |||||
 AGA GGTA GTCCGGAA
 CACAA _
 GAM1023 COL4A3 3' AAGGCCTGATGGAACACAGA 5544 TATAC GG
 TCT TCAT TAGGCCTT
 ||| ||| |||||
 AGA GGTA GTCCGGAA
 CACAA _
 GAM1023 BIVM 5' GCCGACCACAGTATAAGA 19255 CA A
 TCTTATACT TGGT GGC
 ||||| ||| ||
 AGAATATGA ACCA CCG
 C_ G
 GAM1023 DKFZP564F013 3' AAGAATACCATGAATGTAAGA 45199 C GGC
 TCTTATA TCATGGTA CTT
 ||||| ||||| ||
 AGAATGT AGTACCAT GAA
 A AA_
 GAM1023 KCNT1 3' AAGGCCTACGGGTTCAAGA 30970 AT ATG
 TCTT ACTC GTAGGCCTT
 ||| ||| |||||
 AGAA TGGG CATCCGGAA
 CT _
 GAM1023 KIAA0522 3' AGGGCCACCATGAGCCCAAGA 35621 ATA A
 TCTT CTCATGGT GGCCTT
 ||| ||||| |||||
 AGAA GAGTACCA CCGGGA
 CCC _
 GAM1023 LOC145717 3' AAGACCTATCATGCCAAGA 33187 ATACT C
 TCTT CATGGTAGG CTT
 ||| ||||| |||
 AGAA GTACTATCC GAA
 CC_ A
 GAM1023 LOC152925 3' GTCACCACAAAGTATAAGA 39333 CA_ A
 TCTTATACT TGGT GGC
 ||||| ||| ||
 AGAATATGA ACCA CTG
 AAC _
 GAM1023 LOC158301 3' AAGGCCTGTAGTTGAACATAA 39808 AC TG_
 TTAT TCA GTAGGCCTT
 ||| ||| |||||

			AATA AGT TGTCCGGAA		
			CA TGA		
GAM1023	LOC196957	3'	AAGACCTATCATGCCAAGA 42425	ATACT	C
			TCTT CATGGTAGG CTT		
			AGAA GTACTATCC GAA		
			CC__ A		
GAM1023	LOC196961	3'	AAGACCTATCATGCCAAGA 42434	ATACT	C
			TCTT CATGGTAGG CTT		
			AGAA GTACTATCC GAA		
			CC__ A		
GAM1023	LOC197138	3'	AAGACCTATCATGCCAAGA 42452	ATACT	C
			TCTT CATGGTAGG CTT		
			AGAA GTACTATCC GAA		
			CC__ A		
GAM1023	LOC200014	3'	AAGACCTACCATGCTGGGTAGG 42687	ACT_	C
			CTTAT CATGGTAGG CTT		
			GGATG GTACCATCC GAA		
			GGTC A		
GAM1023	LOC202018	3'	AAGGCCTCTTCAGTATAAGG 42956	CAT T	
			TCTTATACT GG AGGCCTT		
			GGAATATGA TC TCCGGAA		
			CT_ _		
GAM1023	LOC245727	3'	AAGACCTATCATGCCAAGA 43794	ATACT	C
			TCTT CATGGTAGG CTT		
			AGAA GTACTATCC GAA		
			CC__ A		
GAM1024	RAI3	3'	ATTCACAGGTCACCCCTCTC 10111	A C	A
			GAGAG GG GACCTGT AGT		
			CTCTC CC CTGGACA TTA		
			C A C		
GAM1024	STARD4	3'	TACAGATCAACTCTCTCA 29172	GC C	
			TGAGAGAG GA CTGTA		
			ACTCTCTC CT GACAT		
			AA A		
GAM1024	TRPM6	3'	ACTACTATTTGTACCTC 19194	C CT A	
			GAGG GAC GTA GTAGT		
			CTCC CTG TAT CATCA		
			A TT _		
GAM1024	GIT2	3'	ACCACTTACAGCTTTCTCA 16598	GCGAC	A
			TGAGAGAG CTGTAAGT GT		

			ACTCTTTC	GACATTCA CA		
			_____	C		
GAM1024	GIT2	3'	ACCACTTACAGCTTTCTCA	27680	GCGAC	A
			TGAGAGAG	CTGTAAGT GT		
			ACTCTTTC	GACATTCA CA		
			_____	C		
GAM1024	GIT2	3'	ACCACTTACAGCTTTCTCA	27693	GCGAC	A
			TGAGAGAG	CTGTAAGT GT		
			ACTCTTTC	GACATTCA CA		
			_____	C		
GAM1024	KIAA1538	3'	ACCTAGGGGAAACCATCTCTC	35420	_ CGA	G A
			GAGAGA GG	CCT TA GT		
			CTCTCT CC	GGG AT CA		
			A AAA	G C		
GAM1024	LOC90408	5'	CTACCATCTCCCTCTCTCA	31396	C CC	TAA
			TGAGAGAGG GA	TG GTAG		
			ACTCTCTCC CT	AC CATC		
			_ CT _			
GAM1025	ANXA7	3'	TGCTTGTTTGCACATGTTGT	10254	C A	TAA C
			AC ACAT TGCAA	CG GCA		
			TG TGTA ACGTT	GT CGT		
			T C	TG_ T		
GAM1025	ANXA7	3'	TGCTTGTTTGCACATGTTGT	6825	C A	TAA C
			AC ACAT TGCAA	CG GCA		
			TG TGTA ACGTT	GT CGT		
			T C	TG_ T		
GAM1025	FGF12	3'	TGCTTGTTGCAATGTGGT	22021	A	C
			ACCACAT TGCAATAA	GCG		
			TGGTGTA ACGTTGTT	CGT		
			- -			
GAM1025	KCNQ1	5'	TGCGCCTGCACATGTGTGT	5725	_ A	ATAAC
			AC CACAT TGCA	GCGCA		
			TG GTGTA ACGT	CGCGT		
			T C	C_		
GAM1025	ATP9A	3'	TGCGTGTGCACATGTGTG	31088	CAATA	
			CACATATG	ACGCGCA		
			GTGTGTAC	TGTGCGT		
			ACG_			
GAM1025	C20orf13	3'	TGCGCGTATGTGCGCACATATG	19301	_____	ATA
	T		ACATAT	GCA ACGCGCA		

	TGTATA CGT TGC	CGT	
	CACG GTA		
GAM1025 DKFZp566H0824	5' CGCACATTAGTGCATACGTG	18976	A A C__
	CAC TATGCA TAA GCG		
	GTG ATACGT ATT CGC		
	C G ACA		
GAM1025 IMPACT	3' TGCATGATTTTGTATATATGGT	20506	C TAA C
	ACCA ATATGCAA CG GCA		
	TGGT TATATGTT GT CGT		
	A TTA A		
GAM1025 KIAA0010	3' GCTGCTGCTTATGTGGT	16132	T ATAAC _
	ACCACATA GCA GC GC		
	TGGTGTAT CGT CG CG		
	T _ _ _ T		
GAM1025 KIAA0978	3' TGCTTGCTGCCATATGTG	34890	_ A C
	CACATATG CA TAA GCG		
	GTGTATAC GT GTT CGT		
	C C _		
GAM1025 KIAA1550	3' GCGCGCCTGTATATGTG	33072	ATAA
	CACATATGCA CGCGC		
	GTGTATATGT GCGCG		
	CC__		
GAM1025 LOC157918	3' TGCGCGTCTGTGCATGTGTG	41900	ATA
	CACATATGCA ACGCGCA		
	GTGTGTACGT TGCGCGT		
	GTC		
GAM1025 LOC202347	3' TGCGCTGTTTCTGCTTATGTGG	43432	T AT _
T	ACCACATA GCA AAC GCGCA		
	TGGTGTAT CGT TTG CGCGT		
	T CT T		
GAM1025 LOC203504	3' TGCTGATTGCATGTGTG	43574	AAC
	CACATATGCAAT GCG		
	GTGTGTACGTTA CGT		
	GT_		
GAM1025 LOC257159	5' TGCGTACATATGTGGT	46417	CAATA
	ACCACATATG ACGCG		
	TGGTGTATAC TGCGT		
	A__		
GAM1025 LOC89919	3' TGCACGTTTCATCTATGTGTG	30466	CAAT C
	CACATATG AACG GCA		

			GTGTGTAT TTGC CGT		
			CTAC A		
GAM1026 CERD4	3'	TCCTTCTGAGACTCTCA	14349	CA C	
		TGAGA TC CAGAAGGG			
		ACTCT AG GTCTTCCT			
		C_ A			
GAM1026 GJB3	3'	CCCCTGGGATGGCTCA	23438	A AA	
		TGAG CATCCCAG GGG			
		ACTC GTAGGGTC CCC			
		G _			
GAM1026 KIF1B	3'	TCTTTTCTAGGAGTGTCTCA	17449	TC _	
		TGAGACA CC AGAAGGGA			
		ACTCTGT GG TCTTTTCT			
		GA A			
GAM1026 POU4F1	3'	AGTGTTTCATCCTGAAATGTCTC	12897	CC AAG	
A		TGAGACAT CAG GGACACT			
		ACTCTGTA GTC CTTGTGA			
		AA CTA			
GAM1026 BNIP2	3'	TGCCCAGTCTGGGATGGCTCA	33163	A A_ A	
		TGAG CATCCCAGA GGG CA			
		ACTC GTAGGGTCT CCC GT			
		G GA _			
GAM1026 C20orf173	5'	AAGTGTGGCTGCCCTTCTGAGA	28092	ACA C	
CCCTCA		AG TC CAGAAGGG ACACTT			
		TC AG GTCTTCCC TGTGAA			
		CC_ A GTCGG			
GAM1026 DJ122O8.2	3'	TGTTTATGGATGTCTCA	21704	CAGAAG	
		TGAGACATCC GGACA			
		ACTCTGTAGG TTTGT			
		TA_			
GAM1026 DKFZp547A023	3'	AAGGCACCTCAAAGATGTCTCA	35941	CCA A GACA	
		TGAGACATC GA GG CTT			
		ACTCTGTAG CT CC GAA			
		AAA _ ACG_			
GAM1026 FLJ10607	3'	AGTGTTCCCTAAGATATCTC	37833	C CCAGA	
		GAGA ATC AGGGACACT			
		CTCT TAG TCCTTGTGA			
		A AA_			
GAM1026 FLJ22795	3'	CCCCCTGGGATGGCTCA	24689	A AA	
		TGAG CATCCCAG GGG			

			ACTC GTAGGGTC CCC			
			G C_			
GAM1026	GABBR1	5'	AAGTGTCCCCCTGAGCTC	22419	ACATCC	AA
			GAG CAG GGGACACTT			
			CTC GTC CCCTGTGAA			
			GA__ CC			
GAM1026	KIAA0377	3'	AGTGCCCCTTCTGCCTCA	16102	ACATCC	A
			TGAG CAGAAGGG CACT			
			ACTC GTCTTCCC GTGA			
			C__ C			
GAM1026	KIAA0546	3'	TCTCCTGGGATGCTCA	35334	A	AA
			TGAG CATCCCAG GGGA			
			ACTC GTAGGGTC CTCT			
			— —			
GAM1026	KIAA1348	3'	TGCTCTTCTAAATGTTTCA	34033	CCC	A
			TGAGACAT AGAAGGG CA			
			ACTTTGTA TCTTCTC GT			
			AAA —			
GAM1026	KIAA1706	3'	AAGCATCGAAATGGGATGTCT	44574	GAAGG	CA
			AGACATCCCA GA CTT			
			TCTGTAGGGT CT GAA			
			AAAG_ AC			
GAM1026	RNP24	3'	AAGCCAATTCTCTGGGTGTCCC	13692	A T	AG GACA
	A		TG GACA CCCAGA G CTT			
			AC CTGT GGGTCT T GAA			
			C _ CT AACC			
GAM1026	LOC145717	3'	CCCCCTGGGATGGCTCA	33192	A	AA
			TGAG CATCCCAG GGG			
			ACTC GTAGGGTC CCC			
			G C_			
GAM1026	LOC145725	5'	CCCCCTGGGATGGCTCA	37948	A	AA
			TGAG CATCCCAG GGG			
			ACTC GTAGGGTC CCC			
			G C_			
GAM1026	LOC145732	5'	CCCCCTGGGATGGCTCA	37957	A	AA
			TGAG CATCCCAG GGG			
			ACTC GTAGGGTC CCC			
			G C_			
GAM1026	LOC196957	5'	CCCCCTGGGATGGCTCA	42429	A	AA
			TGAG CATCCCAG GGG			

			ACTC GTAGGGTC CCC		
			G C_		
GAM1026	LOC196961	5'	CCCCCTGGGATGGCTCA 42438	A	AA
			TGAG CATCCCAG GGG		
			ACTC GTAGGGTC CCC		
			G C_		
GAM1026	LOC197138	5'	CCCCCTGGGATGGCTCA 42456	A	AA
			TGAG CATCCCAG GGG		
			ACTC GTAGGGTC CCC		
			G C_		
GAM1026	LOC220537	3'	CCCCCTGGGATGGCTCA 43622	A	AA
			TGAG CATCCCAG GGG		
			ACTC GTAGGGTC CCC		
			G C_		
GAM1026	LOC245727	5'	CCCCCTGGGATGGCTCA 43797	A	AA
			TGAG CATCCCAG GGG		
			ACTC GTAGGGTC CCC		
			G C_		
GAM1027	BARX1	5'	CGCGCGGCGCCCCGCGGAGC 22236	A_ _	TAC A
			GC CG GG GG CGCCGCGCG		
			CG GC CC CC GCGGCGCGC		
			AG G _ _		
GAM1027	FOX E3	3'	CGCGCGGGCAGGCACCTGTGC 14469		ACGGACG
			GCACGGGT CCGCGCG		
			CGTGTCCA GGCGCGC		
			CGGACG_		
GAM1027	G6PD	5'	CGCGGAGCTGCACCCGTGC 5979	A	ACG
			GCACGGGT CGG CCGCG		
			CGTGCCCA GTC GGCGC		
			C GA_		
GAM1027	GCLM	5'	CGCGCGGCGCCGGCAGCCTCG 7821	_ A_ _	A
			CG GGT CGG CGCCGCGCG		
			GC CCG GCC GCGGCGCGC		
			T ACG _		
GAM1027	RFP	5'	CGGGGCCCATGCCCGTGC 13258	C AC	G
			GCACGGGTA GG GCC CG		
			CGTGCCCGT CC CGG GC		
			A _ G		
GAM1027	SORCS2	5'	CGCGCGGCACGGAGCCAGGC 21877	ACG A_	GAC
			GC GGT CG GCCGCGCG		

CG CCG GC CGGCGCGC
 GA_ AG A_
 GAM1027 C17orf31 5' CGCAGCATACCATGTAGCCCGT 19003 _ _ AC_ C
 GC GCACGGGT AC GG GC GCG
 ||||| || || ||||
 CGTGCCCG TG CC CG CGC
 A TA ATA A
 GAM1027 CENTG2 5' GCGCGGCGGGCTCGCGC 17158 A ACGGA
 GC CGGGT CGCCGCGC
 || |||| |||||
 CG GCTCG GCGGCGCG
 C G_
 GAM1027 DT1P1A10 3' CGCAACAGCTCTGTACCCCTGC 30858 C C C_
 GCA GGGTACGGA GC GCG
 || ||||| || ||
 CGT CCCATGTCT CG CGC
 C _ ACAA
 GAM1027 E2IG3 5' CGCGCGACACTGCGTGCCCGCG 15696 A GACGC_
 C GC CGGGTACG CGCGCG
 || ||||| ||||
 CG GCCCGTGC GCGCGC
 C GTCACA
 GAM1027 EPN2 3' CGCATGTTGCACCTGTGC 17347 A G CC
 GCACGGGT CG ACG GCG
 ||||| || || ||
 CGTGTCCA GT TGT CGC
 C _ A_
 GAM1027 FLJ20400 5' CGCGCGGCGCCGCGCTCGGC 33045 A TA A
 GC CGGG CGG CGCCGCGCG
 || |||| || |||||
 CG GCTC GCC GCGGCGCGC
 _ GC _
 GAM1027 FLJ20979 5' CGCGCCGCCCGTGCCCGCGC 23573 A AC C
 GC CGGGTACGG GC GCGCG
 || ||||| || ||||
 CG GCCCGTGCC CG CGCGC
 C _ C
 GAM1027 FLJ21195 5' CGCGCGGCGCGGGGCGCG 22826 G A_ GA
 CG GT CG CGCCGCGCG
 || || || |||||
 GC CG GC GCGGCGCGC
 G GG _
 GAM1027 FLJ21562 5' CGCGCGGCGTTTACCCAGC 24762 AC CG
 GC GGGTA GACGCCGCGCG
 || |||| |||||
 CG CCCAT TTGCGGCGCGC
 A_ _
 GAM1027 KIAA0415 3' CGCGCGCCATCCGTACCCGGGC 44476 A A_____ CGC
 GC CGGGTACGG CGC G
 || ||||| || |

CG GCCCATGCC GCG C
 G TACCG CGC
 GAM1027 KIAA0683 5' CGCGCGGCGCCTGAGCGCG 18191 G A A
 CG GT CGG CGCCGCGCG
 || ||| |||||
 GC CG GTC GCGGCGCGC
 G A C
 GAM1027 KIAA1643 5' CGCGCCCCCGTACCCGCGT 32240 A ACGCC
 GC CGGGTACGG GCGCG
 || ||||| ||||
 TG GCCCATGCC CGCGC
 C CC__
 GAM1027 MGC10986 5' CGCGCCCTCCTCGTACCCGTGC 24950 ACGCC
 GCACGGGTACGG GCGCG
 ||||| ||||
 CGTGCCCATGCT CGCGC
 CCTCC
 GAM1027 PTDSS2 3' CGCGCGTGTGTACACATGC 25075 CGG G C
 GCA GTACG ACGC GCG
 ||| |||| ||||
 CGT CATGT TGCG CGC
 ACA G _
 GAM1027 LOC254057 5' CGCGGGCTCCCCGTGCCCGT 46344 AC_ G
 ACGGGTACGG GCC CGCG
 ||||| ||||
 TGCCCGTGCC CGG GCGC
 CCT _
 GAM1027 LOC254528 5' CGCGCGGCCGTCGCACCTG 45567 A AC
 CGGGT CGG GCCGCGCG
 |||| ||| |||||
 GTCCA GCT CGGCGCGC
 C GC
 GAM1027 LOC257479 5' CGCGCGGCGGGGTCCCTGC 46052 C T GGA
 GCA GGG AC CGCCGCGCG
 ||| ||| |||||
 CGT CCC TG GCGGCGCGC
 _ _ GG_
 GAM1027 LOC56926 5' CGCGCGGCGCCCGCAGGACCC 36042 A__ A
 GGGT CGG CGCCGCGCG
 ||| ||| |||||
 CCCA GCC GCGGCGCGC
 GGAC C
 GAM1027 LOC56961 5' CGCGCGGCGCCCGCGCCC 31507 TA A
 GGG CGG CGCCGCGCG
 ||| ||| |||||
 CCC GCC GCGGCGCGC
 GC C
 GAM1028 AKAP13 3' AAGGCATCTTTCCAAGTACTCA 43174 T CG GG
 TGA GTACT GG GGATGCCTT
 ||| |||| ||| |||||

ACT CATGA CC TCTACGGAA
 _ A_ TT
 GAM1028 DKFZP434N014 3' AAGACATCCCCCTCCATC 30388 TACTC C
 GATG GGGGGGGATG CTT
 |||| ||||| ||
 CTAC TCCCCCTAC GAA
 C_ _ A
 GAM1028 FLJ23598 3' AAGACACCCCCCTGGACCCATC 24152 TAC A C
 A TGATG TCGGGGGGG TG CTT
 |||| ||||| || ||
 ACTAC GGTCCCCC AC GAA
 CCA _ A
 GAM1028 LOC149086 3' AAGAGCTATTCCCCCGAGTCCA 40945 A T AT _
 CCA TG TG ACTCGGGGGG GC CTT
 || || ||||| || ||
 AC AC TGAGCCCCCTT CG GAA
 C C AT A
 GAM1028 LOC92568 3' AAGGCATCCACATTTAAGTCAC 34572 A T CG GG_
 CA TG TG ACT GG GGATGCCTT
 || || || || |||||
 AC AC TGA TT CCTACGGAA
 C _ AT ACA
 GAM1029 GLRA3 5' ACTGTAAAAATCACCTGCACA 30167 GTATG
 TGTGCAGG TTTTACAGT
 ||||| |||||
 ACACGTCC AAAATGTCA
 ACTA_
 GAM1029 ABCA9 3' TACTATAAAGACACATGCACA 27827 GG ATG C
 TGTGCA GT TTTTA AGTA
 |||| || |||| ||
 ACACGT CA GAAAT TCAT
 A_ CA_ A
 GAM1029 HRH3 3' CTGCACACCCTGCACA 14109 TA TTTA
 TGTGCAGGG TGT CAG
 ||||| || ||
 ACACGTCCC ACA GTC
 C_ C_
 GAM1029 KIAA0892 3' ACTGTCCGACCCCTGCACA 35168 TAT TT
 TGTGCAGGG GTT ACAGT
 ||||| || ||||
 ACACGTCCC CAG TGTCA
 _ CC
 GAM1029 KIAA1546 3' TACTGTAAAACAGTTTTATACA 33715 C GTA
 TGTG AGG TGTTTTACAGTA
 ||| || |||||
 ACAT TTT ACAAATGTCAT
 A TG_
 GAM1029 LOC149832 5' ACTGCCACCACCCTGCACA 41079 AT TTTA
 TGTGCAGGGT GT CAGT
 ||||| || |||

ACACGTCCCA CA GTCA
 C_ CC_
 GAM1029 LOC152274 3' TACCATAAGCACCCCTGCAC 39234 AT TACA
 GTGCAGGGT GTTT GTA
 ||||| ||| ||
 CACGTCCCA CGAA CAT
 _ TAC_
 GAM1029 LOC157247 5' ACTTTTCCACATACCCACACA 39571 CA TTTAC
 TGTG GGGTATGT AGT
 ||| ||||| ||
 ACAC CCCATACA TCA
 _ CCTTT
 GAM1030 LDLR 3' AGAGAAACAGGCCCGGGGGGAC 6125 G AA C
 GTCTC CTCG CCTGTT CTCT
 |||| ||| |||| ||||
 CAGGG GGGC GGACAA GAGA
 _ CC A
 GAM1030 MAP1B 5' AGAGGAGCGGCCGAGCGAGAC 12532 GAAC
 A TGTCTCGCTC CTGTTCTCT
 ||||| |||||
 ACAGAGCGAG GGCGAGGAGA
 GCC_
 GAM1030 RNPEPL1 3' AGAGGAACAAGGACACAGACA 20158 CGCTCGAA _
 TGTCT CCT GTTCCTCT
 |||| ||| |||||
 ACAGA GGA CAAGGAGA
 CACA_ A
 GAM1030 VHL 3' AGAGGAACAAACCAGGGGACA 6158 G CGAACC
 TGTCTC CT TGTTCTCT
 |||| || |||||
 ACAGGG GA ACAAGGAGA
 _ CCAA_
 GAM1030 FLJ00007 3' AGAGGAACAGGCCTTGGG 35305 A_
 CTCGA CCTGTTCTCT
 |||| |||||
 GGGTT GGACAAGGAGA
 CC
 GAM1030 FLJ10298 3' AGAAACAGGTTAGGACA 19807 CGCTCG C
 TGTCT AACCTGTT CT
 |||| ||||| ||
 ACAGG TTGGACAA GA
 A_ A
 GAM1030 PRO1048 3' AGGAACAGGTTAGAAGAGCCA 20556 T GC G
 TG CTC TC AACCTGTTCT
 || ||| |||||
 AC GAG AG TTGGACAAGGA
 C A_ A
 GAM1030 LOC144108 5' AGAAGAACTTAGGGAGCGAGA 37682 GAA _ C
 TCTCGCTC CCT GTTC TCT
 ||||| || ||| |||

AGAGCGAG GGA CAAG AGA
 ____ TT A
 GAM1030 LOC152441 3' AGAGGAACAGGTCAGGGTCAGA 41504 C GA
 CA TGTCT GCTC ACCTGTTCTCT
 ||||| ||| |||||
 ACAGA TGGG TGGACAAGGAGA
 C AC
 GAM1030 LOC153688 3' AGGAACAGAACGAGGCA 41652 CTCGAAC
 TGTCTCG CTGTTCT
 ||||| |||||
 ACGGAGC GACAAGGA
 AA____
 GAM1031 TARBP2 5' AGTGAGTCCTTACCGC 28625 C CA
 GTGGTAAG GGC TCACT
 ||||| ||| |||||
 CGCCATTC CTG AGTGA
 - -
 GAM1031 TARBP2 5' AGTGAGTCCTTACCGC 28627 C CA
 GTGGTAAG GGC TCACT
 ||||| ||| |||||
 CGCCATTC CTG AGTGA
 - -
 GAM1032 ATP11A 3' CCCGTCACCTCGTCCTCA 37804 CGA A
 TGAGGACGA TGACG GG
 ||||| |||||
 ACTCCTGCT ACTGC CC
 CC_ _
 GAM1032 EGFL4 5' CCTCCTCACCAACGTGTCCTCA 30966 G A AC
 TGAGGAC ACG TG GAGGAGG
 ||||| ||| || |||||
 ACTCCTG TGC AC CTCCTCC
 _ A CA
 GAM1032 GALNS 3' CCTCCTCGCCCACGGCGCCTCA 6123 A A A A_
 TGAGG CG CG TG CGAGGAGG
 ||||| ||| || |||||
 ACTCC GC GC AC GCTCCTCC
 _ G _ CC
 GAM1032 GALNS 3' CCTCCTCGCCCACGGCGCCTCA 6122 A A A A_
 TGAGG CG CG TG CGAGGAGG
 ||||| ||| || |||||
 ACTCC GC GC AC GCTCCTCC
 _ G _ CC
 GAM1032 HEM1 5' CCATCATCATGTCCTCA 11807 AC CGA
 TGAGGACG GATGA GG
 ||||| ||||| ||
 ACTCCTGT CTACT CC
 A_ A_
 GAM1032 LIF 3' CCTCCCCATCGTCCCCATCGTC 8094 CGAT ____
 CTC GAGGACGA GACGA GGAGG
 ||||| ||||| |||||

CTCCTGCT CTGCT CCTCC
 ACCC ACC
 GAM1032 MBD3 3' CCTCCTCGGCCCCGTCCCCA 10019 A ACGATGA
 TG GGACG CGAGGAGG
 || |||| |||||
 AC CCTGC GCTCCTCC
 C CCG____
 GAM1032 PROX1 3' CCTCCTCATCACGTTTCTCTCA 8650 AC A C
 TGAGG GACG TGA GAGGAGG
 |||| ||| ||| |||||
 ACTCT TTGC ACT CTCCTCC
 CT _ A
 GAM1032 TRPC6 5' CCTGCTTCACCGTCGTCC 10973 A CG G
 GGACGACG TGA AG AGG
 ||||| ||| || |||
 CCTGCTGC ACT TC TCC
 C _ G
 GAM1032 UBE2V1 3' CCTTTTTCACCGTCACC 9371 AC A A
 GG GACG TG CGAGGAGG
 || |||| || |||||
 CC CTGC AC GTTTTCC
 A_ C _
 GAM1032 UBE2V1 3' CCTTTTTCACCGTCACC 22523 AC A A
 GG GACG TG CGAGGAGG
 || |||| || |||||
 CC CTGC AC GTTTTCC
 A_ C _
 GAM1032 UBE2V1 3' CCTTTTTCACCGTCACC 22770 AC A A
 GG GACG TG CGAGGAGG
 || |||| || |||||
 CC CTGC AC GTTTTCC
 A_ C _
 GAM1032 WHN 3' CCCCTCGTCATTTTCTTTCCCA 9650 A C_ C A
 TG GGA GA GATGACGAGG GG
 || ||| || ||||| ||
 AC CCT CT TTAGTGCTCC CC
 _ TT T _
 GAM1032 YY1 5' CCTCCTCGCCCCGCCCGCCCGCA 9437 A A A_ ATGA
 TG GG CG CG CGAGGAGG
 || ||| || |||||
 AC CC GC GC GCTCCTCC
 G C CC CC_
 GAM1032 E46L 5' CCTCCTCGCCATCCTACTCCTC 14896 CGAC A
 GAGGA GATG CGAGGAGG
 |||| ||| |||||
 CTCCT CTAC GCTCCTCC
 CATC C
 GAM1032 E46L 5' CCTCCTCGTCATCCTCCCCCT 14897 AC C
 AGG GA GATGACGAGGAGG
 ||| || ||||| |||||

		TCC CT CTA	TGCTCCTCC	
		CC C		
GAM1032	FLJ14249	3'	CCCCGAGGCCTTCGTCGTCCTC 22799	TGACGA_ A
	A		TGAGGACGACGA GG GG	
			ACTCCTGCTGCT CC CC	
			TCCGGAG _	
GAM1032	FLJ14249	3'	CCCCGAGGCCTTCGTCGTCCTC 28169	TGACGA_ A
	A		TGAGGACGACGA GG GG	
			ACTCCTGCTGCT CC CC	
			TCCGGAG _	
GAM1032	FLJ22938	3'	CCTCCTCGTCCTCGTCGTCGTC 23986	_____
	CTC		GAGGACGACGAT GACGAGGAGG	
			CTCCTGCTGCTG CTGCTCCTCC	
			CTC	
GAM1032	FOXD4	5'	CCTCCTCGTACATCGCGCTCA 40280	GA A _
			TGAG CG CGATG ACGAGGAGG	
			ACTC GC GCTAC TGCTCCTCC	
			_ _ A	
GAM1032	KIAA0939	3'	CCTCCCCACCATTCCTCGTACTC 31061	G AC ACGA
	A		TGAG ACG GATG GGAGG	
			ACTC TGC TTAC CCTCC	
			A CC CACC	
GAM1032	MGC13170	5'	CCTCCTCAACCTCGTCCTC 26431	CGATGAC
			GAGGACGA GAGGAGG	
			CTCCTGCT CTCCTCC	
			CCAA_	
GAM1032	SIAT8C	5'	CCTCCTCGCCGGCACCCTCA 18026	ACGA ATGA
			TGAGG CG CGAGGAGG	
			ACTCC GC GCTCCTCC	
			CACG C_	
GAM1032	USP24	3'	CCCCTAGCACCTGCCGTCCTCA 43816	A A_ ACG A
			TGAGGACG CG TG AGG GG	
			ACTCCTGC GT AC TCC CC	
			C CC GA_ _	
GAM1032	LOC115330	3'	CCTCCTCGCCTTCAGCCTCCTC 28809	CGAC TGA
	A		TGAGGA GA CGAGGAGG	
			ACTCCT CT GCTCCTCC	
			CCGA TCC	
GAM1032	LOC149650	3'	CCCCCGGTGGTGTCTCA 38792	G G GA A A
			TGAGGAC AC AT CG GG GG	

ACTCCTG TG TG GC CC CC
 _ G _ _ C
 GAM1032 LOC158046 5' CCTCCCCG CAGGTGATCATCCT 29799 C _ A_ A A
 C GAGGA GA CG TG CG GGAGG
 ||||| || || || |||||
 CTCCT CT GT AC GC CCTCC
 A A GG _ C
 GAM1032 LOC220565 5' CCTCCTCGGCTTCCTCCTCA 43633 C CGATGA
 TGAGGA GA CGAGGAGG
 ||||| || |||||
 ACTCCT CT GCTCCTCC
 C TCG__
 GAM1032 LOC222031 3' CCCCATTTACTGTCTGCCCA 45132 A A CGA A
 TG GGACGACG TGA GG GG
 || ||||| || ||
 AC CCTGCTGT ATT CC CC
 C C TA_ _
 GAM1032 LOC222962 3' CCACCTTGTACCCCTCA 44627 ACGACGA A
 TGAGG TGACGAGG GG
 ||||| ||||| ||
 ACTCC ACTGTTCC CC
 C_____ A
 GAM1032 LOC256867 5' CCTCCTTGGCGCCTGTCCCA 45472 A ACGATGA
 TG GGACG CGAGGAGG
 || ||||| |||||
 AC CCTGT GTTCCTCC
 C CCGCG__
 GAM1032 LOC91923 5' CTTGGCATCATGTCCTCA 33544 AC A
 TGAGGACG GATG CGAGG
 ||||| ||||| |||||
 ACTCCTGT CTAC GTTCC
 A_ G
 GAM1032 LOC92299 5' CCTCCTCGCGTTCTTCCCA 34129 A C CG A
 TG GGA GA ATG CGAGGAGG
 || ||| || |||||
 AC CCT CT TGC GCTCCTCC
 C T _ _
 GAM1033 BRF1 3' CCCCCACCCCTGCCTCC 7256 AC CGCA
 GGAGGTAG GGGT GGGG
 ||||| ||||| |||||
 CCTCCGTC CCA CCCC
 _ C_
 GAM1033 CD34 3' CCCCTGCCCCCACTTCC 7533 AGAC TC
 GGAGGT GGG GCAGGGG
 ||||| || |||||
 CCTTCA CCC CGTCCCC
 _ C_
 GAM1033 GAB2 3' CCCTCCACCCACTACCTCC 27844 AC CGC
 GGAGGTAG GGGT AGGG
 ||||| ||||| |||||

			CCTCCATC CCA TCC		
			A_ CC_		
GAM1033	GAB2	3'	CCCTCCACCCACTACCTCC 14648	AC	CGC
			GGAGGTAG GGGT AGGG		
			CCTCCATC CCA TCC		
			A_ CC_		
GAM1033	MLC1	3'	CCCAGCGCCCTCTACCTCC 17521	C T A	
			GGAGGTAGA GGG CGC GGG		
			CCTCCATCT CCC GCG CCC		
			_ _ A		
GAM1033	MLC1	3'	CCCAGCGCCCTCTACCTCC 29215	C T A	
			GGAGGTAGA GGG CGC GGG		
			CCTCCATCT CCC GCG CCC		
			_ _ A		
GAM1033	PTK2B	3'	CGCCCCTGCTGCCATGTACCT 10311	GACG	C_
	CC		GGAGGTA GGT GCAGGGGCG		
			CCTCCAT CCG CGTCCCCGC		
			GTA_ TC		
GAM1033	CPLX1	3'	CGCCCCTGCCAGCACCTCC 13450	AGACG	TC
			GGAGGT GG GCAGGGGCG		
			CCTCCA CC CGTCCCCGC		
			CGA_ _		
GAM1033	DKFZP434B195	5'	CGCCCCCGGGACCCGTCTCCCC 25309	A T	GCA
			GG GG AGACGGGTC GGGGCG		
			CC CC TCTGCCAG CCCCCG		
			_ _ GGC		
GAM1033	FLJ20195	3'	CCCCCGCCCCAGCCTACCTTC 19281	AC_ TC A	
			GGAGGTAG GGG GC GGGG		
			CTTCCATC CCC CG CCCC		
			CGA _ C		
GAM1033	IL18BP	3'	CGCCCCTGTCTGGATCCCCTCC 12252	TAGAC	_
			GGAGG GGGTC GCAGGGGCG		
			CCTCC CCTAG TGTCCCCGC		
			_ _ GTC		
GAM1033	KIAA1196	3'	CGGGGCGCACCCCCAGCTACCT 30820	AC_ T_	AGGG
	CC		GAGGTAG GGG CGC G		
			CTCCATC CCC GCG C		
			GACC ACIII GGGA		
GAM1033	RASD2	3'	CGCCCCTGCTGCCCCACCACC 15605	A AGAC	C
			GG GGT GGGT GCAGGGGCG		

CC CCA CCG CGTCCCCGC
 A C__ T
 GAM1033 SCAMP5 3' CCCCCACCCTCCACCTGCC 29072 _ A C CGCA
 GG AGGT GA GGGT GGGG
 || ||| || ||| |||
 CC TCCA CT CCA CCCC
 G C _ C__
 GAM1033 SIAT8D 5' CCCCCGCGACTATCTCC 12223 AGACG A
 GGAGGT GGTCGC GGGG
 ||||| ||||| |||
 CCTCTA TCAGCG CCCC
 _ C
 GAM1033 TRIP-Br2 5' GCCCCCTCGCCCGCCTCC 16492 TAGA T CA_
 GGAGG CGGG CG GGGGC
 ||||| ||| || |||||
 CCTCC GCCC GC CCCC
 _ _ CTC
 GAM1033 LOC123242 5' CGGGGCGCACCCCCACTACCT 37241 AC__ T__ AGGG
 CC GAGGTAG GGG CGC G
 ||||| ||| ||| |
 CTCCATC CCC GCG C
 ACCC AC||| GGGA
 GAM1033 LOC124245 3' CGCCCCTGATACCCGCCCC 29419 A TAGA CG_
 GG GG CGGGT CAGGGGCG
 || || |||| |||||
 CC CC GCCCA GTCCCCGC
 _ _ CTA
 GAM1033 LOC129303 5' CGCCCCCACTTCCCCATCTACC 36970 C TCGCA_
 TCT GGAGGTAGA GGG GGGGCG
 ||||| || |||||
 TCTCCATCT CCC CCCCCG
 A CTTAC
 GAM1033 LOC130497 3' GCCCCTGCCCCACCCCC 36993 A AGAC TC
 GG GGT GGG GCAGGGGC
 || ||| || |||||
 CC CCA CCC CGTCCCCG
 C _ C_
 GAM1033 LOC150319 3' CCCCCACTCTGCCTCC 38891 CGG CGCA
 GGAGGTAGA GT GGGG
 ||||| || |||
 CCTCCGTCT CA CCCC
 _ C_
 GAM1033 LOC222962 3' CCCCTGCTGTGTCCCATCCCC 44628 TA C T__
 GG GA GGG C GCAGGGG
 || || ||| |||||
 CC CT CCC G CGTCCCC
 CC A T TGT
 GAM1034 PCDHA1 3' CCCGACACCTCACCTTTTCGC 25383 A T CGGG
 GCGAAAG TG GG CGGG
 ||||| || |||

			CGCTTTC AC CC GCCC	
			C T ACA_	
GAM1034	PCDHA1	3'	CCCGACACCTCACCTTTCGC 20864	A T CGGG
			GCGAAAG TG GG CGGG	
			CGCTTTC AC CC GCCC	
			C T ACA_	
GAM1034	PCDHA10	3'	CCCGACACCTCACCTTTCGC 25615	A T CGGG
			GCGAAAG TG GG CGGG	
			CGCTTTC AC CC GCCC	
			C T ACA_	
GAM1034	PCDHA10	3'	CCCGACACCTCACCTTTCGC 20874	A T CGGG
			GCGAAAG TG GG CGGG	
			CGCTTTC AC CC GCCC	
			C T ACA_	
GAM1034	PCDHA11	3'	CCCGACACCTCACCTTTCGC 20884	A T CGGG
			GCGAAAG TG GG CGGG	
			CGCTTTC AC CC GCCC	
			C T ACA_	
GAM1034	PCDHA12	3'	CCCGACACCTCACCTTTCGC 20895	A T CGGG
			GCGAAAG TG GG CGGG	
			CGCTTTC AC CC GCCC	
			C T ACA_	
GAM1034	PCDHA13	3'	CCCGACACCTCACCTTTCGC 20905	A T CGGG
			GCGAAAG TG GG CGGG	
			CGCTTTC AC CC GCCC	
			C T ACA_	
GAM1034	PCDHA2	3'	CCCGACACCTCACCTTTCGC 20915	A T CGGG
			GCGAAAG TG GG CGGG	
			CGCTTTC AC CC GCCC	
			C T ACA_	
GAM1034	PCDHA3	3'	CCCGACACCTCACCTTTCGC 20925	A T CGGG
			GCGAAAG TG GG CGGG	
			CGCTTTC AC CC GCCC	
			C T ACA_	
GAM1034	PCDHA4	3'	CCCGACACCTCACCTTTCGC 20935	A T CGGG
			GCGAAAG TG GG CGGG	
			CGCTTTC AC CC GCCC	
			C T ACA_	
GAM1034	PCDHA5	3'	CCCGACACCTCACCTTTCGC 20945	A T CGGG
			GCGAAAG TG GG CGGG	

			CGCTTTC AC CC GCCC	
			C T ACA_	
GAM1034	PCDHA6	3'	CCCGACACCTCACCTTTCGC 20955	A T CGGG
			GCGAAAG TG GG CGGG	
			CGCTTTC AC CC GCCC	
			C T ACA_	
GAM1034	PCDHA6	3'	CCCGACACCTCACCTTTCGC 25587	A T CGGG
			GCGAAAG TG GG CGGG	
			CGCTTTC AC CC GCCC	
			C T ACA_	
GAM1034	PCDHA7	3'	CCCGACACCTCACCTTTCGC 20965	A T CGGG
			GCGAAAG TG GG CGGG	
			CGCTTTC AC CC GCCC	
			C T ACA_	
GAM1034	PCDHA8	3'	CCCGACACCTCACCTTTCGC 20975	A T CGGG
			GCGAAAG TG GG CGGG	
			CGCTTTC AC CC GCCC	
			C T ACA_	
GAM1034	PCDHA9	3'	CCCGACACCTCACCTTTCGC 25600	A T CGGG
			GCGAAAG TG GG CGGG	
			CGCTTTC AC CC GCCC	
			C T ACA_	
GAM1034	PCDHAC1	3'	CCCGACACCTCACCTTTCGC 20844	A T CGGG
			GCGAAAG TG GG CGGG	
			CGCTTTC AC CC GCCC	
			C T ACA_	
GAM1034	PCDHAC2	3'	CCCGACACCTCACCTTTCGC 20854	A T CGGG
			GCGAAAG TG GG CGGG	
			CGCTTTC AC CC GCCC	
			C T ACA_	
GAM1034	SLC22A12	3'	ACCTGCCCGCCACATCCTCTGC 29402	AAA
			GCG GATGTGGCGGGCGGGT	
			CGT CTACACCGCCCGTCCA	
			CTC	
GAM1035	CRACC	3'	AATGGAGACCTCCCTACCAAGT 22152	CC _ GTA
	GA		TCAC GGTAGGG GGTC TATT	
			AGTG CCATCCC CCAG GTAA	
			AA T AG_	
GAM1035	LOC112885	3'	ATACACTTACCACTGGGTGA 28785	A _ C
			TCACCCGGT GG GGGT GTAT	

AGTGGGTCA CC TTCA CATA
 _ A _
 GAM1036 RAI14 3' TATTGGATAAGGACCAATGACA 17847 CAGAACTG
 TGTCA TTTATCCAATA
 ||||| |||||
 ACAGT GAATAGGTTAT
 AACCAG_
 GAM1036 UVRAG 3' GATTCACTGGTTCTGTAAC 9393 C _ TT
 GT ACAGAACT GT ATC
 || ||||| || |||
 CA TGTCTTGG CA TAG
 A T CT
 GAM1036 ZFP36L1 3' GTAAAAGTTCTGTGACA 11365 G
 TGTCACAGAACT TTTAT
 ||||| |||||
 ACAGTGTCTTGA AAATG
 _
 GAM1036 C1orf34 3' TGGAAGCAGTTCCACCACA 30439 CACA TA
 TGT GAACTGTT TCCA
 ||| ||||| |||
 ACA CTTGACGA AGGT
 CCAC _
 GAM1036 HYPH 3' TATTGAGTAAGTTCTGAAACA 45484 CA GTT TC
 TGT CAGAACT TA CAATA
 ||| ||||| || |||||
 ACA GTCTTGA AT GTTAT
 AA _ GA
 GAM1036 KIAA1719 3' TTGGGAACAGCCCCTGTGACA 33828 AA_ AT
 TGTCACAG CTGTTT CCAA
 ||||| ||||| |||
 ACAGTGTC GACAAG GGTT
 CCC _
 GAM1036 RNF8 3' TGTTGGCAACAGTTCCATGTCA 10100 T CA TAT
 TG CA GAACTGTT CCAATA
 || || ||||| |||||
 AC GT CTTGACAA GGTTGT
 T AC C_
 GAM1036 ZMPSTE24 3' GATGAATCTCTGTGACA 12462 ACT
 TGTCACAGA GTTTATC
 ||||| |||||
 ACAGTGTCT TAAGTAG
 C_
 GAM1036 LOC200301 5' ATTGGAGGATCTGTGACA 42781 A GTTTA
 TGTCACAGA CT TCCAAT
 ||||| || |||||
 ACAGTGTCT GG AGGTTA
 A _
 GAM1036 LOC203286 5' ATTGGATGACCCTGGACA 43494 A AACT T
 TGTC CAG GTT ATCCAAT
 ||| ||| ||| |||||

	ACAG GTC CAG TAGGTTA	
	— C —	
GAM1036 LOC257479 5'	ATTGCACCAAGTTCTGTGACA 46049	GTTTATC
	TGTCACAGAACT CAAT	
	ACAGTGTCTTGA GTTA	
	ACCAC—	
GAM1036 LOC51696 3'	GGGAAACATTCTGTGACA 18312	C A
	TGTCACAGAA TGTTT TCC	
	ACAGTGTCTT ACAA GGG	
	— —	
GAM1036 LOC91907 3'	TATTGGATATGTCATTTCTGT 33521	C TT—
	ACAGAA TG TATCCAATA	
	TGTCTT AC ATAGGTTAT	
	T TGT	
GAM1037 COL11A2 3'	ACCAGGCCACCTGGAATCCCA 27973	AAG GTCATA
CA	TGTGG TC GGCCTGGT	
	ACACC AG CCGGACCA	
	CTA GTCCAC	
GAM1037 COL11A2 3'	ACCAGGCCACCTGGAATCCCA 27978	AAG GTCATA
CA	TGTGG TC GGCCTGGT	
	ACACC AG CCGGACCA	
	CTA GTCCAC	
GAM1037 KIAA0152 3'	CCAAGCCCACCTTCCACA 16332	TC CATA C
	TGTGGAAG GT GGC TGG	
	ACACCTTC CA CCG ACC	
	C_ C_ A	
GAM1037 KIAA1388 3'	ACCAGGCCTAGGATCTCCCCA 44948	T AG GTCA
	TG GGA TC TAGGCCTGGT	
	AC CCT AG ATCCGGACCA	
	C CT G_	
GAM1037 LOC147299 5'	CCAGGCCACGCTCAACA 38330	G A T CATA
	TGT GA G CGT GGCCTGG	
	ACA CT C GCA CCGGACC	
	A _ _ C_	
GAM1038 CAB1 5'	ACAGCGAGGGCCAGCTCCT 21540	T CCA C
	AGG AGT GGCCCTCGC GT	
	TCC TCG CCGGGAGCG CA	
	_ AC_ A	
GAM1038 NAV2 3'	ACAGCGAGAACTGCACTACCTT 30203	C GCC C
	GAGGTAGT CAG CTCGC GT	

			TTCCATCA GTC GAGCG CA			
			C AA_ A			
GAM1038	PML	3'	GCTGCATGCCTGGACCACC	27084	A	CCTC C
			GGT GTCCAGGC GC GT			
			CCA CAGGTCCG CG CG			
			C TA_ T			
GAM1038	PML	3'	GCTGCATGCCTGGACCACC	27080	A	CCTC C
			GGT GTCCAGGC GC GT			
			CCA CAGGTCCG CG CG			
			C TA_ T			
GAM1038	ZNF278	3'	GGGGCCTGGCCACCCCT	25778	A A T	
			AG GGT G CCAGGCCCT			
			TC CCA C GGTCCGGGG			
			C C_			
GAM1038	DKFZP547L112	5'	TGGAGGTCTGGACTACCCCT	33059	A	CT
			AG GGTAGTCCAGGCC CG			
			TC CCATCAGGTCTGG GT			
			C AG			
GAM1038	DKFZP547L112	5'	ACGGCGCTCTCTGGACTACCCC	33055	A	CCCT
	T		AG GGTAGTCCAGG CGCCGT			
			TC CCATCAGGTCT GCGGCA			
			C CTC_			
GAM1038	KIAA0931	3'	AGGACCTAGACTACTTCT	33481	C C	
			AGAGGTAGTC AGG CCT			
			TCTTCATCAG TCC GGA			
			A A			
GAM1038	KIAA1691	3'	AGGGCCTGGACACCCCT	44460	A A	
			AG GGT GTCCAGGCCCT			
			TC CCA CAGGTCCGGGA			
			C _			
GAM1038	KIAA1856	3'	ACAGCGAGGGCCTGTACTACCT	44521	C	C
	C		GAGGTAGT CAGGCCCTCGC GT			
			CTCCATCA GTCCGGGAGCG CA			
			T A			
GAM1038	PRO0386	5'	AGGGCCAGACTACCTCT	20647	CA	
			AGAGGTAGTC GGCCCT			
			TCTCCATCAG CCGGGA			
			A_			
GAM1038	RAP140	3'	CGCAAAGGCTTTACTTCT	17556	TCCA	CTC C
			AGAGGTAG GGCC GC G			

		TCTTCATT TCGG CG C	
		____ AAA A	
GAM1038	SDCCAG3 5'	AGGGACCTGGACTCCCCCT 13434 A T _	
		AG GG AGTCCAGG CCCT	
		TC CC TCAGGTCC GGGA	
		C C A	
GAM1038	LOC122769 5'	ACGGCGAGAACCCGGCCCTGCT 36694 T_ A CC	
		GGTAG CC GG CTCGCCGT	
		TCGTC GG CC GAGCGGCA	
		CC C AA	
GAM1038	LOC256901 5'	CGAATCTGTGACTGCCTCT 46206 _ CCC	
		AGAGGTAGTC CAGG TCG	
		TCTCCGTCAG GTCT AGC	
		T A_	
GAM1039	ADAM12 5'	GCGGCGGCGCGGGCCGTGCGCG 9544 T CTA A	
	AG	CTCGCGCACG CCT CC CCGC	
		GAGCGCGTGC GGG GG GGCG	
		C CGC C	
GAM1039	CDKN2A 3'	CGGCTGGACGTGCGCGA 27758 TCTACCA	
		TCGCGCACGTCC CCG	
		AGCGCGTGCAGG GGC	
		TC_____	
GAM1039	CDKN2B 3'	CGGCTGGACGTGCGCGA 27808 TCTACCA	
		TCGCGCACGTCC CCG	
		AGCGCGTGCAGG GGC	
		TC_____	
GAM1039	CBLN1 5'	GCGGCGGCGGACGTGCGC 10558 TCTA A	
		GCGCACGTCC CC CCGC	
		CGCGTGCAGG GG GGCG	
		C_ C	
GAM1039	KIAA1904 3'	GCGGTGGCAGAGGGTGGTGAG 36380 G GT A	
		CTCGC CAC CCTCT CCACCGC	
		GAGTG GTG GGAGA GGTGGCG	
		_ _ C	
GAM1039	RAI1 5'	GCGAGAGGGAGAGCGTGCGCGA 30254 TC ACCAC	
	G	CTCGCGCACG CTCT CGC	
		GAGCGCGTGC GAGG GCG	
		GA GAGA_	
GAM1039	RINZF 5'	GCGGCCCGAGGCCGTGCGCGAG 23412 T TACCA	
		CTCGCGCACG CCTC CCGC	

GAGCGCGTGC GGAG GGCG
 C CCC__
 GAM1039 SHANK3 5' GGTGGAGGACGCGCAGGAG 32635 GC A
 CTC GC CGTCCTCTACC
 ||| || |||||
 GAG CG GCAGGAGGTGG
 GA C
 GAM1039 LOC201292 5' GCGTGTGCACCGTGC GCGAG 42564 TCCTCTAC _
 CTCGCGCACG CAC CGC
 ||||| ||| |||
 GAGCGCGTGC GTG GCG
 CAC_____ T
 GAM1040 SCNN1A 3' AAGAAACCGCTGATAACCAGGA 6702 CGAG_ CGC
 CA TGTCTGG AGCG TTCTT
 ||||| ||| |||||
 ACAGGACC TCGC AAGAA
 AATAG CA_
 GAM1040 DEGS 3' AAGCTATTTGCCAGGCA 9769 T GCGC
 TG CCTGGCGAGA GCTT
 || ||||| |||
 AC GGACCGCTTT CGAA
 _ AT_
 GAM1040 KIAA0040 3' TGCCACTGCTCACCAGGACA 16099 C _ C_
 TGTCTGG GAG AG GCG
 ||||| ||| |||
 ACAGGACC CTC TC CGT
 A G AC
 GAM1040 TRAF4 3' AAGTTCATCTCCCACCAGGACA 31377 C_ GCGC
 TGTCTGG GAGA GCTT
 ||||| ||| |||
 ACAGGACC CTCT TGAA
 ACC ACT_
 GAM1040 LOC153196 5' AAGACCAGCTCTCTCCAGGACA 41585 C GCGCT
 TGTCTGG GAGAGC TCTT
 ||||| ||||| |||
 ACAGGACC CTCTCG AGAA
 T ACC_
 GAM1041 GRLF1 3' CCACCGTCCCCTCCACA 38410 CA A
 TGT AGTGGGAC GTGG
 || ||||| |||
 ACA TCACCCTG CACC
 CC C
 GAM1041 BA108L7.2 3' CCCACCACCCTACTTGACA 25236 ACA T
 TGTCAAGTGGG GTGGT GG
 ||||| ||||| |||
 ACAGTTCATCC CACCA CC
 _ C
 GAM1041 CDT1 5' GGTCAGCCGCCCCACCTGACA 38068 A ACA
 TGTCA GTGGG GTGGTTGGCT
 ||||| ||||| |||||

[illegible]

			AC GACTCCGT	GGC ACC		
			C	CTG__ C		
GAM1042	LOC255040	5'	TGGTGCCATTGCCTCAGCCA	46110	A	CGTA
			TG CTGAGGCAA	ATCG		
			AC GACTCCGTT	TGGT		
			C	ACCG		
GAM1043	ACADM	3'	GAAGTTTCTTGAAAATCTTA	5452	_ T	C
			TGAGATTT CAA	GGAAG TC		
			ATTCTAAA GTT	CTTTC AG		
			A	_ A		
GAM1043	ADCY9	3'	AGCTGTGGTTAAGATCTCA	6790	C	GGA
			TGAGATTT AAT	AGCT		
			ACTCTAGA TTG	TCGA		
			A	GTG		
GAM1043	ARF1	3'	GAGCTGTGTTGAAATCCA	34991	A	GA
			TG GATTTCAATG	AGCTC		
			AC CTAAAGTTGT	TCGAG		
			_	G_		
GAM1043	ATP1A2	3'	GAGCTTCCAGAAATGCCA	6368	AG	AA
			TG ATTC	TGGAAGCTC		
			AC TAAAG	ACCTTCGAG		
			CG	_		
GAM1043	COL15A1	3'	GAGTTGACACTGAAATCT	7588	A	GA
			AGATTTCA TG	AGCTC		
			TCTAAAGT AC	TTGAG		
			C	AG		
GAM1043	CSNK1G3	3'	AGCCTAAAGAAATCTCA	10609	AA	AA
			TGAGATTTT	TGG GCT		
			ACTCTAAAG	ATC CGA		
			AA	_		
GAM1043	CX3CR1	3'	AGCTTCCAGTCCAATCTCA	34974		TCAA
			TGAGATT	TGGAAGCT		
			ACTCTAA	ACCTTCGA		
			CCTG			
GAM1043	DNMT2	3'	GAGCCTATTACAAGTCTCA	10670	C_	AA
			TGAGATTT	AATGG GCTC		
			ACTCTGAA	TTATC CGAG		
			CA	_		
GAM1043	DSC3	3'	GAGCTACAAAATTTCA	23664	CAA	GA
			TGAGATTT	TG AGCTC		

			ACTTTAAA AC TCGAG	
			___ A_	
GAM1043	DSC3	3'	GAGCTACAAAATTTCA 7653	CAA GA
			TGAGATTT TG AGCTC	
			ACTTTAAA AC TCGAG	
			___ A_	
GAM1043	DSCR3	3'	GTTTCTGAAGTCTCA 12687	ATG
			TGAGATTTCA GAAGC	
			ACTCTGAAGT CTTTG	

GAM1043	DSCR3	3'	GAACTGCCATAAAATCTCA 12686	CA A C
			TGAGATTT ATGG AG TC	
			ACTCTAAA TACC TC AG	
			A_ G A	
GAM1043	EGFR	3'	AGCTGCTCTGAAATCTC 11722	AT A
			GAGATTTCA GG AGCT	
			CTCTAAAGT TC TCGA	
			C_ G	
GAM1043	F2R	3'	GAATTGACATTGAAATCT 7722	GA C
			AGATTTCAATG AG TC	
			TCTAAAGTTAC TT AG	
			AG A	
GAM1043	GALNT7	3'	GAGCTTGTGATGAAATCT 18877	A G
			AGATTTCA TG AAGCTC	
			TCTAAAGT GT TTCGAG	
			A G	
GAM1043	ITM2B	5'	GGAGCTTCCCGAACCTC 22540	AT AAT
			GAG TTC GGAAGCTCC	
			CTC AAG CCTTCGAGG	
			C_ C_	
GAM1043	KIF3C	3'	GAGCTCCCCCAGTCAGATCTCA 8058	CAA A_
			TGAGATTT TGG AGCTC	
			ACTCTAGA ACC TCGAG	
			CTG CCC	
GAM1043	LTBP1	3'	GGAGCATTTTTTGAAATTCA 6243	A T A
			TGAG TTTCAA GGA GCTCC	
			ACTT AAAGTT TTT CGAGG	
			_ _ A	
GAM1043	MN1	3'	GGAGCTTTCAGAAAAACCTCA 8275	A CAA
			TGAG TTT TGGAAGCTCC	

		ACTC AAA ACTTTTCGAGG		
		C AAG		
GAM1043 RBMX	3'	GTCTTCCAAGTGAATCTCA 33857	A_ _	
		TGAGATTTCA TGGAAG C		
		ACTCTAAAGT ACCTTC G		
		CA T		
GAM1043 THY1	3'	GAGCTTCCAGAGCTCT 12977 T AA		
		AGA TTC TGGAAGCTC		
		TCT GAG ACCTTCGAG		
		C _		
GAM1043 ATF3	3'	GGAGTCCTCATTGAATCCTCA 10245 AT AA		
		TGAG TTCAATGG GCTCC		
		ACTC AAGTTACT TGAGG		
		CT CC		
GAM1043 ATP10D	3'	GAAC TTTCAAAATCTCA 36201 CAA C		
		TGAGATTT TGGAAG TC		
		ACTCTAAA ACTTTC AG		
		_ A		
GAM1043 BA108L7.2	3'	GAGCCCCAGGATCTCA 25240 CAA AA		
		TGAGATTT TGG GCTC		
		ACTCTAGG ACC CGAG		
		_ C_		
GAM1043 C15orf5	3'	GGAGCTCAGTGGAATCTC 25214 AATG A		
		GAGATTTC GA GCTCC		
		CTCTAAAG CT CGAGG		
		GTGA _		
GAM1043 CECR1	3'	GAGCTCACAGGAATCTCA 18883 AA GA		
		TGAGATTTC TG AGCTC		
		ACTCTAAGG AC TCGAG		
		_ AC		
GAM1043 CENTA2	3'	GGAAGTGAATGAAATCTCA 20443 ATGGA C		
		TGAGATTTCA AG TCC		
		ACTCTAAAGT TC AGG		
		AAG_ A		
GAM1043 CGGBP1	3'	GAGCTTTAATAAAAAATCTTA 9740 CAATG_		
		TGAGATTT GAAGCTC		
		ATTCTAAA TTTCGAG		
		AAATAA		
GAM1043 DKFZP434P211	3'	GGAGCACTCTGAGATCTCA 15868 AT AA		
		TGAGATTTCA GG GCTCC		

ACTCTAGAGT CT CGAGG
 _ CA
 GAM1043 DKFZP547N043 3' AGGTTTCAAAGTCTCA 25731 CAA G
 TGAGATTT TGGAA CT
 ||||| |||||
 ACTCTGAA ACTTT GA
 _ G
 GAM1043 DKFZP564M182 3' GAGCTTTTGGAAATACTCA 38219 _ AAT
 TGAG ATTTC GGAAGCTC
 ||| ||||| |||||
 ACTC TAAAG TTTTCGAG
 A GT_
 GAM1043 DMTF1 5' GGAGCTTCCATCCTGGTTCT 22116 TT _
 AGA TCA ATGGAAGCTCC
 ||| ||| |||||
 TCT GGT TACCTTCGAGG
 T_ CC
 GAM1043 FBP17 3' GAGCTTCCACTGGAGGCT 36049 A A
 AG TTTCA TGGAAAGCTC
 || ||||| |||||
 TC GAGGT ACCTTCGAG
 G C
 GAM1043 FLJ10392 5' AGCAAGCGTTGAAAATCTCA 19846 A GAA
 TGAG TTTCAATG GCT
 ||| ||||| |||
 ACTC AAAGTTGC CGA
 A GAA
 GAM1043 FLJ10898 5' GAGCCCAGAAAGCCTCA 29893 A_ AA AA
 TGAG TTTC TGG GCTC
 |||| ||| ||| |||
 ACTC AAAG ACC CGAG
 CG _ _
 GAM1043 FLJ11106 3' CTTCTATTAAAATCTCA 20318 C _
 TGAGATTT AAT GGAAG
 ||||| ||| |||||
 ACTCTAAA TTA CCTTC
 A T
 GAM1043 FLJ14166 3' GAGCAGCTGAAAATCTCA 23792 CAA AA
 TGAGATTT TGG GCTC
 ||||| ||| |||||
 ACTCTAAA GTC CGAG
 A_ GA
 GAM1043 FLJ20170 3' AGCTTTCTGGTCAAATCTCA 19259 CAAT_
 TGAGATTT GGAAGCT
 ||||| |||||
 ACTCTAAA CTTTCGA
 CTGGT
 GAM1043 FLJ22690 3' GGAGATGATCAGAAATCTCA 24038 AA AAG_
 TGAGATTTCT TGG CTCC
 ||||| ||| |||||

			ACTCTAAAG ACT GAGG		
			___ AGTA		
GAM1043	GLP	3'	GGAGCTTTTAAATCTCA 20723	CAAT	
			TGAGATTT GGAAGCTCC		
			ACTCTAAA TTTTCGAGG		
			T___		
GAM1043	GOLGIN-67	3'	GGAGCTTTCTAAATCTCA 45536	CAAT	
			TGAGATTT GGAAGCTCC		
			ACTCTAAA CTTTCGAGG		
			T___		
GAM1043	IL17D	3'	GAGTTCCAAAGATCTCA 28699	CAA G	
			TGAGATTT TGGAA CTC		
			ACTCTAGA ACCTT GAG		
			A___ _		
GAM1043	KIAA0152	3'	GGAAGTGTTCAGAAATCTCA 16337	AA _ C	
			TGAGATTTT TGGAA AG TCC		
			ACTCTAAAG ACTT TC AGG		
			___ G A		
GAM1043	KIAA0193	3'	AGCTGCTCTAAAATCTCA 16538	CAA _	
			TGAGATTT TGGAA AGCT		
			ACTCTAAA ATCT TCGA		
			___ CG		
GAM1043	KIAA0254	3'	AGCTTCTGGTAAATCCA 16503	A CAA	
			TG GATTT TGGAAAGCT		
			AC CTAAA GTCTTCGA		
			_ TG_		
GAM1043	KIAA0379	3'	GGAATTTTCTAGAATCTCA 33812	CAAT C	
			TGAGATTT GGAAG TCC		
			ACTCTAAG CTTTT AGG		
			AT___ A		
GAM1043	KIAA0603	3'	GGAACAAACTGTTGAAATCCA 16829	A AAGC_	
			TG GATTTCAATGG TCC		
			AC CTAAAGTTGTC AGG		
			_ AAACA		
GAM1043	KIAA0620	3'	GGAGCCCAAGAAGTCTCA 31122	AA AA	
			TGAGATTTT TGG GCTCC		
			ACTCTGAAG ACC CGAGG		
			A_ _		
GAM1043	KIAA0855	3'	GGAGCTTTCTAAATCTCA 17376	CAAT	
			TGAGATTT GGAAGCTCC		

	ACTCTAAA CTTTCGAGG	
	T__	
GAM1043 KIAA0976	3' GGAGCCCTAATAAATTTCA 17167	CAAT AA
	TGAGATTT GG GCTCC	
	ACTTTAAA CC CGAGG	
	TAAT __	
GAM1043 KIAA1170	3' GGAGCTATACCAAAATCT 34611	CAA A__
	AGATTT TGG AGCTCC	
	TCTAAA ACC TCGAGG	
	__ ATA	
GAM1043 KIAA1361	5' AGCTCTTCACAGATCTCA 31165	CAA _
	TGAGATTT TGGA AGCT	
	ACTCTAGA ACTT TCGA	
	C__ C	
GAM1043 KIAA1789	5' GGAGCTTTTGAAGTCCCA 33311	A T AA
	TG GA TTC TGGAAGCTCC	
	AC CT AAG ATTTTCGAGG	
	C C __	
GAM1043 KIAA1900	3' GGAGTTTCTCAAAATCT 36260	CAAT
	AGATTT GGAAGCTCC	
	TCTAAA TCTTTGAGG	
	AC__	
GAM1043 MGC10940	3' GAACTCCAAGATCTCA 26085	CAA A C
	TGAGATTT TGGA G TC	
	ACTCTAGA ACCT C AG	
	__ _A	
GAM1043 MGC10977	5' AGCTTGTGAAAATCTCA 26402	CA GG
	TGAGATTT AT AAGCT	
	ACTCTAAA TG TTCGA	
	AG __	
GAM1043 MGC12538	5' AGTATTTCCAGAATCTCA 26480	CAA __
	TGAGATTT TGGA GCT	
	ACTCTAAG ACCTT TGA	
	__ TA	
GAM1043 mPA-PLA1	3' GGGTTTTTTGAAATCCCA 29252	A TG
	TG GATTTCAA GAAGCTC	
	AC CTAAAGTT TTTTGGG	
	C __	
GAM1043 NUDT12	3' GAGCATCTTGAAATTCA 25449	A AT A
	TGAG TTTCA GGA GCTC	

		ACTT AAAGT TCT CGAG	
		— — A	
GAM1043	PB1	3' GAGCTTCCACTGCTGTTT 19980	TT A
		AGAT CA TGGAAGCTC	
		TTTG GT ACCTTCGAG	
		TC C	
GAM1043	SDF1	3' GAGCTTCCCTGACTCA 43690	ATT AT
		TGAG TCA GGAAGCTC	
		ACTC AGT CCTTCGAG	
		— C—	
GAM1043	STI2	3' GAGCTCCTGGATCTCA 42877	CAAT A
		TGAGATTT GGA GCTC	
		ACTCTAGG CCT CGAG	
		T— —	
GAM1043	TRIM26	3' GGCCCCCTGAAATCTCA 9501	AT AA
		TGAGATTTCA GG GCT	
		ACTCTAAAGT CC CGG	
		— CC	
GAM1043	USP8	3' AGCTACATTAAAATCTTA 11628	C GA
		TGAGATTT AATG AGCT	
		ATTCTAAA TTAC TCGA	
		A A—	
GAM1043	LOC115131	5' GAGCCACGGAATCTCA 29756	AA GAA
		TGAGATTTT TG GCTC	
		ACTCTAAGG AC CGAG	
		C— —	
GAM1043	LOC116236	3' GGAGCTCTGCAAGTCTCA 36542	CAA A
		TGAGATTT TGGA GCTCC	
		ACTCTGAA GTCT CGAGG	
		C— —	
GAM1043	LOC135398	3' GAGCCTGAGAAATCTTA 37387	AAT AA
		TGAGATTTT GG GCTC	
		ATTCTAAAG TC CGAG	
		AG— —	
GAM1043	LOC143719	5' AGCTTGTGAAAATCTCA 30404	CA GG
		TGAGATTT AT AAGCT	
		ACTCTAAA TG TTCGA	
		AG —	
GAM1043	LOC144438	3' AGCTTCTGTAAATCTCA 37734	CA
		TGAGATTT ATGGAAGCT	

ACTCTAAA TGTCTTCGA

GAM1043 LOC144519 5' AGCTTCCTGAGATCTC 37756 AT
GAGATTTCA GGAAGCT
||||||| |||||
CTCTAGAGT CCTTCGA

GAM1043 LOC145842 5' AGCTGGGTATTGTAAAATCTCA 37996 GA_
TGAGATTT CAATG AGCT
||||||| ||||| |||||
ACTCTAAA GTTAT TCGA
AT GGG

GAM1043 LOC145900 3' GGAGCTTTTTTAAATTTCA 38013 CAAT
TGAGATTT GGAAGCTCC
||||||| |||||
ACTTTAAA TTTTCGAGG
T__

GAM1043 LOC145988 3' GGAGCTTTCTAAATCTC 38041 CAAT
GAGATTT GGAAGCTCC
||||||| |||||
CTCTAAA CTTTCGAGG
T__

GAM1043 LOC146723 3' GGGTGCACCAAATCTCA 38229 CAA AA_
TGAGATTT TGG GCTC
||||||| ||| |||||
ACTCTAAA ACC TGGG
__ ACG

GAM1043 LOC148266 5' AGCTTTCATTAAAATGTCA 38512 G C
TGA ATTT AATGGAAGCT
||| ||||| |||||
ACT TAAA TTACTTTCTGA
G A

GAM1043 LOC150174 3' GGAGCACTCTGAGATCTCA 38874 AT AA
TGAGATTTCA GG GCTCC
||||||| || |||||
ACTCTAGAGT CT CGAGG
__ CA

GAM1043 LOC150213 3' GGAGCACTCTGAGATCTCA 36960 AT AA
TGAGATTTCA GG GCTCC
||||||| || |||||
ACTCTAGAGT CT CGAGG
__ CA

GAM1043 LOC152313 5' AGCTGTTTTCCATAAATCTCA 41471 CA ____
TGAGATTT ATGGA AGCT
||||||| ||||| |||||
ACTCTAAA TACCT TCGA
__ TTTG

GAM1043 LOC152485 3' GGAGCTCCCGGAATCTC 39281 AAT A
GAGATTTT GGA GCTCC
||||||| ||| |||||

	CTCTAAGG	CCT CGAGG		
	C__ _			
GAM1043	LOC154860	5' GAGCCTCGGCTGAAATCCG	41737	A ATG A
		TG GATTTCA GA GCTC		
		GC CTAAAGT CT CGAG		
		_ CGG C		
GAM1043	LOC155006	3' GGAGCCTCCATTTTCTC	39527	TTTC A
		GAGA AATGGA GCTCC		
		CTCT TTACCT CGAGG		
		TT__ C		
GAM1043	LOC158014	3' GGAGATCCATTGAAACTCA	39694	A AG
		TGAG TTTCAATGGA CTCC		
		ACTC AAAGTTACCT GAGG		
		_ A_		
GAM1043	LOC158056	5' GGAGCTTCCACCTTCTCA	39718	TTTCAA
		TGAGA TGGAAGCTCC		
		ACTCT ACCTTCGAGG		
		TCC__		
GAM1043	LOC163882	3' AGCTCCCCTGAGTCTCA	39970	T AT A
		TGAGATT CA GGA GCT		
		ACTCTGA GT CCT CGA		
		_ CC _		
GAM1043	LOC169021	5' AGCTTCCAGGTGTGTCTCA	40257	TT A_
		TGAGAT CA TGGAAGCT		
		ACTCTG GT ACCTTCGA		
		T_ GG		
GAM1043	LOC203523	3' GGAGCTTCCAGATGGGCATC	43054	_ A_
		GAT TTCA TGGAAGCTCC		
		CTA GGGT ACCTTCGAGG		
		C AG		
GAM1043	LOC204301	3' GGAGCTTTTAAATCTCA	43094	CAAT
		TGAGATTT GGAAGCTCC		
		ACTCTAAA TTTTCGAGG		
		T__		
GAM1043	LOC219988	5' AGTCAGCATCGGAATCTCA	44040	A GAA
		TGAGATTTC ATG GCT		
		ACTCTAAGG TAC TGA		
		C GAC		
GAM1043	LOC220534	3' GGAGCTTTTAAATCTCA	43617	CAAT
		TGAGATTT GGAAGCTCC		

		ACTCTAAA	TTTTCGAGG		
		T___			
GAM1043	LOC220538 3'	GGAGCTTTTAAATCTCA	43627	CAAT	
		TGAGATTT	GGAAGCTCC		
		ACTCTAAA	TTTTCGAGG		
		T___			
GAM1043	LOC222234 5'	GAGCTTTCAAATCCCA	45240	A TCAA	
		TG GATT	TGGAAGCTC		
		AC CTAA	ACTTTCGAG		
		C ___			
GAM1043	LOC254358 3'	GGAGCTTTTAAATCTCA	45532	CAAT	
		TGAGATTT	GGAAGCTCC		
		ACTCTAAA	TTTTCGAGG		
		T___			
GAM1043	LOC254936 3'	GGAGCTTTTAAATTTCA	45529	CAAT	
		TGAGATTT	GGAAGCTCC		
		ACTTTAAA	TTTTCGAGG		
		T___			
GAM1043	LOC257286 3'	GGAGCTTTTAAATCTCA	45374	CAAT	
		TGAGATTT	GGAAGCTCC		
		ACTCTAAA	TTTTCGAGG		
		T___			
GAM1043	LOC257464 3'	GGAGCTTCCTGCAATCTCA	43166	T AT	
		TGAGATT CA	GGAAGCTCC		
		ACTCTAA GT	CCTTCGAGG		
		C _			
GAM1043	LOC257494 3'	GGCCCCCTGAAATCTCA	46688	AT AA	
		TGAGATTTCA	GG GCT		
		ACTCTAAAGT	CC CGG		
		_ CC			
GAM1043	LOC58489 3'	GAGCTGATGAAATCTCA	35903	ATGGA	
		TGAGATTTCA	AGCTC		
		ACTCTAAAGT	TCGAG		
		AG___			
GAM1043	LOC92017 5'	AGCCTTCCCTTTGGAATCCCA	33708	A T_ _	
		TG GATTTCAA	GGAAG CT		
		AC CTAAGGTT	CCTTC GA		
		C TC C			
GAM1043	LOC92303 3'	GGAGCTTTGGAAACTTCA	34137	A AATG	
		TGAG TTTC	GAAGCTCC		

ACTT AAAG TTTCGAGG
 C G__
 GAM1043 LOC92822 3' GGAGCTTCCCACCATCTACA 34986 _ TTCAAT
 TG AGAT GGAAGCTCC
 || ||| |||||
 AC TCTA CCTTCGAGG
 A CCAC__
 GAM1044 ALDH1A3 3' CCAAGGCACTTTCTTAAGC 6353 C CCAT
 GC TAAGGG GTGCCTTGG
 || ||||| |||||
 CG ATTCTT CACGGAACC
 A T__
 GAM1044 B4GALT1 3' CAAGGCACAGCCAGGGC 7244 AAG CA
 GCCT GGC TGTGCCTTG
 ||| || |||||
 CGGG CCG ACACGGAAC
 A__ __
 GAM1044 PROK1 3' CCATCATGACATGGTCCCCAGG 26197 AA GCCT_
 CTG CAGCCT GGGCCATGT TGG
 ||||| ||||| |||
 GTCGGA CCTGGTACA ACC
 CC GTACT
 GAM1044 SLC21A2 3' CCATCCATGGCCCCCAGACTG 12158 C AA TGCCT
 CAG CT GGGCCATG TGG
 ||| || ||||| |||
 GTC GA CCCGGTAC ACC
 A CC CT__
 GAM1044 UNC119 3' CAAGACACTGCCTAAGGT 11620 AA CAT C
 GCCT GGGC GTG CTTG
 |||| ||| |||||
 TGGT TCCG CAC GAAC
 A_ T__ A
 GAM1044 UNC119 3' CAAGACACTGCCTAAGGT 27646 AA CAT C
 GCCT GGGC GTG CTTG
 |||| ||| |||||
 TGGT TCCG CAC GAAC
 A_ T__ A
 GAM1044 CENTG1 3' CAACCCAGCCCTTGGGCTG 16564 CATG CC
 CAGCCTAAGGGC TG TTG
 ||||| || |||
 GTCGGGTTCCCG AC AAC
 __ CC
 GAM1044 DOC2B 3' CCAAGGCCTGTGGCCCCCACAC 9636 CCTAA T
 TG CAG GGGCCATG GCCTTGG
 || ||||| |||||
 GTC CCCGGTGT CGGAACC
 ACACC C
 GAM1044 KIAA0767 3' CACATGGCCCCCAGGCTG 30407 AA
 CAGCCT GGGCCATGTG
 ||||| |||||

GTCGGA CCCGGTACAC
 CC
 GAM1044 KIAA1297 3' CCAGCCCTACAACCCCCAGGC 35711 AA CCA CC_
 GCCT GGG TGTG TTGG
 |||| || |||| ||||
 CGGA CCC ACAT GACC
 CC A__ CCC
 GAM1044 KIAA1822 3' GGACATGGCCCCTGGCTG 33554 TAA G
 CAGCC GGGCCATGT CC
 |||| ||||| ||
 GTCGG CCCGGTACA GG
 TC_ _
 GAM1044 NRF 3' CAAGGCACACCACAGCTG 18984 CTAAG CCA
 CAGC GG TGTGCCTTG
 ||| || |||||
 GTCG CC ACACGGAAC
 ACA__ _
 GAM1044 TUB 3' CCAAGCCTGGCCCTTA 9322 TGT C
 TAAGGGCCA GC TTGG
 ||||| || |||
 ATTCCCGGT CG AACC
 C__ _
 GAM1044 LOC127702 3' CACAGCCCTTGGCTG 37180 T CA
 CAGCC AAGGGC TGTG
 |||| |||| |||
 GTCGG TTCCCG ACAC
 _ _
 GAM1044 LOC150407 3' CCAAGGCAACCCCTCAGGGCTG 38950 A_ CCATG
 CAGCCT AGGG TGCCTTGG
 |||| || |||||
 GTCGGG TCCC ACGGAACC
 AC CA__
 GAM1044 LOC166341 3' CAAGGCACCCTCCAGACTG 40210 C AA CCAT
 CAG CT GGG GTGCCTTG
 ||| || |||||
 GTC GA TCC CACGGAAC
 A CC _
 GAM1044 LOC219942 3' CCTTCGCCACAGCCCTTAGAGT 44824 _ CA T CTT
 GC CTAAGGGC TG GC GG
 || ||||| || ||
 TG GATTCCCG AC CG CC
 A AC _ CTT
 GAM1044 LOC253868 5' GGCACACAGCACTTAGGCTG 45751 G CA
 CAGCCTAAG GC TGTGCC
 ||||| || |||||
 GTCGGATTC CG ACACGG
 A AC
 GAM1045 ENAM 3' TCATAGAATTTTCAGCGTTAGA 25633 AAATCAA
 TCTAA AAATTCTATGA
 |||| |||||

			AGATT	TTTAAGATACT		
			GCGAC__			
GAM1045	MXI1	3'	GTCAATGCTATTTTTGTTTTTA	12585	T	TC _
	GA		TCTAAAAA CAAAAAT	TAT GAC		
			AGATTTTT	GTTTTTA	GTA CTG	
			_	TC A		
GAM1045	MXI1	3'	GTCAATGCTATTTTTGTTTTTA	28195	T	TC _
	GA		TCTAAAAA CAAAAAT	TAT GAC		
			AGATTTTT	GTTTTTA	GTA CTG	
			_	TC A		
GAM1045	PCDHB7	3'	TCATAGATGATCATTAAATTTT	21008		CAAAAAAT__
	TAGA		TCTAAAAAT	TCTATGA		
			AGATTTTTTA	AGATACT		
			AATTACTAGT			
GAM1045	RPH3AL	3'	AATTTTTGTATTTTTAGA	13847	_	
			TCTAAAAAT CAAAAATT			
			AGATTTTTTA	GTTTTTAA		
			T			
GAM1045	FHR5	3'	TAGAACTCTGGATTTTTTAGA	25085		AAAAA
			TCTAAAAATC	TTCTA		
			AGATTTTTTAG	AAGAT		
			GTCTC			
GAM1045	FLJ10922	3'	GTCATAGAAGAGGATCTTAGA	20257	AA	AAAAA
			TCTAA ATC	TTCTATGAC		
			AGATT TAG	AAGATACTG		
			C_ GAG__			
GAM1045	FLJ20730	3'	TCTCAGAATTTTAATTTT TAGA	19642	CA	AT
			TCTAAAAAT AAAATTCT	GA		
			AGATTTTTTA	TTTAAAGA	CT	
			A_ CT			
GAM1045	FLJ21820	3'	GTCTTATTTCTGGTTTTT TAGA	22453	A	TCTAT
			TCTAAAAATCA AAAT	GAC		
			AGATTTTTGGT	TTTA	CTG	
			C TT__			
GAM1045	ICK	3'	GTCATTGGTTTGATTTTTGGA	17197		AATTCT
			TCTAAAAATCAAA	ATGAC		
			AGGTTTTTAGTTT	TACTG		
			GGT__			
GAM1045	IPLA2(GAMMA)	5'	GTCATAGAAAATAAATGATTTT	30446		AAAA__
	TA		TAAAAATCA	TTCTATGAC		

	ATTTT TAGT AAGATA CTG	
	AAATAA	
GAM1045 KIAA0276	3' GTCATGGAATACAACCTTTAGA 35136	AATCAAAA
	TCTAAA ATTCTATGAC	
	AGATTT TAAGGTACTG	
	CCAACA__	
GAM1045 moblak	3' TCATAAAGGGTTTGATTTT 28311	AA C
	TAAAAATCAAA TT TATGA	
	ATTTT TAGTTT GA ATACT	
	GG A	
GAM1045 LOC221760	3' GTCATAGAGGCTTGATTTT 45032	AAA
	TAAAAATCAA TTCTATGAC	
	ATTTT TAGTT GAGATACTG	
	CG_	
GAM1045 LOC257422	5' ATAGAACCTTTGATTTT 46189	AA
	AAAAATCAAA TTCTAT	
	TTTTT AGTTT AAGATA	
	CC	
GAM1045 LOC90459	3' TCATAGTCCTTTTGATTTT 31492	ATT
	AAAATCAAAA CTATGA	
	TTTTT AGTTT GATACT	
	CCT	
GAM1046 KCNQ1	3' AGGCACAGGCAGGGCAGGACCA 5721	T AACGA A
	TG GT CCCT CCTGTGCCT	
	AC CA GGGA GGACACGGA	
	_ GGAC_ C	
GAM1046 DKFZP761D0211	5' AGGCACAGATTCCCCGTCCACA 25735	TA ACCCTAC
	TGTG ACG CTGTGCCT	
	ACAC TGC GACACGGA	
	C_ CCCTTA_	
GAM1046 LOC149132	5' AGGCACAGCTCCATCGTTACA 38643	CCCTAC
	TGTAACGA CTGTGCCT	
	ACATTGCT GACACGGA	
	ACCTC_	
GAM1046 LOC255975	5' AGGCACAGCTCCATCATTACA 45887	C CCCTAC
	TGTAA GA CTGTGCCT	
	ACATT CT GACACGGA	
	A ACCTC_	
GAM1047 HOXC13	3' CTGGCCCTCAATTAGCTA 30016	C A_
	TAGCTAATTG AGGG GG	

ATCGATTAAC TCCC TC
 _ GG
 GAM1047 P53AIP1 3' CTACACCTCCCTGGAGGC 22658 AAT G C
 GCT T CAGGGAGG GTAG
 ||| | ||||| |||
 CGG A GTCCCTCC CATC
 _ G A
 GAM1047 VCL 3' CTACCTCCCTGCAACCAACTA 9403 CTAA CG
 TAG TTGCAGGGAGG TAG
 ||| ||||| |||
 ATC AACGTCCCTCC ATC
 AACC _
 GAM1047 VCL 3' CTACCTCCCTGCAACCAACTA 15192 CTAA CG
 TAG TTGCAGGGAGG TAG
 ||| ||||| |||
 ATC AACGTCCCTCC ATC
 AACC _
 GAM1047 ARHGAP5 3' TCTACGTTTGGTTCAATTA 37820 C GG
 TAATTG AG AGGCGTAGA
 ||||| || |||||
 ATTAAC TT TTTGCATCT
 _ GG
 GAM1047 MGC11242 3' TCTTGGCTCCCTGCCATCAGC 23610 A T G T
 GCT AT GCAGGGAG CG AGA
 ||| || ||||| || |||
 CGA TA CGTCCCTC GT TCT
 C C G _
 GAM1048 AP1B1 3' GCTGACCCACATGGTCAA 6797 T
 TTGACCATGTG GTCAGT
 ||||| |||||
 AACTGGTACAC CAGTCG
 C
 GAM1048 PCLO 3' ATGCAACCAACAGTCAA 45213 CATGTG CA
 TTGAC TGT GTTGCAT
 |||| || |||||
 AACTG ACA CAACGTA
 _ AC
 GAM1048 TRHDE 3' AATGCAACTACTCTACAT 15032 T_ C
 ATGTG GT AGTTGCATT
 |||| || |||||
 TACAT CA TCAACGTAA
 CT _
 GAM1048 FLJ10932 3' AATGCTCAGACGACACACA 20262 A _
 TGTGTGTC GTT GCATT
 ||||| || |||||
 ACACACAG CAG CGTAA
 _ ACT
 GAM1048 KIAA0349 3' AATGCAACTGACCCTTTCAATC 44338 CCATGTGT
 AG TTGA GTCAGTTGCATT
 |||| |||||

		GACT	CAGTCAACGTAA		
		AACTTTCC			
GAM1048	KIAA1954	3'	GCAAGACACACACATCAA	38097	CCA_ AG
			TTGA TGTGTGTC TTGC		
			AACT ACACACAG AACG		
			ACAC _		
GAM1048	LOC148443	3'	AGCCAACACATATGGTCAA	38538	CA
			TTGACCATGTGTGT GTT		
			AACTGGTATACACA CGA		
			AC		
GAM1048	LOC149506	3'	GGCCAACACACATGGCCAA	41010	A CA
			TTG CCATGTGTGT GTT		
			AAC GGTACACACA CGG		
			C AC		
GAM1048	LOC157556	3'	AATGGACTAAGACACACATTGT	41819	C _ G
		CAA	TTGAC ATGTGTGTC AGTT CATT		
			AACTG TACACACAG TCAG GTAA		
			T AA _		
GAM1048	LOC203427	3'	CATTTGACACACATACTCAA	43043	CC T
			TTGA ATGTGTGTCAG TG		
			AACT TACACACAGTT AC		
			CA T		
GAM1049	SLC39A1	3'	GGGAAATACTGAGGACCAA	15793	T G AA C
			TTGGT CC TCGG TA TTCCC		
			AACCA GG AGTC AT AAGGG		
			_ _ _ A		
GAM1049	SPG4	3'	GGGAAATACTAGGAACTAA	17261	GTCGGAA C
			TTGGTTCC TA TTCCC		
			AATCAAGG AT AAGGG		
			ATC_ A		
GAM1049	DKFZP434A043	3'	GGAAGTACAGGAACCAG	17702	GTCGGAA
			TTGGTTCC TACTTCC		
			GACCAAGG ATGAAGG		
			AC_		
GAM1049	FLJ12526	3'	GGAAAGATCAAGGAACCAA	24168	GTCG ATA C
			TTGGTTCC GA CTT CC		
			AACCAAGG CT GAA GG		
			AA_ A_ A		
GAM1049	KIAA0513	3'	GGAAAGGGACGGAATCAA	16358	GGAATA C
			TTGGTTCCGTC CTT CC		

			AACTAAGGCAG GAA GG	
			G_____ A	
GAM1049	PLAC3	5'	GGAAATTCAAAGGAACCAA 34366	GTCG AC
			TTGGTTCC GAAT TTCC	
			AACCAAGG CTTA AAGG	
			AAA_ _	
GAM1050	ARL4	5'	GAAGAGAAAAGCATTTC A 12298	A_ GG
			TGAAATGCT TCTC TC	
			ACTTTACGA AGAG AG	
			AA A_	
GAM1050	GEMIN5	5'	AGAAATGACAGCCAGCACCTC 42971	AA AT CG
			GA TGCT CT GTCATTTCT	
			CT ACGA GA CAGTAAAGA	
			CC CC _	
GAM1050	MADD	3'	AGAAATGACTGTAAATATTTCA 28254	CTATCT
			TGAAATG CGGTCATTTCT	
			ACTTTAT GTCAGTAAAGA	
			AAAT_	
GAM1050	MADD	3'	AGAAATGACTGTAAATATTTCA 28239	CTATCT
			TGAAATG CGGTCATTTCT	
			ACTTTAT GTCAGTAAAGA	
			AAAT_	
GAM1050	MADD	3'	AGAAATGACTGTAAATATTTCA 28233	CTATCT
			TGAAATG CGGTCATTTCT	
			ACTTTAT GTCAGTAAAGA	
			AAAT_	
GAM1050	MADD	3'	AGAAATGACTGTAAATATTTCA 9784	CTATCT
			TGAAATG CGGTCATTTCT	
			ACTTTAT GTCAGTAAAGA	
			AAAT_	
GAM1050	MADD	3'	AGAAATGACTGTAAATATTTCA 28249	CTATCT
			TGAAATG CGGTCATTTCT	
			ACTTTAT GTCAGTAAAGA	
			AAAT_	
GAM1050	MADD	3'	AGAAATGACTGTAAATATTTCA 28244	CTATCT
			TGAAATG CGGTCATTTCT	
			ACTTTAT GTCAGTAAAGA	
			AAAT_	
GAM1050	PDAP1	3'	AGAAAGATGCAGGACAGCATTT 44418	A CG_ A
CA			TGAAATGCT TCT GTC TTTCT	

			ACTTTACGA AGG TAG AAAGA		
			C ACG _		
GAM1050	SLC4A7	3'	AAATAATCAAAGATAGCATTCA 9666	A	C_ C
			TGAA TGCTATCT GGT ATTT		
			ACTT ACGATAGA CTA TAAA		
			_ AA A		
GAM1050	C1orf16	3'	AGAAACAGAAGGACAGCATTTTC 16853	A T GG A_	
			GAAATGCT TC C TC TTTCT		
			CTTTACGA AG G AG AAAGA		
			C _ A_ AC		
GAM1050	LOC113612	3'	GAAATGGACAGCATTATCA 36171	_ A TCGGT	
			TGA AATGCT TC CATTTC		
			ACT TTACGA AG GTAAAG		
			A C _		
GAM1050	LOC199920	5'	AAATGACTCTTTGAGCAACTCA 42659	AA ATCTC	
			TGA TGCT GGTCAATT		
			ACT ACGA TCAGTAAA		
			CA GTTTC		
GAM1051	FMO5	3'	TGCCCAGAAATCTACTTTAAT 7193	CT C A	
			ATTAA TAGATTTTC GG CA		
			TAATT ATCTAAAG CC GT		
			TC A C		
GAM1051	TRIM6	3'	TGTTCTCATCTATGTTAATGAA 27713	T TTCC	
			TTCATTAAC TAGAT GGACA		
			AAGTAATTG ATCTA CTTGT		
			T CT_		
GAM1051	LOC152059	3'	TCCAGGGAAGTTAATGGA 39209	TAGAT _	
			TTCATTAAC TTCC GGA		
			AGGTAATTGA AGGG CCT		
			_ A		
GAM1052	BRPF1	3'	CCATCCCACCACCTCTACCTGC 36172	_ C	
	T		AGCAGGTA AGGTGGTGGGA GG		
			TCGTCCAT TCCACCACCCT CC		
			C A		
GAM1052	CASP8	5'	CCACCCCTTCCCTGCTGA 27202	T T	
			TCAGCAGG AAGG GGTGG		
			AGTCGTCC TTCC CCACC		
			C C		
GAM1052	CASP8	5'	CCACCCCTTCCCTGCTGA 27206	T T	
			TCAGCAGG AAGG GGTGG		

			AGTCGTCC TTCC CCACC			
			C C			
GAM1052 CIT	3'	CCATCCCATAGCTCCTGC	34562	TAA G C		
		GCAGG GGT GTGGGA GG				
		CGTCC TCG TACCCT CC				
		___ A A				
GAM1052 DFFB	3'	CCACTGCACCTGACCTGCTGA	42240	A _		
		TCAGCAGGT AGGTG GTGG				
		AGTCGTCCA TCCAC CACC				
		G GT				
GAM1052 G22P1	5'	CCGTCCACATTCCTCACT	7202	A T _		
		GGT AGG GGTG GGACGG				
		TCA TCC TTAC CCTGCC				
		C _ A				
GAM1052 GRM4	3'	CGCCTGCCCTCCTGCCGA	6503	A TA T TG A		
		TC GCAGG AGG GG GG CG				
		AG CGTCC TCC CC CC GC				
		C _ _ GT _				
GAM1052 HTR2C	5'	CTTGCCCTTACCTGCCGA	6533	A T TG		
		TC GCAGGTAAGG GG GG				
		AG CGTCCATTCC CC TC				
		C _ _ GT				
GAM1052 KLHL1	5'	CTGTCCTCCCCACCTGCTGA	21918	AA T TG		
		TCAGCAGGT GG GG GGACGG				
		AGTCGTCCA CC CC CCTGTC				
		_ _ CT				
GAM1052 LHX2	5'	CCACCCCACCAAGGCAACCCCTG	11199	CA AAGG AC		
A		TCAG GGT TGGTGGG GG				
		AGTC CCA ACCACCC CC				
		C_ ACGG CA				
GAM1052 NEK4	5'	CCGCCCGCTGCCCTACCCGC	9137	A A TG A		
		GC GGTA GG GTGGG CGG				
		CG CCAT CC CGCCC GCC				
		C C GT _				
GAM1052 SYNGR1	3'	CCACCAAAAGCCTCTCCTGCTG	11062	TA ____		
A		TCAGCAGG AGGT GGTGG				
		AGTCGTCC TCCG CCACC				
		TC AAAA				
GAM1052 ARFGAP1	3'	CCGTCCCACCACCAAGTTCACC	20109	AA ____		
		GGT GGTGGTGGGACGG				

CCA CCACCACCCTGCC
 CTTGAA
 GAM1052 C20orf124 3' CCGCCCCTCCCTGCTGA 24144 TA T
 TCAGCAGG AGG GGTGG
 ||||| ||| |||||
 AGTCGTCC TCC CCGCC
 C_ _
 GAM1052 CG012 5' CCACCTAACCTACTACTG 40486 C A _
 CAG AGGTA GGT GGTGG
 ||| ||||| ||| |||||
 GTC TCCAT CCA CCACC
 A C AT
 GAM1052 DJ667H12.2 5' CCGCCGCCTCCCCGCTGA 21215 A TA
 TCAGC GG AGGTGGTGG
 ||||| || |||||
 AGTCG CC TCCGCCGCC
 _ CC
 GAM1052 DMWD 3' CCATAACCCTCCCTGCTGA 30528 TAA G
 TCAGCAGG GGT GTGG
 ||||| ||| |||||
 AGTCGTCC CCA TACC
 CTC A
 GAM1052 DMWD 5' CCGCCCCAGTACAGCCTGCTGA 30530 AAG G A
 TCAGCAGGT GTG TGGG CGG
 ||||| ||| ||||| |||
 AGTCGTCCG CAT ACCC GCC
 A_ G C
 GAM1052 EPN2 3' CCTGATCCACCTACCTGCT 17346 A T_
 AGCAGGTA GGTGG GGG
 ||||| ||||| |||
 TCGTCCAT CCACC TCC
 _ TAG
 GAM1052 FLJ10661 3' CCATCCCAGGTCACCACCTGGC 19994 _ AA _ C
 TGA TCAGC AGGT GGTGG TGGGA GG
 ||||| ||||| ||||| ||||| ||
 AGTCG TCCA CCACT ACCCT CC
 G _ GG A
 GAM1052 FLJ12650 3' CCATCCCACCACACTCACTCA 23722 A A _ C
 C GGT AG GTGGTGGGA GG
 | ||| || ||||| ||||| ||
 A TCA TC CACCACCCT CC
 C C A A
 GAM1052 KIAA0356 3' CCACCCCAGTGCGTCTCGCCTG 32891 TA _ G AC
 CTGA TCAGCAGG AG GTG TGGG GG
 ||||| || ||| ||||| ||
 AGTCGTCC TC CGT ACCC CC
 GC TG G CA
 GAM1052 KIAA1464 5' CCACCCCATACCTGCTG 33881 A T
 CAGCAGGTA GG GGTGG
 ||||| || |||||

		GTCGTCCAT CC CCACC		
		A _		
GAM1052	PRO0365	3' CTGTCCCACCCTACCTGC	15388	AA T
		GCAGGT GG GGTGGGACGG		
		CGTCCA TC CCACCCTGTC		
		— —		
GAM1052	SC65	3' CCGCCCTCCTCACTGCTGA	13174	GTA T_
		TCAGCAG AGG GGTGG		
		AGTCGTC TCC CCGCC		
		AC_ TC		
GAM1052	SEPT3	3' CCACCCCTGCCCACTGCTGA	21179	GTA___ T
		TCAGCAG AGG GGTGG		
		AGTCGTC TCC CCACC		
		ACCCCG C		
GAM1052	TED	3' CCACCCCAACCACCTAATCT	17914	AA_ AC
		AGGT GGTGGTGGG GG		
		TCTA CCACCACC CC		
		ATC CA		
GAM1052	LOC129195	5' CCACCCCAATGCCCTCACCTGC	37323	A TGG_ AC
		GCAGGT AGG TGGG GG		
		CGTCCA TCC ACCC CC		
		C CGTA CA		
GAM1052	LOC129195	5' CCACCCCAATGCCCTCACCTGC	37324	A TGG_ AC
		GCAGGT AGG TGGG GG		
		CGTCCA TCC ACCC CC		
		C CGTA CA		
GAM1052	LOC129195	5' CCACCCCAATGCCCTCACCTGC	37325	A TGG_ AC
		GCAGGT AGG TGGG GG		
		CGTCCA TCC ACCC CC		
		C CGTA CA		
GAM1052	LOC146506	3' CCATCCCCACCCACCTGC	38178	AA T C
		GCAGGT GGTGG GGGG GG		
		CGTCCA CCACC CCCT CC		
		C_ _ A		
GAM1052	LOC149606	3' CCATCCCACCACCATGTGCC	38782	A_ C
		GGTA GGTGGTGGGA GG		
		CCGT CCACCACCCT CC		
		GTA A		
GAM1052	LOC150197	3' CCGTCCCCCTACCTTGCT	38866	T
	GA	TCAGCAGGTAAGGTGG GGGACGG		


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AGTCGTCCGTTCCATC CCCTGCC
      C
GAM1052 LOC158490 3' CCATCCCATGTCCACCACCTGGC 39848   _ AA   _   C
      TGA          TCAGC AGGT GGTG GTGGGA GG
                ||||| ||| ||||| ||
                AGTCG TCCA CCAC TACCCT CC
                  G   _   TG   A
GAM1052 LOC220073 5' CCATCCCAGGTCACCACCTGGC 44874   _ AA   _   C
      TGA          TCAGC AGGT GGTGG TGGGA GG
                ||||| ||| ||||| ||
                AGTCG TCCA CCACT ACCCT CC
                  G   _   GG   A
GAM1052 LOC90917 3' CCACCCCAGTGTCTCACTCCAC 32164   CA_ A GT G   AC
      TGA          TCAG GGT AG G TGGG GG
                ||| ||| || ||||| ||
                AGTC TCA TC T ACCC CC
                  ACC C TG G   CA
GAM1052 LOC91069 3' CCATCCCAGGTCACCACCTGGC 32346   _ AA   _   C
      TGA          TCAGC AGGT GGTGG TGGGA GG
                ||||| ||| ||||| ||
                AGTCG TCCA CCACT ACCCT CC
                  G   _   GG   A
GAM1053 OSMR    5' CGACAACCTTCGCAGCCCA 10150   AG   AAA
                TGG TGCGAGGTTG TCG
                ||| ||||| |||
                ACC ACGCTTCAAC AGC
                  CG   _
GAM1053 LOC127943 3' TGACGATTTCAACCTCACAC 36913   C
                GTG GAGGTTGAAATCGTCA
                ||| ||||| |||||
                CAC CTCCAACCTTTAGCAGT
                  A
GAM1053 LOC131873 3' GACAATTCCAGCACTCTA 37365   GA TTGA C
                TGGAGTGC GG AAT GTC
                ||||| || ||| |||
                ATCTCACG CC TTA CAG
                  A_   _   A
GAM1054 ARHE    3' TTGCTCAATGTAATAT 11670   CGTTT
                ATATTACA TTGAGCAA
                ||||| |||||
                TATAATGT AACTCGTT
                _
GAM1054 FLJ11116 3' GTTGTTCAAATATAATATA 40185   CACGTT
                TATATTA TTTGAGCAAC
                ||||| |||||
                ATATAAT AAACCTTGTTG
                  AT_
GAM1054 KIAA1136 3' TTGCTCGACATGTAACATG 43886   A   C   TTT
                TAT TTACA GTT GAGCAA
                ||| ||||| ||| |||||

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GTA AATGT CAG CTCGTT
 C A ____
 GAM1055 ATP11B 3' ATCTCGTGAAGGCTGTAGG 39143 G GC A
 CC ACA GCCTTCAC AGAT
 || ||| ||||| ||||
 GG TGT CGGAAGTG TCTA
 A ____ C
 GAM1055 KIAA0442 3' CTTGTGGAGCCATCGCGA 17843 C CA GCC
 TCGC GA GC TTCACAAG
 |||| || || |||||
 AGCG CT CG AGGTGTTC
 _ AC ____
 GAM1055 MIPOL1 5' ATCTTGTGATGCCACCATCGC 37814 C CAGC_ CT
 GC GA GC TCACAAGAT
 || || || |||||
 CG CT CG AGTGTTCCTA
 _ ACCAC T_
 GAM1055 LOC256789 3' TCCTGTGGAGGCTGCCAGC 46539 CGACA _ A
 GC GC GCCTTCACA GA
 || || ||||| ||
 CG CG CGGAGGTGT CT
 AC__ T C
 GAM1056 LOC148887 3' TGGATGCCCAGGGCGCTGA 40911 A A _
 TCA CGCCTTGG CA CCG
 ||| ||||| || |||
 AGT GCGGGACC GT GGT
 C C A
 GAM1056 LOC90632 5' TGGGCGCCCAAGGCGCTGG 31830 A ACAC
 TCA CGCCTTGG CGTTCG
 ||| ||||| |||||
 GGT GCGGAACC GCGGGT
 C C__
 GAM1057 ITGB1 3' GTCAGAGGGTGGGGTAACCAA 27394 G AAAA C
 TTGGTTAC CCCA TC GAC
 ||||| ||| || |||
 AACCAATG GGGT AG CTG
 _ GGG_ A
 GAM1057 KIAA0258 3' GTCAGATTTTTGCACCAA 16650 TACGCC C
 TTGGT CAAAAATC GAC
 |||| ||||| |||
 AACCA GTTTTCTAG CTG
 C_____ A
 GAM1057 KIAA1819 3' GGTTTGTGTTGGAGTAACCAA 34535 GC AAT_
 TTGGTTAC CCAA CC
 ||||| |||| ||
 AACCAATG GGTTT GG
 A_ GTTT
 GAM1057 LOC255862 3' GGTTGTATTTTGAATGTAACCA 45340 CC ATC
 A TTGGTTACG CAAA CGACC
 ||||| |||| ||||

AACCAATGT GTTTT GTTGG
 AA AT_
 GAM1058 AIM1 3' GGCAATTATGGTCACTGGA 44116 C AATG
 TCCA TGA TCATAATTGCC
 ||||| ||| |||||
 AGGT ACT GGTATTAACGG
 C ____
 GAM1058 ASPH 3' AATTAATATTTTCAGTG 26221 CA
 CACTGAAATGT TAATT
 ||||| |||
 GTGACTTTATA ATTAA

 GAM1058 ASPH 3' AATTAATATTTTCAGTG 26226 CA
 CACTGAAATGT TAATT
 ||||| |||
 GTGACTTTATA ATTAA

 GAM1058 ATRN 3' GGCAATTATCTCTCTTCCAGGG 29301 A AAATGTC_
 A TCC CTG ATAATTGCC
 ||| ||| |||||
 AGG GAC TATTAACGG
 _ CTTCTCTC
 GAM1058 MAT1A 3' GGGCAATGTTAATTTAGTGGA 43669 A TCATA
 TCCACTGAA TG ATTGCCC
 ||||| || |||||
 AGGTGATTT AT TAACGGG
 A TG____
 GAM1058 NRAS 3' TTATAATATTTTCAGTGGA 8363 C
 TCCACTGAAATGT ATAA
 ||||| |||
 AGGTGACTTTATA TATT
 A
 GAM1058 OXCT 3' GGCATGCTGTGACATTTTA 6019 AT_
 TGAAATGTCATA TGCC
 ||||| |||
 ATTTTACAGTGT ACGG
 CGT
 GAM1058 CABYR 3' GCAACATTTTCAGGGA 14478 A CATAAT _
 TCC CTGAAATGT TG C
 ||| ||||| |||
 AGG GACTTTACA AC G
 _ T
 GAM1058 DKFZp434K1210 3' GCAATTTTGTAAATTTTCAG 19101 GT T
 CTGAAAT CA AATTGC
 ||||| || |||||
 GACTTTA GT TTAACG
 AT T
 GAM1058 DKFZP566D1346 3' GGACAAATGCTTTTCAGTG 25137 T T AA _
 CACTGAAA G CAT TTG CC
 ||||| ||| ||| ||

		GTGACTTT C GTA AAC GG	
		__ _ A	
GAM1058	DKFZp586H0623 3'	GGCAATTACTGGCCTCA 18982	AAT _
		TGA GTCA TAATTGCC	
		ACT CGGT ATTAACGG	
		C_ C	
GAM1058	FLJ11383 3'	GGCAATTAATAAATCTCATTGG 24478	C A GTCA
	A	TCCA TGA AT TAATTGCC	
		AGGT ACT TA ATTAACGG	
		T C AATA	
GAM1058	FLJ20694 3'	GGCTTTCAACATGTTTCAGTGGA 19609	_ CATAATT
		TCCACTGAA ATGT GCC	
		AGGTGACTT TACA CGG	
		G ACTTT_	
GAM1058	KIAA1691 3'	GGCATGACCAAACCTCAGTGGA 44469	AAT_ TAAT
		TCCACTGA GTCA TGCC	
		AGGTGACT CAGT ACGG	
		CCAAAC _	
GAM1058	MGC35558 3'	GGGCAAGGGGCTTTCAGTG 29617	T ATAA
		CACTGAAA GTC TTGCC	
		GTGACTTT CGG AACGGG	
		_ GG_	
GAM1058	PRO1843 5'	GCATTAGTGTGGCATTTCAGTG 20573	AT_
	GA	TCCACTGAAATGTCATA TGC	
		AGGTGACTTTACGGTGT ACG	
		GATT	
GAM1058	SH3BGRL 3'	GCAATAGATTCATTTCAGTGGA 31025	AT_ ATA
		TCCACTGAA GTC ATTGC	
		AGGTGACTT TAG TAACG	
		ACT A_	
GAM1058	ZNF387 3'	GGCAATGTCTATTTTCAGGGA 16177	A TCATA
		TCC CTGAAATG ATTGCC	
		AGG GACTTTAT TAACGG	
		_ CTG_	
GAM1058	LOC152627 5'	GGTTC AAGACTTCAGTGGA 39294	AT ATAATT
		TCCACTGAA GTC GCC	
		AGGTGACTT CAG TGG	
		_ AACT_	
GAM1058	LOC162333 5'	GGGCAATTTGTCCTTAGTGGA 42131	AATGT T
		TCCACTGA CA AATTGCC	

AGGTGATT GT TTAACGGG
 CCT__ _
 GAM1058 LOC168082 5' GCACGCATGACATTTTCAGT 40238 AAT
 ACTGAAATGTCAT TGC
 ||||| |||
 TGACTTTACAGTA ACG
 CGC
 GAM1058 LOC90906 5' GGCAATTACCCCGGTGGA 32153 AAATGTCA
 TCCACTG TAATTGCC
 ||||| |||||
 AGGTGGC ATTAACGG
 CCC____
 GAM1059 ADAMTS4 5' TCTGAAAACCTTTGCCTCTG 11568 GTC
 CAGAGG AGTTTTTCAGA
 ||||| |||||
 GTCTCC TCAAAAGTCT
 GTT
 GAM1059 ANGPT1 3' TCTAAAAACTGATTGAATG 6816 GAG C
 CA GGTCAGTTTT AGA
 || ||||| |||
 GT TTAGTCAAAA TCT
 AAG A
 GAM1059 CFTR 3' CTGAAAACCCCTTGCCATGTGC 6101 CA__ CAGT
 GCAC GAGGGT TTTCAG
 ||| ||||| |||||
 CGTG TTCCCA AAAGTC
 TACCG ____
 GAM1059 GAD1 3' TCTGAAAACCTGTTTATGGT 6481 GAGGGT
 ACCA CAGTTTTTCAGA
 ||| |||||
 TGGT GTCAAAAGTCT
 ATTT__
 GAM1059 KCNK3 3' TCTGAAAACCTCTATGCTGG 8034 AG_ TC
 CCAG GG AGTTTTTCAGA
 ||| || |||||
 GGTC TC TCAAAAGTCT
 GTA __
 GAM1059 MFI2 3' AAACGATCACTCTGGTGC 27153 _ A
 GCACCAGAG GGTC GTTT
 ||||| ||| |||
 CGTGGTCTC CTAG CAAA
 A _
 GAM1059 NCOA3 3' TCTGAAAACCCAAGGCCAGGT 13287 AGAG A__
 ACC GGTC GTTTTCAGA
 || ||| |||||
 TGG CCGG CAAAAGTCT
 A__ AACC
 GAM1059 NR2E1 3' TCCGAAAACCTGGTTTCTAGT 9279 C G GT A
 AC AGA G CAGTTTTTC GA
 || ||| | ||||| ||

			TG TCT T GTCAAAAG CT			
			A _TG C			
GAM1059	RDX	3'	TCTGAAAATATCTCTTGTGC 8810	C	GTCA	
			GCAC AGAGG GTTTTCAGA			
			CGTG TCTCT TAAAAGTCT			
			T A__			
GAM1059	SURF4	3'	TCTGGCGTCTGACCCTTCAGTG 27014	CA	TTT	
	C		GCAC GAGGGTCAG TCAGA			
			CGTG TTCCCAGTC GGTCT			
			AC TGC			
GAM1059	UBE2L6	3'	TGTTCTGACCCTCTGTGC 10420	C	TTTT	
			GCAC AGAGGGTCAG CA			
			CGTG TCTCCCAGTC GT			
			_ TT__			
GAM1059	VPS41	3'	CTGAAAACTGAGGGTGC 15738	AGAGGG		
			GCACC TCAGTTTTTCAG			
			CGTGG AGTCAAAAGTC			
			G__			
GAM1059	BC022889	3'	CTGAAAACTTTCCTACTG 40683	A TC		
			CAG GGG AGTTTTTCAG			
			GTC TCC TCAAAAGTC			
			A TT			
GAM1059	DKFZP434P0111	3'	CTGCCTGACCCTCCACTGC 33455	CCA	TTTT	
			GCA GAGGGTCAG CAG			
			CGT CTCCCAGTC GTC			
			CAC C__			
GAM1059	FBXO9	5'	AGGGCTGACGCTCCGGTGC 27256	A G		
			GCACC GAG GTCAGTTTT			
			CGTGG CTC CAGTCGGA			
			C G			
GAM1059	FLJ00001	3'	TCTGAAAGGTCCCTCTG 39787	TCAG		
			CAGAGGG TTTTCAGA			
			GTCTCCC GAAAGTCT			
			TG__			
GAM1059	FLJ10420	3'	TCTGAAAGCACCTCTG 19857	GTCA		
			CAGAGG GTTTTCAGA			
			GTCTCC CGAAAGTCT			
			A__			
GAM1059	FLJ11175	3'	TCTGAAATGCATGCCCTGTGG 20362	G CA _		
			CCA AGGGT GT TTTTCAGA			

GGT TCCCG CG AAAGTCT
 G TA T
 GAM1059 FLJ12747 5' CTGAACTCTGACCCTCCGGGC 25879 A A TT
 GC CC GAGGGTCAG TTCAG
 || || ||||| ||||
 CG GG CTCCCAGTC AAGTC
 _ C TC
 GAM1059 FLJ22679 5' GGGCAACCCTCTGGGC 25952 A CA
 GC CCAGAGGGT GTTT
 || ||||| ||||
 CG GGTCTCCCA CGGG
 _ A_
 GAM1059 GEMIN7 3' CTGAAGATACTCCCCAGTGC 24023 CAGA TCA
 GCAC GGG GTTTTCAG
 ||| || |||||
 CGTG CCC TAGAAGTC
 AC_ TCA
 GAM1059 HIC2 3' CTAAAGAGCCCTCTGGGC 32528 A CAG C
 GC CCAGAGGGT TTTT AG
 || ||||| ||| ||
 CG GGTCTCCCG AGAA TC
 _ _ A
 GAM1059 KIAA0237 3' TCTGAAAAGCCACTCTGG 16455 _ CAG
 CCAGAG GGT TTTTCAGA
 ||||| ||| |||||
 GGTCTC CCG AAAAGTCT
 A _
 GAM1059 KIAA0459 3' TCTGAAAACACTTCCAATGC 30579 CCA GTCA
 GCA GAGG GTTTTCAGA
 ||| ||| |||||
 CGT CTTT CAAAAGTCT
 AAC A_
 GAM1059 KIAA0493 3' TCTGAAAATGCTTCTTGGT 32144 AG CA
 ACCAG GGT GTTTTCAGA
 ||||| ||| |||||
 TGGTT TCG TAAAAGTCT
 CT _
 GAM1059 KIAA0682 3' TCTGAAAACCAGACTCCGGGGC 16903 A AGA A_
 GC CC GGGTC GTTTTCAGA
 || || ||||| |||||
 CG GG CTCAG CAAAAGTCT
 _ GC_ AC
 GAM1059 KIAA0763 3' GAGGACTGCCCCCGGCGC 16968 A AGA T
 GC CC GGG CAGTTTTC
 || || ||| |||||
 CG GG CCC GTCAGGAG
 C CCC _
 GAM1059 KIAA1463 3' TCTGAAAAGTCTGAGGAGTGT 35773 CAGAGGG
 GCAC TCAGTTTTCAGA
 ||| |||||

TGTG AGTCAAAAGTCT
 AGG____
 GAM1059 LOXL4 3' AGGACTGACACCCTAATGC 25926 CC A _
 GCA AG GG GTCAGTTTT
 ||| ||| |||||
 CGT TC CC CAGTCAGGA
 AA _ A
 GAM1059 MBLL39 3' TCTGAAAAGTAGATGCACC 29575 ____ _
 GG GTC AGTTTTTCAGA
 || ||| |||||
 CC TAG TCAAAAGTCT
 ACG A
 GAM1059 PP2447 5' TCTGGTCTGACCCTCTG 24870 TTT
 CAGAGGGTCAG TCAGA
 ||||| ||||
 GTCTCCCAGTC GGTCT
 T____
 GAM1059 PRO1331 3' CTAAATTTGACCCTCTGGGC 25068 A T C
 GC CCAGAGGGTCAG TTT AG
 || ||||| ||| ||
 CG GGTCTCCCAGTT AAA TC
 _ T _
 GAM1059 RPS6KA4 3' CTGGGGGACCCTCTGAAGC 10055 AC AGT TT
 GC CAGAGGGTC T CAG
 || ||||| | |||
 CG GTCTCCCAG G GTC
 AA ____ GG
 GAM1059 SCYD1 3' AAAACTCTCCTCTGCTGC 43707 C TC
 GCA CAGAGGG AGTTTT
 ||| ||||| |||||
 CGT GTCTCCT TCAAAA
 C C_
 GAM1059 SPARCL1 5' TCTGAAATACTCTCTGGTGC 11046 CAGT
 GCACCAGAGGGT TTTCAGA
 ||||| |||||
 CGTGGTCTCTCA AAAGTCT
 T____
 GAM1059 TIX1 3' TCTGAGAAACCACCCAGTGC 30931 CAGA CAG
 GCAC GGGT TTTCAGA
 ||| ||| |||||
 CGTG CCCA AAGAGTCT
 A____ CCA
 GAM1059 TRAF3 3' CTGGAAGCCTGACCCTCTGGT 30044 _
 ACCAGAGGGTCAG TTTCAG
 ||||| |||||
 TGGTCTCCCAGTC GAAGGTC
 C
 GAM1059 LOC115219 3' CTGACACACCCTCTGGTGC 36278 CA TT
 GCACCAGAGGGT GT TCAG
 ||||| || |||

CGTGGTCTCCCA CA AGTC
 _ C_
 GAM1059 LOC133418 5' AGGCGGACCTCTGGCGC 37039 A A
 GC CCAGAGGGTC GTTT
 || ||||| |||
 CG GGTCTCCCAG CGGA
 C G
 GAM1059 LOC143173 5' TCTGAAACTGATAACAGG 30273 AGAGG
 CC GTCAGTTTTCAGA
 || |||||
 GG TAGTCAAAAGTCT
 ACAA_
 GAM1059 LOC149837 5' TCTGAAAATGGGGCCCCGTGC 41102 CAGA A_
 GCAC GGGTC GTTTTCAGA
 ||| ||| |||||
 CGTG CCCGG TAAAAGTCT
 C_ GG
 GAM1059 LOC150271 5' GAATTTCCTCTGGTGC 41169 TC
 GCACCAGAGGG AGTTT
 ||||| |||
 CGTGGTCTCCT TTAAG
 _
 GAM1059 LOC151318 3' CTGAAACTGCTTTTGCTG 39105 C GT
 CA CAGAGG CAGTTTTCAG
 || ||| |||||
 GT GTTTTC GTCAAAAGTC
 C _
 GAM1059 LOC158987 3' TCTGAAACTACGAAACTGG 42050 AGG_ C
 CCAG GT AGTTTTCAGA
 ||| || |||||
 GGTC CA TCAAAAGTCT
 AAAG _
 GAM1059 LOC220954 5' TCTGAAAACACCAGTCT 44737 G_ CA
 AGA GGT GTTTTCAGA
 ||| || |||||
 TCT CCA CAAAAGTCT
 GA _
 GAM1059 LOC254532 3' CTGAAAACCTCTGATGC 46209 C CAGT
 GCA CAGAGGGT TTTCAG
 ||| ||||| |||
 CGT GTCTCCCA AAAGTC
 A _
 GAM1059 LOC255598 5' CTAAAGGAAGCCCTCTGGAGC 46559 A CAG C
 GC CCAGAGGGT TTTT AG
 || ||||| ||| ||
 CG GGTCTCCCG GGAA TC
 A AA_ A
 GAM1060 PCDHA1 3' ATTTTATTTATGGTCCAG 25381 _
 CTG ACCATAAATAAAAT
 ||| |||||

			GAC TGGTATTTATTTTA	
			C	
GAM1060	PCDHA1	3'	ATTTTATTTATGGTCCAG	20862 _
			CTG ACCATAAATAAAAT	
			GAC TGGTATTTATTTTA	
			C	
GAM1060	PCDHA10	3'	ATTTTATTTATGGTCCAG	20872 _
			CTG ACCATAAATAAAAT	
			GAC TGGTATTTATTTTA	
			C	
GAM1060	PCDHA10	3'	ATTTTATTTATGGTCCAG	25613 _
			CTG ACCATAAATAAAAT	
			GAC TGGTATTTATTTTA	
			C	
GAM1060	PCDHA11	3'	ATTTTATTTATGGTCCAG	20882 _
			CTG ACCATAAATAAAAT	
			GAC TGGTATTTATTTTA	
			C	
GAM1060	PCDHA12	3'	ATTTTATTTATGGTCCAG	20893 _
			CTG ACCATAAATAAAAT	
			GAC TGGTATTTATTTTA	
			C	
GAM1060	PCDHA13	3'	ATTTTATTTATGGTCCAG	20903 _
			CTG ACCATAAATAAAAT	
			GAC TGGTATTTATTTTA	
			C	
GAM1060	PCDHA2	3'	ATTTTATTTATGGTCCAG	20913 _
			CTG ACCATAAATAAAAT	
			GAC TGGTATTTATTTTA	
			C	
GAM1060	PCDHA3	3'	ATTTTATTTATGGTCCAG	20923 _
			CTG ACCATAAATAAAAT	
			GAC TGGTATTTATTTTA	
			C	
GAM1060	PCDHA4	3'	ATTTTATTTATGGTCCAG	20933 _
			CTG ACCATAAATAAAAT	
			GAC TGGTATTTATTTTA	
			C	
GAM1060	PCDHA5	3'	ATTTTATTTATGGTCCAG	20943 _
			CTG ACCATAAATAAAAT	

			GAC TGGTATTTATTTTA	
			C	
GAM1060	PCDHA6	3'	ATTTTATTTATGGTCCAG 20953	—
			CTG ACCATAAATAAAAT	
			GAC TGGTATTTATTTTA	
			C	
GAM1060	PCDHA6	3'	ATTTTATTTATGGTCCAG 25585	—
			CTG ACCATAAATAAAAT	
			GAC TGGTATTTATTTTA	
			C	
GAM1060	PCDHA7	3'	ATTTTATTTATGGTCCAG 20963	—
			CTG ACCATAAATAAAAT	
			GAC TGGTATTTATTTTA	
			C	
GAM1060	PCDHA8	3'	ATTTTATTTATGGTCCAG 20973	—
			CTG ACCATAAATAAAAT	
			GAC TGGTATTTATTTTA	
			C	
GAM1060	PCDHA9	3'	ATTTTATTTATGGTCCAG 25598	—
			CTG ACCATAAATAAAAT	
			GAC TGGTATTTATTTTA	
			C	
GAM1060	PCDHAC1	3'	ATTTTATTTATGGTCCAG 20842	—
			CTG ACCATAAATAAAAT	
			GAC TGGTATTTATTTTA	
			C	
GAM1060	PCDHAC2	3'	ATTTTATTTATGGTCCAG 20852	—
			CTG ACCATAAATAAAAT	
			GAC TGGTATTTATTTTA	
			C	
GAM1060	RPA2	3'	ATTTTACAGCTGGACCTAGTTT 8857	A__ TAAA
	CACA		TGTGAAACTG CCA TAAAAT	
			ACACTTTGAT GGT ATTTTA	
			CCA CGAC	
GAM1060	FLJ20079	3'	ATTTTGTTTATGGCCAGTTTCT 19168	T A
	CA		TG GAAACTG CCATAAATAAAAT	
			AC CTTTGAC GGTATTTGTTTTA	
			T C	
GAM1060	GPR88	3'	TTTAGGTACCGTTTCACA 22574	TG_ A
			TGTGAAAC ACC TAAA	

		ACACTTTG TGG ATTT		
		CCA _		
GAM1060	LOC116064 3'	TTTGTGAATGATAGTTTCACA 36498	AC	AA
		TGTGAAACTG CAT ATAAA		
		ACACTTTGAT GTA TGTTT		
		A_ AG		
GAM1060	LOC168448 3'	ATTTTATTTATGGCCAGTTTT 40246	A	
		GAAACTG CCATAAATAAAAT		
		TTTTGAC GGTATTTATTTTA		
		C		
GAM1060	LOC220477 5'	TTTATTTATGGCAGTATTCATA 37411	_	A
		TGTGAA ACTG CCATAAATAAA		
		ATACTT TGAC GGTATTTATTT		
		A _		
GAM1060	LOC83693 3'	TTTATTTATGGTTACCATA 25499	AAAC	
		TGTG TGACCATAAATAAA		
		ATAC ATTGGTATTTATTT		
		C_		
GAM1061	IHPK1 3'	CATTTCCCCAGGCCAAGT 45821	TT	A
		ACTT GC TTGGGGAAATG		
		TGAA CG GACCCCTTTAC		
		C_ _		
GAM1061	MBNL 3'	TCAAAAATGCAAAATGTGA 22032	C	GGG
		TCACA TTTTGCATT GA		
		AGTGT AAAACGTAA CT		
		_ AAA		
GAM1061	SET 3'	TCAATAGGCCAAAAGTGT 8922	A	GG
		ACACTTTTGC TTG GA		
		TGTGAAAACG GAT CT		
		_ AA		
GAM1061	ZNF219 5'	TTCCCAGAACCAAAGAATGTGA 18546	C_	CA_
		TCACA TTTTG TTGGGGA		
		AGTGT GAAAC GACCCTT		
		AA CAA		
GAM1061	C6orf37 3'	CATTTTTTAAAATGTAAAAATG 33511	C	GG
		CA TTTTGCATT GGAAATG		
		GT AAAATGTAA TTTTAC		
		A AA		
GAM1061	ETAA16 5'	TCCCTTTGCAAAATGTGA 21073	C	TT
		TCACA TTTTGCA GGGGA		

AGTGT AAAACGT TCCCT
 _ T_
 GAM1061 FLJ21736 3' CTCGGGCTGCAAAAGGTGA 24459 A _ G
 TCAC CTTTTGCA TT GGG
 ||| ||||| || |||
 AGTG GAAAACGT GG CTC
 _ C G
 GAM1061 KIAA0420 3' ATTCCCCCAATGGACAAGA 31724 _ A
 TTTTG CATTGGGG AAT
 |||| ||||| |||
 AGAAC GTAACCCC TTA
 AG C
 GAM1061 KIAA0644 3' CATTTTTTTTTTTTCAAAAATGT 16782 C CATT
 GA TCACA TTTTG GGGGAAATG
 |||| |||| |||||
 AGTGT AAAAC TTTTTTTAC
 A TTTT
 GAM1061 KIAA1796 3' CATTTCCCTTATCAAAGATGT 43965 C C T
 ACA TTTTG AT GGGGAAATG
 || |||| || |||||
 TGT GAAAC TA TCCCTTTAC
 A _ T
 GAM1061 MARCKS 3' TCTTTATTCAAAAAGTGT 8168 CAT
 ACACTTTTG TGGGGA
 ||||| |||||
 TGTGAAAAC ATTTCT
 TT_
 GAM1061 MGC15634 5' CATTTACAAATGCAAAAATGGA 26496 A C GGGG
 TC CA TTTTGCATT AAATG
 || || ||||| |||||
 AG GT AAAACGTAA TTTAC
 _ A ACA_
 GAM1061 LOC130497 3' CCCC GGAGCCTGCAAAAAGTGT 36992 _
 ACACTTTTGCA TTGGGG
 ||||| |||||
 TGTGAAAACGT GGCCCC
 CCGA
 GAM1061 LOC133418 3' ATTTTTTGCCAAAGTGT 37040 T TTGG
 ACACTTT GCA GGAAAT
 ||||| || |||||
 TGTGAAA CGT TTTTTA
 C _
 GAM1061 LOC144231 5' CATCTCCCCAAAACTAAATGT 40390 C TTGCA A
 GA TCACA TT TTGGGGA ATG
 |||| || ||||| |||
 AGTGT AA AACCCCT TAC
 A TCAAA C
 GAM1061 LOC152426 3' CTCCAGGTTCTGCAAAAAGTTTG 41497 C _
 A TCA ACTTTTGCA TTGGGG
 || ||||| |||||

			AGT TGAAAACGT GACCTC			
			T CTTG			
GAM1061	LOC165693	5'	TTCCAGAACAAAAGTGTGA	40190	CA	
			TCACACTTTTG TTGGGG			
			AGTGTGAAAAC GACCTT			
			AA			
GAM1061	LOC221895	3'	ATTTCCCCCAAAACAAAA	44443	CA	_
			TTTTG TTGGGG AAAT			
			AAAAC AACCCC TTTA			
			AA C			
GAM1061	LOC257354	3'	ATTCCCCCAATGGACAAGA	45577	__	A
			TTTTG CATTGGGG AAT			
			AGAAC GTAACCCC TTA			
			AG C			
GAM1061	LOC257476	3'	CATTTCCCCAGGCCAAGT	30713	TT	A
			ACTT GC TTGGGGAAATG			
			TGAA CG GACCCCTTTAC			
			C_ _			
GAM1062	PPP1CB	3'	TGAGAAACCTGTTAACCTTA	8562		A
			TAAGTTAACAG GTTTTTTA			
			ATTCAATTGTC CAAAGAGT			
			_			
GAM1062	PRO0082	3'	AAAAACTCCTTAACCTTA	20669	CA	
			TAAGTTAA GAGTTTTT			
			ATTCAATT CTCAAAAA			
			C_			
GAM1063	AGRN	3'	CCCTTCCCCACCCCCATCC	38534	ACGT	A
			GGAT GG GTGGGGAAGGG			
			CCTA CC CACCCCTTCCC			
			CC_ _			
GAM1063	ANK1	3'	CCCTCCCCAACCCACATACCTC	30280	_ C	AG A
	C		GGA TA GTGG TGGGGA GGG			
			CCT AT CACC ACCCCT CCC			
			CC A CA _			
GAM1063	ANK1	3'	CCCTCCCCAACCCACATACCTC	21729	_ C	AG A
	C		GGA TA GTGG TGGGGA GGG			
			CCT AT CACC ACCCCT CCC			
			CC A CA _			
GAM1063	ANK1	3'	CCCTCCCCAACCCACATACCTC	5476	_ C	AG A
	C		GGA TA GTGG TGGGGA GGG			

			CCT AT CACC ACCCCT CCC		
			CC A CA _		
GAM1063	CD34	3'	CCCTTCCCCACTGCACACACCT 7534	ATAC	G
			AGG GTG AGTGGGGAAGGG		
			TCC CAC TCACCCCTTCCC		
			ACA_ G		
GAM1063	ELF3	3'	CCCCTCCCCACTCCTCTCC 10719	TACGT	A
			GGA GGAGTGGGGA GGG		
			CCT CCTCACCCCT CCC		
			CT__ C		
GAM1063	FN1	5'	CCCTTCCCCACCCTCTGGCC 7778	ATACGT	A
			GG GG GTGGGGAAGGG		
			CC CC CACCCCTTCCC		
			GGTCT_ _		
GAM1063	FN1	5'	CCCTTCCCCACCCTCTGGCC 27644	ATACGT	A
			GG GG GTGGGGAAGGG		
			CC CC CACCCCTTCCC		
			GGTCT_ _		
GAM1063	FZD7	3'	CCCCTCCCCACCTTTCCACCC 9597	ATAC	A__ A
	C		GG GTGG GTGGGGA GGG		
			CC CACC CACCCCT CCC		
			C__ CTTTC C		
GAM1063	HS2ST1	3'	CCTCCCCCACTCCATTC 14574	TAC	A
			GA GTGGAGTGGGG AGG		
			CT TACCTCACCCC TCC		
			_ C		
GAM1063	ITGA3	3'	CCCTCCCCCATGGGCTGTGTCC 12008	TGGA	A
	TA		TAGGATACG GTGGGG AGGG		
			ATCCTGTGT TACCCC TCCC		
			CGGG C		
GAM1063	ITGA3	3'	CCCTCCCCCATGGGCTGTGTCC 7965	TGGA	A
	TA		TAGGATACG GTGGGG AGGG		
			ATCCTGTGT TACCCC TCCC		
			CGGG C		
GAM1063	PBX2	3'	CCCTTCCCCACCCCACTTGTAT 8447	_	A
			ATAC GTGG GTGGGGAAGGG		
			TATG CACC CACCCCTTCCC		
			TT C		
GAM1063	POLR2E	3'	CCTTCCTCACACATCCCT 30107	ATAC	GA
			AGG GTG GTGGGGAAGG		

			TCC TAC CACTCCTTCC		
			C__ A_		
GAM1063	RNASE1	5'	CCCTTCCCCCATACCTTACCCT 8835	ATACGT A	_
	A		TAGG GG GTGGGG AAGGG		
			ATCC CC TACCCC TTCCC		
			CATT__ A C		
GAM1063	SH3GL1	3'	CCCTTCCCCACTCCATGGCGCC 8961	ATA	
			GG CGTGGAGTGGGGAAGGG		
			CC GTACCTCACCCCTTCCC		
			GCG		
GAM1063	SHANK2	3'	CCTCCCCCACCCTGCCCTG 28421	ATAC TG A	A
			TAGG G G GTGGGG AGG		
			GTCC C C CACCCC TCC		
			__ GT C C		
GAM1063	SLC4A1	3'	CCCTCCCCCACCATTCCACATC 5893	AC __	A
	C		GGAT GTGGA GTGGGG AGGG		
			CCTA CACCT CACCCC TCCC		
			__ TAC C		
GAM1063	SLC4A1	3'	CCCTTCCCCACTCTGCTCC 5894	TAC TG	
			GGA G GAGTGGGGAAGGG		
			CCT C CTCACCCCTTCCC		
			__ GT		
GAM1063	SLC8A2	3'	CCCCCCCCCACTTCACCCC 32968	ATAC	AA
			GG GTGGAGTGGGG GGG		
			CC CACTTCACCCC CCC		
			C__ CC		
GAM1063	SORCS2	3'	CCCCTCCCCACTCCAGAGGCC 21875	ATACG	A
			GG TGAGTGGGGA GGG		
			CC ACCTCACCCCT CCC		
			GGAG_ C		
GAM1063	SORCS3	5'	CCCTCCCCACTCCCCCTA 17363	ATACGT	A
			TAGG GGAGTGGGGA GG		
			ATCC CCTCACCCCT CC		
			C__ C		
GAM1063	ST7	3'	CCCTCTCTCACTCCCCACATCC 22429	ACGT	GA
			GGAT GGAGTGGG AGGG		
			CCTA CCTCACTC TCCC		
			CACC TC		
GAM1063	APELIN	3'	CCCTTCTTCCTGCCCCACACC 18871	ATAC A_ TG	_
	CC		GG GTGG G GG GAAGGG		

			CC CACC C CC CTTCCC			
			CCA_ CC GT TT			
GAM1063	C5orf6	3'	CCCCTCCCCACTAGCTCGATCT 18701	A TGG_	A	
			GGAT CG AGTGGGGA GGG			
			TCTA GC TCACCCCT CCC			
			_ TCGA C			
GAM1063	DJ37E16.5	3'	CCCCTCCCCACTCCCTGATCC 21575	A T	A	
			GGAT CG GGAGTGGGGA GGG			
			CCTA GT CCTCACCCCT CCC			
			_ C C			
GAM1063	DKFZP434L1435	5'	CCCTTCTCCACCCCATATCCT 44267	CGT	A	
	A		TAGGATA GG GTGGGGAAGGG			
			ATCCTAT CC CACCTCTTCCC			
			ACC _			
GAM1063	DKFZP434L1435	5'	CCCTTCTCCACCCCATATCCT 46664	CGT	A	
	A		TAGGATA GG GTGGGGAAGGG			
			ATCCTAT CC CACCTCTTCCC			
			ACC _			
GAM1063	DKFZP434L1435	5'	CCCTTCTCCACCCCATATCCT 46702	CGT	A	
	A		TAGGATA GG GTGGGGAAGGG			
			ATCCTAT CC CACCTCTTCCC			
			ACC _			
GAM1063	DKFZP586N0721	5'	CCCCTCCCCACCTCGCTTCTTC 17707	TAC_ GA	A	
	C		GGA GTG GTGGGGA GGG			
			CCT CGC CACCCCT CCC			
			TCTT TC C			
GAM1063	FLJ10074	5'	CCCCTCCCCACCCCTTTCCT 19719	TACGT A	A	
			AGGA GG GTGGGGA GGG			
			TCCT CC CACCCCT CCC			
			TT_ C C			
GAM1063	FLJ13204	3'	CTCTCCCCACTCCACGCTCC 24116	TA	AG	
			GGA CGTGGAGTGGGGA G			
			CCT GCACCTCACCCCT C			
			C_ CT			
GAM1063	FLJ22671	3'	CCTTCCCCAGGCATCC 24294	AC GGAG		
			GGAT GT TGGGGAAGG			
			CCTA CG ACCCCTTCC			
			_ G_			
GAM1063	GP5	3'	CCCTCCCCACTCCTCCT 10817	TACGT	A	
			AGGA GGAGTGGGGA GG			

TCCT CCTCACCCCT CC
 _____ C
 GAM1063 KIAA0296 3' CCCTCCACCCACCCCCACGACC 16220 ATA A_ GA_
 CC GG CGTGG GTGGG AGGG
 || |||| |||| ||||
 CC GCACC CACCC TCCC
 CCA CC ACC
 GAM1063 KIAA0429 5' CCCTTCCCCACTCCCATCC 16469 ACGT
 GGAT GGAGTGGGGAAGGG
 ||| |||||
 CCTA CCTCACCCCTTCCC
 C____
 GAM1063 KIAA1193 3' CCCTTCCCCACCCCCCGGGCCT 33580 ATA T A
 AGG CG GG GTGGGGAAGGG
 ||| ||| |||||
 TCC GC CC CACCCCTTCCC
 GG_ C C
 GAM1063 KIAA1322 3' CCCTTCTCAGCCACACTTCC 36024 TAC AGTG
 GGA GTGG GGGAAGGG
 ||| ||| |||||
 CCT CACC CTCTTCCC
 TCA GA____
 GAM1063 KIAA1813 5' CCCTTCCCCACTGTTCACTCC 34810 TAC ____
 GGA GTGG AGTGGGGAAGGG
 ||| ||| |||||
 CCT CACT TCACCCCTTCCC
 ____ TG
 GAM1063 MGC19556 5' CCCTTCCCCACCTTTGCCCTCC 27316 TAC TG _
 GGA G GAG TGGGGAAGGG
 ||| | ||| |||||
 CCT C TTC ACCCCTTCCC
 CC_ GT C
 GAM1063 MGC2780 5' CCCCCCCCCACCTCACTCC 24934 TAC GA AA
 GGA GTG GTGGGG GGG
 ||| ||| ||||| |||
 CCT CAC CACCCC CCC
 ____ TC CC
 GAM1063 phospho1 5' CCCTTCCCCACTTCTTACACTC 40061 TACGT_
 C GGA GGAGTGGGGAAGGG
 ||| |||||
 CCT CTTCACCCCTTCCC
 CACATT
 GAM1063 SNRK 3' CCCTTCCCCACTCTTCAGCCCC 19309 ATACGT
 GG GGAGTGGGGAAGGG
 || |||||
 CC TCTCACCCCTTCCC
 CCGACT
 GAM1063 TOR2A 3' CCCTCCCCACCTACCCT 28218 ATAC A A
 AGG GTGG GTGGGGA GG
 ||| ||| ||||| ||

TCC CATC CACCCCT CC
____ _ C
GAM1063 TP53INP1 5' CCTTCCCCGCGCACCCC 27106 ATAC GA
GG GTG GTGGGGAAGG
|| ||| |||||
CC CAC CGCCCCCTCC
C__ G_

GAM1063 ZNF304 3' CCCCCCCCCACTTCACCCCTA 21829 ATAC AA
TAGG GTGGAGTGGGG GGG
|||| ||||| |||
ATCC CACTTCACCCC CCC
CC__ CC

GAM1063 LOC146733 3' CCCTCCCCCACTCCCCACCT 40727 ATACGT A
AGG GGAGTGGGG AGGG
||| ||||| |||
TCC CCTCACCCC TCCC
ACCC__ C

GAM1063 LOC146733 5' CCCTTCCCCACTTCACCTCC 40728 TAC
GGA GTGGAGTGGGGAAGGG
||| |||||
CCT CACTTCACCCCTTCCC
C__

GAM1063 LOC149372 3' CCTTCCCCATCACATCC 38728 AC AGT
GGAT GTGG GGGGAAGG
|||| ||| |||||
CCTA CACT CCCCTTCC
__ AC_

GAM1063 LOC157931 3' CCCTCCCCCACTTGCCACCATC 41902 AC __ A
C GGAT GTGG AGTGGGG AGGG
|||| ||| ||||| |||
CCTA CACC TCACCCC TCCC
C_ GT C

GAM1063 LOC166341 3' CCCTCCCCCTATTACACCCC 40212 ATAC _ A_
GG GTG GAGTGGGG AGGG
|| ||| ||||| |||
CC CAC CTTATCCC TCCC
C__ A CC

GAM1063 LOC220020 5' CCCCTCCCCACTCTGATC 44863 ACG A
GAT TGGAGTGGGGA GGG
||| ||||| |||
CTA GTCTCACCCCT CCC
__ C

GAM1063 LOC222070 5' CCCCTCCCCACCCCTTCTTCC 45178 TACGT A A
GGA GG GTGGGGA GGG
||| || ||||| |||
CCT CC CACCCCT CCC
TCTT_ C C

GAM1063 LOC257490 5' CCCTTCCCCACCCCAAGGTGTCC 46647 G A
TG TAGGATAC TGG GTGGGGAAGGG
||||| ||| |||||

		GTCCTGTG ACC CACCCCTTCCC		
		G C		
GAM1063	LOC90784	5' CCCCTCCCCACCTCCTGCCCCC 32004	ATA T _ A	
		GG CG GGAG TGGGGA GGG		
		CC GT CCTC ACCCCT CCC		
		CCC _ C C		
GAM1064	B4GALT5	3' AACCCATGATGAAGTGTGA 11165	A AT	
		TCACAGTT ATCATG GTT		
		AGTGTCAA TAGTAC CAA		
		G C_		
GAM1064	NEK6	3' AACAGGATTAAGTGTGA 15739	ATGA	
		TCACAGTTAATC TGTT		
		AGTGTCAATTAG ACAA		
		G_		
GAM1064	FLJ13397	3' TGGTATCACTGATTAAGTGT 24502	_ TT	
		ACAGTTAATCA TGATG G		
		TGTCAATTAGT ACTAT T		
		C GG		
GAM1064	KIAA0993	3' CAATACATGATTAAATG 32077	G A	
		CA TTAATCATG TGTTG		
		GT AATTAGTAC ATAAC		
		A _		
GAM1064	NAV3	3' CAACAACACCACGAAACATCTG 17089	TTAA_ A A	
	TG	CACAG TC TG TGTTGTTG		
		GTGTC AG AC ACAACAAC		
		TACAA C C		
GAM1064	STAM2	3' AACAGTCATGCCAAGTGTGA 12457	AAT GT	
		TCACAGTT CATGAT TGTT		
		AGTGTCAA GTACTG ACAA		
		CC_ _		
GAM1064	LOC146452	3' CAACAACATTCTATAACTG 38163	ATCAT	
		CAGTTA GATGTTGTTG		
		GTCAAT TTACAACAAC		
		ATC_		
GAM1064	LOC149153	5' CAACTGATGATAACTGTGA 40963	A GAT	
		TCACAGTTA TCAT GTTG		
		AGTGTCAAT AGTA CAAC		
		_ GT_		
GAM1064	LOC90750	3' CAGGGTTCATGATTACTGTGA 31964	T _ G	
		TCACAGT AATCATGA T TTG		

AGTGTCA TTAGTACT G GAC
 _ T G
 GAM1065 CIT 3' ACGAAACTGTGACTTTCCA 34560 A CCTTGAT
 TG AGAG CAGTTTCGT
 || ||| |||||
 AC TTTC GTCAAAGCA
 C AGT____
 GAM1065 EIF4G2 3' CACAAAAGTATCAGTTTT 7115 CT C
 AGAGC TGATCAGTTT GTG
 |||| ||||| ||
 TTTTG ACTAGTCAAA CAC
 _ A
 GAM1065 NCOA4 3' CACAAGCCTCCAAGGCTCCTTA 11923 A ATCA C
 TGA GAGCCTTG GTTT GTG
 || ||||| ||| ||
 ATT CTCGGAAC CGAA CAC
 C CTC_ _
 GAM1065 FLJ11850 3' CACGAAATCACAACTCTTCA 22948 CC ATCA
 TGAAGAG TTG GTTTCGTG
 ||||| || |||||
 ACTTCTC AAC TAAAGCAC
 A_ AC_
 GAM1065 GOLGA1 3' CACTTTTTGATTAAAGCTCTTC 7859 C TTTC
 A TGAAGAGC TTGATCAG GTG
 ||||| ||||| ||
 ACTTCTCG AATTAGTT CAC
 A TTT_
 GAM1066 RDS 5' ACTGCATTACGGGGATCCCA 5861 A GTT C
 TG GATCCTCG TGGA GCAGT
 || ||||| ||| ||||
 AC CTAGGGGC ACTT CGTCA
 C _ A
 GAM1066 CSMD1 3' CTGCACCTGGAGGATCTCA 36190 GGTTT AC
 TGAGATCCTC GG GCAG
 ||||| || |||
 ACTCTAGGAG CC CGTC
 GT_ A_
 GAM1066 GRWD 3' ACCGCGTCCGGCTCAGGA 25575 C T A
 TCCT GGTT GGACGC GT
 ||| ||| ||||| ||
 AGGA TCGG CCTGCG CA
 C _ C
 GAM1066 LOC257364 3' GTCCAAACCCAGGATCTCA 45524 C
 TGAGATCCT GGTGGGAC
 ||||| |||||
 ACTCTAGGA CCAAACCTG
 C
 GAM1067 B4GALT6 3' GTAAGTTTTATTTTGAAGTGT 30094 _ CTT
 AACT C ATAAACTTAC
 |||| | |||||

		TGTGA G TATTTTGAATG	
		A TTT	
GAM1067 CLK2	3'	GTTTTATAAGGAATTTTGTA 6973	CAC
		TACAA TCCTTATAAAAC	
		ATGTT AGGAATATTTTG	
		TTA	
GAM1067 CNR1	3'	GTAAGTTTTATAAGGTCTG 18164	CT
		CA CCTTATAAACTTAC	
		GT GGAATATTTTGAATG	
		CT	
GAM1067 LAMC1	3'	GTAAGTTTTATAAGGGAGT 8077	_
		ACTCC TTATAAACTTAC	
		TGAGG AATATTTTGAATG	
		G	
GAM1067 KIAA1674	3'	TAAGTTTTTAGTGAGTGT 34114	C T
		ACACTC TTA AAACTTA	
		TGTGAG GAT TTTTGAAT	
		T _	
GAM1067 LOC147093	5'	GTAAGTTTATAAGAGGAG 40804	A _
		CTCCTT TA AAACTTAC	
		GAGGAG AT TTTGAATG	
		A A	
GAM1067 LOC170395	3'	TAAGTTTTTAGTGAGTGT 37546	C T
		ACACTC TTA AAACTTA	
		TGTGAG GAT TTTTGAAT	
		T _	
GAM1067 LOC200609	5'	TAAGTTTTGTTATGTTGTA 43331	CTCCTT
		TACAACA ATAAAACTTA	
		ATGTTGT TGTTTTGAAT	
		AT____	
GAM1068 NR5A2	3'	AGATGGATACCAACACGGT 9914	ACA AGC
		GC TGTTG ATCCATCT	
		TG ACAAC TAGGTAGA	
		GC_ CA_	
GAM1068 PDK4	3'	TAGATGGATACTGAATACTC 46443	CACA G C
		GAG TGTT AG ATCCATCTA	
		CTC ATAA TC TAGGTAGAT	
		____ G A	
GAM1068 PIK3C2B	3'	AGATGGATTTTACATTTGCTC 8504	C T C
		GAGCA ATGT GAG ATCCATCT	

CTCGT TACA TTT TAGGTAGA
T _ _
GAM1068 PTGIS 3' AGATGGATCCACGTGCTC 6665 A TTGAGC
GAGCAC TG ATCCATCT
||||| || |||||
CTCGTG AC TAGGTAGA
C C _ _
GAM1068 BRD3 3' AGATGGATGTCGCACACGCC 14296 A ACA _ G
G GC TGT TGA CATCCATCT
| || ||| ||| |||||
C CG ACA GCT GTAGGTAGA
_ C _ C _
GAM1068 CCNE2 3' ATAGATGAACATGGTGTTC AAC 27710 T _ |||
CTGTGCTC A GTTGAGCATC CATCTA T
| ||||| ||| |
T CAACTTGTGG GTAGAT A
C TACAA |||
GAM1068 CCNE2 3' ATAGATGAACATGGTGTTC AAC 11049 T _ |||
CTGTGCTC A GTTGAGCATC CATCTA T
| ||||| ||| |
T CAACTTGTGG GTAGAT A
C TACAA |||
GAM1068 FLJ21162 3' AGATGGATGATGCACGACTC 24306 CACA TGAG
GAG TGT CATCCATCT
||| ||| |||||
CTC ACG GTAGGTAGA
AGC_ TA_
GAM1068 KIAA0475 3' TAGATGAATACTGGGATTGGCT 16950 A TG G C C
C GAGC CA TT AG AT CATCTA
||||| || ||| |||||
CTCG GT GG TC TA GTAGAT
_ TA G A A
GAM1068 KIAA0931 3' GATGGATGGAGCACTC 33486 CACA GAG
GAG TGTT CATCCATC
||| ||| |||||
CTC ACGA GTAGGTAG
_ G_
GAM1068 PCDH17 3' AGATGAATGCCGAGTGCTT 15810 ATG A C
GAGCAC TTG GCAT CATCT
||||| ||| ||| |||||
TTCGTG AGC CGTA GTAGA
_ _ A
GAM1069 ADAM17 3' ATCAAACCCTTTCCTGCGC 22407 ACCCT A
GTGCA GA GGT TTGAT
||||| || |||||
CGCGT TT CCAA ACTA
CCT_ C
GAM1069 CDH3 3' ACCTGGGCCAGGGTTGCCTCA 7544 T A_
TGAG GCAACCCTG AGGT
||||| ||||| |||

			ACTC CGTTGGGAC	TCCA		
			—	CGGG		
GAM1069	TRPM6	3'	ACCTCAGTGCTGCACTCA	19193	ACC	A
			—	CGGG		
			TGAGTGCA	CTGA GGT		
			ACTCACGT	GACT CCA		
			CGT	—		
GAM1069	CAMP-GEFII	3'	ACCTCAGGGCTGCATTCA	13878	A	A
			—	CGGG		
			TGAGTGCA	CCCTGA GGT		
			ACTTACGT	GGGACT CCA		
			C	—		
GAM1069	FLJ11827	3'	GACCCAGCAGTTGCACTCA	24724	C_	AA
			—	CGGG		
			TGAGTGCAAC	CTG GGT		
			ACTCACGTTG	GAC CCAG		
			AC	—		
GAM1069	FLJ20035	3'	TCAAACAGAGTTGCAATCA	19139	G	C GAAG
			—	CGGG		
			TGA TGCAAC	CT GTTTGA		
			ACT ACGTTG	GA CAAACT		
			A	A	—	
GAM1069	KIAA0319	5'	CAAACCTCTCTTCAGGGCCGCCT	16759	T	AA
			CA	—		
			TGAG GC	CCCTGAAG GTTTG		
			ACTC CG	GGGACTTC CAAAC		
			—	CG		
			—	CC		
			—	TCT		
GAM1069	KIAA0630	5'	ACCCAGATTTGCACTCA	43060	CC	AA
			—	CGGG		
			TGAGTGCAA	CTG GGT		
			ACTCACGTT	GAC CCA		
			TA	—		
GAM1069	KIAA0924	5'	CAAACCTTTTTGACTCA	17063	G	CCCT
			—	CGGG		
			TGAGT CAA	GAAGGTTTG		
			ACTCA GTT	TTTCCAAAC		
			—	CGGG		
GAM1069	YKT6	3'	TCAAACACAGGTGCACTCA	13320	AC	AAG
			—	CGGG		
			TGAGTGCA	CCTG GTTTGA		
			ACTCACGT	GGAC CAAACT		
			—	A		
GAM1069	LOC148413	3'	ACCTGGCCAGACACTGCACTCA	38531	ACC_	A_
			—	CGGG		
			TGAGTGCA	CTG AGGT		
			ACTCACGT	GAC TCCA		
			CACA	CGG		
GAM1069	LOC150225	5'	CCTCCAGGGTTGCACCA	41188	A	A
			—	CGGG		
			TG GTGCAACCCTG	AGG		

AC CACGTTGGGAC TCC
 _ C
 GAM1069 LOC91812 5' ATCAAACCCCAGGTCTGC 33390 AC AA
 GCA CCTG GGTTTGAT
 ||| ||| |||||
 CGT GGAC CCAAATA
 CT C_

GAM1069 LOC91813 5' ATCAAACCCCAGGTCTGC 33396 AC AA
 GCA CCTG GGTTTGAT
 ||| ||| |||||
 CGT GGAC CCAAATA
 CT C_

GAM1070 ANGPT1 3' AAATAACACAAATGCTCA 6812 CTGCAACA
 TGAGTA GTGTTATTT
 ||||| |||||
 ACTCGT CACAATAAA
 AAA_

GAM1070 CDKN2B 3' AATGGCACTGTTGCAAATACTCA 27806 AC
 TGAGT TGCAACAGTGTTATT
 ||||| |||||
 ACTCA ACGTTGTACGGTAA
 A_

GAM1070 ATIP1 3' TAAATAATGCTGGAATACTCA 21862 CTGCAA
 TGAGTA CAGTGTTATTTG
 ||||| |||||
 ACTCAT GTCGTAATAAAT
 AAG_

GAM1070 FLJ11273 3' CAAATAAAGTGGTACAGACTCA 20395 A CAA GTG
 TGAGT CTG CA TTATTTG
 ||||| ||| || |||||
 ACTCA GAC GT AATAAAC
 _ ATG GA_

GAM1070 FLJ20716 3' CAAATATCAACTTGTAATACTC 19630 C CAG T
 A TGAGTA TGCAA TG TATTTG
 ||||| ||||| || |||||
 ACTCAT ATGTT ACATAAAC
 A CA_ T

GAM1070 MGC13138 3' AACAGTGGTCTGTAGCACTCA 27230 A A_ G
 TGAGT CTGCA CA TGTT
 ||||| ||||| || |||
 ACTCA GATGT GTACAA
 C CTG G

GAM1070 QKI 3' CAAATAACAAACTGCAACACT 32616 AC ACAG
 AGT TGCA TGTTATTTG
 ||| ||| |||||
 TCA ACGT ACAATAAAC
 CA CAAA

GAM1070 LOC148188 5' GGCAGTGTGACAGACCCA 38489 A A
 TG GT CTGCAACAGTGTT
 || || |||||

AC CA GACGTTGTCACGG
 C _
 GAM1070 LOC201522 3' ATGACACTGCCGCACACTCA 42585 AC AA
 TGAGT TGC CAGTGTTAT
 ||||| ||| |||||
 ACTCA ACG GTCACAGTA
 C_ CC
 GAM1071 PKIA 5' AATCCAGCGATGCTGCAGCTGT 13696 A A _ A
 AAA TTTACA TT CAGT TTGCT GATT
 ||||| || ||||| |||||
 AAATGT GA GTCG AGCGA CTAA
 C C T C
 GAM1071 LOC253260 3' AGAAAACTGTAATTTTAAA 45908 C G
 TTTA AATTACAGTTT CT
 ||||| ||||| ||||| ||
 AAAT TTAATGTCAAA GA
 T A
 GAM1072 SIGLEC11 3' CAATGAAGAGCTTGAGTTTGAA 27463 C ATAAGA
 TTCA ACTCAAGC CATTG
 ||||| ||||| |||||
 AAGT TGAGTTCG GTAAC
 T AGAA_
 GAM1072 KIAA0977 3' CAATGATGAATCACTTAGTGTG 17081 C CATAAGA_
 AA TTCACACT AAG CATTG
 ||||| ||||| |||||
 AAGTGTGA TTC GTAAC
 _ ACTAAGTA
 GAM1072 SEC24A 3' TTTATGCTTGAATATGAA 40236 CAC
 TTCA TCAAGCATAAG
 ||||| ||||| |||||
 AAGT AGTTCGTATTT
 ATA
 GAM1072 LOC146050 3' CTTATACTGAAGTGTGAA 38054 CA C
 TTCACACT AG ATAAG
 ||||| ||||| |||||
 AAGTGTGA TC TATTC
 AG A
 GAM1073 LIPI 3' ATCCAAACACATGTACACCAAA 38843 AT TGAGAC
 TTTGGT GT GTTTGGAT
 ||||| || |||||
 AAACCA CA CAAACCTA
 _ TGTACA
 GAM1073 PRO0902 5' ATCCAAACAAACAACAAACCAA 27607 A AGAC
 A TTTGGT TGTTG GTTTGGAT
 ||||| ||||| |||||
 AAACCA ACAAC CAAACCTA
 A AAA_
 GAM1073 LOC153937 3' ATCCAAACACCTTGCTGACCAA 39445 ATGTT AC
 TTGGT GAG GTTTGGAT
 ||||| ||||| |||||

			AACCA TTC CAAACCTA GTCG_ CA	
GAM1073	LOC51028	3'	ATGTCTTCAACATACCAAA 18149 TTTGGTATGTTGA GACGT AAACCATACAACCT CTGTA T	—
GAM1074	FGFR2	3'	GGATCTTCAAGTCCCATCATA 23296 TATGATGG ACT ATCC ATACTACC TGA TAGG C_ ACTTC	AAC ATACT
GAM1074	FGFR2	3'	GGATCTTCAAGTCCCATCATA 23290 TATGATGG ACT ATCC ATACTACC TGA TAGG C_ ACTTC	AAC ATACT
GAM1074	FGFR2	3'	GGATCTTCAAGTCCCATCATA 23236 TATGATGG ACT ATCC ATACTACC TGA TAGG C_ ACTTC	AAC ATACT
GAM1074	FGFR2	3'	GGATCTTCAAGTCCCATCATA 23302 TATGATGG ACT ATCC ATACTACC TGA TAGG C_ ACTTC	AAC ATACT
GAM1074	FGFR2	3'	GGATCTTCAAGTCCCATCATA 5640 TATGATGG ACT ATCC ATACTACC TGA TAGG C_ ACTTC	AAC ATACT
GAM1074	FGFR2	3'	GGATCTTCAAGTCCCATCATA 23243 TATGATGG ACT ATCC ATACTACC TGA TAGG C_ ACTTC	AAC ATACT
GAM1074	NAB1	3'	GGATAATACTCCATCATA 12587 TATGATGGA TAT TATCC ATACTACCT ATA ATAGG C_ _	ACAC AC
GAM1074	TCTA	3'	AGTGCACAGTGGCCCCATCATA 22728 TATGATGG CACT TACT ATACTACC GTGA GTGA CCG CAC	AA_ A_
GAM1074	ABHD3	3'	ATAGTATATGTGGACACATA 28740 TATG TG CAC TATACTAT 	A GAA _

		ATAC AC GTG ATATGATA	
		_ AG_ T	
GAM1074	FLJ10781	3' GTAGTAATATTCTATCATA 20137	CACTA
		TATGATGGAA TACTAT	
		ATACTATCTT ATGATG	
		ATA__	
GAM1074	FLJ31737	3' GGAATAATGTTCCATCATG 29591	C ACTA
		TATGATGGAACA TAT TCC	
		GTACTACCTTGT ATA AGG	
		A ____	
GAM1074	HBXAP	3' GACAGTGAAAGTACCATCATA 18655	A ACTA A
		TATGATGG AC TACT TC	
		ATACTACC TG GTGA AG	
		A AAA_ C	
GAM1074	MEGF10	3' ATAGTATAGTAACCACA 26210	A AAC
		TG TGG ACTATACTAT	
		AC ACC TGATATGATA	
		_ AA_	
GAM1074	LOC219333	3' AGTCATAATGTTTCATCATA 44932	G C _
		TATGATG AACA TAT ACT	
		ATACTAC TTGT ATA TGA	
		_ A C	
GAM1074	LOC221405	5' AGAATGGATGCTTCCATCA 45066	_ _ A
		TGATGGAA CA CTAT CT	
		ACTACCTT GT GGTA GA	
		C A A	
GAM1075	KIAA0630	5' CATGTATGATACAGTGAGTCA 43062	CTGGC
		TGACTCGCTGT CATACTATG	
		ACTGAGTGACA GTATGTAC	
		TA__	
GAM1076	INMT	3' TTTAATAACCAGCTCA 13648	T GACTAC
		TGAG CTGGT ATTAATA	
		ACTC GACCA TAATTT	
		_ A____	
GAM1076	SRGAP1	3' GGTTTAATGTAGCCCAGCT 35758	T TGA
		AG CTGG CTACATTAAACC	
		TC GACC GATGTAATTTGG	
		_ C__	
GAM1076	VHL	3' AATGCTTCTATCAGACTCA 6157	ACTA
		TGAGTCTGGTG CATT	

		ACTCAGACTAT GTAA		
		CTTC		
GAM1076	DKFZP566F2124	3' TTTAATGTAGTAACTCA	17891	CTGGTG
		TGAGT ACTACATTA		
		ACTCA TGATGTAATTT		
		A_____		
GAM1076	FLJ13910	3' AATGCAGTTACCAGACCCA	23052	A A
		TG GTCTGGTGA		
		AC CAGACCATTGA GTAA		
		C C		
GAM1076	FLJ22679	3' GGTCTGAAGCCACAGACTCA	19265	G A A TTA
		TGAGTCTG TG CT CA AACC		
		ACTCAGAC AC GA GT TTGG		
		_ C A C_		
GAM1076	PLAGL2	3' GTTTTCATCACTAGACTCA	34879	CTACATT
		TGAGTCTGGTGA AAAC		
		ACTCAGATCACT TTTG		
		ACT_____		
GAM1076	RHOBTB2	3' GGCTTAAATGGCACCAGACTC	30561	A CA A
		GAGTCTGGTG CTA TTAA CC		
		CTCAGACCAC GGT AATT GG		
		_ A_ C		
GAM1076	UCK1	3' GATGTGTCATCAGACTCA	25427	_ T
		TGAGTCTG GTGAC ACATT		
		ACTCAGAC CACTG TGTAG		
		T _		
GAM1076	LOC149465	3' AATGAGTACCAGGCCCA	38758	A A A
		TG GTCTGGTG CT CATT		
		AC CGGACCAT GA GTAA		
		C _ _		
GAM1076	LOC199858	5' GGTCCAGTGGGTCCCCAGACTC	42641	T A AA
	A	TGAGTCTGG GACT CATT ACC		
		ACTCAGACC CTGG GTGA TGG		
		C _ CC		
GAM1076	LOC201182	5' ATGAGTCACCAGGCCCA	43210	A T A
		TG G CTGGTGA		
		AC C GACCACTGA GTA		
		C _ _		
GAM1076	LOC91050	3' AATGTTTATACCAGGCTCA	32331	ACT
		TGAGTCTGGT ACATT		

			ACTCGGACCAT	TGTAA		
			ATT			
GAM1077	KIAA0618	3'	CAAAAACATGTGTTGTA	16832	A	CC
			TACAACA CATGTT	TG		
			ATGTTGT	GTACAA	AC	
			—	AA		
GAM1077	KIAA1467	3'	TAGGAAACATTTTGTGTA	35456	C	—
			TACAACAA ATGTT	CCTG		
			ATGTTGTT	TACAA	GGAT	
			T	A		
GAM1077	MO25	3'	GCAGAGGAATGTTATTGTA	18416	C	G —
			TACAA AACAT	TTC	CTGC	
			ATGTT	TTGTA	AGG	GACG
			A	—	A	
GAM1077	LOC129011	3'	ATGGCACAGTGCATTTGCTGTA	36963	A	C TC C
			TACA CAA ATGT	CTG	GCCAT	
			ATGT	GTT	TACG	GAC CGGTA
			C	—	T	— A
GAM1077	LOC145945	3'	TGGGTCAAACATTGTTGTA	40639	AC	CCT G
			TACAACA ATGTT	GC	CCA	
			ATGTTGT	TACAA	TG	GGT
			—	AC	—	
GAM1077	LOC148534	3'	GCTCTTAACATTTGTTGTA	38549	C	CCT_
			TACAACAA ATGTT	GC		
			ATGTTGTT	TACAA	CG	
			—	TTCT		
GAM1077	LOC150407	3'	ATGATCAGAACTGTTGTTGTA	38949	T	C CGC
			TACAACAACA GTTC	TG	CAT	
			ATGTTGTTGT	CAAG	AC	GTA
			—	—	TA	—
GAM1077	LOC221354	3'	CAAAAACATGTGTTGTA	44392	A	CC
			TACAACA CATGTT	TG		
			ATGTTGT	GTACAA	AC	
			—	AA		
GAM1078	ABR	3'	GACTGCAATAGAAAACCTCCCA	6748	CA	A A
			TGG AGTTTTCTG	TG	AGTC	
			ACC	TCAAAGAT	AC	TCAG
			C	—	A	G
GAM1078	ABR	3'	GACTGCAATAGAAAACCTCCCA	22493	CA	A A
			TGG AGTTTTCTG	TG	AGTC	

		ACC TCAAAGAT AC TCAG		
		C_ A G		
GAM1078 APOBEC1	3'	GACTTCATCTTCAAACTGCCA 12509	A	CT_
		TGGCA GTTTT GATGAAGTC		
		ACCGT CAAAA CTACTTCAG		
		_ CTT		
GAM1078 EFNA1	3'	GACCTCATCTGTGGAGCTGCCA 10703	A	CT_ A
		TGGCA GTTTT GATGA GTC		
		ACCGT CGAGG CTACT CAG		
		_ TGT C		
GAM1078 OLR1	3'	GACTCCTCCCCAGAAAACCACC 8395	CAA	AT _
A		TGG GTTTTCTG GA AGTC		
		ACC CAAAAGAC CT TCAG		
		AC_ CC CC		
GAM1078 OSM	3'	ACTTATATTTAAAACCTTGCC 21753	CT	_
		GGCAAGTTTT GATG AAGT		
		CCGTTCAAAA TTAT TTCA		
		T_ A		
GAM1078 PAX2	5'	ACTTCGCCAACTCGCCA 10136	A	TTTC A
		TGGC AGT TG TGAAGT		
		ACCG TCA AC GCTTCA		
		C _ C		
GAM1078 PAX2	5'	ACTTCGCCAACTCGCCA 10142	A	TTTC A
		TGGC AGT TG TGAAGT		
		ACCG TCA AC GCTTCA		
		C _ C		
GAM1078 PRDM4	3'	ACCTCATCAGAGAAGC 14783	AAG	A
		GC TTTTCTGATGA GT		
		CG AAGAGACTACT CA		
		_ C		
GAM1078 S100B	3'	ACTCCATCAGAACTCGC 12955	A	TT A
		GC AGT TCTGATG AGT		
		CG TCA AGACTAC TCA		
		C _ C		
GAM1078 SH3BP2	3'	GACCTCCCGAGACTTGCCA 8946	CTGAT	A
		TGGCAAGTTTT GA GTC		
		ACCGTTCAGAG CT CAG		
		CC_ C		
GAM1078 DKFZP566K023	3'	TTCTTCAGAAAACCTCCA 17759	CAA	T
		TGG GTTTTCTGA GAA		

ACC CAAAAGACT CTT
 TC_ T
 GAM1078 ELKS 3' ACTTCATCCCAACTTGCT 17419 TTCT
 GGCAAGTT GATGAAGT
 ||||| |||||
 TCGTTCAA CTACTTCA
 CC_
 GAM1078 FLJ20371 3' ACTCCATCAGAACAGCTCCA 19424 CA _ A
 TGG AGTT TTCTGATG AGT
 || ||| ||||| |||
 ACC TCGA AAGACTAC TCA
 _ C C
 GAM1078 FLJ23071 3' GACTGATCGAAAGAAAACCTTGC 24846 GA _
 CA TGGCAAGTTTTCT TGA AGTC
 ||||| ||| |||
 ACCGTTCAAAAGA GCT TCAG
 AA AG
 GAM1078 HSD17B12 3' ACTTGTATGGAGAACTCACCA 18225 CA G _
 TGG AGTTTTCT ATG AAGT
 || ||||| ||| |||
 ACC TCAAGAGG TAT TTCA
 AC _ G
 GAM1078 HT002 3' GACTGCCAGAAAACCCACCA 15282 CAA ATGA
 TGG GTTTTCTG AGTC
 || ||||| |||
 ACC CAAAAGAC TCAG
 AC_ CG_
 GAM1078 KIAA0061 3' ACTTCTGGAAACTTCCA 33891 C TGAT
 TGG AAGTTTTC GAAGT
 || ||||| |||
 ACC TTCAAAGG CTTCA
 _ T_
 GAM1078 KIAA0252 3' ACTTTGGAGAAAACCTCCCA 31447 CA GA
 TGG AGTTTTCT TGAAGT
 || ||||| |||||
 ACC TCAAAGA GTTTCA
 CC G_
 GAM1078 KIAA0729 3' ACTCCAGATGAAAAAACTTGC 45804 _ TGA A
 GCAAGTTT TC TG AGT
 ||||| || |||
 CGTTCAA AG AC TCA
 AAA TAG C
 GAM1078 LIPG 3' ACTTCTTGGAAGGCCA 12653 AAG TG T
 TGGC TTTTC A GAAGT
 ||| |||| | ||||
 ACCG AAAAG T CTTCA
 _ GT_
 GAM1078 SYNPO2 3' GACCTCTCAGAAAACTTGCC 35592 _ T A
 GGCAAGTTTT CTGA GA GTC
 ||||| ||| || |||

CCGTTCAAAA GACT CT CAG
 A _ C
 GAM1078 TBLR1 3' ACTTACAAAACTTGC 23964 CTGA _
 GCAAGTTTT TG AAGT
 ||||| || |||
 CGTTCAAAA AC TTCA
 _ A
 GAM1078 ZNF300 5' GACTGAGGAAAATTTACCA 27439 C GATGA
 TGG AAGTTTTCT AGTC
 || ||||| |||
 ACC TTAAAAGG TCAG
 A AG_
 GAM1078 LOC145757 5' ACTTCATCAAACCTTCAACA 37968 GC_ TTC
 TG AAGTT TGATGAAGT
 || ||| |||||
 AC TTCAA ACTACTTCA
 AAC _
 GAM1078 LOC145945 5' ATTTTTCAGAAAACCTTCCA 40629 C T
 TGG AAGTTTTCTGA GAAGT
 || ||||| |||
 ACC TTCAAAAGACT TTTTA
 _ _
 GAM1078 LOC152190 5' GACTTCATGGCTGACTTGC 34524 TT G
 GCAAGTT CT ATGAAGTC
 ||||| || |||||
 CGTTCAG GG TACTTCAG
 TC _
 GAM1078 LOC201164 3' ACTTCATCATCTTGTCA 42528 TTTTC
 TGGCAAG TGATGAAGT
 ||||| |||||
 ACTGTTCT ACTACTTCA
 T_
 GAM1078 LOC219899 3' ACTCCAGGAAAACCTTGC 43988 GA A
 GCAAGTTTTCT TG AGT
 ||||| || |||
 CGTTCAAAAGG AC TCA
 _ C
 GAM1078 LOC220883 5' ACCTCTTTTAGAAAACCTTGACA 43848 G T_ A
 TG CAAGTTTTCTGA GA GT
 || ||||| || |||
 AC GTTCAAAAGATT CT CA
 A TT C
 GAM1078 LOC255520 3' ACTTCATCAAAGATTTGCT 45877 C
 GGCAAGTTTT TGATGAAGT
 ||||| |||||
 TCGTTTAGAA ACTACTTCA
 _
 GAM1078 LOC255919 3' GACTGAGGAAAACCTCTCCA 45556 CA GATGA
 TGG AGTTTTCT AGTC
 || ||||| |||

		ACC TCAAAGG TCAG		
		TC AG__		
GAM1078	LOC257355 3'	GACCTCATCACTGGATTTGCCA 45321	TC	A
		TGGCAAGTTT TGATGA GTC		
		ACCGTTTAGG ACTACT CAG		
		TC C		
GAM1078	LOC51172 3'	GACCTCATCACTGGATTTGCCA 31720	TC	A
		TGGCAAGTTT TGATGA GTC		
		ACCGTTTAGG ACTACT CAG		
		TC C		
GAM1078	LOC89231 3'	GACTTCATCAGAAAATTTTGTC 44550	_	
A		TGGCAAG TTTTCTGATGAAGTC		
		ACTGTTT AAAAGACTACTTCAG		
		T		
GAM1078	LOC90639 5'	GATATCATCAGAAAATTACCA 31832	CA	A
		TGG AGTTTTCTGATGA GTC		
		ACC TAAAAGACTACT TAG		
		A_ A		
GAM1078	LOC91565 3'	ACTTTTTGGAAACTGCCA 33022	A	TG T
		TGGCA GTTTTC A GAAGT		
		ACCGT CAAAAG T TTTCA		
		_ GT _		
GAM1079	CGTHBA 3'	GGCAGCACCTGCTCTGA 14363	ACG	
		TCAGAGCAG GCTGTT		
		AGTCTCGTC CGACGG		
		CA_		
GAM1079	CLCN6 3'	CAGCAGCCGCCTGCCCTGA 22336	A	A
		TCAG GCAG CGGCTGTTG		
		AGTC CGTC GCCGACGAC		
		C C		
GAM1079	CLCN6 3'	CAGCAGCCGCCTGCCCTGA 6959	A	A
		TCAG GCAG CGGCTGTTG		
		AGTC CGTC GCCGACGAC		
		C C		
GAM1079	CLCN6 3'	CAGCAGCCGCCTGCCCTGA 22341	A	A
		TCAG GCAG CGGCTGTTG		
		AGTC CGTC GCCGACGAC		
		C C		
GAM1079	RECQL 5'	ATCACTGCCCTGCTCTGA 8813	AC	TGTT
		TCAGAGCAG GGC GTGAT		

AGTCTCGTC CCG CACTA
 _ T _
 GAM1079 LBP-9 3' ACAGTGGAGACGTCTGCTCTGA 15873 G_ TG
 TCAGAGCAGACG C TTGT
 ||||| | |||
 AGTCTCGTCTGC G GACA
 AGA GT
 GAM1079 MRPL10 3' ACCAAGCCCTCTGCTCTGA 29767 C GTT
 TCAGAGCAGA GGCT GT
 ||||| || ||
 AGTCTCGTCT CCGA CA
 C AC_
 GAM1079 LOC202126 3' ATCACAGTTGTCTGACCTGA 43411 AG T
 TCAG CAGACGGCTGT GT
 ||| ||||| ||
 AGTC GTCTGTTGACA TA
 CA C
 GAM1080 GALNT1 3' TTTTCATGCTCAGAATTTTCAGG 21726 CGTTA_ A
 T ACC TCT AGCATGAAAA
 ||| ||| |||||
 TGG AGA TCGTACTTTT
 ACTTTA C
 GAM1080 CKAP4 3' TTTTCATGCCCAGTTAAC 13706 T AA
 GTTA CT GCATGAAAA
 ||| || |||||
 CAAT GA CGTACTTTT
 T CC
 GAM1080 FLJ13081 3' GTTTTTCATTTTTATAACTGGTA 24238 C CT C
 TACC GTTAT AAG ATGAAAAC
 ||| ||| ||| |||||
 ATGG CAATA TTT TACTTTTG
 T T_ _
 GAM1080 FLJ23024 3' TTTCTGAGCTAGATAACAGG 24475 C A AT_
 CC GTTATCTA GC GAAA
 || ||||| || |||
 GG CAATAGAT CG CTTT
 A _ AGT
 GAM1080 KIAA0121 5' GTTTTTCATACTCGATCGGG 35971 TT TA C
 CCCG ATC AG ATGAAAAC
 ||| ||| || |||||
 GGGC TAG TC TACTTTTG
 _ C_ A
 GAM1080 SEMA3C 3' TTTTCATGCTTCCAGGTAA 13076 _
 TTATCT AAGCATGAAAA
 ||||| |||||
 AATGGA TTCGTACTTTT
 CC
 GAM1080 SLC26A7 3' GTTTTTCATAATCGAAAGAAACG 27415 A AAGC_
 GGTA TACCCGTT TCT ATGAAAAC
 ||||| ||| |||||

ATGGGCAA AGA TACTTTTG
 _ AAGCTAA
 GAM1080 SPTLC2 3' GTTTTCATACTATAACCAGGTA 11284 C_ CTA C
 TACC GTTAT AG ATGAAAAC
 |||| |||| || |||||
 ATGG CAATA TC TACTTTTG
 AC _ A
 GAM1080 LOC145748 3' TTGGACTTAGATAAGGG 40580 G CA
 CCC TTATCTAAG TGA
 || ||||| ||
 GGG AATAGATTC GTT
 _ AG
 GAM1080 LOC91145 5' GTTTTCATGCTGCTGATAA 32450 TA_
 TTATC AGCATGAAAAC
 |||| |||||
 AATAG TCGTACTTTTG
 TCG
 GAM1081 CAPN10 3' TCTGCCATACGCGGGCGCTGC 23356 CAT A
 GCAGCGCTC TA GGCAGA
 ||||| || |||||
 CGTCGCGGG AT CCGTCT
 CGC A
 GAM1081 ENG 3' CCAGAATGGAGCCTGCT 5591 C AA
 AGCAG GCTCCATT GG
 |||| ||||| ||
 TCGTC CGAGGTAA CC
 _ GA
 GAM1081 LARS2 3' TCTGCCTTAGGCACTTCT 17648 C C CCAT
 AG AG GCT TAAGGCAGA
 || || || |||||
 TC TC CGG ATTCCGTCT
 T A _
 GAM1081 M17S2 5' TTCCGCCCTAATGGAGGT 25610 G A A
 GC CTCCATTA GGC GAA
 || ||||| || ||
 TG GAGGTAAT CCG CTT
 _ C C
 GAM1081 MASP1 3' CTGCCAAGTGCTGCTT 7608 CCATTAA
 AAGCAGCGCT GGCAG
 ||||| ||||
 TTCGTCGTGA CCGTC
 A_
 GAM1081 MLLT2 3' TTGCCTAGAGCGCTGC 12574 CATTA
 GCAGCGCTC AGGCAG
 ||||| ||||
 CGTCGCGAG TCCGTT
 A_
 GAM1081 MNT 3' TCTGCCTCTGGGCAGCCTGCTT 21567 C _ ATTA
 AAGCAG GCT CC AGGCAGA
 ||||| || || |||||

TTCGTC CGA GG TCCGTCT
 _ C GTC_
 GAM1081 MTCP1 5' TCTACCCGGAGGAGCGCT 15489 A AA C
 AGCGCTCC TT GG AGA
 ||||| || || ||
 TCGCGAGG AG CC TCT
 _ GC A
 GAM1081 NCOA6 5' CCTTATGAAGCACTGCT 15288 C C T
 AGCAG GCT CAT AAGG
 |||| |||| ||||
 TCGTC CGA GTA TTCC
 A A _
 GAM1081 NFRKB 5' TCCGCCTCGTCGAGCGCTGCT 12823 CATTA A
 AGCAGCGCTC AGGC GA
 ||||| |||| ||
 TCGTCGCGAG TCCG CT
 CTGC_ C
 GAM1081 PLXNA2 3' TTCTGCCTCTGTGACTGCTGCT 24816 CTC TA
 T AAGCAGCG CAT AGGCAGAA
 ||||| || |||||
 TTCGTCTG GTG TCCGTCTT
 CA_ TC
 GAM1081 SDC2 5' GCTTGGACGCGCTGCT 33327 _ TTAA
 AGCAGCGC TCCA GGC
 ||||| |||| ||
 TCGTCGCG AGGT TCG
 C _
 GAM1081 STS 3' CCCTGGTGAAGCAGCTGCTT 5908 _ C A
 AAGCAGC GCT CATTA GG
 ||||| |||| |||| ||
 TTCGTCTG CGA GTGGT CC
 A A C
 GAM1081 TCF2 3' TTCTACCTGAGGAGGCTGC 13203 G ATTA C
 GCAGC CTCC AGG AGAA
 |||| |||| |||| ||
 CGTCG GAGG TCC TCTT
 _ AG_ A
 GAM1081 TCTA 3' TTCTGCCTCTTAAGCCTGCT 22732 C CCATTA
 AGCAG GCT AGGCAGAA
 |||| || |||||
 TCGTC CGA TCCGTCTT
 _ ATTC_
 GAM1081 C20orf110 3' TTCTGCCTTGGGGGCG 38839 AT
 CGCTCC TAAGGCAGAA
 |||| |||||
 GCGGGG GTTCCGTCTT
 _
 GAM1081 C20orf42 3' TCTGCCTTGAGACTGC 19216 CG CATT
 GCAG CTC AAGGCAGA
 |||| || |||||

CGTC GAG TTCCGTCT
A_ ____

GAM1081 DGKZ 3' CTGCCTTGCTTGGCACCCGCT 9722 CT__ T_
AGCG CCA TAAGGCAG
|||| ||| |||||||
TCGC GGT GTTCCGTC
CCAC TC

GAM1081 FLJ10097 3' CTGAGGTTAATGTGAACACTGC 33989 CGC _ GG_
TT AAGCAG TC CATTAA CAG
||||| || ||||| |||
TTCGTC AG GTAATT GTC
ACA T GGA

GAM1081 FLJ20686 3' TTCTGCCTCTGTGGAAACTAC 19597 C CGC TA
TT AAG AG TCCAT AGGCAGAA
||| || ||||| |||||||
TTC TC AGGTG TCCGTCTT
A AAA TC

GAM1081 GOLGA1 3' TCTGCCTTCCAGAGGCCGCTT 7865 A G CATT
AAGC GC CTC AAGGCAGA
|||| ||| |||||||
TTCG CG GAG TTCCGTCT
C _ ACC_

GAM1081 KCNV1 5' TTCTGCCACTTGTGCGCTGCTT 15713 TC TTAA
AAGCAGCGC CA GGCAGAA
||||||| || |||||||
TTCGTGCGG GT CCGTCTT
T_ TCA_

GAM1081 LAT1-3TM 3' CTGTTTTGGAGACTGC 25252 CG TTA
GCAG CTCCA AGGCAG
|||| ||||| |||||||
CGTC GAGGT TTTGTC
A_ ____

GAM1081 MCF2L 3' TTCTGCCTCTGGACGGTGCTT 30510 G C TTA
AAGCA CG TCCA AGGCAGAA
||||| || ||||| |||||||
TTCGT GC AGGT TCCGTCTT
G _ C_

GAM1081 MGC5601 5' TTCTATGTGATGGAGTACTGC 24927 CG AGGC
GCAG CTCCATTA AGAA
|||| ||||||| |||
CGTC GAGGTAGT TCTT
AT GTA_

GAM1081 NBR2 5' TTCCGCCCTAATGGAGGT 12426 G A A
GC CTCCATTA GGC GAA
|| ||||||| ||| |||
TG GAGGTAAT CCG CTT
_ C C

GAM1081 PEMT 5' CTGACCACAGAGCGCTGCT 14014 CATTAA _
AGCAGCGCTC GG CAG
||||||| || |||

	TCGTCGCGAG	CC GTC	
	ACA__ A		
GAM1081 PPP2R3A	5' CCTGGAGGCAAGCGCTGC	8586	__ A A
	GCAGCGCT CC TT AGG		
	CGTCGCGA GG AG TCC		
	AC _ G		
GAM1081 LOC119188	5' CTGCTTTGGAGGCTGC	36612	G TTA
	GCAGC CTCCA AGGCAG		
	CGTCG GAGGT TTCGTC		
	— —		
GAM1081 LOC143153	3' CTGCCTTGCCAGCCTGCT	37579	C CCAT
	AGCAG GCT TAAGGCAG		
	TCGTC CGA GTTCCGTC		
	_ CC_		
GAM1081 LOC143154	3' CTGCCTTGCCAGCCTGCT	37586	C CCAT
	AGCAG GCT TAAGGCAG		
	TCGTC CGA GTTCCGTC		
	_ CC_		
GAM1081 LOC148195	5' CCTTTTCATAGAGCGCTGTTT	40874	CATT__
	AAGCAGCGCTC AAGG		
	TTTGTGCGGAG TTCC		
	ATACTT		
GAM1081 LOC149010	3' TTCTGCCTCAATGTTTACTGT	38630	CGCTC A
	GCAG CATT AGGCAGAA		
	TGTC GTAA TCCGTCTT		
	ATTT_ C		
GAM1081 LOC149182	5' CTGCTCTGGGAATGCTGCTT	40970	C ATTAA
	AAGCAGCG TCC GGCAG		
	TTCGTCTGT AGG TCGTC		
	A GTC_		
GAM1081 LOC150159	3' CTCCAAATGGAGCTCTACTT	29180	C C AA C
	AAG AG GCTCCATT GG AG		
	TTC TC CGAGGTAA CC TC		
	A T A_ _		
GAM1081 LOC197423	5' CTGTTTTGGAGACTGC	38142	CG TTA
	GCAG CTCCA AGGCAG		
	CGTC GAGGT TTTGTC		
	A_ _		
GAM1081 LOC200597	3' TCTGTCCTGGGCGCTGC	42826	T TTAA
	GCAGCGC CCA GGCAGA		

		CGTCGCG GGT CTGTCT		
		_ C__		
GAM1081	LOC204970 3'	CTGCCTGCAGAGCGCTGC 43069	CATTA	
		GCAGCGCTC AGGCAG		
		CGTCGCGAG TCCGTC		
		ACG__		
GAM1081	LOC219294 3'	CTGCCTTGCCGGCCTGCT 44686	C CCAT	
		AGCAG GCT TAAGGCAG		
		TCGTC CGG GTTCCGTC		
		_ CC__		
GAM1081	LOC219295 3'	CTGCCTTGCCGGCCTGCT 44681	C CCAT	
		AGCAG GCT TAAGGCAG		
		TCGTC CGG GTTCCGTC		
		_ CC__		
GAM1081	LOC219513 5'	TCTGCCCTGTGGCTGCTT 45296	GCTC TAA	
		AAGCAGC CAT GGCAGA		
		TTCGTCTG GTG CCGTCT		
		___ TC_		
GAM1081	LOC221641 5'	TCCGCCACATTGTGGAGCGTGC 45009	G TAA__ A	
	TT	AAGCA CGCTCCAT GGC GA		
		TTCGT GCGAGGTG CCG CT		
		_ TTACA C		
GAM1082	SLC30A3 3'	TCCGCTGCAGCTCCACCAAT 9529	C CTAT	
		ATTG GT TTGCAGCGGA		
		TAAC CA GACGTCGCCT		
		_ CCTC		
GAM1082	FLJ20294 3'	TCCACTGCGAGTTGACCAAT 19351	C T C	
		ATTG GTC ATTTGCAG GGA		
		TAAC CAG TGAGCGTC CCT		
		_ T A		
GAM1082	LOC149721 5'	TCCCACAACAACGCAATGA 38812	CTAT CAGC	
		TCATTGCGT TTG GGA		
		AGTAACGCA AAC CCT		
		AC__ AC__		
GAM1083	HNF3G 3'	TACTTACTGTGATGACTGCTGT 35809	C T AC__	
	CT	AGACAGCA TC TCA AAGTA		
		TCTGTCGT AG AGT TTCAT		
		C T GTCA		
GAM1083	LBR 3'	TGTAAAGGAGTGCTGTCTTA 29855	CA	
		TAAGACAGCACTCTT ACA		

		ATTCTGTCGTGAGGA TGT	
		AA	
GAM1083 MCL1	3'	TACATGGGAAGAGTGCT 22489	AA A
		AGCACTCTTC CA GTA	
		TCGTGAGAAG GT CAT	
		G_ A	
GAM1083 T	3'	ACCTGCAGTAGCGGTGCTGTC 9153	_ TCAA A
		GACAGCACT CT CA GT	
		CTGTCGTGG GA GT CA	
		C TGAC C	
GAM1083 TGM4	3'	ACCTGTCAACTGGAGTGCTCTC 9235	C TCA__ A
T		AGA AGCACTCT ACA GT	
		TCT TCGTGAGG TGT CA	
		C TCAAC C	
GAM1083 CGGBP1	5'	ACTTGTTGAAAACTGATTTG 9738	A CACTC
		TAAG CAG TTCAACAAGT	
		GTTT GTC AAGTTGTTCA	
		A AAA__	
GAM1083 ELF4	3'	TACTTGTTGGTCTGTATCTTA 7127	CA CTCT
		TAAGA GCA TCAACAAGTA	
		ATTCT TGT GGTTGTTTCA	
		A_ CT__	
GAM1083 MGC4832	3'	TACTTGCTCAGTGCTGTCT 29701	CTTCAA
		AGACAGCACT CAAGTA	
		TCTGTCGTGA GTTCAT	
		CTC__	
GAM1083 P2RXL1	3'	CTTGGTAGGGTGCTGCCT 11931	A TCAA
		AG CAGCACTCT CAAG	
		TC GTCGTGGGA GTTC	
		C TG__	
GAM1083 TRIP-Br2	3'	ACTTGTCAAGGCTGTTTGA 16482	A CTTC
		TAAGACAGC CT ACAAGT	
		ATTTTGTCTG GA TGTTCA	
		_ AC__	
GAM1084 FMOD	3'	TGCCATCACATCCCTGATA 7773	A CAA
		TATCA GGA TGATGGCA	
		ATAGT CCT ACTACCGT	
		C AC_	
GAM1084 RNH	5'	CTTGCCACTGTCCTTG 8846	ATGA
		CAAGGACA TGGCAAGG	

			G TTCCTGT ACCGTTTC		
			C__		
GAM1084	RNH	5'	CTTTGCCACTGTCCTTG 29995	ATGA	
			CAAGGACA TGGCAAGG		
			G TTCCTGT ACCGTTTC		
			C__		
GAM1084	ZNF266	3'	CCCTGTCTCCACCTTGATA 42600	ACAA AT A	
			TATCAAGG TG GGCA GG		
			ATAGTTCC AC CTGT CC		
			____ CT C		
GAM1084	ELKS	3'	ACCCTGCTAGCTTTGCCCTTGA 17418	A TGA A	
			TCAAGG CAA TGGCA GGT		
			AGTTCC GTT ATCGT CCA		
			C TCG C		
GAM1084	FLJ22313	5'	CCTCAGTCCATCCTTGTA 22761	CAAT GGCA	
			TATCAAGGA GAT AGG		
			ATGGTTCCT CTG TCC		
			AC__ AC__		
GAM1084	FLJ23519	5'	CTTTGCCACTGTCCTTG 34309	ATGA	
			CAAGGACA TGGCAAGG		
			G TTCCTGT ACCGTTTC		
			C__		
GAM1084	MGC4309	3'	CCCTGCCATAGCCTTGATG 23567	ACAATG A	
			TATCAAGG ATGGCA GG		
			G TAGTTCC TACCGT CC		
			GA__ C		
GAM1084	ZNF33A	3'	CCTACAGCTAACATTATCCTTG 43897	C A A__	
	ATG		TATCAAGGA AATG TGGC AGG		
			G TAGTTCCT TTAC ATCG TCC		
			A A ACA		
GAM1084	LOC152503	5'	CCTTTAATCGTCTTTGATA 41517	AAT GGC	
			TATCAAGGAC GAT AAGG		
			ATAGTTTCTG CTA TTCC		
			____ AT__		
GAM1084	LOC51236	3'	ACCCTGCCCTCAACCCTTG 18569	ACAA T A	
			CAAGG TGA GGCA GGT		
			G TTCC ACT CCGT CCA		
			CA__ C C		
GAM1085	HCS	3'	TCATGACTTTTTTATGTGTACC 21015	A TTTC C	
	A		TG TACGCATGA AG CATGA		

AC ATGTGTATT TC GTACT
 C TTT_ A
 GAM1085 FLJ11164 3' CATGGCTGGGAATTGCCTACCA 20356 A C TGA TT
 TG TA GCA T CAGCCATG
 || ||| | |||||
 AC AT CGT A GTCGGTAC
 C C TA_ GG
 GAM1085 MAPKAPK3 3' TCATGGCTGATCAGAGC 11011 A_ TT
 GC TGA TCAGCCATGA
 || ||| |||||
 CG ACT AGTCGGTACT
 AG _
 GAM1085 SE57-1 3' TCATGGCTGCCTCACCACACAT 24892 ACGCA_ TTT
 CA TGAT TGA CAGCCATGA
 ||| ||| |||||
 ACTA ACT GTCGGTACT
 CACACC CC_
 GAM1085 LOC143920 5' CACGGCCACCATGGCGTATCA 37638 _ ATTTCA A
 TGATACGC ATG GCC TG
 ||||| ||| |||
 ACTATGCG TAC CGG AC
 G CAC_ C
 GAM1085 LOC157317 3' TCATGACTTTTTTATGTGTACC 39585 A TTTC C
 A TG TACGCATGA AG CATGA
 || ||||| || |||
 AC ATGTGTATT TC GTACT
 C TTT_ A
 GAM1085 LOC203429 3' CATGGCTGAAGCAAGCATCA 43049 AC A A
 TGAT GC TG TTTCAGCCATG
 ||| ||| |||||
 ACTA CG AC GAAGTCGGTAC
 _ A _
 GAM1085 LOC203429 3' CATGGCTGGAGCAAGTATCA 43050 GCA A
 TGATAC TG TTTCAGCCATG
 |||| || |||||
 ACTATG AC GAGGTCGGTAC
 A_ _
 GAM1086 RSN 3' TAAGCCAGTATAAAACAC 8864 CATTGG
 GTG TTGTACTGGCTTA
 ||| |||||
 CAC AATATGACCGAAT
 AA_
 GAM1086 CBCIP2 3' GCTTGTACAACCAAACAC 26606 CA T
 GTG TTGGTTGTAC GGC
 ||| ||||| |||
 CAC AACCAACATG TCG
 A_ T
 GAM1086 CNNM1 3' AGTATTGTACAACCAAACAC 21604 CA TG_
 GTG TTGGTTGTAC GCT
 ||| ||||| |||

		CAC AACCAACATG TGA	
		___ TTA	
GAM1086	FLJ00024	3' GTGAAACAAACCAATGCAC 31897	GTAC GC
		GTGCATTGGTT TG TTAC	
		CACGTAACCAA AC AGTG	
		___ AA	
GAM1086	FLJ13984	3' AGTAAACCAGTTCCCAAACAC 24130	CA TTGT C
		GTG TTGG ACTGG TTACT	
		CAC AACC TGACC AATGA	
		A_ CT_ A	
GAM1086	LOC196485	3' TAAACCAGGGGCACAATGCAC 42382	GT A_ C
		GTGCATTG TGT CTGG TTA	
		CACGTAAC ACG GACC AAT	
		___ GG A	
GAM1086	LOC202986	3' TAAACCAGGGACACAATGCAC 43473	GT A_ C
		GTGCATTG TGT CTGG TTA	
		CACGTAAC ACA GACC AAT	
		___ GG A	
GAM1086	LOC221354	3' TAAACCAGAGGCACAATGTAC 44393	_ GTA C
		GTGCATTG GTT CTGG TTA	
		CATGTAAC CGG GACC AAT	
		A A_ A	
GAM1086	LOC90333	3' AGTAATGCTACAACCATTGCAC 31219	T ACT _
		GTGCA TGGTTGT GGC TTACT	
		CACGT ACCAACA TCG AATGA	
		T _ T	
GAM1087	PAG	3' CAGCTTTTCCTACACTGA 20509	A C
		TCA TGTAGGAAAA CTG	
		AGT ACATCCTTTT GAC	
		C C	
GAM1087	PEA15	3' CTGCATTTTCCTACATTGA 9848	CC
		TCAATGTAGGAAAA TGTAG	
		AGTTACATCCTTTT ACGTC	

GAM1087	XPC	3' CCACTACAGGCCCCACACCTGC 10999	AAAA_
		GTAGG CCTGTAGTGG	
		CGTCC GGACATCACC	
		ACACCCC	
GAM1087	BRD3	3' CTGCAGGTTTCCATACACTGA 14297	A _ A
		TCA TGTA GGAAA CCTGTAG	

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AGT ACAT CCTTT GGACGTC
  C  A  _
GAM1087 C21orf108 3' CACTTCTTCCTACATTGA 42766 AACCTGT
                   TCAATGTAGGAA AGTG
                   ||||| |||
                   AGTTACATCCTT TCAC
                   CT_____
GAM1087 FLJ22965 3' CCATTGATTCTCCTACATT 22644 AAACCTG
                   AATGTAGGA TAGTGG
                   ||||| ||||
                   TTACATCCT GTTACC
                   CTTA____
GAM1087 KIAA0895 3' CCAGAGAGGTTTTCTACA 44546 GTAG
                   TGTAGGAAAACCT TGG
                   ||||| |||
                   ACATCCTTTTGGA ACC
                   GAG_
GAM1087 KIAA1305 5' CCAAGCCTGCTCTCCTACATT 24681 AAACCT ____
                   AATGTAGGA GTAG TGG
                   ||||| ||| |||
                   TTACATCCT CGTC ACC
                   CT_____ CGA
GAM1087 MGC4737 3' CCACGCCCTTCCTACACTG 25505 A AACCT A
                   CA TGTAGGAA GT GTGG
                   || ||||| || |||
                   GT ACATCCTT CG CACC
                   C CCC_ _
GAM1087 LOC163812 5' CCACTGTGGTTTGCCACACTGA 39967 A A A TGT
                   TCA TGT GG AAACC AGTGG
                   ||| ||| ||||| ||||
                   AGT ACA CC TTTGG TCACC
                   C _ G TG_
GAM1088 CTLA4 3' CCAGTGATGCTAAAGGTTGTAT 11711 CTCAA C
      T          GATGTAACC CA CACTGG
                   ||||| || |||||
                   TTATGTTGG GT GTGACC
                   AAATC A
GAM1088 NRCAM 3' CCAACGGTCCAAGGGATTACAT 11448 _ CAAC AC
      CT          GGATGTAA CCCT ACC TGG
                   ||||| ||| ||| |||
                   TCTACATT GGGG TGG ACC
                   A ACC_ CA
GAM1088 FLJ21432 3' CCAGTGGTGACATGACCACTCC 23766 T AACCC A__
                   GGA GT TCA CACCACTGG
                   ||| || ||| |||||
                   CCT CA AGT GTGGTGACC
                   _ CC_ ACA
GAM1088 PP1628 5' CCAGTGGTGCCAGGTGCCACC 24857 A TA CTCAA
                   GG TG ACC CACCACTGG
                   || || ||| |||||

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CC AC TGG GTGGTGACC
 _ CG ACC_
 GAM1088 LOC159199 5' CCAGACACTGAGGGTTCCATCC 39979 T ACACCA
 GGATG AACCTCA CTGG
 ||||| ||||| ||||
 CCTAC TTGGGAGT GACC
 C CACA_
 GAM1089 HAS3 3' CAAGTGCAGAGTTCAGACTTC 11802 AGACTC C
 GAAGT CTCTGCAC TG
 ||||| ||||| ||
 CTTCA GAGACGTG AC
 GACTT_ A
 GAM1089 C21orf25 3' AGGTGCACTCTATTCA 31796 G CTCCTC
 TGAA TAGA TGCACCT
 ||||| ||||| |||||
 ACTT ATCT ACGTGGG
 _ C_
 GAM1089 ERG-1 5' TCAGGTAATGGGAGTCTCTCCA 22557 A T CTGC
 TG AG AGACTCCT ACCTGA
 || ||||| |||||
 AC TC TCTGAGGG TGGACT
 C _ TAA_
 GAM1089 FLJ13590 5' CAGGTGTGAGCCACTTCA 24250 AGA CTCT
 TGAAGT CTC GCACCTG
 ||||| || |||||
 ACTTCA GAG TGTGGAC
 CC_ _
 GAM1089 FLJ14810 3' CAGGATGGTGGAGTCTGCCCA 26632 AA T GCA
 TG GTAGACTCC CT CCTG
 || ||||| || |||||
 AC CGTCTGAGG GG GGAC
 CC T TA_
 GAM1089 INA 3' TCAGGTGCAGAGGAAGTAC 26454 GAC
 GTA TCCTCTGCACCTGA
 || ||||| |||||
 CAT AGGAGACGTGGACT
 GA_
 GAM1089 INSM2 3' AGGAAGAGCTACTTCA 26326 ACTC GCA
 TGAAGTAG CTCT CCT
 ||||| ||||| ||
 ACTTCATC GAGA GGA
 _ A_
 GAM1089 KIAA0261 3' CAGGTGCAAAGGCAGCTTA 33830 T A _ C
 G AG CT CCT TGCACCTG
 | || ||||| |||||
 A TC GA GGA ACGTGGAC
 T _ C A
 GAM1089 KIAA1483 3' TCAGTTAAGAAATCTACTTTA 34617 CTCC GCAC
 TGAAGTAGA TCT CTGA
 ||||| || |||||

			ATTCATCT AGA GACT		
			AA__ ATT__		
GAM1089	KIAA1530	3'	TGGAGAGGAGTCTATTCA 33737	G	G
			TGAA TAGACTCCTCT CA		
			ACTT ATCTGAGGAGA GT		
			__ G		
GAM1089	MRPL35	3'	CAAGTGCGTGTCTACTT 18733	TCCTC	C
			AAGTAGAC TGCAC TG		
			TTCATCTG GCGTG AC		
			T__ A		
GAM1089	NAPG	3'	CAGGTGCAGCCTCCTTCA 46251	T	ACTCCT
			TGAAG AG CTGCACCTG		
			ACTTC TC GACGTGGAC		
			C C__		
GAM1089	SLC26A1	3'	TCAGGTGCAGTGGCCCTAC 22567	ACT	T
			GTAG CC CTGCACCTGA		
			CATC GG GACGTGGACT		
			CC_ T		
GAM1089	STK29	3'	CAGGCTCGGGGGAGCCTCCTCC 42317	A T A	CA
	A		TG AG AG CTCCTCTG CCTG		
			AC TC TC GAGGGGGC GGAC		
			C C C TC		
GAM1089	LOC162165	5'	TCAGGTGCCCCTGAGTCCACCT 42117	A A	CTCT
	TA		TGA GT GACTC GCACCTGA		
			ATT CA CTGAG CGTGGACT		
			C C TCCC		
GAM1089	LOC196527	3'	GCCTAGCAGTCTACTTCA 42400	C	CT
			TGAAGTAGACT CT GC		
			ACTTCATCTGA GA CG		
			C TC		
GAM1089	LOC221002	3'	CAGCTAGAGGAGCACACTCCA 43972	A AGA	CAC
			TG AGT CTCCTCTG CTG		
			AC TCA GAGGAGAT GAC		
			C CAC C__		
GAM1090	BCL11A	3'	CACATTGGAACAGTGA 19752	G	TTAATA
			TCACTG TC CAATGTG		
			AGTGAC AG GTTACAC		
			A ____		
GAM1090	BCL11A	3'	CACATTGGAACAGTGA 28852	G	TTAATA
			TCACTG TC CAATGTG		

AGTGAC AG GTTACAC
 A _____
 GAM1090 DVL3 3' CCCACATTACTGAAACCA 10692 C ATAC
 TGGT TTA AATGTGGG
 |||| ||| |||||
 ACCA AGT TTACACCC
 A CA__
 GAM1090 SWAP70 3' CAGGTGTATTAGACCA 35346 T A G
 TGGTCT AATACA T TG
 ||||| ||||| | ||
 ACCAGA TTATGT G AC
 _ _ G
 GAM1090 AK5 3' CCTTGCATTAAACCAGTGA 14394 C A TGT
 TCACTGGT TTAAT CAA GG
 ||||||| ||||| ||| ||
 AGTGACCA AATTA GTT CC
 _ C _____
 GAM1090 CHRFAM7A 3' CCTCATTAAGACCAGT 45553 ATACA T
 ACTGGTCTTA ATG GG
 ||||||| ||| ||
 TGACCAGAAT TAC CC
 _____ T
 GAM1090 FLJ13215 3' CTAAATATCAAGACCAGGA 24576 A A CAATG
 TC CTGGTCTT ATA TGG
 || ||||| ||| |||
 AG GACCAGAA TAT ATC
 _ C AA____
 GAM1090 KIAA1430 3' CCCACATTTAAAGACCTAGT 39357 _ AATAC
 ACT GGTCTT AATGTGGG
 ||| ||||| |||||
 TGA CCAGAA TTACACCC
 T AT____
 GAM1090 PRO2955 3' CCCACATTACACTAATCATTGA 20620 C CTTAATAC
 TCA TGGT AATGTGGG
 ||| ||| |||||
 AGT ACTA TTACACCC
 T ATCACA__
 GAM1090 LOC148014 3' TTGTATTAAGAGCCAATGA 38442 C _
 TCA TGG TCTTAATACAA
 ||| ||| |||||
 AGT ACC AGAATTATGTT
 A G
 GAM1090 LOC90917 3' CCCAAGATATTAAACCAGTGA 32165 C CAATG
 TCACTGGT TTAATA TGGG
 ||||||| ||||| |||
 AGTGACCA AATTAT ACCC
 _ AGA____
 GAM1091 MGC13057 5' GACCCCACGGCTGTCCGGACGT 26125 _ _ ACGAA
 GCCA TGGCACGTC GA AGCTG GTC
 ||||||| || ||||| |||

ACCGTGCAG CT TCGGC CAG
 GC G ACCC_
 GAM1092 GAB3 3' AAGACACGAAGCGACCTACCCA 27926 A GAAAGC
 TGG TAGGTTGTT GTCTT
 ||| ||||| ||||
 ACC ATCCAGCGA CAGAA
 C AGCA_
 GAM1092 LOC147093 3' CTTTGCAACAACCTACCCA 40802 A _
 TGG TAGGTTGTTG AAAG
 ||| ||||| ||||
 ACC ATCCAACAAC TTTC
 C G
 GAM1092 LOC169943 5' ATGTCTTCCAACAACCTACCCA 42184 ATA A _
 TGG GGTGTTG AAG CGT
 ||| ||||| ||| |||
 ACC TCAACAAC TTC GTA
 CA_ C T
 GAM1092 LOC222128 5' ACGCTTCCATCTTTATCCA 44538 TTGT A
 TGGATAGG TG AAGCGT
 ||||| || |||||
 ACCTATTT AC TTCGCA
 CT_ C
 GAM1093 AF9Q34 3' ACAAAGCCCGCTTGCTCGC 26274 GA GA_
 GCGAGCAAGC GGGT TGT
 ||||| ||| |||
 CGCTCGTTCCG CCG ACA
 _ AAA
 GAM1093 C20orf54 5' GACAGGCCCGCTTGCTGCA 27228 G GAG GA
 TGC AGCAAGC GGT TGTC
 ||| ||||| ||| |||
 ACG TCGTTCCG CCG ACAG
 _ _ G_
 GAM1093 FLJ20034 3' GGAAGTGTCCCTCGCTTGCTCC 19134 C T _
 A TG GAGCAAGCGAGGG GAT GTCC
 || ||||| ||| |||||
 AC CTCGTTCCGCTCCC CTG CAGG
 _ _ T
 GAM1093 KIAA0853 5' GACATCACTCATCTTCCTCACA 17438 C C CGA
 TG GAG AAG GGGTGATGTC
 || ||| ||| |||||
 AC CTC TTC CTCACTACAG
 A C TA_
 GAM1093 MGC13071 3' ACATCACCTGCCTGCCGGCA 26408 GA A GA
 TGC GCA GC GGGTGATGT
 ||| ||| || |||||
 ACG CGT CG TCCACTACA
 GC C _
 GAM1093 NGEF 5' GGACACACCATCCTGCTCGCA 34278 A C G A
 TGCAGCA G GA GGTG TGTCC
 ||||| || ||| |||||

ACGCTCGT C CT CCAC ACAGG

-- A _

GAM1093 POLR2D 3' ACATCACTGCTGCTCG 11227 A GAG
CGAGCA GC GGTGATGT
||||| || |||||
GCTCGT CG TCACTACA

- - -

GAM1093 WASL 5' ACGAGCTCTCGCCCACTCGC 10051 CAA GA
GCGAG GCGAGGGT TGT
|||| | ||||| ||
CGCTC CGCTCTCG GCA
ACC A_

GAM1093 LOC151512 5' GTCACCCTCACCTGTCGCA 41362 G AGC
TGCGA CA GAGGGTGAT
|||| | |||||
ACGCT GT CTCCCACTG
_ CCA

GAM1093 LOC153277 3' GGACATCACCGGCTGCACGCA 41605 A A GAG
TGCG GCA GC GGTGATGTCC
||| ||| || |||||
ACGC CGT CG CCACTACAGG
A _ G_

GAM1094 LOC153937 5' AACAGCTCAAATCCATTTTTTA 39443 T_ C
C GTGG TGGATT GAGCTGTT
||| |||| | |||||
CATT ACCTAA CTCGACAA
TTTT A

GAM1095 ACCN1 3' TCGCTCCGGCCACGTCCAACA 6753 _ T _
TGTTGGAC TG GT GCGA
||||| || || |||
ACAACCTG AC CG CGCT
C _ GCCT

GAM1095 DAG1 3' GCTTTGTCCTAACAGTCCACA 10636 T GTGC A
TGT GGA CTGT GA CAAAGC
|| ||||| || |||||
ACA CCTGACA CT GTTTCG
_ ATC_ _

GAM1095 FYCO1 3' TCCAGGCCAAGTCCAACA 23714 _ G C
TGTTGGACT GT TG GA
||||| || || ||
ACAACCTGA CG AC CT
AC G _

GAM1095 SEPT6 3' CTTTCAAAGCACACAGTCAAAC 17494 G GAAC
A TGTT GACTGTGTGC AAAG
||| ||||| |||
ACAA CTGACACACG TTTC
A AAAC

GAM1095 LOC91445 3' GCTTTGTCAGGTCAGCCCAAC 30371 A _ G CGA
GTTGG CTG T TG ACAAAGC
|||| ||| || |||||

			CAACC GAC G AC TGTTCG	
			C T G ____	
GAM1096	ARF1	3'	TTATAGCTATTAGAATAAAATC 34994	CC TCCA_
	TC		GAGATTTTA CT CTATAA	
			CTCTAAAAT GA GATATT	
			AA TTATC	
GAM1096	CHD2	3'	AGTGGGAAAATTTC A 6934 TACCC	
			TGAGATTT TTCCACT	
			ACTTTAAA AGGGTGA	

GAM1096	ITGA4	3'	TGCAAGGGGAAAATCTCA 6584 A C	
			TGAGATTTT CCCTT CA	
			ACTCTAAAA GGGAA GT	
			G C	
GAM1096	KIAA1319	3'	TTATAGTGGAAGGATGGTC 21869 TTAC	
			GATT CCTTCCACTATAA	
			CTGG GGAAGGTGATATT	
			TA__	
GAM1096	KIAA1361	5'	TATAGTGGAAGCAGTCT 31171 TTACCC	
			AGATT TTCCACTATA	
			TCTGA AAGGTGATAT	
			CGA__	
GAM1096	SH3BGRL2	3'	TGAGAAAGGAAAATCTCA 25533 A C _	
			TGAGATTTT CC TTC CA	
			ACTCTAAAA GG AAG GT	
			_ A A	
GAM1096	LOC152008	3'	GGTGGAAGAGCAAACTCA 39197 A ACC	
			TGAG TTTT CTTCCACT	
			ACTC AAAA GAAGGTGG	
			_ CGA	
GAM1096	LOC57826	3'	AGTGAAAGGTAAAATCTCA 22159 C C	
			TGAGATTTTACC TTC ACT	
			ACTCTAAAATGG AAG TGA	
			A _	
GAM1096	LOC90333	3'	ATAGTGAGAGAAACCTTA 31220 A ACCC	
			TGAG TTTT TTCCACTAT	
			ATTC AAAG GAGGTGATA	
			C A__	
GAM1096	LOC90982	5'	TAGTTGAAAAATAAAATCTC 32234 CCC C	
			GAGATTTTA TTC ACTA	

CTCTAAAAT AAG TGAT
 AAA T
 GAM1097 AAT1 3' TCAACATGGAGTCCAAGTAA 39228 ACA TAG
 TTAC GGCT CCATGTTGA
 ||| ||| |||||
 AATG CTGA GGTACAACT
 AAC ____
 GAM1097 ACP33 3' TCTCCACTAAGCCTGTGTAA 18745 CCA TT
 TTACACAGGCTTAG TG GA
 ||||| || ||
 AATGTGTCCGAATC AC CT
 ____ CT
 GAM1098 ARNT2 3' TGTGAATGAGGCCACCC 16938 A ACG
 GGT GGCCTCA TTTACA
 || ||||| |||||
 CCA CCGGAGT AAGTGT
 C ____
 GAM1098 SLC14A2 5' CTGTAAGTTTCCTGAGGCCTCC 14010 T ACG__
 C GG AGGCCTCA TTTACAG
 || ||||| |||||
 CC TCCGGAGT GAATGTC
 C CCTTT
 GAM1098 SLC6A8 3' CTGTGAGCCCTACCTTA 12149 CCTCAAC
 TAAGGTAGG GTTTACAG
 ||||| |||||
 ATTCCATCC CGAGTGTC

 GAM1098 TIAM1 5' CTGTGGACTGAGACCCACCTT 9260 A C AC
 AAGGT GG CTCA GTTTACAG
 |||| || ||| |||||
 TTCCA CC GAGT CAGGTGTC
 C A ____
 GAM1098 ESDN 3' TGTAACATGACCCACTT 28155 A CC AC
 AGGT GG TCA GTTTACA
 |||| || || |||||
 TTCA CC AGT CAAATGT
 C __ A_
 GAM1098 LIN-28 3' CTGTGAGATCACCGCAAACCTA 23980 CCTCAACG__
 CCTTA TAAGGTAGG TTTACAG
 ||||| |||||
 ATTCCATCC GAGTGTC
 AAACGCCACTA
 GAM1098 SNPH 3' TGGGGCCAAGGCCTACC 16303 CAAC A
 GG TAGGCCT GTTT CA
 ||||| ||| ||
 CCATCCGGA CGGG GT
 AC__ _
 GAM1098 LOC146488 3' CTGTGAGCCCTACCTTA 35045 CCTCAAC
 TAAGGTAGG GTTTACAG
 ||||| |||||

ATTCCATCC CGAGTGTC

GAM1098 LOC147229 5' CTGTGAACTCAAGGCCTTCCCT 38318 T_ CAAC
AGG AGGCCT GTTTACAG
||| ||||| |||||
TCC TCCGGA CAAGTGTC
CT ACT_

GAM1098 LOC200942 3' CTGGAGTTGACCAGGCCTACC 42871 ____ GTTTA
GGTAGGCC TCAAC CAG
||||||| ||||| |||
CCATCCGG AGTTG GTC
ACC AG__

GAM1099 EIF1A 3' GAATAACAACTCAGTGAA 42722 A A
TTCA TGA TTGTTATTC
||| ||| |||||
AAGT ACT AACAATAAG
G C

GAM1099 MYB 3' ACATGAACTTTTCATGAA 29943 A TT AT
TTCA TGAA GTT TCATGT
||| ||| ||| |||||
AAGT ACTT CAA AGTACA
_ TT _

GAM1099 MGC20253 3' CGGCTACAACAATTCATAGAA 29395 A ATTCAT
TTC ATGAATTGTT GTCG
||| ||||| |||||
AAG TACTTAACAA CGGC
A CAT__

GAM1099 STK38L 3' CGTAGATAACAATACTGAA 34289 A A TC
TTCA TG ATTGTTAT ATG
||| ||| ||||| |||
AAGT AC TAACAATA TGC
C A GA

GAM1100 EN2 3' ACCTTGTCTTTCAAAAGAACTC 7143 ATTCC
A TGGGTTCTTT GGACAAGGT
||||||| |||||
ACTCAAGAAA TCTGTTCCA
ACTT_

GAM1100 SMG1 3' TCCAAAATAAAAACCCA 17482 C CC
TGGGTT TTTATT GGA
||||| ||||| |||
ACCCAA AAATAA CCT
_ AA

GAM1100 FKSG42 3' CCTTGTCCAGTGGAGCCCA 25732 TTATTCC
TGGGTTCT GGACAAGG
||||||| |||||
ACCCGAGG CCTGTTCC
TGA__

GAM1100 KIAA0940 3' CCTTGTCCAGAAAACC 17147 CTTTA C
GGTT TTC GGACAAGG
||| ||| |||||

		CCAA AAG CCTGTTCC		
		_____ A		
GAM1100	POLM	3' CCCTGCCCAGAATGCCCA 43784	TCTTT	C A A
		TGGGT ATTG GG CA GG		
		ACCCG TAAG CC GT CC		
		_____ A C C		
GAM1100	RACGAP1	3' CCTTGTCCAGTGGAGCCCA 14942	TTATTCC	
		TGGGTTCT GGACAAGG		
		ACCCGAGG CCTGTTCC		
		TGA_____		
GAM1100	LOC201626	5' ACCTTATCCAGAAGGAACTCA 42887	TTA	C C
		TGGGTTCT TTC GGA AAGGT		
		ACTCAAGG AAG CCT TTCCA		
		_____ A A		
GAM1100	LOC91522	3' CCTATCCAAGAAGACCCA 32962	T ATTCC	CA
		TGGGT CTTT GGA AGG		
		ACCCA GAAG CCT TCC		
		_____ AA_____ A_		
GAM1101	HRASLS	5' GCGAGGCCAAGAGAGACCCC 21658	CC	G C
		GG GTTT TCT GGCCTCGC		
		CC CAGA AGA CCGGAGCG		
		C_ G A		
GAM1101	SLC7A5	3' CGAAGCCGGACACGGCTTCA 9576	TT T	C
		TGAGGCCGT GTC CGGC TCG		
		ACTTCGGCA CAG GCCG AGC		
		_____ A		
GAM1101	WHSC1	3' GCGTTCCTGGACAAACAGCCTC 28465	C	C CCT
	A	TGAGGC GTTTGTCT GG CGC		
		ACTCCG CAAACAGG CC GCG		
		A T TT_		
GAM1101	WHSC1	3' GCGTTCCTGGACAAACAGCCTC 28476	C	C CCT
	A	TGAGGC GTTTGTCT GG CGC		
		ACTCCG CAAACAGG CC GCG		
		A T TT_		
GAM1101	WHSC1	3' GCGTTCCTGGACAAACAGCCTC 17184	C	C CCT
	A	TGAGGC GTTTGTCT GG CGC		
		ACTCCG CAAACAGG CC GCG		
		A T TT_		
GAM1101	WHSC1	3' GCGTTCCTGGACAAACAGCCTC 28448	C	C CCT
	A	TGAGGC GTTTGTCT GG CGC		

ACTCCG CAAACAGG CC GCG
 A T TT_
 GAM1101 C21orf93 5' AGGCCGAGTGGACTCTCA 29739 CC TT T
 TGAGG GT G CTCGGCCT
 |||| | | |||||
 ACTCT CA T GAGCCGGA
 _ GG_
 GAM1101 CLIC5 3' AGGCCAAGGACAAACGCC 18845 C C_
 GGC GTTTGTCT GGCCT
 || ||||| ||||
 CCG CAAACAGG CCGGA
 _ AA
 GAM1101 L3MBTL 3' GCGAGGCCACGACAGGCCTCA 34457 GTT TC
 TGAGGCC TGTC GGCCTCGC
 |||| | |||||
 ACTCCGG ACAG CCGGAGCG
 _ CA
 GAM1101 LOC149576 5' CGAGACGAAAACGGCCCCG 38776 A GTC GC
 TG GGCCGTTT TCG CTCG
 || ||||| || ||||
 GC CCGGCAAA AGC GAGC
 C _ A_
 GAM1101 LOC149668 5' CGAGGCCGCCTGACGCCTCA 41029 C TGTCT
 TGAGGC GTT CGGCCTCG
 |||| | |||||
 ACTCCG CAG GCCGGAGC
 _ TCC_
 GAM1101 LOC221489 5' GCAAGGAGCAAATGGCCTCA 44983 _ CG
 TGAGGCCGTTTG TCT GC
 ||||| || ||
 ACTCCGGTAAAC AGG CG
 G AA
 GAM1101 LOC84570 5' GCGAAGCCGAGACGGCC 26266 GTTT C
 GGCC GTCTCGGC TCGC
 || | ||||| ||||
 CCGG CAGAGCCG AGCG
 _ A
 GAM1102 PTBP2 3' TTTAGGGCACACTGTTATA 22168 C AC
 TAT ACA GTGCCCTAAG
 || | |||||
 ATA TGT CACGGGATTT
 T CA
 GAM1102 ZFP36L2 3' CACAACAGGGCAGTTGTGATA 13753 G AAGA
 TATCACAAC TGCCCT TGTG
 ||||| |||| |
 ATAGTGTTG ACGGGA ACAC
 _ CA_
 GAM1103 GFAP 3' CCCAGAAGGACCTCCTGAGCGA 7813 A G AAAC TAG
 TC CT AG CTTTCTGGG
 || || | |||||

AG GA TC GGAAGACCC
 C G CTCCA__
 GAM1103 HIP2 3' CCCAACTTAGTTTTTCAGTGA 11814 CTTTC
 TCACTGAGAAACTAG TGGG
 ||||| |||
 AGTGACTTTTTGATT ACCC
 CA__
 GAM1103 IL15RA 3' CCCAGGGCCCAGCTTCCCAGGA 7946 A A A A_ TT
 TC CTG GAA CT GCT CTGGG
 || ||| || ||| |||||
 AG GAC CTT GA CGG GACCC
 _ C C CC _
 GAM1103 LIMK1 3' CCCAGAGGACGTTCTCAAGGA 18795 AC A TAG T
 TC TGAG AAC CTT CTGGG
 || ||| ||| ||| |||||
 AG ACTC TTG GGA GACCC
 GA C CA_ _
 GAM1103 PODXL 3' CCAGCGAGTTTCCCAGGA 11871 A A A TTCT
 TC CTG GAAACT GCT GG
 || ||| ||||| ||| ||
 AG GAC CTTTGA CGA CC
 _ C G ____
 GAM1103 COE2 3' CCAGAAAGCCAGCTTGGT 32126 TG AAA A
 AC AG CT GCTTTCTGG
 || || || |||||
 TG TC GA CGAAAGACC
 GT _ C
 GAM1103 DKFZp547H236 5' CCCTGGCTAGCTTCCCAGAGA 38405 A A A TTCT
 TC CTG GAA CTAGCT GGG
 || ||| ||| ||||| |||
 AG GAC CTT GATCGG CCC
 A C C T__
 GAM1103 ELSPBP1 5' CCCAGAAGAAGCTCTCTCAAAGA 22704 AC AACTAG T
 TC TGAGA CTT CTGGG
 || |||| ||| |||||
 AG ACTCT GAA GACCC
 AA CTCAA_ _
 GAM1103 EVI5 3' CCAGAAAGCTATCAATG 12210 C GAAAC
 CA TGA TAGCTTTCTGG
 || ||| |||||
 GT ACT ATCGAAAGACC
 A ____
 GAM1103 FLJ10853 3' CCCAGGAGTAATTTCTCAG 20214 CTA T
 CTGAGAAA GCTT CTGGG
 ||||| ||| |||||
 GACTCTT TGAG GACCC
 AA_ _
 GAM1103 FLJ12770 3' CCCTGAACTATTCCTCAGTGA 25885 A C CT T
 TCACTGAG AA TAG TTC GGG
 ||||| || ||| ||| |||

AGTGA CTC TT ATC AAG CCC
 C _ _ T
 GAM1103 FLJ13491 5' CCAGGAGAGTCCTCAG 23887 AA AGC
 CTGAG ACT TTTCTGG
 ||||| ||| |||||
 GACTC TGA GAGGACC
 C_ _
 GAM1103 FLJ14166 3' CCCAGAAAGAGGCGTCCCA 23791 A AA AG
 TG GA CT CTTTCTGGG
 || || || |||||
 AC CT GG GAAAGACCC
 C GC A_
 GAM1103 FLJ14564 3' CCAACTCAGTCTTCAGTGA 37595 AA _ CTTTC
 TCACTGAG ACT AG TGG
 ||||| ||| |||
 AGTGACTT TGA TC ACC
 C_ C A_
 GAM1103 FLJ20315 3' CCCAGAGGCCAGCTCCCCAGT 19378 A_ AACTA T
 ACTG GA GCTT CTGGG
 ||| || ||| |||||
 TGAC CT CGGA GACCC
 CC CGACC _
 GAM1103 HTCD37 3' CCAGAAAGGCCTTAATGA 33617 C AACTA _
 TCA TGAG GC TTTCTGG
 ||| ||| || |||||
 AGT ATTC CG AAAGACC
 A _ _ G
 GAM1103 KIAA0040 3' CCCAGAAACTCACTTCTCAGT 16096 ACT C
 ACTGAGAA AG TTTCTGGG
 ||||| || |||||
 TGA CT TC AAAGACCC
 CAC _
 GAM1103 KIAA0682 3' CCCAGGGAAGCCTCCAGCGG 18289 A A AACTA _
 TC CTG GA GCTTTC TGGG
 || ||| || ||||| |||||
 GG GAC CT CGAAGG ACCC
 C C C_ _ G
 GAM1103 KIAA1297 5' CCCAGAAGGCCACCCCCCAGTG 35712 AGAAACTA
 G TCACTG GCTTTCTGGG
 ||||| |||||
 GGTGAC CGGAAGACCC
 CCCCCAC_
 GAM1103 KIAA1854 3' CCAGAAAAAGTGCCAGTGA 35525 AGAA AGC
 TCACTG ACT TTTCTGG
 ||||| ||| |||||
 AGTGAC TGA AAAGACC
 CG_ A_
 GAM1103 My015 3' CCCAGATTTTGGTTTCCA 33105 A CTT
 TG GAACTAG TCTGGG
 || ||||| |||||

	AC CTTTGGTT AGACCC	
	— TT—	
GAM1103 LOC122553 3'	CCCTCTTCTGCTTCTCAGTGA 36689	AACT TTTCT—
	TCACTGAGA AGC GGG	
	AGTGACTCT TCG CCC	
	— TCTTCT	
GAM1103 LOC149146 5'	AAAGCCGGTTTCTCAGTGA 38654	TA
	TCACTGAGAAAC GCTTT	
	AGTGACTCTTTG CGAAA	
	GC	
GAM1103 LOC150279 3'	CCTGTGGGCTAGTCTCCAG 38899	A A TCT
	CTG GA ACTAGCTT GG	
	GAC CT TGATCGGG CC	
	— C TGT	
GAM1103 LOC150951 5'	CCCAGAAGCAGGTCCTCCAGTG 41278	A A_ A T
A	TCACTG GA ACT GCTT CTGGG	
	AGTGAC CT TGG CGAA GACCC	
	— CC A —	
GAM1103 LOC158549 5'	CCAGGAACCAGTTCCTTAATGA 42005	C A AGC
	TCA TGAG AACT TTTCTGG	
	AGT ATTC TTGA AAGGACC	
	A C CC—	
GAM1103 LOC255252 3'	CCAGAGCATCCTCAGTGA 45545	AAACTA TT
	TCACTGAG GC TCTGG	
	AGTGACTC CG AGACC	
	CTA— —	
GAM1103 LOC255452 3'	CCCAGAAAGCAGAACCCAGGA 46573	A AGAAA A
	TC CTG CT GCTTTCTGGG	
	AG GAC GA CGAAAGACCC	
	— CCAA— —	
GAM1103 LOC257428 5'	CAGGAGTAACTTCTCAGTGA 45260	AC T
	TCACTGAGAA TAGCTT CTG	
	AGTGACTCTT ATTGAG GAC	
	CA —	
GAM1103 LOC55831 5'	CTGGGAACCAGCTTTTCAGTGA 20516	AAACT — G
	TCACTGAG AGCT TTCT GG	
	AGTGACTT TCGA AAGG TC	
	— CC G	
GAM1103 LOC91050 3'	CCCAGAGTGGTAGCCTCTCAGT 32334	AA GCT
GA	TCACTGAGA CTA TTCTGGG	

		AGTGACTCT GAT GAGACCC		
		CC GGT		
GAM1103	LOC91149	5' CCGTCGAGTCTCTCAGTGA	32456	AACTA TC
		TCACTGAGA GCTT TGG		
		AGTGACTCT TGAG GCC		
		C_____ CT		
GAM1103	LOC91748	3' CCCAGAAGAGAGTCCCCAAGTG	33286	GAGAA AG T
	A	TCACT ACT CTT CTGGG		
		AGTGA TGA GAA GACCC		
		ACCCC GA _		
GAM1103	LOC91759	3' CCCAGAGACACCCAGTTTCTCA	33303	AGC__
	GTG	CACTGAGAACT TTTCTGGG		
		GTGACTCTTTGA AGAGACCC		
		CCCAC		
GAM1104	MGC15854	5' ACACCATCGGGGACCGAGGACC	29642	_ _ C C
		GGTC TCG TCCCCGA GG GT		
		CCAG AGC AGGGGCT CC CA		
		G C A A		
GAM1105	COPA	5' TCACCTGCTAGTAGGACG	10591	A_
		CGTC GCTGGCAGGTGA		
		GCAG TGATCGTCCACT		
		GA		
GAM1105	FOXD1	5' CCTCAGCTGACGGGGCA	10779	A GC
		TGCC CGTCAGCTG AGG		
		ACGG GCAGTCGAC TCC		
		G _		
GAM1105	GYG	3' TTCAGAAGCAGACATGGCA	10340	C A GGCAGG
		TGCCA GTC GCT TGAA		
		ACGGT CAG CGA ACTT		
		A A AG__		
GAM1105	PTPRF	3' TCATAAACCAATGTGGCA	8724	CAGC CAG
		TGCCACGT TGG GTGA		
		ACGGTGTA ACC TACT		
		_____ AAA		
GAM1105	PTPRF	3' TCATAAACCAATGTGGCA	28198	CAGC CAG
		TGCCACGT TGG GTGA		
		ACGGTGTA ACC TACT		
		_____ AAA		
GAM1105	RARA	3' CACCTGCCCTCCCGGGCA	6686	A TC CT
		TGCC CG AG GGCAGGTG		

ACGG GC TC CCGTCCAC
 _ CC _
 GAM1105 SGK 3' CCGCCAGCTGACAGGACA 12138 _ AC A
 TG CC GTCAGCTGGC GG
 || || ||||| ||
 AC GG CAGTCGACCG CC
 A A_ _
 GAM1105 ATP9A 3' CTTACCTGCCACCTCGT 31081 TC C
 ACG AG TGGCAGGTGAAG
 ||| || ||||| |||||
 TGC TC ACCGTCCACTTC
 _ C
 GAM1105 C20orf59 3' CACCTGCCAGCGGGCTCGGC 22623 AC A
 GCC GTC GCTGGCAGGTG
 ||| ||| ||||| |||||
 CGG CGG CGACCGTCCAC
 CT G
 GAM1105 FLJ31300 3' TCACCTGCCAGCCATGGCA 29463 CGTCA _
 TGCCA GCTGG CAGGTGA
 |||| |||| |||||
 ACGGT CGACC GTCCACT
 AC_ C
 GAM1105 GGA2 3' CTTGCCAGCTGACGTCACA 28920 CC
 TG ACGTCAGCTGGCAGG
 || ||||| |||||
 AC TGCAGTCGACCGTTC
 AC
 GAM1105 GGA2 3' CTTGCCAGCTGACGTCACA 17399 CC
 TG ACGTCAGCTGGCAGG
 || ||||| |||||
 AC TGCAGTCGACCGTTC
 AC
 GAM1105 HSJ001348 3' CTTACCCACCAGCTGGC 31132 CA
 GTCAGCTGG GGTGAAG
 ||||| |||||
 CGGTCGACC CCACTTC
 AC
 GAM1105 KIAA1061 3' CTTACCTACTGACATG 35266 C CTGGC
 CA GTCAG AGGTGAAG
 || |||| |||||
 GT CAGTC TCCACTTC
 A A_
 GAM1105 MGC16386 3' TCACTGGCTGATGCAGCA 27960 CA GGCA
 TGC CGTCAGCT GGTGA
 ||| ||||| |||||
 ACG GTAGTCGG TCACT
 AC _
 GAM1105 MGC2835 3' ATCCCAGCTAACGTGGCA 23501 C CA
 TGCCACGT AGCTGG GGT
 ||||| ||||| |||

ACGGTGCA TCGACC CTA
 A _
 GAM1105 PALM 3' CACCTGCCAGCTCTACTGGGC 8436 ACGTC_
 GCC AGCTGGCAGGTG
 ||| |||||
 CGG TCGACCGTCCAC
 GTCATC
 GAM1105 VMP1 3' TTATACCAGCTGAATGGCA 25206 CG CAG
 TGCCA TCAGCTGG GTGA
 |||| ||||| |||
 ACGGT AGTCGACC TATT
 A_ A_
 GAM1105 LOC147299 3' TCACCTGCTCACGGGCA 38333 A CAGCT
 TGCC CGT GGCAGGTGA
 ||| ||| |||||
 ACGG GCA TCGTCCACT
 _ C_
 GAM1105 LOC147429 3' TCTGCCAGCCAAGTGGCA 38339 GTCA
 TGCCAC GCTGGCAGG
 |||| |||||
 ACGGTG CGACCGTCT
 AAC_
 GAM1105 LOC151512 5' TCACCTGCCAGGTGAGGACA 41364 _ ACG G
 TG CC TCA CTGGCAGGTGA
 || || ||| |||||
 AC GG AGT GACCGTCCACT
 A _ G
 GAM1105 LOC151525 5' TCACCTGCGCGGCACGTG 39131 CA _
 CACGT GCTG GCAGGTGA
 |||| ||| |||||
 GTGCA CGGC CGTCCACT
 _ G
 GAM1105 LOC158055 3' CTTCAGTCCGGCTGACGTGGCA 39703 CAGG
 TGCCACGTGACGTGG TGAAG
 ||||| |||||
 ACGGTGCAAGTCGGCC ACTTC
 TG_
 GAM1105 LOC255104 3' CCCACCAGCTGACAGGCA 45683 AC CA
 TGCC GTCAGCTGG GG
 ||| ||||| ||
 ACGG CAGTCGACC CC
 A_ AC
 GAM1105 LOC256364 5' TCACCTGCGGCCACGACCGGCA 45445 AC A_ G
 TGCC GTC GCTG CAGGTGA
 ||| ||| ||| |||||
 ACGG CAG CGGC GTCCACT
 C_ CAC _
 GAM1105 LOC51236 3' TCACCTGCCAGTTATGTGGC 18573 C
 GCCACGT AGCTGGCAGGTGA
 ||||| |||||

CGGTGTA TTGACCGTCCACT

GAM1106	PALM	3'	CACTCCCCCGAACCA	8437	C A
			TGGTTCGGGGGG GG TG		
			ACCAAGCCCCCC TC AC		
GAM1107	APM1	3'	CAGTCCTGGGGAGCTTCACA	11207	CAACA A_
			TGTG CT CCAGGACTG		
			ACAC GA GGTCTGAC		
			TTC_ GG		
GAM1107	BAIAP3	3'	TCAGTCCTGCCAGCAGCCGCA	10036	CAACA AC
			TGTG CT CAGGACTGA		
			ACGC GA GTCCTGACT		
			CGAC_ CC		
GAM1107	CD1D	3'	CAGTCCTGGTCTGCTCA	38790	T AACT
			TG GCA ACCAGGACTG		
			AC CGT TGGTCCTGAC		
			T C_		
GAM1107	CDS2	3'	TCTGGAAGACAGTGTGCCCCA	9910	T A_
			TG GCAACACT CCAGG		
			AC CGTTGTGA GGTCT		
			C CAGAA		
GAM1107	DGKI	3'	TCATTGGAATGTTGCACA	11081	CTA _
			TGTGCAACA CCAG GA		
			ACACGTTGT GGTT CT		
			AA_ A		
GAM1107	FLRT2	3'	CAGTCTTGGCTGCACA	14878	ACACTA
			TGTGCA CCAGGACTG		
			ACACGT GGTCTGAC		
			C_		
GAM1107	FOX11	3'	TCAGCCCTGGTGGCCCTGCA	14475	ACA A
			TGCA CTACCAGG CTGA		
			ACGT GGTGGTCC GACT		
			CCC C		
GAM1107	GARP	3'	CAGTCCTGGTTGGGATCACA	12031	CAACA _
			TGTG CTA CCAGGACTG		
			ACAC GGT GGTCTGAC		
			TAG_ T		
GAM1107	RNMT	3'	CCATGTAGACATGTTGCACA	9883	_ CA
			TGTGCAACA CTAC GG		

ACACGTTGT GATG CC
 ACA TA
 GAM1107 SPHK2 3' TCAGTCCTGACGCTTGCCA 21314 T CACTAC
 TG GCAA CAGGACTGA
 || ||| |||||
 AC CGTT GTCCTGACT
 _ CGCA_
 GAM1107 C20orf20 3' TCAGCCCTGGTGGCGGCA 20247 AACA A
 TGC CTACCAGG CTGA
 ||| ||||| |||
 ACG GGTGGTCC GACT
 GC_ C
 GAM1107 C5orf6 3' TCTTGAGTAGAGTTGCACA 18706 A _
 TGTGCAAC CTAC CAGGA
 ||||| ||| |||
 ACACGTTG GATG GTTCT
 A A
 GAM1107 CAP350 3' TCAGTGGGCAGGGTTGCACA 16772 A A AGG
 TGTGCAAC CT CC ACTGA
 ||||| || |||
 ACACGTTG GA GG TGACT
 G C G_
 GAM1107 COTL1 3' TCAGTCCTGCGTCTGCAC 42468 AACT _
 GTGCA AC CAGGACTGA
 ||| || |||||
 CACGT TG GTCCTGACT
 C_ C
 GAM1107 FEM-2 3' CAGTCCTGGTCGGCCACA 16007 _ AACACT
 TGTG C ACCAGGACTG
 ||| | |||||
 ACAC G TGGTCCTGAC
 C GC_
 GAM1107 FLJ10815 3' CAGTCCTGGCAGTGCCGT 20169 AA A
 GC CACT CCAGGACTG
 || ||| |||||
 TG GTGA GGTCTGAC
 CC C
 GAM1107 FLJ11783 3' TCAGCCAGTGGCGTTGCGCA 24366 A CA A
 TGTGCAAC CTAC GG CTGA
 ||||| ||| |||
 ACGCGTTG GGTG CC GACT
 C A_ _
 GAM1107 FLJ20105 5' TCAGTCTTTGCATGCTGCTCA 19210 T A CTACC
 TG GCA CA AGGACTGA
 || ||| || |||||
 AC CGT GT TTCTGACT
 T C ACGT_
 GAM1107 FLJ20477 5' TCAATCCTGGTAGCAACAC 19504 CAACA C
 GTG CTACCAGGA TGA
 ||| ||||| |||

		CAC GATGGTCCT ACT	
		AAC__ A	
GAM1107 FLJ21736	3'	CAGTCCTGGCCCCTGCACA 24458	ACACTA
		TGTGCA CCAGGACTG	
		ACACGT GGCCTGAC	
		CCCC__	
GAM1107 FLJ22009	3'	TCAGAGCCAATGTTGTACA 30245	CTACCA A_
		TGTGCAACA GG CTGA	
		ACATGTTGT CC GACT	
		AA__ GA	
GAM1107 FLJ22419	5'	CAGTCCTGATGTCACA 24007	CA CTAC
		TGTG ACA CAGGACTG	
		ACAC TGT GTCCTGAC	
		__ A__	
GAM1107 H11	3'	TCTTGATGAAAATGTTGCACA 15693	C__ C
		TGTGCAACA TA CAGGA	
		ACACGTTGT GT GTTCT	
		AAAA A	
GAM1107 HEYL	3'	CAGTGGGACCAGTGTGCCA 15928	T A__ AGG
		TG GCAACACT CC ACTG	
		AC CGTTGTGA GG TGAC	
		_ CCA G__	
GAM1107 KIAA0016	3'	CATGTGCTAATGTTGCACA 16530	CTACC G _
		TGTGCAACA AG AC TG	
		ACACGTTGT TC TG AC	
		AA__ G T	
GAM1107 PRO1048	3'	TCAGTCCTGATTTGTCTGCCA 20561	T _ CTAC
		TG GCA ACA CAGGACTGA	
		AC CGT TGT GTCCTGACT	
		_ C TTA_	
GAM1107 TREX1	5'	TCACGGTGATGTTGCACA 27340	C AG
		TGTGCAACA TACC GA	
		ACACGTTGT GTGG CT	
		A CA	
GAM1107 TREX1	5'	TCACGGTGATGTTGCACA 27347	C AG
		TGTGCAACA TACC GA	
		ACACGTTGT GTGG CT	
		A CA	
GAM1107 LOC129080	3'	TCAGTCCTGGCACCATGCACA 28541	ACACTA
		TGTGCA CCAGGACTGA	

	ACACGT GGCCTGACT	
	ACCAC_	
GAM1107 LOC143785 3'	CAAGCTTTGTAGTGGTTGCACA 37632	_ C AC
	TGTGCAAC ACTAC AGG TG	
	ACACGTTG TGATG TTC AC	
	G T GA	
GAM1107 LOC146714 5'	CAGCCCTAGCATGTTGTTGCAT 40719	_ TACC_ A
A	TGTGCAACA C AGG CTG	
	ATACGTTGT G TCC GAC	
	T TACGA C	
GAM1107 LOC149301 3'	TCAGTCTTCAGATGTTACATA 38692	C _ ACC
	TGTG AACA CT AGGACTGA	
	ATAC TTGT GA TTCTGACT	
	A A C_	
GAM1107 LOC151277 5'	TCTATAGAATGTTGCACA 39094	_ CC
	TGTGCAACA CTA AGG	
	ACACGTTGT GAT TCT	
	AA A_	
GAM1107 LOC221486 5'	CCGGGACAGTGTGTACA 43742	A_ A
	TGTGCAACACT CC GG	
	ACATGTTGTGA GG CC	
	CA G	
GAM1107 LOC254205 5'	TCAGCCCTGCGGTCCTGCCGCG 46219	AA CT _ A
CA	TGTGC CA ACC AGG CTGA	
	ACGCG GT TGG TCC GACT	
	CC CC CG C	
GAM1108 KCNJ5 3'	CTCAGAGTGCTTCTAATCA 6587	CG G CG C
	TGA TAGAAG C ACTC GAG	
	ACT ATCTTC G TGAG CTC	
	A_ _ _ A	
GAM1108 FLJ10352 3'	GAGAGCCATTCTATGTCA 25826	_ CGA
	TGACGTAGAA GGC CTC	
	ACTGTATCTT CCG GAG	
	A A_	
GAM1108 KIAA0254 3'	CTCAGATCCTCCTTCTAC 16506	CC C C
	GTAGAAGG GA TC GAG	
	CATCTTCC CT AG CTC	
	TC _ A	
GAM1108 N4BP3 3'	TCTCGGAGCTGGATCCCCGTCA 32938	TA AGG A
	TGACG GA CCG CTCCGAGA	

ACTGC CT GGT GAGGCTCT
 CC A__ C
 GAM1109 LAMB1 5' AAGAAAGGGCAGGCGGCTCGGC 8072 G CAGACGGA
 G CG CGAGCCGCC TCTT
 || ||||| ||||
 GC GCTCGGCGG AGAA
 G ACGGGAA_
 GAM1109 LOC90719 5' CCGAGCGCGGGCGGCTCCCCG 31947 C AGA__
 CGG GAGCCGCC CGG
 ||| ||||| |||
 GCC CTCGGCGGG GCC
 C CGCGA
 GAM1110 CYFIP2 5' GCGCAGCGGAGCGGGGCAGAG 36439 C G _ A
 CTTTGCCCC G TTT CT CGC
 ||||| | ||| |||
 GAGACGGGG C AGG GA GCG
 _ G C C
 GAM1110 RAI14 3' GCACAGAAATGCTGCAGAGTA 17846 CCCC G AC
 TACTTTGC GTTTCT GC
 ||||| ||||| ||
 ATGAGACG TAAAGA CG
 TCG__ CA
 GAM1110 TP63 3' GCATAGAAACCACTAGAAAGTG 9816 GCCCCC C
 TACTTT GGTTCCTA GC
 ||||| ||||| ||
 GTGAAA CCAAAGAT CG
 GATCA_ A
 GAM1110 WWOX 3' CGCAGAACTACCAGGTGGCAAA 18504 _ C _ A
 GTA TACTTTGCC CC GGT TTCT CG
 ||||| || ||| ||||| ||
 ATGAAACGG GG CCA AAGA GC
 T A TC C
 GAM1110 DKFZP434N1511 5' GCGGCTCTGCCGGGGACAAAG 43938 C TTCTA
 CTTTG CCCC GGT CGC
 ||||| ||||| |||
 GAAAC GGGGCCG GCG
 A TCTCG
 GAM1111 ATP2C1 3' ACTTTGATATCATATTCCT 15717 C TTCT
 AGGAA ATGATATT GT
 ||||| ||||| ||
 TCCTT TACTATAG CA
 A TTT_
 GAM1111 GNRHR 5' ACAGAAAAAGTTCCTA 5982 ATGATA
 TAGGAAC TTTTCTGT
 ||||| ||||| |||||
 ATCCTTG AAAAGACA
 A____
 GAM1111 MUC3B 5' TACAGAAACCTCATCCCT 45256 AAC TAT
 AGG ATGA TTTCTGTA
 ||| ||| |||||

			TCC TACT AAAGACAT		
			C__ CC_		
GAM1111	POLS	3'	ACAGGTACCATGTTCC	13863	A TTT
			GGAACATG TAT CTGT		
			CCTTGTAC ATG GACA		
			C ____		
GAM1111	KIAA1161	5'	ACAGAGCCATCATCATGTTCC	39745	ATT__
			GGAACATGAT TTCTGT		
			CCTTGTACTA GAGACA		
			CTACC		
GAM1111	KLHL6	3'	TACAAATATCACGTTCTTAT	28213	A TTC
			ATAGGAAC TGATATT TGTA		
			TATTCTTG ACTATAA ACAT		
			C ____		
GAM1111	RASAL2	3'	GTACAGAAAATATCACTGT	11251	_
			ACA TGATATTTTCTGTAC		
			TGT ACTATAAAAGACATG		
			C		
GAM1111	SNAPC1	3'	GCAGACCATATCCCTAT	9056	AACAT TT
			ATAGG GATAT TCTGT		
			TATCC CTATA AGACG		
			____ CC		
GAM1111	LOC149483	3'	GTACAGAAAACCAGTTCC	38757	A ATA
			GGAAC TG TTTTCTGTAC		
			CCTTG AC AAAAGACATG		
			_ C__		
GAM1111	LOC150397	3'	ACAGAAAATATGTTCC	38957	TGA
			GGAACA TATTTTCTGT		
			CCTTGT ATAAAAGACA		

GAM1111	LOC152627	5'	ACAGAAAATAATATTCCT	39291	AC A
			AGGA ATG TATTTTCTGT		
			TCCT TAT ATAAAAGACA		
			__ A		
GAM1111	LOC219529	3'	GCAAGGATATCACACTCCTA	44672	ACA C
			TAGGA TGATATTTT TGT		
			ATCCT ACTATAGGA ACG		
			CAC _		
GAM1112	DKFZP434J193	3'	AGAGGACCAGTATTTTCATTTC	35161	C TA_____
			CATAAA TTA GGAGATGAAA TCCTCT		

		AAT CCTTTACTTT	AGGAGA	
		A	TATGACC	
GAM1112	KIAA1548	3'	TAGATTTGACTTCAACTCCGTA	21927 A ATATCC
	AA		TTTACGGAG TGAA TCTA	
			AAATGCCTC ACTT AGAT	
			A CAGTTT	
GAM1112	LOC150998	3'	TAGAGAGACCCCATCTCTG	41287 AAATA _
			CGGAGATG TC CTCTA	
			GTCTCTAC AG GAGAT	
			CCC__ A	
GAM1113	AK2	3'	GAACAACAGCAGTGTTATTGT	15075 _ TC
			ACAATAACAC GCT TGTTT	
			TGTTATTGTG CGA ACAAG	
			A CA	
GAM1113	CALM2	3'	GAACGTGCAGCATGTTGTTGTT	7480 C TCT_
			AACAATAACA GCT GTTC	
			TTGTTGTTGT CGA CAAG	
			A CTGT	
GAM1113	HMMR	3'	AACACCTTGGCTTGTTATTG	14862 C TC__
			CAATAACA GCT TGTT	
			GTTATTGT CGG ACAA	
			T TTCC	
GAM1113	HMMR	3'	AACACCTTGGCTTGTTATTG	14860 C TC__
			CAATAACA GCT TGTT	
			GTTATTGT CGG ACAA	
			T TTCC	
GAM1113	LAMP2	3'	GAACAGGGGCTGGTATT	15184 A C
			AATA CA GCTTCTGTTC	
			TTAT GT CGGGGACAAG	
			G _	
GAM1113	MTMR8	3'	AACAGGAGTAATGTTTCGTT	17741 AAT C_
			AAC AACA GCTTCTGTT	
			TTG TTGT TGAGGACAA	
			CT_ AA	
GAM1113	PTX3	3'	GAACAGAGGGACAATTGTT	8747 AACACG
			AACAAT CTTCTGTTC	
			TTGTTA GGAGACAAG	
			ACAG__	
GAM1113	CCR7	3'	AACAGAGGCTATTGT	7576 ACAC
			ACAATA GCTTCTGTT	

TGTTAT CGGAGACAA

GAM1113 CNOT7 3' AACAGAGGGTATTATTTGTT 14998 _ C G
AACAA TAA AC CTTCTGTT
||||| ||| || |||||
TTGTT ATT TG GGAGACAA
T A _

GAM1113 FLJ12363 3' GACTGTGCCTGTTATTGTT 25868 C TTCT
ACAATAACA GC GTT
||||||| || |||
TTGTTATTGT CG CAG
C TGT_

GAM1113 FLJ13912 3' AACTGAGCTTGTTATTG 23025 C CT
CAATAACA GCTT GTT
||||||| ||| |||
GTTATTGT CGAG CAA
T T_

GAM1113 FLJ20340 3' GAACAGATCAGTTGTTGT 19396 ACGCT
ACAATAAC TCTGTTC
||||||| |||||
TGTTGTTG AGACAAG
ACT_

GAM1113 FLJ21240 3' GAACAGAAGTTTAAGTTATTGT 24279 AC_
T AACATAAC GCTTCTGTTC
||||||| |||||
TTGTTATTG TGAAGACAAG
AATT

GAM1113 FLJ23022 3' GAACAGGAAGTGCCTTGT 24647 TAA GC
ACAA CAC TTCTGTTC
||| ||| |||||
TGTT GTG AGGACAAG
CC_ A_

GAM1113 KIAA0748 3' AACAGAAGTTGATTTTGT 16698 TAA C
AACAA CA GCTTCTGTT
||||| || |||||
TTGTT GT TGAAGACAA
TTA _

GAM1113 MCM10 3' GAACAGAGGGTATCATTG 20594 AAC G
CAAT AC CTTCTGTTC
||||| || |||||
GTTA TG GGAGACAAG
CTA _

GAM1113 MGC15438 3' GAACAGAAACGGATTATGTT 26693 A CA C
AACAA TAA CG TTCTGTTC
||||| ||| || |||||
TTGT ATT GC AAGACAAG
_ AG A

GAM1113 MGC22014 3' AACAGGAGTGATGTCATTTC 32213 C A _
A AAT ACA CGCTTCTGTT
| ||| ||| |||||

			C TTA TGT GTGAGGACAA		
			T C A		
GAM1113	PMAIP1	3'	AACAGTTCAGTGCATTGTTGTT 22098	CA	T__
			AACAATAA CGCT CTGTT		
			TTGTTGTT GTGA GACAA		
			AC CTT		
GAM1113	SSR3	3'	GAACAGAAGCTTAATGTT 13971	A	CAC
			AACA TAA GCTTCTGTTC		
			TTGT ATT CGAAGACAAG		
			A ____		
GAM1113	TBX21	3'	GAACAGAAACAGTGTTATT 14996	GC	_
			AATAACAC TTCTGTTC		
			TTATTGTG AAGACAAG		
			ACA		
GAM1113	LOC58489	3'	GAACAGAAGAGTCCTCTGTT 35902	ATAAC	G
			AACA AC CTTCTGTTC		
			TTGT TG GAAGACAAG		
			CTCC_ A		
GAM1113	LOC92267	3'	GACTGTGCCTGTTATTGTT 34055	C	TTCT
			AACAATAACA GC GTT		
			TTGTTATTGT CG CAG		
			C TGT_		
GAM1113	LOC92482	5'	GAACAACGTGGTTATTGT 34432	A	TTC
			ACAATAAC CGC TGTTC		
			TGTTATTG GTG ACAAG		
			_ CA_		
GAM1114	GPRK7	3'	ATAAACATCCATGACATC 29226	C	_
			GAT TCATGGAT TTTAT		
			CTA AGTACCTA AAATA		
			C C		
GAM1114	SLC12A7	3'	AATAAAATCCTATGAAATC 13372	C	_
			GAT TCAT GGATTTTATT		
			CTA AGTA CCTAAAATAA		
			A T		
GAM1114	SLC4A7	3'	AAATGTAATCATCCCAAAGATC 9667	CAT	TTT
			GATCT GGAT ATTACATTT		
			CTAGA CCTA TAATGTAAA		
			AAC C__		
GAM1114	KIAA0391	3'	AAATGTAATAAAATTTGAGA 16134	TG	
			TCTCA GATTTTATTACATTT		

AGAGT TTAAAATAATGTAAA

GAM1114 KIAA1884 3' AAATGTAATAAAATGTAT 36289 G
ATG ATTTTATTACATTT
||| |||||||||
TAT TAAAATAATGTAAA
G

GAM1114 PP1201 3' AAATGTAATAAAATTTATG 22709
CATGGATTTTATTACATTT
|||||||||||
GTATTTAAAATAATGTAAA

GAM1114 PRO0659 3' AAATGCAATGTGCTGCCCTGAG 15404 T ATTT_ A
ATC GATCTCA GG TATT CATTT
||||| || ||| ||||
CTAGAGT CC GTAA GTAAA
C GTCGT C

GAM1114 LOC148824 3' AAATGTAGATGCCTCCATGAGT 40905 T TTTTA
TC GA CTCATGGA TTACATTT
|| ||||| |||||
CT GAGTACCT GATGTAAA
T CCGTA

GAM1114 LOC203286 5' AAATGTAGACCTCCATGA 43492 TTTTA
TCATGGA TTACATTT
||||| |||||
AGTACCT GATGTAAA
CCA__

GAM1114 LOC221543 3' GTGATAAATATCCATGAAATC 45014 C _
GAT TCATGGAT TTTATTAC
||| ||||| |||||
CTA AGTACCTA AAATAGTG
A T

GAM1114 LOC257596 3' GTGATAAATATCCATGAAATC 46754 C _
GAT TCATGGAT TTTATTAC
||| ||||| |||||
CTA AGTACCTA AAATAGTG
A T

GAM1115 ITGA3 3' ATCCAGCCAGACCCCA 7964 C CTAGCT
TGG GGTCT GCTGGAT
||| |||| |||||
ACC CCAGA CGACCTA
_ C__

GAM1115 ITGA3 3' ATCCAGCCAGACCCCA 12007 C CTAGCT
TGG GGTCT GCTGGAT
||| |||| |||||
ACC CCAGA CGACCTA
_ C__

GAM1115 PTEN 5' CATCCAGCAGCCGCCGC 5851 CTCTA
GCGGT GCTGCTGGATG
|||| |||||||

			CGCCG	CGACGACCTAC		
			C_____			
GAM1115	BSPECV	5'	CATCCAGCAGCTCCTCATCCCC	18748	C	TCTCT_
	A		TGG GG AGCTGCTGGATG			
			ACC CC TCGACGACCTAC			
			_ TACTCC			
GAM1115	CAPN6	3'	TCACCCAGCAGCCAGAGCCG	15571	T	A A
			CGG CTCT GCTGCTGG TGA			
			GCC GAGA CGACGACC ACT			
			_ C C			
GAM1115	HRD1	3'	TCACCCAGCAGCCACTGCC	34474	CTCTA	A
			GGCGGT GCTGCTGG TGA			
			CCGTCA CGACGACC ACT			
			C_____ C			
GAM1115	KIAA0293	3'	CATCAAAGTAGAGACCCCA	30394	C	CTGCTG
			TGG GGTCTCTAG GATG			
			ACC CCAGAGATC CTAC			
			_ AAA_____			
GAM1115	KIAA0712	5'	TCATCCAGCAGCTCCCCCACC	16266	C	TCTCT
	A		TGG GG AGCTGCTGGATGA			
			ACC CC TCGACGACCTACT			
			A CCCC_			
GAM1115	KIAA0889	3'	CACCCACCAGAGACTGCCA	17675	AGCT C	A
			TGGCGGTCTCT G TGG TG			
			ACCGTCAGAGA C ACC AC			
			_____ C C			
GAM1115	KIAA1853	3'	CCATGGGGCTAGAGACTGCCA	34384	GC_	
			TGGCGGTCTCTAGCT TGG			
			ACCGTCAGAGATCGG ACC			
			GGT			
GAM1115	MGC1842	5'	CATCCAGCAGCTCTACC	32686	CTCT	
			GGT AGCTGCTGGATG			
			CCA TCGACGACCTAC			
			TC_			
GAM1115	MGC20460	5'	CCCAGCTAGAGACCCCA	27588	C	CT
			TGG GGTCTCTAGCTG GG			
			ACC CCAGAGATCGAC CC			
			_ _			
GAM1115	MIDORI	3'	CACCCAGCAGCAGACCAACCA	36527	C_	CTA A
			TGG GGTCT GCTGCTGG TG			

ACC CCAGA CGACGACC AC
 AA ____ C
 GAM1115 PRO2533 3' CATCCAGCAGCCAAGAC 20701 CTA
 GTCT GCTGCTGGATG
 |||| |||||
 CAGA CGACGACCTAC
 AC_
 GAM1115 ZNF384 3' TCATCCAGCAGCCTCCCCTCC 28546 C TCTCTA
 GG GG GCTGCTGGATGA
 || || |||||
 CC CC CGACGACCTACT
 T CCTC_
 GAM1115 LOC147976 5' TCATAGTGCCAGAGACACCA 38428 CG A T _
 TGG GTCTCT GC GCTG GA
 || |||| || ||||
 ACC CAGAGA CG TGAT CT
 A_ C _ A
 GAM1115 LOC153565 5' CACCAGGACTAAAGGCCGCCA 39402 C CTG A
 TGGCGGTCT TAG CTGG TG
 ||||| || ||||
 ACCGCCGA ATC GACC AC
 A AG_ _
 GAM1115 LOC202908 5' CCACCGGTCCCAGAACCCGCCA 42995 TC A__ C
 TGGCGG TCT GCTG TGG
 |||| || ||||
 ACCGCC AGA TGGC ACC
 CA CCC C
 GAM1115 LOC222057 5' CCACCAGTCCCAGAACCCGCCA 44571 TC A__ C
 TGGCGG TCT GCTG TGG
 |||| || ||||
 ACCGCC AGA TGAC ACC
 CA CCC C
 GAM1115 LOC255975 5' CCACCAGTCCCAGAACCCGCCA 45888 TC A__ C
 TGGCGG TCT GCTG TGG
 |||| || ||||
 ACCGCC AGA TGAC ACC
 CA CCC C
 GAM1115 LOC256878 5' CCACCAGTCCCAGAACCCGCCA 46306 TC A__ C
 TGGCGG TCT GCTG TGG
 |||| || ||||
 ACCGCC AGA TGAC ACC
 CA CCC C
 GAM1116 HBP1 3' TCGTGTGACCATAAGATACTGA 14564 C A ATG
 TCAGTGTC TATG TCA ACGA
 ||||| |||| ||||
 AGTCATAG ATAC AGT TGCT
 A C G_
 GAM1116 PSR 3' CATCATCATAGAGACTGA 32500 G C CA
 TCAGT TC TATGAT ATG
 |||| || |||| ||

		AGTCA AG ATACTA TAC		
		G _ C_		
GAM1117	KIAA1841	3' CAAACTATAACCATATAATA 39025	T _	
		TATTATATG TTG AGTTTG		
		ATAATATAC AAT TCAAAC		
		C A		
GAM1117	LOC150468	5' AAACAAACCCAAATATTAA 38974	T A	
		TTA ATGTTTG GTTTGTTT		
		AAT TATAAAC CAAACAAA		
		_ C		
GAM1117	LOC54557	3' AAACAAACTCAAAACATA 36054	_	
		TATGTTT GAGTTTGTTT		
		ATACAAA CTCAAACAAA		
		A		
GAM1118	SULT1C1	3' AACAAATGTCAGTGTTAAA 6718	A C	
		TTTAACAT TGATATT GTT		
		AAATTGTG ACTGTAA CAA		
		_ _		
GAM1118	CXorf1	3' AACGAATTGCATGCATGTTGAA 11052	_ AT	
		TTTAACAT ATG ATTCGTT		
		AAGTTGTA TAC TAAGCAA		
		CG GT		
GAM1118	KIAA1211	3' GAATGATCACTATGTTAAA 34164	_ _	
		TTTAACATA TGAT ATTC		
		AAATTGTAT ACTA TAAG		
		C G		
GAM1118	SH3BGRL	3' AATGTTTATGATATGTTAAA 31022	G TT	
		TTTAACATAT ATA CGTT		
		AAATTGTATA TAT GTAA		
		G TT		
GAM1118	LOC221143	3' AACGATGTTTATATGTTAAG 44940	TAT	
		TTTAACATATGA TCGTT		
		GAATTGTATATT AGCAA		
		TGT		
GAM1119	COL6A1	3' AAACCCTGTCTCCACCCCTC 7583	AT AAC _	
		GAG GT GGGG ACAGGGTTT		
		CTC CA CCCT TGTCCCAAA		
		CC _ CC		
GAM1119	IL15RA	3' AAACCCTGCCCGAATCTT 7945	GTAA AA	
		GAGAT CGGG CAGGGTTT		

		TTCTA GCCC GTCCCAAA	
		A__ C_	
GAM1119	CAMKK1	3' AAACCCGGATCCCGCTGCATCT 26062	A ACA
	C	GAGATGTA CGGGA GGGTTT	
		CTCTACGT GCCCT CCCAAA	
		C AGG	
GAM1119	KIAA1399	3' AAACCCTGCCCCAATGCACCT 34795	A AC AA
		AG TGTA GGG CAGGGTTT	
		TC ACGT CCC GTCCCAAA	
		C AA C_	
GAM1119	LOC153937	5' AAACCCTGCTACTACTCCTCT 39442	AT ACG AA
		AGAG GTA GG CAGGGTTT	
		TCTC CAT TC GTCCCAAA	
		CT CA_ _	
GAM1119	LOC222234	5' AACCCCTGACTTACGTCTC 45238	CGGGAA
		GAGATGTAA CAGGGTT	
		CTCTGCATT GTCCCAA	
		CA_	
GAM1119	LOC255565	3' AAACCCGAAACCGTTACATCT 45586	GAACA
		AGATGTAACGG GGGTTT	
		TCTACATTGCC CCCAAA	
		AAAG_	
GAM1120	FGF5	3' ACTAGTAAACATATGTTTCCTAA 10769	_ CA_
		TTAGGAAC TATGTT TGGT	
		AATCCTTG ATACAA ATCA	
		T ATG	
GAM1120	FGF5	3' ACTAGTAAACATATGTTTCCTAA 26996	_ CA_
		TTAGGAAC TATGTT TGGT	
		AATCCTTG ATACAA ATCA	
		T ATG	
GAM1120	PCSK2	3' GATACCATACTCATTTCTAA 8457	ACT TTC
		TTAGGA ATG ATGGTATC	
		AATCTT TAC TACCATAG	
		_ TCA	
GAM1120	PDGFRA	3' GATACTTACATGTTCC 12884	T TCAT
		GGAAC ATGT GGTATC	
		CCTTG TACA TCATAG	
		_ T_	
GAM1120	FLJ10996	3' CGTGTAACACAGTTCCTA 21127	A _
		TAGGAACT TGTT CATG	

		ATCCTTGA ACAA GTGC	
		C AAT	
GAM1120	LOC146713 3'	GGATACCAGCTCAGTTCC 40715	AT TCA
		GGA ACT GT TGGTATCC	
		CCTTGA CG ACCATAGG	
		CT _	
GAM1120	LOC150271 3'	GACACCATTCAAGTTCTTAA 41170	ATG TTC A
		TTAGGAACT ATGGT TC	
		AATTCTTGA TACCA AG	
		CT _ C	
GAM1120	LOC199926 3'	ATCATGAACACAATTCTAA 43260	ACTA
		TTAGGA TGTTTCATGGT	
		AATCTT ACAAGTACTA	
		AAC _	
GAM1120	LOC202316 3'	ATCATGAACACAATTCTAA 43425	ACTA
		TTAGGA TGTTTCATGGT	
		AATCTT ACAAGTACTA	
		AAC _	
GAM1121	ADAMTS1 3'	AAAACTTCAGATTGTTCA 13850	GT
		TG CGATCTGAAGTTTT	
		AC GTTAGACTTCAAAA	
		TT	
GAM1121	ATP7B 3'	TAAAACTTTTAGGACCAT 5508	GATCT
		ATGGTC GAAGTTTTA	
		TACCAG TTTCAAAAT	
		GAT _	
GAM1121	BANK 3'	AAAACTTCAGATTTC A 19623	TC
		TGG GATCTGAAGTTTT	
		ACT TTAGACTTCAAAA	
		_	
GAM1121	KLHL4 3'	TAAAACTTCAAATATCTCACCA 21197	C_ C_
		TGGT GAT TGAAGTTTTA	
		ACCA CTA ACTTCAAAAT	
		CT TAA	
GAM1121	TEB4 3'	TAAAACTTCAAATAAAACCA 30428	CG_ C
		TGGT AT TGAAGTTTTA	
		ACCA TA ACTTCAAAAT	
		AAA A	
GAM1122	CALU 3'	AGCTTCTGGTTTCACATG 6882	AT T
		CATG TGAG CCAGAAGCT	

		GTAC ACTT GGTCTTCGA	
		— T	
GAM1122	RAF1	3' AGCTTCTGGAGGAATGCATGTC 39245	ATTGAG
	A	TGACATG TCCAGAAGCT	
		ACTGTAC AGGTCTTCGA	
		GTAAGG	
GAM1122	DKFZp761P1010	3' AGCTTCTAATTTTCAATCA 20477	TCC_
		TGATTGAG AGAAGCT	
		ACTAACTT TCTTCGA	
		TTAA	
GAM1122	HTMP10	3' CTGGCTCAATCATGTCA 27049	T
		TGACATGATTGAG CCAG	
		ACTGTACTAACTC GGTC	
		—	
GAM1122	KIAA0471	3' AGCTTCTGGAAGGCCATGTT 16907	ATTGAG
		GACATG TCCAGAAGCT	
		TTGTAC AGGTCTTCGA	
		CGGA_	
GAM1122	KIAA1676	3' AGCTTCTGGTGCTTAACCACAT 44726	CA A _
	C	GA TG TTGAGT CCAGAAGCT	
		CT AC AATTCG GGTCTTCGA	
		AC C T	
GAM1122	LOC115294	3' AGCTTCTAGCATCAGATCA 36143	CA TGA CC
		TGA TGAT GT AGAAGCT	
		ACT ACTA CG TCTTCGA	
		AG _ A_	
GAM1122	LOC121536	3' CTTCTGAGTACTCAATCAATCA 36664	CA C_
		TGA TGATTGAGT CAGAAG	
		ACT ACTAACTCA GTCTTC	
		A_ TGA	
GAM1122	LOC148936	3' AGCCTCTGTAATCATGT 40929	AGTC A
		ACATGATTG CAGA GCT	
		TGTACTAAT GTCT CGA	
		_ C	
GAM1122	LOC148938	3' AGCCTCTGTAATCATGT 40922	AGTC A
		ACATGATTG CAGA GCT	
		TGTACTAAT GTCT CGA	
		_ C	
GAM1122	LOC152674	5' AGTGTAACCTCAATTATGTCA 41536	CCAGAA
		TGACATGATTGAGT GCT	

			ACTGTATTA	ACTCA	TGA	
			ATG			
GAM1122	LOC254100	3'	CTCCTGGACTCAAGT	GATC	46127	_ GA A
			GA CAT	TTGAGTCCAG	AG	
			CT GTG	AACTCAGGTC	TC	
			A		C	
GAM1122	LOC92249	5'	TAGCTTCTGGACTAACATC		34024	TG_
			GAT	AGTCCAGAAGCTA		
			CTA	TCAGGTCTTCGAT		
			CAA			
GAM1123	CASP2	3'	GTGAAGTTGTAAACACA		6890	CAGCA
			TGTGTT	ACAACTTCAT		
			ACACAA	TGTTGAAGTG		
			A			
GAM1123	CASP2	3'	GTGAAGTTGTAAACACA		26853	CAGCA
			TGTGTT	ACAACTTCAT		
			ACACAA	TGTTGAAGTG		
			A			
GAM1123	CASP2	3'	GTGAAGTTGTAAACACA		26858	CAGCA
			TGTGTT	ACAACTTCAT		
			ACACAA	TGTTGAAGTG		
			A			
GAM1123	CASP2	3'	GTGAAGTTGTAAACACA		26863	CAGCA
			TGTGTT	ACAACTTCAT		
			ACACAA	TGTTGAAGTG		
			A			
GAM1123	CYP8B1	3'	ATGATCATTGCTGAACTCA		10622	T CAACT
			TG GTTCAGCAA	TCAT		
			AC CAAGTCGTT	AGTA		
			T	ACT		
GAM1123	EIF1A	3'	ATGGAGTTCGTGAACACA		42720	G AAC
			TGTGTTCA C	AACTTCAT		
			ACACAAGT G	TTGAGGTA		
				C		
GAM1123	FRAP1	3'	ATGGAGGTGCTGAACACA		11403	ACAA
			TGTGTTCA	CTTCAT		
			ACACAAGTCGT	GAGGTA		
			G			
GAM1123	HMG20A	3'	ATGAAGTTACAGGCTAGCACA		20073	C AAC_
			TGTGTT AGC	AACTTCAT		

		ACACGA TCG TTGAAGTA	
		_ GACA	
GAM1123 RELN	3'	ATGAAGTTGTACAACAC 45280	CAGCA
		GTGTT ACAACTTCAT	
		CACAA TGTGAAGTA	
		CA__	
GAM1123 DCOHM	3'	ATGAAGTTGCTAGTTAACAC 25842	C AA_
		GTGTT AGC CAACTTCAT	
		CACAA TTG GTTGAAGTA	
		_ ATC	
GAM1123 HTGN29	3'	ATGAAGTTGTTTGTATACATA 21432	TCA _
		TGTGT GCAA CAACTTCAT	
		ATACA TGTG GTTGAAGTA	
		TA_ T	
GAM1123 KIAA1728	3'	ATGAAGTTCCTGTGAACAT 33949	G AC
		GTGTTCA CA AACTTCAT	
		TACAAGT GT TTGAAGTA	
		_ CC	
GAM1123 LOC145483	3'	AAGTAATTGCCATGAACACA 37879	__ CA
		TGTGTTCA GCAA ACTT	
		ACACAAGT CGTT TGAA	
		AC AA	
GAM1123 LOC145757	5'	AAGTTGTTGCTTTGGAAT 37967	__
		GTTC AGCAACAACTT	
		TAAG TCGTTGTTGAA	
		GTT	
GAM1123 LOC153883	3'	ATGAAGTTGTCTGTACA 39429	T CA
		TGT CAG ACAACTTCAT	
		ACA GTC TGTGAAGTA	
		T _	
GAM1123 LOC166793	5'	AAGTAATGCTGGACACA 29804	ACA
		TGTGTT CAGCA ACTT	
		ACACAGGTCGT TGAA	
		AA_	
GAM1123 LOC219699	5'	ATGAGGAGACCCTGAACACA 46100	CAACAA
		TGTGTT CAG CTTCAT	
		ACACAAGTC GGAGTA	
		CCAGA_	
GAM1123 LOC51054	5'	GAGTTTGCTGAAAACA 18043	G CA
		TGT TTCAGCAA ACTT	

		ACA AAGTCGTT TGAG	
		A _	
GAM1123	LOC51691 3'	ATGAAAGTAATATGAACACA 18291	GCAACA _
		TGTGTTCA ACTT CAT	
		ACACAAGT TGAA GTA	
		ATAA_ A	
GAM1123	LOC90786 5'	TGAAGTTGTGGTAACA 32015	CA A
		TGTT GC ACAACTTCA	
		ACAA TG TGTGAAGT	
		_ G	
GAM1123	LOC92465 5'	ATGAAGTGAAGTGAACACA 34393	G AA A
		TGTGTTCA C CA CTTCAT	
		ACACAAGT G GT GAAGTA	
		_ AA _	
GAM1124	DDX34 3'	AACTCCTGCAATTCACGGCATC 16158	_ A TTA
		GATGCCGT AA TGT AGTT	
		CTACGGCA TT ACG TCAA	
		C A TCC	
GAM1124	EDG2 5'	GACACCTACAGCATCAGG 27669	C AA
		TCTGATGC GTA TGTT	
		GGACTACG CAT ACAG	
		A CC	
GAM1124	ICK 3'	AACTCGTTATCTAAAGCATCAG 17191	CG A TTTA
	A	TCTGATGC TA ATG AGTT	
		AGACTACG AT TAT TCAA	
		AA C TGC_	
GAM1124	LOC112687 3'	AACTTAAACATCTGTGGAACCA 36064	ATG A
		TG CCGTA ATGTTTAAGTT	
		AC GGTGT TACAAATTCAA	
		CAA C	
GAM1124	LOC220692 5'	AGACATTCAGGCATCAGA 43831	GTA
		TCTGATGCC AATGTTT	
		AGACTACGG TTACAGA	
		AC_	
GAM1125	BCL11B 3'	GCAAAACAAAAACAATT 23165	C
		AATTGTTTTTG TTTTGT	
		TTAACAAAAAC AAAACG	
		_	
GAM1125	COL4A4 3'	ACGAAACAAAGACAATTTA 5550	C
		TAAATTGTTTTTG TTTTGT	

ATTTAACAGAAAC AAAGCA

GAM1125 ENC1 3' CTTTGAAGCAAATACAATT 9699 T TGT
AATTGT TTTGCTTT GG
||||| ||||| ||
TTAACA AAACGAAG TC
T TT_

GAM1125 GPR23 3' CTATAAAGCAAAAACATTTA 30363 T T
TAAAT GTTTTTGCTTT GTGG
||||| ||||| |||||
ATTTA CAAAAACGAAA TATC

GAM1125 SLA2 3' CCCACAAGGTAGAAACAA 25942 T
TTGTTTTTGCTTT GTGGG
||||| |||||
AACAAAGATGGAA CACCC

GAM1125 SRR 3' CCCACAAAATGTAAACCCA 22476 TT _
TG TTTGC TTTTGTGGG
|| ||||| |||||
AC AAATG AAAACACCC
CC T

GAM1125 WSX1 3' CATCAAAAACAAAACAATT 11255 C _
AATTGTTTTTG TTTTG TG
||||| ||||| ||
TTAACAAAAC AAAAC AC
A T

GAM1125 BHMT 3' CCCTTAGTAACAAACACAATTT 7444 T CTT T
A TAAATTGT TTTG TTG GGG
||||| ||||| |||||
ATTTAACA AAAC GAT CCC
C AAT T

GAM1125 CCR5 3' CCCACAAAAGTACAATTTA 6184 TTTT
TAAATTGT GCTTTTGTGGG
||||| ||||| |||||
ATTTAACA TGAAAACACCC

GAM1125 CEP3 3' GCCCTGTTTGCAAAAACAATTT 13159 TTTTGT
A TAAATTGTTTTTGC GGGC
||||| ||||| |||||
ATTTAACAAAACG CCCG
TTTGT_

GAM1125 KIAA1948 3' CCCACAAAACATGAGATA 40080 _ C
TGTTTT TG TTTTGTGGG
||||| ||||| |||||
ATAGAG AC AAAACACCC
T A

GAM1125 ZNF185 3' CCCACAAAAGCAAGCATTGATT 14001 TT_
T AAATTG TTTGCTTTTGTGGG
||||| ||||| |||||

TTTAGT GAACGAAAACACCC
 TAC
 GAM1125 LOC126964 3' CCCCAGCAAGCAAAAACATTTA 36883 T _ T
 TAAAT GTTTTTGCTT TTG GGG
 |||| ||||||| ||| |||
 ATTTA CAAAAACGAA GAC CCC
 _ C _
 GAM1125 LOC150848 5' ACAAAGCATAAACAATTTA 41250 T T
 TAAATTGTTT TGCTTT GT
 ||||||| ||||| ||
 ATTTAACAAA ACGAAA CA
 T _
 GAM1125 LOC151248 3' ACAAAAACAAAAACATTTT 39083 T C
 TAAA TGTTTTTG TTTTGT
 ||| ||||||| |||||
 ATTT ACAAAAAC AAAACA
 T A
 GAM1125 LOC153222 3' TAAACAAAAACAATTTA 39367 C
 TAAATTGTTTTTG TTTTG
 ||||||||| |||||
 ATTTAACAAAAAC AAAAT
 _
 GAM1126 AK1 3' CAACCCTCCGTTCTCCT 6086 CAGA
 AGGAG GATGGAGGGTTG
 |||| |||||||||
 TCCTC TTGCCTCCCAAC
 C__
 GAM1126 ALPI 3' CAACCCCCACCCTGCCTCT 7342 GA AGA A
 AG GCAG TGG GGGTTG
 || |||| ||| |||||
 TC CGTC ACC CCCAAC
 TC CC_ _
 GAM1126 AP2B1 3' CAACCCATGAACTCTTCACTCC 6950 C__ ATGGA
 T AGGAG AGAG GGGTTG
 |||| ||| |||||
 TCCTC TCTC CCCAAC
 ACT AAGTA
 GAM1126 ATP8A2 3' CAACCCTTGGTCTACTGCT 44917 _ G
 AGCAG AGAT GAGGGTTG
 |||| ||| |||||||
 TCGTC TCTG TTCCAAC
 A G
 GAM1126 AXL 3' CAACCCTCCACCTGGTACTCC 22441 __ AGA
 GGAG CAG TGGAGGGTTG
 ||| ||| |||||||
 CCTC GTC ACCTCCAAC
 ATG C__
 GAM1126 AXL 3' CAACCCTCCACCTGGTACTCC 7420 __ AGA
 GGAG CAG TGGAGGGTTG
 |||| ||| |||||||

			CCTC GTC ACCTCCCAAC		
			ATG C__		
GAM1126	BAZ2A	3'	CAACCCACCCCTGCCCT 15117	A	AGAT A
			AGG GCAG GG GGGTTG		
			TCC CGTC CC CCCAAC		
			_ CC_ A		
GAM1126	BMP3	5'	CAACCCTCGGCTCCGCCGCC 6865	A_ A	ATG
			GG GC GAG GAGGGTTG		
			CC CG CTC CTCCCAAC		
			GC C GG_		
GAM1126	CRHR1	3'	CAGTCACCTCCTGCTCCT 10606	A T	AG GT
			AGGAGCAG GA GG G TG		
			TCCTCGTC CT CC C AC		
			_ _ A_ TG		
GAM1126	CX3CR1	3'	CAACCCTTTTGTCTGCCTCT 34975	GA	GAT
			AG GCAGA GGAGGGTTG		
			TC CGTCT TTTCCCAAC		
			TC GT_		
GAM1126	DAB2	3'	ATTATTCATCTCTCCTCC 7022	C	GG
			GGAG AGAGATGGA GT		
			CCTC TCTCTACTT TA		
			C AT		
GAM1126	EGFL4	5'	ACTGCCAGCTCTGCTCC 30960	A	AG
			GGAGCAGAG TGG GGT		
			CCTCGTCTC ACC TCA		
			G G_		
GAM1126	FBXL11	3'	CAAATTTGCACTCTGCTCC 14679	A G	G
			GGAGCAGAG TG AGG TTG		
			CCTCGTCTC AC TTT AAC		
			_ G A		
GAM1126	FLOT2	3'	CAACCCAATCCTCTGTCTCCT 10792	_	ATGGA
			AGGAG CAGAG GGGTTG		
			TCCTC GTCTC CCCAAC		
			T CTAA_		
GAM1126	FXVD6	3'	ATCACCTTCTGCTCCT 22546	AT	AG
			AGGAGCAGAG GG GGT		
			TCCTCGTCTT CC CTA		
			_ A_		
GAM1126	GFI1	3'	CAACCCTGACTGCTCCT 11768	AGA	A
			AGGAGCAG TGG GGGTTG		

		TCCTCGTC GTC CCCAAC		
		A _ _		
GAM1126 IGF2	5'	CAACCTTCCCTTCGCTCC 6214	AG AT	
		GGAGC AG GGAGGGTTG		
		CCTCG TC CCTCCAAC		
		CT _		
GAM1126 INPP1	5'	CAACCCTCGTCCTCTGCGCCT 7950	A ATG	
		AGG GCAGAG GAGGGTTG		
		TCC CGTCTC CTCCCAAC		
		G CTG		
GAM1126 L1CAM	3'	CTTTGCCATCTCTGCTCC 23430	_	
		GGAGCAGAGATGG AGGG		
		CCTCGTCTCTACC TTTC		
		G		
GAM1126 L1CAM	3'	CTTTGCCATCTCTGCTCC 6002	_	
		GGAGCAGAGATGG AGGG		
		CCTCGTCTCTACC TTTC		
		G		
GAM1126 MFRP	3'	ACCCTCCCTGCTCCT 25430	AGAT	
		AGGAGCAG GGAGGGT		
		TCCTCGTC CCTCCA		

GAM1126 NGFR	3'	CAACCCTCCCTCAGCCCCT 8330	A A AT	
		AGG GC GAG GGAGGGTTG		
		TCC CG CTC CCTCCAAC		
		C A _		
GAM1126 NGFR	3'	CAACCCTCCTATCACCTCC 8331	CA GAT	
		GGAG GA GGAGGGTTG		
		CCTC CT CCTCCAAC		
		CA AT_		
GAM1126 NRXN1	3'	CAAAATATATCTCTGCTCTT 28993	GAGGG	
		AGGAGCAGAGATG TTG		
		TTCTCGTCTCTAT AAC		
		ATAA_		
GAM1126 NRXN1	3'	CAAAATATATCTCTGCTCTT 11222	GAGGG	
		AGGAGCAGAGATG TTG		
		TTCTCGTCTCTAT AAC		
		ATAA_		
GAM1126 PCDH11X	3'	CAACCTATTTCTCTACTCTT 26788	C TGGA	
		AGGAG AGAGA GGGTTG		

		TTCTC TCTCT TCCAAC		
		A TTA_		
GAM1126	PCDH11X	3' CAACCTATTTCTCTACTCTT	26803	C TGGA
		AGGAG AGAGA GGGTTG		
		TTCTC TCTCT TCCAAC		
		A TTA_		
GAM1126	PCDH11Y	3' CAACCTATTTCTCTACTCTT	26822	C TGGA
		AGGAG AGAGA GGGTTG		
		TTCTC TCTCT TCCAAC		
		A TTA_		
GAM1126	PCTK3	3' GGCCCCCACCCTCCACTCCT	36126	CA A_ A
		AGGAG GAG TGG GGGTT		
		TCCTC CTC ACC CCCGG		
		AC CC _		
GAM1126	PPP2R5B	3' CCCACCCTCTGCTCCT	12913	AT A
		AGGAGCAGAG GG GGG		
		TCCTCGTCTC CC CCC		
		_ A		
GAM1126	PSCD4	3' CAACCCTTCCCTGTCTCCT	15036	G AGAT
		AGGA CAG GGAGGGTTG		
		TCCT GTC CTTCCCAAC		
		_ CC_		
GAM1126	PYCR1	3' ACCACCTCCTGCTCCT	34728	A T AG
		AGGAGCAG GA GG GGT		
		TCCTCGTC CT CC CCA		
		_ _ A_		
GAM1126	SLC2A3	3' ACTGTTCCCTCTGCTCCT	13816	AT G
		AGGAGCAGAG GGA GGT		
		TCCTCGTCTC CTT TCA		
		C_ G		
GAM1126	SNL	3' CAACCCTCCCTGCTAACCCT	9059	_____ AGAT
		AGG AGCAG GGAGGGTTG		
		TCC TCGTC CCTCCCAAC		
		CCAA _____		
GAM1126	TGFB3	3' CAACCCTCTCCTGTCTGCCCT	9233	A GAT_
		AGG GCAGA GGAGGGTTG		
		TCC CGTCT TCTCCCAAC		
		_ GTCC		
GAM1126	TLR5	5' CAACCAGGGACCCTCTGCCCCT	9276	A AT AG_____
		AGG GCAGAG GG GGTG		

TCC CGTCTC CC CCAAC
 C _ AGGGA
 GAM1126 UBE4A 3' CAACCCCCATGCTGCCTCC 11195 _ AG A
 GGAG CAG ATGG GGGTTG
 |||| ||| |||| |||||
 CCTC GTC TACC CCCAAC
 C G_ _
 GAM1126 ABLIM 3' AACCCCTCCTGTGTCCT 8110 G G GAT
 AGGA CA A GGAGGGTT
 |||| ||| |||||
 TCCT GT T CCTCCCAA
 _ G _
 GAM1126 ABLIM 3' AACCCCTCCTGTGTCCT 13543 G G GAT
 AGGA CA A GGAGGGTT
 |||| ||| |||||
 TCCT GT T CCTCCCAA
 _ G _
 GAM1126 C20orf110 3' CAACCCTTCTTGCCTACTCCT 38831 C AGAT
 AGGAG AG GGAGGGTTG
 |||| || |||||
 TCCTC TC CTCCCAAC
 A CGTT
 GAM1126 CALN1 3' CAACCCTTGCATTCCACCCT 25512 AGCAGA _
 AGG GATG GAGGGTTG
 || |||| |||||
 TCC TTAC TTCCCAAC
 CACC_ G
 GAM1126 CLIC2 3' CAATCTCACCTGCTCCT 6966 AGAT A_
 AGGAGCAG GG GGGTTG
 ||||| || |||||
 TCCTCGTC CC TCTAAC
 _ AC
 GAM1126 CLSTN2 3' TTTTCCATCTCCATCCT 22695 GCA
 AGGA GAGATGGAGGG
 |||| |||||
 TCCT CTCTACCTTTT
 AC_
 GAM1126 D15Wsu75e 3' CAACCCTCACCTTCCCTCC 33100 CA ATG
 GGAG GAG GAGGGTTG
 |||| ||| |||||
 CCTC TTC CTCCCAAC
 CC CA_
 GAM1126 DKFZP564L2423 3' CAACCCTTATTCCAAGTGCCT 31258 A A_ TG
 GG GCAG GA GAGGGTTG
 || |||| || |||||
 TC CGTC CT TTCCCAAC
 _ AC TA
 GAM1126 DKFZp761G0313 3' CAGAGGCCATCTCTACTACT 32739 G C AGGG
 AG AG AGAGATGG TTG
 || || ||||| |||

		TC TC TCTCTACC GAC	
		A A GGA_	
GAM1126	FER1L4	3' CAACCCTTCAATGCCTGCTCCT 24872	AGA_
		AGGAGCAG TGGAGGGTTG	
		TCCTCGTC ACTTCCCAAC	
		CGTA	
GAM1126	FLJ11000	5' CAACCCTGATTTCCTGCTTCT 20284	A TGG_
		AGGAGCAG GA AGGGTTG	
		TCTTCGTC CT TCCCAAC	
		_ TTAG	
GAM1126	FLJ12294	5' CAACCCACCTCCCGTGCCCC 24742	A GA_ T A
		GG GCA GA GG GGGTTG	
		CC CGT CT CC CCAAC	
		C GCC _ A	
GAM1126	FLJ12595	5' CAAAGTGCCCTCTGCTCCT 24557	AT AGGG
		AGGAGCAGAG GG TTG	
		TCCTCGTCTC CC AAC	
		_ GTGA	
GAM1126	FLJ13204	3' CAAAATTAATTTCTGCCCCT 24113	A GG GG
		AGG GCAGAGAT AG TTG	
		TCC CGTCTTTA TT AAC	
		C A_ AA	
GAM1126	FLJ13391	5' AACTTCTCTGCTCCT 25894	TGGAG
		AGGAGCAGAGA GGTT	
		TCCTCGTCTCT TCAA	

GAM1126	FLJ13881	3' CAACCCATTCCCTCTGCTTCT 24065	AT _
		AGGAGCAGAG GGA GGGTTG	
		TCTTCGTCTC CCT CCAAC	
		_ TA	
GAM1126	FLJ20128	5' CAACCCTCGGCTCTCTCCT 19222	C ATG
		AGGAG AGAG GAGGGTTG	
		TCCTC TCTC CTCCCAAC	
		_ GG_	
GAM1126	FLJ20489	3' GGGTTTCCATCCCCGCTGCC 19506	_ AGA G
		GG AGC GATGGAGG TT	
		CC TCG CTACCTTT GG	
		G CCC G	
GAM1126	FLJ22169	3' CAACCTTCCCTAGCCCC 23520	A AG AT
		GG GC AG GGAGGGTTG	

CC CG TC CCTTCCAAC
 C A_ _
 GAM1126 FLJ30663 3' AACTGTCATCTCTACCCT 38461 AGC AG
 AGG AGAGATGG GGTT
 ||| ||||| |||
 TCC TCTCTACT TCAA
 CA_ G_
 GAM1126 GP5 3' CAACCCCTCCTCTCTGTCCC 10816 AG T_ _
 GG CAGAGA GGAGGG TTG
 || ||||| ||||| |||
 CC GTCTCT CCTCCC AAC
 CT CT C
 GAM1126 HCCA2 5' CCCTCCTCCCTGCTCCT 33202 A T
 AGGAGCAG GA GGAGGG
 ||||| || |||||
 TCCTCGTC CT CCTCCC
 C _
 GAM1126 KIAA0237 3' CAACTTTCCCTCCCTCC 16439 CA AT
 GGAG GAG GGAGGGTTG
 ||| || |||||
 CCTC CTC CCTTTCAAC
 C_ _
 GAM1126 KIAA0285 3' CAACCCTCACCTCCTCC 16749 CA ATG
 GGAG GAG GAGGGTTG
 ||| || |||||
 CCTC CTC CTCCCAAC
 _ CCA
 GAM1126 KIAA0397 3' CGACCCACCTCTGTTCTCCT 30894 A AG
 AGGAGCAGAG TGG GGTTG
 ||||| || |||||
 TCCTTGCTCTC ACC CCAGC
 C _
 GAM1126 KIAA0427 3' CAACCTGCCCTCTGGTCC 16572 G AT A
 GGA CAGAG GG GGGTTG
 || |||| || |||||
 CCT GTCTC CC TCCAAC
 G _ G
 GAM1126 KIAA0471 3' CAACCAAGTGTCTTCTGCCCCT 16908 A _ GAG
 AGG GCAGA GATG GGTTG
 || |||| ||| |||||
 TCC CGTCT CTGT CCAAC
 C T GA_
 GAM1126 KIAA0481 3' CAACCTGTGCTCTCTGGCCCC 35567 A _ _ G
 GG GC AGAGA TG AGGGTTG
 || || |||| || |||||
 CC CG TCTCT GT TCCCAAC
 C G C G
 GAM1126 KIAA0563 3' AACTCTCCCTTCTCCT 16839 C AGAT
 AGGAG AG GGAGGGTT
 |||| || |||||

			TCCTC TC CCTCTCAA		
			T ____		
GAM1126	KIAA0978	3'	CAAAGCCATGCCTGCTCCT 34886	AG	AGGG
			AGGAGCAG ATGG TTG		
			TCCTCGTC TACC AAC		
			CG GA__		
GAM1126	KIAA1465	3'	CAACCTTCACCTACTCCT 30500	C	AGATG
			AGGAG AG GAGGGTTG		
			TCCTC TC CTTCCAAC		
			A CA__		
GAM1126	KIAA1554	3'	CAACCCTGACCTTCCCCCTCC 45608	CAGA	T ____
			GGAG GA GG AGGGTTG		
			CCTC CT CC TCCCAAC		
			CCC_ T AG		
GAM1126	KIAA1727	3'	GACCCATCTCTGCCCT 32032	A	GGA
			AGG GCAGAGAT GGGTT		
			TCC CGTCTCTA CCCAG		
			— —		
GAM1126	KIAA1909	5'	CAGAATTCATTCTGCTCC 36557	A	GGG
			GGAGCAGAG TGGA TTG		
			CCTCGTCTT ACTT GAC		
			_ AA_		
GAM1126	KIAA1944	3'	CAACCTTAGCCCTCTCCCCT 37226	AGCA	T ____
			AGG GAGA GG AGGGTTG		
			TCC CTCT CC TTCCAAC		
			C__ C GA		
GAM1126	MGC1136	3'	CAAAGGGGCCATCTCTGCCCT 23452	A	AGGG_
			AGG GCAGAGATGG TTG		
			TCC CGTCTCTACC AAC		
			GGGAA		
			—		
GAM1126	MGC13170	5'	CAACCTCGTCCTCTGCCCCT 26430	A	_ GA
			AGG GCAGAG ATG GGGTTG		
			TCC CGTCTC TGC TCCAAC		
			C C _		
GAM1126	MGC17998	3'	CAATAACATGTCTGCTCC 29602	G	GAGG
			GGAGCAGA ATG GTTG		
			CCTCGTCT TAC TAAC		
			G AA__		
GAM1126	MRPL20	3'	CAACCCTCCAGGGCTACT 19695	G	AGAGA
			AG AGC TGGAGGGTTG		

		TC TCG ACCTCCCAAC		
		A GG__		
GAM1126	OPRL1	3' CAACCCAGCCCTGCTTCT 6614	AGAT A_	
		AGGAGCAG GG GGGTTG		
		TCTTCGTC CC CCCAAC		
		__ GA		
GAM1126	PDZD2	5' CAACCCATGACTGCTCCT 39389	AG GGA	
		AGGAGCAG AT GGGTTG		
		TCCTCGTC TA CCCAAC		
		AG __		
GAM1126	PME-1	3' GGCTCCCCTGCTCCT 18232	AGAT A	
		AGGAGCAG GG GGGTT		
		TCCTCGTC CC CTCGG		
		__ -		
GAM1126	PRO0132	5' CAACATCTATCTCTGCTGCC 15368	_ GG	
		GG AGCAGAGATGGA GTTG		
		CC TCGTCTCTATCT CAAC		
		G A_		
GAM1126	SDC3	3' GGCCTTCCCTGCCCT 16088	A AGAT	
		AGG GCAG GGAGGGTT		
		TCC CGTC CCTTCCGG		
		C __		
GAM1126	SEP15	3' CAACAGATTGCCTGCTCCT 10453	A_ GGAGG	
		AGGAGCAG GAT GTTG		
		TCCTCGTC TTA CAAC		
		CG GA__		
GAM1126	SFXN5	3' AGCTCACCCCTGCTCCT 29384	AGAT A	
		AGGAGCAG GG GGGTT		
		TCCTCGTC CC CTCGA		
		__ A		
GAM1126	SKIP	3' CAACCTTCCCTCCCTACTC 28260	C A T	
		GAG AG GA GGAGGGTTG		
		CTC TC CT CCTTCCAAC		
		A C _		
GAM1126	SKIP	3' CAACCTTCCCTCCCTACTC 18597	C A T	
		GAG AG GA GGAGGGTTG		
		CTC TC CT CCTTCCAAC		
		A C _		
GAM1126	SLC38A5	5' CAACCACTCTCTGCCCCT 27295	A TG _	
		AGG GCAGAGA GAG GGTG		

TCC CGTCTCT CTC CCAAC
 C _ A
 GAM1126 SMC1L1 3' CAACCTTCCCCCTACCTCCT 35617 CAG AT
 AGGAG AG GGAGGGTTG
 |||| || |||||
 TCCTC TC CCTTCCAAC
 CA_ CC
 GAM1126 SMCR5 3' CAACCCTCCGGACTCTCC 29561 C AGA
 GGAG AG TGGAGGGTTG
 |||| || |||||
 CCTC TC GCCTCCCAAC
 _ AG_
 GAM1126 SNPH 3' CAACCCGGCCCCTCTGTCCC 16289 AG AT A_
 GG CAGAG GG GGGTTG
 || |||| || ||||
 CC GTCTC CC CCCAAC
 CT C_ GG
 GAM1126 STAT5A 5' CAACTTTTCCCTCCTCC 9126 CA AT
 GGAG GAG GGAGGGTTG
 |||| || |||||
 CCTC CTC CTTTCAAC
 _ C_
 GAM1126 SYT12 5' CAACCCTGATCCTGTCCT 45429 G A GG
 AGGA CAG GAT AGGGTTG
 |||| |||| || |||||
 TCCT GTC CTA TCCCAAC
 _ _ G_
 GAM1126 ZFP91 3' CAACCCTCCATATGGCTCT 27572 AGAG
 GGAGC ATGGAGGGTTG
 |||| |||||
 TCTCG TACCTCCCAAC
 GTA_
 GAM1126 LOC116071 3' ACCACCCTCTGCTCCT 28815 AT AG
 AGGAGCAGAG GG GGT
 ||||| || ||
 TCCTCGTCTC CC CCA
 _ A_
 GAM1126 LOC118738 3' CAACCCTGTGGCTGCCCT 37194 A AGAT G
 AGG GCAG G AGGGTTG
 || |||| | |||||
 TCC CGTC T TCCCAAC
 _ GG_ G
 GAM1126 LOC127702 3' CAACCCTCCTCCCCTGCCC 37179 A A_ T
 GG GCAG GA GGAGGGTTG
 || |||| || |||||
 CC CGTC CT CCTCCCAAC
 _ CC _
 GAM1126 LOC130644 3' CAACCTCTTCATCCTGCCCC 37304 A A _
 GG GCAG GATGGAG GGTG
 || |||| ||||| ||||

CC CGTC CTACTTC CCAAC
 C _ T
 GAM1126 LOC132166 3' CTTTCTACCTCTGCTCCT 37020 A
 AGGAGCAGAG TGGAGGG
 ||||| |||||
 TCCTCGTCTC ATCTTTC
 C
 GAM1126 LOC145761 5' CAACCTTCATTCTCTGACTCC 40582 _ TG
 GGAG CAGAGA GAGGGTTG
 ||| ||||| |||||
 CCTC GTCTCT CTTCCAAC
 A TA
 GAM1126 LOC145989 3' CAACCCTCCCTGCTAACCCT 29947 ____ AGAT
 AGG AGCAG GGAGGGTTG
 || ||||| |||||
 TCC TCGTC CCTCCCAAC
 CCAA ____
 GAM1126 LOC147071 3' AACTCTCCCTTCTCCT 36132 C AGAT
 AGGAG AG GGAGGGTT
 ||||| || |||||
 TCCTC TC CCTCTCAA
 T ____
 GAM1126 LOC148894 5' CAACCCAGCTCTCTCTGCTC 40917 T A__
 GAGCAGAGA GG GGGTTG
 ||||| || |||||
 CTCGTCTCT TC CCAAC
 C GAC
 GAM1126 LOC151068 5' CAACCCTCATCTCCCTCC 41296 CA G
 GGAG GAGATG AGGGTTG
 ||| ||||| |||||
 CCTC CTCTAC TCCAAC
 C_ _
 GAM1126 LOC152286 3' CAACCCCCCATTCCCTCC 41461 CAGA A
 GGAG GATGG GGGTTG
 ||| ||||| |||||
 CCTC TTACC CCAAC
 CC_ C
 GAM1126 LOC152915 5' CAACCCGGCACACCTGCTCCT 33268 AGA GA
 AGGAGCAG TG GGGTTG
 ||||| || |||||
 TCCTCGTC AC CCAAC
 CAC GG
 GAM1126 LOC153338 3' ATTTGGCCATCTCGCTCCT 41608 A A_
 AGGAGC GAGATGG GGGT
 ||||| ||||| |||
 TCCTCG CTCTACC TTTA
 _ GG
 GAM1126 LOC158230 3' CTTTCCACCTCCCTCCT 39766 CA A
 AGGAG GAG TGGAGGG
 |||| ||| |||||

TCCTC CTC ACCTTTC
 C_ C
 GAM1126 LOC158969 3' CAACCCCTCTTTCCTGCTCCT 39919 A T _
 AGGAGCAG GA GGAGGG TTG
 ||||| || ||||| ||
 TCCTCGTC CT TCTCCC AAC
 _ T C
 GAM1126 LOC200982 3' CAACAGGGCCCTCTGCTCCT 43372 AT AGG_
 AGGAGCAGAG GG GTTG
 ||||| || ||||
 TCCTCGTCTC CC CAAC
 _ GGA
 GAM1126 LOC201173 3' AACTCTCCCTTCTCCT 42211 C AGAT
 AGGAG AG GGAGGGTT
 |||| || |||||
 TCCTC TC CCTCTCAA
 T _
 GAM1126 LOC201220 3' AACTCTCCCTTCTCCT 42219 C AGAT
 AGGAG AG GGAGGGTT
 |||| || |||||
 TCCTC TC CCTCTCAA
 T _
 GAM1126 LOC201229 3' CCCTCCTCTGCTCCT 42542 GAT
 AGGAGCAGA GGAGGG
 ||||| ||||
 TCCTCGTCT CCTCCC
 _
 GAM1126 LOC203197 3' CAACCCTGCTGCTCTCTGCCTC 43009 _ _ _
 CT AGGAG CAGAGA TGG AGGGTTG
 |||| ||||| || |||||
 TCCTC GTCTCT GTC TCCCAAC
 C C G
 GAM1126 LOC205693 5' CAATGGCCATCCCTGCTCCT 43608 A AGG
 AGGAGCAG GATGG GTTG
 ||||| |||| ||||
 TCCTCGTC CTACC TAAC
 C GG_
 GAM1126 LOC220766 5' ACTTAGGCAGCTCTGCTCCT 43647 A GA_
 AGGAGCAGAG TG GGGT
 ||||| || ||||
 TCCTCGTCTC AC TTCA
 G GGA
 GAM1126 LOC221463 3' CAACCCTCCAGTCCCCT 44200 AGCA GA
 AGG GA TGGAGGGTTG
 || || |||||
 TCC CT ACCTCCCAAC
 C_ G_
 GAM1126 LOC223073 5' CAACCCTCTGGATCACCTCT 45316 CA GA
 GGAG GA TGGAGGGTTG
 |||| || |||||

		TCTC CT GTCTCCCAAC		
		CA AG		
GAM1126	LOC257054	5' AGCACCGTCTGCTCCT	45780	GA AGG
		AGGAGCAGA TGG GTT		
		TCCTCGTCT GCC CGA		
		__ A__		
GAM1126	LOC51236	3' CAGCCACCCTCTGCCCCT	18570	A AT AG
		AGG GCAGAG GG GGTTG		
		TCC CGTCTC CC CCGAC		
		C __ A__		
GAM1126	LOC51308	3' CAACCCTCCATCCTAGGCTCT	18707	AGA_
		GGAGC GATGGAGGGTTG		
		TCTCG CTACCTCCCAAC		
		GATC		
GAM1126	LOC56961	5' CAACCCTCCCCCTGCCC	31505	A AGAT
		GG GCAG GGAGGGTTG		
		CC CGTC CCTCCCAAC		
		_ CC__		
GAM1126	LOC91373	3' CAACTCATCCTCTGCCCC	32751	A GAT _
		GG GCAGA GGA GGGTTG		
		CC CGTCT CCT CTCAAC		
		C __ A		
GAM1127	CORO2A	3' GTTTAGAACCAAACCACA	27408	_ C
		TGTGGTTTG TTC AAAT		
		ACACCAAAC AAG TTTG		
		C A		
GAM1127	FBLN5	3' AGAGAAGGCTATGTAAACAAAC	13021	C_ AATA _
	CACA	TGTGGTTTGTG CA CT CTCT		
		ACACCAAACAA GT GA GAGA		
		AT ATCG A		
GAM1127	PIGA	3' GAGAACATTTAAGCCAC	21708	TTCCA AC
		GTGGTTTG AAT TCTC		
		CACCGAAT TTA AGAG		
		__ CA		
GAM1127	PIGA	3' GAGAACATTTAAGCCAC	8497	TTCCA AC
		GTGGTTTG AAT TCTC		
		CACCGAAT TTA AGAG		
		__ CA		
GAM1127	PIGA	3' GAGAACATTTAAGCCAC	21715	TTCCA AC
		GTGGTTTG AAT TCTC		

CACCGAAT TTA AGAG
_____ CA
GAM1127 AF311304 3' AGTAGAAGAAACCACA 25259 G CAAA
TGTGGTTT TTC TACT
||||||| ||| ||||
ACACCAAA AAG ATGA
G _____
GAM1127 APOL2 3' AGAGAGTATCTGAGAACCAACC 25159 T _ A
A TGGTT GTTC CA ATACTCTCT
||||| |||| || |||||||
ACCAA CAAG GT TATGAGAGA
C A C
GAM1127 JDD1 3' AGAAAGCAGCATGAACAGAACC 31668 _ CAAATA C
ACA TGTGGT TTGTTC CT TCT
||||| |||||| || |||
ACACCA GACAAG GA AGA
A TACGAC A
GAM1127 MAB21L2 3' TAGAGAGCAACCCAACCAAAAC 13152 CCAAATA_____ |||
AAATCACA TTGTT CTCTCT A
||||| |||||| |
AACAA GAGAGA T
AACCAACCCAAC |||
GAM1127 LOC254413 5' AGAGAGTACCTGACTTCAGACC 46398 TTC_ AA
AC GTGGTTTG CA TACTCTCT
||||||| || |||||||
CACCAGAC GT ATGAGAGA
TTCA CC
GAM1128 CELSR2 3' AACGTCCATCTGAGGA 7105 TAAAG C
TTCTCAGA TGG CGTT
||||||| ||| ||||
AGGAGTCT ACC GCAA
_____ T
GAM1128 LEP 3' GAACAAGGTTCCCTCTGAGAA 5736 TAAAGT _
TTCTCAGA GGCC GTTC
||||||| |||| ||||
AAGAGTCT TTGG CAAG
CCC_ AA
GAM1128 TCF3 3' GAACGGCCACTCGAGA 35008 A TAA
TCTC GA GTGGCCGTTC
|||| || |||||||||
AGAG CT CACCGGCAAG
- _____
GAM1128 C20orf162 5' TGGTACCACCCCATCTGAGAA 27921 AAA CCGTT
TTCTCAGAT GTGG CCA
||||||| |||| |||
AAGAGTCTA CACC GGT
CCC AT____
GAM1128 DKFZp434K1210 3' AATGGTACCTTGTCTGA 19100 A G
TCAGATAA GTG CCGTT
||||||| ||| |||||

		AGTCTGTT CAT GGTA	
		C _	
GAM1128	FLJ10737	3' AACTGCTTTTTATCTGAGAA 20063	T C
		TTCTCAGATAAAG GGC GTT	
		AAGAGTCTATTTT TCG CAA	
		_ T	
GAM1128	FLJ10956	3' GGAACAACCTCCATTTTATCT 20277	CC__
		AGATAAAGTGG GTTCC	
		TCTATTTTACC CAAGG	
		TCAA	
GAM1128	GFPT1	3' TGGACCCTCCACTTCAATCTGA 7819	A_ CCGT
	GAA	TTCTCAGAT AAGTGG TCCA	
		AAGAGTCTA TTCACC AGGT	
		AC TCCC	
GAM1128	GIT2	3' AATCGCACCTTATCTGA 16597	A G C
		TCAGATAA GTG C GTT	
		AGTCTATT CAC G TAA	
		C _ C	
GAM1128	GIT2	3' AATCGCACCTTATCTGA 27692	A G C
		TCAGATAA GTG C GTT	
		AGTCTATT CAC G TAA	
		C _ C	
GAM1128	GIT2	3' AATCGCACCTTATCTGA 27679	A G C
		TCAGATAA GTG C GTT	
		AGTCTATT CAC G TAA	
		C _ C	
GAM1128	KIAA1941	3' AATTGCCCCCATTTGAGAA 36950	AAAGT C
		TTCTCAGAT GGC GTT	
		AAGAGTTTA CCG TAA	
		CCC__ T	
GAM1128	MGC13198	5' GAAAGCTCATTATCTGAGAA 26410	AGT CG
		TTCTCAGATAA GGC TTC	
		AAGAGTCTATT TCG AAG	
		AC_ A_	
GAM1128	SPEC1	3' AATCGCCTCCATTTGAGAA 21507	AAAGT C
		TTCTCAGAT GGC GTT	
		AAGAGTTTA CCG TAA	
		CCT__ C	
GAM1128	LOC146819	3' GAAATATACTTTATCTGA 38253	GCCG
		TCAGATAAAGTG TTC	

	AGTCTATTTTCAT	AAG	
	ATA_		
GAM1128 LOC146821 3'	GAAATATACTTTATCTGA	38251	GCCG
	TCAGATAAAGTG	TTC	
	AGTCTATTTTCAT	AAG	
	ATA_		
GAM1128 LOC153218 5'	GAACAGGTGCGACTTCTGAGAA	39364	TAAA G _
	TTCTCAGA	GTG CC GTTC	
	AAGAGTCT	CGT GG CAAG	
	TCAG	_ A	
GAM1128 LOC253187 5'	GAATCTGCATCTGAGAA	46393	AAA TG CC
	TTCTCAGAT	G G GTTC	
	AAGAGTCTA	C C TAAG	
	__	GT __	
GAM1128 LOC253613 3'	AACTCCCTCATCTGAGAA	46006	AA T CC
	TTCTCAGAT	AG GG GTT	
	AAGAGTCTA	TC CC CAA	
	C_	_ T_	
GAM1128 LOC54466 3'	TGGAAAGTACTTTATCCAGAA	21075	CA GCCG
	TTCT	GATAAAGTG TTCCA	
	AAGA	CTATTTTCAT AAGGT	
	C_	GA__	
GAM1128 LOC91963 5'	TGGCCACCTCCTCTGAGAA	33628	TAAA
	TTCTCAGA	GTGGCCG	
	AAGAGTCT	CACCGGT	
	CCTC		
GAM1129 DAG1 3'	GCCCACGACCAAGGGGTCTTCA	10633	A_ T ACC__
	TGAAGG	CCTTG GT GC	
	ACTTCT	GGAAC CA CG	
	GG	_ GCACC	
GAM1129 ATP1B4 3'	TGCCTGGCAAGGTCCTTC	14327	GTACC
	GAAGGACCTTG	GCA	
	CTTCCTGGAACG	CGT	
	GTC__		
GAM1129 DKFZP564C196 3'	GCTTGCGGCAGTACAATGCCCC	34712	AA ACC TA_
CA	TG GG TTGTG	CCGCAAGC	
	AC CC AACAT	GGCGTTTCG	
	CC GT_	GAC	
GAM1129 PP1057 3'	CTTGTCTCAGAAAGTCCCTCA	25311	A C G TACC
	TGA GGAC	TT TG GCAAG	

		ACT CCTG AA AC TGTT	
		C A G TC__	
GAM1129	LOC143920 3'	GCTTACGTTGCCATGATCCCTC 37642	A CCT T C C
	A	TGA GGA TG GTA CG AAGC	
		ACT CCT AC CGT GC TTCG	
		C AGT _ T A	
GAM1129	LOC154881 3'	GCTTGCGGCCTGCAGGCACTCC 39499	C__ TA
		GGA CTTGTG CCGCAAGC	
		CCT GGACGT GGCGTTCG	
		CAC CC	
GAM1129	LOC255152 5'	GCTTGCGGCCCGCTGGCTCCTC 46534	A _ TT TA
	A	TGA GGA CC GTG CCGCAAGC	
		ACT CCT GG CGC GGCGTTCG	
		_ C T_ CC	
GAM1129	LOC255481 3'	GCCTGCAGTATGCAGAGCCCC 45330	AC _ C A
		GG CT TGTGTAC GCA GC	
		CC GA ACGTATG CGT CG	
		CC G A C	
GAM1129	LOC91301 5'	GCCCGCGGTTTGAGGTCCTTC 32648	GTGT AA
		GAAGGACCTT ACCGC GC	
		CTTCCTGGAG TGGCG CG	
		TT__ CC	
GAM1130	NDRG2 3'	CCTTTAACCCGTGATTCC 18378	TT AAA
		GGAATT AC GTTAAAGG	
		CCTTAG TG CAATTTCC	
		_ CC_	
GAM1130	AD022 3'	CCTTATGGCTTAAAATTCCTTA 43737	CAA _
		TAAGGAATTTTA AGTTA AAGG	
		ATTCCTTAAAAT TCGGT TTCC	
		_ _ A	
GAM1130	KIAA0534 3'	GACTTTGAAAAATTCCTTA 35384	A
		TAAGGAATTTT CAAAGTT	
		ATTCCTTAAAA GTTTCAG	
		A	
GAM1130	OSBPL2 5'	AAGTTTGTAATAATTCCTTA 16848	G
		TAAGGAATTTTACAAA TT	
		ATTCCTTAAAATGTTT AA	
		G	
GAM1130	OSBPL2 5'	AAGTTTGTAATAATTCCTTA 29316	G
		TAAGGAATTTTACAAA TT	

ATTCCTTAAATGTTT AA
 G
 GAM1130 PPP1R16B 3' CCTTTAGTCTGTAAACTCCT 30774 A AAG
 AGGA TTTTACA TTAAAGG
 |||| ||||| |||||
 TCCT AAAATGT GATTTC
 C CT_
 GAM1130 TUBB5 3' CCTTTAACTTTGCAGACCTTCC 12729 T_ A
 TT AAGGAA TTT CAAAGTTAAAGG
 ||||| ||| |||||
 TTCCTT AGA GTTTCAATTTC
 CC C
 GAM1130 LOC157657 3' CCTTTAATGCCTAAACTCC 39625 A CAAA
 GGA TTTTA GTTAAAGG
 || ||||| |||||
 CCT AAAAT TAATTTC
 C CCG_
 GAM1131 MTMR8 3' TTAAACACTCTGACCA 17751 CGC G
 TGGTCAGAG TGT TAGA
 ||||| ||| |||
 ACCAGTCTC ACA ATTT
 _ A
 GAM1131 FLJ10520 3' TTGTCCAGCCTGACCAA 19909 AGC TG
 TTGGTCAG GCTG TAG
 ||||| ||| |||
 AACCAGTC CGAC GTT
 _ CT
 GAM1131 FLJ31564 5' AGGATCTCAGCACTCTGACC 29541 C TGT _
 GGTCAGAG GCTG AGA CCT
 ||||| ||| ||| |||
 CCAGTCTC CGAC TCT GGA
 A _ A
 GAM1131 MGC13114 3' GCCCAGGGCCTGACCAA 26153 A G T
 TTGGTCAG GC CTG GT
 ||||| || ||| ||
 AACCAGTC CG GAC CG
 _ G C
 GAM1131 LOC145836 5' GGGCAAACGCTCCGACCAA 40614 A CTG AGA
 TTGGTC GAGCG TGT CC
 ||||| |||| ||| ||
 AACCAG CTCGC ACG GG
 C AA_ _
 GAM1131 LOC221466 3' GGCCACATGTCTGACCA 44996 G C TAGA
 TGGTCAGA CG TGTG CC
 ||||| || ||| ||
 ACCAGTCT GT ACAC GG
 _ _ CC_
 GAM1131 LOC57086 5' TCTACACAGGTTGCCAA 21617 CAG G
 TTGGT AGC CTGTGTAGA
 |||| ||| |||||

AACCG TTG GACACATCT

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GAM1132 FGF2   3' CCTTCTCTGTACCCATACAGCA 7736   TG__ GTC
                TGCTGTAT ATAG AGAAGG
                ||||| ||| |||||
                ACGACATA TGTC TCTTCC
                CCCA ____
GAM1132 LDHB   5' TCCTTCTGACCACACACAGACA 8089   _ AT ATA
                TG CTGT TG GGTCAGAAGGA
                || ||| || |||||
                AC GACA AC CCAGTCTTCCT
                A C_ A__
GAM1132 PCDH11X 3' TCCTCTGTGATATCATACAGCA 26794   T GGT A
                TGCTGTAT GATA CAGA GGA
                ||||| ||| ||| |||
                ACGACATA CTAT GTCT CCT
                _ AGT _
GAM1132 PCDH11X 3' TCCTCTGTGATATCATACAGCA 26809   T GGT A
                TGCTGTAT GATA CAGA GGA
                ||||| ||| ||| |||
                ACGACATA CTAT GTCT CCT
                _ AGT _
GAM1132 PCDH11Y 3' TCCTCTGTGATATCATACAGCA 26828   T GGT A
                TGCTGTAT GATA CAGA GGA
                ||||| ||| ||| |||
                ACGACATA CTAT GTCT CCT
                _ AGT _
GAM1132 AFAP   3' TCCCCCTGACCTGGGCACAGGC 22294   GTAT A_ AA
      A
                TGCT TG TAGGTCAG GGA
                ||| || ||||| |||
                ACGG AC GTCCAGTC CCT
                AC_ GG CC
GAM1132 FLJ12484 3' CCCTCCCTGTCAGCACAGCA 23017   A TCA A
                TGCTGT TTGATAGG GA GG
                |||| ||||| || ||
                ACGACA GACTGTCC CT CC
                C _ C
GAM1132 FLJ12484 3' CCCTCCCTGTCAGCACAGCA 34515   A TCA A
                TGCTGT TTGATAGG GA GG
                |||| ||||| || ||
                ACGACA GACTGTCC CT CC
                C _ C
GAM1132 FLJ20154 5' TCCCTCTGACCTACCAGT 36108   A A
                ATTG TAGGTCAGA GGA
                ||| ||||| |||
                TGAC ATCCAGTCT CCT
                C C
GAM1132 KIAA0040 5' TCCTTCTGACCACACACAGACA 16098   _ AT ATA
                TG CTGT TG GGTCAGAAGGA
                || ||| || |||||
```

	AC GACA AC CCAGTCTTCCT	
	A C_ A__	
GAM1132 PRO1048	3' TCCTTCCTCAATCAATACAG 20562	A TCA
	CTGTATTGAT GG GAAGGA	
	GACATAACTA CT CTCCT	
	A C__	
GAM1132 LOC149117	3' TCCTCCAAACCAAATACAGCA 40955	GATA CAGA
	TGCTGTATT GGT AGGA	
	ACGACATAA CCA TCCT	
	A__ AACC	
GAM1132 LOC220929	5' CCTTCTGGAACAATACAG 43929	ATAGG
	CTGTATTG TCAGAAGG	
	GACATAAC GGTCTTCC	
	AA__	
GAM1133 SLC2A1	3' AGATCACCAGCCCGGCCTG 13264	C_ CCAC
	CAGGCC GC GGTGATCT	
	GTCCGG CG CCACTAGA	
	CC A__	
GAM1133 C21orf25	3' GAGCACAGCGGGCCTGT 31800	CCACG A
	ACAGGCCCGC GTG TC	
	TGTCCGGGCG CAC AG	
	A__ G	
GAM1133 FLJ10849	3' GCACGAAGCAGGCCTGTTA 20204	C CCA _
	TAACAGGCC GC CG GT	
	ATTGTCCGG CG GC CG	
	A AA_ A	
GAM1133 MSC	3' AGATCACCGCAGGCGGGTTT 37533	CA
	AGGCCCGCC CGGTGATCT	
	TTTGGGCGG GCCACTAGA	
	AC	
GAM1133 RASSF2	3' AGATCACCATAAGCGTCCCTG 16389	CC CCAC
	CAGG CGC GGTGATCT	
	GTCC GCG CCACTAGA	
	CT AATA	
GAM1133 ZNF337	3' ACCAAGGCAGGCCTGTTA 33770	C CAC
	TAACAGGCC GCC GGT	
	ATTGTCCGG CGG CCA	
	A AA_	
GAM1133 LOC154834	3' AGATGTGCATGTGAGCAAGCTT 41730	CC C _ _
	GTTA TAACAGGC GC CACG GTG ATCT	

ATTGTTTCG CG GTGT CGT TAGA
 AA A A G
 GAM1133 LOC200720 5' GGTTCCTGGGCAGCC 43342 CC T
 GGC GCCCACGG GATC
 ||| ||||| |||
 CCG CGGGTGCC TTGG
 A_ _
 GAM1133 LOC91461 3' GGTTCCTGGGCAGCC 32869 CC T
 GGC GCCCACGG GATC
 ||| ||||| |||
 CCG CGGGTGCC TTGG
 A_ _
 GAM1134 AWP1 5' CATCAACCTCAACTGTGTGTGC 21077 A TC
 A TGC GCA AC GTTGAGGTTGATG
 ||||| || |||||
 ACGTGT TG CAACTCCAACTAC
 G T_
 GAM1134 LOC199796 5' CAACCCAGTTTTGTCCGCTGC 36806 _ AA TCG_ A
 A TGC GC AC TTG GGTTG
 ||| || ||| |||||
 ACG CG TG GAC CCAAC
 T CC TTTT C
 GAM1134 LOC257464 3' CAACCTCAGTGTCTGAGCA 43163 G A TCG
 TGC CA AC TTGAGGTTG
 ||| || ||| |||||
 ACG GT TG GACTCCAAC
 A C T_
 GAM1134 LOC51313 3' CATCAACCTCAAGCCCGTTTAG 18718 GC TC _
 CA TGC AAAC GTT GAGGTTGATG
 ||| |||| ||| |||||
 ACG TTTG CGA CTCCAACCTAC
 A_ CC A
 GAM1135 ABCC3 3' GTTCTGGCCCTGTCTCCTCA 21294 T _ A_
 A GGGA GACG GGCCAGAAC
 | |||| |||||
 A TCCT CTGT CCGGTCTTG
 C A CC
 GAM1135 ABCD1 3' GCCCTGTCCCTCCCACTCC 5472 A _ A
 GGA TGGGA GACG GGC
 ||| |||| ||| |||
 CCT ACCCT CTGT CCG
 C CC C
 GAM1135 ADRA2A 3' CTGGCTAATCCCCTTCCA 6337 T ACGA
 TGGAA GGGAG GGCCAG
 |||| |||| |||||
 ACCTT CCCTT TCGGTC
 C AA_
 GAM1135 B4GALT6 5' TCTGGCCTCCCATTC 30096 GACGA
 GAATGGGA GGCCAGA
 ||||| |||||

CTTACCCT CCGGTCT

GAM1135 CARD10 3' TCTGGCCTCTCACCCCA 15872 AAT A C
TGG GGG GA GAGGCCAGA
||| ||| || |||||
ACC CCC CT CTCCGGTCT

___ A _

GAM1135 DAAM2 3' CGTTCCAGCCTCTCCCTACTCC 44329 AC___ CA |||
CATCCCA TGGGAG GAGGC GAAC G
||||| ||||| ||| |
ACCCTC CTCCG CTTG C

ATCCCT AC |||

GAM1135 EN2 5' CTGGCCTCGCGTCTCTCA 7144 _
TGGGAGAC GAGGCCAG
||||||| |||||
ACTCTCTG CTCCGGTC
CG

GAM1135 EXTL1 5' GCTCTGGTCTCCCGCCCA 10757 AA G _
TGG TGGGAGAC AG GC
||| ||||| || ||
ACC GCCCTCTG TC CG
CC G T

GAM1135 HDAC7A 3' CTGGCTGTGGCCCCATTCC 17712 AGA A
GGAATGGG CG GGCCAG
||||||| || |||||
CCTTACCC GT TCGGTC
CCG G

GAM1135 HDAC7A 3' CTGGCTGTGGCCCCATTCC 18682 AGA A
GGAATGGG CG GGCCAG
||||||| || |||||
CCTTACCC GT TCGGTC
CCG G

GAM1135 MSN 3' TTCTGGCCTAGTCCCTTCCA 30231 T GACG
TGGAA GGGA AGGCCAGAA
||||| ||||| |||||
ACCTT CCCT TCCGGTCTT
_ GA_

GAM1135 PPIL1 5' TTCTTCTCGTCTCCACCCCA 18135 AA CC
TGG TGGGAGACGAGG AGAA
||| ||||| ||||| |||||
ACC ACCCTCTGCTCT TCTT
CC _

GAM1135 PSG4 3' TTCTACTAGTTCCTCCAATTCC 8671 G _ GA CC
A TGGAAT GGAG AC GG AGAA
||||| ||||| || || |||||
ACCTTA CCTC TG TC TCTT
A CT A_ A_

GAM1135 PSG7 3' TTCTACTAGTTCCTCCAATTCC 8672 G _ GA CC
A TGGAAT GGAG AC GG AGAA
||||| ||||| || || |||||

ACCTTA CCTC TG TC TCTT
 A CT A_ A_
 GAM1135 PTP4A2 3' TTCTCTCCTCTCCCATCCCA 9557 A C GCC
 TGG ATGGGAGA GAG AGAA
 ||| ||||| || ||||
 ACC TACCCTCT CTC TCTT
 C C ____
 GAM1135 SMURF1 3' GTTTAATCCCCCATTCCA 44415 A CG
 TGAATGGG GA AGGC
 ||||| || ||||
 ACCTTACCC CT TTTG
 C AA
 GAM1135 STXBP1 3' TCTCTCCCGTCTCCCTCCCA 9141 AAT A CC
 TGG GGGAGACG GG AGA
 ||| ||||| || ||||
 ACC CCCTCTGC CC TCT
 CT_ C TC
 GAM1135 SWAP70 3' CTCCAGTATCCCTCATTCCA 35348 _ G _
 TGAAT GGGA AC GAG
 ||||| |||| || ||||
 ACCTTA CCCT TG CTC
 CT A AC
 GAM1135 TFAP4 3' GTCTCATCTTCCACCCCA 9225 AA C
 TGG TGGGAGA GAGGC
 ||| ||||| |||||
 ACC ACCTTCT CTCTG
 CC A
 GAM1135 UCP2 5' GTTTCGTCTCCCACCCA 9382 AA
 TGG TGGGAGACGAGGC
 ||| ||||| |||||
 ACC ACCCTCTGCTTTG
 C_
 GAM1135 AP1GBP1 3' CCTTAGATCTCCCTTCCA 14116 T C_
 TGGAA GGGAGA GAGG
 ||||| ||||| ||||
 ACCTT CCCTCT TTCC
 _ AGA
 GAM1135 AP1GBP1 3' CCTTAGATCTCCCTTCCA 27871 T C_
 TGGAA GGGAGA GAGG
 ||||| ||||| ||||
 ACCTT CCCTCT TTCC
 _ AGA
 GAM1135 AP1GBP1 3' CCTTAGATCTCCCTTCCA 27879 T C_
 TGGAA GGGAGA GAGG
 ||||| ||||| ||||
 ACCTT CCCTCT TTCC
 _ AGA
 GAM1135 C11orf11 3' TTCTGGCCCCCGGCTCCC 44791 A A_
 GGGAG CG GGCCAGAA
 ||||| || |||||

			CCCTC GC CCGGTCTT			
			G CC			
GAM1135	C20orf173	5'	CTGGCCTCTTCCACCCCA	28093	AA	CGA
			TGG TGGGAGA GGCCAG			
			ACC ACCTTCT CCGGTC			
			CC ____			
GAM1135	CALN1	3'	CCTGGTCTCCCATGCCCA	25513	A_	G
			TGG ATGGGAGAC AGG			
			ACC TACCCTCTG TCC			
			CG G			
GAM1135	CBLN1	3'	CTCGCCTCCCCCATTCCA	10555	AGAC	C
			TGGAATGGG GAGGC AG			
			ACCTTACCC CTCCG TC			
			C__ C			
GAM1135	CHERP	3'	GCCAGCGCCTTCCACTCCA	13091	A	A A_
			TGGA TGGGAG CG GGC			
			ACCT ACCTTC GC CCG			
			C C GA			
GAM1135	DDX37	3'	CTGGCCTCACAGCCGTCCCA	26389	A	GAGAC
			TGG ATGG GAGGCCAG			
			ACC TGCC CTCCGGTC			
			C GACA_			
GAM1135	DOCK3	3'	GCCAGCCGTCTCCTACTCCA	33035	A	A__
			TGGA TGGGAGACG GGC			
			ACCT ATCCTCTGC CCG			
			C CGA			
GAM1135	EDR2	3'	TCTTGGCCTCCCACTCCCA	30341	AC_	_
			TGGGAG GAGGCCA GA			
			ACCCTC CTCCGGT CT			
			ACC T			
GAM1135	ERMAP	3'	TTCTGGCCTCTGCCCCCA	20609	AAT	AGAC
			TGG GGG GAGGCCAGAA			
			ACC CCC CTCCGGTCTT			
			C__ GT__			
GAM1135	FLJ12681	3'	GCTCTGATCTCCCATCCA	23037	A	_ AG
			TGGA TGGGAGA CG GC			
			ACCT ACCCTCT GT CG			
			_ A CT			
GAM1135	FLJ12704	3'	TTCTGACGTGTCCATTCCA	24567	AG	AGGC
			TGGAATGGG ACG CAGAA			

ACCTTACCT TGC GTCTT
 G_ A_
 GAM1135 FLJ22501 5' TCTGGCCTCCATCCTCCA 24083 ATG GAC
 TGGG GGA GAGGCCAGA
 ||| ||| |||||
 ACCT CCT CTCCGGTCT
 _ AC_
 GAM1135 FRAG1 3' TTCTGGCCTTCCCCACCCCA 15834 AA A CG
 TGG TGGG GA AGGCCAGAA
 ||| |||| || |||||
 ACC ACCC CT TCCGGTCTT
 CC _ _
 GAM1135 HIP-55 3' TCTGTGCTCCCCACTCCA 15277 A A CGAG _
 TGGG TGGG GA GC CAGA
 ||| |||| || |||||
 ACCT ACCC CT CG GTCT
 C _ _ T
 GAM1135 KIAA0552 3' CTGGCGACCACTGCCCATTCCTCA 16345 _ ACGAG
 TGGGATGGG AG GCCAG
 ||||| || |||||
 ACCTTACCC TC CGGTC
 G ACCAG
 GAM1135 KIAA1193 3' GCCTCGCCTTCCCACCCCA 33583 AA A_
 TGG TGGGAG CGAGGC
 ||| ||||| |||||
 ACC ACCCTT GCTCCG
 CC CC
 GAM1135 KIAA1196 3' CTGGCCTCACCTCCACCCA 30822 AATG AC
 TGG GGAG GAGGCCAG
 ||| |||| |||||
 ACC CCTC CTCCGGTC
 CA_ CA
 GAM1135 KIAA1434 3' TCTGTGCTCTCCCATCCA 34491 A GGC
 TGGG TGGGAGACGA CAGA
 ||| ||||| |||||
 ACCT ACCCTCTGCT GTCT
 _ _
 GAM1135 KIAA1485 3' CTGTTGCGCTCCCATTCCTA 43002 A GC
 TGGGATGGGAG CGAG CAG
 ||||| ||||| |||||
 ATCTTACCCTC GCTT GTC
 C _
 GAM1135 LASP1 3' CTGGCCTCACTTGATTC 12796 G G AC
 GAAT G AG GAGGCCAG
 |||| | || |||||
 CTTA T TC CTCCGGTC
 G_ A_
 GAM1135 LASP1 3' TCTGGGAGTCCCCATCCCA 12803 A A GAGG
 TGG ATGGG GAC CCAGA
 ||| ||||| ||| |||||

ACC TACCC CTG GGTCT
 C _ AG__
 GAM1135 PTPNS1 3' CTGGCCTCCCCCATCCC 28054 A AGAC
 GG ATGGG GAGGCCAG
 || |||| |||||
 CC TACCC CTCCGGTC
 C C__
 GAM1135 SEMA4G 3' TTCTGACTGAGCTCCCCCATTC 19565 A CGA_ C
 C GGAATGGG GA GG CAGAA
 ||||| || || ||||
 CCTTACCC CT TC GTCTT
 C CGAG A
 GAM1135 SEMA4G 3' TTCTGACTGAGCTCCCCCATTC 45416 A CGA_ C
 C GGAATGGG GA GG CAGAA
 ||||| || || ||||
 CCTTACCC CT TC GTCTT
 C CGAG A
 GAM1135 TP53INP1 3' TCTGGCCTCTGTTTCCCCCA 36119 AAT _
 TGG GGGAGAC GAGGCCAGA
 || ||||| |||||
 ACC CCCTTTG CTCCGGTCT
 _ T
 GAM1135 TP53INP1 3' TCTGGCCTCTGTTTCCCCCA 27110 AAT _
 TGG GGGAGAC GAGGCCAGA
 || ||||| |||||
 ACC CCCTTTG CTCCGGTCT
 _ T
 GAM1135 TTC4 3' CTGGCCTCAAGTTATTTCA 32960 GAGAC
 TGGAATGG GAGGCCAG
 ||||| |||||
 ACTTTATT CTCCGGTC
 GAA__
 GAM1135 WBSCR17 3' GTTCTCCTCCACATCTCCCATC 39549 A C__ CC
 CCA TGG ATGGGAGA GAGG AGAAC
 || ||||| || ||||
 ACC TACCCTCT CTCC TCTTG
 C ACAC _
 GAM1135 LOC113444 3' TTCTGGCCCTTCCACACCA 28790 AA ACGA
 TGG TGGGAG GGCCAGAA
 || ||||| |||||
 ACC ACCCTT CCGGTCTT
 AC C__
 GAM1135 LOC146733 5' TCCATCTTCACCCTCCATTCCA 40732 AGAC CCA
 TGGAATGGG GAGG GA
 ||||| || ||
 ACCTTACCT CTTC CT
 CCCA TAC
 GAM1135 LOC146784 5' TTCTGACCCCTGTGCCTCCCA 38241 A _ C__
 TGGGAG CG AGG CAGAA
 ||||| || || ||||

ACCCTC GT TCC GTCTT
 C G CCA
 GAM1135 LOC148932 3' GTCTTGTCTCCCATCCCA 38624 A
 TGG ATGGGAGACGAGGC
 ||| |||||
 ACC TACCCTCTGTTCTG
 C
 GAM1135 LOC158263 3' TTCTGGTCCCCCATCC 39801 A AGACGA
 GGA TGGG GGCCAGAA
 ||| ||| |||||
 CCT ACCC CTGGTCTT
 _ C _
 GAM1135 LOC162333 5' GTTCTGGCCCTAGACCACGTCC 42133 A_ GAGACGA
 A TGA TGG GGCCAGAAC
 ||| ||| |||||
 ACCT ACC CCGGTCTTG
 GC AGATC_
 GAM1135 LOC200830 3' TTTGGCTCCTCCCCACCCCA 43351 AA A C G
 TGG TGGG GA GAG CCAGA
 ||| ||| ||| |||
 ACC ACCC CT CTC GGTTT
 CC C C _
 GAM1135 LOC219621 3' TTTTGCTATCTCCCATCCCA 43969 A CGA C
 TGG ATGGGAGA GGC AGAA
 ||| ||||| ||| |||
 ACC TACCCTCT TCG TTTT
 C A_ _
 GAM1135 LOC221466 5' TTCTGGCCTCTCATCCCA 44998 _ C
 TGGGA GA GAGGCCAGAA
 ||||| ||| |||||
 ACCCT CT CTCCGGTCTT
 A _
 GAM1135 LOC221833 3' CTGGCTTTCCCTTTCCA 44456 T ACGA
 TGGAA GGGAG GGCCAG
 ||||| ||||| |||||
 ACCTT CCCTT TCGGTC
 T _
 GAM1135 LOC254428 3' TCTAACCTCACCTCATTCT 45719 AGAC CC
 GGAATGGG GAGG AGA
 ||||| ||| |||
 TCTTACTC CTCC TCT
 CA_ AA
 GAM1135 LOC256997 5' GCTGTGTCTCCCATCCCA 45652 A
 TGGAAATGGGAGACG GGC
 ||||| ||||| |||
 ACCTTACCCTCTGT TCG
 G
 GAM1135 LOC51267 3' TCTGATAATTGTCTCCCCTCCA 18591 AT GGC_
 TGA GGGAGACGA CAGA
 ||| ||||| |||

ACCT CCCTCTGTT GTCT
 C_ AATA
 GAM1135 LOC59346 5' CTGGCCTCGTCCGCGGCCCA 22272 A____
 TGGG GACGAGGCCAG
 ||| |||||
 ACCC CTGCTCCGGTC
 GGCGC
 GAM1136 SORCS2 3' CCAGCATCTGTCTTTTC 21873 T_ CG
 GAA GGC AGATGCTGG
 ||| ||| |||||
 CTT CTG TCTACGACC
 TT ____
 GAM1136 TAP2 3' CCTCTTCCGGCCATTCTTCA 6140 C A TGCT
 TGA GAATGGCCG GA GG
 ||| ||||| || ||
 ACT CTTACCGGC CT CC
 T _ TCT_
 GAM1136 RIN3 3' CCAGCATCTCAGGAGCACCTC 24230 A_ G_ _
 GA TG CC GAGATGCTGG
 || || || |||||
 CT AC GG CTCTACGACC
 CC GA A
 GAM1136 LOC145623 3' CCAGCATCTTCACTTGTGCATA 40544 A GCC
 TATGACGA TG GAGATGCTGG
 ||||| || |||||
 ATACTGTT AC TTCTACGACC
 C ____
 GAM1136 LOC197335 5' CCAGCATCTCATTTTCCCCCAT 42479 AC_ TGGCC
 A TATG GAA GAGATGCTGG
 ||| ||| |||||
 ATAC CTT CTCTACGACC
 CCC TTA____
 GAM1137 A2BP1 5' CAGCTTCCTTGATCGGACTCA 20804 A AACTC
 TGAG TCCGATCAAG GTTG
 ||| ||||| |||
 ACTC AGGCTAGTTC CGAC
 _ CTT____
 GAM1137 NPD009 3' CAACAAGTTCTTGTTGACTCA 45561 A CGAT C
 TGAG TC CAAGAACT GTTG
 ||| || ||||| |||
 ACTC AG GTTCTTGA CAAC
 _ TT__ A
 GAM1138 AK1 3' AGAAATAAACAGGAGTTCA 6085 CCAA TAC
 TGAGCTCC GTTT TTCT
 ||||| ||| |||
 ACTTGAGG CAAA AAGA
 A__ TA_
 GAM1138 HOXD4 5' AGAAGCCCAGTGGGGAGCTC 15978 AGTTTTA
 GAGCTCCCCA CTTCT
 ||||| |||

		CTCGAGGGGT GAAGA	
		GACCC__	
GAM1138 KDR	3'	AGAAGTAGCAGTACCTGGGGAG 8052	A T__
CT		AGCTCCCCA GT TTACTTCT	
		TCGAGGGGT CA GATGAAGA	
		C TGAC	
GAM1138 KLF8	5'	GAGAAATAGGGGAGTGGGGGCC 14124	A T AG_ C
CA		TG GC CCCCCA TTTTA TTCTC	
		AC CG GGGGT GGGAT AAGAG	
		C _ GAG A	
GAM1138 MIPOL1	5'	AGAAGGCTAAAGGAGCTCA 37813	CCA TTTA
		TGAGCTCC AGT CTTCT	
		ACTCGAGG TCG GAAGA	
		AAA _	
GAM1138 PPP1R8	5'	AGAAACCCGGGGTTGGGGGCTC 28853	T G TAC_
A		TGAGC CCCCAG TTT TTCT	
		ACTCG GGGGTT GGG AAGA	
		_ G CCCA	
GAM1138 PPP1R8	5'	AGAAACCCGGGGTTGGGGGCTC 8567	T G TAC_
A		TGAGC CCCCAG TTT TTCT	
		ACTCG GGGGTT GGG AAGA	
		_ G CCCA	
GAM1138 PPP2R4	3'	GAGAAGCACAGCACAGGGGCTC 30375	CCAA TTA
A		TGAGCTCC GTT CTTCTC	
		ACTCGGGG CGA GAAGAG	
		ACA_ CAC	
GAM1138 PRX	3'	GAGAAGTGGCCGAAGAGGCTCA 21937	CCCCAA TT
		TGAGCT GT TACTTCTC	
		ACTCGG CG GTGAAGAG	
		AGAAGC _	
GAM1138 SAR1	3'	AGAAGCTGCTGTGAGGAGCTCA 21351	C _ TTTA
		TGAGCTCC CA AGT CTTCT	
		ACTCGAGG GT TCG GAAGA	
		A G TC__	
GAM1138 WHSC1	3'	AAGTGACAACCTTAGGGAGC 28439	C _
		GCTCCC AAGTT TTA	
		CGAGGG TTCAA AGTGAA	
		A C	
GAM1138 WHSC1	3'	AAGTGACAACCTTAGGGAGC 28456	C _
		GCTCCC AAGTT TTA	

CGAGGG TTCAA AGTGAA
A C

GAM1138 WHSC1 3' AAGTGACAACCTTAGGGAGC 17175 C _
GCTCCC AAGTT TTA CTT
||||| ||||| |||||
CGAGGG TTCAA AGTGAA
A C

GAM1138 ATP1B4 3' GAGAAGCAGATTTGGAGAGATC 14324 G C TA
A TGA CTC CCAAGTTT CTTCTC
||| ||| ||||| |||||
ACT GAG GGTTTAGA GAAGAG
A A C_

GAM1138 C6.1A 3' AGAAGAAAACTTGGAGGACTC 23638 C _ A
A TGAG TCC CCAAGTTTT CTTCT
||||| ||| ||||| |||||
ACTC AGG GGTTCAAAA GAAGA
_ A A

GAM1138 CDC14A 3' GAGAAGTAGGGGAAAGGGAATC 9765 GC CAAG
A TGA TCCC TTTTACTTCTC
||| ||||| ||||| |||||
ACT AGGG GGGATGAAGAG
A_ AAAG

GAM1138 CNOT7 3' GAACTACTGAGGAGCTTA 15002 C _
TGAGCTCC CA AGTTTT
||||||| || |||||
ATTCGAGG GT TCAAAG
A CA

GAM1138 DKFZP434J193 3' GAGAAGTAAGACAGAGAAGCCG 35166 A CCCCCA
TG GCT GTTTTACTTCTC
|| ||| ||||| |||||
GC CGA CAGAATGAAGAG
_ AGAGA_

GAM1138 DKFZp761H2121 5' AAGTGGGGTGGGGAAGTCA 28738 C AG
TGAG TCCCCA TTTTACTT
||||| ||||| |||||
ACTC AGGGGT GGGGTGAA
A _

GAM1138 FLJ10716 3' AGGTAGAAGTTGAGAACTCA 20044 C CC
TGAG TC CAAGTTTTACTT
||||| || ||||| |||||
ACTC AG GTTCAAGATGGA
A A_

GAM1138 FLJ10738 3' AGAAGTGAACAAGGAGTCA 20068 G CCAA T
TGA CTCC GTTT ACTTCT
||| ||||| ||| |||||
ACT GAGG CAAG TGAAGA
_ AA_ _

GAM1138 FLJ22301 5' GAGAAGTAAACTTAGCTGCA 24241 _ CCCC
TG AGCT AAGTTTTACTTCTC
|| ||||| ||||| |||||

AC TCGA TTCAAATGAAGAG
 G _____
 GAM1138 KIAA0182 3' AAGTAAAAGAGCTTA 35642 CCCAAG
 TGAGCTC TTTTACTT
 ||||| |||||
 ATTCGAG AAAATGAA

 GAM1138 KIAA0494 3' AAGTTATCCATTGGGGAGCTC 16586 GTTTT_
 GAGCTCCCAA ACTT
 ||||| |||
 CTCGAGGGGT TGAA
 ACCTAT
 GAM1138 KIAA0660 3' AAGTAGAGCAAAGAGCCA 14656 A CCCAA
 TG GCTC GTTTTACTT
 || ||| |||||
 AC CGAG CGAGATGAA
 _ AAA_
 GAM1138 RNF9 3' AGAAATAAACTGCTCA 27410 TCCCA C
 TGAGC AGTTTTA TTCT
 ||| ||||| |||
 ACTCG TCAAAT AAGA
 _____ A
 GAM1138 LOC124222 3' GAAACTGACACAGGGAGCTCA 36741 CA____
 TGAGCTCCC AGTTTT
 ||||| |||||
 ACTCGAGG TCAAAG
 ACACAG
 GAM1138 LOC131870 3' GAGAAGTTGGCCTTCAAGGGGC 37017 CC_ T TT
 TCA TGAGCTCC AAG T ACTTCTC
 ||||| ||| |||||
 ACTCGGGG TTC G TGAAGAG
 AAC C GT
 GAM1138 LOC150213 3' GAGAAATATGGATGGGGAGC 36959 AGTTT C
 GCTCCCA TA TTCTC
 ||||| || |||||
 CGAGGGGT AT AAGAG
 AGGT_ A
 GAM1138 LOC150236 5' GAGAAATATGGATGGGGAGC 38905 AGTTT C
 GCTCCCA TA TTCTC
 ||||| || |||||
 CGAGGGGT AT AAGAG
 AGGT_ A
 GAM1138 LOC220840 3' GAGAAGTAACAGGGAAGCTACA 43658 _ C AAGTT
 TG AGCT CCC TTTACTTCTC
 || ||| ||| |||||
 AC TCGA GGG AATGAAGAG
 A A AC____
 GAM1138 LOC221914 3' AGGTGGGGGGGTGCTCA 45099 T AAGT
 TGAGC CCCC TTTACTT
 |||| ||| |||||

ACTCG GGGG GGGTGGGA
 T ____
 GAM1138 LOC257277 5' AGAAGTCGTGGGGGGCCCA 45640 A AGTTTT
 TG GCTCCCCA ACTTCT
 || ||||| |||||
 AC CGGGGGGT TGAAGA
 C GC____
 GAM1138 LOC91464 3' AAGTAGGACGGAAAGCTC 32872 CC AA
 GAGCT CC GTTTTACTT
 |||| | |||||
 CTCGA GG CAGGATGAA
 AA ____
 GAM1139 C20orf36 3' GGCTCTGACGAAACACTGA 20221 G TAG T
 TCAGTGTT TCGTCA G GCC
 ||||| |||| | |||
 AGTCACAA AGCAGT C CGG
 - ____T
 GAM1139 DKFZp586l021 5' GCACCTACAAGCAGCACTG 26027 CGTCA
 CAGTGTTGT TAGGTGC
 ||||| |||||
 GTCACGACG ATCCACG
 AAC____
 GAM1139 LOC154834 3' GCTTTCCAACACCAACACTGA 41732 TC CAT_
 TCAGTGTTG GT AGGT
 ||||| || |||
 AGTCACAAC CA TTCG
 CA ACCT
 GAM1139 LOC169026 5' ACCTACCAACAACACTGA 40261 CGTCA
 TCAGTGTTGT TAGGT
 ||||| |||||
 AGTCACAACA ATCCA
 ACC____
 GAM1139 LOC201292 5' GCACACGACAGCACTGA 42563 CATAG
 TCAGTGTTGTCGT GTGC
 ||||| |||||
 AGTCACGACAGCA CACG

 GAM1140 ATP11A 3' AAGGCCACGCCGGCAGCT 37800 GAT
 AGCTGCCGGCGT GGCTTT
 ||||| |||||
 TCGACGGCCGCA CCGGAA

 GAM1140 FLJ22056 5' CGAAAGCCTGCTCACCAGCCGC 22868 C ____ T_
 CA TG CGGC GTGA GGCTTTCTG
 || ||| ||| |||||
 AC GCCG CACT CCGAAAGC
 C AC CGT
 GAM1140 LOC253461 3' GAAAACATGCCGGAAGC 46073 G ATGGC
 GCT CCGGCGTG TTTC
 || ||||| |||

			CGA GGCCGTAC	AAAG		
			A	A__		
GAM1141	TRPC6	5'	GAACCCTCCGCACCGGGTCCC	10975	AGAC	A
			GGGATCCG	GCG AGGGTTC		
			CCCTGGGC	CGC TCCCAAG		
			CA__	C		
GAM1141	NTT73	5'	AACCCAGCCCCGGGTCCC	19820	AGAC	GAA
			GGGATCCG	GC GGGTT		
			CCCTGGGC	CG CCCAA		
			CC__	A__		
GAM1142	LANCL1	3'	AAGGGAATACTATCTAACCA	12692	C	GGTGA
			TGG TAGGTAGTA	CCTT		
			ACC ATCTATCAT	GGAA		
			A	AAG__		
GAM1142	PCDH9	5'	GAGGACTATCTAACCA	40294	C	AGGTGA
			TGG TAGGTAGT	CCTT		
			ACC ATCTATCA	GGAG		
			A	_____		
GAM1142	RFX5	3'	GGTGACCTTAAAGACTTCCTAG	6048	T T_____	TGA
	CCA		GGCTAGG AG	AGG CC		
			CCGATCC TC	TCC GG		
			T AGAAIIIT	AGT		
GAM1142	C17orf26	3'	AAGGTCACCTATAGAAGC	29183	AGGTA	
			GCT GTAGGTGACCTT			
			CGA TATCCACTGGAA			
			AGA__			
GAM1142	CABYR	3'	AAGGTCACCCATCACCGCCA	14476	TA	A A
			TGGC GGT GT GGTGACCTT			
			ACCG CCA TA CCACTGGAA			
			__	C C		
GAM1142	FLJ10579	3'	AAGATCATACCTTACCTACCA	19944	C	TAG C
			TGG TAGGTAG	GTGA CTT		
			ACC ATCCATT	TACT GAA		
			_	CCA A		
GAM1142	FLJ11618	3'	AAGGTCATAACCTCACCAGCCA	22790	A	_ TAG
			TGGCT GGT AG	GTGACCTT		
			ACCGA CCA TC	TACTGGAA		
			_	C CAA		
GAM1142	HAPIP	3'	AAGACCACCCTACCAGCC	10066	A	TA AC
			GGCT GGTAG	GGTG CTT		

CCGA CCATC CCAC GAA
 _ _ CA
 GAM1142 KIAA0515 3' AAGGTCACCTGTTCTCCAGCC 31915 A T _
 GGCT GG AG TAGGTGACCTT
 ||| ||| |||||
 CCGA CC TC GTCCACTGGAA
 _ _ TT
 GAM1142 NPD009 5' AAGGTCACCTGCACTCCCAGCC 45559 A TA_
 GGCT GG GTAGGTGACCTT
 ||| || |||||
 CCGA CC CGTCCACTGGAA
 C TCA
 GAM1142 PELI2 3' AAGGCCAGATTTTACCTACCA 22227 C TAGG A
 TGG TAGGTAG TG CCTT
 || ||||| || |||
 ACC ATCCATT AC GGAA
 _ TTAG C
 GAM1142 LOC116411 5' AAGGTCAGTACCTTGCCA 36563 T AGTA
 TGGC AGGT GGTGACCTT
 ||| ||| |||||
 ACCG TCCG TCACTGGAA
 T A_
 GAM1142 LOC51094 3' CACCAACTTTTACCTAGCC 18088 _ A
 GGCTAGGT AGT GGTG
 ||||| || |||
 CCGATCCA TCA CCAC
 TTT A
 GAM1143 ECM2 3' ACACAGATGAACAACC 7085 A GCTG
 GGT GTT CGTCTGTGT
 ||| ||| |||||
 CCA CAA GTAGACACA
 A _
 GAM1143 GPRC5B 3' ACACAGACACGTAATACC 18348 G T C
 GGTA TTGC G GTCTGTGT
 ||| ||| | |||||
 CCAT AATG C CAGACACA
 _ _ A
 GAM1143 LILRB4 3' ACACAGACACACACACAC 13716 A _ C C
 GT GT TG TG GTCTGTGT
 || ||| || |||||
 CA CA AC AC CAGACACA
 _ C _ A
 GAM1143 KIAA1161 5' CACACACTGACAACCTACC 39749 CT C C
 GGTAGTTG G GT TGTG
 ||||| | || |||
 CCATCAAC T CA ACAC
 AG _ C
 GAM1144 CCNF 3' ACAACACACCCTGCTGCCA 7522 G CTCTA
 TGGC AGCAGGGT GTTGT
 ||| ||||| |||

ACCG TCGTCCCA CAACA
 _ CA____
 GAM1144 TAF7L 3' TTAAAGACCCCACTCGACCA 24339 _ CA C
 TGG CGAG GGGTCT TAG
 ||| ||| ||||| |||
 ACC GCTC CCCAGA ATT
 A AC A
 GAM1144 FER1L4 3' ACCGGAGACCCTGCCCCCA 24871 CGA TA
 TGG GCAGGGTCTC GT
 ||| ||||| ||| ||
 ACC CGTCCCAGAG CA
 CC_ GC
 GAM1144 KIAA0040 3' CACAACTGCCACTGCTCACCA 16094 C _ CTCT
 TGG GAGCAG GGT AGTTGTG
 ||| ||||| ||| |||||
 ACC CTCGTC CCG TCAACAC
 A A ____
 GAM1144 LHX6 3' CAGGGAGAGACCCTACCCCCA 15697 CGAGC AG
 TGG AGGGTCTCT TTG
 ||| ||||| ||| |||
 ACC TCCCAGAGA GAC
 CCCA_ GG
 GAM1144 LOC160414 3' TGGGGACCCCGCTCACCA 42106 C A
 TGG GAGC GGGTCTCTA
 ||| ||| ||||| |||
 ACC CTCG CCCAGGGGT
 A C
 GAM1144 LOC51716 3' CACAACTAGAAAGTGTACC 18403 C G GGGTC
 GG GA CA TCTAGTTGTG
 || ||| ||||| |||
 CC CT GT AGATCAACAC
 A _ GAA____
 GAM1145 B3GNT7 3' GCATCTGCCCCGGTGAAG 35238 ATGGTG
 TTTCAC GGGGCAGATGC
 ||||| ||||| |||
 GAAGTG CCCCCGTCTACG
 G____
 GAM1145 CHST4 3' GCACATCCCACCAAGTGAAA 12338 A GCAGA
 TTTCAC TGGTG GGGG TGC
 ||||| ||||| ||| |||
 AAAGTG ACCACCCT ACG
 _ AC____
 GAM1145 CLIC4 3' CATCTGACACCATGTAGAA 15128 _ GGGG
 TTC ACATGGTG CAGATG
 ||| ||||| ||| |||||
 AAG TGTACCAC GTCTAC
 A A____
 GAM1145 FLJ11274 3' CATGGTTCCCACCATGT 20398 AG
 ACATGGTG GGGGGC ATG
 ||||| ||||| ||| |||

		TGTACCACCCTTG TAC	
		G_	
GAM1145	FLJ12903	3' AGCATCCTTCGGACCTCACCAC 22976	ACA GCA_____
		GCGAAA TTC TGGTGGGG GATGCT	
		AAG ACCACTCC CTACGA	
		CGC AGGCTTC	
GAM1146	ACT	3' ATGAGGTTTTTCATACCT 21735	CAA
		AGGTATGAAAA TTCAT	
		TCCATACTTTT GAGTA	
		TG_	
GAM1146	BRCA1	3' ATGAATATTTTCATATCT 14161	ACA
		AGGTATGAAA ATTCAT	
		TCTATACTTT TAAGTA	
		A_	
GAM1146	BRCA1	3' ATGAATATTTTCATATCT 14167	ACA
		AGGTATGAAA ATTCAT	
		TCTATACTTT TAAGTA	
		A_	
GAM1146	BRCA1	3' ATGAATATTTTCATATCT 14173	ACA
		AGGTATGAAA ATTCAT	
		TCTATACTTT TAAGTA	
		A_	
GAM1146	BRCA1	3' ATGAATATTTTCATATCT 14179	ACA
		AGGTATGAAA ATTCAT	
		TCTATACTTT TAAGTA	
		A_	
GAM1146	BRCA1	3' ATGAATATTTTCATATCT 14186	ACA
		AGGTATGAAA ATTCAT	
		TCTATACTTT TAAGTA	
		A_	
GAM1146	BRCA1	3' ATGAATATTTTCATATCT 14192	ACA
		AGGTATGAAA ATTCAT	
		TCTATACTTT TAAGTA	
		A_	
GAM1146	BRCA1	3' ATGAATATTTTCATATCT 14198	ACA
		AGGTATGAAA ATTCAT	
		TCTATACTTT TAAGTA	
		A_	
GAM1146	BRCA1	3' ATGAATATTTTCATATCT 14206	ACA
		AGGTATGAAA ATTCAT	

			TCTATACTTT TAAGTA		
			A__		
GAM1146	BRCA1	3'	ATGAATATTTTCATATCT 14212	ACA	
			AGGTATGAAA ATTCAT		
			TCTATACTTT TAAGTA		
			A__		
GAM1146	BRCA1	3'	ATGAATATTTTCATATCT 14218	ACA	
			AGGTATGAAA ATTCAT		
			TCTATACTTT TAAGTA		
			A__		
GAM1146	CASP2	3'	ATGTTATTGTTTTCAACCT 26852	A	T_
			AGGT TGAAAACAAT CAT		
			TCCA ACTTTTGTTA GTA		
			TT		
GAM1146	CASP2	3'	ATGTTATTGTTTTCAACCT 26857	A	T_
			AGGT TGAAAACAAT CAT		
			TCCA ACTTTTGTTA GTA		
			TT		
GAM1146	CASP2	3'	ATGTTATTGTTTTCAACCT 26862	A	T_
			AGGT TGAAAACAAT CAT		
			TCCA ACTTTTGTTA GTA		
			TT		
GAM1146	CASP2	3'	ATGTTATTGTTTTCAACCT 6889	A	T_
			AGGT TGAAAACAAT CAT		
			TCCA ACTTTTGTTA GTA		
			TT		
GAM1146	CRMP1	3'	ATGGTGTTTTTCATTCC 6998	T	AT
			GG ATGAAAACA TCAT		
			CC TACTTTTGT GGTA		
			T		
GAM1146	DUSP5	3'	ATGGACATTTTCATACCT 10683	ACAA	
			AGGTATGAAA TTCAT		
			TCCATACTTT AGGTA		
			AC__		
GAM1146	HOXA7	3'	GTATAAATTGTTTTCATACTT 13770		C
			AGGTATGAAAACAATT ATAC		
			TTCATACTTTTGTTAA TATG		
			A		
GAM1146	IL12B	3'	GTATGGAATGTTTCATACT 7942	A A	
			GGTATGAAA CA TTCATAC		

		TCATACTTT GT AGGTATG	
		_ A	
GAM1146 MLLT3	3'	TATGAATTGCTGTCTAGCCT 10871	AT AAA
		AGGT GA CAATTCATA	
		TCCG CT GTTAAGTAT	
		AT GTC	
GAM1146 NOV	3'	TATGAGGACCTTTCATATCT 8346	ACAA
		AGGTATGAAA TTCATA	
		TCTATACTTT GAGTAT	
		CCAG	
GAM1146 PFN2	3'	TATGAACTCGCTTTTATACCT 27582	AACAA
		AGGTATGAA TTCATA	
		TCCATATTT AAGTAT	
		CGCTC	
GAM1146 PIGA	3'	TATGAACTGTTTTATATC 21712	A A
		GGTATGAAA CA TTCATA	
		CTATATTTT GT AAGTAT	
		_ C	
GAM1146 PIGA	3'	TATGAACTGTTTTATATC 21719	A A
		GGTATGAAA CA TTCATA	
		CTATATTTT GT AAGTAT	
		_ C	
GAM1146 PIGA	3'	TATGAACTGTTTTATATC 8499	A A
		GGTATGAAA CA TTCATA	
		CTATATTTT GT AAGTAT	
		_ C	
GAM1146 STS	3'	ATGATTTTGTTCATCC 5906	T T_
		GG ATGAAAACAA TCAT	
		CC TACTTTTGTT AGTA	
		TT	
		_	
GAM1146 CCR5	3'	ATGGCTTAGTTTTTCATAC 6183	_ TT
		GTATGAAAAC AA CAT	
		CATACTTTTG TT GTA	
		A CG	
GAM1146 CLSTN2	3'	GTATGCCCATGTCTATCATACC 22693	AA_ ATT_
		AGGTATGA ACA CATAC	
		TCCATACT TGT GTATG	
		ATC ACCC	
GAM1146 CPR2	3'	GTATGAGTATTCATTCCT 25176	T AACAA
		AGG ATGAA ATTCATAC	

TCC TACTT TGAGTATG
 T A__
 GAM1146 MGC4730 3' GTATGAATTGCTGATACTT 32133 GAAAA
 AGGTAT CAATTCATAC
 ||||| |||||
 TTCATA GTTAAGTATG
 GTC__
 GAM1146 ODZ2 3' TATGAATTGTTTCATCG 35097 T AA
 G ATGA ACAATTCATA
 ||||| |||||
 G TACT TGTTAAGTAT
 C __
 GAM1146 TA-KRP 3' TGTGAAGTTTATACCT 26254 ACAA
 AGGTATGAAA TTCATA
 ||||| |||||
 TCCATATTTT AAGTGT
 G__
 GAM1146 WDR7 3' GTATGAATTGTTTCTAAC 17611 A A
 GT TG AAACAATTCATAC
 || || |||||
 CA AT TTTGTTAAGTATG
 _ C
 GAM1146 LOC154739 5' GTGTGATATTTTCATAC 41721 CAAT
 GTATGAAAA TCATAC
 ||||| |||||
 CATACTTTT AGTGTG
 AT__
 GAM1146 LOC158401 5' GTATGAATTCTTAATACCT 39837 GAAAAC
 AGGTAT AATTCATAC
 ||||| |||||
 TCCATA TTAAGTATG
 ATTC__
 GAM1146 LOC90488 3' TATGAAGGTTTCTCATACTT 31559 _ AA
 AGGTATGA AAAC TTCATA
 ||||| |||||
 TTCATACT TTTG AAGTAT
 C G_
 GAM1146 LOC91115 3' TGAATTGTTCCCATAGCT 32403 G AA
 AG TATG AACAATTCA
 || ||||| |||||
 TC ATAC TTGTTAAGT
 G CC
 GAM1147 HLCS 3' ACGGAATATAGAAGACATGG 5988 A GCGAA
 CTAT TCTTCTATA TGT
 ||| ||||| |||
 GGTA AGAAGATAT GCA
 C AAG__
 GAM1147 TNFSF4 3' ACATTTTCAATAGAGGATA 9327 AGC
 TATCTTCTAT GAATGT
 ||||| |||||

	ATAGGAGATA TTTACA	
	ACT	
GAM1147 FLJ23511 3'	TTCTTAAAGAAGATATAGTA 25969	A C
	TACTATATCTTCT TAG GAA	
	ATGATATAGAAGA ATT CTT	
	A _	
GAM1147 LOC120196 3'	ACATTACTTTAGAAGATATG 37218	T CG
	TATATCTTCTA AG AATGT	
	GTATAGAAGAT TC TTACA	
	T A_	
GAM1148 DAB2 3'	CTTAGACACTTTGGAATC 7023	_ C
	GATTCCAA TGTC AAG	
	CTAAGGTT ACAG TTC	
	TC A	
GAM1148 FLJ11269 3'	TGAACAGTTATCACATTTAA 35955	TCCAA C
	TTAAATGTGAT TGT CA	
	AATTTACACTA ACA GT	
	TTG_ A	
GAM1148 KIAA0016 3'	TTGAACAAATCACATTT 16536	CCAA C
	AAATGTGATT TGT CAA	
	TTTACACTAA ACA GTT	
	_ A	
GAM1148 KIAA1431 3'	CTTGTTTAAAAATCACATTTA 31551	CCAA TC
	TAAATGTGATT TG CAAG	
	ATTTACACTAA AT GTTC	
	AA_ TT	
GAM1148 PCDH19 3'	TTGGTAAAATTACATTTAA 31866	CCAATGT
	TTAAATGTGATT CCAA	
	AATTTACATTAA GGTT	
	AAT_	
GAM1148 LOC221300 3'	TTTGTGACCAGAACACATTTAA 44150	A CAAT _
	TTAAATGTG TTC GTC CAAG	
	AATTTACAC AAG CAG GTTT	
	_ AC_ T	
GAM1148 LOC222499 5'	CTTGGACATCCTGAACAT 45303	A CA_
	GTG TTC ATGTCCAAG	
	TAC AAG TACAGGTTC	
	_ TCC	
GAM1148 LOC90321 3'	CTTGAGTAGGATTCACATTTAA 31210	T AA TC
	TTAAATGTGA TCC TG CAAG	

AATTTACACT AGG AT GTTC
 T _ GA
 GAM1149 LPL 3' ACACAGAGGTTTTAAAC 5747 TTGATA
 GTTTAAA CTCTGTGT
 ||||| |||||
 CAAATTT GAGACACA
 TG____
 GAM1149 DICER1 5' ACACAGAGATCTCAAAC 24963 AAATT A
 GTTT GATCTCTGTGT
 ||| ||| |||||
 CAAA CTA GAGACACA
 CT_____
 GAM1149 FLJ11040 3' ACACAGAGTAATAATCAAAC 20294 AA A
 GTTT ATTG TACTCTGTGT
 ||| ||| |||||
 CAAA TAAT ATGAGACACA
 C_ A
 GAM1149 TCL6 5' GACACAGAGTATTTTAAAAGA 21770 G ATT
 TC TTTAA GATACTCTGTGTC
 || ||||| |||||
 AG AAATT TTATGAGACACAG
 A _
 GAM1149 TCL6 5' GACACAGAGTATTTTAAAAGA 21761 G ATT
 TC TTTAA GATACTCTGTGTC
 || ||||| |||||
 AG AAATT TTATGAGACACAG
 A _
 GAM1149 TCL6 5' GACACAGAGTATTTTAAAAGA 14843 G ATT
 TC TTTAA GATACTCTGTGTC
 || ||||| |||||
 AG AAATT TTATGAGACACAG
 A _
 GAM1149 TCL6 5' GACACAGAGTATTTTAAAAGA 15767 G ATT
 TC TTTAA GATACTCTGTGTC
 || ||||| |||||
 AG AAATT TTATGAGACACAG
 A _
 GAM1149 LOC200609 5' ACACAGAGTCAGTGTTAAAT 43322 _ TA
 GTTTAA ATTGA CTCTGTGT
 ||||| ||||| |||||
 TAAATT TGA CT GAGACACA
 G _
 GAM1149 LOC253747 5' ACACAGAGGGACAACTCAAAC 46551 AAA_ ATA
 GTTT TTG CTCTGTGT
 ||| ||| |||||
 CAAA AAC GAGACACA
 CTCA AGG
 GAM1150 ITGB1 3' CCGTGCAAATCCCACAACA 7977 A GTTA
 TGTTGTGG ATT ACGG
 ||||| ||| |||

ACAACACC TAA TGCC
C ACG_

GAM1150 LRAT 3' CCACTAATTTGCCACAACAA 30182 AATT AC
TTGTTGTGG GTTA GG
||||||| ||| ||
ACAACACC TAAT CC
CGTT CA

GAM1150 FLJ20281 5' GTTAACATCCCACAACAAC 43728 AAT
GTTGTTGTGG TGTTAAC
||||||| |||||
CAACAACACC ACAATTG
CT_

GAM1150 RP4-622L5 3' CCATGGACATCCCCAACAAC 21200 T AT AAC
GTTGTTG GGA TGTT GG
||||||| ||| ||| ||
CAACAAC CCT ACAG CC
C _ GTA

GAM1150 LOC129566 5' CCGCGGACCTTCCACAACGAC 37280 TT AA
GTTGTTGTGGAA GTT CGG
||||||| ||| |||
CAGCAACACCTT CAG GCC
C_ GC

GAM1150 LOC154386 5' CCGTAATGCTCACAACAAC 39472 AAT A
GTTGTTGTGG TGTTA CGG
||||||| ||||| |||
CAACAACACT GTAAT GCC
C_ _

GAM1151 AGPAT2 3' TTCTGTCACTGGTCTCA 13120 T AG
TGAGACCA TGA AGAG
||||||| ||| |||
ACTCTGGT ACT TCTT
C G_

GAM1151 ARHGEF6 3' CTCCCTCTCTCTTCTCTTTCTC 33846 CCATT AA
GAGA GAAGAGAGA GAG
||| ||||| |||
CTCT CTTCTCTCT CTC
TTCT_ CC

GAM1151 ARHGEF6 3' CTCTCTCTCTCTCCCTCTCTC 33847 CCATT A A
GAGA GA GAGAGA AGAG
||| || ||||| |||
CTCT CTCTCTCT TCTC
CTCC_ _ C

GAM1151 ATP8A2 3' TCTTTCTCCCAGGCCTCA 44924 A AT AAGA
TGAG CC TG GAGAAAGA
||| || || |||||
ACTC GG AC CTCTTTCT
C _ C_

GAM1151 BSN 3' CTTTCTCTCTTCTCTTGGCTCA 9517 A TT_
TGAG CCA GAAGAGAGAAAG
||| ||| |||||

ACTC GGT CTTCTCTCTTTC
 _ TCT
 GAM1151 DPYSL2 5' CTCCTTCTCTCTCTCTCTC 7063 CCATT _ A
 GAGA GA AGAGAGAA GAG
 ||| || ||||| |||
 CTCT CT TCTCTCTT CTC
 CT__ C C
 GAM1151 ENO2 3' TCTTTCTCTCTTCCCTCA 7706 ACCATT
 TGAG GAAGAGAGAAAGA
 ||| ||||| |||||
 ACTC CTTCTCTCTTTCT
 C____
 GAM1151 FTSJ2 3' CTCTCTCTCTCTTTCTCTCTC 15044 CCATT A
 GAGA GAAGAGAGA AGAG
 ||| ||||| |||
 CTCT TTTCTCTCT TCTC
 CTC__ C
 GAM1151 GAC1 3' CTCTTTCTCTGTACAGTCTCA 13037 CAT AAG
 TGAGAC TG AGAGAAAGAG
 ||||| || ||||| |||
 ACTCTG AC TCTCTTTCTC
 __ ATG
 GAM1151 GLUD1 3' CTTTCTCTCCTGACTCA 11774 AC TTGAA
 TGAG CA GAGAGAAAG
 ||| || ||||| |||
 ACTC GT CTCTCTTTC
 A_ C____
 GAM1151 HCN4 3' TCTCTCCCATCTCTGGTCTCA 11979 TT A____
 TGAGACCA GA GAGAGA
 ||||| || ||||| |||
 ACTCTGGT CT CTCTCT
 CT ACCC
 GAM1151 HMGA2 3' CTCTCCCTCTCCCTCTCTC 9566 CCATT A_ AA
 GAGA GA GAGAG AGAG
 ||| || ||||| |||
 CTCT CT CTCTC TCTC
 ____ CC CC
 GAM1151 HMGA2 3' CTCTCTCTCTCTCCCTCTC 9567 CCATT A A
 GAGA GA GAGAGA AGAG
 ||| || ||||| |||
 CTCT CT CTCTCT TCTC
 CC__ _ C
 GAM1151 IGF1R 3' CTTTCTCTCCTCTC 6557 CCATT A
 GAGA GA GAGAGAAAG
 ||| || ||||| |||
 CTCT CT CTCTCTTTC
 C____ _
 GAM1151 KIF3B 3' CTTTCTCTCCTCTCTC 11216 CCATT A
 GAGA GA GAGAGAAAG
 ||| || ||||| |||

CTCT CTCTCTTTC
 _____ C
 GAM1151 LPL 3' TCTCTCCCCCTTCTTTTTTGTC 5754 CATT__ ____
 TCA TGAGAC GAA GAGAGA
 ||||| ||| |||||
 ACTCTG CTT CTCTCT
 TTTTTT CCCC
 GAM1151 MEIS1 3' CTCTTTCTCTCTCTTTTCCTC 8218 ACCATT A
 GAG GA GAGAGAAAGAG
 ||| || |||||
 CTC CT CTCTCTTTCTC
 CTTT_ _
 GAM1151 NFIA 5' CTCTCTCTCTCTTCTCTCTC 34841 CCATT A
 GAGA GAAGAGAGA AGAG
 ||| ||||| |||
 CTCT CTTCTCTCT TCTC
 CTC_ C
 GAM1151 NFIA 5' CTCTCTCCCTCTTTCTCCTCTC 34840 CCATT A A
 GAGA GAAGAG GA AGAG
 ||| ||||| |||
 CTCT TTTCTC CT TCTC
 CCTC_ C C
 GAM1151 NPR1 5' CTTTCTCTCTCTCTCTC 42235 CCATT _
 GAGA GA AGAGAGAAAG
 ||| || |||||
 CTCT CT TCTCTCTTC
 CT_ C
 GAM1151 NTRK2 3' CTCTTTCTCTCTTTCCATCTC 12843 CCATT
 GAGA GAAGAGAGAAAGAG
 ||| |||||
 CTCT TTTCTCTCTTTCTC
 ACC_
 GAM1151 PAX5 3' TCTTCCTCTCTTCCTC 18792 ACCATT A
 GAG GAAGAGAG AAGA
 ||| ||||| |||
 CTC CTTCTCTC TTCT
 _____ C
 GAM1151 PCDHA1 3' CTCTTTCTCTCTCTCTCTC 20866 CCATT _
 GAGA GA AGAGAGAAAGAG
 ||| || |||||
 CTCT CT TCTCTCTTTCTC
 CT_ C
 GAM1151 PCDHA1 3' TCTCTCTCTCTTTTCT 20869 CCATT A
 AGA GAAGAGAGA AGA
 ||| ||||| |||
 TCT TTTCTCTCT TCT
 _____ C
 GAM1151 PCDHA1 3' CTCTTTCTCTCTCTCTCTC 25385 CCATT _
 GAGA GA AGAGAGAAAGAG
 ||| || |||||

CTCT CT TCTCTCTTTCTC
 CT__ C
 GAM1151 PCDHA1 3' TCTCTCTCTCTTTTCT 25388 CCATT A
 AGA GAAGAGAGA AGA
 ||| ||||| |||
 TCT TTTCTCTCT TCT
 ____ C
 GAM1151 PCDHA10 3' CTCTTTCTCTCTCTCTCTC 25617 CCATT _
 GAGA GA AGAGAGAAAGAG
 ||| || ||||| |||
 CTCT CT TCTCTCTTTCTC
 CT__ C
 GAM1151 PCDHA10 3' TCTCTCTCTCTTTTCT 25620 CCATT A
 AGA GAAGAGAGA AGA
 ||| ||||| |||
 TCT TTTCTCTCT TCT
 ____ C
 GAM1151 PCDHA10 3' CTCTTTCTCTCTCTCTCTC 20876 CCATT _
 GAGA GA AGAGAGAAAGAG
 ||| || ||||| |||
 CTCT CT TCTCTCTTTCTC
 CT__ C
 GAM1151 PCDHA10 3' TCTCTCTCTCTTTTCT 20879 CCATT A
 AGA GAAGAGAGA AGA
 ||| ||||| |||
 TCT TTTCTCTCT TCT
 ____ C
 GAM1151 PCDHA11 3' CTCTTTCTCTCTCTCTCTC 20886 CCATT _
 GAGA GA AGAGAGAAAGAG
 ||| || ||||| |||
 CTCT CT TCTCTCTTTCTC
 CT__ C
 GAM1151 PCDHA11 3' TCTCTCTCTCTTTTCT 20890 CCATT A
 AGA GAAGAGAGA AGA
 ||| ||||| |||
 TCT TTTCTCTCT TCT
 ____ C
 GAM1151 PCDHA12 3' CTCTTTCTCTCTCTCTCTC 20897 CCATT _
 GAGA GA AGAGAGAAAGAG
 ||| || ||||| |||
 CTCT CT TCTCTCTTTCTC
 CT__ C
 GAM1151 PCDHA12 3' TCTCTCTCTCTTTTCT 20900 CCATT A
 AGA GAAGAGAGA AGA
 ||| ||||| |||
 TCT TTTCTCTCT TCT
 ____ C
 GAM1151 PCDHA13 3' CTCTTTCTCTCTCTCTCTC 20907 CCATT _
 GAGA GA AGAGAGAAAGAG
 ||| || ||||| |||

CTCT CT TCTCTCTTTCTC
 CT__ C
 GAM1151 PCDHA13 3' TCTCTCTCTCTTTTCT 20910 CCATT A
 AGA GAAGAGAGA AGA
 ||| ||||| |||
 TCT TTTCTCTCT TCT
 ____ C
 GAM1151 PCDHA2 3' CTCTTTCTCTCTCTCTCTC 20917 CCATT _
 GAGA GA AGAGAGAAAGAG
 ||| || ||||| |||
 CTCT CT TCTCTCTTTCTC
 CT__ C
 GAM1151 PCDHA2 3' TCTCTCTCTCTTTTCT 20920 CCATT A
 AGA GAAGAGAGA AGA
 ||| ||||| |||
 TCT TTTCTCTCT TCT
 ____ C
 GAM1151 PCDHA3 3' CTCTTTCTCTCTCTCTCTC 20927 CCATT _
 GAGA GA AGAGAGAAAGAG
 ||| || ||||| |||
 CTCT CT TCTCTCTTTCTC
 CT__ C
 GAM1151 PCDHA3 3' TCTCTCTCTCTTTTCT 20930 CCATT A
 AGA GAAGAGAGA AGA
 ||| ||||| |||
 TCT TTTCTCTCT TCT
 ____ C
 GAM1151 PCDHA4 3' CTCTTTCTCTCTCTCTCTC 20937 CCATT _
 GAGA GA AGAGAGAAAGAG
 ||| || ||||| |||
 CTCT CT TCTCTCTTTCTC
 CT__ C
 GAM1151 PCDHA4 3' TCTCTCTCTCTTTTCT 20940 CCATT A
 AGA GAAGAGAGA AGA
 ||| ||||| |||
 TCT TTTCTCTCT TCT
 ____ C
 GAM1151 PCDHA5 3' CTCTTTCTCTCTCTCTCTC 20947 CCATT _
 GAGA GA AGAGAGAAAGAG
 ||| || ||||| |||
 CTCT CT TCTCTCTTTCTC
 CT__ C
 GAM1151 PCDHA5 3' TCTCTCTCTCTTTTCT 20950 CCATT A
 AGA GAAGAGAGA AGA
 ||| ||||| |||
 TCT TTTCTCTCT TCT
 ____ C
 GAM1151 PCDHA6 3' CTCTTTCTCTCTCTCTCTC 20957 CCATT _
 GAGA GA AGAGAGAAAGAG
 ||| || ||||| |||

CTCT CT TCTCTCTTTCTC
 CT__ C
 GAM1151 PCDHA6 3' TCTCTCTCTCTTTTCT 20960 CCATT A
 AGA GAAGAGAGA AGA
 ||| ||||| |||
 TCT TTTCTCTCT TCT
 ____ C
 GAM1151 PCDHA6 3' CTCTTTCTCTCTCTCTCTC 25589 CCATT _
 GAGA GA AGAGAGAAAGAG
 ||| || ||||| |||
 CTCT CT TCTCTCTTTCTC
 CT__ C
 GAM1151 PCDHA6 3' TCTCTCTCTCTTTTCT 25592 CCATT A
 AGA GAAGAGAGA AGA
 ||| ||||| |||
 TCT TTTCTCTCT TCT
 ____ C
 GAM1151 PCDHA7 3' CTCTTTCTCTCTCTCTCTC 20967 CCATT _
 GAGA GA AGAGAGAAAGAG
 ||| || ||||| |||
 CTCT CT TCTCTCTTTCTC
 CT__ C
 GAM1151 PCDHA7 3' TCTCTCTCTCTTTTCT 20970 CCATT A
 AGA GAAGAGAGA AGA
 ||| ||||| |||
 TCT TTTCTCTCT TCT
 ____ C
 GAM1151 PCDHA8 3' CTCTTTCTCTCTCTCTCTC 20977 CCATT _
 GAGA GA AGAGAGAAAGAG
 ||| || ||||| |||
 CTCT CT TCTCTCTTTCTC
 CT__ C
 GAM1151 PCDHA8 3' TCTCTCTCTCTTTTCT 20980 CCATT A
 AGA GAAGAGAGA AGA
 ||| ||||| |||
 TCT TTTCTCTCT TCT
 ____ C
 GAM1151 PCDHA9 3' CTCTTTCTCTCTCTCTCTC 25603 CCATT _
 GAGA GA AGAGAGAAAGAG
 ||| || ||||| |||
 CTCT CT TCTCTCTTTCTC
 CT__ C
 GAM1151 PCDHA9 3' TCTCTCTCTCTTTTCT 25606 CCATT A
 AGA GAAGAGAGA AGA
 ||| ||||| |||
 TCT TTTCTCTCT TCT
 ____ C
 GAM1151 PCDHAC1 3' CTCTTTCTCTCTCTCTCTC 20846 CCATT _
 GAGA GA AGAGAGAAAGAG
 ||| || ||||| |||

CTCT CT TCTCTCTTTCTC
 CT__ C
 GAM1151 PCDHAC1 3' TCTCTCTCTCTTTTCT 20849 CCATT A
 AGA GAAGAGAGA AGA
 ||| ||||| |||
 TCT TTTCTCTCT TCT
 ____ C
 GAM1151 PCDHAC2 3' CTCTTTCTCTCTCTCTCTC 20856 CCATT _
 GAGA GA AGAGAGAAAGAG
 ||| || ||||| |||
 CTCT CT TCTCTCTTTCTC
 CT__ C
 GAM1151 PCDHAC2 3' TCTCTCTCTCTTTTCT 20859 CCATT A
 AGA GAAGAGAGA AGA
 ||| ||||| |||
 TCT TTTCTCTCT TCT
 ____ C
 GAM1151 PCK1 3' CTCTTTCTCTCCTGCAGTCCCG 12872 A CAT AA_
 TG GAC TG GAGAGAAAGAG
 || ||| || ||||| |||
 GC CTG AC CTCTCTTTCTC
 C __ GTC
 GAM1151 PCK1 3' CTCTTTCTCTCCTGCAGTCCCG 26907 A CAT AA_
 TG GAC TG GAGAGAAAGAG
 || ||| || ||||| |||
 GC CTG AC CTCTCTTTCTC
 C __ GTC
 GAM1151 PCK1 3' CTCTTTCTCTCCTGCAGTCCCG 26913 A CAT AA_
 TG GAC TG GAGAGAAAGAG
 || ||| || ||||| |||
 GC CTG AC CTCTCTTTCTC
 C __ GTC
 GAM1151 PPOX 5' CTCCTTCTCCCTCATTTTCTCT 5847 CCAT_ A A A
 CA TGAGA TGA G GAGAA GAG
 |||| ||| ||||| |||
 ACTCT ACT C CTCTT CTC
 CTTT _ C C
 GAM1151 PPT2 3' CTCTCTCTCTCTTTATTTTCA 29061 CCAT A
 TGAGA TGAAGAGAGA AGAG
 |||| ||||| ||||
 ACTTT ATTTCTCTCT TCTC
 T__ C
 GAM1151 PTK2B 3' TTCCTCTTCGGCCCTCA 10313 A_ ATT A
 TGAG CC GAAGAG GAA
 |||| || ||||| |||
 ACTC GG CTTCTC CTT
 CC __ _
 GAM1151 RUNX3 3' CTTTCCCCTAGGTGGTCTCA 10550 GA AGA
 TGAGACCATT AG GAAAG
 ||||| || ||||

ACTCTGGTGG TC CTTTC
 A_ CC_
 GAM1151 SH3BP5 3' CTCTTTCTCTTCTCACCCTCA 11257 ACCAT AG
 TGAG TGA AGAGAAAGAG
 |||| ||| |||||
 ACTC ACT TCTCTTTCTC
 CC__ CT
 GAM1151 SIX2 3' CTTTCTCTCTCCTTCTC 18850 CCATT A
 GAGA GA GAGAGAAAG
 |||| |||||
 CTCT CTCTCTTTCTC
 TC__ _
 GAM1151 SLC7A6 3' CTCCCCCTCCCTTGTGGTTTCA 10129 TG A AAA
 TGAGACCAT AAG GAG GAG
 ||||| ||| ||| |||
 ACTTTGGTG TTC CTC CTC
 _ C CCC
 GAM1151 TBL1X 3' CTCTTTCTCTCTCTCTCTC 12183 CCATT _
 GAGA GA AGAGAGAAAGAG
 |||| |||||
 CTCT CTCTCTCTTTCTC
 _ C
 GAM1151 TGFBR2 3' CTCTTTTATATCAAAAAGTCTC 9239 CA AGAG
 A TGAGAC TTGA AGAAAGAG
 |||| ||| |||||
 ACTCTG AACT TTTTCTC
 AA ATA_
 GAM1151 TNFSF5 3' CTCTCTCTCTCCATCTC 5519 CCAT A A
 GAGA TG AGAGAGA AG
 |||| ||||| ||
 CTCT AC TCTCTCT TC
 _ C C
 GAM1151 TRPS1 5' CTCTTTCTCTCTCTCTCTCTC 15352 CCATT _
 GAGA GA AGAGAGAAAGAG
 |||| |||||
 CTCT CTCTCTCTTTCTC
 CT__ C
 GAM1151 ACTR1A 3' TCTTTCTCCCTTTTCCTC 31535 ACCATT A
 GAG GAAG GAGAAAGA
 || |||||
 CTC TTTC CTCTTTCT
 CT__ C
 GAM1151 BCL2L1 3' CTCCCTCTCTCTTCTGCTC 28893 ACCATT AA
 GAG GAAGAGAGA GAG
 || ||||| |||
 CTC CTTCTCTCT CTC
 GT__ CC
 GAM1151 BIRC5 3' CTCTCTCTCTCTTTTGGGGG 6836 A__ TT A
 CTCA TGAG CCA GAAGAGAGA AGAG
 |||| ||| ||||| ||||

ACTC GGT TTTCTCTCT TCTC
 GGG TT C
 GAM1151 C1QR1 3' CTCTTTCTCTCTCTCTCTC 14333 CCATT _
 GAGA GA AGAGAGAAAGAG
 ||| || |||||
 CTCT CT TCTCTCTTTCTC
 CT__ C
 GAM1151 C2orf139 3' CTTTCTCTGTCTCA 41105 CATTGA
 TGAGAC AGAGAGAAAG
 |||| | |||||
 ACTCTG TCTCTCTTC

 GAM1151 C6orf9 3' TTCCTTGCCACTGGTCTCA 22656 T AA A
 TGAGACCA TG GAG GAA
 ||||| || |||
 ACTCTGGT AC TTC CTT
 C CG _
 GAM1151 CRK7 3' CTCTTTCTCTCTCTCTCTC 18586 CCATT _
 GAGA GA AGAGAGAAAGAG
 ||| || |||||
 CTCT CT TCTCTCTTTCTC
 CT__ C
 GAM1151 CRK7 3' CTCTCTCTCTTTCTCTCTC 18585 CCATT A
 GAGA GAAGAGAGA AGAG
 ||| ||||| |||
 CTCT TTTCTCTCT TCTC
 CTC__ C
 GAM1151 dA141H5.1 3' CTCCTTCTCTCTCTCTCTC 29748 CCATT _ A
 GAGA GA AGAGAGAA GAG
 ||| || ||||| |||
 CTCT CT TCTCTCTT CTC
 CT__ C C
 GAM1151 DCTD 3' TTCTCTTTAATCTCA 7637 CCA
 TGAGA TTGAAGAGAG
 |||| |||||
 ACTCT AATTCTCTT

 GAM1151 FLJ12572 3' TTCTCTTCAACAGTTCA 23202 A CA
 TGAG C TTGAAGAGAG
 |||| | |||||
 ACTT G AACTTCTCTT
 _ AC
 GAM1151 FLJ13154 3' CTCCTCTCTCTTCCTCTC 23837 CCATT AA
 GAGA GAAGAGAGA GAG
 ||| ||||| |||
 CTCT CTTCTCTCT CTC
 C__ C_
 GAM1151 FLJ13154 3' CTCTTCCTCTCCTCTCTCTC 23838 CCATT A A
 GAGA GA GAGAG AAGAG
 ||| || |||| ||||

		CTCT	CT CTCTC TTCTC		
		CT__	C C		
GAM1151	FLJ13154	3'	CTCTTCCTCTCCTCTCTCTC	23839	CCATT A A
			GAGA GA GAGAG AAGAG		
			CTCT CT CTCTC TTCTC		
			CT__	C C	
GAM1151	FLJ13154	3'	CTCTTCCTCTCCTCTCTCTC	23840	CCATT A A
			GAGA GA GAGAG AAGAG		
			CTCT CT CTCTC TTCTC		
			CT__	C C	
GAM1151	FLJ13154	3'	CTCTTCCTCTCCTCTCTCTCTC	23841	CCATT A A
			GAGA GA GAGAG AAGAG		
			CTCT CT CTCTC TTCTC		
			CTCT_	C C	
GAM1151	FLJ13154	3'	CTCTTCCTCTCCTCTCTTCCTC	23842	ACCATT A A
			GAG GA GAGAG AAGAG		
			CTC CT CTCTC TTCTC		
			CTTCT_	C C	
GAM1151	FLJ13154	3'	CTCTTTCTCTCCTCTGTCTC	23843	CATT A
			GAGAC GA GAGAGAAAGAG		
			CTCTG CT CTCTCTTTCTC		
			T__	C	
GAM1151	FLJ13154	3'	TCTTCCTCTCCTCTCTC	23845	CCATT A A
			GAGA GA GAGAG AAGA		
			CTCT CT CTCTC TTCT		
			__	C C	
GAM1151	FLJ13154	3'	TCTTCCTCTCTTCTCTC	23846	CCATT A
			GAGA GAAGAGAG AAGA		
			CTCT CTTCTCTC TTCT		
			__	C	
GAM1151	FLJ14594	3'	CTCTTTCTCCCTCCCGCCTC	26566	ACCATT A A
			GAG GA G GAGAAAGAG		
			CTC CT C CTCTTTCTC		
			CGCC_ _	C	
GAM1151	FLJ22671	3'	CTCCCCCTCTCCTTTTGCTCTC	24295	C TT A AAA
			GAGA CA GA GAGAG GAG		
			CTCT GT TT CTCTC CTC		
			C T_	C CCC	
GAM1151	FLJ22679	3'	CTCTTTCTCTCTCTCCTCA	19262	ACCATT _
			TGAG GA AGAGAGAAAGAG		

ACTC CT TCTCTCTTTCTC
 CT___ C
 GAM1151 FLJ23263 5' CTCCTTCCCTCTTCAGCGGATC 24766 _ A A A
 GA CC TTGAAGAG GAA GAG
 || || ||||| || ||
 CT GG GACTTCTC CTT CTC
 A C C C
 GAM1151 FLJ30574 3' CTCTCTCTCTCTTTTTTTTCTC 29448 CCATT A
 GAGA GAAGAGAGA AGAG
 ||| ||||| |||
 CTCT TTTCTCTCT TCTC
 TTTT_ C
 GAM1151 HSPC065 3' CTCTTTCTCTCTTTCTTTTCTC 15452 CCATT
 GAGA GAAGAGAGAAAGAG
 ||| |||||
 CTCT TTTCTCTCTTTCTC
 TTC_
 GAM1151 HTATSF1 5' CTTTCTCTGCTCAGCTC 15837 ACCA AG
 GAG TTGA AGAGAAAG
 || ||| |||||
 CTC GACT TCTCTTTC
 ___ CG
 GAM1151 JIK 3' TCTCTCTCTCTTACTCTTA 18408 CCATTG A
 TGAGA AAGAGAGA AGA
 |||| ||||| ||
 ATTCT TTCTCTCT TCT
 CA___ C
 GAM1151 KIAA0210 5' CTCTCCCTCATGGTTTCA 16423 T A_
 TGAGACCAT GA GAGAG
 ||||| || ||||
 ACTTTGGTA CT CTCTC
 _ CC
 GAM1151 KIAA0450 3' CTCTCTCTCTTCTGCTTCTC 16032 CCATT A
 GAGA GAAGAGAGA AG
 ||| ||||| ||
 CTCT CTTCTCTCT TC
 TCGT_ C
 GAM1151 KIAA0721 3' CTCTTTCTCTCCCTCCTCCTC 22319 ACCATT A_
 GAG GA GAGAGAAAGAG
 || || |||||
 CTC CT CTCTCTTTCTC
 CTC___ CC
 GAM1151 KIAA0721 3' CTCTTTCTCTCCCTCCTCCTC 45926 ACCATT A_
 GAG GA GAGAGAAAGAG
 || || |||||
 CTC CT CTCTCTTTCTC
 CTC___ CC
 GAM1151 KIAA1029 3' CTCTCTCTCTCTCTCA 14144 CCATT A A
 TGAGA GA GAGAGA AG
 |||| || ||||| ||

ACTCT CTCTCTCT TC
 _____ C
 GAM1151 KIAA1029 3' CTCTTTCTCTCTCTCTCTC 14145 CCATT _
 GAGA GA AGAGAGAAAGAG
 |||| || |||||
 CTCT CT TCTCTCTTTCTC
 CT__ C
 GAM1151 KIAA1076 3' CTCTCTCTCTTCTCTGTCTC 32639 CATT A
 GAGAC GAAGAGAGA AG
 |||| |||||
 CTCTG CTTCTCTCT TC
 TCT_ C
 GAM1151 KIAA1181 3' TCTTCCTCTCTTCTCCTC 33924 ACCATT A
 GAG GAAGAGAG AAGA
 || |||||
 CTC CTTCTCTC TTCT
 CT__ C
 GAM1151 KIAA1384 5' CTCTCTCTCTCCCTCTCTC 32259 CCATT A_ A
 GAGA GA GAGAGA AGAG
 |||| || |||||
 CTCT CT CTCTCT TCTC
 _____ CC C
 GAM1151 MGC10765 3' CTCTTTCCCTCTCCCTGTCCCT 23644 AC_ TT A A
 C GAG CA GA GAG GAAAGAG
 || || || |||||
 CTC GT CT CTC CTTTCTC
 CCT CC _ C
 GAM1151 MGC10812 3' CTCTTTCTCCCCGCTGTGCCTC 25410 AC TGAAGA
 GAG CAT GAGAAAGAG
 || || |||||
 CTC GTG CTCTTTCTC
 C_ TCGCCC
 GAM1151 MGC11115 3' CTCCCTCTCTCTCCCTCTCTC 26094 CCATT A AA
 GAGA GA GAGAGA GAG
 |||| || |||||
 CTCT CTCTCTCT CTC
 CTCC_ _ CC
 GAM1151 MGC11115 3' CTCCCTCTCTCTTTACCCTC 26095 ACCAT AA
 GAG TGAAGAGAGA GAG
 || |||||
 CTC ATTTCTCTCT CTC
 CC__ CC
 GAM1151 MGC13053 3' CTCTCTCTCTCTTTCTCTCTC 26423 CCATT A
 GAGA GAAGAGAGA AGAG
 |||| |||||
 CTCT TTTCTCTCT TCTC
 CTC__ C
 GAM1151 MGC13053 3' TCTTTCTCTCTCTCTCTC 26424 CCATT _
 GAGA GA AGAGAGAAAGA
 |||| || |||||

CTCT CT TCTCTCTTTCT
 _____ C
 GAM1151 MGC14798 3' CTCCTTCTCTCTTTCTTGCTCC 27938 A C TT A
 A TG GA CA GAAGAGAGAA GAG
 || || || || || || || || ||
 AC CT GT TTTCTCTCTT CTC
 _ C TC C
 GAM1151 MGC15827 3' TTCTCTTCAACGGTTTCA 26703 A
 TGAGACC TTGAAGAGAG
 || || || || || || || || ||
 ACTTTGG AACTTCTCTT
 C
 GAM1151 MGC4796 3' TCTTTCTCTCCCGTCTCA 30835 CATTGAA
 TGAGAC GAGAGAAAGA
 || || || || || || || || ||
 ACTCTG CTCTCTTTCT
 CC_____
 GAM1151 MOST2 5' CTCTCCCTCTTCAGGTCTCA 21552 AT A A
 TGAGACC TGAAGAG GA AG
 || || || || || || || || ||
 ACTCTGG ACTTCTC CT TC
 _ C C
 GAM1151 NPD009 5' TCTTCCTCTCTTTTGCTCA 45564 ACCATT A
 TGAG GAAGAGAG AAGA
 || || || || || || || || ||
 ACTC TTTCTCTC TTCT
 GT____ C
 GAM1151 NRN1 5' TCTTTCTCTCCTCCCTC 18664 ACCATT A
 GAG GA GAGAGAAAGA
 || || || || || || || || ||
 CTC CT CTCTCTTTCT
 C____ C
 GAM1151 OR7C1 5' CTCTTTCTCTCTCTCTCTC 18962 CCATT _
 GAGA GA AGAGAGAAAGAG
 || || || || || || || || ||
 CTCT CT TCTCTCTTTCTC
 _____ C
 GAM1151 PFTK1 3' CTCTTTCTCCCCCAAACCCCT 14752 ACCA AAGA
 C GAG TTG GAGAAAGAG
 || || || || || || || || ||
 CTC AAC CTCTTTCTC
 CCCA CCCC
 GAM1151 PFTK1 3' TCTCTCTCTCTGTCTC 14753 CATT A A
 GAGAC GA GAGAGA AGA
 || || || || || || || || ||
 CTCTG CT CTCTCT TCT
 T____ C
 GAM1151 RFX3 5' CTCTCTCTCTCCTCTCTC 8823 CCATT A A
 GAGA GA GAGAGA AGAG
 || || || || || || || || ||

			CTCT CTCTCTCTCTC		
			CTCC_ _ C		
GAM1151	RFX3	5'	CTCTCTCTCTCTCCCTCTCTC 28670	CCATT A	A
			GAGA GA GAGAGA AGAG		
			CTCT CTCTCTCTCTC		
			CTCC_ _ C		
GAM1151	RGS7	3'	CTCTCTCTCTCTCTCA 8828	CCATT A	A
			TGAGA GA GAGAGA AG		
			ACTCT CTCTCTCTTC		
			_____ C		
GAM1151	SSH2	3'	CTCTCTCTCTCCTCTCTCTCTC 31181	CCATT A	A
			GAGA GA GAGAGA AGAG		
			CTCT CTCTCTCTCTC		
			CTCT_ C C		
GAM1151	TRIM15	5'	CTCTCTCTCTCTTTCTCTCTC 27074	CCATT	A
			GAGA GAAGAGAGA AGAG		
			CTCT TTTCTCTCTCTC		
			CTC_ _ C		
GAM1151	TRIM15	5'	CTCTTTCTCTCTCTCTGTCTC 27075	CATT A	
			GAGAC GA GAGAGAAAGAG		
			CTCTG CTCTCTTTCTC		
			TCT_ _		
GAM1151	UPLC1	3'	CTCTTTCTCTTGGTCAACTCA 19284	ACCA A_	
			TGAG TTGA GAGAGAAAGAG		
			ACTC AACT TTCTCTTTCTC		
			_____ GG		
GAM1151	LOC112868	3'	CTCTCTCTCTCCTCTCTTTCTC 36080	CCATT A	A
			GAGA GA GAGAGA AGAG		
			CTCT CTCTCTCTCTC		
			TTCT_ C C		
GAM1151	LOC112868	3'	CTCTTTCTCTCTCTCCCTCTC 36081	CCATT A	
			GAGA GA GAGAGAAAGAG		
			CTCT CTCTCTCTTTCTC		
			CCCT_ _		
GAM1151	LOC112868	3'	TCTCTCTCTCTCCTCTC 36086	CCATT A	A
			GAGA GA GAGAGA AGA		
			CTCT CTCTCTCTCT		
			C_ _ _ C		
GAM1151	LOC112868	3'	TCTCTCTCTCTCTCCTC 36087	ACCATT _	A
			GAG GA AGAGAGA AGA		

	CTC	CT TCTCTCT TCT		
	_____	C C		
GAM1151 LOC113612 3'	CTCTCTCTCTCTTTTCATCCTC	36169	ACC T	A
	GAG AT GAAGAGAGA AGAG			
	CTC TA TTTCTCTCT TCTC			
	C_ C C			
GAM1151 LOC113612 3'	CTTTCTCTCTCTCTCTC	36170	CCATT _	
	GAGA GA AGAGAGAAAG			
	CTCT CT TCTCTCTTTC			
	_____	C		
GAM1151 LOC116411 5'	CTTTCTCTCTCCTTAGTG	36570	___	
	CATTGA AGAGAGAAAG			
	GTGATT TCTCTCTTTC			
	CC			
GAM1151 LOC129285 3'	CTCTCTCTCTCTTTCTTCTCTC	36968	CCATT	A
	GAGA GAAGAGAGA AGAG			
	CTCT CTTCTCTCT TCTC			
	CTTT_ C			
GAM1151 LOC131034 5'	TCCCTCCCTCTTTTCTCA	28316	CCATT	A AA
	TGAGA GAAGAG GA GA			
	ACTCT TTTCTC CT CT			
	_____	C CC		
GAM1151 LOC144231 5'	CTCTTTCTCCCTTCTGCTC	40392	ACCATT	A
	GAG GAAG GAGAAAGAG			
	CTC CTC CTCTTTCTC			
	GT_ C			
GAM1151 LOC144262 5'	CTTTCTCTCTCATAGTCTTA	37704	CAT	A
	TGAGAC TGA GAGAGAAAG			
	ATTCTG ACT CTCTCTTTC			
	AT_ _			
GAM1151 LOC146839 5'	CTCTTTCTCTCTTTTTCCTC	40754	ACCATT	
	GAG GAAGAGAGAAAGAG			
	CTC TTTCTCTCTTTCTC			
	CTT_			
GAM1151 LOC150577 3'	CTCTTTCTCTCTCTCTCTC	41221	CCATT _	
	GAGA GA AGAGAGAAAGAG			
	CTCT CT TCTCTCTTCTC			
	CT_ C			
GAM1151 LOC151742 3'	CTCCCTGGTGGTCTTA	29243	GA	A
	TGAGACCATT AG GAG			

ATTCTGGTGG TC CTC
 _ C
 GAM1151 LOC154761 3' CTCTTTCTCTCCACCAAAGCTC 39484 ACCA AA_
 A TGAG TTG GAGAGAAAGAG
 ||| ||| |||||
 ACTC AAC CTCTCTTTCTC
 GA_ CAC
 GAM1151 LOC201617 5' CTCTCTCTCTTTCTCTGCCTCA 43381 ACCATT A
 TGAG GAAGAGAGA AG
 ||| ||||| ||
 ACTC TTTCTCTCT TC
 CGTCTC C
 GAM1151 LOC201799 3' CTTTCTCTCTTTAGGTATC 42917 G AT
 GA ACC TGAAGAGAGAAAAG
 || ||| |||||
 CT TGG ATTTCTCTCTTC
 A _
 GAM1151 LOC221477 3' TCTTTCTCTGTGGGTCTCA 44261 ATTGAAG
 TGAGACC AGAGAAAGA
 ||||| |||||
 ACTCTGG TCTCTTTCT
 GTG____
 GAM1151 LOC221662 3' CTCTTTCCCTCCCAATTTTCCA 44388 A CC AA A
 TG GA ATTG GAG GAAAGAG
 || || ||| ||| |||||
 AC CT TAAC CTC CTTTCTC
 _ TT C_ C
 GAM1151 LOC253847 5' CTCCCCAGCTGCAGTGGTCCC 45940 A A AGAGAAA
 A TG GACCATTG AG GAG
 || ||||| || |||
 AC CTGGTGAC TC CTC
 C G GACCC_ _
 GAM1151 LOC254945 5' CTCCTTCTCTCTGTCTACCTCA 46305 ACCATTGA A
 TGAG AGAGAGAA GAG
 ||| ||||| |||
 ACTC TCTCTCTT CTC
 CATCTG_ C
 GAM1151 LOC51008 5' CTCCTTCTCTTTGATGATTCA 18063 AC TG AAA
 TGAG CAT AAGAGAG GAG
 ||| ||| ||||| |||
 ACTT GTA TTCTCTT CTC
 A_ GT C_
 GAM1151 LOC56930 5' TCTTCCTCTCTTTTCATTC 31092 CC T A
 GA AT GAAGAGAG AAGA
 || ||| ||||| |||
 CT TA TTTCTCTC TTCT
 _ C C
 GAM1151 LOC91812 5' CTCTCTCCCTTTTCAGTGTC 33392 C A A
 GAC ATTGAAGAG GA AGAG
 ||| ||||| || |||

		CTG TGACTTTTC CT TCTC		
		— C C		
GAM1151	LOC91813	5' CTCTCTCCCTTTTCAGTGTC 33400	C	A A
		GAC ATTGAAGAG GA AGAG		
		CTG TGACTTTTC CT TCTC		
		— C C		
GAM1152	EPHA3	3' TCACTTACTATTGTTGCT 11743	CAATA	TA
		AGCAGCAATAG TA TGA		
		TCGTTGTTATC AT ACT		
		_____ TC		
GAM1152	GABRP	3' TCATTCTGTCATTGCTGCT 15479	AG	ATATAT
		AGCAGCAAT CA ATGA		
		TCGTCGTTA GT TACT		
		CT CT_____		
GAM1152	TUFT1	3' GTTGCTGCCATTGCTGCT 21318	_____	
		AGCAGCAAT AGCAAT		
		TCGTCGTTA TCGTTG		
		CCG		
GAM1152	ABLM	3' GTCATATACTCTGCATCACTGT 13550	CA A	ATA
		GCAG AT GCA TATATGAC		
		TGTC TA CGT ATATACTG		
		AC _ CTC		
GAM1152	ABLM	3' GTCATATACTCTGCATCACTGT 8117	CA A	ATA
		GCAG AT GCA TATATGAC		
		TGTC TA CGT ATATACTG		
		AC _ CTC		
GAM1152	dJ309H15.1	3' GTCATATATATCACTCAGGC 28889	AAT	CA
		GC AG ATATATATGAC		
		CG TC TATATATACTG		
		GAC AC		
GAM1152	KIAA0565	3' TCTGTAATTGCTATTGC 33220	A	T
		GCAATAGCAAT TATA GA		
		CGTTATCGTTA ATGT CT		
		— —		
GAM1152	KIAA0635	3' CATATATAACGTGTTATTGC 16054	A	_____
		GCAATAGCA TATATATG		
		CGTTATTGT ATATATAC		
		GCA		
GAM1152	MacGAP	3' TCATATATACTGTAATATATGC 27289	GCA A	A
	T	AGCA AT GCA TATATATGA		

TCGT TA TGT ATATATACT
ATA A C

GAM1152 MGC13130 5' GTCAGTTGCCGCTGTTGCTACT 26713 C AATATATA
AG AGCAATAGC TGAC
|| ||||| |||
TC TCGTTGTCG ACTG
A CCGTTG__

GAM1152 LOC131368 3' TATATTGCTATTGTCACT 37355 CA
AG GCAATAGCAATATA
|| |||||
TC TGTTATCGTTATAT
AC

GAM1152 LOC153077 3' TCATATATAGCATCTCTGCT 41569 CA A AA
AGCAG AT GC TATATATGA
|||| ||| |||||
TCGTC TA CG ATATATACT
TC _ _

GAM1152 LOC256207 3' TCTGTAATTGCTATTGC 45621 A T
GCAATAGCAAT TATA GA
||||||| ||| ||
CGTTATCGTTA ATGT CT

GAM1152 LOC90288 3' GTCAGGATTGCTATTCTGCT 31112 C ATATA
AGCAG AATAGCAAT TGAC
|||| ||||| |||
TCGTC TTATCGTTA ACTG
C GG__

GAM1153 ALTE 3' TGTCTAGGAGGGATGACCCAC 11107 ATA GA _
TCA TGA GGGTTATC TTC AGACA
||| ||||| ||| |||||
ACT CCCAGTAG AGG TCTGT
CAC GG A

GAM1153 FLJ23598 5' TGTCAGTGGCAAACAACCCTAT 24158 A ATCGAT _
CCA TG ATAGGGTT TCA GACA
|| ||||| ||| |||
AC TATCCCAA GGT CTGT
C CAAAC_ GA

GAM1153 HMP19 3' GTCTGAACCGATATTTCT 42273 T A
AGGG TATCG TTCAGAC
|||| ||||| |||||
TCTT ATAGC AAGTCTG
T C

GAM1153 KIAA1710 3' TGCCTAAATTGCCACACCTATT 31332 _ TAT C A
CA TGAATAGG GT CGATT AG CA
||||||| || ||||| |||
ACTTATCC CA GTTAA TC GT
A CC_ A C

GAM1153 LOC143943 3' TCTGTGGTAACCCTGCCCA 40384 AA ATT
TG TAGGGTTATCG CAGA
|| ||||| |||||

			AC GTCCCAATGGT GTCT		
			CC _____		
GAM1153	LOC58489	3'	TCTGTTTCTCAACCTTATCCA 35905	A	ATC TT
			TG ATAGGGTT GA CAGA		
			AC TATTCCAA CT GTCT		
			C CT_ TT		
GAM1154	CNGB3	3'	ACAAAATATAACAAGTTTT 21175		GTGAA
			AAAAC TTGT ATTTGT		
			TTTTGAACA TAAAACA		
			ATA_		
GAM1154	CALN1	3'	GCCCTGTTACACAAATTTT 25517	C	ATTTT
			AAAA TTGTGTGAA GT		
			TTTT AACACACTT CG		
			A GTCC_		
GAM1155	COL19A1	3'	ATTGCGTGTTGATCCAA 7594		_ _
			TTGGATCT AAC TGTAGT		
			AACCTAGA TTG GCGTTA		
			C T		
GAM1155	ERBB2IP	5'	TATTCAGCTGGATCCAA 20774	A	T
			TTGGATCTA CTG AGTA		
			AACCTAGGT GAC TTAT		
			C _		
GAM1155	MGAT5	5'	GAGTACCATGTGAGATTCAA 8239	A	TGTA
			TTGGATCT AC GTACTC		
			AACTTAGA TG CATGAG		
			G TAC_		
GAM1155	RXRB	3'	GAGACTTGCAGTTAGACTCAA 22501	GA	_ A
			TTG TCTAACTGTA GT CTC		
			AAC AGATTGACGT CA GAG		
			TC T _		
GAM1155	FLJ23598	5'	AGTACTACAAGAACAA 24153	GA	AAC
			TTG TCT TGTAGTACT		
			AAC AGA ACATCATGA		
			A_ _		
GAM1155	KIAA1128	3'	AGTACTACAGCCTTCCAG 33965		TCTAA
			TTGGA CTGTAGTACT		
			GACCT GACATCATGA		
			TCC_		
GAM1155	KLHL6	3'	AGTGAGGAGGCTGGATCCAA 28209	A	G TAG
			TTGGATCTA CT TACT		

		AACCTAGGT GG GTGA		
		C AGGA		
GAM1155	MGC10966	5' AGTACTACAGCTTCTTCGA	25535	TCTAA
		TTGGA CTGTAGTACT		
		AGCTT GACATCATGA		
		CTTC_		
GAM1155	MGC15873	3' GAGTTGGACACAAGATCCAA	26742	AAC AGT
		TTGGATCT TGT ACTC		
		AACCTAGA ACA TGAG		
		AC_ GGT		
GAM1155	PDGFC	3' AGTAGACATTCAGATCCAG	18301	AAC AG
		TTGGATCT TGT TACT		
		GACCTAGA ACA ATGA		
		CTT G_		
GAM1155	POPX1	3' GAATACTACAGTTTTGTCCA	17121	CT C
		TGGAT AACTGTAGTA TC		
		ACCTG TTGACATCAT AG		
		TT A		
GAM1155	SAMHD1	3' AGTCTGCAGTTAGAGCCAA	30733	A T
		TTGG TCTAACTGTAG ACT		
		AACC AGATTGACGTC TGA		
		G _		
GAM1155	SCYD1	3' GAGTACTACAGTCCTCCCA	43711	ATCTA
		TGG ACTGTAGTACTC		
		ACC TGACATCATGAG		
		CTCC_		
GAM1155	SIAT9	3' AGCACTTAAGTGTTAGATCTAA	9976	TGT__ A
		TTGGATCTAAC AGT CT		
		AATCTAGATTG TCA GA		
		TGAAT C		
GAM1155	LOC127534	3' GAGCACTGGAACCTCAGATCCA	37171	AACTG__ A
	G	TTGGATCT TAGT CTC		
		GACCTAGA GTCA GAG		
		CTCCAAG C		
GAM1155	LOC130535	3' AGTCCTAAATTGGATCCAA	37475	CTG T
		TTGGATCTAA TAG ACT		
		AACCTAGGTT ATC TGA		
		AAA C		
GAM1155	LOC221395	3' TATGTCATTAGATCCAA	44185	C TA
		TTGGATCTAA TG GTA		

AACCTAGATT AC TAT
 _ TG
 GAM1155 LOC91947 3' AGTACTACAGTTTTCA 33569 TCT
 TGG AACTGTAGTACT
 ||| |||||
 ACTT TTGACATCATGA

 GAM1156 BDG-29 3' GCCATTACAGTGGCCTGGATA 35816 AGA CT
 TATCCAG TAT TGTAATGGC
 ||||| || |||||
 ATAGGTC GTG ACATTACCG
 CG_ _

GAM1156 C21orf6 3' GCCATTGCCTGTCTCT 18855 TCTT
 AGAGATA GTAATGGC
 ||||| |||||
 TCTCTGT CGTTACCG
 C_ _

GAM1156 DKFZp434D177 3' ACCAGATATCTCTGGGTA 26007 T
 TATCCAGAGATATCT GT
 ||||| ||||| ||
 ATGGGTCTCTATAGA CA
 C

GAM1156 HSA249128 3' GCCAAATTA ACTCTCTGGA 19027 TATC TAA
 TCCAGAGA TTG TGGC
 ||||| || |||
 AGGTCTCT AAT ACCG
 C_ _ TAA

GAM1156 KIAA1634 3' CCACCAACTATTTCTGGATA 31751 TC TAA
 TATCCAGAGATA TTG TGG
 ||||| || |||
 ATAGGTCTTTAT AAC ACC
 C_ C_ _

GAM1156 KIAA1941 3' GCCCCCCAAAAATGTCTCTAGA 36951 C C GTAAT
 TC AGAGATAT TT GGC
 || ||||| || |||
 AG TCTCTGTA AA CCG
 A A ACCC_

GAM1156 PRO2533 3' CCATTACAAAATGTAATGG 20702 GAG C
 CCA ATAT TTGTAATGG
 || ||| |||||
 GGT TGTA AACATTACC
 AA_ A

GAM1156 LOC151201 3' TGTAAAATACCTCTGGATA 41323 A C
 TATCCAGAG TAT TTGTA
 ||||| || |||||
 ATAGGTCTC ATA AATGT
 C A

GAM1157 NTRK2 3' AAAAGAAAACCTGTGTTCAATC 12841 ATACT A
 GAT CACAA TTTTCTTTT
 || |||| |||||

		CTA GTGTT AAAAGAAAA		
		ACTT_ C		
GAM1157	LOC116143 3'	AAAAAAAAATTTGCTGGGTGTC 36516	T _ C	
	A	A ATACTCA CAAATTTT TTTT		
		I		
		A TGTGGGT GTTTAAAA AAAA		
		C C A		
GAM1157	LOC151121 5'	AAAGGGGGGATTGTGACATATC 39050	AC A TT	
	A	TGATAT TCACAA TT CTTT		
		ACTATA AGTGTT GG GGAAA		
		C_ A GG		
GAM1157	LOC203429 3'	AAAAGAAATTGGGAGAGTATAT 43046	ACAAAT	
	CA	TGATATACTC TTTCTTTT		
		ACTATATGAG AAAGAAAA		
		AGGGTT		
GAM1158	AS3 3'	TATTAATCTACTGTATCA 18051	CCAAA	
		TGATACA GGATTAATA		
		ACTATGT TCTAATTAT		
		CA__		
GAM1158	MAN1A1 3'	TATTAATTCAGCCAGTGTATC 44136	CAAA_	
		GATACAC GGATTAATA		
		CTATGTG CTTAATTAT		
		ACCGA		
GAM1158	NOS1 3'	TATTAATCCCTCGTGTGTC 6234	CAAA	
		GATACAC GGATTAATA		
		CTGTGTG CCTAATTAT		
		CTC_		
GAM1158	B3GNT1 3'	TTGGTTTCCTGGTGGTATCATA 13344	_ AA	
		TATGATAC ACCA GGATTAA		
		ATACTATG TGGT TTTGGTT		
		G CC		
GAM1158	B3GNT1 3'	TTGGTTTCCTGGTGGTATCATA 27087	_ AA	
		TATGATAC ACCA GGATTAA		
		ATACTATG TGGT TTTGGTT		
		G CC		
GAM1158	FLJ21313 3'	TAATTGTTTAGGGTATCATA 23410	A _ G	
		TATGATAC CC AAA GATTA		
		ATACTATG GG TTT TTAAT		
		_ A G		
GAM1158	GTPBG3 3'	TGTTTGTCTTGTGTATCATA 26336	CAA T	
		TATGATACAC AGGAT AATA		

		ATACTATGTG TTCTG TTGT		
		____ T		
GAM1158	KIAA0792	3' ATTGGTCTGGTGCAGCATA 16213	ATA	AAG
		TATG CACCA GATTAAT		
		ATAC GTGGT CTGGTTA		
		GAC ____		
GAM1158	KIAA0979	3' TATTAATCTACTGTATCA 17389	CCAAA	
		TGATACA GGATTAATA		
		ACTATGT TCTAATTAT		
		CA ____		
GAM1158	KIAA0981	3' ATTTTATAGGGTATCATA 30796	A	A
		TATGATAC CC AAGGAT		
		ATACTATG GG TTTTA		
		_ A		
GAM1158	KIAA1462	3' ATCTTAAATTGTTGTATCATA 43919	C	____
		TATGATACA CAA AGGAT		
		ATACTATGT GTT TTCTA		
		T AAA		
GAM1158	ZAK	3' TATTGGTCACCCAGTGATCATA 18779	A	CAAAG
		TATGAT CAC GATTAATA		
		ATACTA GTG CTGGTTAT		
		_ ACCCA		
GAM1158	LOC138515	5' ATCTGCATTTGGTGTATCA 37395	____	
		TGATACACCAAA GGAT		
		ACTATGTGGTTT TCTA		
		ACG		
GAM1158	LOC254249	5' TATTATGCTCTTGGTGTACCA 45713	A	AG AT
		TG TACACCAA G TAATA		
		AC ATGTGGTT C ATTAT		
		C CT GT		
GAM1159	C7	3' TCTACAAAATGACTAGGATA 6191	_	GTGAA
		TATCCTAG CATT GTAGA		
		ATAGGATC GTAA CATCT		
		A AA ____		
GAM1159	FKBP1A	3' GTTCCACTCCACTTTGTATAG 6475	_	TT A A
		CTA GCA GTG AGT GAAC		
		GAT TGT CAC TCA CTTG		
		A TT C C		
GAM1159	PKHD1	3' CTAGTTCAATGCTAGG 28941	TG	G
		CCTAGCAT TGAA TAG		

		GGATCGTA ACTT ATC		
		___ G		
GAM1159	FENS-1	3' TTCTACTTCTTGTTC	21896	CT___ TTGT
		TATC AGCA GAAGTAGAA		
		GTAG TTGT CTTCATCTT		
		AACC T___		
GAM1159	FLJ12592	5' GTTCTACTTTTGGCCAAGGA	25874	A_ ATTGT
		TCCT GC GAAGTAGAAC		
		AGGA CG TTTCATCTTG		
		AC GT___		
GAM1159	FLJ20079	3' TCTACCTTCCGTAAAATGCTAG	19179	GT___ _
		CTAGCATT GAAG TAGA		
		GATCGTAA CTTC ATCT		
		AATGC C		
GAM1159	KIAA0143	3' TCTTCTTCACAATAATAGGA	32352	GC T
		TCCTA ATTGTGAAG AGA		
		AGGAT TAACACTTC TCT		
		AA T		
GAM1159	KIAA0420	3' CTACAAGTATGCTGGGATA	31726	TGTGAA
		TATCCTAGCAT GTAG		
		ATAGGGTCGTA CATC		
		TGAA___		
GAM1159	PRO2266	3' CTGGCACAATCCTAGGATA	20597	C A_
		TATCCTAG ATTGTG AG		
		ATAGGATC TAACAC TC		
		C GG		
GAM1159	SCYD1	3' GTTCTACCCAGGTGCTAGGA	43713	GTGAA
		TCCTAGCATT GTAGAAC		
		AGGATCGTGG CATCTTG		
		ACC___		
GAM1159	LOC115265	3' TCCACTTCACATGCTGGAGA	36310	_ T A
		TC CTAGCAT GTGAAGT GA		
		AG GGTGCGTA CACTTCA CT		
		A _ C		
GAM1159	LOC164375	5' TTCTGACCACAATGCCAG	42158	A AAG
		CT GCATTGTG TAGAA		
		GA CGTAACAC GTCTT		
		C CA_		
GAM1159	LOC253776	3' GTTCTACTTCTCAGGCTGG	46526	A T
		CTAGC TTG GAAGTAGAAC		

GGTCG GAC CTTTCATCTTG
_ T
GAM1159 LOC255696 5' TCCACTTCACAGATGAGGA 46568 AGCA A
TCCT TTGTGAAGT GA
|||| ||||||| ||
AGGA GACACTTCA CT
GTA_ C
GAM1159 LOC257354 3' CTACAAGTATGCTGGGATA 45579 TGTGAA
TATCCTAGCAT GTAG
||||||| |||
ATAGGGTCGTA CATC
TGAA_
GAM1160 BTEB1 5' CACCGAAGCCGTTCTGACTGGC 6870 TGAATT A
A TGCCA ACGGCTTCG TG
|||| ||||||| ||
ACGGT TGCCGAAGC AC
CAGTCT C
GAM1160 DKFZP434I1735 3' CATCCCTGTAATTCCAGCA 42420 CAT CTTC
TGC GAATTACGG GATG
||| ||||||| |||
ACG CTTAATGTC CTAC
AC_ C_
GAM1160 FLJ23598 3' CATGGCACACTTCATGGCA 24154 TTACG TCG
TGCCATGAA GCT ATG
||||||| ||| |||
ACGGTACTT CGG TAC
CACA_ _
GAM1160 LOC149711 3' TCAAAGCCAGTAATTCATAGCA 41074 C _ C
TGC ATGAATTAC GGCTT GA
||| ||||||| ||||| ||
ACG TACTTAATG CCGAA CT
A A A
GAM1160 LOC199988 5' CACCGAAGCCGCTGTGGACA 43268 _ GAATTA A
TG CCAT CGGCTTCG TG
|| ||| ||||||| ||
AC GGTG GCCGAAGC AC
A TCC_ C
GAM1161 LOC203276 3' GACGCAGGCGCCATTGCAC 43486 _ A ATCGAA
GTGCAATG C CC CGTT
||||||| | || |||
CACGTTAC G GG GCAG
C C AC_
GAM1161 LOC203305 3' GACGCAGGCGCCATTGCAC 43510 _ A ATCGAA
GTGCAATG C CC CGTT
||||||| | || |||
CACGTTAC G GG GCAG
C C AC_
GAM1161 LOC254243 3' GACGCAGGCGCCATTGCAC 46512 _ A ATCGAA
GTGCAATG C CC CGTT
||||||| | || |||

		CACGTTAC G GG	GCAG	
		C C AC__		
GAM1161	LOC90038	3' GACGCAGGCGCCATTGCAC	30649	_ A ATCGAA
		GTGCAATG C CC	CGTT	
		I		
		CACGTTAC G GG	GCAG	
		C C AC__		
GAM1162	BPAG1	3' TCTGACAGCCACAGCACTACA	17811	CAAATA CA
		TGTAGTGCT	CT TCAGA	
		ACATCACGA	GA AGTCT	
		CACC__ C_		
GAM1162	CSMD1	3' CTGATGAGTATCCGATCCTG	36189	TGC AA
		TAG TC	ATACTCATCAG	
		GTC AG	TATGAGTAGTC	
		CT_ CC		
GAM1162	KIAA1987	3' TCTGGTGCCACCTGAGCACTCA	42501	T AATACT
		TG AGTGCTCA	CATCAGA	
		AC TCACGAGT	GTGGTCT	
		_ CCACC_		
GAM1162	LGI2	3' TCTGATGAGCATTGCGTA	20002	CA A
		TGCT AAT	CTCATCAGA	
		ATGG TTA	GAGTAGTCT	
		C_ C		
GAM1162	VEST1	5' TCTGATTTTTTTGAGCACTA	27519	TACTC
		TAGTGCTCAA	ATCAGA	
		ATCACGAGTTT	TAGTCT	
		TT__		
GAM1162	LOC145945	5' TCTGATGAGTATCTCTCTGCA	40638	TGCTCAA
		TGTAG	ATACTCATCAGA	
		ACGTC	TATGAGTAGTCT	
		TCTC__		
GAM1162	LOC149013	3' CTGACTCATTCCAGCACTACA	38632	CA ACTCA
		TGTAGTGCT AAT	TCAG	
		ACATCACGA TTA	AGTC	
		CC CTC__		
GAM1163	ATP10B	3' CCAGGCAATATCTCAGGATA	31735	A CT AA
		TATCC GAGATAT	TGT TGG	
		ATAGG CTCTATA	ACG ACC	
		A _ G_		
GAM1163	BDG-29	3' CCATTACAGTGGCCTGGATA	35815	AGA CT
		TATCCAG	TAT TGTAATGG	

ATAGGTC GTG ACATTACC
 CG_ _
 GAM1163 GW112 3' CCACTTACTTAGATATCTGCAG 13131 CAG T_ _
 ATA TATC AGATATCT GTAA TGG
 ||| ||||| ||| |||
 ATAG TCTATAGA CATT ACC
 ACG TT C
 GAM1163 HSPB7 3' CCATTACAACAGCTCCAGGA 15780 A_ ATATC
 TCC GAG TTGTAATGG
 ||| ||| |||||
 AGG CTC AACATTACC
 AC GAC_
 GAM1163 KIAA1464 3' CCAGTATTTATCTCTGGA 33882 TCTT A
 TCCAGAGATA GTA TGG
 ||||| ||| |||
 AGGTCTCTAT TAT ACC
 T_ G
 GAM1163 KIAA1634 3' CCACCAACTATTTCTGGATA 31752 TC TAA
 TATCCAGAGATA TTG TGG
 ||||| ||| |||
 ATAGGTCTTTAT AAC ACC
 C_ C_
 GAM1163 NETO1 3' CCATCATCTCATCTCTGGATG 29097 ATCT TA
 TATCCAGAGAT TG ATGG
 ||||| || |||
 GTAGGTCTCTA AC TACC
 CTCT _
 GAM1163 PRO2533 3' CCATTACAAAATGTAATGG 20703 GAG C
 CCA ATAT TTGTAATGG
 ||| ||| |||||
 GGT TGTA AACATTACC
 AA_ A
 GAM1163 LOC151201 3' TGTAAAATACCTCTGGATA 41324 A C
 TATCCAGAG TAT TTGTA
 ||||| ||| |||
 ATAGGTCTC ATA AATGT
 C A
 GAM1164 NTRK2 3' AAAAGAAAACCTGTGTTCAATC 12841 ATACT A
 GAT CACAA TTTTCTTTT
 ||| ||| |||||
 CTA GTGTT AAAAGAAAA
 ACTT_ C
 GAM1164 LOC116143 3' AAAAAAAATTTGCTGGGTGTC 36516 T _ C
 A A ATACTCA CAAATTTT TTTT
 | ||||| ||||| |||
 A TGTGGGT GTTTAAAA AAAA
 C C A
 GAM1164 LOC151121 5' AAAGGGGGGATTGTGACATATC 39050 AC A TT
 A TGATAT TCACAA TT CTTT
 ||||| ||||| || |||

		ACTATA AGTGTT GG GGAAA		
		C_ A GG		
GAM1164	LOC203429	3' AAAAGAAATTGGGAGAGTATAT 43046		ACAAAT
	CA	TGATATACTC TTTCTTTT		
		ACTATATGAG AAAGAAAA		
		AGGGTT		
GAM1165	APOBEC1	3' CCTGTTTAAAGATTTC 12508		CTTGAT
		TGAAATCTTTA CAGG		
		ACTTTAGAAAT GTCC		
		TT____		
GAM1165	BIN3	3' TATTTTTTCAAGTAAAATTTTC 20762	TC	TC
	A	TGAAA TTTACTTGA AGGATA		
		ACTTT AAATGAACT TTTTAT		
		TA T_		
GAM1165	DDX6	3' ATCCCAAGTAAAAATTC 10642	C	ATCA
		GAAAT TTTACTTG GGAT		
		CTTTA AAATGAAC CCTA		
		A ____		
GAM1165	F8	3' TATCCTGATCAAGCATGGA 5617	TTA	
		TCT CTTGATCAGGATA		
		AGG GAACTAGTCCTAT		
		TAC		
GAM1165	FGF2	3' CCTAACAAAGTAAAGTTTTCA 7735	T	GATC
		TGAAA CTTTACTT AGG		
		ACTTT GAAATGAA TCC		
		T ACAA		
GAM1165	PPP3CA	3' TATCCTGACTAAAAAATTTCA 6645	C AC A	
		TGAAAT TTT TTG TCAGGATA		
		ACTTTA AAA AAT AGTCCTAT		
		A _ C		
GAM1165	RAD50	3' TATCCCAAGAATGCAAGATTTC 12297	TA__	ATCA
	A	TGAAATCTT CTTG GGATA		
		ACTTTAGAA GAAC CCTAT		
		CGTAA ____		
GAM1165	RAD50	3' TATCCCAAGAATGCAAGATTTC 28555	TA__	ATCA
	A	TGAAATCTT CTTG GGATA		
		ACTTTAGAA GAAC CCTAT		
		CGTAA ____		
GAM1165	SORCS1	3' TATCATTAAGTAAAGATTT 27487		GATCAG
		AAATCTTTACTT GATA		

TTTAGAAATGAA CTAT
 ATTA__
 GAM1165 KIAA0268 3' TATCCATTACAGTAAAGGATTT 34688 _ _ CA
 CA TGAAATC TTTACT TGAT GGATA
 ||||| ||||| ||| |||||
 ACTTTAG AAATGA ATTA CCTAT
 G C _
 GAM1165 MGC22014 3' TATCCTGATCCCTGAATTTC 32222 CT CTT
 GAAAT TTA GATCAGGATA
 |||| | |||||
 CTTTA AGT CTAGTCCTAT
 _ CC_
 GAM1166 RAD54B 3' CTTAACCTCATTGGAGGATCTC 28675 AACGCAAAA
 A TGAGATCTTT TTAAG
 ||||| |||||
 ACTCTAGGAG AATTC
 GTTACTCC_
 GAM1166 SIM2 3' TTTTGCTTAAAGATCTCA 11519 C
 TGAGATCTTTAA GCAAAA
 ||||| |||||
 ACTCTAGAAATT CGTTTT
 _
 GAM1166 TAPBP 3' CTTAATTTTGTTATAAAATCTC 9180 C AC
 A TGAGAT TTTA GCAAAATTAAG
 |||| | |||||
 ACTCTA AAAT TGTTTTAATTC
 _ AT
 GAM1166 FHR5 3' CTTAATCACCTTCTAAAGATCT 25084 ACGCAAA
 CA TGAGATCTTTA ATTAAG
 ||||| |||||
 ACTCTAGAAAT TAATTC
 CTTCCAC
 GAM1166 LOC145739 3' TAATTTTGCATTAGTCTC 37963 CTT C
 GAGAT TAA GCAAAATTA
 |||| | |||||
 CTCTG ATT CGTTTTAAT
 _ A
 GAM1167 DLG5 3' GCATAATGGTTATTGTCACTA 40337 CA CT_
 TGG ACAATAACCA TGC
 || ||||| |||
 ATC TGTTATTGGT ACG
 AC AAT
 GAM1167 HTR4 3' AGGTGTCAGTTATTGTTTCCA 6539 C _
 TGG AACAATAAC CACTT
 || ||||| |||||
 ACC TTGTTATTG GTGGA
 T ACT
 GAM1167 GHITM 3' CAAGTGGTCATTGTTACA 15725 GC A
 TG AACAAT ACCACTTG
 || ||||| |||||

		AC TTGTTA TGGTGAAC		
		A_ C		
GAM1167 MKRN2	3'	GGGTAGCAATCTTGTTGCCA 35857	TAACCAC	_
		TGGCAACAA TTGC ACTT		
		ACCGTTGTT AACG TGGG		
		CT_____ A		
GAM1167 NETO2	3'	AAGTACAAGTGGTTAATGTACC 19860	CA A	C
A		TGG ACA TAACCACTTG ACTT		
		ACC TGT ATTGGTGAAC TGAA		
		A_ A A		
GAM1168 IL2RA	3'	AGTATAAAGAAAAGTAGG 5998	AG	
		CTTA TTTCTTTATACT		
		GGAT AAAGAAATATGA		
		GA		
GAM1168 SPON1	3'	TATAAAGAAACACAAGATTTA 31304	C AA	
		A AATCTT GTTTCTTTATA		
		A TTAGAA CAAAGAAATAT		
		T CA		
GAM1168 TRIM34	3'	TATAAATTGGGATTTAAGACTG 22252	A TT__	
TA		TACA TCTTAAGT C TTTATA		
		ATGT AGAATTTA G AAATAT		
		C GG TT		
GAM1168 TRIM34	3'	TATAAATTGGGATTTAAGACTG 28176	A TT__	
TA		TACA TCTTAAGT C TTTATA		
		ATGT AGAATTTA G AAATAT		
		C GG TT		
GAM1168 PMAIP1	3'	GTATTACTTAAGATTGT 22102	TTCTTT	
		ACAATCTTAAGT ATAC		
		TGTTAGAATTCA TATG		
		T_____		
GAM1168 SLC5A7	3'	AGTACAAAAAAGTTTAAGATTG 22386	GT C A	
		CAATCTTAA TT TTT TACT		
		GTTAGAATT AA AAA ATGA		
		TG A C		
GAM1168 LOC56959	5'	GGAAAGACTCAAGATTGTA 39840	A C	
		TACAATCTT AGTTT TTT		
		ATGTTAGAA TCAGA AGG		
		C A		
GAM1169 ACK1	5'	GGAGGAGGAGGTGGTGAAGTGGC 12361	G A G _	
A		TG CA TCACCA CCTCCTCC CC		

AC GT AGTGGT GGAGGAGG GG
 G C _ A
 GAM1169 ADAMTS13 3' GGAGGAGGTGTGGTCACCA 29130 CA CA
 TGG ATCAC GCCTCCTCC
 ||| |||| |||||
 ACC TGGTG TGGAGGAGG
 AC _
 GAM1169 ADCY8 5' GGAGGAGGTGGTGACCACCA 6789 CAA G
 TGG TCACCA CCTCCTCC
 ||| |||| |||||
 ACC AGTGGT GGAGGAGG
 ACC _
 GAM1169 CDC2L2 5' GGAGGAGGAAGGGAGCACCA 27300 CAA A AG
 TGG TC CC CCTCCTCC
 ||| || |||||
 ACC AG GG GGAGGAGG
 ACG _ AA
 GAM1169 CKTSF1B1 3' GAGGAGAAATGAGATTGCCA 15025 AC GC_
 TGGCAATC CA CTCCTC
 ||||| || |||||
 ACCGTTAG GT GAGGAG
 A_ AAA
 GAM1169 CREB1 3' GAAGAAGTGTGATTGCCA 10601 CCA C C
 TGGCAATCA GC TC TC
 ||||| || || ||
 ACCGTTAGT TG AG AG
 TG_ A A
 GAM1169 DBP 5' GGAGTGTGCTGGTGATCGC 7031 A CTC
 GC ATCACCAGC CTCC
 || ||||| |||
 CG TAGTGGTCG GAGG
 C TGT
 GAM1169 DLEC1 3' GAGTGAGCTGGTGACCA 14266 CAA C _
 TGG TCACCAGC TC CTC
 ||| ||||| || |||
 ACC AGTGGTCG AG GAG
 _ _ T
 GAM1169 DLEC1 3' GAGTGAGCTGGTGACCA 14273 CAA C _
 TGG TCACCAGC TC CTC
 ||| ||||| || |||
 ACC AGTGGTCG AG GAG
 _ _ T
 GAM1169 DUOX2 3' GGAGGAGGAGGCTGGGATCC 15308 CA A _
 GG ATC CCAGCCTCCTCC CC
 || ||| ||||| || ||
 CC TAG GGTCTGGAGGAGG GG
 _ _ A
 GAM1169 DVL1 3' GGGGGAGGAGGCGACCCTGTCA 29844 ATCACCA
 TGGCA GCCTCCTCCCC
 |||| |||||

			ACTGT	CGGAGGAGGGGG		
			CCCAG__			
GAM1169	FRZB	5'	AGGAAGCGGTGATTGCC	7198	A C	
			GGCAATCACC GC TCCT			
			CCGTTAGTGG CG AGGA			
			_ A			
GAM1169	FZD8	3'	GGAGGAGGGGTGACCGCCA	25625	AA AG	
			TGGC TCACC CCTCCTCC			
			ACCG AGTGG GGAGGAGG			
			CC _			
GAM1169	GAS7	3'	GGGAGAGAGCTGGTGATTCCA	9717	C _ C	
			TGG AATCACCAGC CTC TCCC			
			ACC TTAGTGGTCG GAG AGGG			
			_ A _			
GAM1169	GJB3	3'	GGAGGAGGCTGGGGTGGAACC	23440	CA__ A	
			GG ATC CCAGCCTCCTCC			
			CC TGG GGTCGGAGGAGG			
			AAGG _			
GAM1169	GORASP1	3'	GGGGAGGAAGCTGTTCTCCCCA	25647	CAATCAC C	
			TGG CAGC TCCTCCCC			
			ACC GTCG AGGAGGGG			
			CCTCTT_ A			
GAM1169	LUZP1	5'	AGAAGATTGTGTTGCCA	27350	C GC C	
			TGGCAATCAC A CT CT			
			ACCGTTGGTG T GA GA			
			_ TA A			
GAM1169	MMP8	3'	GGGGAGGAGGCCGTGTGA	8259	CA_	
			TCAC GCCTCCTCCCC			
			AGTG CGGAGGAGGGG			
			TGC			
GAM1169	MPZ	3'	GGAGGAAGAGGCTGCACTGC	6131	ATCAC C _	
			GCA CAGCCTC TCC CC			
			CGT GTCGGAG AGG GG			
			CAC__ A A			
GAM1169	P4HB	3'	GGAAGAGGAGCTGGTGGCTGCC	6629	AT C CC	
	A		TGGCA CACCAGC TCCTC CC			
			ACCGT GTGGTCG AGGAG GG			
			CG _ AA			
GAM1169	RAD54B	3'	GGAGGAGGAAGTACTGCTA	28677	ATC CAG	
			TGGCA AC CCTCCTCC			

			ATCGT TG GGAGGAGG		
			CA_ AA_		
GAM1169 RB1CC1	5'	GGAGGAGGCGTTGCC	16631	CACCA	
		GGCAAT GCCTCCTCC			
		CCGTTG CGGAGGAGG			
GAM1169 RELN	3'	AGGACTTGGTGATTACC	45278	C CC	
		GG AATCACCAG TCCT			
		CC TTAGTGGTT AGGA			
		A C_			
GAM1169 SOX4	3'	GGGGAGGAGGCCAGCCA	9075	AATCACCA	
		TGGC GCCTCCTCCCC			
		ACCG CGGAGGAGGGG			
		AC_____			
GAM1169 STC1	3'	GGGAGGAGGGGTAGGACTGC	9136	A __ AG	
		GCA TC ACC CCTCCTCCC			
		CGT AG TGG GGAGGAGGG			
		C GA _			
GAM1169 TGFA	3'	GGAGAAAAAGATGGGATTGCCA	9231	A GC C__	
		TGGCAATC CCA CT CTCC			
		ACCGTTAG GGT GA GAGG			
		_ A_ AAAA			
GAM1169 TIAM1	5'	GGAAGAGGAGGCTGGTTGGTAC	9261	CA _ CC	
CA		TGG ATCA CCAGCCTCCTC CC			
		ACC TGGT GGTCGGAGGAG GG			
		A_ T AA			
GAM1169 TJP1	5'	GGAGGAGGAGGTACCGCCA	9265	AATC AG	
		TGGC ACC CCTCCTCC			
		ACCG TGG GGAGGAGG			
		CCA_ A_			
GAM1169 AKAP8	3'	GGAAAGAAAACCTTGATGTGATT	12465	__ CC__ C_	
GCC		GGCAATCAC CAG TC TCC			
		CCGTTAGTG GTT AG AGG			
		TA CAAA AA			
GAM1169 BLR1	3'	GGGGAAGGAGGCTGGCTTGTC	7447	TCA _	
		GGCAA CCAGCCTCCT CCCC			
		CTGTT GGTCGGAGGA GGGG			
		C_ A			
GAM1169 BLR1	3'	GGGGAAGGAGGCTGGCTTGTC	26777	TCA _	
		GGCAA CCAGCCTCCT CCCC			

CTGTT GGTCTGGAGGA GGGG
 C__ A
 GAM1169 CDC14B 3' GGAAGGAGGCTGGCTGGCTCA 27170 _ AATCA C
 TG GC CCAGCCTCCT CC
 || || ||||| ||
 AC CG GGTCTGGAGGA GG
 T GTC__ A
 GAM1169 CLIC2 5' GGAGGCAGGAGGCTGACAACTG 6967 G ATCAC _ _
 GCA TG CA CAGCCTCCT CC CC
 || || ||||| || ||
 AC GT GTCGGAGGA GG GG
 G CAACA C A
 GAM1169 CNM2 3' GAGGGAACCTTTGGGGATTGCCA 19155 A CC__
 TGGCAATC CCAG TCCTC
 ||||| ||| ||||
 ACCGTTAG GGTT GGGAG
 G TCAA
 GAM1169 DDX34 3' GGAGGAGGAGGATACGCCA 16165 A_ ACCAG
 TGGC ATC CCTCCTCC
 ||| || |||||
 ACCG TAG GGAGGAGG
 CA GA__
 GAM1169 DDX35 3' GGGATTGGTGATTGACA 22454 G CCTCC
 TG CAATCACCAG TCCC
 || ||||| |||
 AC GTTAGTGGTT AGGG
 A _____
 GAM1169 DKFZP434L187 3' GGAGAGAAGGCTGGAGGCTGAC 34121 G AT A C C
 A TG CA C CCAGCCT CTC CC
 || || | ||||| ||| ||
 AC GT G GGTCTGGA GAG GG
 A CG A A A
 GAM1169 DKFZP434N178 5' GGAGGCGGCTGGTGCCGCCA 35598 AAT T
 TGGC CACCAGCC CCTCC
 ||| ||||| ||||
 ACCG GTGGTCGG GGAGG
 CC_ C
 GAM1169 DKFZP586I2223 3' GGAGGCTGATGCCTGCCA 17732 AT C
 TGGCA CA CAGCCTCC
 |||| || |||||
 ACCGT GT GTCGGAGG
 CC A
 GAM1169 FLJ13710 3' GGGGAAACCAGGTGATTGCC 24206 AGCCTCC
 GGCAATCACC TCCCC
 ||||| |||
 CCGTTAGTGG AGGGG
 ACCAA__
 GAM1169 FLJ20154 3' GGAAGGAGGCTGGGACTGTGCC 36106 ATCA_ C
 GGCA CCAGCCTCCT CC
 ||| ||||| ||

		CCGT GGTCTGGAGGA GG	
		GTCAG A	
GAM1169 GS3955	5'	GGGGGAGACGGGGTGATTGC 22305	AG TC
		GCAATCACC CC CTCCCC	
		CGTTAGTGG GG GAGGGGG	
		__ CA	
GAM1169 KIAA0296	3'	GGGAGGAGCCAGTTTGCCA 16222	TC CA C
		TGGCAA AC GC TCCTCCC	
		ACCGTT TG CG AGGAGGG	
		__ AC _	
GAM1169 KIAA0337	3'	GGGGGCAGTGATTGCCA 16655	CA
		TGGCAATCAC GCCTCC	
		ACCGTTAGTG CGGGGG	
		A_	
GAM1169 KIAA0415	3'	GGGGGAGGGTTGCAAGCGCCA 44477	AATCAC TC
		TGGC CAGCC CTCCCC	
		ACCG GTTGG GAGGGGG	
		CGAAC_ _	
GAM1169 KIAA0472	3'	GGGGAATTGGTGATTACA 35580	GC CCTCC
		TG AATCACCAG TCCCC	
		AC TTAGTGGTT AGGGG	
		A_ A_	
GAM1169 KIAA0668	3'	GGGGGAAGAGGCTGGCAGA 33053	A_ C
		TC CCAGCCTC TCCCC	
		AG GGTCTGGAG AGGGGG	
		AC A	
GAM1169 KIAA1023	3'	GAGGAGGCTCTGCATGTCCA 19090	_ AT CC
		TGG CA CA AGCCTCCTC	
		ACC GT GT TCGGAGGAG	
		T AC C_	
GAM1169 KIAA1184	3'	AGGAGGGTCCTGATTGCCA 22893	CCAG
		TGGCAATCA CCTCCT	
		ACCGTTAGT GGAGGA	
		CCTG	
GAM1169 KIAA1374	3'	AGGAGAATAGTGGTTGCCA 30709	CAGC
		TGGCAATCAC CTCCT	
		ACCGTTGGTG GAGGA	
		ATAA	
GAM1169 KIAA1464	3'	GGAAAGACTGAGATGGTTGCCA 33884	C_ C CC
		TGGCAATCA CAG CT TCC	

			ACCGTTGGT GTC GA AGG		
			AGA A A_		
GAM1169 KIAA1674	3'	GGGAGGGGTGACAGCCA	34113	AA	AGCCT
		TGGC TCACC CCTCCC			
		ACCG AGTGG GGAGGG			
		AC _____			
GAM1169 LRBA	5'	GAGGAGGAGGGCGACGCCA	13557	AA A AG	
		TGGC TC CC CCTCCTC			
		ACCG AG GG GGAGGAG			
		C_ C GA			
GAM1169 MAGE-E1	3'	GGGAGAAGAGGCTGGCTCAGTG	25108	ATCA_	__
	CC	GGCA CCAGCCTC CTCCC			
		CCGT GGTCCGAG GAGGG			
		GA CTC AA			
GAM1169 MDS006	3'	GAAAAGGTGGTGATTGCCA	21502	G CC	
		TGGCAATCACCA CCT TC			
		ACCGTTAGTGGT GGA AG			
		_ AA			
GAM1169 MGC2663	5'	GAGGAATGGAGATTGCCA	23551	A GCC	
		TGGCAATC CCA TCCTC			
		ACCGTTAG GGT AGGAG			
		A A_			
GAM1169 MGC33371	5'	GGAGGAGGAGACTGAGGAGC	29480	AA AC C	_
		GC TC CAG CTCCTCC CC			
		CG AG GTC GAGGAGG GG			
		_ GA A A			
GAM1169 MKNK1	5'	GGAGAACTGAAGATTGCCA	9794	AC C_	
		TGGCAATC CAG CTCC			
		ACCGTTAG GTC GAGG			
		AA AA			
GAM1169 MMPL1	3'	GGGAAGAGGCTGGGAGC	10348	AA A C	
		GC TC CCAGCCTC TCCC			
		CG AG GGTCGGAG AGGG			
		_ _ A			
GAM1169 N4BP3	3'	AGGAGGCTGGGGGATCACC	32930	CA A_	
		GG ATC CCAGCCTCCT			
		CC TAG GGTCGGAGGA			
		AC GG			
GAM1169 NAG14	3'	GGGAGGGGAATTGCCA	22705	CACCAGC	
		TGGCAAT CTCCTCCC			

ACCGTTA GGGGAGGG
 A_____
 GAM1169 PIP3-E 3' GGAGGAGGCGTGTCCA 33180 C T CA
 TGG AA CAC GCCTCCTCC
 ||| || ||| |||||
 ACC TT GTG CGGAGGAGG

— — —
 GAM1169 PTPNS1 3' GGAGGCTGACGTTGCCA 28055 CAC
 TGGCAAT CAGCCTCC
 ||||| |||||
 ACCGTTG GTCGGAGG
 CA_

GAM1169 RANBP8 5' GGAAGAGGAGGCTGAGAGGGTC 13094 AA AC CC
 A
 TGGC TC CAGCCTCCTC CC
 ||| || ||||| ||
 ACTG AG GTCGGAGGAG GG
 GG A_ AA

GAM1169 SNRPD1 3' GGCTGAAACTTAGTGATTGCCA 13821 _____
 TGGCAATCAC CAGCC
 ||||| |||
 ACCGTTAGTG GTCGG
 ATTCAAA

GAM1169 TED 3' GGGAAGGAGGCTGCTCACCCA 17920 CAATCAC C
 TGG CAGCCTCCT CCC
 ||| ||||| |||
 ACC GTCGGAGGA GGG
 CACTC_ A

GAM1169 TU12B1-TY 3' GGAGGAGGAAGATGGCCA 18648 A ACCAG
 TGGC ATC CCTCCTCC
 ||| ||| |||||
 ACCG TAG GGAGGAGG
 G AA_

GAM1169 UBCE7IP5 3' GGGGGCTGGTGATTCCCA 17273 C
 TGG AATCACCAGCCTCC
 ||| |||||
 ACC TTAGTGGTCGGGGG
 C

GAM1169 LOC127294 3' GGAGGAGGCTAAGGCTGCC 36894 AT ACC
 GGCA C AGCCTCCTCC
 ||| | |||||
 CCGT G TCGGAGGAGG
 CG AA_

GAM1169 LOC129676 5' GGAGGAGGAGGCCAGGGA 37285 A A_ _
 TC CC GCCTCCTCC CC
 || || ||||| ||
 AG GG CGGAGGAGG GG
 _ AC A

GAM1169 LOC138389 3' GGGAGGAGGGTGACACCCA 37507 CAA AGC
 TGG TCACC CTCCTCCC
 || ||| |||||

		ACC AGTGG GAGGAGGG		
		CAC ____		
GAM1169	LOC144970 5'	GGGATGCTGGTGAATTCCA	37793	C C
		TGG AATCACCAGC TCCT		
		ACC TTAGTGGTCG AGGG		
		T T		
GAM1169	LOC145623 3'	GGGAGGAGAGGTTGGAAGCTGC	40545	ATCA C _
	CA	TGGCA CCAGCCTC TCC CCC		
		ACCGT GGTGAG AGG GGG		
		CGAA _ A		
GAM1169	LOC146520 5'	GGAGGAGGAGGGATGCCA	38186	A A AG
		TGGCA TC CC CTCCTCC		
		ACCGT AG GG GGAGGAGG		
		_ _ A_		
GAM1169	LOC147912 5'	GGGGGAGGAGGCTGGGGAAAGC	38418	AA A
	C	GGC TC CCAGCCTCCTCCCC		
		CCG AG GGTCGGAGGAGGGG		
		AA G		
GAM1169	LOC148946 5'	GGAACGAGCAATGATTGCCA	40940	CCA C C_
		TGGCAATCA GC TC TCC		
		ACCGTTAGT CG AG AGG		
		AA_ _ CA		
GAM1169	LOC151009 5'	AGGAGGGCGAGCCGATTGCCA	41289	ACCA_ _
		TGGCAATC GCC TCCT		
		ACCGTTAG CGG AGGA		
		CCGAG G		
GAM1169	LOC152283 3'	GGAGGAGGAGGCTGTGGATGAC	41487	GCA AC _
	A	TG ATC CAGCCTCCTCC CC		
		AC TAG GTCGGAGGAGG GG		
		AG_ GT A		
GAM1169	LOC155179 3'	GAGGAGGCTCTGCATGTCCA	39557	_ AT CC
		TGG CA CA AGCCTCCTC		
		ACC GT GT TCGGAGGAG		
		T AC C_		
GAM1169	LOC164714 5'	GGGAGGAGGCCGGGAGC	42182	AA A A
		GC TC CC GCCTCCTCCC		
		CG AG GG CGGAGGAGGG		
		_ _ C		
GAM1169	LOC196047 5'	AGGAGCGCCAAGATTGCCA	43143	ACCA_ _
		TGGCAATC GC CTCCT		

ACCGTTAG CG GAGGA
 AAC_ C
 GAM1169 LOC196472 5' GGAAGAAGAGCAGTGGGATTGC 42375 A _ _ _ C
 CA TGGCAATC CCA GC CT C TCC
 ||||| || || || ||
 ACCGTTAG GGT CG GA G AGG
 _ GA A A A
 GAM1169 LOC199858 3' GGGAGGCTGTAATTGTCA 42639 CAC
 TGGCAAT CAGCCTCCT
 ||||| |||||
 ACTGTTA GTCGGAGGG
 AT_
 GAM1169 LOC200597 5' GGAGGAGGCTGGGCAGGGCC 42825 AATCA
 GGC CCAGCCTCCTCC
 || |||||
 CCG GGTGGAGGAGG
 GGACG
 GAM1169 LOC203636 3' GGGGAGGAAGCTGCCAGTCA 43077 AATCAC C
 TGGC CAGC TCCTCCCC
 ||| ||| |||||
 ACTG GTCG AGGAGGGG
 ACC_ A
 GAM1169 LOC219686 5' GGAGGAGGAGGCCGAGGCGCC 43674 AA_ ACCA _
 GGC TC GCCTCCTCC CC
 ||| || ||||| ||
 CCG AG CGGAGGAGG GG
 CGG C_ A
 GAM1169 LOC219899 3' AGGAAATTGGTAATAGCCA 43989 A C CC
 TGGC AT ACCAG TCCT
 |||| |||| ||||
 ACCG TA TGGTT AGGA
 A A AA
 GAM1169 LOC220018 5' GGGAAGGAGGCTGCTGGGTAGC 44856 A AC_ C
 GC ATC CAGCCTCCT CCC
 || ||| ||||| |||
 CG TGG GTCGGAGGA GGG
 A GTC A
 GAM1169 LOC220906 5' GGGAGGAGAATCTGATTCCA 43926 C CCAGC
 TGG AATCA CTCCTCCC
 || |||| |||||
 ACC TTAGT GAGGAGGG
 T CTAA_
 GAM1169 LOC222486 5' GGAGGAGGAGGGGATCGCC 45300 A A AG
 GGC ATC CC CCTCCTCC
 ||| ||| || |||||
 CCG TAG GG GGAGGAGG
 C _ GA
 GAM1169 LOC254532 5' GGAGGAGGAGGGGGACCAGCCA 46212 AA_ A AG
 TGGC TC CC CCTCCTCC
 ||| ||| || |||||

ACCG AG GG GGAGGAGG
 ACC G GA
 GAM1169 LOC256950 5' GGAGAGGAGGCTGAGGCC 45701 AATCAC C
 GGC CAGCCTCCTC CC
 ||| ||||| ||
 CCG GTCGGAGGAG GG
 GA_____ A
 GAM1169 LOC92299 5' GGAAGAGGGGGTGGCCGCCA 34131 AA AG C
 TGGC TCACC CCTC TCC
 ||| ||| ||| |||
 ACCG GGTGG GGAG AGG
 CC G_ A
 GAM1169 LOC92973 5' GGAGGTGTCAGTGATTGCCA 35185 CA_
 TGGCAATCAC GCCTCC
 ||||| |||||
 ACCGTTAGTG TGGAGG
 ACTG
 GAM1170 B3GALT5 3' CATGAAGTCACTGATTAGTT 27037 G C AATA
 GA TAA CAGT ACTTCATG
 || ||| ||| |||||
 TT ATT GTCA TGAAGTAC
 G A C_
 GAM1170 B3GALT5 3' CATGAAGTCACTGATTAGTT 12699 G C AATA
 GA TAA CAGT ACTTCATG
 || ||| ||| |||||
 TT ATT GTCA TGAAGTAC
 G A C_
 GAM1170 B3GALT5 3' CATGAAGTCACTGATTAGTT 27022 G C AATA
 GA TAA CAGT ACTTCATG
 || ||| ||| |||||
 TT ATT GTCA TGAAGTAC
 G A C_
 GAM1170 B3GALT5 3' CATGAAGTCACTGATTAGTT 27027 G C AATA
 GA TAA CAGT ACTTCATG
 || ||| ||| |||||
 TT ATT GTCA TGAAGTAC
 G A C_
 GAM1170 B3GALT5 3' CATGAAGTCACTGATTAGTT 27032 G C AATA
 GA TAA CAGT ACTTCATG
 || ||| ||| |||||
 TT ATT GTCA TGAAGTAC
 G A C_
 GAM1170 IL1F5 3' ATGAAGTCCTGTCACTCA 14596 AAC TAATA
 TGAGT CAG ACTTCAT
 |||| | |||||
 ACTCA GTC TGAAGTA
 CT_ C_
 GAM1170 DKFZP434L187 5' CATGGATTTGCTCACTGGTTAC 34118 AA_ C
 TCA TGAGTAACCACT TAA TTCATG
 ||||| ||| |||||

ACTCATTGGTCA GTT AGGTAC
 CTC T
 GAM1170 NCUBE1 3' ATGAGTATTACTAGTTACTCA 18092 C AC
 TGAGTAAC AGTAATA TTCAT
 ||||| ||||| |||||
 ACTCATTG TCATTAT GAGTA
 A _
 GAM1170 LOC145773 3' GGCTATTACTGTTTACCCA 37983 A C A
 TG GTAA CAGTAATA CT
 || ||| ||||| ||
 AC CATT GTCATTAT GG
 C T C
 GAM1170 LOC145899 5' CATGAAGTTTCAGTCACTCA 40623 A CAGTAAT
 TGAGT AC AACTTCATG
 |||| || |||||
 ACTCA TG TTGAAGTAC
 C ACT____
 GAM1171 AXL 3' AGATTCTAGATCAGATGCTCCA 7418 AA AGC
 TGG A CATCT TCTAGAATCT
 ||| |||| |||||
 ACCT GTAGA AGATCTTAGA
 C_ CT_
 GAM1171 AXL 3' AGATTCTAGATCAGATGCTCCA 22439 AA AGC
 TGG A CATCT TCTAGAATCT
 ||| |||| |||||
 ACCT GTAGA AGATCTTAGA
 C_ CT_
 GAM1171 ETV5 3' CTAGAGCTAGCAGTTCCCA 10748 A AT
 TGG AAC CTAGCTCTAG
 ||| ||| |||||
 ACC TTG GATCGAGATC
 C AC
 GAM1171 RGS5 3' AGACTGTGGGTCAAATGTTTCC 9677 CTA _ AA
 A TGGAAACAT GCTC TAG TCT
 ||||| ||| ||| |||
 ACCTTTGTA TGGG GTC AGA
 AAC T _
 GAM1171 KIAA0298 3' AGATTCTAGTTCTCAACCTCTC 37624 AACATCT CT
 CA TGGA AG CTAGAATCT
 ||| || |||||
 ACCT TC GATCTTAGA
 CTCCAAC TT
 GAM1171 KIAA1229 3' AGATTCTAAGAAAATGTTTCA 31094 GA CTAG C
 TG AACAT CT TAGAATCT
 || |||| || |||||
 AC TTGTA GA ATCTTAGA
 AC AAA_ _
 GAM1171 LOC129607 3' ATTCTAGAGCCAAGTGTTC 36972 A CTA
 GGAA CAT GCTCTAGAAT
 |||| ||| |||||

CCTT GTG CGAGATCTTA
 _ AAC
 GAM1171 LOC130639 5' ATTCTACTGCAGGTGTTTCCA 37001 A TC
 TGGAACATCT GC TAGAAT
 ||||| || |||||
 ACCTTTGTGGA CG ATCTTA
 _ TC
 GAM1171 LOC200339 3' ATTCTAGAGAGGCATCCA 43297 AACAA AG
 TGGA TCT CTCTAGAAT
 ||| || |||||
 ACCT GGA GAGATCTTA
 AC__ __
 GAM1171 LOC257465 3' AGATTCTGATTTATATGTTCCC 39664 A C C T
 A TGG AACAT TAG TC AGAATCT
 || |||| || |||||
 ACC TTGTA ATT AG TCTTAGA
 C T T _
 GAM1172 FBXL3A 3' TAAGTTCATAATCATATTTTTC 14456 CATCT_
 GA TGATTATGAACTTA
 || |||||
 CT ACTAATACTTGAAT
 TTTTAT
 GAM1172 CECR1 3' AAGTTCATGTCACTGTCT 18881 TCT T
 AGACA TGAT ATGAACTT
 |||| || |||||
 TCTGT ACTG TACTTGAA
 C__ _
 GAM1172 CORTBP2 3' AGTTTTAATCAAGATGTTCA 27250 A T
 A GACATCTTGATTA GAACT
 | ||||| |||||
 A TTGTAGAACTAAT TTTGA
 C _
 GAM1172 KIAA1900 3' AAGTAACTCTCAGATGTCTTA 36257 T TTATGA
 TAAGACATCT GA ACTT
 ||||| || |||
 ATTCTGTAGA CT TGAA
 _ CTCAA_
 GAM1172 MKRN2 3' AAGTTCTCTCAAGTGTC 35856 T TTAT
 GACA CTTGA GAACTT
 ||| |||| |||||
 CTGT GAACT CTTGAA
 _ CT__
 GAM1172 LOC144182 3' TTCATGATCAACATCTCT 29168 C C
 AGA AT TTGATTATGAA
 ||| || |||||
 TCT TA AACTAGTACTT
 C C
 GAM1172 LOC151878 5' TAAGTCCATGAGGGATGTC 39171 GA A
 GACATCTT TTATG ACTTA
 ||||| |||| |||||

CTGTAGGG AGTAC TGAAT
 — C
 GAM1173 ADAMTS13 5' GTCTGTGGGTTTCTGGTCC 29125 C TA A
 A ACCAGAAATCC ACA AC
 | ||||| ||| ||
 C TGGTCTTTGGG TGT TG
 C — C
 GAM1173 ADAMTS13 5' GTCTGTGGGTTTCTGGTCC 29127 C TA A
 A ACCAGAAATCC ACA AC
 | ||||| ||| ||
 C TGGTCTTTGGG TGT TG
 C — C
 GAM1173 ADAMTS13 5' GTCTGTGGGTTTCTGGTCC 29131 C TA A
 A ACCAGAAATCC ACA AC
 | ||||| ||| ||
 C TGGTCTTTGGG TGT TG
 C — C
 GAM1173 AK3 3' TTTGTCCCAGGCTTTCTGGTGT 15074 T A__
 ACACCAGAAA CCT ACAAA
 ||||| ||| ||||
 TGTGGTCTTT GGA TGTTT
 C CCC
 GAM1173 CEBPA 3' TTTGTTTGGTTTTCTCGG 10573 _ T T
 CC AGAAA CC AACAAA
 || |||| || |||||
 GG TCTTT GG TTGTTT
 C T T
 GAM1173 HSPA4 3' TTGTTAATTTTGGTGT 42977 ATCC
 ACACCAGAA TAACAA
 ||||| |||||
 TGTGGTTTT ATTGTT
 A__
 GAM1173 HSPD1 3' TGTTAAATCAGGATTTT TAGT 30208 C AACA__
 G CAC AGAAATCCT AACA
 || ||||| |||
 GTG TTTT TAGGA TTGT
 A CTAAAA
 GAM1173 KMO 3' TTGTTTGT TAGCAGGTGT 9783 AGAAATC
 ACACC CTAACAAACAA
 |||| |||||
 TGTGG GATTGTTTGT
 AC____
 GAM1173 NR3C2 3' TGTTTGT TGGCACTGATG 6599 C AAAT T
 CA CAG CC AACAAACA
 || ||| || |||||
 GT GTC GG TTGTTTGT
 A AC__ T
 GAM1173 ORC2L 3' TTTGTTTGCTATTCTGTGTGT 12864 _ ATCC A
 ACAC CAGAA TA CAAACAAA
 ||| |||| || |||||

			TGTG GTCTT AT GTTTGTTT		
			T ____ C		
GAM1173	PACE	3'	TTGCTTGTTGGGATTCTG 8428	A	A
			CAG AATCCTAACAA CAA		
			GTC TTAGGGTTGTT GTT		
			C C		
GAM1173	PCDH11X	3'	TTGTTTGTGTCTCTCTGCTGT 26796	C	AATCCTA
			ACA CAGA ACAAACAA		
			TGT GTCT TGT TTGTT		
			C CTCTG__		
GAM1173	PCDH11X	3'	TTGTTTGTGTCTCTCTGCTGT 26811	C	AATCCTA
			ACA CAGA ACAAACAA		
			TGT GTCT TGT TTGTT		
			C CTCTG__		
GAM1173	PCDH11Y	3'	TTGTTTGTGTCTCTCTGCTGT 26830	C	AATCCTA
			ACA CAGA ACAAACAA		
			TGT GTCT TGT TTGTT		
			C CTCTG__		
GAM1173	PPP1R11	3'	TGTTATTTAGGATTTCTG 22485		CA
			CAGAAATCCTAA AACA		
			GTCTTTAGGATT TTGT		
			TA		
GAM1173	UBE2G2	3'	TTTGTGACTTAGGATTTTGATG 32378	CCA	CAA
	T		ACA GAAATCCTAA ACAA		
			TGT TTTTAGGATT TGT TT		
			AG_ CAG		
GAM1173	AGTRL2	5'	TGTTTAAACACTGAACTCTGGT 11648		AA CTAAC__
	GT		ACACCAGA TC AAACA		
			TGTGGTCT AG TTTGT		
			CA TCACAAA		
GAM1173	ARP3BETA	3'	TTTGTTTGAACTTTCTGG 21687		TCCTAA
			CCAGAAA CAAACAAA		
			GGTCTT GTTTGTTT		
			CAA__		
GAM1173	DCOHN	3'	TGTTTGTCTTTGGTGT 25852		AATCCTA
			ACACCAGA ACAAACA		
			TGTGGTTT TGT TTGT		
			C_____		
GAM1173	DKFZp566H0824	5'	TGTTTTATGTATTTCTGGTG 18981		CCTAAC
			CACCAGAAAT AAACA		

GTGGTCTTTA TTTGT
 TGTAT_
 GAM1173 EFA6R 3' TTTGTTTGCTAAAGGATGGGG 17628 AGAA AA__
 CC ATCCT CAAACAAA
 || |||| |||||
 GG TAGGA GTTTGTTT
 GG__ AATC
 GAM1173 EREG 3' TTGTACAAACAGTATTTCTGGT 7158 C AACAA_
 GT ACACCAGAAAT CT ACAA
 ||||| || ||||
 TGTGGTCTTTA GA TGTT
 T CAAACA
 GAM1173 FLJ10656 3' TTGTTTGTATTTCTTCAGGT 19992 __ CCTA
 ACC AGAAAT ACAAACAA
 || |||| |||||
 TGG TCTTTA TGTTTGTT
 ACT ____
 GAM1173 FLJ10891 3' TTTGTGACAAGGATTTCTGGGTG 20227 A AACAA
 T ACACC GAAATCCT ACAA
 |||| |||| ||||
 TGTGG CTTTAGGA TGTTT
 G ACAG_
 GAM1173 FLJ21106 3' TTGTTTGTCTTCTGG 24739 TCCTA
 CCAGAAA ACAAACAA
 |||| |||||
 GGTCTT TGTTTGTT

 GAM1173 FLJ23511 3' TTTGGGGAAAATCTTCTGGTGT 25970 A__ AA
 ACACCAGAA TCCT CAAA
 ||||| ||| ||||
 TGTGGTCTT AGGG GTTT
 CTA__
 GAM1173 KIAA0152 3' TTGTTTGTAGTTTGCCTGG 16343 AAATC
 CCAG CTAACAAACAA
 ||| |||||
 GGTC GATTGTTTGTT
 CGTTT
 GAM1173 KIAA0940 3' TTGTTTGTGTTGTGGTGT 17150 G ATCC
 ACACCA AA TAACAAACAA
 |||| || |||||
 TGTGGT TT GTTGTTTGTT
 G ____
 GAM1173 KIAA0940 3' TTTGTTTGTCTTCTATGT 17151 CC TCCT
 ACA AGAAA AACAAACAAA
 || |||| |||||
 TGT TCTTT TTGTTTGTTT
 A_ TT_
 GAM1173 MGC10765 3' TTTGTTGATTTTGGTGT 23647 A CT
 ACACCAGAA TC AACAAA
 ||||| || |||||

TGTGGTTTT AG TTGTTT

GAM1173 MRPS10 3' TGTGGTTAGGAGATGTCT 19941 AA__
AGA TCCTAACAAACA
||| |||||
TCT AGGATTGTTTGT
GTAG

GAM1173 SDS3 3' TTGTTTGTAGCCTTGACTG 34322 A_ TC
CAG AA CTAACAAACAA
||| || |||||
GTC TT GATTGTTTGT
AG CC

GAM1173 STK3 3' TTTGTTTTTTTGATTTTGTATG 36495 C CT C
T ACA CAGAAATC AA AAACAAA
||| ||||| || |||||
TGT GTTTTTAG TT TTTGTTT
A T_ T

GAM1173 TUCAN 3' TTTGTATGTTAGGACTTT 17322 A A
GAA TCCTAACA ACAA
||| ||||| |||||
TTT AGGATTGT TGTTT
C A

GAM1173 ZNF340 3' TGTGGTATTTTGGTGT 41036 ATCCTA
ACACCAGAA ACAAACA
||||| |||||
TGTGGTTTT TGTTTGT
A_____

GAM1173 LOC143785 3' TTTGCAGGGAGATTTCTGATG 37633 C _ AA_
CA CAGAAATC CT CAAA
|| ||||| || |||||
GT GTCTTTAG GG GTTT
A A GAC

GAM1173 LOC144453 3' TTTGTTTGAGGCTTTCT 37749 T AA
AGAAA CCT CAAACAAA
||| || |||||
TCTTT GGA GTTTGTTT
C _

GAM1173 LOC148824 3' TTTGTTTGTTCCTTTGTGGT 40910 G TCCT
ACCA AAA AACAAACAAA
||| || |||||
TGGT TTT TTGTTTGT
G CCT_

GAM1173 LOC200471 5' TGTTTGATTTTCTGGTGT 43305 TCCTAA
ACACCAGAAA CAAACA
||||| |||||
TGTGGTCTTT GTTTGT
TA_____

GAM1173 LOC201696 3' TTGTTTGTTCCTTCTGG 31628 ATCCT_
CCAGAA AACAAACAA
||| |||||

GGTCTT TTGTTTGT
CCTTTT
GAM1173 LOC257465 3' TTGTCATTGGAGAATTTCTGGT 39668 __ CAA
ACCAGAAAT C CTAA ACAA
||||||| | ||| |||
TGGTCTTTA G GGTT TGTT
A A AC_
GAM1173 LOC91408 3' TTTGTTTGGGGTATTTTGGTG 32794 _ AA
T ACACCAGAAAT CCT CAAACAAA
||||||| ||| |||||
TGTGGTTTTTA GGG GTTTGTTT
T _
GAM1174 LHPP 3' CCACACAGTGAGAACTGTAGC 22674 T C A
GCT ATAG TCTCACTGT TGG
||| ||| ||||| |||
CGA TGTC AGAGTGACA ACC
_ A C
GAM1174 LOC151584 3' CCATACAGCAAAGGAGAAGC 41376 ATAG CA_
GCTT CTCT CTGTATGG
||| ||| |||||
CGAA GAGG GACATACC
_ AAAC
GAM1174 LOC201799 3' CCATACAATGAAAGCTATAACT 42914 C C C
A TAG TTATAGCT TCA TGTATGG
||| ||||| ||| |||||
ATC AATATCGA AGT ACATACC
_ A A
GAM1175 LFNG 3' GTTCCAGTGGCCCCACGA 44510 AA _
TCGT GGGCCACT AAC
||| ||||| |||
AGCA CCCGGTGA TTG
C_ CC
GAM1175 MGC3178 3' TTGGATGTCTTCCTTAGA 25132 G CCACTA
TC TAAGGG ACATCCAA
|| ||||| |||||
AG ATTCTT TGTAGGTT
_ TC_
GAM1175 TOB2 3' TTGGATGCTGCCTTAC 45772 GCCAC A
GTAAGG TA CATCCAA
||||| || |||||
CATTCC GT GTAGGTT
_ C
GAM1175 LOC145501 3' GGATGCCAGTGGCCCTCGCGA 37883 TA AA
TCG AGGGCCACT CATCC
||| ||||| |||||
AGC TCCCGGTGA GTAGG
GC CC
GAM1175 LOC147671 3' TTGGATGCTGCCTTAC 38379 GCCAC A
GTAAGG TA CATCCAA
||||| || |||||

CATTCC GT GTAGGTT
 _____ C
 GAM1175 LOC157273 3' TGAATGTTAGTGCCTT 41788 C C
 AAGGGC ACTAACAT CA
 ||||| ||||| ||
 TTCCTG TGATTGTA GT
 _____ A
 GAM1175 LOC91380 5' TGGTATGGATGGCCCTTAGA 32759 G CTAA _
 TC TAAGGGCCA CAT CCA
 || ||||| || |||
 AG ATTCCCGGT GTA GGT
 _____ AG__ T
 GAM1176 AP2B1 3' TCTCAGGTCCAGTTCAA 6955 C CT
 TTG AGCT GACCTGAGA
 ||| ||| |||||
 AAC TTGA CTGGACTCT
 _____ C_
 GAM1176 CBFA2T2 3' TCCCAGGTCAGTAGACCAA 11552 CAG _ A
 TTG CT CTGACCTG GA
 ||| || ||||| ||
 AAC GA GACTGGAC CT
 CA_ T C
 GAM1176 COL4A6 5' TCTCCTGAGTGCTGCAAGTT 27360 T GACCT
 AACTTGCAGC CT GAGA
 ||||| || |||
 TTGAACGTCG GA CTCT
 T GTC__
 GAM1176 EPHB1 3' CTCAGTGGGCTGCAGTT 10728 T TGAC
 AACT GCAGCTC CTGAG
 ||| ||||| ||||
 TTGA CGTCGGG GACTC
 _____ T__
 GAM1176 GNB3 5' TCCCAGGAACCGGAGCTGGAA 7854 G A__ A
 TT CAGCTCTG CCTG GA
 || ||||| ||| ||
 AA GTCGAGGC GGAC CT
 G CAA C
 GAM1176 GPC1 3' CTCAGGTCAGCTGGGAG 7871 G CT
 CTT CAGCT GACCTGAG
 ||| ||| |||||
 GAG GTCGA CTGGACTC
 G _
 GAM1176 IL1F5 5' CTCAGGTCCTGGCAAGTT 14600 AGCTCT
 AACTTGC GACCTGAG
 ||||| |||||
 TTGAACG CTGGACTC
 GTC__
 GAM1176 MMP19 5' TCTCAGGTCAGAGGCACGG 23080 _ AG
 CT TGC CTCTGACCTGAGA
 || ||| |||||

GG ACG GAGACTGGACTCT
C _
GAM1176 NXF2 5' TCCCAGGTTGGTTCCAAGT 22591 C CT A
ACTTG AGCT GACCTG GA
||||| ||| ||||| ||
TGAAC TTGG TTGGAC CT
C _ C
GAM1176 OPHN1 3' TCCCAGGCTCCTATGCAAGTT 8406 GCTCT _ A
AACTTGCA GA CCTG GA
||||||| || ||||| ||
TTGAACGT CT GGAC CT
ATC_ C C
GAM1176 PODXL 3' CTCAGGTCTGCTGCAA 11873 TCT
TTGCAGC GACCTGAG
||||||| |||||
AACGTCG CTGGACTC
T_
GAM1176 RNASE1 5' TCTCAGACACCAAGCTGCAG 8837 C AC_
TTGCAGCT TG CTGAGA
||||||| || |||||
GACGTCGA AC GACTCT
_ CACA
GAM1176 CARD14 5' CTGCACACAGACTGCAAGT 27407 C ACC _
ACTTGCACTCTG TG AG
||||||| ||| |||
TGAACGTC AGAC AC TC
_ AC_ G
GAM1176 CHST3 3' CTTATAGAGCTGCAA 10482 ACC
TTGCAGCTCTG TGAG
||||||| |||
AACGTCGAGAT ATTC

GAM1176 DKFZP586B2420 3' CTCACCCAAGCTGCAGTT 37010 T C ACC
AACT GCAGCT TG TGAG
||| ||||| || |||
TTGA CGTCGA AC ACTC
_ _ CC_
GAM1176 DKFZp586I021 3' CTCAGAGGAGCTGCAAG 26023 GAC
CTTGCAGCTCT CTGAG
||||||| |||||
GAACGTCGAGG GACTC
A_
GAM1176 DRIL2 3' CTCAGCCCGGTAAGCTGCAG 13186 _ AC
TTGCAGCT CTG CTGAG
||||||| ||| |||||
GACGTCGA GGC GACTC
AT CC
GAM1176 FLB6421 5' CTCAAGCAACAGAGCTGCAG 21301 AC_ _
TTGCAGCTCTG CT GAG
||||||| ||| |||

			GACGTCGAGAC	GA	CTC		
			AAC	A			
GAM1176	FLJ10521	3'	CTCAGAGGGGCACAGCTGCAGG	19910		C	AC__
			CTTGCAGCT	TG	CTGAG		
			GGACGTCGA	AC	GA	CTC	
			C	GGGA			
GAM1176	FLJ10620	3'	TCATACAGAGCTGCAGTT	19975	T		ACC
			AACT	GCAGCTCTG	TGA		
			TTGA	CGTCGAGAC	ACT		
			_	AT_			
GAM1176	FLJ10751	3'	CAAATCAGAGCTCACAGT	20090	_	C	CC
			ACT	TG	AGCTCTGA	TG	
			TGA	AC	TCGAGACT	AC	
			C	_	AA		
GAM1176	FLJ10751	3'	CAAATCAGAGCTCACAGT	20189	_	C	CC
			ACT	TG	AGCTCTGA	TG	
			TGA	AC	TCGAGACT	AC	
			C	_	AA		
GAM1176	FLJ10842	3'	TCCCAGGTGATTCTGTAAAGTT	20188		CTCTG	A
			AACTTGCAG	ACCTG	GA		
			TTGAATGTC	TGGAC	CT		
			TTAG_	C			
GAM1176	FLJ12547	3'	CTCATTGTGGAGCTGCAA	24547		ACC	
			TTGCAGCTCTG	TGAG			
			AACGTCGAGGT	ACTC			
			GTT				
GAM1176	FLJ31709	5'	TCTCAGGGACGGGCTGCAG	29459		TGA	
			TTGCAGCTC	CCTGAGA			
			GACGTCGGG	GGA	CTCT		
			CAG				
GAM1176	HIC2	3'	TCTCAGGTTCCAGCAAGT	32533		AGCTCT	
			ACTTGC	GACCTGAGA			
			TGAACG	TTGGA	CTCT		
			ACC__				
GAM1176	KIAA0317	5'	CTCGTTTAAAGCTGCAG	16794		C	CC
			TTGCAGCT	TGA	TGAG		
			GACGTCGA	ATT	GCTC		
			A	T_			
GAM1176	KIAA0417	3'	TCTGGCCACAGAGCTGCAG	35292		A__	T
			TTGCAGCTCTG	CC	GA		

GACGTCGAGAC GG CT
 ACC T
 GAM1176 KIAA0574 3' CTCAGACATGGCTGCAA 34344 C AC
 TTGCAGCT TG CTGAG
 ||||| || ||||
 AACGTCGG AC GACTC
 T A_

GAM1176 KIAA0939 3' TCTCAGGGTGAGGAGCTGCCAG 31066 T GA__
 T ACT GCAGCTCT CCTGAGA
 || ||||| |||||
 TGA CGTCGAGG GGA CTCT
 C AGTG

GAM1176 KIAA1211 3' TAGATCAGAGCTACAAGTT 34166 C C
 AACTTG AGCTCTGA CTG
 |||| ||||| ||
 TTGAAC TCGAGACT GAT
 A A

GAM1176 KIAA1580 5' AGATCAAAGCTGCAGTT 34407 T C C
 AACT GCAGCT TGA CT
 ||| ||||| ||| ||
 TTGA CGTCGA ACT GA
 _ A A

GAM1176 KIAA1879 3' CTCAGGCAGCTGCAG 36415 CT A
 TTGCAGCT G CCTGAG
 ||||| | |||||
 GACGTCGA C GGA CTCT

GAM1176 LANCL2 3' CTCAGAGTGCAGTGCAG 20776 CTC _ _
 TTGCAG TG AC CTGAG
 ||||| || || |||||
 GACGTC AC TG GACTC
 _ G A

GAM1176 MAC30 5' CTCAAAGGAAGCTGCAAGT 31405 _ GACC
 ACTTGCAGCT CT TGAG
 ||||| || |||
 TGAACGTCGA GG ACTC
 A AA_

GAM1176 MAP3K3 3' TCCCAGGTTGGCTCTGCCAGT 8224 T CT TG A
 ACT GCAG C ACCTG GA
 || ||| | ||||| ||
 TGA CGTC G TGGAC CT
 C TC GT C

GAM1176 MGC4368 3' CTCAGTAGTGGCTGCCAGT 23699 T _ AC
 ACT GCAGCT CTG CTGAG
 || ||||| || |||||
 TGA CGTCGG GAT GACTC
 C T _

GAM1176 NIFU 5' CTCAAACGCAAAGAAAAGTGC 33437 C_ GACC_
 GGT ACTTGCAG TCT TGAG
 ||||| || |||

TGGACGTC AGA ACTC
 AAA AACGCAA
 GAM1176 RALGPS1A 3' CAGGCACAGAGCTGCAGTT 16017 T A_
 AACT GCAGCTCTG CCTG
 |||| ||||| ||||
 TTGA CGTCGAGAC GGAC
 _ AC
 GAM1176 TED 3' CTCAGGGAGCTGCAA 17916 TGA
 TTGCAGCTC CCTGAG
 ||||| |||||
 AACGTCGAG GGA CTC

 GAM1176 LOC115129 3' TCCCAGGCCCATAGCTGCAA 36254 C A_ A
 TTGCAGCT TG CCTG GA
 ||||| || |||||
 AACGTCGA AC GGAC CT
 T CC C
 GAM1176 LOC124977 5' TCTCAGGCCAAGAGCTGCAGG 37448 GA_
 CTTGCAGCTCT CCTGAGA
 ||||| |||||
 GGACGTCGAGA GGA CTC
 ACC
 GAM1176 LOC138399 5' TCCCAGGTGCAACTGCAG 37132 CTC _ A
 TTGCAG TG ACCTG GA
 ||||| || |||||
 GACGTC AC TGGAC CT
 A_ G C
 GAM1176 LOC142941 5' TCTCAGGTCAGTGGCAG 40323 AGCT
 TTGC CTGACCTGAGA
 |||| |||||
 GACG GACTGGACTCT
 GT_
 GAM1176 LOC144481 3' TCCCAGCAGGCTGCAA 40420 T AC A
 TTGCAGC CTG CTG GA
 ||||| || |||||
 AACGTCG GAC GAC CT
 _ _ C
 GAM1176 LOC146138 3' TCCCAGGTCAGAGAGGAGAGT 40657 GCAG A
 ACTT CTCTGACCTG GA
 |||| ||||| |||||
 TGAG GAGACTGGAC CT
 AGGA C
 GAM1176 LOC146333 5' TCTTCGTAGAGCCCAAGT 40045 CA ACCT
 ACTTG GCTCTG GAGA
 |||| ||||| |||||
 TGAAC CGAGAT TTCT
 C_ GC_
 GAM1176 LOC149175 3' TCCCAGGTCAGAGGTCAGCA 38663 AG_ A
 TGC CTCTGACCTG GA
 |||| ||||| |||||

	ACG GAGACTGGAC CT	
	ACTG C	
GAM1176 LOC153883 5'	TCTCAGTTCACTGCAA 39432	CTC C
	TTGCAG TGA CTGAGA	
	AACGTC ACT GACTCT	
	___ T	
GAM1176 LOC157931 3'	TCCCAGAGTTGCTGCAAG 41905	TCT _ A
	CTTGCAGC GAC CTG GA	
	GAACGTCG TTG GAC CT	
	___ A C	
GAM1176 LOC196759 5'	TCCCAGGCACAGCTGCAG 42296	C A A
	TTGCAGCT TG CCTG GA	
	GACGTCGA AC GGAC CT	
	C _ C	
GAM1176 LOC199864 5'	TCCCAGGCACAGCTGCAG 43252	C A A
	TTGCAGCT TG CCTG GA	
	GACGTCGA AC GGAC CT	
	C _ C	
GAM1176 LOC200734 3'	TCCCATGTAAGCTGCAGTT 42842	T CTG C A
	AACT GCAGCT AC TG GA	
	TTGA CGTCGA TG AC CT	
	_ A__ T C	
GAM1176 LOC202934 5'	CAGCAATGTAGAACTGTAAGT 43454	C AC__
	ACTTGCAG TCTG CTG	
	TGAATGTC AGAT GAC	
	A GTAAC	
GAM1176 LOC220776 3'	TCCCAGGCAGAGCTGCAG 33937	A A
	TTGCAGCTCTG CCTG GA	
	GACGTCGAGAC GGAC CT	
	_ C	
GAM1176 LOC253868 5'	CTCAGTGGGGGATACTGCAAGT 45749	___ G C
T	AACTTGCAG CTCT AC TGAG	
	TTGAACGTC GGGG TG ACTC	
	ATA G _	
GAM1176 LOC254045 3'	TCCCAGCAGGCTGCAA 46162	T AC A
	TTGCAGC CTG CTG GA	
	AACGTCG GAC GAC CT	
	_ _ C	
GAM1176 LOC255465 5'	CAGCAATGTAGAACTGTAAGT 46448	C AC__
	ACTTGCAG TCTG CTG	

TGAATGTC AGAT GAC
 A GTAAC
 GAM1176 LOC91351 3' TCTCAAATGAGCTTAAACTGCA 32699 _____ TGACC
 AGT ACTTGCA GCTC TGAGA
 ||||| ||| |||||
 TGAACGT CGAG ACTCT
 CAAATT TAA__
 GAM1177 MSN 3' ATGGTGCCAATGGAACCTC 30226 C
 GAG TTCCATTGGCACCGT
 ||| |||||
 CTC AAGGTAACCGTGGTA
 C
 GAM1177 RAD52 3' ACGCACCAGCGGAAGCTC 28642 A CAC
 GAGCTTCC TTGG CGT
 ||||| ||| |||
 CTCGAAGG GACC GCA
 C AC_
 GAM1177 RAD52 3' ACGCACCAGCGGAAGCTC 28652 A CAC
 GAGCTTCC TTGG CGT
 ||||| ||| |||
 CTCGAAGG GACC GCA
 C AC_
 GAM1177 RAD52 3' ACGCACCAGCGGAAGCTC 28661 A CAC
 GAGCTTCC TTGG CGT
 ||||| ||| |||
 CTCGAAGG GACC GCA
 C AC_
 GAM1178 FLJ10508 3' TGGCTCTTATCATCATCT 19896 T
 AGATG ATGATAAGAGCCA
 ||||| |||||
 TCTAC TACTATTCTCGGT
 -
 GAM1178 LOC136288 3' ACACTTGGCTAACAAACA 37098 A ATAAG
 TGT TG AGCCAAGTGT
 ||| ||| |||||
 ACA AC TCGGTCACA
 A AA__
 GAM1178 LOC51333 3' ACACTTGGCCCTTGGTTACGTC 18749 TGA A
 GATGTA TAAG GCCAAGTGT
 ||||| ||| |||||
 CTGCAT GTTC CGGTCACA
 TG_ C
 GAM1179 ARPP-19 3' AATATGTCTTAACTATT 13417 G
 AATAGT TAAGACATATT
 ||||| |||||
 TTATCA ATTCTGTATAA
 -
 GAM1179 LOC51141 3' TATTGAATATGTGTACAC 34051 AG
 GTGTA ACATATTCAATA
 ||||| |||||

		CACAT TGTATAAGTTAT		
		G_		
GAM1179	LOC91050	3' ATTGGGTGGGTCTCCCACTA	32332	TA A
		TAGTG AGAC TATTCAAT		
		ATCAC TCTG GTGGGTTA		
		CC G		
GAM1180	ATP6V1G2	3' TGATACTGTGTTCCCT	28225	TTGTT
		AGGGAAT CAGTATCA		
		TCCCTTG GTCATAGT		
		T____		
GAM1180	ATP6V1G2	3' TGATACTGTGTTCCCT	28698	TTGTT
		AGGGAAT CAGTATCA		
		TCCCTTG GTCATAGT		
		T____		
GAM1180	BACH1	3' ATACTGTTTTTTTCCTTTA	6856	TTTGTT
		TAAAGGGAA CAGTAT		
		ATTCCTTT GTCATA		
		TTTT__		
GAM1180	HLA-DQA1	3' GAAGCAACAAATTCCTTTA	46726	CA A
		TAAAGGGAATTTGTT GT TC		
		ATTCCTTAAACAA CG AG		
		__ A		
GAM1180	CG018	3' TGATACTGATTTTCCTTT	27405	TTTGT
		AAGGGAA TCAGTATCA		
		TTTCCTT AGTCATAGT		
		TT__		
GAM1180	E2F6	3' GTGATAATTGAAACTCCTTT	7676	ATTTG _
		AAGGGA TTCAGT ATCAC		
		TTTCCT AGGTTA TAGTG		
		CAA__ A		
GAM1180	FLJ10261	3' TGATACTAAACAACCTCTCT	19789	AT C
		AGGGA TTGTT AGTATCA		
		TCTCT AACAA TCATAGT		
		C_ A		
GAM1180	LOC92573	5' GATACTGAAGAACTCCC	34600	A G
		GGGA TTT TTCAGTATC		
		CCCT AAA AAGTCATAG		
		C G		
GAM1181	FLJ14600	5' TTATTAACCTTCAGCCTTCGA	26576	A TAAA
		TC AAGGCTGA TTAATAA		

AG TTCCGACT AATTATT
 C TCC_
 GAM1181 KIAA0596 3' TTATTAATTTATTTCCCT 31465 CT
 AGG GATAAATTAATAA
 ||| |||||
 TCC TTATTTAATTATT
 CT
 GAM1181 KIAA1373 3' ATTAATTTACAGACATTTGAA 35123 GG_ A
 TTCAAA CTG TAAATTAAT
 ||||| ||| |||||
 AAGTTT GAC ATTTAATTA
 ACA _
 GAM1181 SPTLC2 3' TTATTAATTTAGGCCT 11288 GA
 AGGCT TAAATTAATAA
 ||||| |||||
 TCCGG ATTTAATTATT

 GAM1182 HMGA2 3' AATGGAAGCAATTGCTCA 9559 C T C
 C AGC GGTTGCT CCATT
 | ||| ||||| |||||
 A TCG TTAACGA GGTA
 C _ A
 GAM1182 IFI16 5' AGAATAGGAGCAAGCCAGCACT 35281 CA__ _ C
 AGTCA TGAC GCTGGTT GCTCC ATTCT
 ||||| ||||| ||||| |||||
 ACTG CGACCGA CGAGG TAAGA
 ATCA A A
 GAM1182 NEO1 3' AGAATGAGCCAGCAGACTGGCC 8314 A _ GTT CC
 A TG CCAG CTG GCTC ATTCT
 || ||||| ||| |||||
 AC GGTC GAC CGAG TAAGA
 C A GAC _
 GAM1182 TIRAP 5' AGAACAGTTTCCTCAGCTGGTCA 27473 _TT CCCA
 TGACCAGCTG G GCT TTCT
 ||||| ||| ||| |||||
 ACTGGTCGAC C TGA AAGA
 T CT C__
 GAM1182 BTBD2 3' AGAATGGGGCCCCAGCCGG 19438 A TT T
 CC GCTGG GC CCCATTCT
 || ||||| || |||||
 GG CGACC CG GGGTAAGA
 C C_ _
 GAM1182 FGD3 3' GGGGCAACCACTGGCCA 36092 A C
 TG CCAG TGGTTGCTCC
 || ||||| |||||
 AC GGTC ACCAACGGGG
 C _
 GAM1182 FLJ21791 3' AGAATAAAGGCAACCACT 30808 CCC
 GCTGGTTGCT ATTCT
 ||||| |||||

			TGACCAACGG	TAAGA		
			AAA			
GAM1182	GBTS1	3'	AGGATGGGGAGCTGGCA	29726	A	GGTTGC
			TG CCAGCT	TCCCATTCT		
			AC GGTCGA	GGGGTAGGA		
			—	—		
GAM1182	KIAA1257	3'	AGAACGGGTCAGCTCAGCAGGC	31428	A A	_ CT A
			CA	TG CC GCTG GTTG CCC TTCT		
				AC GG CGAC CGAC GGG AAGA		
				C A T T_ C		
GAM1182	SBBI26	3'	AGAATAGAAGATTGGCTCATCA	20829	CC	TG GC CC
				TGA AGC GTT TC ATTCT		
				ACT TCG TAG AG TAAGA		
				AC GT A_ A_		
GAM1182	LOC124602	3'	AATGGGAGCAGTCCATGGTGCA	36756	_	GC _
				TG ACCA TGG TTGCTCCCATT		
				AC TGGT ACC GACGAGGGTAA		
				G _ T		
GAM1182	LOC132235	5'	AGAACGGGACAGAGCAGCTGCC	37479	AC	G GC A
			CA	TG CAGCTG TT TCCC TTCT		
				AC GTCGAC AG AGGG AAGA		
				CC G AC C		
GAM1182	LOC158295	5'	AGAATGAGAAGCCAGT	41936	GC	C
				GCTGGTT TC CATTCT		
				TGACCGA AG GTAAGA		
				_ A		
GAM1182	LOC200940	3'	AATGAGAGAGGCGGCCGCGC	42874	_	C
				GCTGGTTGC TC CATT		
				CGGCCGCG AG GTAA		
				GAG A		
GAM1182	LOC201685	5'	AGAATAAGAAAGCAGCCAGC	43383	CCC_	
				GCTGGTTGCT ATTCT		
				CGACCGACGA TAAGA		
				AAGAA		
GAM1182	LOC203397	3'	AATGGGAGCAGTCCATGGTGCA	43036	_	GC _
				TG ACCA TGG TTGCTCCCATT		
				AC TGGT ACC GACGAGGGTAA		
				G _ T		
GAM1182	LOC254413	5'	AGAATAGCTACAAACAACACTGGT	46397	C _	T CCC
			CA	TGACCAG TG GT GCT ATTCT		

			ACTGGTC AC CA CGA TAAGA		
			A AAA T ____		
GAM1182	LOC57228	5'	AGAACAAAGGCAGCTACGTCA 21705	CAGC	CCCA
			TGAC TGGTTGCT TTCT		
			ACTG ATCGACGG AAGA		
			C____ AAAC		
GAM1183	FGF2	3'	AGAATTATATAATCACTGCTTT 7732	A AC T	
			AAAGCAGT ATTA TA TTCT		
			TTTCGTCA TAAT AT AAGA		
			C AT T		
GAM1183	PDE4D	3'	GAAATATATACTGCTTT 36431	ATTAAC	
			AAAGCAGTA TATTC		
			TTTCGTCAT ATAAAG		
			AT____		
GAM1183	PTGS2	3'	AGAAATAGTCAATATGCTT 6682	GTA A	
			AAGCA ATT ACTATTTCT		
			TTCGT TAA TGATAAAGA		
			A__ C		
GAM1183	RAD50	3'	AGATAATTACTGCCTTGA 12292	A A	
			TCAA GCAGTAATTA CT		
			AGTT CGTCATTAAT GA		
			C A		
GAM1183	RAD50	3'	AGATAATTACTGCCTTGA 28549	A A	
			TCAA GCAGTAATTA CT		
			AGTT CGTCATTAAT GA		
			C A		
GAM1183	SH3GL2	3'	GGTTAACCCTGCTTTGG 8967	AA	
			TCAAAGCAGT TTAAT		
			GGTTTCGTCA AATTGG		
			CC		
GAM1183	SRRM1	3'	AGAAATAAGACCACTGTTTTGA 12448	AATTAAC	
			TCAAAGCAGT TATTTCT		
			AGTTTTGTCA ATAAAGA		
			CCAGA__		
GAM1183	SUV39H2	3'	AGAAACAGTTAATTTGGGC 23973	AGT A	
			GC AATTAAT TTTCT		
			CG TTAATTGA AAAGA		
			GGT C		
GAM1183	UBE4A	3'	AGAAATGGGTGTCACTGCTT 11194	A TAA	
			AAGCAGT AT CTATTTCT		

		TTCGTCA TG GGTAAGA		
		C TG_		
GAM1183	FLJ25422	5' GAAATAGTTAATTTGT	29603	GT
		GCA AATTAAC TATTC		
		TGT TTAATTGATAAAG		
		—		
GAM1183	KIAA1254	3' AAATGTGTTTACTGCTTT	34695	TTA T
		AAAGCAGTAA AC ATTT		
		TTTCGTCATT TG TAAA		
		TG_ _		
GAM1183	MGC3040	3' AGATGATTACTGCTTTGA	33195	A
		TCAAAGCAGTAATTA CT		
		AGTTTCGTCATTAGT GA		
		A		
GAM1183	MGC32043	3' AGAAATAGTTTTTGCTGTT	29390	TT
		AGCAGTAA AACTATTTCT		
		TTGTCGTT TTGATAAAGA		
		T_		
GAM1183	OBTP	3' AGAAATAACAGTGCTGTTTT	19076	ATTAAC
		AAAGCAGTA TATTTCT		
		TTTTGTCGT ATAAAGA		
		GACA_		
GAM1183	PTP4A1	5' AGAAACTGATTACTGCT	9530	ACTA
		AGCAGTAATTA TTTCT		
		TCGTCATTAGT AAAGA		
		C_		
GAM1183	RRN3	3' GAAATTTTTATTGCTTT	20487	TTAACT
		AAAGCAGTAA ATTC		
		TTTCGTTATT TAAAG		
		TT_		
GAM1183	LOC150848	5' TAGTTCTACTGCTTGA	41256	A ATT
		TCAA GCAGTA AACTA		
		AGTT CGTCAT TTGAT		
		_ C_		
GAM1183	LOC161734	3' GGTTATTAACACTGCTTTGA	42110	AAT_
		TCAAAGCAGT TAACT		
		AGTTTCGTCA ATTGG		
		CAATT		
GAM1183	LOC220930	3' GAATAAATTACTGCTTT	44734	AAC
		AAAGCAGTAATT TATTT		

TTTCGTCATTAA ATAAG

GAM1183 LOC221663 5' AGAAAGTCATCATTACTGCTTT 45038 TAACTA
GA TCAAAGCAGTAAT TTTCT
||||||| ||||
AGTTTCGTCATTA AAAGA
CTACTG

GAM1184 FGFR2 5' GAGCCTTCGCAACTCGCGA 23246 _ GAT
TCGCGAGTTG GAA GGCTT
||||||| || ||||
AGCGCTCAAC CTT CCGAG
G _

GAM1184 FGFR2 5' GAGCCTTCGCAACTCGCGA 23248 _ GAT
TCGCGAGTTG GAA GGCTT
||||||| || ||||
AGCGCTCAAC CTT CCGAG
G _

GAM1184 FGFR2 5' GAGCCTTCGCAACTCGCGA 23239 _ GAT
TCGCGAGTTG GAA GGCTT
||||||| || ||||
AGCGCTCAAC CTT CCGAG
G _

GAM1184 FGFR2 5' GAGCCTTCGCAACTCGCGA 23249 _ GAT
TCGCGAGTTG GAA GGCTT
||||||| || ||||
AGCGCTCAAC CTT CCGAG
G _

GAM1184 FGFR2 5' GAGCCTTCGCAACTCGCGA 23295 _ GAT
TCGCGAGTTG GAA GGCTT
||||||| || ||||
AGCGCTCAAC CTT CCGAG
G _

GAM1184 FGFR2 5' GAGCCTTCGCAACTCGCGA 5639 _ GAT
TCGCGAGTTG GAA GGCTT
||||||| || ||||
AGCGCTCAAC CTT CCGAG
G _

GAM1184 FGFR2 5' GAGCCTTCGCAACTCGCGA 23235 _ GAT
TCGCGAGTTG GAA GGCTT
||||||| || ||||
AGCGCTCAAC CTT CCGAG
G _

GAM1184 FGFR2 5' GAGCCTTCGCAACTCGCGA 23242 _ GAT
TCGCGAGTTG GAA GGCTT
||||||| || ||||
AGCGCTCAAC CTT CCGAG
G _

GAM1184 FGFR2 5' GAGCCTTCGCAACTCGCGA 23247 _ GAT
TCGCGAGTTG GAA GGCTT
||||||| || ||||

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AGCGCTCAAC CTT CCGAG
      G ____
GAM1184 FGFR2  5' GAGCCTTCGCAACTCGCGA 23289  _ GAT
      TCGCGAGTTG GAA GGCTT
      ||||| ||| ||||
      AGCGCTCAAC CTT CCGAG
      G ____
GAM1184 FGFR2  5' GAGCCTTCGCAACTCGCGA 23301  _ GAT
      TCGCGAGTTG GAA GGCTT
      ||||| ||| ||||
      AGCGCTCAAC CTT CCGAG
      G ____
GAM1184 LOH11CR2A 5' AAGCCATCTCCCAGGGC 15983  GAG A
      GC TTGG AGATGGCTT
      || ||| |||||
      CG GACC TCTACCGAA
      G__ C
GAM1184 HSJ1   3' GAACTGCTTTCCAACCTC 13587  AT C
      GAGTTGGAAG GG TTC
      ||||| || |||
      CTCAACCTTT TC AAG
      CG _
GAM1184 KIAA0802 5' GAAGCCATCGGAGGCCAGCGA 31349  GA GGAA
      TCGC GTT GATGGCTTC
      ||| ||| |||||
      AGCG CGG CTACCGAAG
      AC AGG_
GAM1184 L3MBTL2 5' GAGCTACTCCTCCAACCTC 42789  A _
      GAGTTGGA GA TGGCTT
      ||||| || |||||
      CTCAACCT CT ATCGAG
      C C
GAM1184 LAP1B   5' AAGCCATCTTCGCGATCG 32261  G _
      CGA TTG GAAGATGGCTT
      ||| ||| |||||
      GCT AGC CTTCTACCGAA
      _ G
GAM1184 STK38L  3' AAGCCATCTTCCATAGTTG 34285  GT_
      CGA TGGAAGATGGCTT
      ||| |||||
      GTT ACCTTCTACCGAA
      GAT
GAM1184 LOC149182 5' AAGCCATCAAATCTCGTGA 40967  TTGGAA
      TCGCGAG GATGGCTT
      ||||| |||||
      AGTGCTC CTACCGAA
      TAAA_
GAM1185 ADD2   3' GCAAATGGAGGCCAACCTCA 18933  AAAACAC CC
      TGAG GGCCTCCA TGC
      ||| ||||| |||

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			ACTC	CCGGAGGT	ACG		
			CAA_____	AA			
GAM1185	ADD2	3'	GCAAATGGAGGCCAACCTCA	18938	AAAACAC	CC	
			TGAG	GGCCTCCA	TGC		
			ACTC	CCGGAGGT	ACG		
			CAA_____	AA			
GAM1185	ADD2	3'	GCAAATGGAGGCCAACCTCA	18946	AAAACAC	CC	
			TGAG	GGCCTCCA	TGC		
			ACTC	CCGGAGGT	ACG		
			CAA_____	AA			
GAM1185	CGTHBA	3'	GCAGGTGGGCGCTCGCGTCTC	14360	AAA A _ C		
			GAGA	C CG GC	TCCACCTGC		
			CTCT	G GC CG	GGGTGGACG		
			___ C T C				
GAM1185	DHCR7	3'	GCAGGTGGGCTCTGCTTCCCG	7040	A AA C TC		
			TG GAA	CA GGCC	CACCTGC		
			GC CTT	GT TCGG	GTGGACG		
			C C_ C _				
GAM1185	LYPLA1	3'	GCAGGTAGCTTCTTTTTTCTCA	13028	CAC_ CTCC		
			TGAGAAAA	GGC	ACCTGC		
			ACTCTTTT	TCG	TGGACG		
			TTCT	A___			
GAM1185	MMP19	3'	GCAGGTGGGTCAATGCTCTC	8268	AAACAC TC		
			GAGA	GGCC	CACCTGC		
			CTCT	CTGG	GTGGACG		
			CGTAA_ _				
GAM1185	MMP19	3'	GCAGGTGGGTCAATGCTCTC	23076	AAACAC TC		
			GAGA	GGCC	CACCTGC		
			CTCT	CTGG	GTGGACG		
			CGTAA_ _				
GAM1185	PLA2G2D	3'	GCAGGTGGAGGCCATGCCTGTC	14771	AAA_ C		
	TT		GAGA	CA GGCCTCC	CACCTGC		
			TTCT	GT CCGGAGGT	TGGACG		
			GTCC	A			
GAM1185	PPAT	3'	GCAGGTGGTCACTGACATTTCC	8550	A ACA CCT		
	CA		TG GAAA	CGG	CCACCTGC		
			AC CTTT	GTC	GGTGGACG		
			C ACA	ACT			
GAM1185	STMN1	3'	CAGGTGGGGCATGTCCTCA	12091	AAA CG T		
			TGAG	ACA GCC	CCACCTG		

		ACTC TGT CGG GGTGGAC		
		C__ A_ _		
GAM1185	BTN2A1	3' GCAATACCGGGCCGTGTCCTC	27803	AAA CCACC
		GAG ACACGGCCT TGC		
		CTC TGTGCCGGG ACG		
		C__ CCATA		
GAM1185	CLIC4	3' CAGGTCACCAATTTTCTCA	15127	CAC CCTCC
		TGAGAAAA GG ACCTG		
		ACTCTTTT CC TGGAC		
		AA_ AC__		
GAM1185	FLJ12875	3' CAGATGGGGCTGTTTTT	23755	CG T C
		GAAAACA GCC CCA CTG		
		CTTTTGT CGG GGT GAC		
		_ _ A		
GAM1185	KIAA1052	3' GCAGGCACTGTGTTTTCTCA	17312	_ CCTCCA
		TGAG AAAACACGG CCTGC		
		ACTC TTTTGTGTC GGACG		
		C AC__		
GAM1185	TGOLN2	3' GCAGGTGGAAGTGCTTTTCT	32026	_ GGCC
		AGAAAA CAC TCCACCTGC		
		TCTTTT GTG AGGTGGACG		
		C A__		
GAM1185	LOC113763	3' CAGGTGGGATATGTCCTCA	28801	AAAAC GCC
		TGAG ACG TCCACCTG		
		ACTC TGT GGGTGGAC		
		C__ ATA		
GAM1185	LOC116113	3' GCAGGTGGAGCCAAGCTCTC	44286	AAACAC C
		GAGA GGC TCCACCTGC		
		CTCT CCG AGGTGGACG		
		CGAA_ _		
GAM1185	LOC124842	3' GCAGGTGGAGGGCTCTTCCTC	37262	AAAACAC _
		GAG GGCC TCCACCTGC		
		CTC TCGG AGGTGGACG		
		CTTC__ G		
GAM1185	LOC149271	5' CAGGTGGCCATTTTCTCA	38679	CAC TCC
		TGAGAAAA GGCC ACCTG		
		ACTCTTTT CCGG TGGAC		
		TA_ _		
GAM1185	LOC150271	3' CAGGTGGCACCTTCTCA	41167	AACAC CCT
		TGAGAA GG CCACCTG		

		ACTCTT CC GGTGGAC		
		_____ AC_		
GAM1185	LOC152573 3'	CAGGTGGAGCCCTGCTC 39287	AAAA C C	
		GAG CA GGC TCCACCTG		
		CTC GT CCG AGGTGGAC		
		_____ C _		
GAM1185	LOC158158 5'	GCAGGTGGCCCCGTCTTCCA 39734	A AAC CCT	
		TG GAA ACGG CCACCTGC		
		AC CTT TGCC GGTGGACG		
		_ CC_ CC_		
GAM1185	LOC200860 3'	GCAGGTGGAGGCCATGTCATTT 43355	AA C	
	C	GAGA ACA GGCCTCCACCTGC		
		CTTT TGT CCGGAGGTGGACG		
		AC A		
GAM1186	INPP5D 3'	TGCTGAGGCTGGAAGAAAAAC 40307	C _ ATA	
		GTTTTTCT CCA CC AGCA		
		CAAAAAGA GGT GG TCGT		
		A C AG_		
GAM1186	MAML1 3'	TGCCCATGGTGGGAGCGTGGTC 16500	GT TTT AA	
		G T CTCCCACCAT GCA		
		C G GAGGGTGGTA CGT		
		TG TGC CC		
GAM1186	TFDP1 3'	TGCTTATGGTAAAATTTGCCTG 13978	TTTTCTCCC	
		TAGGT ACCATAAGCA		
		GTCCG TGGTATTCGT		
		TTTAAAA_		
GAM1186	BRAG 3'	CTCATGGTATGGAAAACC 16941	TCCC A	
		GGTTTTTC ACCAT AG		
		CCAAAAGG TGGTA TC		
		TA_ C		
GAM1186	KIAA0820 3'	TGCTCATGGTATGTCAAACCT 34221	TTCTCCC A	
		AGGTTT ACCAT AGCA		
		TCCAAA TGGTA TCGT		
		CTGTA_ C		
GAM1186	KIAA0984 3'	TGCTAAATCATAGGAGAAAAAT 32646	CACCATA_	
	CTA	TAGGTTTTTCTCC AGCA		
		ATCTAAAAAGAGG TCGT		
		ATACTAAA		
GAM1186	KIAA1858 3'	TGCTCTGCGGGAGAAAAGCC 33331	AC TA	
		GGTTTTTCTCCC CA AGCA		

CCGAAAAGAGGG GT TCGT
C_ C_
GAM1186 PSMF1 3' GCTTTGGAGAAAGACC 13688 CACCAT
GGTTTTTCTCC AAGC
||||||| |||
CCAGAAAGAGG TTCG
T____
GAM1186 LOC115129 5' TGCGACCATGAGAGAAAAACCT 36256 C CCATAA
G TAGGTTTTTCTC CA GCA
||||||| || |||
GTCCAAAAGAG GT CGT
A ACCAG_
GAM1186 LOC255045 3' GCTCATTTTCAGGAAAACCTA 46032 CCCACC A
TAGGTTTTTCT AT AGC
||||||| || |||
ATCCAAAAGGA TA TCG
CTT___ C
GAM1187 CACNA1C 3' CTCCCGGCCAGCCGCGGCCCG 6380 AGT ___ T A
C GC GCCGGCGGC GCC G GGAG
|| ||||| ||| |||
CG CGGCCGCG CGG C CCTC
CC_ AC __
GAM1187 CACNG8 5' CCCCAGCCGCGGCACGGC 35595 A GCC A
GC GTGCCGGCGGC TG GG
|| ||||| || ||
CG CACGGCCGCG AC CC
G ___ C
GAM1187 EGFL3 5' CCTCCCGCCCGCCGGCCT 31374 T C CT
AG GCCGGCGG GC GAGG
|| ||||| || |||
TC CGGCCGCC CG CTCC
_ _ CC
GAM1187 FGFR1 3' CCTCCCTGCCACCAGGCACTGC 17976 _ C CCT
GCAGTGCC GG GGCG GAGG
|||||| || ||| |||
CGTCACGG CC CCGT CTCC
A A CC_
GAM1187 FGFR1 3' CCTCCCTGCCACAGGCACTGC 23370 GGC CCT
GCAGTGCC GGCG GAGG
|||||| ||| |||
CGTCACGG CCGT CTCC
ACA CC_
GAM1187 FGFR1 3' CCTCCCTGCCACCAGGCACTGC 6205 _ C CCT
GCAGTGCC GG GGCG GAGG
|||||| || ||| |||
CGTCACGG CC CCGT CTCC
A A CC_
GAM1187 GPC1 5' CCGGGGGCGCCGCGGCCCGC 7870 AGT GA
GC GCCGGCGGCGCCT GG
|| ||||| || ||

CG CGGCCGCCGCGGG CC
CCC GG
GAM1187 GRM7 5' CTCCAGCGCCGCGCCGCCACC 6517 A C __ AG
GC GC GTG CGGCGGCG C CTG G
|| ||| ||||| | ||| |
CG CAC GCCGCCGC G GAC C
C C C C CT
GAM1187 MAPRE3 3' CCTCGGGCACCAGCCTGC 14711 C _ C
GC GGC GG GCCTGAGG
|| ||| || |||||
CG CCG CC CGGGCTCC
T A A
GAM1187 MPDU1 3' CTCCCCATCTGAGCCAGCCTGC 11297 T C GG CC A
GCAG GC GGC CG TG GGAG
|||| || ||| || || ||||
CGTC CG CCG GT AC CCTC
_ A A_ CT C
GAM1187 NRXN1 5' CCCCACCCGCCGGCACGC 28994 A CGCC A
GC GTGCCGGCGG TG GG
|| ||||| || ||
CG CACGGCCGCC AC CC
_ C__ C
GAM1187 PLXNB2 3' CTCCCCAAGGGTGCCGGCACT 14776 G G GA_
AGTGCCGGCG C CCT GGAG
||||||| | ||| ||||
TCACGGCCGT G GGA CCTC
__ ACC
GAM1187 PTMS 5' CCGAGCGCGCCGGCACCGC 8695 A G CTGA
GC GTGCCGGCG CGC GG
|| ||||| || ||
CG CACGGCCGC GCG CC
C _ AG_
GAM1187 SKI 3' CCGCAGCGCCGCCGACAACGC 8987 AG C C A
GC TG CGGCGGCGC TG GG
|| || ||||| || ||
CG AC GCCGCCGCG AC CC
CA A _ G
GAM1187 SQSTM1 3' CCTCAGCTCCCCGGCACTGC 9989 C C C
GCAGTGCCGG GG GC TGAGG
||||||| || || ||||
CGTCACGGCC CC CG ACTCC
_ T _
GAM1187 TR2 5' CCTCAGGCCCGTCCCGGCGCC 35794 A _ C
GC GTGCCGG CGG GCCTGAGG
|| ||||| || |||||
CG CGCGGCC GCC CGGACTCC
C CT C
GAM1187 YWHAG 3' TCCTCAGGGATCACACTGC 14858 CCGGC CG
GCAGTG GG CCTGAGGA
||||| || |||||

			CGTCAC	CT	GGA	CTCCT		
			A			AG		
GAM1187	CCNE1	5'	CTCCCGGCGCCGCGCCGCCAC	6906	C			A
	TGC		GCAGTG CGGCGGCG C CTG GGAG					
			CGTCAC GCCGCCGC G GGC CCTC					
			C		C	C		
GAM1187	CEP3	5'	CCCGCGCCGCGGCCCGC	13156	AGT			CT A
			GC GCCGGCGGCGC G GG					
			CG CGGCCGCCGC C CC					
			CCC					
GAM1187	FLJ14525	3'	CCTCAGGGCTAACGGCACTGT	26549			GC	G
			GCAGTGCCG GGC CCTGAGG					
			TGTCACGGC TCG GGA					
			AA					
GAM1187	FLJ20507	3'	CTCCTCAGGACTGCAGCACTG	19512			CG	CG
			CAGTGC GCGG CCTGAGGAG					
			GTCACG CGTC GGA					
			A			A		
GAM1187	FLJ20507	3'	CTCCTCAGGACTGCAGCACTG	30220			CG	CG
			CAGTGC GCGG CCTGAGGAG					
			GTCACG CGTC GGA					
			A			A		
GAM1187	KIAA0545	3'	CCTCAGGCCGTGGCCCTGC	31634	T	G		GC
			GCAG GCCG CGGC CTGAGG					
			CGTC CGGT GCCG GACTCC					
			C					
GAM1187	KIAA0669	5'	CCTCACGCCGCGCCACCGC	16625	A	C		CC
			GC GTG CGGCGGCG TGAGG					
			CG CAC GCCGCCGC ACTCC					
			C			C		
GAM1187	KIAA0997	5'	CCGCGCGCCGCCCACTGC	17279			C	CTGA
			GCAGTG CGGCGGCG GG					
			CGTCAC GCCGCCGC CC					
			C			CG		
GAM1187	MACMARCKS	5'	CCTCGGGCGCCAGCCCCAC	23271			CC	
			GTG GGC GGCGCCTGAGG					
			CAC CCG CCGCGGGCTCC					
			C			A		
GAM1187	MGC10966	5'	CTCCTCAGCATCCGGCAC	25537			CGGC	C
			GTGCCG GC TGAGGAG					

CACGGCC CG ACTCCTC
TA__ _
GAM1187 OAZIN 5' CTCCTTCGGCCGCCGCCGCCAC 18020 C _ T
TGC GCAGTG CGGCGGCG CC GAGGAG
||||| ||||| || |||||
CGTCAC GCCGCCGC GG TTCCTC
C C C
GAM1187 POLR3F 5' CCCCAGGCGTCAGGAACTGC 30115 G GGC A
GCAGT CC GGCGCCTG GG
||||| || ||||| ||
CGTCA GG CTGCGGAC CC
A A__ C
GAM1187 RNF10 5' CCCCACGCGCCGCCACCGC 16962 A C CC A
GC GTG CGGCGGCG TG GG
|| ||| ||||| || ||
CG CAC GCCGCCGC AC CC
C C A_ C
GAM1187 SERPINA1 5' CTCCTCAGCTTCAGGCAC 5839 GGC GCC
GTGCC GGC TGAGGAG
||||| ||| |||||
CACGG TCG ACTCCTC
ACT ____
GAM1187 TOR2A 3' CTCCCGCTCCAGCGGCAC 28220 GC C CT A
GTGCCG GG GC G GGAG
||||| || || | ||||
CACGGC CC CG C CCTC
GA T ____
GAM1187 LOC157226 5' CTCAGCGCCGCCGACAC 31976 C C
GTG CGGCGGCGC TGAG
||| ||||| ||||
CAC GCCGCCGCG ACTC
A _
GAM1187 LOC158373 5' CTCAGCGCCGCCGACAC 35190 C C
GTG CGGCGGCGC TGAG
||| ||||| ||||
CAC GCCGCCGCG ACTC
A _
GAM1188 DUOX1 5' TCTCCATTTTGGGACATT 18889 TCC C
AATGTCCCG GGA GGAGA
||||||| ||| |||||
TTACAGGGT TTT CCTCT
__ A
GAM1188 PLCB2 3' CCATCCCCTGGGACATTT 10917 TCC C
AAATGTCCCG GGA GG
||||||| ||| ||
TTTACAGGGT CCT CC
CAC A
GAM1188 DCLRE1A 3' TCCCCAGACCAAAGGAAACATT 34281 __ C__ C AC
TCA TGAAATG TCC GTC GG GGA
||||||| ||| ||| |||

ACTTTAC AGG CAG CC CCT
 AA AAAC A _
 GAM1188 FLJ22419 5' TCTCCACGCCGGGGACATTTC 24008 GTC AC_
 GAAATGTCCC CGG GGAGA
 ||||| ||| ||||
 CTTTACAGGG GCC CCTCT
 _ GCA
 GAM1188 KIAA0930 3' CTCCAACCTGGGACATCCCA 34915 AA TCC AC
 TG ATGTCCCG GG GGAG
 || ||||| || ||||
 AC TACAGGGT CC CCTC
 CC _ AA
 GAM1188 MGC35558 3' TCTTTGTCAGATGGGACACTTC 29619 A CG
 A TGAA TGTCCCGTC GACGGAGA
 ||| ||||| |||||
 ACTT ACAGGGTAG CTGTTTCT
 C A_
 GAM1188 PHRET1 3' CTCCGTCCAGAAATGCCTCTCA 22175 AAT CCCG C
 TGA GT TC GGACGGAG
 ||| || |||||
 ACT CG AG CCTGCCTC
 CTC TAA_ A
 GAM1188 RIG-I 5' CTCCGTCCGGCCTCATTTTC 15614 TCCC T
 GAAATG G CCGGACGGAG
 ||||| | |||||
 CTTTAC C GGCCTGCCTC
 TC__
 GAM1188 WBSCR20A 5' CTCCACATCTGTGGGATATCTC 25860 A TC C_
 A TGA ATGTCCCG CGGA GGAG
 ||| ||||| ||| ||||
 ACT TATAGGGT GTCT CCTC
 C _ ACA
 GAM1188 LOC144600 3' CTCCAACCTGGGACATCCCA 40447 AA TCC AC
 TG ATGTCCCG GG GGAG
 || ||||| || ||||
 AC TACAGGGT CC CCTC
 CC _ AA
 GAM1188 LOC150622 5' TCTCCACCTTCAGGACAAAAGC 38997 CCC_ _ C_
 ATTTCA GAAATGT GTCC GGA GGAGA
 ||||| ||| ||| ||||
 CTTTACG CAGG CTT CCTCT
 AAAA A CCA
 GAM1188 LOC204285 3' TCTGGCCAGAAAGACATTTCA 43090 CCG C A
 TGAAATGTC TC GG CGGA
 ||||| || |||
 ACTTTACAG AG CC GTCT
 AA_ A G
 GAM1189 ACP1 5' CCCACCCCCGCAGCT 10508 AG T
 AGCTGC GGGGGT GGG
 ||||| ||||| |||

Accession	Gene	Strand	Sequence	Position	Context
GAM1189	ACP1	5'	CCCCACCCCCG	13958	AG T
GAM1189	ADAM11	3'	CCCCACCCACCTCCTGCGGCT	22240	GT C
GAM1189	ADAM11	3'	CCCCACCCACCTCCTGCGGCT	8207	GT C
GAM1189	AGRN	3'	CCCCACCCCCAGCCCCAGC	38533	GCAGG C__
GAM1189	B4GALT3	5'	CCCCGGGACCCCTGGAGC	9864	G GTTGGG
GAM1189	BCL7B	3'	CCCCACAGTACCCCTTCAGCT	7435	C GG GGC
GAM1189	BMP1	3'	CCCCACCCAGTACCGCATCT	12769	C AGG GG C
GAM1189	BMP1	3'	CCCCACCCAGTACCGCATCT	12772	C AGG GG C
GAM1189	CHST6	5'	CCCCACCGTGCCGCTGCAGCT	22246	G GGT GC
GAM1189	CRAT	5'	CCCCGCCCCCGCCCCACAGC	6406	CA _ TT

			CGAC CCCC CC CCCGCCCC			
			A_ G _			
GAM1189	CYLN2	3'	CCCCACCCTCCGGCAGCT	9422	A	T
			AGCTGC GGGGGGT GGG			
			TCGACG CCTCCCA CCC			
			G C			
GAM1189	DBH	3'	CCCCGCCCCCGCCCCGCTGC	6439	G	T_
			GCAG GGGGT GGGCGGGG			
			CGTC CCCC CGCCGCCCC			
			G CC			
GAM1189	DEDD	3'	CCCACCCCTCCCTGCA	26879	TTG	C
			TGCAGGGGGG GG GGG			
			ACGTCCCTCC CC CCC			
			_ A			
GAM1189	DNMT3L	5'	CCCCAAGTGACCCCCCGCAGCT	15018	A	GGC
			AGCTGC GGGGGGTTG GGGG			
			TCGACG CCCCCCAGT CCCC			
			_ GAA			
GAM1189	DVL3	3'	CCCCTTACTCCCCTCTGCA	10693	T_	C
			TGCAGGGGGG TGGG GGG			
			ACGTCTCCCC ATTC CCC			
			TC _			
GAM1189	EFNB1	3'	CCCACCCAACCCAGCT	10706	GCAGGG	C
			AGCT GGGTTGGG GGG			
			TCGA CCAACCC CCC			
			_ A			
GAM1189	EMS1	3'	CCCCAAGGTCCCCCCACAGCT	11736	CA	TTGGGC
			AGCTG GGGGGG GGGG			
			TCGAC CCCCC CCCC			
			A_ TGGAA_			
GAM1189	EMS1	3'	CCCCAAGGTCCCCCCACAGCT	28867	CA	TTGGGC
			AGCTG GGGGGG GGGG			
			TCGAC CCCCC CCCC			
			A_ TGGAA_			
GAM1189	ENG	5'	CCCCGGTGCCCGCCCGCAGC	5592	A _	TGGG
			GCTGC GGG GGGT CGGGG			
			CGACG CCC CCG GCCCC			
			_ G TG_			
GAM1189	ENG	3'	CCCGGCCCCCGCGCT	5593	T A	
			AGC GC GGGGGGTTGGG			

TCG CG CCCCCCGGCC

GAM1189 EPHA8 3' CCCACCGTGTGCCCCCTGCCA 21745 GT__ GC
GC GCTG CAGGGGG TGG GGGG

||||| ||| |||
CGAC GTCCCCC GCC CCCC
C GTGT A_

GAM1189 ESR1 3' CCCC GCCCGTTCCCTACCGC 5599 TGCA GG T
GC GGGG T GGGCGGGG

|| ||| | |||||
CG TCCC G CCGCCCC
CCA_ TT C

GAM1189 FAAH 5' CCCC GCTCCGCCCCCGCCGC 23597 T A T
GC GC GGGGGGT GGGCGGGG

|| || ||||| |||||
CG CG CCCCCCG CTCGCCCC
C _ C

GAM1189 FMNL 5' CCCC GCCTCTCCCTGGCAGC 12511 A TT
GCTGC GGGGGG GGGCGGGG

||||| |||||
CGACG TCCCTC TCCGCCCC
G _

GAM1189 FOSB 3' CCCGCCGTTCCTGCGCTT 13582 T GTTG
AAGC GCAGGGGG GGC GGG

||||| |||||
TTCG CGTCCCTT CCGCCC
_ G__

GAM1189 GNB1 3' CCCC GCCCCCCGCACT 7849 C A T
AG TGC GGGGGGT GGG

|| ||| ||||| |||
TC ACG CCCCCCG CCC
_ _ C

GAM1189 GRM6 5' CCCC GCCCCTCTGTCTCCCCGC 6506 A TT__
AGC GCTGC GGGGGG GGGCGGGG

||||| |||||
CGACG CCCCTC CCGCCCC
_ TGTCTC

GAM1189 GTF2IRD1 5' CCCC GCCCTCCGCCGAGC 18451 A G TT
GCTGC GG GGG GGGCGGGG

||||| ||| |||||
CGACG CC CCT CCGCCCC
_ G _

GAM1189 HCN2 3' CCCACCGTGGCCCCCACGC 6864 A_ _ C
GC GGGGGGTTG GG GGGG

|| ||||| || |||
CG CCCCCCGGT CC CCCC
CA G A

GAM1189 IL2RB 3' CCCACCCAGTCCTGCA 6570 GGG C
TGCAGGG TTGGG GGGG

||||| ||||| |||

			ACGTCCT GACCC CCCC		
			_____ A		
GAM1189 IL6R	5'	CCCCGCCCCGCCCTGC	6172	GGTT	
		GCAGGGG GGGCGGGG			
		CGTCCCC CCGCCCC			
		GC__			
GAM1189 ITGA4	5'	CCCAGCGCCCCCTGCAGC	6580	_	
		GCTGCAGGGGG GTTGGG			
		CGACGTCCCCC CGACCC			
		G			
GAM1189 ITGB4	5'	CCCCCAACCCCCCGCGC	5710	T A C	
		GC GC GGGGGGTTGGG GGG			
		CG CG CCCCCCAACCC CCC			
		— — —			
GAM1189 LAD1	3'	CCCCACAAGCCCCCTCCA	12085	C G GGC	
		TG AGGGGG TTG GGGG			
		AC TCCCC AAC CCCC			
		C G A__			
GAM1189 LIMK1	3'	CCCCAACTGCCCCCGAGCTT	18796	GCA TGGGC	
		AAGCT GGGGGGT GGGG			
		TTCGA CCCCCG CCCC			
		G__ TCAAA			
GAM1189 LPIN2	3'	CCCCGCCCGCCCCCAACAACT	16061	C CAG T	
		AG TG GGGGGT GGGCGGGG			
		TC AC CCCCCG CCGCCCC			
		A AA_ C			
GAM1189 MLC1	3'	CCCCACCTCCCTGCAGCTT	17522	T	
		AAGCTGCAGGGGGGT GGG			
		TTCGACGTCCCTCCA CCC			
		C			
GAM1189 MLC1	3'	CCCCACCTCCCTGCAGCTT	29216	T	
		AAGCTGCAGGGGGGT GGG			
		TTCGACGTCCCTCCA CCC			
		C			
GAM1189 MPHOSPH1	3'	CCCCACCTCCCCCTGCA	18287	GTT C	
		TGCAGGGGG GGG GGGG			
		ACGTCCCCC TCC CCCC			
		_____ A			
GAM1189 PSD	5'	CCCCACCCGGGGCCCAGAGCT	8669	GCAG GG C	
		AGCT GGG TTGGG GGGG			

		TCGA CCC GGCCC CCCC		
		GA__ GG A		
GAM1189 PTMS	5'	CCCGCCTCCCCGCCAGC 8694	CA	GGTT
		GCTG GGGG GGGCGGG		
		CGAC CCCC TCCGCCC		
		CG ____		
GAM1189 PVT1	3'	CCCCACCCAACCCCTATGTTAG 32661	_ G	C
TT		AGCTG CA GGGGGTTGGG GGGG		
		TTGAT GT TCCCCAACCC CCCC		
		T A A		
GAM1189 PYGO2	3'	CCCCACCCCCACCCCGCTGC 31998	G T_ C	
		GCAG GGGGT GGG GGGG		
		CGTC CCCC A CCC CCCC		
		G CC A		
GAM1189 SCRT1	3'	CCCACCCCTTCCCAAGC 25345	GCA TT C	
		GCT GGGGGG GGG GGG		
		CGA CCCTTC CCC CCC		
		A__ _ A		
GAM1189 SLC12A7	3'	CCCCGCCCTGGGCTGCAGC 13373	GGGGGT	
		GCTGCAG GGGCGGGG		
		CGACGTC CCGCCCC		
		GGGT__		
GAM1189 SLC6A8	3'	CCCCACCCACAGTGCTGCACT 12146	C GGGG T C	
		AG TGCAG GT GGG GGGG		
		TC ACGTC CA CCC CCCC		
		_ GTGA _ A		
GAM1189 SYNGR1	3'	CCCCACTCTAGACCCCCC 11063	_ C	
		GGGGGGTT GGG GGGG		
		CCCCCCAG CTC CCCC		
		AT A		
GAM1189 TCF1	3'	CCCGGCACCCCCTGCAGCTT 6145	_	
		AAGCTGCAGGGGG GTTGGG		
		TTCGACGTCCCC CGGCC		
		A		
GAM1189 TCF7	3'	CCCCACAGGCCCCCCGCAGC 9192	A GGGC	
		GCTGC GGGGGGT GGGG		
		CGACG CCCCCCGG CCCC		
		_ ACA_		
GAM1189 TGFB1	3'	CCCCGCCCGCCCCCGCTGC 6319	_ T	
		GCAG GGGGGT GGGCGGGG		

CGTC CCCCCG CCGCCCC
G C

GAM1189 TNFAIP2 3' CCCACGGCCCCTACAGGCT 12981 GCAG GGC
AGCT GGGGGTTG GGG
|||| ||||| ||
TCGG TCCCCGGC CCC
ACA_ A_

GAM1189 UBTF 3' CCCACCCACTTCTGCACTT 15496 C GGT C
AAG TGCAGGGG TGGG GGG
||| ||||| ||| |||
TTC ACGTCTTC ACCC CCC
_ _ A

GAM1189 ZNF42 5' CCCACGCTTGCCCTACAGC 9466 C G GTTG _
GCTG AGGG G GGCG GGG
|||| ||| | ||| |||
CGAC TCCC T TCGC CCC
A G_ A

GAM1189 AGPAT1 3' CCCACCCAGCCCCCTGCAGC 13116 G C
GCTGCAGGGGG TTGGG GGGG
||||||| ||| |||
CGACGTCCCCC GACCC CCCC
_ A

GAM1189 AGPAT1 3' CCCACCCAGCCCCCTGCAGC 26472 G C
GCTGCAGGGGG TTGGG GGGG
||||||| ||| |||
CGACGTCCCCC GACCC CCCC
_ A

GAM1189 C1orf17 5' CCCC GGCCGCCCTCGCAGC 33853 A T G
GCTGC GGGGGGT GG CGGGG
|||| ||||| || |||||
CGACG CTCCCCG CC GCCCC

GAM1189 C5orf6 3' CCCACCCCCCTCCCCACTAGCT 18700 CA TT C
AGCTG GGGGGG GGG GGGG
|||| ||||| || |||||
TCGAT CCCCTC CCC CCCC
CA C_ A

GAM1189 C8orf2 3' CCCACCCCCCCCCCGC 14021 A TT C
GC GGGGGG GGG GGGG
|| ||||| || |||||
CG CCCCCC CCC CCCC
C C_ A

GAM1189 Cab45 3' CCCACCTCTTCCCTGCCGC 18277 T TT C
GC GCAGGGGGG GGG GGGG
|| ||||| || |||||
CG CGTCCCTTC TCC CCCC
C _ A

GAM1189 CBX6 3' CCCACCCCTTGCCCCAGC 15574 AG T_ C
GC GGGGGT GGG GGGG
|| ||||| || |||||

CG CCCCCG CCC CCCC
A_ TT A
GAM1189 CDCA4 3' CCCC GCCTACCCCACATGC 19661 GG_ T
GCA GGGGT GGGCGGGG
||| ||||| |||||
CGT CCCCCA TCCGCCCC
ACA C
GAM1189 CPLX1 3' CCCC GCCCTCCCCCTACAG 13447 C TT
CTG AGGGGGG GGGCGGGG
||| ||||| |||||
GAC TCCCCCT CCGCCCC
A C_
GAM1189 CRELD1 5' CCCCACCCATCCCCACAGC 17774 CAG T C
GCTG GGGGGT GGG GGGG
||| ||||| ||| |||
CGAC CCCCTA CCC CCCC
A_ _ A
GAM1189 CXYorf1 3' CCCCACCACCACCCCAGCT 39905 CA _ T GC
AGCTG GGGG GGT GG GGGG
||||| ||| ||| ||| |||
TCGAC CCCC CCA CC CCCC
_ A _ A_
GAM1189 DCAMKL1 5' CCCC GCCGCGCCCCCAGC 11114 A TG_
GC GGGGGGT GGC GGGG
|| ||||| |||||
CG CCCCCCG CCGCCCC
A CCG
GAM1189 DKFZp434C0328 5' CCCCACGAAACCCCCTAAAGC 19010 GCA GGGC
GCT GGGGGGT GGGG
||| ||||| |||
CGA TCCCCCAA CCCC
AA_ AGCA
GAM1189 EFNA5 3' CCCGCCCCACCCCCAGC 7685 AG T
GC GGGGGT GGGCGGG
|| ||||| |||||
CG CCCCCA CCGCCC
A_ C
GAM1189 FLJ10637 5' CCCGCCAGCCAGCAGC 34042 AGGGG
GCTGC GGTTGGGCGGG
||||| |||||
CGACG CCGACCCGCCC
A____
GAM1189 FLJ10700 3' CCCTAACTACCTCCCCACAGC 20019 CA T GC
GCTG GGGGGGT GG GGGG
||| ||||| ||| |||
CGAC CCCTCCA TC TCCC
AC C AA
GAM1189 FLJ10743 3' CCCACCTGCCCTGCACT 20076 C G T
AG TGCAGGG GG TGGG
|| ||||| || |||

TC ACGTCCC TC ACCC
 _ G C
 GAM1189 FLJ13204 5' CCCACCTGCCCCGAGCT 24114 GCAGG T C
 AGCT GGGGT GGG GGG
 |||| |||| ||||
 TCGA CCCCCG TCC CCC
 G _ _ A
 GAM1189 FLJ13322 3' CCCCACCCCTCCCTGCAGCTT 24058 TTG C
 AAGCTGCAGGGGGG GG GGGG
 ||||| ||||
 TTCGACGTCCCTCC CC CCCC
 _ A
 GAM1189 FLJ13881 3' CCCCACCTGGGTCCCCTGCA 24066 G TG C
 TGCAGGGGG T GG GGGG
 ||||| | ||||
 ACGTCCCCT G CC CCCC
 G GT A
 GAM1189 FLJ14100 3' CCTGGGAAGCCCCCGCAGC 24614 A GGG
 GCTGC GGGGGGTT CGGG
 |||| ||||| ||||
 CGACG CCCCCCGA GTCC
 _ AGG
 GAM1189 FLJ14327 3' CCCCACCCAGCTGCCCTCAGC 24424 C G C
 GCTG AGGG GGTTGGG GGGG
 |||| |||| ||||| ||||
 CGAC TCCC TCGACCC CCCC
 _ G A
 GAM1189 FLJ20257 5' CCCGTGCCGCCACAGC 21222 CA G TGG
 GCTG GGG GGT GCGGG
 |||| |||| ||||
 CGAC CCC CCG TGCCC
 A _ G _
 GAM1189 FLJ22301 5' CCCC GCCCAGTCCCGCAGTCC 24240 A AGG GT _
 A GCTGC GGG TGGG CGGGG
 | |||| || |||| ||||
 C TGACG CCC ACCC GCCCC
 C _ TG C
 GAM1189 FLJ31300 3' CCCACCTCCCTGCACT 29462 C T
 AG TGCAGGGGGG TGGG
 || ||||| ||||
 TC ACGTCCCTCC ACCC
 _ C
 GAM1189 GABARAPL1 5' CCCC GAACCCCCCTGCA 25390 TTGGG
 TGCAGGGGGG CGGGG
 ||||| ||||
 ACGTCCCCC GCCCC
 CAA_
 GAM1189 GBTS1 3' CCCCACTGACCCCGCTGC 29727 _ TG GC
 GCAG GGGGGT G GGGG
 |||| |||| | ||||

CGTC CCCCCA C CCCC
G GT A_
GAM1189 HS6ST 3' CCCACCCACTCCCTACAGTCC 31071 A C GT C
A GCTG AGGGGG TGGG GGGG
| ||| ||||| ||| ||||
C TGAC TCCCTC ACCC CCCC
C A _ A
GAM1189 HS6ST1 3' CCCACCCACTCCCTACAGTCC 11229 A C GT C
A GCTG AGGGGG TGGG GGGG
| ||| ||||| ||| ||||
C TGAC TCCCTC ACCC CCCC
C A _ A
GAM1189 HSPC195 3' CCCAGGGGGGCCCCCTGCGGC 39421 G GGGC
GCTGCAGGGGG TT GGGG
||||||| || ||||
CGGCGTCCCCC GG CCCC
G GGA_
GAM1189 HYP C 5' CCCACCCCAGTGCCCACAGGC 32272 GCAG G C_
GCT GGG GTTGGG GGGG
||| ||| ||||| ||||
CGG CCC TGACCC CCCC
ACA_ G CA
GAM1189 ISL2 3' CCCGCCCTGCCCCAGCT 35080 GCAGG T
AGCT GGGGT GGGCGGG
|||| ||||| |||||
TCGA CCCC G CCGCCC
_ T
GAM1189 KIAA0140 3' CCCACCTCCCCGCAAGCT 16107 _ A T
AGCT GC GGGGGGT GGG
|||| ||| ||||| |||
TCGA CG CCCTCCA CCC
A C C
GAM1189 KIAA0227 3' CCCACCCCCATTCCCAAGC 30451 AG T_ C
GC GGGGGT GGG GGGG
|| ||||| ||| ||||
CG CCCTTA CCC CCCC
AA CC A
GAM1189 KIAA0415 3' CCCCGCCCCCAATCCCCCATAG 44474 CA _
CT AGCTG GGGGGGT GGGCGGGG
|||| ||||| |||||
TCGAT CCCCCTAA CCGCCCC
A_ CC
GAM1189 KIAA0446 3' CCCACCCCCCACCTGCCAGC 34148 _ _ TT C
GCTG CAGGG GGG GGG GGGG
|||| ||||| ||| ||||
CGAC GTCCC CCC CCC CCCC
C A _ A
GAM1189 KIAA0481 3' CCCAGGGGCCCCCTGAGC 35569 G GGGC
GCT CAGGGGGGT GGGG
||| ||||| ||| ||||

CGA GTCCCCCCGG CCCC
 _ GA_
 GAM1189 KIAA0841 3' CCCACCCGACCTGCAGTCC 35360 A GGGGT C
 A GCTGCAGG TGGG GGGG
 | ||||| ||| |||
 C TGACGTCC GCCC CCCC
 C AC_ A
 GAM1189 KIAA0939 3' CCCACCCGGAGGACCCCTGCG 31060 GG_ C
 GC GCTGCAGGGG TTGGG GGGG
 ||||| ||| |||
 CGGCGTCCCC GGCCC CCCC
 AGGA A
 GAM1189 KIAA0963 5' CCCACCCCGCCTGCCGC 17342 T _ T
 GC GCAGG GGGGT GGG
 || ||| ||| |||
 CG CGTCC CCCCA CCC
 C G C
 GAM1189 KIAA1138 3' CCCACCCGGCCCGCAGC 31125 AGGG C
 GCTGC GGGTTGGG GGGG
 ||| ||||| |||
 CGACG CCCGGCCC CCCC
 _ A
 GAM1189 KIAA1138 3' CCCACCCCTCTGCCCCCGAGC 31126 A T_ C
 GC GGGGGGT GGG GGGG
 || ||| ||| |||
 CG CCCCCCG CCC CCCC
 A TCT A
 GAM1189 KIAA1205 3' CCCCAAGTCCCCCCTGCAG 34704 TTGGGC
 CTGCAGGGGGG GGGG
 ||||| |||
 GACGTCCCCC CCCC
 TGAA_
 GAM1189 KIAA1441 3' CCCCGCCCAACCCCAACTCACT 42627 C C G_
 AG TG AG GGGGTGCGGGG
 || || |||||
 TC AC TC CCCCAACCCGCCCC
 _ _ AA
 GAM1189 KIAA1453 3' CCTGCAACCCCTTCAGC 24713 C GG
 GCTG AGGGGGGT GCGGG
 ||| ||||| |||
 CGAC TCCCCCAA CGTCC
 T _
 GAM1189 KIAA1553 3' CCCAGCCCTCACAGCTT 44142 CA
 AAGCTG GGGGGGTG
 |||| |||||
 TTCGAC CTCCCCGACCC
 A_
 GAM1189 KIAA1580 5' CCCCGCCCCCGCACT 34411 C A T
 AG TGC GGGGGGT GGG
 || ||| ||||| |||

			TC ACG CCCCCCG CCC		
			— — C		
GAM1189	KIAA1813	5'	CCCAGCTCCCCGCAGCT 34808	A	
			AGCTGC GGGGGGTTGGG		
			TCGACG CCCCTCGACCC		
			—		
GAM1189	KIAA1893	3'	CCCCACTGTCCCCTCACAGC 36245	CA	TTG C
			GCTG GGGGGG GG GGGG		
			CGAC CTCCCC TC CCCC		
			A_ TG_ A		
GAM1189	KIAA1904	3'	CCCGGAACCCCCTGCAGCT 36373		GTTGGG
			AGCTGCAGGGGG CGGG		
			TCGACGTCCCCC GCCC		
			AAG__		
GAM1189	KIAA1924	3'	CCCGGGGGCCCCCCAGC 36473	CA	GGG
			GCTG GGGGGGTT CGGG		
			CGAC CCCCCCGG GCCC		
			— G_		
GAM1189	LGALS12	5'	CCCGCCCAGCCAGAGCT 26947		GCAGGGG
			AGCT GGTTGGGCGGG		
			TCGA CCGACCCGCC		
			GA_____		
GAM1189	MGC10966	5'	CCCGAGACCCACCTGCAGC 25536	G	GGG
			GCTGCAGG GGGTT CGGG		
			CGACGTCC CCCAG GCCC		
			A A_		
GAM1189	MGC2705	3'	CCCACCCCTGCCCCAGC 26415	CA	G TT C
			GCTG GGG GG GGG GGG		
			CGAC CCC TC CCC CCC		
			— G — A		
GAM1189	MGC2827	5'	CCCGCCCGTACCTGCACTT 23425	C	GGGGT
			AAG TGCAGG TGGGCGGG		
			TTC ACGTCC GCCCGCCC		
			— AT__		
GAM1189	MGEA6	5'	CCCCAGCTCCCCCGCAGC 12559	A	TTG _
			GCTGC GGGGGG GGC GGGG		
			CGACG CCCCCC TCG CCCC		
			— — A		
GAM1189	N4BP3	3'	CCCGCCCCACCCCAGC 32932	GCAGG	T
			GCT GGGGT GGGCGGG		

			CGA	CCCCA	CCCGCCC		
			_____	C			
GAM1189	NFASC	3'	CCCAATGACCCCCCTTCAGC	34828	C	GGC	
			GCTG AGGGGGGTTG	GGG			
			CGAC TCCCCCCAGT	CCC			
			T	AA_			
GAM1189	NOPAR	5'	CCCCACCCCCATCCTGCGC	27570	T	GG TT C	
			GC GCAGG GG GGG GGGG				
			CG CGTCC CC CCC CCCC				
			_	TA	_	A	
GAM1189	OS4	5'	CCCCGCCCAGGCCCCCCAGC	12287	CA	G	
			GCTG GGGGG TTGGGCGGGG				
			CGAC CCCCC GACCCGCCCC				
			_	G			
GAM1189	P17.3	5'	CCCCGCCCCTGAGACCCTGCAG	21138		GGGTT_	
	C		GCTGCAGGG GGGCGGGG				
			CGACGTCCC CCGCCCC				
			AGAGTC				
GAM1189	PAK6	3'	CCCCACCCTCTGCCCTTCAGC	21389	C	G TT C	
			GCTG AGGG GG GGG GGGG				
			CGAC TCCC TC CCC CCCC				
			T G T_ A				
GAM1189	PLA2G6	3'	CCCCACCCCGAGAACCCTCAGC	33030	C	GGG C_	
	T		AGCTG AGGG TTGGG GGGG				
			TCGAC TCCC AGCCC CCCC				
			_	AAG	CA		
GAM1189	PRKWNK2	5'	CCCCGCAGCCCCTGCAGC	43519		GGTTGG	
			GCTGCAGGGG GCGGGG				
			CGACGTCCCC CGCCCC				
			GA_____				
GAM1189	PTPRU	3'	CCCCACTGCCCCCTGCAGC	28399		GTTG C	
			GCTGCAGGGGG GG GGGG				
			CGACGTCCCCC TC CCCC				
			G_ A				
GAM1189	PTPRU	3'	CCCCACTGCCCCCTGCAGC	28404		GTTG C	
			GCTGCAGGGGG GG GGGG				
			CGACGTCCCCC TC CCCC				
			G_ A				
GAM1189	PTPRU	3'	CCCCACTGCCCCCTGCAGC	12254		GTTG C	
			GCTGCAGGGGG GG GGGG				

CGACGTCCCC TC CCCC
G__ A
GAM1189 RASD2 3' CCCACCCACTGCCTGAGC 15602 G G GT C
GCT CAGG GG TGGG GGGG
||| ||| || ||| |||
CGA GTCC TC ACCC CCCC
_ G _ A
GAM1189 SEC61A1 3' CCCCATAGTCCCGCCTGCAGC 14983 G TTGGGC
GCTGCAGG GGG GGGG
||||| ||| |||
CGACGTCC CCC CCCC
G TGATA_
GAM1189 SEMA3C 5' CCCC GCCCGGTCCGCCCGCCGCG 13072 A _ _
GCT AGCTGC GGGG GG TTGGGCGGGG
||||| ||| ||| ||| |||
TCGGCG CCCC CC GGCCCGCCCC
C G T
GAM1189 STMN3 3' CCCACCCCCGCCCCAGCTT 18037 CA _ TT C
AAGCTG GGGG GG GGG GGGG
||||| ||| ||| |||
TTCGAC CCCC CC CCC CCCC
_ G _ A
GAM1189 LOC115051 3' CCCACCCACTCCCTACAGTCC 30158 A C GT C
A GCTG AGGGGG TGGG GGGG
| ||| ||||| ||| |||
C TGAC TCCCTC ACCC CCCC
C A _ A
GAM1189 LOC144114 5' CCCCGCACCTCCCCACAGC 39994 CA TT _
GCTG GGGGGG GG GCGGGG
||| ||||| ||| |||
CGAC CCCCTC CC CGCCCC
A_ _ A
GAM1189 LOC146268 3' CCCGCCCTCCCCAGCT 38120 GCAG TT
AGCT GGGGG GGGCGGG
||| ||||| |||||
TCGA CCCCC CCGCCC
_ T_
GAM1189 LOC146488 3' CCCACCCACAGTGCTGCACT 35042 C GGGG T C
AG TGCAG GT GGG GGGG
|| |||| || ||| |||
TC ACGTC CA CCC CCCC
_ GTGA _ A
GAM1189 LOC146895 5' CCCC GCCCCACCCCGCA 40759 AG T
TGC GGGGGT GGGCGGGG
||| ||||| |||||
ACG CCCCCA CCGCCCC
_ C
GAM1189 LOC157349 5' CCCACCCGCACCCCTGCACCT 39589 C G T C
AG TGCAGGGG GT GGG GGGG
|| ||||| || ||| |||

TC ACGTCCCC CG CCC CCCC
 C A _ A
 GAM1189 LOC159090 5' CCCC GCCCGTCCCCAAGC 39939 AG TT_
 GC GGGGG GGGCGGGG
 || |||| |||||
 CG CCCCT CCCGCCCC
 AA GCC
 GAM1189 LOC196500 5' CCCCACCATGCCCGCA 42388 A G T GC
 TGC GGGG GT GG GGGG
 ||| ||| || || |||
 ACG CCCC TA CC CCCC
 _ G _ A_
 GAM1189 LOC199786 3' CCCC GCCCCCAACCCACAGC 42617 CA _ TT
 T AGCTG GGG GGG GGGCGGGG
 |||| ||| ||| |||||
 TCGAC CCC CCC CCCGCCCC
 AC AA _
 GAM1189 LOC199800 5' CCCC GCCCCATTTCACGCT 43249 _ CA GG T
 T AAGC TG GGG GT GGGCGGGG
 |||| || ||| || |||||
 TTCG AC CCC TA CCCGCCCC
 C _ TT C
 GAM1189 LOC200093 3' CCCCACCACACCCCCAGCT 31597 CA _ T GC
 AGCTG GGGG GGT GG GGGG
 |||| ||| ||| || |||
 TCGAC CCCC CCA CC CCCC
 _ A _ A_
 GAM1189 LOC201245 5' CCCC GCCCTATCCCCTACGC 42229 A_ T
 GC GGGGGGT GGGCGGGG
 || ||||| |||||
 CG TCCCCTA CCCGCCCC
 CA T
 GAM1189 LOC205095 3' CCCCAGAAGCCCCTCACAGC 43603 CA GGGC
 GCTG GGGGGGT GGGG
 ||| ||||| |||
 CGAC CTCCCCGA CCCC
 A_ AGA_
 GAM1189 LOC219513 5' CCTGGGTCAACCGCCCTGCAGC 45291 G G_
 GCTGCAGGG GGTG CGGG
 ||||| |||| |||
 CGACGTCCC CCAACT GTCC
 G GG
 GAM1189 LOC221424 5' CCCC GCCCGCGGCCACC 44977 _ _
 GG GGGGT TGGGCGGGG
 || |||| |||||
 CC CCCC GCCCGCCCC
 A GC
 GAM1189 LOC222183 3' CCCCACAGCCTCCCCAAGCT 45183 GCA GGC
 AGCT GGGGGGTG GGGG
 ||| ||||| |||

TCGA CCCTCCGAC CCCC
 ACC A__
 GAM1189 LOC256867 5' CCCACGCCCCCGCAGC 45471 AG GGC
 GCTGC GGGGGTTG GGG
 |||| ||||| ||
 CGACG CCCCCGGC CCC
 __ A__
 GAM1189 LOC257451 3' CCCCACCCCCACCCCGCTGC 45741 G T_ C
 GCAG GGGGT GGG GGGG
 |||| |||| || ||||
 CGTC CCCC A CCC CCCC
 G CC A
 GAM1189 LOC90768 5' CCCC GCCCGCCGGCCCTCCAG 31986 C __ T
 C GCTG AGGGG GGT GGGCGGGG
 |||| |||| || |||||
 CGAC TCCCC CCG CCGCCCCC
 C GG _
 GAM1189 LOC91040 3' CCCCACCACCACCCCAGCT 32315 CA _ T GC
 AGCTG GGGG GGT GG GGGG
 |||| |||| || || ||||
 TCGAC CCCC CCA CC CCCC
 __ A _ A__
 GAM1189 LOC91149 5' CCCGCCACCCGCAGC 32455 AGGG T G
 GCTGC GGGT GG CGGG
 |||| |||| || ||||
 CGACG CCCA CC GCCC
 __ _ G
 GAM1190 BIG1 3' ATATCCCTACTGACAGTAACTA 13136 C C _ GT
 CCT AGG AGT ATTG CGG GGGATAT
 |||| |||| || |||||
 TCC TCA TGAC GTC CCCTATA
 A A A AT
 GAM1190 KCNK6 3' CACCCTGGACAAGTGACTGCC 11238 GC____
 GGCAGTCATT GGGTG
 ||||| ||||
 CCGTCAGTGA CCCAC
 ACAGGT
 GAM1190 LDOC1 3' ATCCCACCTACAGACTACC 14691 C AT CG
 GG AGTC TG GGTGGGAT
 || |||| || |||||
 CC TCAG AC CCACCCTA
 A _ AT
 GAM1190 MGC27382 3' TACCCCTATGACTGCCT 29524 TGC
 AGGCAGTCAT GGGTG
 ||||| ||||
 TCCGTCAGTA CCCAT
 TC_
 GAM1190 MIG 3' ATCCCACTCACAACAGCTGCCT 8244 CA C
 AGGCAGT TTG GGGTGGGAT
 ||||| || |||||

			TCCGTCG AAC CTCACCCTA		
			AC A		
GAM1190	SDFR1	3'	CACCACAATGACTGTCT 14802	CG	
			AGGCAGTCATTG GGTG		
			TCTGTCAGTAAC CCAC		
			A_		
GAM1190	SDFR1	3'	CACCACAATGACTGTCT 18929	CG	
			AGGCAGTCATTG GGTG		
			TCTGTCAGTAAC CCAC		
			A_		
GAM1190	LOC146429	5'	CCCACCCAGGTTCTGCCT 40695	TC GC	
			AGGCAG ATT GGGTGGG		
			TCCGTC TGG CCCACCC		
			CT A_		
GAM1191	CARD15	3'	CTCCAGCTGGGATCACA 22715	G C	
			TGTGATCCCAGT GG AG		
			ACACTAGGGTCG CC TC		
			A _		
GAM1191	HD	3'	TTGCCCACTAGGATCCCA 7899	T C	
			TG GATCC AGTGGGCAG		
			AC CTAGG TCACCCGTT		
			C A		
GAM1191	LIMK1	3'	CTGCCACTGGGCCACACA 18802	AT G	
			TGTG CCCAGTGG CAG		
			ACAC GGGTCACC GTC		
			CC _		
GAM1191	STAC	3'	AGCTGTCCCCCAGGATCCCA 9117	T CAGT	
			TG GATCC GGGCAGCT		
			AC CTAGG CCTGTCTGA		
			C ACCC		
GAM1191	STIM1	3'	AGCATGGCCTGGGATCTCA 30201	T GT G _	
			TG GATCCCA GG CA GCT		
			AC CTAGGGT CC GT CGA		
			T _ G A		
GAM1191	BMF	3'	TGGAACCCAGCAGGATCACA 27283	CAG CAG	
			TGTGATCC TGGG CTA		
			ACACTAGG ACCC GGT		
			ACG AA_		
GAM1191	CDC14B	3'	GCAGCCCTACTGGAACACA 9760	ATC _ A	
			TGTG CCAGT GGGC GC		

ACAC GGTCA CCCG CG
 AA_ T A
 GAM1191 CDC14B 3' GCAGCCCTACTGGAACACA 27164 ATC _ A
 TGTG CCAGT GGGC GC
 ||| |||| ||| ||
 ACAC GGTCA CCCG CG
 AA_ T A
 GAM1191 FLJ20758 3' TAGCTGCTGGAATCACA 19655 C GTGG
 TGTGAT CCA GCAGCTA
 ||||| ||| |||||
 AACTA GGT CGTCGAT
 A ____
 GAM1191 MGC12992 5' GCAGCTCGCGGGTCACA 26136 T A A
 TGTGA CCC GTGGGC GC
 ||||| ||| ||||| ||
 AACT GGG CGCTCG CG
 _ _ A
 GAM1191 TRIM2 3' TCGTAGCTACATACGTACCACA 17603 ATCCCA GGC
 TGTG GTG AGCTACGA
 ||| ||| |||||
 ACAC CAT TCGATGCT
 CATG_ ACA
 GAM1191 LOC92080 5' CGTCCCCACTGGGCCACACA 33757 AT CAGCT
 TGTG CCCAGTGGG ACG
 ||| ||||| |||
 ACAC GGGTCACCC TGC
 CC C____
 GAM1192 FLJ12888 3' GATTATATTGAATGATTTAAAA 24495 ATAC_
 CT AGTTT CATTCAATATAATC
 |||| |||||
 TCAA GTAAGTTATATTAG
 ATTTA
 GAM1192 FLJ22794 5' GATTATAGTTGGTGAATAAACT 44032 _ TTCAA
 A TAGTTTAT ACCA TATAATC
 ||||| ||| |||||
 ATCAAATA TGGT ATATTAG
 AG TG____
 GAM1192 MEP50 3' ATTATATTGAAAGTAAAT 23547 ACCA
 GTTTAT TTCAATATAAT
 |||| |||||
 TAAATG AAGTTATATTA
 A____
 GAM1192 LOC256846 5' GATTGGAGAATGGTACAACTG 45698 A AATA
 TAGTTT TACCATTG TAATC
 |||| ||||| |||
 GTCAAA ATGGTAAG GTTAG
 C AG____
 GAM1192 LOC90355 3' ATTGAATGATTAACTA 27062 TAC
 TAGTTTA CATTCAAT
 ||||| |||||

		ATCAAAT GTAAGTTA		
		TA_		
GAM1193	SLC1A4	3' GAGAAAACCATGTACTAA	8997	A ____
		TTAG TACATGG TCTC		
		AATC ATGTACC AGAG		
		_ AAA		
GAM1193	BC008967	5' ACTTCTCTCTAGCTGTATCTAA	30476	__ TCTC
		TTAGATACA TGG AGAAGT		
		AATCTATGT ATC TCTTCA		
		CG TC__		
GAM1193	LOC158722	3' CTACTCCTGACCACTGTATTTA	39889	_ TC A
	A	TTAGATACA TGGTC AG AGTAG		
		AATTTATGT ACCAG TC TCATC		
		C _ C		
GAM1193	LOC91650	5' ACTTCTGGGTATATATC	33200	C GT
		GATA ATG CTCAGAAGT		
		CTAT TAT GGGTCTTCA		
		A _		
GAM1194	ED1	3' TCGAGAGCCTTACTTCA	7101	A A A
		TGAAGTAA GT TCT CGA		
		ACTTCATT CG AGA GCT		
		C _ _		
GAM1194	OSR1	3' CGTTAGTAAACTTACTTCATA	11590	AG_ CT
		TATGAAGTAA TAT ACG		
		ATACTTCATT ATG TGC		
		CAA AT		
GAM1194	PACE4	5' CGCAGGCCCTTTACTTCA	28726	TA A
		TGAAGTAAAG TCT CG		
		ACTTCATTTT GGA GC		
		CC C		
GAM1194	KIAA1462	3' CGTATGATTTTATTTTATA	43921	ATC
		TATGAAGTAAAGT TACG		
		ATACTTTATTTTA ATGC		
		GT_		
GAM1194	LOC145945	3' TCATAGATACAATACTTTA	40636	AA C
		TGAAGTA GTATCTA GA		
		ATTTTAT CATAGAT CT		
		AA A		
GAM1194	LOC219401	5' TCGTGGGCCCCGCACTTCATA	44595	AAAGTA
		TATGAAGT TCTACGA		

		ATACTTCA GGGTGCT	
		CGCCC_	
GAM1195 DHFR	3'	ACCTGCTACAGTGAGCTGCCA 6445	C TTCC
		TGGCAGCTCGC GT TAGGT	
		ACCGTCGAGTG CA GTCCA	
		A TC_	
GAM1195 EMS1	3'	ACCCAGAGCACAGGAGCTGCCA 11734	GCC TTC A
		TGGCAGCTC GT CT GGT	
		ACCGTCGAG CA GA CCA	
		GA_ CGA C	
GAM1195 EMS1	3'	ACCCAGAGCACAGGAGCTGCCA 28865	GCC TTC A
		TGGCAGCTC GT CT GGT	
		ACCGTCGAG CA GA CCA	
		GA_ CGA C	
GAM1195 GNAI3	3'	CCCAGGGCAGCTGCCA 13240	C GTTTC A
		TGGCAGCT GCC CT GG	
		ACCGTCGA CGG GA CC	
		_ _ _ _ C	
GAM1195 TFCP2	5'	TGGGAAGCAGCAAGCCACCA 12192	CA C C
		TGG GCT GC GTTTCCTA	
		ACC CGA CG CGAAGGGT	
		AC A A	
GAM1195 WHSC1L1	5'	ACCCAGGCCGGGCTGCCA 19408	CCGTTT A
		TGGCAGCTCG CCT GGT	
		ACCGTCGGGC GGA CCA	
		C_ _ _ C	
GAM1195 WHSC1L1	5'	ACCCAGGCCGGGCTGCCA 23315	CCGTTT A
		TGGCAGCTCG CCT GGT	
		ACCGTCGGGC GGA CCA	
		C_ _ _ C	
GAM1195 FLJ12355	3'	TACCTAGGAACAAAGAAACGCC 24545	AGC GCC T
A		TGGC TC GTT CCTAGGTA	
		ACCG AG CAA GGATCCAT	
		CAA AAA _	
GAM1195 KIAA1922	3'	TACCTAAGAAAGCTCAAGGCTG 36458	C_ _ CG C
CCA		TGGCAGCT GC TTTC TAGGTA	
		ACCGTCGG CG AAAG ATCCAT	
		AACT _ A	
GAM1195 RNF24	3'	TACCTAGGACACCAGCTGCCA 14089	CGCC T
		TGGCAGCT GT TCCTAGGTA	

ACCGTCGA CA AGGATCCAT
 C__ C
 GAM1195 SEC14L1 3' ACCTGGGACGGAAGCTGCCA 8899 CG TT
 TGGCAGCT CCG TCCTAGGT
 ||||| || |||||
 ACCGTCGA GGC AGGGTCCA
 A_ _
 GAM1195 SEZ6 3' ACCTAGGAGGAGATGCCA 36770 G GCCGT
 TGGCA CTC TTCCTAGGT
 |||| || |||||
 ACCGT GAG GAGGATCCA
 A _ _ _
 GAM1195 WSB1 3' ACCCAAGAAGTTCAGGAGCTGC 28613 GCCG_ CTA
 C GGCAGCTC TTTC GGT
 ||||| ||| ||
 CCGTCGAG GAAG CCA
 GACTT AAC
 GAM1195 LOC150183 5' ACCTAGCCTAGAGGCGGCTGCC 41153 T GTTTC_
 A TGGCAGC CGCC CTAGGT
 ||||| ||| |||||
 ACCGTCG GCGG GATCCA
 _ AGATCC
 GAM1195 LOC150184 5' ACCTAGCCTAGAGGCGGCTGCC 41154 T GTTTC_
 A TGGCAGC CGCC CTAGGT
 ||||| ||| |||||
 ACCGTCG GCGG GATCCA
 _ AGATCC
 GAM1195 LOC150185 5' ACCTAGCCTAGAGGCGGCTGCC 41150 T GTTTC_
 A TGGCAGC CGCC CTAGGT
 ||||| ||| |||||
 ACCGTCG GCGG GATCCA
 _ AGATCC
 GAM1195 LOC255654 5' ACCCAGGAGGGATGACGGAGCT 46300 _C _ A
 GCCA TGGCAGCTC G CGTT TCCT GGT
 ||||| ||| ||| |||
 ACCGTCGAG C GTAG AGGA CCA
 G A GG C
 GAM1195 LOC91069 3' ACCTGCAGCTGAGCTGCCA 32343 _C TTCCT
 TGGCAGCTC GC GT AGGT
 ||||| || || |||
 ACCGTCGAG CG CG TCCA
 T A _ _ _
 GAM1196 BMP6 3' TGTACTCTTTGCTAGTACCAAA 7455 C _ CA
 TTTGGTAT AGCGA GAG GCA
 ||||| |||| || |||
 AAACCATG TCGTT CTC TGT
 A T A_
 GAM1196 C20orf18 3' TGCGCTGCCCCAGTGCCAGA 25277 CAGCGAGA A
 TTTGGTAT GCAGC CA
 ||||| |||| ||

		AGACCGTG	CGTCG GT	
		ACCCC_	C	
GAM1196	FLJ10921	3'	TGCTGCTCTCTACCAGA	20250 TCAGC
			TTTGGTA GAGAGCAGCA	
			AGACCAT CTCTCGTCGT	
GAM1196	LOC220038	5'	TGTACTGTGTAGCATAATACCA	44082 CA_ GAGA C
		AA	TTTGGTAT GC GCAG ACA	
			AAACCATA CG TGTC TGT	
			ATA ATG_ A	
GAM1197	DAZL	3'	CAAGAGGGCTTTATTACACCTC	33799 AC CG T
		A	TGAGGT AAT GGTT CTCTTG	
			ACTCCA TTA TCGG GAGAAC	
			CA TT _	
GAM1197	FANCG	5'	CAAGAGGACCAACCGCAGCCCA	11000 A ACAATCG T
			TG GGT GGTT CTCTTG	
			AC CCG CCAG GAGAAC	
			_ ACGCCAA _	
GAM1197	REG1A	5'	AGAGATTCATTGCAGCTCA	42827 GTA C
			TGAG CAAT GGGTTTCT	
			ACTC GTTA CTTAGAGA	
			GAC _	
GAM1197	SCML1	3'	AGAAATATTGTACCGCA	13592 A CGG
			TG GGTACAAT GTTTCT	
			AC CCATGTTA TAAAGA	
			G _	
GAM1197	BANK	3'	AAGAGGAAACTACACCTTA	19625 ACAATCG _
			TGAGGT GGTTTC TCTT	
			ATTCCA TCAAAG AGAA	
			CA_ G	
GAM1197	KIAA0553	3'	AAGAGGAATTACCACCTCA	34632 ACAATCG
			TGAGGT GGTTTCTCTT	
			ACTCCA TTAAGGAGAA	
			CCA_	
GAM1197	PRO0097	5'	AGAGATCTATTGTACTTCA	15363 C
			TGAGGTACAAT GGGTTTCT	
			ACTTCATGTTA TCTAGAGA	
GAM1198	POLH	5'	ATTTTCGGCAACCGCTGCT	13248 TACC G
			AGCAGT GC CGAGAAT	

		TCGTCG CG GCTTTTA	
		CCAA _	
GAM1198	NMT1	3' CATCCTCGAGCAACTGCTGT 22047	ACC G A
		ACAGCAGTT GC CGAG ATG	
		TGTCGTCAA CG GCTC TAC	
		_ A C	
GAM1198	LOC150208	5' TCAGGCAGATAACTGCTGTA 41157	CC_ GC
		TACAGCAGTTA GC GA	
		ATGTCGTCAAT CG CT	
		AGA GA	
GAM1198	LOC255631	5' TCATCACCAGCGACTGCTGTA 46039	TAC GC_ _
		TACAGCAGT CGC GA GA	
		ATGTCGTCA GCG CT CT	
		_ ACCA A	
GAM1199	CD164	3' AACCAATCTGTATCATGT 12628	A C
		ACGT GTGC AGATTGGTT	
		TGTA TATG TCTAACCAA	
		C _	
GAM1199	LOC157226	5' AGCCCGGCACTACGGG 31974	A AGATT
		CC CGTAGTGCC GGTT	
		GG GCATCACGG CCGA	
		_ C_	
GAM1199	LOC91974	5' AGCTGGTCTGACACTACG 33650	C TG
		CGTAGTG CAGAT GTT	
		GCATCAC GTCTG CGA	
		A GT	
GAM1200	ADCY6	5' TACTAGTGGTGGCAGTGGC 17590	A TG C
		GTCAC GTT ACCAC AGTA	
		CGGTG CGG TGGTG TCAT	
		A _ A	
GAM1200	ALDH1B1	3' TACTGACACATGCTGTGAC 6349	T ACCAC
		GTCACAGT TG CAGTA	
		CAGTGTCTG AC GTCAT	
		T ACA_	
GAM1200	DAAM2	3' ACTGGGGAAGTGTGAC 44327	TGA A
		GTCACAGTT CC CCAGT	
		CAGTGTCAA GG GGTCA	
		_ _	
GAM1200	FGF2	3' TACTAATGGAATAAACTGT 7742	A_ CC
		ACAGTTTG CCA AGTA	

			TGTCAAAT GGT TCAT		
			AA AA		
GAM1200	GAS7	3'	ACTGGTGGGCACTGGAC 9713	A	TTGA
			GTC CAGT CCACCAGT		
			CAG GTCA GGTGGTCA		
			_ CG_		
GAM1200	KERA	5'	TACTAATGAATTGAACTGTGA 13909	TG C_ CC	
			TCACAGTT A CA AGTA		
			AGTGTCAA T GT TCAT		
			GT AA AA		
GAM1200	MMP25	3'	ACTGGTGGGGACCTGGGAC 22820	A T GA	
			GTC CAG TT CCACCAGT		
			CAG GTC AG GGTGGTCA		
			G C G_		
GAM1200	PPL	3'	TACTGGTGGCACACCAGAC 8553	ACA T A	
			GTC GT TG CCACCAGTA		
			CAG CA AC GGTGGTCAT		
			AC_ C _		
GAM1200	TCF19	3'	TACCAAGTGTGATGGCTGTGAC 46711	TGAC CA	
			GTCACAGTT CAC GTA		
			CAGTGTCGG GTG CAT		
			TAGT AC		
GAM1200	TCF19	3'	TACCAAGTGTGATGGCTGTGAC 46662	TGAC CA	
			GTCACAGTT CAC GTA		
			CAGTGTCGG GTG CAT		
			TAGT AC		
GAM1200	TMPRSS2	3'	ACTGGCGGTCAAGTGTGG 12194	G A	
			TCACA TTTGACC CCAGT		
			GGTGT GAACTGG GGTCA		
			_ C		
GAM1200	C11orf23	3'	ACTGGTGGCACACGTGGC 20299	A T A	
			GTCAC GT TG CCACCAGT		
			CGGTG CA AC GGTGGTCA		
			_ C _		
GAM1200	DC-TM4F2	3'	TACTGGTGGCTGTTGATGAC 25198	_ TTTGA	
			GTCA CAG CCACCAGTA		
			CAGT GTT GGTGGTCAT		
			A GTC_		
GAM1200	Di-Ras2	3'	TACTGGCCCCAACTGTGGC 19044	TGACCA	
			GTCACAGTT CCAGTA		

			CGGTGTCAA	GGTCAT	
			CCCC__		
GAM1200	EML4	3'	TACTGGCTCAGACTGT	21145	CCA
			ACAGTTTGA	CCAGTA	
			TGTCAGACT	GGTCAT	
			C__		
GAM1200	FLJ12542	3'	ACTGATAAATTGTGAT	24382	ACCAC
			GTCACAGTTTG	CAGT	
			TAGTGTTAAAT	GTCA	
			A____		
GAM1200	FLJ12800	3'	TACTGGTGGTTGAGTCAGGAC	23193	ACAG TG
			GTC TT	ACCACCAGTA	
			CAG GA	TGGTGGTCAT	
			GACT	GT	
GAM1200	FLJ13693	3'	ACTGGTGGGGAGACCATGGC	24186	CA GA
			GTCA GTTT	CCACCAGT	
			CGGT CAGA	GGTGGTCA	
			AC	GG	
GAM1200	FLJ20730	3'	TACTAATTCAAGCTGTGAC	19641	CCACC
			GTCACAGTTTGA	AGTA	
			CAGTGTCGAACT	TCAT	
			TAA__		
GAM1200	FLJ22127	3'	ACCAGTGGCAGCTGGTGAC	23040	_ T A CA
			GTCAC AGTT G	CCAC GT	
			CAGTG TCGA C	GGTG CA	
			G _ _	AC	
GAM1200	FLJ23191	5'	ACTGGTGCCTGCTGTGGC	23801	TTGAC
			GTCACAGT	CACCAGT	
			CGGTGTCG	GTGGTCA	
			TCC__		
GAM1200	GMPPB	3'	TACTGGTGGGAAGCACTGTG	45818	_ GA
			CACAGT TT	CCACCAGTA	
			GTGTCA GA	GGTGGTCAT	
			C AG		
GAM1200	KIAA1854	3'	TACTGAATATCAACTGTGA	35536	T CCAC
			TCACAGTT GA	CAGTA	
			AGTGTCAA CT	GTCAT	
			_ ATAA		
GAM1200	KIAA1912	3'	ACTAGTAGGAGACTGTGA	36311	GA _ C
			TCACAGTTT	CC AC AGT	

		AGTGTGTCAGA GG TG TCA	
		— A A	
GAM1200	KLHL4	3' TATTGATACAACTGTGAC 21198	ACCAC
		GTCACAGTTTG CAGTA	
		CAGTGTCAAAC GTTAT	
		ATA__	
GAM1200	MR	5' ACTGGTGGCAGGTGAT 25254	AGT A
		GTCAC TTG CCACCAGT	
		TAGTG GAC GGTGGTCA	
		— —	
GAM1200	LOC129831	3' TACTGGTGACAGTGTGA 36980	GT AC
		TCACA TTG CACCAGTA	
		AGTGT GAC GTGGTCAT	
		— A_	
GAM1200	LOC130644	5' ACTGGTGGCCAGCGTGG 37301	A T A
		TCAC GTT G CCACCAGT	
		GGTG CGA C GGTGGTCA	
		— _C	
GAM1200	LOC151121	5' ACTGGGGTAATTGTGAC 39051	TG A
		GTCACAGTT ACC CCAGT	
		CAGTGTTAA TGG GGTCA	
		— —	
GAM1200	LOC151778	5' ACTGGTGGCAGGCTGTGGC 35397	A
		GTCACAGTTTG CCACCAGT	
		CGGTGTCGGAC GGTGGTCA	
		—	
GAM1200	LOC153396	3' ACCAGTATCTGACTGTGGC 39371	T CC CA
		GTCACAGTT GA AC GT	
		CGGTGTCAG CT TG CA	
		T A_ AC	
GAM1200	LOC155340	5' ACTGGTGGCAGGCTGTGGC 36316	A
		GTCACAGTTTG CCACCAGT	
		CGGTGTCGGAC GGTGGTCA	
		—	
GAM1200	LOC157867	5' TACTGGATGGGTCAAAC 41856	A__
		AGTTTGACC CCAGTA	
		TCAAAC 2GG GGTTCAT	
		GTA	
GAM1200	LOC158345	5' TACTGGCAGAGCTGTGGC 32132	GACCA
		GTCACAGTTT CCAGTA	

		CGGTGTCGAG	GGTCAT		
		AC__			
GAM1200	LOC159193	5'	ACTTGCTCACA	ACTGTGAC	39976 _ C CC
			GTCACAGTT	TGA CA AGT	
			CAGTGTCAA	ACT GT TCA	
			C C		
GAM1200	LOC255620	5'	ACTGGTGGC	AGGCTGTGGC	46378 A
			GTCACAGTTTG	CCACCAGT	
			CGGTGTCGGAC	GGTGGTCA	
GAM1200	LOC256598	5'	ACTGGTGGC	AGGCTGTGGC	46097 A
			GTCACAGTTTG	CCACCAGT	
			CGGTGTCGGAC	GGTGGTCA	
GAM1200	LOC91759	5'	ACTGGTCAGGGA	ACTGTGGC	33301 GA _
			GTCACAGTTT	CC ACCAGT	
			CGGTGTCAAG	GG TGGTCA	
GAM1201	EXTL2	5'	TGCAATCTACTG	CACTCGA	7164 A C_
			TC AGTGCAGTAG	TGCA	
			AG TCACGTCATC	ACGT	
			C	TA	
GAM1201	KIAA1580	5'	CAAAGCTGCAGTTG	CATTTGA	34409 GTA A
			TCAAGTGCA	GCTGCA CTTTG	
			AGTTTACGT	TGACGT GAAAC	
GAM1201	KIAA1879	3'	CAAAATTGCACCA	CTGCACT	36410 AGC C
			AGTGCAGT	TGCAA TTTG	
			TCACGTCA	ACGTT AAAC	
			CC_	A	
GAM1201	SEMA4F	3'	CAAAGTTAAAGG	ACCACTGCCC	10455 A T AG_ GC_
	TGA		TCA G GCAGT	CT AACTTTG	
			AGT C CGTCA	GG TTGAAAC	
			_C	CCA AAA	
GAM1201	LOC127534	5'	CAAGGAAGCAGCT	ACTGGAC	37163 G AA
			GT CAGTAGCTGC	CTTTG	
			CA GTCATCGACG	GGAAC	
			G	AA	
GAM1201	LOC151178	5'	AAGTTCAACCA	CTGCACT	39067 AGC C
			AGTGCAGT	TG AACTT	

	TCACGTCA AC TTGAA	
	CCA _	
GAM1201 LOC158987 3'	CAAAGACTGTGCCACTGCACT 42045	A T A_
	AGTGCAGT GC GCA CTTTG	
	TCACGTCA CG TGT GAAAC	
	C _ CA	
GAM1201 LOC221833 3'	CAAAGTTACTTTGACTGCATT 44454	AGCTGC
	AGTGCAGT AACTTTG	
	TTACGTCA TTGAAAC	
	GTTTCA	
GAM1201 LOC91661 3'	AAAGTCAAGCTGCACT 28750	AGC CA
	AGTGCAGT TG ACTTT	
	TCACGTCA AC TGAAA	
	A _ _	
GAM1202 PRPS1 3'	ACTAGCAACAAAGGCAACCCA 8653	C ACATG
	TGGGTTGCCTTT TTG AGT	
	ACCCAACGGAAA AAC TCA	
	C GA _	
GAM1202 KIAA0237 3'	GCTCCAAGAAAGGCCACCCA 16450	T ACAT
	TGGGT GCCTTTCTTG GAGT	
	ACCCA CGGAAAGAAC CTCG	
	C _	
GAM1203 LOC149296 5'	CCACTGCTACAGTCACCACCA 38694	CACAC AAT
	TGG GTGG TAGCAGTGG	
	ACC CACT ATCGTCACC	
	AC _ GAC	
GAM1203 LOC149721 3'	CCACCTCTGTCCACGTGCACC 38810	CA AT CA
	GG CACGTGGA TAG GTGG	
	CC GTGCACCT GTC CACC	
	AC _ TC	
GAM1203 LOC153338 5'	CCACTGCTAACTATGCAGGGCC 41611	ACA_ AA
A	TGGC CGTGG TTAGCAGTGG	
	ACCG GTATC AATCGTCACC	
	GGAC _	
GAM1203 LOC254413 5'	CCACTGCTGGGGAAAATGTGCC 46400	CGTGGAA
A	TGGCACA TTAGCAGTGG	
	ACCGTGT GGTCGTCACC	
	AAAAGG_	
GAM1203 LOC254755 3'	CACTGCTAATTCGGGCC 46487	ACACGTG
	GGC GAATTAGCAGTG	

CCG CTTAATCGTCAC
 GG____
 GAM1204 CYP24 5' CAACCTCGCCCCACCCC 6424 T AG AA
 GG GGTGGG GCGA TTG
 || ||||| ||| |||
 CC CCACCC CGCT AAC
 _ _ CC
 GAM1204 EIF2C1 3' TCAACCTCATGTCCCCACCCC 14504 T A _ AA
 TCA TGAGG GGTGGG GGC GA TTGA
 ||||| ||||| ||| || |||||
 ACTCC CCACCC CTG CT AACT
 _ C TA CC
 GAM1204 EZH1 3' TCAACCCCTCCCCACCACGTCA 7717 G _ CGAAA
 TGA GTGGTGGG AGG TTGA
 ||| ||||| ||| |||||
 ACT CACCACCC TCC AACT
 G C CC____
 GAM1204 GLRX 3' TCAACTCCACCCCATCCCATCC 7831 T _ CGAAA_
 C GG GGTGGGA GG TTGA
 || ||||| || |||||
 CC CTACCCT CC AACT
 _ A CCACCTC
 GAM1204 LGALS3BP 3' CAGGAGTTCTCCCACCACCTCA 34357 _ GAAA
 TGAGGTGGTGGGAGG C TTG
 ||||| ||||| ||| |||||
 ACTCCACCACCCTCT G GAC
 T AG____
 GAM1204 NR4A1 5' CAACCCCGCCTCTTCCTCC 7912 T T AAA
 GG GG GGGAGGCG TTG
 || || ||||| ||| |||||
 CC CC TTCTCCGC AAC
 T _ CCC
 GAM1204 PCSK2 3' TCAATCCCAAAAGTCACCACTC 8459 AG GA _ C AA
 CA TG GTGGTGG GG GA TTGA
 || ||||| ||| ||| |||||
 AC CACCACT CC CT AACT
 CT GAAAA _ _
 GAM1204 RFX1 3' CGTCCTCCCACCACCCCA 8822 A _
 TG GGTGGTGGGAGG CG
 || ||||| ||||| ||| |||||
 AC CCACCACCCTCC GC
 C T
 GAM1204 SARDH 5' CAGGACCCCCACACCACCCCA 13961 A _ A CGAAA
 TG GGTGGTG GG GG TTG
 || ||||| ||| ||| |||||
 AC CCACCAC CC CC GAC
 C A _ CAG____
 GAM1204 TOX 3' TCAATTCTGAACCACCACC 16327 GAGG A
 GGTGGTGG CG AATTGA
 ||||| || |||||

CCACCACC GT TTAAC
 AA__ C
 GAM1204 ZNF278 3' TCCTTCTCCACCACCCA 25776 A _ C
 TG GGTGGTGG GAGG GA
 || ||||| ||| ||
 AC CCACCACC CTTC CT
 _ T _
 GAM1204 ZNF278 3' TCCTTCTCCACCACCCA 25786 A _ C
 TG GGTGGTGG GAGG GA
 || ||||| ||| ||
 AC CCACCACC CTTC CT
 _ T _
 GAM1204 ZNF278 3' TCCTTCTCCACCACCCA 15627 A _ C
 TG GGTGGTGG GAGG GA
 || ||||| ||| ||
 AC CCACCACC CTTC CT
 _ T _
 GAM1204 ASB16 5' TCAAGCGATCCTCCCACCACCT 34654 CGAAA
 CA TGAGGTGGTGGGAGG TTGA
 ||||| ||| |||
 ACTCCACCACCTCC AACT
 TAGCG
 GAM1204 C11orf21 5' TCCCCCACCACCTCA 15427 A C
 TGAGGTGGTGGG GG GA
 ||||| || ||
 ACTCCACCACCC CC CT
 _ _
 GAM1204 C11orf25 5' CAACCCCGCTCAACGCCACCC 25399 T A__ AAA
 CTCA TGAGG GGTGGG GGCG TTG
 |||| ||| ||| |||
 ACTCC CCACCC TCGC AAC
 _ GCAAC CCC
 GAM1204 DKFZp434J0226 5' TCCCCCACCACCCCA 35806 A A C
 TG GGTGGTGGG GG GA
 || ||||| || ||
 AC CCACCACCC CC CT
 C _ _
 GAM1204 FLJ11753 3' TCCCTGCCACCACCCCA 23963 A G C
 TG GGTGGTGG AGG GA
 || ||||| ||| ||
 AC CCACCACC TCC CT
 C G _
 GAM1204 GW112 3' CAATTCCACCCCCACCAACC 13129 _ A CGA
 GGT GGTGGG GG AATTG
 ||| |||| || ||||
 CCA CCACCC CC TTAAC
 A C ACC
 GAM1204 KIAA1644 3' TTGCCCCCACCACCCCA 41203 A A
 TG GGTGGTGGG GGCGA
 || ||||| ||||

AC CCACCACCC CCGTT
 C C
 GAM1204 MGC20235 3' TTACCTCCCACCCCCTCA 29671 T CG
 TGAGG GGTGGGAGG A
 ||||| ||||| |
 ACTCC CCACCCTCC T
 C AT
 GAM1204 STK39 3' TTTCCTCCCACCCCCTCA 14895 T C
 TGAGG GGTGGGAGG GA
 ||||| ||||| ||
 ACTCC CCACCCTCC TT
 C T
 GAM1204 LOC146146 5' TCTGACTCCCTCCACCTCA 38074 T GC_
 TGAGGTGG GGGAG GA
 ||||| |||| |
 ACTCCACC CCCTC CT
 T AGT
 GAM1204 LOC149448 3' TCCCTCCCACCACCCCA 40990 A C
 TG GGTGGTGGGAGG GA
 || ||||| |||| |
 AC CCACCACCCTCC CT
 C _
 GAM1204 LOC169693 3' TCAATTTCCCTCCCATCACCTC 42207 C
 A TGAGGTGGTGGGAGG GAAATTGA
 ||||| ||||| |||||
 ACTCCACTACCCTCC CTTTAACT
 _
 GAM1205 AMT 3' TGAGTGACGGACCAGCTCA 6090 CT GGT G
 TGAGCTGG CGTT G TCA
 ||||| |||| | |||
 ACTCGACC GCAG T AGT
 AG _ G
 GAM1205 DDEF2 3' TGACCACCTGGTGCCAGCT 9969 TCGTT
 AGCTGGC GGTGGTCA
 ||||| |||||
 TCGACCG CCACCAGT
 TGGT_
 GAM1205 GNAS 3' ACCCCGAGAACCAGTTCA 18677 C G T
 TGAGCTGG TC TTGG GGT
 ||||| || |||| |
 ACTTGACC AG AGCC CCA
 A _ _
 GAM1205 HR 3' ACCACAGTGCCACCAAGCTCA 11615 _ CTC TG_
 TGAGCT GG GT GTGGT
 ||||| || || ||||
 ACTCGA CC CG CACCA
 A AC_ TGA
 GAM1205 PCLO 3' ACCAAGACCAAAGCCAGCT 45211 CG _
 AGCTGGCT TTGGT GGT
 ||||| |||| | |||

		TCGACCGA AACCA CCA	
		___ GAA	
GAM1205 PTPRA	5'	TGACCCTTCGGAATCAGCCCA 8716	A GC GTT T
		TG GCTG TC GG GGTCA	
		AC CGAC AG TC CCAGT	
		C TA GCT _	
GAM1205 TGFBR3	3'	ACCCGGCCCAACCCAGCCCA 9247	A CTC T__
		TG GCTGG GTTGG GGT	
		AC CGACC CAACC CCA	
		C ___ CGGC	
GAM1205 TNFRSF8	3'	ACCACGAGCCACAGCCCA 6908	A ___ CGT
		TG GCT GGCT TGGTGGT	
		AC CGA CCGG ACCACCA	
		C CAC _	
GAM1205 WHSC1	3'	TGACCGTCTGAGCCCAGCTCA 17188	_ TT GT
		TGAGCTGG CTCG G GGTCA	
		ACTCGACC GAGT C CCAGT	
		C _ TG	
GAM1205 WHSC1	3'	TGACCGTCTGAGCCCAGCTCA 28469	_ TT GT
		TGAGCTGG CTCG G GGTCA	
		ACTCGACC GAGT C CCAGT	
		C _ TG	
GAM1205 WHSC1	3'	TGACCGTCTGAGCCCAGCTCA 28477	_ TT GT
		TGAGCTGG CTCG G GGTCA	
		ACTCGACC GAGT C CCAGT	
		C _ TG	
GAM1205 WHSC1	3'	TGACCGTCTGAGCCCAGCTCA 28452	_ TT GT
		TGAGCTGG CTCG G GGTCA	
		ACTCGACC GAGT C CCAGT	
		C _ TG	
GAM1205 WWOX	3'	TGACCAAGACTGAGCCAGCTTA 18506	_ GG
		TGAGCTGGCTC GTT TGGTCA	
		ATTCGACCGAG CAG ACCAGT	
		T A_	
GAM1205 CLIPR-59	3'	GACCACCAAGGACAGCTCA 17789	GC G
		TGAGCTG TC TTGGTGGTC	
		ACTCGAC AG AACCACCAG	
		_ G	
GAM1205 DDX17	5'	TGACTATCCAAACAGCTCA 25157	GCTCG _
		TGAGCTG TTGG TGGTCA	

		ACTCGAC	AACC ATCAGT		
		A___	T		
GAM1205	FLJ20452	3'	TGACCATGCCTGAACCAAGTCA	19491	G C TTG
			TGA CTGG TCG GTGGTCA		
			ACT GACC AGT TACCAGT		
			_ A CCG		
GAM1205	FLJ32865	3'	TGACAGCTACGAGCCAGCCCA	29432	A T G
			TG GCTGGCTCGT GGT GTCA		
			AC CGACCGAGCA TCG CAGT		
			C _ A		
GAM1205	KIAA0630	3'	GACCTCAAACCAAGCTTA	43063	CTCG T
			TGAGCTGG TTGG GGTC		
			ATTCGACC AACT CCAG		
			A___ _		
GAM1205	KIAA1029	5'	TGACCACCCCTCCAGCTC	14146	CTCGTT
			GAGCTGG GGTGGTCA		
			CTCGACC CCACCAGT		
			CTCC__		
GAM1205	MGC10870	5'	GACCCCAAGAGCCGGCCCA	26081	A GT T
			TG GCTGGCTC TGG GGTC		
			AC CGGCCGAG ACC CCAG		
			C _ _		
GAM1205	MGC26954	3'	ACCACCAACCAAGGTCA	29637	G CTCG
			TGA CTGG TTGGTGGT		
			ACT GACC AACCACCA		
			G _		
GAM1205	MGC4643	3'	TGACCACTCAGGCCAGCCCA	26443	A CGTT
			TG GCTGGCT GGTGGTCA		
			AC CGACCGG TCACCAGT		
			C AC__		
GAM1205	NUP160	3'	TGACCACCAAAAGCAGTCA	42329	G G CG
			TGA CTG CT TTGGTGGTCA		
			ACT GAC GA AACCACCAGT		
			_ _ A_		
GAM1205	PTPNS1	3'	TGACGTTGCCAAACCAAGCCA	28058	A CTCG G__
			TG GCTGG TTGGT GTCA		
			AC CGACC AACCG CAGT		
			_ A__ TTG		
GAM1205	RA-GEF-2	3'	TGCTAACGAACAGCTCA	18467	GC
			TGAGCTG TCGTTGGTG		

		ACTCGAC AGCAATCGT	
		A_	
GAM1205	URG4	3' TGACCTCACAGACCAGCTCA 19579	C GT T
		TGAGCTGG TC TGG GGTCA	
		ACTCGACC AG ACT CCAGT	
		_ AC _	
GAM1205	LOC115110	3' CAACGGCTGAGCCAGCCCA 35505	A _ G
		TG GCTGGCTC GTTG TG	
		AC CGACCGAG CGGC AC	
		C T A	
GAM1205	LOC147174	5' TGACCACCACCATCCACCAGTT 32342	CTCGT_
		CA TGAGCTGG TGGTGGTCA	
		ACTTGACC ACCACCAGT	
		ACCTACC	
GAM1205	LOC157376	3' GGAAACACAGCCAGCTCA 39600	C TG GG
		TGAGCTGGCT GT GT TC	
		ACTCGACCGA CA CA GG	
		_ _ AA	
GAM1205	LOC164397	3' ACCACCAACTCCTCACTCA 40148	C CTC
		TGAG TGG GTTGGTGGT	
		ACTC ACT CAACCACCA	
		_ CCT	
GAM1205	LOC202451	5' ACCACCAACAACGTTC 43435	T CTC
		GAGC GG GTTGGTGGT	
		CTTG TC CAACCACCA	
		_ AA_	
GAM1205	LOC220002	3' GACCACTCTGCAGCTCA 44049	G TCGTT
		TGAGCTG C GGTGGTC	
		ACTCGAC G TCACCAG	
		_ TC_	
GAM1205	LOC253292	5' TGA CTGCACAAATCAGCTCA 46340	CTCG _ TG
		TGAGCTGG TTG G GTCA	
		ACTCGACT AAC C CAGT	
		A_ A GT	
GAM1205	LOC255294	5' ACCAGGAGAACCTAGCTCA 45337	_ G
		TGAGCTGG CTC TTGGT	
		ACTCGATC GAG GACCA	
		CAA _	
GAM1205	LOC90784	5' ACCACCAAAATAGCTACA 32001	_ GCTCG
		TG AGCTG TTGGTGGT	

AC TCGAT AACCACCA
 A AA____
 GAM1206 XK 3' CATGCACTCTTCATGTAATCA 22056 CG T T
 TGA TACATGAA AGT GCATG
 ||| ||||| ||| |||||
 ACT ATGTACTT TCA CGTAC
 A_ C _
 GAM1206 PDCD7 3' AACTATCCATGTAGTCA 35695 G A
 TGAC TACATG ATAGTT
 |||| ||||| |||||
 ACTG ATGTAC TATCAA
 _ C
 GAM1206 LOC255104 3' TCATGCAACATCTGGAC 45686 A T ATA
 GT CA GA GTTGCATGA
 || ||| |||||
 CA GT CT CAACGTACT
 G _ A_
 GAM1207 SKI 3' CACCCGGGGAAGCCATCACAGC 8986 _ AA _ TTC
 TCA TGAGCTGT AT CT CCCT GTG
 ||||| || || ||| |||
 ACTCGACA TA GA GGGG CAC
 C CC A CC_
 GAM1207 DKFZP434O047 5' CACGAAAGGGTACCAAGCCCA 17863 A GTATAACT
 TG GCT CCCTTTCGTG
 || ||| |||||
 AC CGA GGGAAAGCAC
 C ACCAT____
 GAM1207 DKFZP761E2110 3' CATGGGGGAGAACATACAGCCC 25222 A AA_ TT
 A TG GCTGTAT CTCCCT CGTG
 || ||||| ||||| |||
 AC CGACATA GAGGGG GTAC
 C CAA _
 GAM1207 PRO2266 3' CATGCTGGGCCATACAGCTCA 20596 AACT TTT
 TGAGCTGTAT CCC CGTG
 ||||| ||| |||
 ACTCGACATA GGG GTAC
 CC_ TC_
 GAM1207 ZAK 3' TGAAAGCCTACAGCTCA 28608 TAACTCC
 TGAGCTGTA CTTTCG
 ||||| |||||
 ACTCGACAT GAAAGT
 CC____
 GAM1207 LOC147463 3' CACGAAGTCAAGAACCAAACAG 38341 ATAAC CC_
 CTCA TGAGCTGT TC TTTCGTG
 ||||| || |||||
 ACTCGACA AG GAAGCAC
 AACCA AACT
 GAM1208 BN51T 3' CAAGGCCAGAACCAGCAGG 42282 C_ _
 CCTGCTGG CT CTTTG
 ||||| || |||||

			GGACGACC GA GGAAC		
			AA CC		
GAM1208	CLASP1	3'	ACACTTTAAAGGACAGCA 32538	GC T	T
			TGCTG C CTTTGAG TGT		
			I		
			ACGAC G GAAATTT ACA		
			A__ C		
GAM1208	ITGA6	3'	ACAACCCAAAAGGTTTAAG 5699	GCT	C A
			CT GGCCT TTTG GTTGT		
			GA TTGGA AAAC CAACA		
			AT_ _ C		
GAM1208	FLJ20695	3'	CAAAGCAGGACCAGCAGG 19611	_ _	
			CCTGCTGG CCT CTTTG		
			GGACGACC GGA GAAAC		
			A C		
GAM1208	KIAA1023	3'	ACAGGCCAGAAACCAGCAG 19083	CCTC	AG
			CTGCTGG TTTG TTGT		
			GACGACC AGAC GACA		
			AA__ CG		
GAM1208	LOC114971	3'	ACAACTCAAAAAACATTTAGCA 36207	CCTC__	
			TGCTGG TTTGAGTTGT		
			ACGATT AAACTCAACA		
			TACAAA		
GAM1208	LOC155179	3'	ACAGGCCAGAAACCAGCAG 39551	CCTC	AG
			CTGCTGG TTTG TTGT		
			GACGACC AGAC GACA		
			AA__ CG		
GAM1208	LOC201516	5'	ACAACTCAAAAAGAGCAGAGC 42580	G_ _ C	
			GCT GC CT TTTGAGTTGT		
			CGA CG GA AAACTCAACA		
			GA A A		
GAM1208	LOC222865	3'	ACAATAATGAGGCCAGAAGTA 44620	CTG	TTTGA
			TAC CTGGCCTC GTTGT		
			ATG GACCGGAG TAACA		
			AA_ TAA__		
GAM1208	LOC257464	3'	AGCTTCAAAGAGGCCAAAAG 43161	GC	_
			CT TGGCCTCTTTGA GTT		
			GA ACCGGAGAAACT CGA		
			AA T		
GAM1209	GRIN2A	3'	CACTTCATAGCACCAACA 6489	GC	GTTTTG
			TG TGGTG ATGAAGTG		

			AC ACCAC TACTTCAC		
			A_ GA_____		
GAM1209	TCF2	3'	CCACCTCAGTGCCCACAGCCA 13201	GT	TTTGA A
			TGGCTG GGT TGA GTGG		
			ACCGAC CCG ACT CACC		
			AC TG____ C		
GAM1209	TP53	3'	CACTTCACCGTACTAACCA 6151	_	TT A
			TGGT GGT TG TGAAGTG		
			ACCA TCA GC ACTTCAC		
			A T_ C		
GAM1209	TRIM34	3'	CCACCCCCATGACCACCACCA 22249	C	T ATGAA
			TGG TGGTGGTT TG GTGG		
			ACC ACCACCAG AC CACC		
			_ T CCC__		
GAM1209	TRIM34	3'	CCACCCCCATGACCACCACCA 28173	C	T ATGAA
			TGG TGGTGGTT TG GTGG		
			ACC ACCACCAG AC CACC		
			_ T CCC__		
GAM1209	KIAA0574	3'	CCAGCGAGGCCAAGACCACCAG 34342		ATGAA _
			CCA TGGCTGGTGGTTTTG G TGG		
			ACCGACCACCAGAAC C ACC		
			CGGAG G		
GAM1209	KIAA1016	5'	CCACTTCATCATCCCCACCACC 44085	C	TTT
			A TGG TGGTGG TGATGAAGTGG		
			ACC ACCACC ACTACTTCACC		
			_ CCT		
GAM1209	LEC3	3'	CACCGAGAACCACCAGCCA 17566		GATGAA
			TGGCTGGTGGTTTT GTG		
			ACCGACCACCAAGA CAC		
			GC_____		
GAM1209	MGC22014	5'	CCACTCCTCACCACCAGC 32217		TTT T A
			GCTGGTGGT GA GA GTGG		
			CGACCACCA CT CT CACC		
			__ C _		
GAM1209	POMT1	3'	CACCTGAACCACGAGCCA 14016	G	TGATGAA
			TGGCT GTGGTTT GTG		
			ACCGA CACCAAG CAC		
			G TC_____		
GAM1209	LOC143173	5'	CCACTTCACCTCATCCCAGCCA 30269	T	TTTGA
			TGGCTGG GGT TGAAGTGG		

ACCGACC CTA ACTTCACC
 _ CTCC_
 GAM1209 LOC202451 5' CCACCCTTTTCAACCACCAACA 43437 GC TT T A_
 TG TGGTGGT TGA GA GTGG
 || ||||| ||| ||||
 AC ACCACCA ACT TT CACC
 A_ _ T CC
 GAM1210 BDG-29 3' GCCATTACAGTGGCCTGGATA 35816 AGA CT
 TATCCAG TAT TGTAATGGC
 ||||| ||| |||||
 ATAGGTC GTG ACATTACCG
 CG_ _
 GAM1210 C21orf6 3' GCCATTGCCTGTCTCT 18855 TCTT
 AGAGATA GTAATGGC
 ||||| |||||
 TCTCTGT CGTTACCG
 C_
 GAM1210 DKFZp434D177 3' ACCAGATATCTCTGGGTA 26007 T
 TATCCAGAGATATCT GT
 ||||| ||||| ||
 ATGGGTCTCTATAGA CA
 C
 GAM1210 HSA249128 3' GCCAAATTA ACTCTCTGGA 19027 TATC TAA
 TCCAGAGA TTG TGGC
 ||||| ||| ||||
 AGGTCTCT AAT ACCG
 C_ TAA
 GAM1210 KIAA1634 3' CCACCAACTATTTCTGGATA 31751 TC TAA
 TATCCAGAGATA TTG TGG
 ||||| ||| |||
 ATAGGTCTTTAT AAC ACC
 C_ C_
 GAM1210 KIAA1941 3' GCCCCCCAAAAATGTCTCTAGA 36951 C C GTAAT
 TC AGAGATAT TT GGC
 || ||||| || |||
 AG TCTCTGTA AA CCG
 A A ACCC_
 GAM1210 PRO2533 3' CCATTACAAAATGTAATGG 20702 GAG C
 CCA ATAT TTGTAATGG
 ||| ||| |||||
 GGT TGTA AACATTACC
 AA_ A
 GAM1210 LOC151201 3' TGTAAAATACCTCTGGATA 41323 A C
 TATCCAGAG TAT TTGTA
 ||||| ||| ||||
 ATAGGTCTC ATA AATGT
 C A
 GAM1211 NDRG3 3' ACTGTAACATTCCAACATCT 22845 G ATCA T
 AGA GTTGGAAT AC AGT
 ||| ||||| || |||

			TCT CAACCTTA	TG TCA		
			A	CAA_ _		
GAM1211	NDRG3	3'	ACTGTAACATTCCAACATCT	25720	G	ATCA T
			AGA GTTGGAAT	AC AGT		
			TCT CAACCTTA	TG TCA		
			A	CAA_ _		
GAM1211	SARM	3'	CAACTAGCTGACAAAGCTTC	17453		GGAATA A
			GAGGTT	TCA CTAGTTG		
			CTTCGA	AGT GATCAAC		
			AAC_ _	C		
GAM1212	F3	3'	AAGACTACTATACAAACTACAG	33296	A	ATA _ _
	A		TCT TAGTTTGTA	TGG AG CTT		
			AGA ATCAAACAT	ATC TC GAA		
			C	_ _ A A		
GAM1212	STK6	3'	AAGCTCCACATCAATAAAC	9654	A_ A	
			GTTTGT	AT TGGAGCTT		
			CAAATA	TA ACCTCGAA		
			AC C			
GAM1212	FLJ10719	3'	AAGCTCCACGGGAGCAAATACA	31339	ATA	AATA_
	GA		TCT GTTTGT	TGGAGCTT		
			AGA TAAACG	ACCTCGAA		
			CA_	AGGGC		
GAM1212	FLJ23323	3'	AAGCTCCACGGCCACCATAGA	23953	A TT	AATA
			TCTAT GT GT	TGGAGCTT		
			AGATA CA CG	ACCTCGAA		
			C C_ GC_			
GAM1212	LOC149721	3'	AGTCCATTACAAACT	38808	AT	G
			AGTTTGTA	ATGGA CT		
			TCAAACAT	TACCT GA		
			_ _			
GAM1212	LOC202459	3'	AAGCTCCATATTTACAGCTATA	29814	T	_
			TATAGTT GTAA	TATGGAGCTT		
			ATATCGA CATT	ATACCTCGAA		
			_ T			
GAM1212	LOC254735	5'	CCATCTATACAAACTATA	45837	AT_	
			TATAGTTTGTA	ATGG		
			ATATCAAACAT	TACC		
			ATC			
GAM1213	PIP5K1B	3'	TAGGTCTGCCTTCACTTTA	9605	TAA	A
			TAAAGTGA	GCA ACCTA		

ATTTCACT CGT TGGAT
 TC_ C
 GAM1213 KIAA1463 3' ACAATAGGCCTTTTCTTTATCA 35767 A C ____
 TTCA A AGTGATAAG AAA CCTATTGT
 | ||||| ||| |||||
 A TTACTATTT TTT GGATAACA
 C C TCC
 GAM1213 RERG 3' ACATCTGATTTGTTTATCACCT 26737 A CCTAT
 TA TAA GTGATAAGCAAA TGT
 ||| ||||| |||
 ATT CACTATTTGTTT ACA
 C AGTCT
 GAM1213 LOC221474 5' AGGCCTGCTCTCACTTTA 44378 TA AA
 TAAAGTGA AGCA CCT
 ||||| ||| |||
 ATTTCACT TCGT GGA
 C_ CC
 GAM1214 DMPK 3' GTCCTGTGTACCGGGCCCGCC 10667 CA T
 GGTGGGCCCCGGT GC GGAC
 ||||| || |||
 CCGCCCGGGCCA TG CCTG
 TG T
 GAM1214 EPHA8 3' CCAGCACCAGGCCACC 21744 C CA
 GGTGGGCC GGT GCTGG
 ||||| || |||
 CCACCCGG CCA CGACC
 A ____
 GAM1214 FANCA 3' CCGGACACCAAGCCCGCCTCC 5630 A CC CAG
 A AGGTGGGC GGT CTGG
 | ||||| ||| |||
 C TCCGCCCCG CCA GGCC
 C AA CA_
 GAM1214 GLI2 5' TCCAGCCCTCACCCACCTT 24936 CCC TCA
 AAGGTGGG GG GCTGGA
 ||||| || |||||
 TTCCACCC CC CGACCT
 ACT ____
 GAM1214 HOXD1 3' CCAGCTGCCAGCCCAGCTCC 23696 A G CC T
 A AG TGGGC GG CAGCTGG
 | || |||| || |||||
 C TC ACCCG CC GTCGACC
 C G A_ _
 GAM1214 KLF8 5' CCAGCGAACCCACTTT 14123 CCCGG A
 AAGGTGGG TC GCTGG
 ||||| || |||||
 TTTCACCC AG CGACC
 A____ _
 GAM1214 LENG4 5' CCAGCCCACCCACCTT 23581 CCC TCA
 AAGGTGGG GG GCTGG
 ||||| || |||||

TTCCACCC CC CGACC
 A__ __
 GAM1214 NF1 5' CCAGGGCGCCGGCCCACC 5812 C CAG
 GGTGGGCC GGT CTGG
 ||||| ||| |||
 CCACCCGG CCG GACC
 _ CGG
 GAM1214 OAS3 3' CCAGCTGAGAATGCCCCCTCC 12859 A T CCGG
 A AGG GGGC TCAGCTGG
 | ||| ||| |||||
 C TCC CCCG AGTCGACC
 C _ TAAG
 GAM1214 PDE4A 3' TCCTCCGGACCCACCTT 12876 C_ TCAGCT
 AAGGTGGG CCGG GGA
 ||||| ||| |||
 TTCCACCC GGCC CCT
 CA T____
 GAM1214 SLC24A1 5' GTCCAGCTTCAGACCCACTCTT 11102 _ CCC TC
 T AAAG GTGGG GG AGCTGGAC
 ||| ||| || |||||
 TTTC CACCC CT TCGACCTG
 T AGA __
 GAM1214 AGTRL2 5' CCAGAGGAAAGCCCATCTCC 11645 A CCGG AG
 A AGGTGGGC TC CTGG
 | ||||| || |||
 C TCTACCCG AG GACC
 C AA__ GA
 GAM1214 C1orf16 3' CCAGCTGCAGTCTCCCAGCCTC 16854 A _ CCCG_ T
 C A AGG TGGG G CAGCTGG
 | ||| ||| | |||||
 C TCC ACCC C GTCGACC
 C G TCTGA_
 GAM1214 C21orf93 3' CCCTGTGCCCGGCCACCTT 29740 C _ CT
 AAGGTGGGCC GGT CAG GG
 ||||| ||| ||| |||
 TTCCACCCGG CCG GTC CC
 C T __
 GAM1214 CNNM1 3' CCAGCTGACCACTGGCCC 21607 C__
 GGGCC GGTCAGCTGG
 |||| |||||
 CCCGG CCAGTCGACC
 TCA
 GAM1214 DKFZP434H132 5' CCAGCTGGCCCAGCCCCT 36447 T CC
 GG GGGC GGTCAGCTGG
 || ||| |||||
 TC CCCG CCGGTCGACC
 _ AC
 GAM1214 DKFZP434I216 5' GCCCCGAGCAGGCCACCTTT 38100 ____ TCA
 AAAGGTGGGCC CGG GC
 ||||| ||| |||

TTTCCACCCGG GCC CG
 ACGA C__
 GAM1214 DKFZP586G1122 3' GTCCAGTCCAAGCCCACC 30726 CC TCA
 GGTGGGC GG GCTGGAC
 ||||| || |||||
 CCACCCG CC TGACCTG
 AA ____
 GAM1214 DKFZP761E2110 3' CCAAGGCTGCTAGGCCACC 25224 CG T ____
 GGTGGGCC G CAGCT GG
 ||||| | |||| ||
 CCACCCGG C GTCGG CC
 AT_ AA
 GAM1214 FLJ22746 3' CCAGCTATGGGTGCCACCT 24164 _ G C
 AGGTGGGC CC GT AGCTGG
 ||||| || || |||||
 TCCACCCG GG TA TCGACC
 T G _
 GAM1214 FLJ23022 3' CCGGGCCCGGGCCACCTT 24646 TCAG
 AAGGTGGGCCCGG CTGG
 ||||| |||| ||||
 TTCCACCCGGGCC GGCC
 CG__
 GAM1214 FLJ23420 5' CCACACCAAGGCCACCT 24660 C_ CAGC
 AGGTGGGCC GGT TGG
 ||||| ||| |||
 TCCACCCG CCA ACC
 AA C__
 GAM1214 FUSIP1 3' TCCAGCTAAGAGGGCCCATCT 13410 GGTC
 AGGTGGGCC AGCTGGA
 ||||| |||||
 TCTACCCGGG TCGACCT
 AGAA
 GAM1214 KIAA0152 3' TCCAGTGATGGTCCCACCTTT 16340 C G G
 AAAGGTGGG CCG TCA CTGGA
 ||||| ||| ||| |||||
 TTTCCACCC GGT AGT GACCT
 T _ _
 GAM1214 KIAA0930 3' GCCCCGGCCGGGCCAGCC 34916 _ A__
 GG TGGGCCCGGTC GC
 || ||||| ||
 CC ACCCGGGCCGG CG
 G CCC
 GAM1214 KIAA1029 5' CCAGTGACCACCCCTCC 14143 T CCC
 GG GGG GGTCAGCTGG
 || ||| |||||
 CC CCC CCAGTCGACC
 T CA_
 GAM1214 KIAA1157 3' CCTGCACACCATAGCCCACCT 35749 CC_ CA T
 AGGTGGGC GGT GC GG
 ||||| ||| |||

TCCACCCG CCA CG CC
 ATA CA T
 GAM1214 KIAA1602 3' GCCCCAGGGCCCACCTTT 32277 _ TCA
 AAAGGTGGGCCC GG GC
 ||||| || ||
 TTTCCACCCGGG CC CG
 A C__
 GAM1214 KIAA1656 3' GTCCAGCTCAAAGGCCACCTCC 32736 A G CGGTC
 A AGGTGG CC AGCTGGAC
 | |||| || |||||
 C TCCACC GG TCGACCTG
 C _ AAAC_
 GAM1214 KIAA1854 3' CCAGCTGACCAGGCAAGACCT 35526 GG_ C
 AGGT GCC GGTCAGCTGG
 ||| || |||||
 TCCA CGG CCAGTCGACC
 GAA A
 GAM1214 MAPK8IP3 3' CCAGCCCTGCCACCTGGGCCCA 27218 A _ _ _
 CCTCC A AGGTGGGCCC GGT CA GCTGG
 | ||||| || || ||||
 C TCCACCCGGG CCA GT CGACC
 C T CC CC
 GAM1214 MESDC2 3' CCAGGAGGCCACCT 35891 CGG AG
 AGGTGGGCC TC CTGG
 ||||| || |||
 TCCACCCGG AG GACC
 _ _
 GAM1214 MSE55 5' CCAAGCCCAGCCCACCTCC 13924 A CC TCA _
 A AGGTGGGC GG GCT GG
 | ||||| || |||
 C TCCACCCG CC CGA CC
 C A_ _ A
 GAM1214 N4BP3 3' CCCCTCCCCGCACCCACCTCC 32931 A CC TC CT
 A AGGTGGG CGG AG GG
 | ||||| || ||
 C TCCACC GCC TC CC
 C AC CC C_
 GAM1214 PRIC285 3' CCAAAGCCAGGGGCCACC 30802 _ CAGC
 GGTGGGCC GGT TGG
 ||||| || |||
 CCACCCGGG CCG ACC
 GA AA_
 GAM1214 RASD2 3' CCACTTAGACCACGCCACCTC 15601 A CC _ C
 C A AGGTGGGC GGTC AG TGG
 | ||||| || || |||
 C TCCACCCG CCAG TT ACC
 C CA A C
 GAM1214 TM4SF11 3' GTCCAAGACTGGGGCCCACC 18085 _ AGC
 GGTGGGCC GGTC TGGAC
 ||||| || |||

CCACCCGGG TCAG ACCTG
 G A__
 GAM1214 TNRC9 5' CCGGCCCCGGGCCAGCTT 35321 G TCA
 AAG TGGGCCCGG GCTGG
 ||| ||||| ||||
 TTC ACCCGGGCC CGGCC
 G C__
 GAM1214 ZNF340 3' CCAGGACCCAGGCCGCCTCC 41032 A C_ AG
 A AGGTGGGCC GGTC CTGG
 | ||||| ||| ||||
 C TCCGCCCGG CCAG GACC
 C AC __
 GAM1214 LOC127281 3' GTCCAGCTTCTTGCCACCTTT 36890 G C TC
 AAAGGTGG CC GG AGCTGGAC
 ||||| || |||||
 TTTCCACC GG TC TCGACCTG
 _ T T_
 GAM1214 LOC143153 3' GTCCAGAGACAGGCCCTCCTCC 37581 A T CG AG
 A AGG GGGCC GTC CTGGAC
 | ||| ||| |||||
 C TCC CCCGG CAG GACCTG
 C T A_ A_
 GAM1214 LOC143196 3' CCAGTTGACCCACCTT 40330 CCGG
 AAGGTGGG GTCAGCTGG
 ||||| |||||
 TTCCACCC CAGTTGACC

 GAM1214 LOC144600 5' GCCCCGGCCGGGCCAGCC 40448 _ A__
 GG TGGGCCCGGTC GC
 || ||||| ||
 CC ACCCGGGCCGG CG
 G CCC
 GAM1214 LOC147093 3' CCAGCTGAGCCCCTCCTTT 40800 T_ CCGG
 AAAGG GGGC TCAGCTGG
 |||| ||| |||||
 TTTCC CCG AGTCGACC
 TC _____
 GAM1214 LOC149566 3' CCATGCTCAGGCCACCTCC 41015 A C GTC _
 A AGGTGGGCC G AGC TGG
 | ||||| | ||| |||
 C TCCACCCGG C TCG ACC
 C A__ T
 GAM1214 LOC151171 5' TCCAGCTTCACCGACCTCC 39066 T CC C_
 GG GGG CGGT AGCTGGA
 || ||| ||| |||||
 CC TCC GCCA TCGACCT
 _ A_ CT
 GAM1214 LOC163682 3' GTCCAGCTCCTGGGCCACC 42098 TC
 GGTGGGCCCGG AGCTGGAC
 ||||| |||||

CCACCCGGGTC TCGACCTG
 C_
 GAM1214 LOC164714 3' TCCAGCCCCGCCCACTTCC 42183 A CC TCA
 A AGGTGGGC GG GCTGGA
 | ||||| || |||||
 C TTCACCCG CC CGACCT
 C _ C_
 GAM1214 LOC203260 3' CCAGCTGGACCCCTTT 43023 T CCCGG
 AAAGG GGG TCAGCTGG
 ||||| || |||||
 TTTCC CCC GGTCGACC
 _ A_
 GAM1214 LOC204254 5' CCAGAGCTGGAGTCCACCTT 43582 _ CAG
 AAGGTGGGC CCGGT CTGG
 ||||| ||||| |||||
 TTCCACCTG GGTCG GACC
 A A_
 GAM1214 LOC205095 3' CCACCTCCCGGGCCCCCT 43602 T TC C
 AGG GGGCCCCG AG TGG
 || ||||| || |||||
 TCC CCCGGGCC TC ACC
 C C_ C
 GAM1214 LOC254617 5' CCAGCTTCTGGGCCCCACT 46518 TC
 GGTGGGCCCCG AGCTGG
 ||||| |||||
 TCACCCGGGTC TCGACC
 T_
 GAM1214 LOC255299 5' CCAGCCCCACCGCCACCT 46547 CC CA_
 AGGTGGGC GGT GCTGG
 ||||| || |||||
 TCCACCCG CCA CGACC
 _ CCC
 GAM1214 LOC256946 3' TCCAGCTAAGAGGGCCCATCT 45360 GGTC
 AGGTGGGCCC AGCTGGA
 ||||| |||||
 TCTACCCGGG TCGACCT
 AGAA
 GAM1214 LOC51152 3' CCAGCTGACTGAGCCCCCT 18283 T C
 AGG GGGC CGGTCAGCTGG
 || ||||| |||||
 TCC CCCG GTCAGTCGACC
 _ A
 GAM1214 LOC91963 3' CCAACTGAGACTCCCATCTTT 33626 CCCGG C
 AAAGGTGGG TCAG TGG
 ||||| |||||
 TTTCTACCC AGTC ACC
 TCAG_ A
 GAM1214 LOC92230 5' CCAGCCCCTTGCCACCT 34006 CC TCA
 AGGTGGGC GG GCTGG
 ||||| || |||||

TCCACCCG CC CGACC
 TT C__
 GAM1214 LOC93259 5' GTCCAGCTGAGCTCCACCT 35560 _ CCGG
 AGGTGG GC TCAGCTGGAC
 ||||| || |||||
 TCCACC CG AGTCGACCTG
 T ____
 GAM1215 FMOD 3' TCCACTTCACCCACTCCA 7771 _ CTTTCT
 TGGAGTGG TGA GTGGA
 ||||| || |||||
 ACCTCACC ACT CACCT
 C T____
 GAM1215 NDRG3 3' AGTCCATCCTTCAAATGACCAC 22846 GACTTTCT__
 TCCA TGGAGTGGT GTGGACT
 ||||| |||||
 ACCTCACCA TACCTGA
 GTAAACTTCC
 GAM1215 NDRG3 3' AGTCCATCCTTCAAATGACCAC 25722 GACTTTCT__
 TCCA TGGAGTGGT GTGGACT
 ||||| |||||
 ACCTCACCA TACCTGA
 GTAAACTTCC
 GAM1215 PCSK2 3' TCCCAAAAGTCACCACTCCA 8460 C T
 TGGAGTGGTGACTTT TG GGA
 ||||| |||||
 ACCTCACCAGTAAA AC CCT
 - -
 GAM1215 RAB40A 5' TCCATCAAAGCCACCACCTCA 39931 GA A CT
 TG GTGGTG CTTT GTGGA
 || ||||| |||||
 AC CACCAC GAAA TACCT
 TC C C_
 GAM1215 LOC150150 5' CCACAAAAAGTCATTCCCCCA 41134 AGT C
 TGG GGTGACTTT TGTGG
 || ||||| |||||
 ACC TTAAGTAAA ACACC
 CCC A
 GAM1216 ATRN 3' GTCCATCTCTTTTGATCA 29302 CTCA
 TGATCAAAA GTGGAC
 ||||| |||||
 ACTAGTTTT TACCTG
 CTC_
 GAM1216 B3GALT5 3' GTCCCTTGTTTTTGATCA 27038 CT T
 TGATCAAAA CAG GGAC
 ||||| |||||
 ACTAGTTTT GTT CCTG
 T_ C
 GAM1216 B3GALT5 3' GTCCCTTGTTTTTGATCA 27023 CT T
 TGATCAAAA CAG GGAC
 ||||| |||||

		ACTAGTTTT GTT CCTG	
		T_ C	
GAM1216 B3GALT5	3'	GTCCCTTGTTTTTGATCA 27028	CT T
		TGATCAAAA CAG GGAC	
		ACTAGTTTT GTT CCTG	
		T_ C	
GAM1216 B3GALT5	3'	GTCCCTTGTTTTTGATCA 27033	CT T
		TGATCAAAA CAG GGAC	
		ACTAGTTTT GTT CCTG	
		T_ C	
GAM1216 B3GALT5	3'	GTCCCTTGTTTTTGATCA 12700	CT T
		TGATCAAAA CAG GGAC	
		ACTAGTTTT GTT CCTG	
		T_ C	
GAM1216 BACH1	3'	CCCTTTTGTGATCAGG 6858	CTC T
		TCTGATCAAAA AG GG	
		GGACTAGTTTT TC CC	
		— —	
GAM1216 CHC1L	3'	ATTGAATGTTCTGATCAGA 6929	A —
		TCTGATCA AAC TCAGT	
		AGACTAGT TTG AGTTA	
		C TA	
GAM1216 CTNS	3'	GTCCACTGAGTTTCCTTC 11385	TCA
		GA AACTCAGTGGAC	
		CT TTTGAGTCACCTG	
		TCC	
GAM1216 CYP3A43	3'	GTCCTCCTGAGCTGTGATCAGA 27663	AAA T_
		TCTGATCA CTCAG GGAC	
		AGACTAGT GAGTC CCTG	
		GTC CT	
GAM1216 DTNA	3'	TTCAAGTTGTTGATCAGA 7084	_ CAG
		TCTGATCAA AACT TGGA	
		AGACTAGTT TTGA ACTT	
		G —	
GAM1216 DTNA	3'	TTCAAGTTGTTGATCAGA 26841	_ CAG
		TCTGATCAA AACT TGGA	
		AGACTAGTT TTGA ACTT	
		G —	
GAM1216 DTNA	3'	TTCAAGTTGTTGATCAGA 26851	_ CAG
		TCTGATCAA AACT TGGA	

		AGACTAGTT TTGA ACTT	
		G _	
GAM1216 DTNA	3'	TTCAAGTTGTTGATCAGA 26846	_ CAG
		TCTGATCAA AACT TGGA	
		AGACTAGTT TTGA ACTT	
		G _	
GAM1216 ELMO1	3'	GTCCACTGGTGGGACAAGA 28203	GA AAA T
		TCT TC AC CAGTGGAC	
		AGA AG TG GTCACCTG	
		AC GG_ _	
GAM1216 FGF2	3'	CTGAGTAGTTTTGATCAG 7738	_
		CTGATCAAA ACTCAG	
		GACTAGTTT TGAGTC	
		TGA	
GAM1216 GABRE	3'	TCCCTCTCCTTTGGTCAGA 22533	ACTC T
		TCTGATCAAA AG GGA	
		AGACTGGTTT TC CCT	
		CCTC _	
GAM1216 GABRE	3'	TCCCTCTCCTTTGGTCAGA 22511	ACTC T
		TCTGATCAAA AG GGA	
		AGACTGGTTT TC CCT	
		CCTC _	
GAM1216 GABRE	3'	TCCCTCTCCTTTGGTCAGA 22515	ACTC T
		TCTGATCAAA AG GGA	
		AGACTGGTTT TC CCT	
		CCTC _	
GAM1216 GABRE	3'	TCCCTCTCCTTTGGTCAGA 11409	ACTC T
		TCTGATCAAA AG GGA	
		AGACTGGTTT TC CCT	
		CCTC _	
GAM1216 KLHL2	3'	CCATGTGTGTTGATCAGA 14112	A TCA
		TCTGATCAA AC GTGG	
		AGACTAGTT TG TACC	
		G TG_	
GAM1216 TGFBR3	3'	CCCTGAGTTTTACCCAGA 9249	ATC T
		TCTG AAAACTCAG GG	
		AGAC TTTTGAGTC CC	
		CCA _	
GAM1216 AK5	3'	TCCACTGGTGGCTCAGA 14395	_ AAAC
		TCTGA TCA TCAGTGGA	

	AGACT GGT GGTCACCT	
	C ____	
GAM1216 BHLHB2	3' GTCTGTGGCTTTGATCAGA 9755	A CA TG
	TCTGATCAAA CT G GAC	
	AGACTAGTTT GG T CTG	
	C __ GT	
GAM1216 C20orf139	3' GTCTCTTGGTTTTGACAGA 41108	A T T
	TCTG TCAAAAC CAG GGAC	
	AGAC AGTTTTG GTT TCTG	
	- - C	
GAM1216 FLJ13782	3' CCACTTTCTGGTCAGA 24435	A CTC
	TCTGATCA AA AGTGG	
	AGACTGGT TT TCACC	
	C ____	
GAM1216 FLJ20151	3' TCCACTGGCTGAATGATCAGG 19245	AAAC_
	TCTGATCA TCAGTGGA	
	GGACTAGT GGTCACCT	
	AAGTC	
GAM1216 FLJ22329	3' TCAAGCAGTTACTGATCAGA 23959	A_ CAG
	TCTGATCA AACT TGG	
	AGACTAGT TTGA ACT	
	CA CGA	
GAM1216 HTCD37	3' GTCTTCTGTCCTGATCAGG 33619	AAACT T
	TCTGATCA CAG GGAC	
	GGACTAGT GTC TCTG	
	CCT__ T	
GAM1216 KIAA0295	3' GTCAAGAGTATTTGATCAGA 33784	_ AGTG
	TCTGATCAAA ACTC GAC	
	AGACTAGTTT TGAG CTG	
	A AA__	
GAM1216 KIAA0483	3' GTCCTTAGATTTTGATCA 17529	C AGT
	TGATCAAAA TC GGAC	
	ACTAGTTTT AG CCTG	
	_ ATT	
GAM1216 KIAA0483	3' CCATGTGATCATTGATCAGA 17527	AAC _
	TCTGATCAA TCA GTGG	
	AGACTAGTT AGT TACC	
	ACT G	
GAM1216 KIAA0847	3' CCTGAAGAGTCATTGATCAGA 38046	A_ AGT_
	TCTGATCAA ACTC GG	

		AGACTAGTT TGAG CC	
		AC AAGT	
GAM1216 KIAA0934	3'	GTCCACTGAAGCGTGCAGA 32120	AT AAAC
		TCTG CA TCAGTGGAC	
		AGAC GT AGTCACCTG	
		__ GCGA	
GAM1216 KIAA1522	3'	CCACTGAGTTGGGGAAAGA 32416	GA AA
		TCT TC AACTCAGTGG	
		AGA GG TTGAGTCACC	
		AA GG	
GAM1216 KIAA1530	3'	CCACAGTGCCTTGATCAG 33731	A__ CA
		CTGATCAA ACT GTGG	
		GACTAGTT TGA CACC	
		CCG __	
GAM1216 KIAA1908	5'	CCAGTGATTTGATCGGA 36332	AC G
		TCTGATCAAA TCA TGG	
		AGGCTAGTTT AGT ACC	
		__ G	
GAM1216 MKP-7	3'	CCATTGAGTTTTGATCAG 33005	
		CTGATCAAAACTCAGTGG	
		GACTAGTTTTGAGTTACC	
GAM1216 NCOA2	3'	GTCCCTTTTAGTTTGATCAGA 13296	ACTC_ T
		TCTGATCAAA AG GGAC	
		AGACTAGTTT TC CCTG	
		GATTT _	
GAM1216 PACSIN2	3'	GTCTACTGTTTTAATGAGA 14098	G C TC
		TCT AT AAAAC AGTGGAC	
		AGA TA TTTTG TCATCTG	
		G A _	
GAM1216 PDE4DIP	3'	GTCCACTGGAGGGTCCAGA 45709	_ AAAAC
		TCTG ATC TCAGTGGAC	
		AGAC TGG GGTCACCTG	
		C GA__	
GAM1216 SERHL	3'	GTCCACGGATATTTTGATC 45758	C_ A
		GATCAAAA TC GTGGAC	
		CTAGTTTT AG CACCTG	
		AT G	
GAM1216 UMP-CMPK	3'	TCATTGCACTTTGGTCAGA 18428	ACT
		TCTGATCAAA CAGTGG	

		AGACTGGTTT GTTACT		
		CAC		
GAM1216	USP22	3' GTCCACTGAGAAATTAGA	33753	CAAAA
		TCTGAT CTCAGTGGAC		
		AGATTA GAGTCACCTG		
		AA__		
GAM1216	LOC128954	5' TCCTTGCCTTGATCAGG	37321	AACT T
		TCTGATCAA CAG GGA		
		GGACTAGTT GTT CCT		
		CC__ _		
GAM1216	LOC133926	3' GTCTGAGCAGTTTTGATTAGA	37060	CAG
		TCTGATCAAAACT TGGAC		
		AGATTAGTTTTGA GTCTG		
		CGA		
GAM1216	LOC146756	3' CCTTGGGGTTTTGATCAG	40734	AGT
		CTGATCAAAACTC GG		
		GACTAGTTTTGGG CC		
		GTT		
GAM1216	LOC147632	5' GTCTTCAGCTTGATCAGA	28827	AA CAGT
		TCTGATCAA CT GGAC		
		AGACTAGTT GA TCTG		
		C_ CT__		
GAM1216	LOC152343	3' GTCCATTTTTTAATCAGG	39263	C CTC
		TCTGAT AAAA AGTGGAC		
		GGACTA TTTT TTACCTG		
		A ____		
GAM1216	LOC220514	3' GTCTACTGTTTTAATGAGA	30322	G C TC
		TCT AT AAAAC AGTGGAC		
		AGA TA TTTTG TCATCTG		
		G A ____		
GAM1216	LOC254015	3' CCTTGGGGTTTTGATCAG	46242	AGT
		CTGATCAAAACTC GG		
		GACTAGTTTTGGG CC		
		GTT		
GAM1216	LOC257464	3' TCTACATTCTGATCAGA	43169	A CTCA
		TCTGATCA AA GTGA		
		AGACTAGT TT CATCT		
		C A__		
GAM1216	LOC91813	5' CCAGGAGTTTTGACCAGG	33398	A AG
		TCTG TCAAAACTC TGG		

			GGAC AGTTTTGAG ACC		
			C G_		
GAM1216	LOC92181	3'	GTCTCTTGAGTTTCAACAGA 33944	ATCA	T
			TCTG AAAC TCAG GGAC		
			AGAC TTTGAGTT TCTG		
			AAC_ C		
GAM1217	ABL1	3'	CCACAAACGGAGCCCCTG 11637	TG	_
			CAGGGGCTCC TTG GG		
			GTCCCCGAGG AAC CC		
			CA A		
GAM1217	ABL1	3'	CCACAAACGGAGCCCCTG 14226	TG	_
			CAGGGGCTCC TTG GG		
			GTCCCCGAGG AAC CC		
			CA A		
GAM1217	FEN1	3'	GGCAGAAAGCTGGAGCCCCTGG 10320	T	GGGATA
	A		TCCAGGGGCTCC GTT CC		
			AGGTCCCCGAGG CGA GG		
			T AAGAC_		
GAM1217	HUNK	3'	GTAAGCAGCAAACCCCTGGA 15951	CTCC	GGA
			TCCAGGGG TGTTG TAC		
			AGGTCCCC ACGAC ATG		
			AA_ GA_		
GAM1217	IGFBP3	3'	ATCCCAACGCATGCTCCTGGA 6197	TCC	
			TCCAGGGGC TGTTGGGAT		
			AGGTCCTCG GCAACCCTA		
			TAC		
GAM1217	IL10RA	3'	TATCTCAGGAGCCCC 29999	TTG	
			GGGGCTCCTG GGATA		
			CCCCGAGGAC TCTAT		

GAM1217	IRS2	5'	GGCATCCTCAGGAGCCCC 30033	TT	A
			GGGGCTCCTG GGGAT CC		
			CCCCGAGGAC TCCTA GG		
			_ C		
GAM1217	LUZP1	3'	ATCTGGAGAAGCCCCTGGG 27352	C	GT G
			TCCAGGGGCT CT T GGAT		
			GGGTCCCCGA GA G TCTA		
			A _ G		
GAM1217	MRC1	3'	TATTTTAAGGAGCTCCC 8281	_	GT
			GGG GCTCCT TGGGATA		

CCC CGAGGA ATTTTAT
 T _
 GAM1217 ZNF38 5' GTACCATGATACCCCTGGA 45311 CTCC _ A
 TCCAGGGG TGTTG GG TAC
 ||||| |||| ||||
 AGGTCCCC ATAGT CC ATG
 _ _ A _
 GAM1217 AASDHPPT 3' TTTTAACAAAAGCCTCCAGA 17725 CA CC
 TC GGGGCT TGTTGGGA
 || ||||| |||||
 AG CTCCGA ACAATTTT
 AC AA
 GAM1217 C20orf81 5' CCGCGGAGCCCCGGGA 23003 A T T
 TCC GGGGCTCC GT GG
 ||| ||||| || ||
 AGG CCCCAGAGG CG CC
 G _ _
 GAM1217 CDT1 3' ATCCCTGGAGCCTCCAGA 38065 CA TGTT
 TC GGGGCTCC GGGAT
 || ||||| ||||
 AG CTCCGAGG CCCTA
 AC T _
 GAM1217 DKFZP586A0522 3' GGTATCCTAGGTAAGAGCCCCT 15263 CTG_
 AGGGGCTC TTGGGATACC
 ||||| |||||
 TCCCCGAG GATCCTATGG
 AATG
 GAM1217 DKFZp586I021 3' GGGATACCAGCACGGAGGAGCC 26029 GTT_____ GATA
 CCCGG GGGGCTCCT GG CC
 ||||| || ||
 CCCCAGGA CC GG
 GGCACGAI|| ATAG
 GAM1217 FLJ10261 3' ATCCCAGTTATCCCTGGA 19788 CTCCTG
 TCCAGGGG TTGGGAT
 ||||| |||||
 AGGTCCCT GACCCTA
 ATT _
 GAM1217 FLJ13855 3' GGTACCTTTACAGGAGCACCTA 23344 C G T_ A
 GA TC AGG GCTCCTGT GGG TACC
 || ||| ||||| || ||||
 AG TCC CGAGGACA TCC ATGG
 A A TT _
 GAM1217 FLJ14451 5' CCCACAGGAGCCCCGGA 26540 A T
 TCC GGGGCTCCTGT GGG
 ||| ||||| ||||| ||||
 AGG CCCCAGGACA CCC
 _ _
 GAM1217 HSPB7 5' GTCCTCAGGAGCCCCCAGG 15783 A_ TT
 CC GGGGCTCCTG GGGAT
 || ||||| |||||

GG CCCCCGAGGAC TCCTG
AC ____
GAM1217 KIAA0211 3' GTATCCCCCAGCCCCAGGA 15993 A CCTGTT
TCC GGGGCT GGGATAC
||| ||||| |||||
AGG CCCCCGA CCCTATG
A CC____
GAM1217 KIAA0546 3' TATCCCAACATGCCTGG 35333 GGCTCC
CCAGG TGTTGGGATA
||||| |||||
GGTCC ACAACCCTAT
GT____
GAM1217 KIAA0710 3' TATCCAGGCAGAGAAGCTCCTG 16993 __ TG
GA TCCAGGGGCT C CTGT GGATA
||||||| | ||| |||||
AGGTCCTCGA G GACG CCTAT
A A GA
GAM1217 KIAA1045 3' TTGAGCAAGGGCCCCTAGA 35205 C C G
TC AGGGGCTC TGTT GG
|| ||||| ||| ||
AG TCCCCGGG ACGA TT
A A G
GAM1217 KIAA1423 3' GGCATCATAGAAGGCCCTGGA 30922 G C TGG A
TCCAGGG CT CTGT GAT CC
|||||| || ||| ||| ||
AGGTCCC GA GATA CTA GG
G A ____ C
GAM1217 MGC2628 3' ATCAAGCAGGAACCCCTGGA 23507 C GG
TCCAGGGG TCCTGTT GAT
|||||| ||||| |||
AGGTCCCC AGGACGA CTA
A A_
GAM1217 MGC3020 3' GTGACTAAAAGCCCCCTG 23484 CCTG GA
CAGGGGCT TTGG TAC
|||||| ||| |||
GTCCCCGA AATC GTG
A__ A_
GAM1217 MSP 3' GATACCAGCATCTGGAGCCCCT 25761 _ ____ T__ GATA
AGG AGGGGCTCC TGT GG C
|||||| ||| || |
TCCCCGAGG ACG CC G
A TCT A||| ATAG
GAM1217 USP3 5' CCAGACGGAGCCTCCGGA 43171 A TG
TCC GGGGCTCC TTGG
||| ||||| |||
AGG CTCCGAGG GACC
C CA
GAM1217 LOC131873 5' CCGAAAGAGGAGCCCCTGGA 37363 G_ T____
TCCAGGGGCTCCT T GG
||||||| ||| ||

	AGGTCCCCGAGGA A CC	
	GA AGIII	
GAM1217 LOC145231 3'	TATCCATTTCCGAGTCCCTGGA 40521	CTGTTG
	TCCAGGGGCTC GGATA	
	AGGTCCCTGAG CCTAT	
	CCTTTA	
GAM1217 LOC146237 3'	GGCAAGCCCAGGGACCCCTGGA 40670	C GT ATA_
	TCCAGGGG TCCT TGGG CC	
	AGGTCCCC AGGG ACCC GG	
	GAAC	
GAM1217 LOC146713 3'	TCGGAAGGAGCCCCCAGG 40717 A_ G	
	CC GGGGCTCCT TTGG	
	GG CCCCAGGA GGCT	
	AC A	
GAM1217 LOC147664 3'	ATTTCACACAGAGCCCCT 38351 C _ GG	
	AGGGGCTC TGT TG AT	
	TCCCCGAG ACA AC TA	
	_ C TT	
GAM1217 LOC151031 5'	GGCATCCGCCTCAGAGCTCCCT 42156 _ C TTG_ A	
GGA	TCCAGGG GCTC TG GGAT CC	
	AGGTCCC CGAG AC CCTA GG	
	T _ TCCG C	
GAM1217 LOC166341 3'	CACACAGGAGCACCTGGA 40211 G _	
	TCCAGG GCTCCTGT TG	
	AGGTCC CGAGGACA AC	
	A C	
GAM1217 LOC196529 3'	GGTATCCTAGGTAAGAGCCCCT 42410 CTG_	
	AGGGGCTC TTGGGATAACC	
	TCCCCGAG GATCCTATGG	
	AATG	
GAM1217 LOC205313 5'	CATCGGGAAGCCCCTGGG 43593 _ T	
	TCCAGGGGCT CCTG TG	
	GGGTCCCCGA GGGC AC	
	A T	
GAM1217 LOC253612 3'	TATCCTAAGCCTCCTGGA 46256 _ CCTGT	
	TCCAGG GGCT TGGGATA	
	AGGTCC CCGA ATCCTAT	
	T _____	
GAM1217 LOC256683 5'	CGGCAAGCAGCCCCTGGA 46070 C _	
	TCCAGGGGCT CT GTTG	

				AGGTCCCCGA GA CGGC			
				C A			
GAM1217	LOC90288	3'	GTCACACAGGAGCCCTGGA	31111	G	TGG	
			TCCAGGG CTCCTGT GAT				
			AGGTCCC GAGGACA CTG				
			— CA_				
GAM1218	LOC124976	3'	AGCACGATCTGCAGCTTTGAA	36780	CT	TT	A
			TTCAAAGT TGCG ATCGT CT				
			AAGTTTCG ACGT TAGCA GA				
			— C_ C				
GAM1219	COX15	3'	TGGATCAAGAATGCATTAA	27791			
			TTAATGCGTTCTTGATCTA				
			AATTACGTAAGAACTAGGT				
GAM1219	CYP39A1	3'	TTAGTTCAAGAACACATT	18681	C	T	
			AATG GTTCTTGA CTAA				
			TTAC CAAGAACT GATT				
			A T				
GAM1220	C1orf1	3'	AAGAGGTTACTTCCTCCCA	6873	A	CGTC	GT
			TGG AGGGAG G CTCTT				
			ACC TCCTTC T GAGAA				
			C A__ TG				
GAM1220	CNGA3	3'	GAAGAGACATCCCCTCC	6978	A	GCGTCG	
			GGA GGGG GTCTCTTC				
			CCT CCCT CAGAGAAG				
			C A_____				
GAM1220	CUTL1	3'	GGAAGACGCTTCCTTCCA	7629		GG	
			TGGAAGGGAGCGTC TCT				
			ACCTTCCTTCGCAG AGG				
			A_				
GAM1220	ITGA5	3'	GGATTCTTCAAACGCTCCCTCC	30723	A	CGGTCTCT	
	CA		TGG AGGGAGCGT TCC				
			ACC TCCCTCGCA AGG				
			C AACTTCTT				
GAM1220	NAP1L4	3'	GGAAGAAACGCCGCTCCCTGCC	12590	A	T	GTC
	A		TGG AGGGAGCG CG TCTTCC				
			ACC TCCCTCGC GC AGAAGG				
			G C AA_				
GAM1220	THBD	3'	GAAGAGACAAACACCTCCC	5919	C_	CG	
			GGGAG GT GTCTCTTC				

			CCCTC CA CAGAGAAG		
			CA AA		
GAM1220 IMPACT	3'	AGAAACAACCCTCCCCCCA	20500	AA	C CG C
		TGG GGGAG GT GT TCT			
		ACC CCCTC CA CA AGA			
		CC C A_ A			
GAM1220 KIAA0193	3'	GGAAGAAAGGGACCCCTCTCCA	16544	_	AGC GGTC
		TGGA AGGG GTC TCTTCC			
		ACCT TCCC CAG AGAAGG			
		C _ GGAA			
GAM1220 KIAA0476	3'	GGAAGAACTGGTGCCCCCTCCA	16905	A A	GT C
		TGGA GGG GC CGGT TCTTCC			
		ACCT CCC CG GTCA AGAAGG			
		C _ TG _			
GAM1220 KIAA1337	3'	GAAGAGACCAGCCCTCCTCCCA	35984	AA	C C
		TGG GGGAG GT GGTCTCTTC			
		ACC TCCTC CG CCAGAGAAG			
		C_ C A			
GAM1220 MGC4415	3'	GAAGAGCACTCCCTTCC	25569	C	TCGGT
		GGAAGGGAG G CTCTTC			
		CCTTCCCTC C GAGAAG			
		A _			
GAM1220 PI4KII	3'	GGAAGGAACATCTCCCTTCCA	20481	CGTCG	CT
		TGGAAGGGAG GT CTTCC			
		ACCTTCCCTC CA GAAGG			
		TA_ AG			
GAM1220 TGOLN2	5'	GAAGAGGCTCGCCTCCC	32025	C C	
		GGGAG GT GGTCTCTTC			
		CCCTC CG TCGGAGAAG			
		_ C			
GAM1220 LOC126353	3'	AAGAGACCCGCTCCTCCA	36828	AG	TC
		TGGA GGAGCG GGTCTCTT			
		ACCT CCTCGC CCAGAGAA			
		_ _			
GAM1220 LOC151475	5'	AGGCCACACTGCCCTCCCA	41353	A _	C C
		TGG AGGG AG GT GGTCT			
		ACC TCCC TC CA CCGGA			
		C G A _			
GAM1220 LOC197423	5'	GGAAGAGACGTGCCTCCCCTT	38143	A _	T G
CA		TGGA GGGAG CG CG TCTCTTCC			

ACTT CCCTC GC GC AGAGAAGG
 C C T _
 GAM1220 LOC200138 5' GAAGAGACAGATCTCCTCCA 43279 AG C G
 TGGA GGAG GTC GTCTCTTC
 |||| ||| |||||
 ACCT CCTC TAG CAGAGAAG
 _ _ A
 GAM1220 LOC220753 5' GGAAAAGGAAATGCGCTCCCCT 44663 A CGG_ C
 CCA TGGA GGGAGCGT TCT TTCC
 |||| ||||| ||| ||||
 ACCT CCCTCGCG GGA AAGG
 C TAAA A
 GAM1220 LOC254559 5' GAAAGATAAGACGCCCCCTTTC 46195 A G_ C
 A TGGAAGGG GCGTC GTCT TTC
 ||||| |||| ||| |||
 ACTTTCCC CGCAG TAGA AAG
 C AA _
 GAM1220 LOC57795 5' AAGAGACATCCGCTCCCTCTCA 34358 GA TCG
 TG AGGGAGCG GTCTCTT
 || ||||| |||||
 AC TCCCTCGC CAGAGAA
 TC CTA
 GAM1220 LOC90120 5' GGCCGACGCCTCCCCCA 30853 AA _
 TGG GGGAG CGTCGGTC
 ||| |||| |||||
 ACC CCCTC GCAGCCGG
 C_ C
 GAM1220 LOC93613 5' GAGAGTCTCAACAGCCCCTTCC 35994 A _ C _ T
 A TGGAAGGG GC GT G G CTCTT
 ||||| || ||| |||||
 ACCTTCCC CG CA C C GAGAG
 _ A A T T
 GAM1221 DPH2L2 3' GGATATGCCATCATGGCA 7059 AA ATG
 TGCCATGGT CA GTTC
 ||||| || ||||
 ACGGTACTA GT TAGG
 CC A_
 GAM1221 DYRK1A 3' TGCATCATCACCATGGTA 28166 AACA T
 TGCCATGGT ATGGT CG
 ||||| |||| ||
 ATGGTACCA TACTA GT
 C_ C
 GAM1221 IL2RB 3' ACGAATTAATTACCTGGCA 6568 T CAA
 TGCCA GGTA TGGTTCGT
 |||| |||| |||||
 ACGGT CCATT ATTAAGCA
 _ A_
 GAM1221 VPS26 3' ACCTGTTTTACTACTATGGCA 11324 _ AT
 TGCCATGGTA ACA GGT
 ||||| ||| |||

ACGGTATCAT TGT CCA
 CATTT _
 GAM1221 CST7 5' ACAAACCATTTGCCCGGCA 9725 AT TAA C
 TGCC GG CAATGGTT GT
 ||| || ||||| ||
 ACGG CC GTTACCAA CA
 C_ _ A
 GAM1221 FOXD4 5' CGCGCTCATCACCATGGC 40281 AACAA _ T
 GCCATGGT ATG GT CG
 ||||| ||| ||
 CGGTACCA TAC CG GC
 C_ _ T C
 GAM1221 KIAA0427 3' ACGGCCTTTGTCAGCCATGGCA 16570 A_ T T
 TGCCATGGT ACAA GGT CGT
 ||||| ||| ||| ||
 ACGGTACCG TGTT CCG GCA
 AC T _
 GAM1221 KIAA0794 3' GGACTATTTCCATGACA 39182 C TAAC
 TG CATGG AATGGTTC
 || ||| |||||
 AC GTACC TTATCAGG
 A T_ _
 GAM1221 KIAA0820 3' AGCTCATAATTACCATGACA 34216 C CA _
 TG CATGGTAA ATG GTT
 || ||||| ||| ||
 AC GTACCATT TAC CGA
 A AA T
 GAM1221 KIAA1024 3' AATCATTACCATGGC 34233 ACA
 GCCATGGTA ATGGTT
 ||||| ||||
 CGGTACCAT TACTAA
 _
 GAM1221 KIAA1265 3' ACGAGAATGTTACCATGCA 35030 C ATGG
 TGC ATGGTAACA TTCGT
 || ||||| |||
 ACG TACCATTGT GAGCA
 _ AA_ _
 GAM1221 MGC2487 5' ACCTGCCACCAGCCATGGCA 23422 AACAA TC
 TGCCATGGT TGGT GT
 ||||| ||| ||
 ACGGTACCG ACCG CA
 ACC_ _ TC
 GAM1221 MRPS11 5' ACGAACCATTTCGCATATGG 23126 GTAAC
 CCATG AATGGTTCGT
 ||| |||||
 GGTAT TTACCAAGCA
 ACGC_
 GAM1221 MRPS11 5' ACGAACCATTTCGCATATGG 45376 GTAAC
 CCATG AATGGTTCGT
 ||| |||||

GGTAT TTACCAAGCA
ACGC_
GAM1221 PRO2015 5' ACAAACCAGTACCATGG 20584 ACAA C
CCATGGTA TGGTT GT
||||| |||||
GGTACCAT ACCAA CA
G__ A
GAM1221 TCL6 5' AGCTATTGCTCCATGACA 21758 C TAA
TG CATGG CAATGGTT
|| ||| |||||
AC GTACC GTTATCGA
A TC_
GAM1221 TCL6 5' AGCTATTGCTCCATGACA 21766 C TAA
TG CATGG CAATGGTT
|| ||| |||||
AC GTACC GTTATCGA
A TC_
GAM1221 TCL6 5' AGCTATTGCTCCATGACA 14841 C TAA
TG CATGG CAATGGTT
|| ||| |||||
AC GTACC GTTATCGA
A TC_
GAM1221 TCL6 5' AGCTATTGCTCCATGACA 15764 C TAA
TG CATGG CAATGGTT
|| ||| |||||
AC GTACC GTTATCGA
A TC_
GAM1221 LOC115265 3' ATGAACCATTTCACCATGGCA 36306 AAC
TGCCATGGT AATGGTTCGT
||||| |||||
ACGGTACCA TTACCAAGTA
CT_
GAM1221 LOC152674 5' ATTATTTCACTTACCATGGCA 41537 C__
TGCCATGGTAA AATGGT
||||| |||||
ACGGTACCATT TTATTA
CACT
GAM1221 LOC163782 3' GCCTGTCACCATGGCA 39966 A AT
TGCCATGGT ACA GGT
||||| ||| |||
ACGGTACCA TGT CCG
C _
GAM1221 LOC56965 5' GACTTGTTACCACCGCA 21456 CA AT
TGC TGGTAACA GGTT
||| ||||| |||
ACG ACCATTGT TCAG
CC _
GAM1222 RAD52 3' TCATTCTGAACCTTATCA 8790 CG A
TGA AG TTCAGAAATGA
||| || |||||

			ACT TC AAGTCTTACT			
			AT C			
GAM1222	RAD52	3'	TCATTCTGAACCTTATCA	28647	CG A	
			TGA AG TTCAGAAATGA			
			ACT TC AAGTCTTACT			
			AT C			
GAM1222	RAD52	3'	TCATTCTGAACCTTATCA	28655	CG A	
			TGA AG TTCAGAAATGA			
			ACT TC AAGTCTTACT			
			AT C			
GAM1222	RAD52	3'	TCATTCTGAACCTTATCA	28664	CG A	
			TGA AG TTCAGAAATGA			
			ACT TC AAGTCTTACT			
			AT C			
GAM1222	KIAA0193	3'	CCACAGAGTAGTGAATCTCTCA	16542	C	GA GACC
			TGA GAGATTCA AT GTGG			
			ACT CTCTAAGT TG CACC			
			_ GA AGA_			
GAM1222	KIAA0286	3'	CCAGGGCTCTGGATCTCATCA	33907	C	ATGA G
			TGA GAGATTGAGA CC TGG			
			ACT CTCTAGGTCT GG ACC			
			A C__ G			
GAM1222	LOXL4	3'	CCAGTCATCCCTGAATCTTGCC	25929	A	A_ CG
	A		TG CGAGATTCAG ATGAC TGG			
			AC GTTCTAAGTC TACTG ACC			
			C CC _			
GAM1222	LOC201696	3'	CCACTGGCATCTGAATTCATCA	31622	C A	A A _
			TGA GAG TTCAGA TG CC GTGG			
			ACT CTT AAGTCT AC GG CACC			
			A _ _ _ T			
GAM1223	B3GNT3	3'	AATAGGACCGCCCCCTC	15531	T A	
			GA GG GCGGTCCTGTT			
			CT CC CCGCCAGGATAA			
			C _			
GAM1223	CERD4	3'	GTGCCAGGACCACCCCACCT	14348	A A C	TT
			AG TGG GG GGTCTG GC			
			TC ACC CC CCAGGAC TG			
			C _ A CG			
GAM1223	CRY2	3'	AGGTTGGCAGGACCACCTCCGC	35730	A C	CT
	CT		AG TGGAGG GGTCTGTTG CT			

		TC GCCTCC CCAGGACGGT GA	
		C A TG	
GAM1223	NUP98	3' AGCATTTCCCACCCTCCATCT 18439	C_ TCCTGT
		AGATGGAGG GG TGCT	
		TCTACCTCC CC ACGA	
		CA CTTT__	
GAM1223	C20orf103	3' AGAACAACAAAAGCACTTTTCC 14568	CG_ CC_ C
		ATCT AGATGGAGG GT TGTTG TCT	
		TCTACCTTT CG ACAAC AGA	
		TCA AAA A	
GAM1223	CAMP-GEFII	3' AGCAACAGTTTGTCTCCAGTC 13879	_ TC
		GA TGGAGGCGG CTGTTGCT	
		CT ACCTCTGTT GACAACGA	
		G T_	
GAM1223	FIGN	3' AGAGCAACAGTATTCCTCAATC 45775	G C C
		GAT GAGG GGT CTGTTGCTCT	
		CTA CTCC TTA GACAACGAGA	
		A _ T	
GAM1223	FLJ10044	3' ACAGGACCCACCTCCATC 19709	C_
		GATGGAGG GGTCTGT	
		CTACCTCC CCAGGACA	
		AC	
GAM1223	FLJ22283	5' GGGCCAGACCGCCTCCACCT 25946	A C TT
		AG TGGAGGCGGTC TG GCTC	
		TC ACCTCCGCCAG AC CGGG	
		C _ _	
GAM1223	KIAA0939	3' AGAGCAAGCACATCTCCATCT 31056	CG C GT
		AGATGGAGG GT CT TGCTCT	
		TCTACCTCT CA GA ACGAGA	
		A_ C _	
GAM1223	KIAA1111	3' AACATCCCCCACCTCCATTT 46017	C TCC__
		AGATGGAGG GG TGTT	
		TTTACCTCC CC ACAA	
		A CCCCT	
GAM1223	PTPRN2	3' GAAAACGCACCTCCATC 28373	CG CCT GC
		GATGGAGG GT GTT TC	
		CTACCTCC CG CAA AG	
		A_ _ A_	
GAM1223	PTPRN2	3' GAAAACGCACCTCCATC 28368	CG CCT GC
		GATGGAGG GT GTT TC	

CTACCTCC CG CAA AG
 A_ _ A_
 GAM1223 LOC143188 5' AGCAACAGATTCTCCAGCT 40327 A CG C
 AG TGGAGG GTC TGTTGCT
 || ||||| || |||||
 TC ACCTCT TAG ACAACGA
 G _ _
 GAM1223 LOC146880 3' AACAAATCCCTTCATC 38256 C CC
 GATGGAGG GGT TGTT
 ||||| || |||
 CTACTTCC CTA ACAA
 _ CA
 GAM1223 LOC151507 3' AACAACTGCTCCATCT 39125 G CC
 AGATGGAG CGGT TGTT
 ||||| || |||
 TCTACCTC GTCA ACAA
 _ _
 GAM1223 LOC168576 5' GGCCAGGCCACCTCCATC 40254 C T TT
 GATGGAGG GG CCTG GCT
 ||||| || ||| |||
 CTACCTCC CC GGAC CGG
 A C _
 GAM1223 LOC196955 3' GACCTGGCCGCCTCCATC 37935 CT
 GATGGAGGCGGTC GTT
 ||||| ||||| |||
 CTACCTCCGCCGG CAG
 TC
 GAM1224 AKAP13 3' TCCTTCCCTCCCCACCCCG 43181 A ATTAA AAA
 CG GGT GGGGA AAGGA
 || ||| ||||| |||||
 GC CCA CCCCT TTCCT
 C C _ CCC
 GAM1224 BCL2L2 3' CCTCCTTTCCCCTGCCCTTG 10260 TATTA AA
 CGAGG AGGGGAAA AGG
 ||||| ||||| |||
 GTTCC TCCCCTTT TCC
 CG _ CC
 GAM1224 CD244 3' CCTTTTCTCCCCTCTC 18525 GTATTA A
 GAG AGGGGA AAAAGG
 ||| ||||| |||||
 CTC TCCCCT TTTTCC
 _ C
 GAM1224 CDC5L 5' CCTTTCAGCCACCCAATATCTC 6923 AA _ AAA
 G CGAGGTATT GG GG AAAGG
 ||||| || || |||||
 GCTCTATAA CC CC TTTCC
 C_ A GAC
 GAM1224 DACH 5' CCTTTTTCCTTCCCCTC 28037 TATT
 GAGG AAGGGGAAAAAAGG
 |||| ||||| |||||

			CTCC	TTCCCCTTTTTTCC			
			CC__				
GAM1224	DACH	5'	TCCTTTTCTCCCCCTTCTC	28041	TATTAA	A	
			GAGG	GGGGA AAAAGGA			
			CTCT	CCCCT TTTTCCT			
			TC__	C			
GAM1224	DGKE	3'	TCCTTTTTTCAGCAAAATACTT	9724	AAGGG		
	C		GAGGTATT	GAAAAAAGGA			
			CTTCATAA	CTTTTTTCCT			
			AACGA				
GAM1224	EIF4G2	5'	CCTTCCCTCCCCCTTTTTTTTG	7116	TATT	AAAA_	
			CGAGG	AAGGGG AAGG			
			GTTTT	TTCCCC TTCC			
			TT__	CTCCC			
GAM1224	ELMO1	3'	TCCTCCTTTCCCTCTCTC	28205	TATTA	AA	
			GAGG	AGGGGAAA AGGA			
			CTCT	TCCCCTTT TCCT			
			C__	CC			
GAM1224	FKBP1A	3'	TCCTCTTCCCCTTTCTCCTCG	6476	TATT	AAA	
			CGAGG	AAGGGGAA AGGA			
			GCTCC	TTCCCCTT TCCT			
			TCT_	C__			
GAM1224	GFRA2	3'	TCCTCCTTTCCCCTTTCTCTTT	7242	TATT__	AA	
	CCTC		GAGG	AAGGGGAAA AGGA			
			CTCC	TTCCCCTTT TCCT			
			TTTCTCT	CC			
GAM1224	GRM6	3'	TCCTTTCTTCTCTTGCCTCG	6510	TTA	A	
			CGAGGTA	AGGGGAA AAAGGA			
			GCTCCGT	TCTCCTT TTTTCCT			
			__	C			
GAM1224	IGHMBP2	3'	CCCTTCCCCTTACTCCCCG	7938	A TAT	AAAA	
			CG GG	TAAGGGGAA GG			
			GC CC	ATTCCCCTT CC			
			C TC_	C__			
GAM1224	LFG	3'	TCCTCTCCTCCGGGCCCTC	37697	TA AA	AAAA	
			GAGG	TT GGGGA AGGA			
			CTCC	GG CTCCT TCCT			
			CC GC	C__			
GAM1224	LMO1	5'	TCCTCTTTTCCCCTTCTCTCT	8129	TATTAA	A	
	C		GAGG	GGGGAAAA AGGA			

		CTCT CCCCTTTT TCCT		
		CTCTTC C		
GAM1224 PGD	3'	CCCTTTTTCCTTTACTC 38524 GTAT AA		
		GAG TAAGGGGAAAA GG		
		CTC ATTCCTTTT CC		
		_____ C_		
GAM1224 PMX1	5'	TCCTCTCTCCCCTTGTTATT 22918 T AAAAA		
		GGTA TAAGGGG AGGA		
		TTAT GTTCCCC TCCT		
		T CTCTC		
GAM1224 PMX1	5'	TCCTCTCTCCCCTTGTTATT 13783 T AAAAA		
		GGTA TAAGGGG AGGA		
		TTAT GTTCCCC TCCT		
		T CTCTC		
GAM1224 PTGS1	3'	TCCCCTCTTCTGCTAATACCTC 6678 _____		
		GAGGTATTA AGGGGA		
		CTCCATAAT TCCCCT		
		CGTCTTC		
GAM1224 PTGS1	3'	TCCCCTCTTCTGCTAATACCTC 27899 _____		
		GAGGTATTA AGGGGA		
		CTCCATAAT TCCCCT		
		CGTCTTC		
GAM1224 PYGM	5'	TCCTCTCCTCCCCTTGCCCTC 12129 TAT AAAAA		
		GAGG TAAGGGGA AGGA		
		CTCC GTTCCCCT TCCT		
		C_ CCTC		
GAM1224 RBBP5	3'	CCTCTCCCCAGATACCTC 11485 AA AAAAA		
		GAGGTATT GGGGA AGG		
		CTCCATAG CCCCT TCC		
		A_ C_		
GAM1224 REQ	3'	CCTTTCTTCCCTTGACGCTCG 12950 _ ATTA A		
		CGAG GT AGGGGAA AAAGG		
		GCTC CA TTCCCTT TTTCC		
		G CG_ C		
GAM1224 RORB	5'	TCCTTTTTCCCCCTTGTTCT 13787 TAT _		
		AGG TAAGGGG AAAAAAGGA		
		TCC GTTCCCC TTTTTCCT		
		TT_ C		
GAM1224 RUNX1	3'	CCTCTCTTCCCCCAATATCTC 7496 AA AAA		
		GAGGTATT GGGGAA AGG		

CTCTATAA CCCCTT TCC
 CC CTC
 GAM1224 SC5DL 3' TCCTCTTCTCCCCTCACTTT 43696 ATTA A A
 GAGGT AGGGGA AA AGGA
 |||| ||||| || ||||
 TTTCA TCCCCT TT TCCT
 C__ C C
 GAM1224 SIAT1 5' CCTTCTCCCATACCTTG 8974 TAAG AAA
 CGAGGTAT GGGG AAGG
 ||||| ||| ||||
 GTTCCATA CCCT TTCC
 ____ C__
 GAM1224 SOX4 3' CCTCTTTTCCCCTTGCCCCCTC 9074 TAT A
 GAGG TAAGGGGAAAA AGG
 ||| ||||| |||
 CTCC GTTCCCCTTTT TCC
 CCC C
 GAM1224 TBL1X 3' CCTCTCCTCCCCTTGCGCTCG 12181 _ TTA AAAA
 CGAG GTA AGGGGA AGG
 ||| ||| ||||| |||
 GCTC CGT TCCCCT TCC
 G _ CCTC
 GAM1224 TIAL1 3' TCCTCCCCCTGTAATACCTC 22742 _ AAAAA
 GAGGTATTA AGGGG AGGA
 ||||| |||| |||
 CTCCATAAT TCCCC TCCT
 G C__
 GAM1224 ARHGEF2 3' CCTTTCTCCTCTCCCCTC 11090 TATTA AA
 GAGG AGGGGA AAAGG
 ||| ||||| ||||
 CTCC TCTCCT TTTCC
 CC__ C_
 GAM1224 CECR1 3' TCCTTCTTTCCCCTTTTGTCTT 18885 GT TT A
 G CGAG A AAGGGGAAA AAGGA
 ||| | ||||| ||||
 GTTC T TTCCCCTTT TTCCT
 TG T_ C
 GAM1224 DKFZp761K1824 3' CCTTCCTCCCCTTTCTC 19059 TATT AAA
 GAGG AAGGGGA AAGG
 ||| ||||| |||
 CTCT TTCCCCT TTCC
 ____ CC_
 GAM1224 EIF4B 3' TCCTTTTTTTTTTTTAACCCC 37401 TA
 GG TTAAGGGGAAAAAAGGA
 || ||||| |||||
 CC AATTTTTTTTTTTTCCT
 CC
 GAM1224 FBXO21 3' TCCTTTTTTCTTAGACACATC 27326 ATTAAG
 GGT GGGAAAAAAGGA
 ||| ||||| |||||

CTA TTCTTTTTTCCT
 CACAGA
 GAM1224 FLJ11715 5' TCCCCTTTTCCTCTTATCCC 23789 TAT AA
 GG TAAGGGGAAAA GGA
 || ||||| ||
 CC ATTCTCCTTTT CCT
 CT_ CC
 GAM1224 FLJ11939 3' CCTCTTCTCTTATCCTC 23990 TAT AAAA
 GAGG TAAGGGGA AGG
 ||| ||||| ||
 CTCC ATTCTCTT TCC
 T_ C_
 GAM1224 FLJ12619 5' TCCCTTTTTCCCGTCTGACCCC 25211 TA AG_ A
 GG TTA GGGAAAAA GGA
 || ||| ||||| ||
 CC AGT CCCTTTTTT CCT
 CC CTG C
 GAM1224 FLJ12700 3' TCCTCTTTCCTCTAAACCTC 24416 ATTA AA
 GAGGT AGGGGAAA AGGA
 |||| ||||| ||
 CTCCA TCTCCTTT TCCT
 AA_ C_
 GAM1224 FLJ20739 3' CCTTTTTTCCCCTACC 33704 ATTA
 GGT AGGGGAAAAAAGG
 ||| |||||
 CCA TCCCCTTTTTTCC

 GAM1224 FLJ21945 3' TCCTTTTCCCCCCTTCCTT 24868 TATT AA
 GAGG AAGGGG AAAAGGA
 |||| ||||| |||||
 TTCC TTCCCC TTTTCCT
 _____ CC
 GAM1224 FLJ30567 3' CCCTTTTTTCTATACCT 29629 TAAG A
 AGGTAT GGGAAAAA GG
 |||| ||||| ||
 TCCATA TCCTTTTTT CC
 _____ C
 GAM1224 KIAA0010 3' CCTCCTTTCCCCTGGGCTGCG 16130 A ATTA AA
 CG GGT AGGGGAAA AGG
 || ||| ||||| ||
 GC TCG TCCCCTTT TCC
 G GG_ CC
 GAM1224 KIAA0237 3' TCCAGCCCTCCTAATACCTC 16454 A_ AAAAAA
 GAGGTATTA GGGG GGA
 ||||| ||| ||
 CTCCATAAT TCCC CCT
 CC GA____
 GAM1224 KIAA0426 3' CCTCTTTTCCCCCTAGAAGAAC 16309 A_ A A
 C GGT TTA GGGGAAAA AGG
 ||| ||| ||||| |||

CCA GAT CCCCTTTT TCC
 AGAA C C
 GAM1224 KIAA0427 5' CCTCCCTTCCCCTTCCCTGCC 16573 TT_ AAA
 GGTA AAGGGGAA AGG
 ||| ||||| |||
 CCGT TTCCCCTT TCC
 CCC CCC
 GAM1224 KIAA0792 5' TCCTTCCTTCCCCTAGTGTCTG 16215 G GT A AA
 G C AG ATTA GGGGAA AAGGA
 || ||| ||||| |||||
 G TC TGAT CCCCTT TTCCT
 G TG _ CC
 GAM1224 KIAA1052 3' CCTCCTTCCCCCTTTGACTT 17310 ATT A AA
 AGGT AAGGGG AA AGG
 ||| ||||| |||
 TTCA TTCCCC TT TCC
 GT_ C CC
 GAM1224 KIAA1205 3' CCTCTCCCCTTGCCCCG 34705 A TTA AAAA
 CG GGTA AGGGGA AGG
 || ||| ||||| |||
 GC CCGT TCCCCT TCC
 C _ C_
 GAM1224 KIAA1322 3' CCAGGGTCCCTTAACACCTCG 36021 A AAAAAA
 CGAGGT TTAAGGGG GG
 ||||| ||||| |||
 GCTCCA AATTCCT CC
 C GGGA_
 GAM1224 KIAA1467 3' CCCTTTTCCTTAGACCCCG 35452 A A GG AAAA
 CG GGT TTAAGG AA GG
 || ||| ||||| |||
 GC CCA GATTCC TT CC
 C _ TT C_
 GAM1224 KIAA1674 3' CCTCCTTTCCCCTGGGGGCCCT 34110 TA A_ AA
 C GAGG TT AGGGGAAA AGG
 ||| || ||||| |||
 CTCC GG TCCCCTTT TCC
 CG GG CC
 GAM1224 KIAA1819 5' TCCTCTCTATTAATACCTC 34536 _
 GAGGTATTA AGGGGA
 ||||| |||||
 CTCCATAAT TCTCCT
 TATC
 GAM1224 KIAA1918 3' TCCTTTTCTCCCCTCATTTCT 36218 TATTA A
 C GAGG AGGGGA AAAAGGA
 ||| ||||| |||||
 CTCC TCCCCT TTTTCCT
 TTTAC C
 GAM1224 KIAA1949 5' CCTCCTTTCCCCTCTTCCCTGG 44209 G TATTA AA
 C AGG AGGGGAAA AGG
 ||| ||||| |||

G TCC TCCCCTTT TCC
 G CTTC_ CC
 GAM1224 KIAA1949 5' CCTCCTTTCCCCTCTTCCCTGG 46668 G TATTA AA
 C AGG AGGGGAAA AGG
 ||| ||||| |||
 G TCC TCCCCTTT TCC
 G CTTC_ CC
 GAM1224 KIAA1949 5' CCTCCTTTCCCCTCTTCCCTGG 46713 G TATTA AA
 C AGG AGGGGAAA AGG
 ||| ||||| |||
 G TCC TCCCCTTT TCC
 G CTTC_ CC
 GAM1224 MAB21L2 3' CCTTCTTTCCCCCTATCCT 13151 T TAA A
 AGG AT GGGGAAA AAGG
 ||| ||||| |||
 TCC TA CCCCTTT TTCC
 _ TC_ C
 GAM1224 MGC16491 5' TCCTCCTCCCCTTAACCACC 27502 A_ AAAA
 GGT TTAAGGGGA AGGA
 ||| ||||| |||
 CCA AATTCCCCT TCCT
 CC CC_
 GAM1224 MYO18B 3' TCCTCCATGCTCCCTTAATCCC 26332 T _AAAAA
 GG ATTAAGGG G AGGA
 || ||||| | |||
 CC TAATTCCC C TCCT
 C TGTACC
 GAM1224 OSBPL2 3' CCTTTCTTCTCACACGTCG 29319 G ATTAAG A
 CGA GT GGGAA AAAGG
 ||| || |||| |||||
 GCT CA CTCTT TTTCC
 G CA_ C
 GAM1224 OSBPL2 3' CCTTTCTTCTCACACGTCG 16851 G ATTAAG A
 CGA GT GGGAA AAAGG
 ||| || |||| |||||
 GCT CA CTCTT TTTCC
 G CA_ C
 GAM1224 P66 3' CCTTTTCTCCCCACTCCTC 21845 TATTAA A
 GAGG GGGGA AAAAGG
 ||| |||| |||||
 CTCC CCCCT TTTTCC
 TCA_ C
 GAM1224 phospho1 5' CCTGCGCCCCAATACCTC 40062 AA AAAAA
 GAGGTATT GGGG AGG
 ||||| ||| |||
 CTCCATAA CCCC TCC
 _ GCG_
 GAM1224 SDS3 3' CCCCTTTTCCCTGAACCACG 34319 A ATTAA AA
 CG GGT GGGGAAAA GG
 || ||| ||||| ||

			GC CCA TCCCTTTT CC		
			A AG__ CC		
GAM1224	SIMRP7	3'	TCCTCTTTTCCCCTGGAAACCT 44373	A A	A
		C	GAGGT TT AGGGGAAAA AGGA		
			CTCCA AG TCCCCTTTT TCCT		
			A G C		
GAM1224	SP192	5'	TCCCCTTTTCCCCTTTCCCCT 22299	TATT	AA
			AGG AAGGGGAAAA GGA		
			TCC TTCCCCTTTT CCT		
			CCT_ CC		
GAM1224	STMN3	3'	TCCTTCTTTCCCTTGGACGCC 18039	TA A	A
			GG TT AGGGGAAA AAGGA		
			CC AG TTCCCTTT TTCCT		
			GC G C		
GAM1224	LOC126917	3'	CCTCTCCTCTGACCCCTC 36868	TA A	AAAA
			GAGG TTA GGGGA AGG		
			CTCC AGT CTCCT TCC		
			CC _ C__		
GAM1224	LOC144114	5'	TTTCCCCTCAATGCCCG 39995	A A	
			CG GGTATT AGGGGAAA		
			GC CCGTAA TCCCCTTT		
			C C		
GAM1224	LOC144473	3'	TCCTCTTTTCCCCCTTTTC 40415	TATTAA	A
			GAGG GGGGAAAA AGGA		
			CTTT CCCCTTTT TCCT		
			TC__ C		
GAM1224	LOC144866	5'	CCTTTTTTCCTTTTCACC 40478	ATT	
			GGT AAGGGGAAAAAAGG		
			CCA TTTTCCTTTTTTCC		
			C__		
GAM1224	LOC145815	5'	CCTCTTTTCCCCCATGCT 40603	TAA	A
			GGTAT GGGGAAAA AGG		
			TCGTA CCCCTTTT TCC		
			CC_ C		
GAM1224	LOC146823	3'	TCCTCTTCTCCTACAAATACCT 40750	A__	AAA
		C	GAGGTATT AGGGGAA AGGA		
			CTCCATAA TCCTCTT TCCT		
			ACA C__		
GAM1224	LOC153146	5'	CCTCCTCCCAGATACCTC 41577	AAG	AAAA
			GAGGTATT GGGA AGG		

		CTCCATAG CCCT TCC		
		A__ CC__		
GAM1224	LOC155072 5'	CCTTCTTCCCCTTATCC	41759	TAT AA
		GG TAAGGGGAA AAGG		
		CC ATTCCCCTT TTCC		
		T__ C__		
GAM1224	LOC155072 3'	TCCTCCTTTCCCCTCTCCTT	41762	TATTA AA
		GAGG AGGGGAAA AGGA		
		TTCC TCCCCTTT TCCT		
		TC__ CC		
GAM1224	LOC202868 5'	CCTTCTTCCCCTTATCC	43446	TAT AA
		GG TAAGGGGAA AAGG		
		CC ATTCCCCTT TTCC		
		T__ C__		
GAM1224	LOC202868 3'	TCCTCCTTTCCCCTCTCCTT	43450	TATTA AA
		GAGG AGGGGAAA AGGA		
		TTCC TCCCCTTT TCCT		
		TC__ CC		
GAM1224	LOC203260 3'	CCTTTTTTCCCTTATCCCC	43024	TATTA
		GG AGGGGAAAAAAGG		
		CC TTCCCTTTTTTCC		
		CCTA_		
GAM1224	LOC221431 3'	TCCTCAAATACCTCAAATACCT	44227	AA GAAAAA
	C	GAGGTATT GGG AGGA		
		CTCCATAA TCC TCCT		
		AC ATAAAC		
GAM1224	LOC221814 5'	TCCTTTTTTTGTAAATACCT	45097	AAGGG
		AGGTATT GAAAAAAGGA		
		TCCATAA TTTTTTTCCT		
		AATG_		
GAM1224	LOC254532 5'	TCCTCCCCTCCCCTTCCCTTG	46214	TATT AAAA
		CGAGG AAGGGGA AGGA		
		GTTCC TTCCCCT TCCT		
		C__ CCCC		
GAM1224	LOC89944 3'	TCCCCTTTCCTTCCCCTCG	44004	GTATTA AAA
		CGAG AGGGGAAA GGA		
		GCTC TTCCCTTT CCT		
		ACCC__ CC__		
GAM1225	KCNA6 5'	ATCCCCAGCGCCAGGTCACC	8016	CAT AGA AA
		GG CC GGGCGCTG GAT		

CC GG CCCGCGAC CTA
 ACT A__ CC
 GAM1225 MGAM 3' CTCATTCTGGATCCA 35823 C GGCGC A
 TGG ATCCAGAG TGA G
 ||| ||||| |||
 ACC TAGGTCTT ACT C
 _ _ _ C
 GAM1225 C16orf5 3' TCAGTGCTGATGCCA 15056 CAGAG
 TGGCATC GGCGCTGA
 ||||| |||||
 ACCGTAG TCGTGA CT

 GAM1225 KIAA1303 3' CTCCAGGTCTCTGGACTCCA 32833 CA G G A
 TGG TCCAGAGG C CTG AG
 ||| ||||| | |||
 ACC AGGTCTCT G GAC TC
 TC _ _ C
 GAM1225 NFASC 3' CTTCAGCCCCGGGTGCCA 34829 AGA C
 TGGCATCC GGG GCTGAAG
 ||||| ||| |||||
 ACCGTGGG CCC CGACTTC

 GAM1225 NIR3 3' ATCTCCAAGTGTCTGCTGCTGCCA 32925 CAG GA_
 TGGCATC AGGGCGCT AGAT
 ||||| ||||| |||
 ACCGTGG TCCTGTGA TCTA
 _ ACC
 GAM1225 NYD-SP25 3' TCTCCACTTTCTGGAACCA 27294 CA CGC A
 TGG TCCAGAGGG TG AGA
 ||| ||||| |||
 ACC AGGTCTTTC AC TCT
 A_ _ C
 GAM1225 LOC132422 5' ATCCCCAGCGCCCTGCGGGCC 37369 AT AG AA
 GGC CC AGGGCGCTG GAT
 ||| ||| ||||| |||
 CCG GG TCCGCGAC CTA
 _ CG CC
 GAM1225 LOC143915 3' ATCTTCAGCAGCTCTGGATGCT 40376 GGC
 GGCATCCAGAG GCTGAAGAT
 ||||| |||||
 TCGTAGGTCTC CGACTTCTA
 GA_
 GAM1225 LOC151178 5' ATCTCCTGTCTCTGGACAACA 39070 GCA G CT A
 TG TCCAGAGG CG GA GAT
 || ||||| ||| |||
 AC AGGTCTCT GT CT CTA
 AAC _ C_ _
 GAM1225 LOC166042 5' ATCTTCAGTTAGGCCTGACACC 40197 CA CAGA _
 A TGG TC GGGC GCTGAAGAT
 ||| || ||| |||||

ACC AG TCCG TGA CTTCTA
 AC ____ GAT
 GAM1225 LOC196759 3' ATCTCCAAGTTTCTGGGCGCCA 42293 AT G GC A
 TGGC CCAGAGG C TG AGAT
 |||| ||||| | ||||
 ACCG GGTCTTT G AC TCTA
 CG _A_ C
 GAM1225 LOC197201 3' AGACGCCCTCTGAAGCCA 42460 ATC _
 TGGC CAGAGGGCG CT
 |||| ||||| ||
 ACCG GTCTCCCGC GA
 AA_ A
 GAM1225 LOC254755 3' ATCCTCAGCGCCTGCCAGGAGC 46486 A AGA_ A
 CA TGGC TCC GGGCGCTGA GAT
 |||| || ||||| ||
 ACCG AGG TCCGCGACT CTA
 _ ACCG C
 GAM1226 ARCN1 3' AACAAAGTATATCTAACCCA 7364 A C GC CAC
 TG GGT AG AT ACTTGTT
 || ||| || |||||
 AC CCA TC TA TGAACAA
 _ A TA ____
 GAM1226 CCND2 3' AACAAAGTGTGATGCCATATC 7510 CA
 GGT GGCATCACACTTGTT
 ||| |||||
 CTA CCGTAGTGTGAACAA
 TA
 GAM1226 LIFR 3' AACAAAGTGTGACACTGACC 8098 GCA
 GGTCAG TCACACTTGTT
 ||||| |||||
 CCAGTC AGTGTGAACAA
 AC_
 GAM1226 MYCBP 3' GAATGTCCGTGATGCCTACCTC 14724 C ACT
 A TGAGGT AGGCATCAC TGTTT
 ||||| ||||| ||||
 ACTCCA TCCGTAGTG GTAAG
 _ CCT
 GAM1226 WARS 5' AACAAATCCTCTGACCTCA 33412 CATCACAC
 TGAGGTCAGG TTGTT
 ||||| ||||
 ACTCCAGTCT AACAA
 CCTA____
 GAM1226 KLK15 3' AACAAAGAGGCCCAATCTCA 23262 CA ATCACA
 TGAGGT GGC CTTGTT
 ||||| || |||||
 ACTCTA CCG GAACAA
 AC GA____
 GAM1226 KLK15 3' AACAAAGAGGCCCAATCTCA 28860 CA ATCACA
 TGAGGT GGC CTTGTT
 ||||| || |||||

ACTCTA CCG GAACAA
 AC GA____
 GAM1226 LOC118738 3' ACAAGTCCCTGCCTCA 37191 T CATCAC
 TGAGG CAGG ACTTGT
 ||||| |||| |||||
 ACTCC GTCC TGAACA
 _ C____
 GAM1226 LOC132241 5' GTCTGGAACGCCTGACCTCA 37022 A__ C
 TGAGGTCAGGC TCA AC
 ||||| |||| ||||
 ACTCCAGTCCG GGT TG
 CAA C
 GAM1226 LOC158434 3' GAACAAATATCAAACACTGACC 41984 GCATCACAC_
 TCA TGAGGTCAG TTGTTC
 ||||| ||||
 ACTCCAGTC AACAAG
 ACAAACTATA
 GAM1226 LOC158549 5' GAGCCATGACGCCTGGCCTCA 42008 A CACTT
 TGAGGTCAGGC TCA GTTC
 ||||| |||| ||||
 ACTCCGGTCCG AGT CGAG
 C AC____
 GAM1227 HK1 5' ATGCAACAAGGACTTCA 27268 TAGA T
 TGAAGTTCT TGTT GCAT
 ||||| |||| ||||
 ACTTCAGGA ACAA CGTA

 GAM1227 HK1 5' ATGCAACAAGGACTTCA 27274 TAGA T
 TGAAGTTCT TGTT GCAT
 ||||| |||| ||||
 ACTTCAGGA ACAA CGTA

 GAM1227 HK1 5' ATGCAACAAGGACTTCA 27271 TAGA T
 TGAAGTTCT TGTT GCAT
 ||||| |||| ||||
 ACTTCAGGA ACAA CGTA

 GAM1227 HPIP 3' CTATGCAAATGCATGCAAATAC 21738 A TC AG ____
 TCCA TG AGT TT ATGT TTGCATAG
 || ||| || ||||| |||||
 AC TCA AA TACG AACGTATC
 C TA CG TA
 GAM1228 CELSR2 3' CTGGGGGGCCTGCCCTCA 7106 ATGA A
 TGAG CAGGCTTC TTAG
 ||| ||||| ||||
 ACTC GTCCGGGG GGTC
 CCC_ _
 GAM1228 ERAP140 3' CTCCTTTCTGCCATCATCTCA 37085 CA TTCATTA
 TGAGATGA GGC GAAG
 ||||| || ||||

ACTCTACT CCG CTTC
 A_ TCTTTC_
 GAM1228 FLJ13910 3' CTTCTGCAAAGCGTATCATCTC 23055 CAG CAT
 A TGAGATGA GCTT TAGAAG
 ||||| ||| |||||
 ACTCTACT CGAA GTCTTC
 ATG AC_
 GAM1228 HCA127 3' TCATTAGAAGCTCCTACCCTCA 20759 C_ G_ ATTA
 TCTCA GATGA AG CTTC GA
 |||| || |||| ||
 CTACT TC GAAG CT
 CCCA CTC||| ATTA
 GAM1228 KIAA1009 3' CTTCTAGTGTACCCATCATCCA 17052 A CA CTT
 TG GATGA GG CATTAGAAG
 || |||| || |||||
 AC CTACT CC GTGATCTTC
 _ AC AT_
 GAM1228 Kv6.3 3' TCTCTGAGCCTGTCTCCCA 28566 A T T TT
 TG GA GACAGGCT CA AGA
 || ||||| || |||
 AC CT CTGTCCGA GT TCT
 C _ _ C_
 GAM1228 PRO0365 5' CTTCTAATGAAAACCTTGGTCAT 15389 _ GC
 CTT GAGATGAC AG TTCATTAGAAG
 ||||| || |||||
 TTCTACTG TC AAGTAATCTTC
 GT AA
 GAM1228 LOC152742 3' CTTCTAATGGTGACTTCCATCT 41544 AC GCT
 CA TGAGATG AG TCATTAGAAG
 ||||| || |||||
 ACTCTAC TC GGTAATCTTC
 CT AGT
 GAM1229 CYR61 3' ACTGCAAACAGAAATCAGGTGT 7276 _ AAGACA
 T AACAC TGATT TTGCAGT
 |||| |||| |||||
 TTGTG ACTAA AACGTCA
 G AGACA_
 GAM1229 LRP4 5' ACTGCAATGTTAACAACGGT 32195 ATTAA
 ACTG GACATTGCAGT
 ||| |||||
 TGGC TTGTAACGTCA
 AACAA
 GAM1229 NFE2L1 3' GACTACAATGTCTTTATT 9198 T C
 GAT AAGACATTG AGTC
 || ||||| |||
 TTA TTCTGTAAC TCAG
 T A
 GAM1229 TMOD2 3' ATTGTATCTTAATCA 15859 CAT
 TGATTAAGA TGCAGT
 ||||| |||||

ACTAATTCT ATGTTA

GAM1229 ACTR1A 3' GACTGCAGT GCGCTTAACCA 31533 A A_
TG TTAAG CATTGCAGTC
|| |||| |||||
AC AATTC GTGACGTCAG
C GC

GAM1229 C20orf130 3' ACTGGCCTTGATCAGTGT 30934 ACATTG
ACACTGATTAAG CAGT
||||||| |||
TGTGACTAGTTC GTCA
CG____

GAM1229 FLJ22087 5' GACTGGTACCTCTTAATCAG 22613 CATTG
CTGATTAAGA CAGTC
||||||| |||
GACTAATTCT GTCAG
CCATG

GAM1229 KIAA0940 3' GACTGCATGTTTACTTAATCAG 17148 A ____ T
GTT AAC CTGATTAAG ACAT GCAGTC
|| ||||| ||| |||||
TTG GACTAATTC TGTA CGTCAG
_ ATT _

GAM1229 KIAA1463 3' GACCAGCATGCTAATCAGTGT 35771 A A T A_
ACACTGATTA G CAT GC GTC
||||||| | ||| |||
TGTGACTAAT C GTA CG CAG
_ _ _ AC

GAM1229 MGC2541 3' CTGTAGCTCAATCAGTGT 27963 A ACA
ACACTGATT AG TTGCAG
||||||| || |||||
TGTGACTAA TC GATGTC
C ____

GAM1229 MIL1 3' ACCAAAATAGTCCTAATCAGT 17665 A _ GCA
ACTGATTA GAC ATT GT
||||||| ||| ||| |||
TGACTAAT CTG TAA CA
C A AAC

GAM1229 MUC17 3' GACTGCAACATCTTTCA 45259 TT CA
TGA AAGA TTGCAGTC
||| ||| |||||
ACT TTCT AACGTCAG
_ AC

GAM1229 PRO1257 3' ACTGCTGTTAAGCAATGTT 20656 C ATTAA TT
AACA TG GACA GCAGT
||| || ||| |||||
TTGT AC TTGT CGTCA
A GAA__ _

GAM1229 RNF2 3' ACTGCAATTATTCAGT 14074 T AGAC
ACTGA TA ATTGCAGT
||||| || |||||

T G A C T A T T A A C G T C A
 T ____
 GAM1229 LOC164397 5' ACAGCATCCTCATCAGTGT 40147 T A A C A T A
 A C A C T G A T G A T G C G T
 ||||||| || ||| ||
 T G T G A C T A C T A C G C A
 ____ C C T A
 GAM1230 ACP2 3' AA A C T G G C A G T C A G T G T T 7318 A G T G
 A A C A C T A C T G C G T T T
 ||||| ||||| | |||||
 T T G T G A T G A C G C A A A
 C _ G T
 GAM1230 AGRN 3' G G G G C C A G C C A G T G T C T G 38536 C T A
 C A A C T G G C T G G T T T T
 || |||||||||
 G T T G A C C G A C C G G G G
 C T G
 GAM1230 E2F3 3' A A A T C C T A C C A G T T A T G T 7664 C C T T
 A C A T A A C T G G G G T T T
 ||| ||||| || |||
 T G T A T T G A C C C C A A A
 _ A T T
 GAM1230 LIMD1 3' T G A A G C C A G C C A A T G T G T T 15502 T A A C
 A A C A C T G G C T G G T T T T A
 ||||| |||||||||
 T T G T G A C C G A C C G A A G T
 T A ____
 GAM1230 NCALD 3' T A A A A C C A G C C T G T G A T G T T 25745 C T A T
 A A C A A C G G C T G G T T T T A
 ||||| || |||||||||
 T T G T T G C C G A C C A A A A T
 A G _ T
 GAM1230 SHANK2 3' G G A G C C A G C C A G C G T G 14684 T A A
 C A C C T G G C T G G T T T T
 ||| |||||||||
 G T G G A C C G A C C G A G G
 C ____
 GAM1230 SIM2 3' A C C A G C A G T G T T T A A 11516 A A C T G
 T T A A A C A C T G C T G G T
 ||||||| |||||
 A A T T T G T G A C G A C C A

 GAM1230 SPON1 3' T A A A A C C A G G T T A A T G G C T A A 31303 A A C T G G
 T T A C A T A A C C T G G T T T T A
 ||| || ||||| |||||||
 A A T G T A T T G G A C C A A A A T
 C G A ____
 GAM1230 DKFZP564L0864 3' C A G C C A T T T A G C A T T T A A 35919 C A C
 T T A A A C T A A T G G C T G
 ||||| ||||| |||||

AATTT GATT ACCGAC
 AC T
 GAM1230 DKFZp761B1514 3' TAAAAAATGACAGTTTGTGTTT 26047 T GCTGG
 AA TTAACAC AACTG TTTTA
 ||||| |||| ||||
 AATTTGTG TTGAC AAAAT
 T AGTAA
 GAM1230 FBXO9 3' CAGTCCTATTAGTGTTTAA 27258 CT _
 TTAAACACTAA GG CTG
 ||||| || ||||
 AATTTGTGATT CC GAC
 AT T
 GAM1230 KDELR3 3' TAAACAGAAAAGTGTTTAG 13724 AACTGG
 TTAAACACT CTGGTTTAA
 ||||| |||||
 GATTGTGA GACCAAAAT
 AAA__
 GAM1230 KIAA0914 3' ATTACCAGTTAGCTTTTAA 17034 CA C
 TTAAA CTAAGTGG TGGT
 |||| ||||| ||||
 AATTT GATTGACC ATTA
 TC _
 GAM1230 SKIP 3' TGAAACCAGCTAGTGTGT 28264 TA
 ACAC ACTGGCTGGTTTAA
 ||| |||||
 TGTG TGATCGACCAAAGT
 _
 GAM1230 SKIP 3' TGAAACCAGCTAGTGTGT 18600 TA
 ACAC ACTGGCTGGTTTAA
 ||| |||||
 TGTG TGATCGACCAAAGT
 _
 GAM1230 ZER6 3' AAAACCAGCCAAGATCTGTT 31738 CTAAC
 AACA TGGCTGGTTT
 ||| |||||
 TTGT ACCGACCAAAA
 CTAGA
 GAM1230 LOC146856 3' AAATCCTACCAGTTATGT 40297 C CT T
 ACA TAACTGG GG TTT
 ||| ||||| || ||||
 TGT ATTGACC CC AAA
 _ AT T
 GAM1230 LOC200609 5' AAAACACAGAGTCAGTGTT 43321 A GG _
 AACACT ACT CTG GTTTT
 ||||| || ||| |||||
 TTGTGA TGA GAC CAAAA
 C _ A
 GAM1231 ECM2 3' TCAACTGAATACTGGTGTT 7087 C AATCTT
 AGCACCAG ATT TTGA
 ||||| || ||||

			TTGTGGTC TAA AACT	
			A GTTC__	
GAM1231	MBNL	3'	GTCAAAAGACTATAAATGCT 22031	AA__
			AGCATT TCTTTTGAC	
			TCGTAA AGAAAACTG	
			ATATC	
GAM1231	PARK2	3'	TCAAAAGATTAACAACACTGC 15161	CCAGCA
			GCA TTAATCTTTTGA	
			CGT AATTAGAAAAC	
			CACAAC	
GAM1231	PARK2	3'	TCAAAAGATTAACAACACTGC 10907	CCAGCA
			GCA TTAATCTTTTGA	
			CGT AATTAGAAAAC	
			CACAAC	
GAM1231	PARK2	3'	TCAAAAGATTAACAACACTGC 15154	CCAGCA
			GCA TTAATCTTTTGA	
			CGT AATTAGAAAAC	
			CACAAC	
GAM1231	TMOD3	3'	TCAAAAGGGATGTTGCTGGT 15858	TTAA_
			ACCAGCA TCTTTTGA	
			TGGTCGT GGAAAAC	
			TGTAG	
GAM1231	DKFZP434L187	5'	TTGGAATGAATGCTGGTACTT 34127	C AATC TG
			AAG ACCAGCATT TTT A	
			TTC TGGTCGTAA AAG T	
			A GT__ GT	
GAM1231	FLJ11004	5'	TCAAAAGTCAGTGCTAATGTT 20288	CC AAT
			AGCA AGCATT CTTTGA	
			TTGT TCGTGA GAAAAC	
			AA CT_	
GAM1231	KIAA0495	5'	GTCAGTGCCAACGCTGGTGTTT 31360	ATTAATCTT
			AAGCACCAGC TTGAC	
			TTTGTGGTCG GACTG	
			CAACCGT__	
GAM1231	KIAA1600	3'	TCAAAAGATTATGAATAGC 35395	ACCAG T
			GC CAT AATCTTTTGA	
			CG GTA TTAGAAAAC	
			ATAA_ _	
GAM1231	LEPROTL1	3'	CAAGTGTTAATGCCCATGC 17649	CCA CT
			GCA GCATTAAT TTTG	

CGT CGTAATTG GAAC
 ACC T_
 GAM1231 LOC142955 3' AGACTATATGCTGGTGCT 37570 _ A
 AGCACCAGCAT TA TCT
 ||||| || ||
 TCGTGGTCGTA AT AGA
 T C
 GAM1231 LOC257103 5' GTCACAGTTAATGCCAGTGCT 45754 CA CTTT
 AGCAC GCATTAAT TGAC
 |||| ||||| ||||
 TCGTG CGTAATTG ACTG
 AC AC_
 GAM1231 LOC90148 3' TCAAAAGAAAGCCTGGTGGTT 30892 G CATTAA
 AA CACCAG TCTTTTGA
 || ||||| |||||
 TT GTGGTC AGAAAACT
 G CGAA_
 GAM1232 GRIN2B 5' CCAACATGCTCACTCCCTTA 6491 C _
 TAAGGGAG GAGC TGTTGG
 ||||| |||| |||||
 ATTCCCTC CTCG ACAACC
 A T
 GAM1232 LAPTM5 3' AATCCAATGCTCACCT 13615 _ GAGCT
 AGG GAGC GTTGGATT
 ||| |||| |||||
 TCC CTCG TAACCTAA
 A _
 GAM1232 D15Wsu75e 3' CCCTCACCTTCCCTCCCTTA 33101 C _ C TT
 TAAGGGAG GA G TG GG
 ||||| || || ||
 ATTCCCTC CT C AC CC
 C T C TC
 GAM1232 LOC146452 3' ATAATCTCAAGACTCCTCCCTT 38161 C _ GTT
 A TAAGGGAG GAG CT GGATTAT
 ||||| |||| |||||
 ATTCCCTC CTC GA TCTAATA
 _ A AC_
 GAM1232 LOC149461 3' CCCACAGCTCACTCCACT 38761 _ C T
 AG GGAG GAGCTGT GG
 || |||| ||||| ||
 TC CCTC CTCGACA CC
 A A C
 GAM1232 LOC222057 3' GGTCCAGCTCCTCCCT 44573 C GTT
 AGGGAG GAGCT GGATT
 ||||| |||| |||||
 TCCCTC CTCGA CCTGG
 _ _
 GAM1233 DFFB 3' AGAGGTGTCATGCTTTGG 42238 ACC TCA
 CCAGA TGA CACCTCT
 |||| || |||||

			GGTTT ACT GTGGAGA		
			CGT ____		
GAM1233	DIO3	3'	AAGAGAGGTGGGGGGAGAGCCT 7041	AAC GA A	
	G		CAG CT TC CACCTCTCTT		
			GTC GA GG GTGGAGAGAA		
			CGA GG G		
GAM1233	EDAR	5'	AGAGAGGTGTGCCAGGT 22744	AT	
			ACCTG CACACCTCTCT		
			TGGAC GTGTGGAGAGA		
			C_		
GAM1233	IGFBP5	5'	AGAGGTGTTAGGGTTTGG 6201	A ATC	
			CCAGA CCTG ACACCTCT		
			GGTTT GGAT TGTGGAGA		
			G ____		
GAM1233	ITSN1	3'	GGTCTGATCAGGCCCTGG 8957	AA C	
			CCAG CCTGATCA ACC		
			GGTC GGACTAGT TGG		
			CC C		
GAM1233	RBM3	5'	AAGAGAGGTGTCTGTCTAGCCC 34892	AACCT C_	
	TG		CAG GAT ACACCTCTCTT		
			GTC CTG TGTGGAGAGAA		
			CCGAT TC		
GAM1233	RGS3	3'	AAGAGAGGCCCCAGGCTACTGG 19422	AA_ ATCACA	
			CCAG CCTG CCTCTCTT		
			GGTC GGAC GGAGAGAA		
			ATC CC____		
GAM1233	RGS3	3'	AAGAGAGGCCCCAGGCTACTGG 22086	AA_ ATCACA	
			CCAG CCTG CCTCTCTT		
			GGTC GGAC GGAGAGAA		
			ATC CC____		
GAM1233	RGS3	3'	AAGAGAGGCCCCAGGCTACTGG 29307	AA_ ATCACA	
			CCAG CCTG CCTCTCTT		
			GGTC GGAC GGAGAGAA		
			ATC CC____		
GAM1233	RGS3	3'	AAGAGAGGCCCCAGGCTACTGG 28281	AA_ ATCACA	
			CCAG CCTG CCTCTCTT		
			GGTC GGAC GGAGAGAA		
			ATC CC____		
GAM1233	RGS3	3'	AAGAGAGGCCCCAGGCTACTGG 28667	AA_ ATCACA	
			CCAG CCTG CCTCTCTT		

			GGTC GGAC GGAGAGAA		
			ATC CC_____		
GAM1233	RGS3	3'	AAGAGAGGCCCGGCTACTGG	29305	AA_ ATCAC
			CCAG CCTG CCTCTCTT		
			GGTC GGAC GGAGAGAA		
			ATC CC_____		
GAM1233	SERPINA5	3'	AAGAGAGGTCCAGAGTCCTGG	6239	A _ ATCAC
			CCAG AC CTG ACCTCTCTT		
			GGTC TG GAC TGGAGAGAA		
			C A C_____		
GAM1233	TFE3	3'	AAGAGGAGATGTGATCAGG	13275	C _
			CCTGATCACA CTC TCTT		
			GGA CTAGTGT GAG AGAA		
			A G		
GAM1233	TSSC4	5'	AAGAGAGGTGTGGCGTGGCCCT	12258	AA _ A
	GG		CCAG CC TG TCACACCTCTCTT		
			GGTC GG GC GGTGTGGAGAGAA		
			CC T _		
GAM1233	ABCC13	3'	AGAAGTGGTCAGACTCTGG	28969	AC ACC
			CCAGA CTGATCAC TCT		
			GGTCT GACTGGTG AGA		
			CA A_		
GAM1233	EDG1	3'	GGGTGGAGATCAGGTCCCGG	29841	AGA A_
			CC ACCTGATC CACCT		
			GG TGGACTAG GTGGG		
			CCC AG		
GAM1233	FLJ12568	3'	AGAGAGGTTAAATTCTGG	24551	CC ATCAC
			CCAGAA TG ACCTCTCT		
			GGTCTT AT TGGAGAGA		
			AA _____		
GAM1233	LENG1	5'	AAGAGAGGCAAGAGAAAGCTCT	40860	AC GA_ ACA
	GG		CCAGA CT TC CCTCTCTT		
			GGTCT GA AG GGAGAGAA		
			C_ AAG AAC		
GAM1233	LIG-1	3'	AAGAGAGGTAGGAGAGGCTG	31949	AA GA AC
			CAG CCT TC ACCTCTCTT		
			GTC GGA AG TGGAGAGAA		
			_ G_ GA		
GAM1233	MGC10999	5'	AAGAGAGGCATCGGATTCTCA	26087	C C CACA
			C AGAA CTGAT CCTCTCTT		

A TCTT GGCTA GGAGAGAA
 C A C___
 GAM1233 MGC2603 3' AAGAGAGGTAGAATGGTGCT 23470 A TGA AC
 AG ACC TC ACCTCTCTT
 || ||| || |||||
 TC TGG AG TGGAGAGAA
 G TA_ A_
 GAM1233 MGC3113 3' AAGAGAGGCTCTCAAACCTTTG 23467 ACC TCACA
 CAGA TGA CCTCTCTT
 ||| ||| |||||
 GTTT ACT GGAGAGAA
 CAA CTC___
 GAM1233 SIMRP7 3' AAGAGAAAGGAGTCAGGTTT 44367 CACA ___
 GAACCTGAT CC TCTCTT
 ||||| || |||||
 TTTGGACTG GG AGAGAA
 A___ AA
 GAM1233 TSGA14 3' AGAGGTGTGACAGGCTCT 20792 A A
 AGA CCTG TCACACCTCT
 || ||| |||||
 TCT GGAC AGTGTGGAGA
 C _
 GAM1233 LOC122416 5' AGAGAGGTATGGGACCTG 36683 AA TGAT C
 CAG CC CA ACCTCTCT
 ||| || || |||||
 GTC GG GT TGGAGAGA
 CA ___ A
 GAM1233 LOC145439 5' AAGAGAGGGTCGCAGACCTG 37863 AAC ATC A
 CAG CTG AC CCTCTCTT
 ||| ||| || |||||
 GTC GAC TG GGAGAGAA
 CA_ GC_ _
 GAM1233 LOC149842 3' AGAGAGGTGTCAATTCTG 41088 CC TCA
 CAGAA TGA CACCTCTCT
 |||| ||| |||||
 GTCTT ACT GTGGAGAGA
 A_ ___
 GAM1233 LOC153338 5' AAGAGAGATACTCTGCACAGGT 41606 AT CAC___
 TTTGG CCAGAACCTG CA CTCTCTT
 ||||| || |||||
 GGT TTTGGAC GT GAGAGAA
 AC CTCATA
 GAM1233 LOC158654 3' AGAGAGGCGACAGCTGTGG 39874 GAAC A ACA
 CCA CTG TC CCTCTCT
 ||| ||| || |||||
 GGT GAC AG GGAGAGA
 GTC_ _ C_
 GAM1233 LOC162333 5' AAGAAAGGCATCATTTAGGTTC 42119 TCACA_ C
 GAACCTGA CCT TCTT
 ||||| ||| |||

CTTGGATT GGA AGAA
 TACTAC A
 GAM1233 LOC254659 5' AGGCATCAGGTTCTGG 45599 CACA
 CCAGAACCTGAT CCT
 ||||| |||
 GGTCTTGGACTA GGA
 C____
 GAM1234 REQ 3' GTCCCATTCCACCCACCCCA 12952 A C ATGCT
 TG GGT GGGT AATGGGAC
 || ||| |||||
 AC CCA CCA TTACCCTG
 C C CC____
 GAM1234 CD109 3' CCCACCCCAACCCACCCCA 28570 A C A CTAA
 TG GGT GGGT TG TGGG
 || ||| ||| |||
 AC CCA CCA AC ACCC
 C _ _ CCC_
 GAM1234 RIN3 3' TCCCCACACCCACCCCA 24235 A C A CTAAT
 TG GGT GGGT TG GGA
 || ||| ||| |||
 AC CCA CCA AC CCCT
 C _ C C____
 GAM1234 LOC113655 5' CCCACCTGGAACCCGACCTC 28795 ATG A_
 GAGGTCGGGT CTA TGGG
 ||||| ||| |||
 CTCCAGCCCA GGT ACCC
 A__ CC
 GAM1234 LOC145501 3' CCGGCATGCCCAACCTCA 37882 C AAT
 TGAGGT GGGTATGCT GG
 ||||| ||||| ||
 ACTCCA CCCGTACGG CC
 A ____
 GAM1234 LOC148046 3' CCCACTCCTGACCTCA 40866 TA CTAAT
 TGAGGTCGGG TG GGG
 ||||| ||| |||
 ACTCCAGTCC AC CCC
 TC ____
 GAM1234 LOC196985 5' CCCATCTTTGAGCCCGGCCCA 43158 A ATGCTA
 TG GGTGCGGT ATGGG
 || ||||| |||
 AC CCGGCCCG TACCC
 C AGTTTC
 GAM1234 LOC89919 5' TCCCATCATGGGGGCCCATCCT 30464 TC ATG ____
 CA TGAGG GGGT CTA ATGGGA
 |||| ||| ||| |||||
 ACTCC CCG GGT TACCCT
 TA GG_ AC
 GAM1235 ADD2 3' ACCCTGGACCACATTCGG 18935 A ATCCTG
 TC AATGTGG CCAGGGT
 || ||||| |||||

GG TTACACC GGTCCCA
C A____
GAM1235 ADD2 3' ACCCTGGACCACATTCGG 18940 A ATCCTG
TC AATGTGG CCAGGGT
|| ||||| |||||
GG TTACACC GGTCCCA
C A____
GAM1235 ADD2 3' ACCCTGGACCACATTCGG 18943 A ATCCTG
TC AATGTGG CCAGGGT
|| ||||| |||||
GG TTACACC GGTCCCA
C A____
GAM1235 ADD2 3' ACCCTGGACCACATTCGG 18948 A ATCCTG
TC AATGTGG CCAGGGT
|| ||||| |||||
GG TTACACC GGTCCCA
C A____
GAM1235 EHD2 3' ACCCTGGCAGGGGACCCCA 15959 T A_
TG GG TCCTGCCAGGGT
|| || |||||
AC CC GGGACGGTCCCA
C AG
GAM1235 PCOLN3 3' ACCGTCACTCAGATCCACATT 8662 C CCAG_
AATGTGGATC TG GGT
||||||| || |||
TTACACCTAG AC CCA
_ TCACTG
GAM1235 TCF3 3' GACCCCGGGCTTCATCCACAT 35009 CCT A_
ATGTGGAT GCC GGGTC
|||||| || |||||
TACACCTA CGG CCCAG
CTT GC
GAM1235 DKFZp547I224 5' ATGTTGAGAATCCACATATGA 21473 A C GC G
TCA ATGTGGAT CT CAG GT
|| ||||| || ||| ||
AGT TACACCTA GA GTT TA
A A _ G
GAM1235 FIGN 5' ACCCTGGCAGCCTTCCTTGA 19848 ATGT TC_
TCAA GGA CTGCCAGGGT
||| || |||||
AGTT CCT GACGGTCCCA
_ TCC
GAM1235 FLJ12891 3' GACCCTGGCATAACATT 24510 GGATCC
AATGT TGCCAGGGTC
|||| |||||
TTACA ACGGTCCCAG
AT____
GAM1235 FLJ22865 5' ACCCTGGCTGACCACTTTGA 24758 T A CT
TCAAA GTGG TC GCCAGGGT
|||| ||| || |||||

AGTTT CACC AG CGGTCCCA
 _ _ T_
 GAM1235 KIAA0295 3' GACCCTGGAACCCTACACTTGA 33782 A ATCCTG
 TCAA TGTGG CCAGGGTC
 ||| ||| |||||
 AGTT ACATC GGTCCCAG
 C CCAA_
 GAM1235 KIAA1280 5' GACTGCAAAGTCCACATCCGA 34554 AA CC CAG
 TC ATGTGGAT TGC GGTC
 || ||||| || |||
 AG TACACCTG ACG TCAG
 CC AA _
 GAM1235 KIAA1987 3' ACCTGGACCCACATTTG 42493 A TGCCA
 CAAATGTGG TCC GGGT
 ||||| || |||
 GTTTACACC AGG TCCA
 C _
 GAM1235 LASP1 3' CCCTGGCCTCACTTGA 12794 AT ATCCT
 TCAA GTGG GCCAGGG
 ||| ||| |||||
 AGTT CACT CGGTCCC
 _ C_
 GAM1235 PDE4DIP 3' ACTCACAGATCCACACCTGA 45708 AA C CCA
 TCA TGTGGATC TG GGGT
 || ||||| || |||
 AGT ACACCTAG AC CTCA
 CC _ A_
 GAM1235 PRO1496 3' GCCAGGGTCAATCAGGATCCCC 20680 T T_____ CAGG
 ATTTGA ATG GGATCC GC GT
 ||| |||| || ||
 TAC CCTAGG TG CG
 C ACTAAIIC GGAC
 GAM1235 LOC219920 5' GACCCTGGCAAGCGGAGAAGC 44807 GGA _
 GT TCC TGCCAGGGTC
 || ||| |||||
 CG AGG ACGGTCCCAG
 AAG CGA
 GAM1235 LOC92568 3' GACCAAGGCATCCACATTT 34578 TCC AG
 AAATGTGGA TGCC GGTC
 ||||| ||| |||
 TTTACACCT ACGG CCAG
 _ AA
 GAM1236 SCML2 3' CTACACTTTGAAAGATATATT 12735 T
 AATGT TTTTCAAAGTGTAG
 |||| |||||
 TTATA AGAAAGTTTCACATC
 T
 GAM1236 TRAM 3' CTATGAATGAAAAAATATTTT 15591 AAG
 A TAAAATGTTTTTTCA TGTAG
 ||||| |||||

	ATTTTATAAAAAAAGT GTATC	
	AA_	
GAM1236 KIAA0831	3' CTACACTCTAGTAAACATTTT 17206	TTTTCAA
	AAAATGTTT AGTGTAG	
	TTTTACAAA TCACATC	
	TGATC_	
GAM1236 KIAA1300	3' CTACTGACCAAAAAAGAACATT 31480	CAAAGT_
	TTA TAAAATGTTTTTT GTAG	
	ATTTTACAAGAAAA CATC	
	AACCAGT	
GAM1236 LOC130813	3' ACACTTCTAGGGTAAAGCATTT 37306	T A_
	TA TAAAATGTTTT TTC AAGTGT	
	ATTTTACGAAA GGG TTCACA	
	T ATC	
GAM1237 CBFA2T2	3' GGACACATCTTGCCACCA 11551	C
	TGGTGGCAAGATGT TCC	
	ACCACCGTTCTACA AGG	
	C	
GAM1237 RAB5B	3' GATGGCCTCAGCCCCAGCCACC 8773	AAGA_ TCTC
	ATA TATGGTGGC TG CCATC	
	ATACCACCG AC GGTAG	
	ACCCCG TCC_	
GAM1237 SORBS1	5' GACGACTTGTCTGCCACCA 17688	A _ _
	TGGTGGCA GAT GTC TC	
	ACCACCGT CTG CAG AG	
	C TT C	
GAM1237 C20orf18	3' ATGGGATTCCTTGCCACC 25274	ATGTC
	GGTGGCAAG TCCCAT	
	CCACCGTTC AGGGTA	
	CTT_	
GAM1237 C20orf30	3' ATGGAAAAGTGTTGCCTGCCA 15430	_ G GTCTC
	TGGT GGCAA AT CCAT	
	ACCG CCGTT TG GGTA	
	T G AAAA_	
GAM1237 FLJ13612	3' GGAGGAACAGCATGCCACCA 24864	AGA _
	TGGTGGCA TGT CTCC	
	ACCACCGT ACA GAGG	
	ACG AG	
GAM1237 GHITM	3' GATAAGAAACATGTCATCATA 15726	AGA C CC
	TATGGTGGCA TGT TC ATC	

		ATACTACTGT ACA AG TAG		
		___ A AA		
GAM1237	KIAA0700	3' GATGGCTCCTGCCCCATA 35660	T A T _	
		TATGG GGCA GA GTC TC		
		ATACC CCGT CT CGG AG		
		_ C _ T		
GAM1237	KIAA1877	3' GGGAGACACCTTGCTCC 32884	T A	
		GG GGCAAG TGTCTCCC		
		CC TCGTTC ACAGAGGG		
		_ C		
GAM1237	RASSF2	3' GATAGGAGACAGGAGATCACCA 16394	CAAGA C	
	TA	TATGGTGG TGTCTCC ATC		
		ATACCACT ACAGAGG TAG		
		AGAGG A		
GAM1237	SPEC1	3' GGAAACATCCTGTTTTATTAT 21512	_ A C	
		ATGGTG GCA GATGT TCC		
		TATTAT TGT CTACA AGG		
		TT C A		
GAM1237	LOC143425	3' AGACATCCTCCACCATA 42348	CAA	
		TATGGTGG GATGTCT		
		ATACCACC CTACAGA		
		TC_		
GAM1237	LOC149832	5' GATGGGATTGTCAGCCACCA 41082	AA TC	
		TGGTGGC GATG TCCCATC		
		ACCACCG CTGT AGGGTAG		
		A_ T_		
GAM1237	LOC150319	3' GATGCCACCTCCTGCCACCA 38895	A T CTCC	
		TGGTGGCA GA GT CATC		
		ACCACCGT CT CA GTAG		
		C C CC_		
GAM1238	AXUD1	3' AACAGGAAGCCCAGAGAGGGC 26916	AGG A_	
		GCC CTC GGCTTCCTGTT		
		CGG GAG CCGAAGGACAA		
		GA_ AC		
GAM1238	CACNA2D2	3' AGGACCTGAGCTGGC 12647	G CT	
		GCCAG CTCAGG TCCT		
		CGGTC GAGTCC AGGA		
		_ _		
GAM1238	CX3CR1	3' CAGGGCCTGAGCCAAGCTA 34977	CA TT	
		TAGC GGCTCAGGC CCTG		

			ATCG CCGAGTCCG GGAC		
			AA _		
GAM1238	PEX10	3'	AACAGAAAGCTGTCCCTGGCTG 8478	CT G C	
			TAGCCAGG CAG CTT CTGTT		
			GTCGGTCC GTC GAA GACAA		
			CT _ A		
GAM1238	RRM2B	3'	AGGTAGCCTGAGCCTAGTTA 33687	C T	
			TAGC AGGCTCAGGCT CCT		
			ATTG TCCGAGTCCGA GGA		
			A T		
GAM1238	TACSTD2	3'	AACAGGAAACCTGACTGGGGC 8157	A_ C C	
			GCC GG TCAGG TTCCTGTT		
			CGG TC AGTCC AAGGACAA		
			GG _ A		
GAM1238	DKFZP564D116	3'	ACAGAAAACCTGCTGGCTG 35733	GCT GC C	
			TAGCCAG CAG TTC TGT		
			GTCGGTC GTC AAG ACA		
			_ AA _		
GAM1238	FLJ14855	3'	AACAGGAAGCCTGCATGTGACT 27057	C GGCT	
	G		TAG CA CAGGCTTCCTGTT		
			GTC GT GTCCGAAGGACAA		
			A GTAC		
GAM1238	FLJ21709	3'	AGGAGCCTGAGCTGGC 38166	G T	
			GCCAG CTCAGGCT CCT		
			CGGTC GAGTCCGA GGA		
			- -		
GAM1238	FLJ22477	3'	AACAGAGAGAACGAGCCTGG 24074	AGG TC	
			CCAGGCTC CT CTGTT		
			GGTCCGAG GA GACAA		
			CAA GA		
GAM1238	GGA2	3'	AGGAACCTGAGCCTGGCTG 17396	C	
			TAGCCAGGCTCAGG TTCCT		
			GTCGGTCCGAGTCC AAGGA		
			-		
GAM1238	GGA2	3'	AGGAACCTGAGCCTGGCTG 28916	C	
			TAGCCAGGCTCAGG TTCCT		
			GTCGGTCCGAGTCC AAGGA		
			-		
GAM1238	KIAA0449	3'	AACAGGCGGAGCCTGGC 19049	AGGCTT	
			GCCAGGCTC CCTGTT		

		CGGTCCGAG	GGACAA	
		GC_____		
GAM1238	MGC16075	3' AACAGGAAGCCTGTGGAGGACT	26503	_ AGGCT
	G	TAG CC CAGGCTTCCTGTT		
		GTC GG GTCCGAAGGACAA		
		A AGGT_		
GAM1238	POPX1	3' AACAGCAGACCAGCCTGGC	17115	CA _ TC
		GCCAGGCT GG CT CTGTT		
		CGGTCCGA CC GA GACAA		
		_ A C_		
GAM1238	RALGPS1A	3' AACAGGAAGCCACTTGCAAGC	16013	CAG TCA_
		GC GC GGCTTCCTGTT		
		CG CG CCGAAGGACAA		
		AA_ TTCA		
GAM1238	RSP3	5' AACAGAGCTGGGAGCCTGGCTG	25671	A_ TC
		TAGCCAGGCTC GGCT CTGTT		
		GTCGGTCCGAG TCGA GACAA		
		GG _		
GAM1238	LOC138399	5' ACAGGACACCCTGGCTA	37129	CTCAG CT
		TAGCCAGG G TCCTGT		
		ATCGGTCC C AGGACA		
		_ AC		
GAM1238	LOC139231	5' AGGGAGCCCGAGCCAGGC	37141	A A
		GCC GGCTC GGCTTCCT		
		CGG CCGAG CCGAGGGA		
		A C		
GAM1238	LOC149706	5' AACAGGGCAGAGCCTGGCTG	41056	AG TT
		TAGCCAGGCTC GC CCTGTT		
		GTCGGTCCGAG CG GGACAA		
		A_ _		
GAM1238	LOC150282	5' AACAGAACGTTCTGAGTCTG	38918	_ TTC
		CAGGCTCAGG C CTGTT		
		GTCTGAGTCT G GACAA		
		T CAA		
GAM1238	LOC221474	5' AACAGAAAGCCTGAGAACCAGC	44376	CA _ C
	T	AGC GG CTCAGGCTT CTGTT		
		TCG CC GAGTCCGAA GACAA		
		A_ AA A		
GAM1238	LOC93589	3' AACAGGAAACCAATCACCTGGC	35974	CTCA_ C
		GCCAGG GG TTCCTGTT		

		CGGTCC CC AAGGACAA		
		ACTAA A		
GAM1239	COL3A1	3' CTGTAAAGGTCAACAATAAA 5543	T	GC_
		TTTATTGTT ACCT TAG		
		AAATAACAA TGGA GTC		
		C AAT		
GAM1239	CXYorf1	5' ATCTCCCAGCAGGTAGAGCAG 39903	_	AGA
		TTGTTT ACCTGCT AGAT		
		GACGAG TGGACGA TCTA		
		A CCC		
GAM1239	TRIP-Br2	3' CTTTGTGGTAAACAATGAA 16490		TGCTA
		TTTATTGTTTACC GAAG		
		AAGTAACAAATGG TTTC		
		TG__		
GAM1239	LOC199725	3' ATCCCCTAGCAGGTGCCACACA 43241	T__	AA
	G	TTGT TACCTGCTAG GAT		
		GACA GTGGACGATC CTA		
		CACC CC		
GAM1239	LOC200093	5' ATCTCCCAGCAGGTAGAGCAG 31595	_	AGA
		TTGTTT ACCTGCT AGAT		
		GACGAG TGGACGA TCTA		
		A CCC		
GAM1239	LOC91040	5' ATCTCCCAGCAGGTAGAGCAG 32312	_	AGA
		TTGTTT ACCTGCT AGAT		
		GACGAG TGGACGA TCTA		
		A CCC		
GAM1239	LOC91464	3' AGCAAACATAACAATAAA 32873	CC_	
		TTTATTGTTTA TGCT		
		AAATAACAAAT ACGA		
		CAA		
GAM1240	ARNT2	3' AAAAAAGGCACAAAAATAGGT 16931	AC C	A
		ACC AT TTTGTGTC TTTT		
		TGG TA AAACACGG AAAAA		
		A_ A A		
GAM1240	AVPR1A	3' TTAAAAGTCACATAAAATGCGG 6377	A C	C
		CC CAT TTTGTGT ATTTTAA		
		GG GTA AAATACA TGAAAATT		
		C _ C		
GAM1240	KLHL2	3' TTAAAAATGACCAAAACATGT 14113	C_	T
		ACAT TTTG GTCATTTTAA		

			TGTA AAAC CAGTAAAAATT		
			CA _		
GAM1240	MRC1	3'	AAGTGGCATAAAAAATGTAGT 8280	C C	
			AC ACAT TTTGTGTCATTT		
			TG TGTA AAATACGGTGAA		
			A A		
GAM1240	MYH11	3'	TTAAAAATAAGCTGGGCGTGGT 8303	AT TT GTC	
			ACCAC CT GT ATTTTTAA		
			TGGTG GG CG TAAAAATT		
			CG T_ AA_		
GAM1240	MYH11	3'	TTAAAAATAAGCTGGGCGTGGT 23145	AT TT GTC	
			ACCAC CT GT ATTTTTAA		
			TGGTG GG CG TAAAAATT		
			CG T_ AA_		
GAM1240	OSR1	3'	AAAGATACACAAAGATGGG 11585	A C	
			CC CATCTTTGTGT ATTTTT		
			GG GTAGAAACACA TAGAAA		
			— —		
GAM1240	CG018	3'	TAAAAATGTGAGATGTG 27402	TGTGT	
			CACATCTT CATTTTAA		
			GTGTAGAG GTAAAAAT		
			T_____		
GAM1240	DKFZP434B172	3'	AAAAATGAAAGTGTGGT 34701	T TGTG	
			ACCACA CTT TCATTTTT		
			TGGTGT GAA AGTAAAAA		
			— ———		
GAM1240	DKFZP564M182	3'	AAAAATAAGCTGGGTGTGGT 38217	TT GTC	
			ACCACATCT GT ATTTTT		
			TGGTGTGGG CG TAAAAA		
			T_ AA_		
GAM1240	FLJ10830	3'	TTAAAAATGAGCCAAGTGTGGT 20185	CT TG	
			ACCACAT TTG TCATTTTAA		
			TGGTGTG AAC AGTAAAAATT		
			— CG		
GAM1240	FLJ12572	3'	TAAAAACGTGTAAGATGTGGT 23200	T TG CA	
			ACCACATCTT G T TTTTAA		
			TGGTGTAGAA T G AAAAAT		
			GT C		
GAM1240	FLJ12592	3'	TTAAAAATGAAACAAGTGTGGT 25877	CT G	
			ACCACAT TTGT TCATTTTAA		

			TGGTGTG	AACA	AGTAAAAATT		
			—	A			
GAM1240	HSPC043	3'	TTAAAAATAATAGGGAATGTGG	33638		—	GTC
		T	ACCACAT CTTTGT	ATTTTTAA			
			TGGTGTA GGGATA	TAAAAATT			
			A	A	—		
GAM1240	KIAA0052	3'	TTAAAAACTACATACAAAGTTG	33693	T	CA	—
		TG	CACA CTTTGTGT	TTTTTAA			
			GTGT GAAACATA	AAAAATT			
			T	CATC			
GAM1240	KIAA0532	3'	AAAGTGACAAAAACGTGT	35020	C	G	
			ACAT TTT TGTCATTTT				
			TGTG AAA ACAGTGAAA				
			C	A			
GAM1240	KIAA1719	3'	TAAAAAAAGCAAAGATG	33823		GTCA	
			CATCTTTGT	TTTTTA			
			GTAGAAACG	AAAAAT			
			AA	—			
GAM1240	KLK7	3'	TTAAAAATGATACTTAGA	29276	TT		
			TCT GTGTCATTTTTAA				
			AGA CATAGTAAAAATT				
			TT				
GAM1240	KLK7	3'	TTAAAAATGATACTTAGA	11479	TT		
			TCT GTGTCATTTTTAA				
			AGA CATAGTAAAAATT				
			TT				
GAM1240	MCF2L	3'	TTAAAGAAAATACAAAGATGCA	30509	CA	CA	
		GT	AC CATCTTTGTGT	TTTTTAA			
			TG GTAGAAACATA	AGAAATT			
			AC	AA			
GAM1240	MGC27382	5'	AAAAATGAACAAAGAAATG	29522	CA	G	
			CA TCTTTGT TCATTTT				
			GT AGAAACA AGTAAAAA				
			AA	—			
GAM1240	MISS	3'	TTAAAAATCTAAGATGTGG	29383		TGTGTC	
			CCACATCTT	ATTTTTAA			
			GGTGTAGAA	TAAAAATT			
			TC	—			
GAM1240	NLN	3'	TTAAAAATTATAAAGATGT	21858		TC	
			ACATCTTTGTG	ATTTTTAA			

TGTAGAAATAT TAAAAATT

GAM1240 PRO0097 5' AAAAATGACATGTGT 15362 CTTT
ACAT GTGTCATTTTT
|||| ||||||||
TGTG TACAGTAAAAA

GAM1240 RERG 5' AAGATTCAACAATGATATGGT 26736 C T TC
ACCA ATC TTGTG ATTTT
|||| ||| |||| ||||
TGGT TAG AACAC TAGAA
A T T_

GAM1240 LOC123435 5' TTAAAAATGAACGGTGATTTGG 36724 C T G
CCA ATC TTGT TCATTTTTAA
||| ||| |||| ||||||||
GGT TAG GGCA AGTAAAAATT
T T _

GAM1240 LOC147837 3' TAAAAATGACATATTTGGT 38394 CATCTT
ACCA TGTGTCATTTTAA
|||| |||||||||
TGGT ATACAGTAAAAAT
TT_____

GAM1240 LOC153894 3' TTAAAAATCTAAGATGTGG 39428 TGTGTC
CCACATCTT ATTTTTAA
||||||| |||||||
GGTGTAGAA TAAAAATT
TC_____

GAM1240 LOC154442 3' TAGGGAAACACGAAGAT 41707 CA
ATCTTTGTGT TTTTAA
||||||| |||||
TAGAAGCACA AGGGAT
A_

GAM1240 LOC255328 3' AAGATGCACTAAGATGTGGT 46177 T T
ACCACATCTT GTG CATTTT
||||||| ||| |||||
TGGTGTAGAA CAC GTAGAA
T _

GAM1240 LOC51696 3' AATGCACAAAGCTGTAGT 18305 C T T
AC ACA CTTTGTG CATT
|| ||| |||||| |||
TG TGT GAAACAC GTAA
A C _

GAM1240 LOC91012 5' TAAAAATGACTTTGGGAT 32284 TGT
ATCTT GTCATTTTAA
|||| |||||||||
TAGGG CAGTAAAAAT
TTT

GAM1240 LOC91380 5' TTAAAAATGACACTCTGA 32760 TTT
TC GTGTCATTTTAA
|| |||||||||

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AG CACAGTAAAAATT
TCT
GAM1241 PORIMIN 5' CGCCGCCCGGCTGCGCACGCG 27492 A TA A_ A
TG CGTGCGCA GTTG GCG CG
|| ||||| ||| ||| ||
GC GCACGCGT CGGC CGC GC
_ _ CC C
GAM1242 CROT 3' AGTCCATCTTTCAAGCACTTTA 22122 ATAGT
TGAAGTGC GAAGATGGACT
||||| |||||
ATTTACAG TTTCTACCTGA
AAC_
GAM1242 DYRK1A 3' CCATCTTCATGGATAGCTCA 7093 A GCATA
TGA GT GTGAAGATGG
||| || |||||
ACT CG TACTTCTACC
_ ATAGG
GAM1242 DYRK1A 3' CCATCTTCATGGATAGCTCA 28186 A GCATA
TGA GT GTGAAGATGG
||| || |||||
ACT CG TACTTCTACC
_ ATAGG
GAM1242 DYRK1A 3' CCATCTTCATGGATAGCTCA 28163 A GCATA
TGA GT GTGAAGATGG
||| || |||||
ACT CG TACTTCTACC
_ ATAGG
GAM1242 TFDP2 3' ATCCAAGCTATGCATTTCA 12973 GAA
TGAAGTGCATAGT GAT
||||||| |||
ACTTTACGTATCG CTA
AAC
GAM1242 UNC5C 3' TCCAGATGAGACCAATGCACTT 9821 A_ GAAGA_
CA TGAAGTGCAT GT TGGA
||||||| || |||
ACTTCACGTA CA ACCT
AC GAGTAG
GAM1242 KIAA0599 3' AGTCCATCCCCTCCGCCCTTCA 37853 T AT TGAA
TGAAG GC AG GATGGACT
||||| || || |||||
ACTTC CG TC CTACCTGA
C CC CC_
GAM1242 MGC11266 3' AGTCCATGAGTGTGCACTTCA 23611 GTGAAG
TGAAGTGCATA ATGGACT
||||||| |||||
ACTTCACGTGT TACCTGA
GAG_
GAM1242 TUSP 5' TTTTCACTATGCATTCA 21539 G
TGAA TGCATAGTGAAGA
||| |||||

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GAM1242	ZNF262	3'	AGTCCATCTCCCTCATCTC	11556	AG	CAT	T	A
			GA TG AG GA GATGGACT					
			CT AC TC CT CTACCTGA					
			CT _ C _					
GAM1242	LOC147072	3'	TCCAAACCACTATGCTCTTCA	30301	T			AAGA
			TGAAG GCATAGTG TGGA					
			ACTTC CGTATCAC ACCT					
			T CAA_					
GAM1242	LOC147976	3'	TCCCTCACTATGCCTTCA	38429	T			AGAT
			TGAAG GCATAGTGA GGA					
			ACTTC CGTATCACT CCT					
			_ C_					
GAM1242	LOC148645	5'	TCCATTCTATGCACCTC	40891	A			TGAA
			GA GTGCATAG GATGGA					
			CT CACGTATC TTACCT					
			C _					
GAM1242	LOC164397	5'	GCCATCTTCAACTTCA	40153		GCATAG		A
			TGAAGT TGAAGATGG C					
			ACTTCA ACTTCTACC G					
			_ C					
GAM1242	LOC253985	5'	CCATGCTCTACAGCACTTCA	46151		ATA	A	_
			TGAAGTGC GTG AG ATGG					
			ACTTCACG CAT TC TACC					
			A_ C G					
GAM1242	LOC93444	3'	AGCCCATCTCCTGTCTTGCAGT	35843	G	_	T	A A
			TCA TGAA TGCA TAG GA GATGG CT					
			ACTT ACGT GTC CT CTACC GA					
			G TCT _ _ C					
GAM1243	LHCGR	3'	AAGCACATTTCAGCCTATTTGC	5744				TTACA
	TTA		TAAGCAAAT TGAG TGCTT					
			ATTCGTTTA ACTT ACGAA					
			TCCG TAC_					
GAM1243	TDG	3'	AAGCATGTAAGTATGCT	9205	_	TG		
	T		AAGCAA AT AGTTACATGCTT					
			TTCGTT TG TCAATGTACGAA					
			A GA					
GAM1243	KIAA1497	5'	AAACATGTAAGTCTGCTT	33522	AATT			C
			AAGCA GAGTTACATG TT					

TTCGT CTCAATGTAC AA
 _____ A
 GAM1243 MGC12679 3' GAAGCATGTGAAAATTCA 26458 ____
 TGAGT TACATGCTTC
 |||| |||||
 ACTTA GTGTACGAAG
 AAA
 GAM1244 CXADR 3' AGCCAGATCAAGGATGTAGTA 7018 CG CA CT
 TACTACA CT GATT TGGCT
 ||||| || ||| ||||
 ATGATGT GG CTAG ACCGA
 A_ AA _
 GAM1244 MEIS2 3' AGCCAAGGAGCAGCATATAGT 21345 CAC CAGA
 ACTA GCT TTCTTGGCT
 ||| ||| |||||
 TGAT CGA AGGAACCGA
 ATA CG_
 GAM1244 DKFZP564D172 3' CTTGTGAATCTGAGCTGTAG 25751 C TT_
 CTACA GCTCAGATTC GG
 |||| ||||| ||
 GATGT CGAGTCTAAG TC
 _ TGT
 GAM1244 HSMPP8 3' AGAATCTAAGATGTAGTA 44901 CG C
 TACTACA CT AGATTCT
 ||||| || |||||
 ATGATGT GA TCTAAGA
 A_ A
 GAM1244 LGI4 5' AGCCAGGGCCGAGCGTGCCAG 29287 A_ AGAT
 CT CACGCTC TCTTGGCT
 || ||||| |||||
 GA GTGCGAG GGGACCGA
 CC CC_
 GAM1244 MAPK6 5' AGCACGGTAATCTGAGTGCACA 8625 ACA C _
 GTA TACT CGCTCAGATT TTG GCT
 ||| ||||| ||| |||
 ATGA GTGAGTCTAA GGC CGA
 CAC T A
 GAM1245 ARSD 3' AGCCTGGGCAACATAGTGAG 14316 A A CTC
 CTCACTAT TT CTT GCT
 ||||| || ||| |||
 GAGTGATA AA GGG CGA
 C C TC_
 GAM1245 ERBB4 3' TAGCAAGAAATATTTTAATATA 11746 C_____ C III
 GTGAAATG ACTATATTA TTCT GCT A
 ||||| ||| ||| |
 TGATATAAT AAGA CGA T
 TTTATA A III
 GAM1245 GALR1 3' GAGAAGTAATATTGTGAACT 7215 C T
 AG TCAC ATATTACTTCTC
 || ||| ||||| |||||

		TC AGTG TATAATGAAGAG		
		A T		
GAM1245	FLJ10204	3' AGGGGTAATATTGTGAGCTG	19765	T
		CAGCTCAC ATATTACTTCT		
		GTCGAGTG TATAATGGGGA		
		T		
GAM1245	FLJ21272	3' AGCCTGGGCAACATAGTGAGT	24629	A A CTC
		GCTCACTAT TT CTT GCT		
		TGAGTGATA AA GGG CGA		
		C C TC_		
GAM1245	KIAA0461	3' AGCACACTATAATATAGTGAAC	35072	C CTTCTC
	TG	CAG TCACTATATTA GCT		
		GTC AGTGATATAAT CGA		
		A ATCACA		
GAM1245	LOC150139	3' GCGAGGCTTCAGTGAGCTG	38858	ATATTACT
		CAGCTCACT TCTCGC		
		GTCGAGTGA GGAGCG		
		CTTC_____		
GAM1245	LOC150481	3' AAGTAATACAGTAGCTG	38978	C A
		CAGCT ACT TATTACTT		
		GTCGA TGA ATAATGAA		
		_ C		
GAM1246	ABCC12	5' TGGCCACACTCCCCTAC	27073	AA T
		GTA GGAGT GTGGTTA		
		CAT CCTCA CACCGGT		
		CC _		
GAM1246	BECN1	3' TAACCCCATGGACTCCTTT	9843	___ T
		AAAGGAGT TG GGTTA		
		TTTCCTCA AC CCAAT		
		GGT C		
GAM1246	CDO1	5' TGGCTCGCTCAGCTCCTCCAC	7556	AA T TAA
		GT AGGAGTTG GGT AGCCA		
		CA TCCTCGAC TCG TCGGT		
		CC _ C_		
GAM1246	DBN1	3' TGGCCCCTCCCCAACTCCTT	10640	T TTAAA
		AAGGAGTTG GG GCCA		
		TTCTCAAC CC CGGT		
		C TCCC_		
GAM1246	DBN1	3' TGGCCCCTCCCCAACTCCTT	28125	T TTAAA
		AAGGAGTTG GG GCCA		

			TTCCTCAAC CC CGGT		
			C TCCC_		
GAM1246 DDX6	3'	TAGCCCTAACTCCTTAAC	10648	A	T
		GT AAGGAGTTG GGTTA			
		CA TTCCTCAAT CCGAT			
		A C			
GAM1246 FUS1	3'	TGGCTTTGCACCAAATCCTCC	14138	TTG_ _	
		GGAG TGGT TAAAGCCA			
		CCTC ACCA GTTTCGGT			
		CTAA C			
GAM1246 PPP4R1	3'	GCTCTGAGGTGCAACTTCTTCA	11610	A	G AA_
C		GT AAGGAGTTGTG TT AGC			
		CA TTCTTCAACGT GA TCG			
		C G GTC			
GAM1246 RAI3	3'	GCCTCAACCACAATTCTT	10113	AAA	
		AGGAGTTGTGGTT GC			
		TTCTTAACACCAA CG			
		CTC			
GAM1246 TCF19	3'	GGCCCCAAAACCTTCCCTAC	46660	AA	G TTAAA
		GTA GGAGTT TGG GCC			
		CAT CTTCAA ACC CGG			
		CC A C_			
GAM1246 TCF19	3'	GGCCCCAAAACCTTCCCTAC	46709	AA	G TTAAA
		GTA GGAGTT TGG GCC			
		CAT CTTCAA ACC CGG			
		CC A C_			
GAM1246 UPF3A	3'	GCTTCAACTATTGCCCTTT	27986	A T	A
		AAAGG GT GTGGTT AAGC			
		TTTCC CG TATCAA TTCG			
		_ T C			
GAM1246 UPF3A	3'	GCTTCAACTATTGCCCTTT	23275	A T	A
		AAAGG GT GTGGTT AAGC			
		TTTCC CG TATCAA TTCG			
		_ T C			
GAM1246 C20orf3	3'	GGCCTCAAAGTTCTTCTTTAC	33765	_ T	
		GTAAAGGAG TTG GGTT			
		CATTTCTTC AAC CCGG			
		TTGA T			
GAM1246 ELF4	3'	TAACCCTGACTCCTTCAC	7126	A	T
		GT AAGGAGTTG GGTTA			

	CA TTCCTCAGT CCAAT	
	C C	
GAM1246 FLJ12747	3' TGGCTTTAACTCTCAGCTCCTT 25881	T_
	AAGGAGTTG GGTAAAGCCA	
	TTCCTCGAC TCAATTCGGT	
	TC	
GAM1246 FLJ20313	5' TAACTTCAAAATCTCCTTTAT 19377	___ T
	GTAAAGGAG TTG GGTTA	
	TATTTCTC AAC TCAAT	
	TAA T	
GAM1246 KIAA0237	3' GCTCAACCAACTCCTTTA 16449	TG AA
	TAAAGGAGT TGGTT AGC	
	ATTTCTCA ACCAA TCG	
	___ C_	
GAM1246 RNF10	5' GGCTCCAACAGCTCCTCCGC 16964	AA _ TTAA
	GT AGGAGTTGT GG AGCC	
	CG TCCTCGACA CC TCGG	
	CC A ____	
GAM1246 SLC31A2	3' TGGCCTCAATGCCCTCCTTTAT 30194	TTGT TAAA__
	GTAAAGGAG GGT GCCA	
	TATTTCTC CCG CGGT	
	___ TAACTC	
GAM1246 LOC115297	3' TGGCTTTTTTAACTCCTTT 36074	GTGGTT
	AAAGGAGTT AAAGCCA	
	TTTCCTCAA TTTCGGT	
	ATT__	
GAM1246 LOC115817	5' GCCCTAACCTGCCTCCTTTGC 28814	TTGT AA
	GTAAAGGAG GGTTA GC	
	CGTTTCCTC CCAAT CG	
	CGT_ CC	
GAM1246 LOC126755	3' TGGCCCCAGAGAGCTCCTTCAC 36858	A _ G TTAAA
	GT AAGGAGT T TGG GCCA	
	CA TTCCTCG A ACC CGGT	
	C AG G C_	
GAM1246 LOC200014	3' GCTCTAAAGGTTTCTCCTTTGC 42692	TTGTGG A
	GTAAAGGAG TTA AGC	
	CGTTTCCTC AAT TCG	
	TTTGGA C	
GAM1247 ANKH	3' TGAGAAGATTAAAAAAATCT 27638	G GTG
CA	TGAGATTTTT TTTAAT TTCA	

		ACTCTAAAAA AAATTA GAGT		
		A GAA		
GAM1247	PCDHB4	3' CATCTTAAAAAAAATCTCA 21005	G	T
		TGAGATTTTT TTAA GTG		
		ACTCTAAAAA AAATT TAC		
		A C		
GAM1247	ZNF266	3' AACACATCAGAAATCTCA 42598	TTTA	
		TGAGATTTTTG ATGTGTT		
		ACTCTAAAGAC TACACAA		

GAM1247	KIAA0293	3' AAGACTCTAAACAAAAACCTC 30391	A	AT G
		GAG TTTTGTTTA GT TT		
		CTC AAAAACAAAT CA AA		
		C CT G		
GAM1247	LOC163026	5' ACCTGTAACAAAAATCTCA 40071	TAAT	
		TGAGATTTTTGTT GT		
		ACTCTAAAAACAA CA		
		TGTC		
GAM1248	BDG-29	3' GCCATTACAGTGGCCTGGATA 35816	AGA	CT
		TATCCAG TAT TGTAATGGC		
		ATAGGTC GTG ACATTACCG		
		CG_ _		
GAM1248	C21orf6	3' GCCATTGCCTGTCTCT 18855	TCTT	
		AGAGATA GTAATGGC		
		TCTCTGT CGTTACCG		
		C_ _		
GAM1248	DKFZp434D177	3' ACCAGATATCTCTGGGTA 26007	T	
		TATCCAGAGATATCT GT		
		ATGGGTCTCTATAGA CA		
		C		
GAM1248	HSA249128	3' GCCAAATTA ACTCTCTGGA 19027	TATC	TAA
		TCCAGAGA TTG TGGC		
		AGGTCTCT AAT ACCG		
		C_ _ TAA		
GAM1248	KIAA1634	3' CCACCAACTATTTCTGGATA 31751	TC	TAA
		TATCCAGAGATA TTG TGG		
		ATAGGTCTTTAT AAC ACC		
		C_ C_		
GAM1248	KIAA1941	3' GCCCCCAAAAATGTCTCTAGA 36951	C	C GTAAT
		TC AGAGATAT TT GGC		

		AG TCTCTGTA AA CCG	
		A A ACCC_	
GAM1248	PRO2533	3' CCATTACAAAATGTAATGG 20702	GAG C
		CCA ATAT TTGTAATGG	
		GGT TGTA AACATTACC	
		AA_ A	
GAM1248	LOC151201	3' TGTAATAACCTCTGGATA 41323	A C
		TATCCAGAG TAT TTGTA	
		ATAGGTCTC ATA AATGT	
		C A	
GAM1249	BPAG1	3' TCTGACAGCCACAGCACTACA 17811	CAGATA CA
		TGTAGTGCT CT TCAGA	
		ACATCACGA GA AGTCT	
		CACC_ C_	
GAM1249	CSMD1	3' CTGATGAGTATCCGATCCTG 36189	TGC A
		TAG TC GATACTCATCAG	
		GTC AG CTATGAGTAGTC	
		CT_ C	
GAM1249	KIAA1987	3' TCTGGTGCCACCTGAGCACTCA 42501	T ATACT
		TG AGTGCTCAG CATCAGA	
		AC TCACGAGTC GTGGTCT	
		_ CACC_	
GAM1249	SH3BGRL2	3' TCTGACGAGTATCTGAAGGCAT 25532	_ A
		GTGC TCAGATACTC TCAGA	
		TACG AGTCTATGAG AGTCT	
		GA C	
GAM1249	LOC123242	5' TGAGCACTGACCCACAGCACTA 37247	_____ ATA
	CA	TGTAGTGC TCAG CTCA	
		ACATCACG AGTC GAGT	
		ACACCC AC_	
GAM1249	LOC145945	5' TCTGATGAGTATCTCTCTGCA 40638	TGCTC
		TGTAG AGATACTCATCAGA	
		ACGTC TCTATGAGTAGTCT	
		TC_	
GAM1249	LOC149013	3' CTGACTCATTCCAGCACTACA 38632	CA TACTCA
		TGTAGTGCT GA TCAG	
		ACATCACGA CT AGTC	
		C_ TACTC_	
GAM1249	LOC253001	5' TGAGCACTGACCCACAGCACTA 46061	_____ ATA
	CA	TGTAGTGC TCAG CTCA	

		ACATCACG AGTC GAGT	
		ACACCC AC_	
GAM1250	GRINL1A	3' CATTAATGTTTGATAAGG 34444	AC
		CTTTGT GACATTAATG	
		GGAATA TTGTAATTAC	
		GT	
GAM1250	FHX	3' TAGCATTGCTGGACACAAAGTG 20462	_ ACGA T
	TA	TAC CTTTGT CA TAATGCTA	
		ATG GAAACA GT GTTACGAT	
		T CAG_ C	
GAM1250	FLJ13611	3' AGCATTAATGTAACAAAAAG 24486	GTACG
		CTTT ACATTAATGCT	
		GAAA TGTAATTACGA	
		AACAA	
GAM1250	KIAA0746	5' TAGCATTCCTCGTGACAAA 34416	ACATT
		TTTGTACG AATGCTA	
		AAACATGT TTACGAT	
		GCCC_	
GAM1250	KIAA1363	3' TAGCATTTTATGTACAAA 34335	ACATT
		TTTGTACG AATGCTA	
		AAACATGT TTACGAT	
		ATT_	
GAM1250	LOC220766	5' TAGCATTAACATCTGCAAG 43655	C CA
		TTTGTA GA TTAATGCTA	
		GAACGT CT AATTACGAT	
		_ AC	
GAM1250	LOC221964	3' AGCATTAACGTACCTGGG 45111	TT AC A
		CCT GT GAC TTAATGCT	
		GGG CA CTG AATTACGA	
		TC _ C	
GAM1250	LOC92181	3' AGCATTAATCCCAAAGG 33942	TACGAC
		CCTTTG ATTAATGCT	
		GGAAAC TAATTACGA	
		CC_	
GAM1251	DMXL1	3' TTGAGACGTCAGTGATAAATGA 12024	CATG CA
	G	TTCAT TGC ACGTCTCAA	
		GAGTA GTG TGCAGAGTT	
		AATA AC	
GAM1251	HTLF	5' TGAGTCAGCAGATGATGAA 7933	G CAACGT
		TTCATCAT TGC CTCA	

			AAGTAGTA ACG	GAGT	
			G ACT__		
GAM1251	SFRS2IP	5'	ATGTTGTACATGAGAA	11086	A C
			TTC TCATGTGC AACGT		
			AAG AGTACATG TTGTA		
			— —		
GAM1251	SLC21A9	3'	TTGAGACTTTCCCACATGAT	14129	CC C
			ATCATGTG AA GTCTCAA		
			TAGTACAC TT CAGAGTT		
			CC T		
GAM1251	AKT3	3'	TGAAACGTTATGATGA	11960	TGCCA C
			TCATCATG ACGT TCA		
			AGTAGTAT TGCA AGT		
			— A		
GAM1251	BTN2A1	3'	TTGAGACGCCTTACAAATGATG	27805	G CCAA_
	GA		TTCATCAT TG CGTCTCAA		
			AGGTAGTA AC GCAGAGTT		
			A ATTCC		
GAM1251	CBX6	3'	TTGAGACGTTTCATTTAATGAA	15581	CAT CC
			TTCAT GTG AACGTCTCAA		
			AAGTA TAC TTGCAGAGTT		
			ATT —		
GAM1251	DCOHN	3'	TGAGACGTTAGGGGCATAT	25851	—
			ATGTGCC AACGTCTCA		
			TATACGG TTGCAGAGT		
			GGA		
GAM1251	FLJ22009	3'	TTGAGACGTCAATGGGACG	30246	G —
			TGT CCA ACGTCTCAA		
			GCA GGT TGCAGAGTT		
			G AAC		
GAM1251	KIAA0193	3'	TGAAACGGGCAGAGATGATGAA	16547	G_ AA C
			TTCATCAT TGCC CGT TCA		
			AAGTAGTA ACGG GCA AGT		
			GAG — A		
GAM1251	KIAA1364	3'	GATTTAGCCATGATGAA	31814	T C C
			TTCATCATG GC AA GTC		
			AAGTAGTAC CG TT TAG		
			— A —		
GAM1251	NTN4	3'	AGATGACAGCCATGATGAA	31509	T CAA
			TTCATCATG GC CGTCT		

		AAGTAGTAC CG GTAGA		
		_ ACA		
GAM1251	PRO0943	5' GCTTAGCACAATGATGAA 20650	_	C C
		TTCATCAT GTGC AA GT		
		AAGTAGTA CACG TT CG		
		A A _		
GAM1251	PTPNS1	3' TTGAGACGCTAATGTTTCATGA 28060	T	CAA__
		TCATG GC CGTCTCAA		
		AGTAC TG GCAGAGTT		
		T TAATC		
GAM1251	LOC147632	5' GATAAGGCACATGTGAA 28825	T	AAC
		TTCA CATGTGCC GTC		
		AAGT GTACACGG TAG		
		_ AA_		
GAM1251	LOC152426	3' TGGGAATTGGCAATGATGAA 41501	G	CG
		TTCATCAT TGCCAA TCTCA		
		AAGTAGTA ACGGTT AGGGT		
		_ A_		
GAM1251	LOC165741	3' TTGAAACAGCACATGAAGAA 42193	A	CAAC C
		TTC TCATGTGC GT TCAA		
		AAG AGTACACG CA AGTT		
		A A__ A		
GAM1251	LOC200728	3' GGTGGGGGCAATGATGAA 43343	G	AA T
		TTCATCAT TGCC CG CT		
		AAGTAGTA ACGG GT GG		
		_ GG T		
GAM1251	LOC51112	5' TGAACGAACACATGATGGA 18113	CCAA	C
		TTCATCATGTG CGT TCA		
		AGGTAGTACAC GCA AGT		
		AA__ _		
GAM1252	ABCC3	3' GCGCAACGGCTCCTTTGCCA 21293		ATAGAGG
		TGGCAAAGGAGCC GCGT		
		ACCGTTTCCTCGG CGCG		
		CAA__		
GAM1252	CLN2	3' CGCCCTTCCTCCCTTGC 5965	A	CCATA
		GCAA GGAG GAGGGCG		
		CGTT CCTC TTCCCGC		
		C C__		
GAM1252	ITPKB	3' ACGCCCTCCCTGGCCCCCGCC 7980	AAA A	TA
		GGC GG GCCA GAGGGCGT		

CCG CC CGGT CTCCCGCA
 CC_ _ CC
 GAM1252 DKFZP586P0123 3' ACGCCCCCAGTGTCTTGACA 45463 GCA GC AGA_
 TG AAGGA CAT GGGCGT
 || |||| || ||||
 AC TTCCT GTG CCCGCA
 AG_ _ ACCC
 GAM1252 DLAT 5' TCCTGGCTCCTTCACCA 33503 CA TAGA
 TGG AAGGAGCCA GGG
 || ||||| ||
 ACC TTCCTCGGT CCT
 AC _
 GAM1252 FLJ10350 3' ACACCAGGAGAATGGCTTCTCC 45728 CAA AGAG_ C
 ACCA TGG AGGAGCCAT GG GT
 || ||||| ||
 ACC TCTTCGGTA CC CA
 ACC AGAGGA A
 GAM1252 FLJ20337 3' ACACCCTCAAGTCTCTTTGCCA 19391 GA CATA C
 TGGCAAAG GC GAGGG GT
 ||||| || ||||
 ACCGTTTC TG CTCCC CA
 TC AA_ A
 GAM1252 HRH3 3' CGCCCTCCTCCCTCCGCTA 14108 AAA CCATA
 TGGC GGAG GAGGGCG
 ||| ||| |||||
 ATCG CCTC CTCCCGC
 _ CCTC_
 GAM1252 KIAA0284 3' CGCCCTTGCCCCCTCGTCA 31617 AAA A CATA
 TGGC GG GC GAGGGCG
 ||| ||| |||||
 ACTG CC CG TTCCCGC
 CTC C _
 GAM1252 KIAA0284 3' ACGCTTCATCCACGGCTCCTTC 31616 CA ATA _
 CCA TGG AAGGAGCC GA GGGCGT
 || ||||| || |||||
 ACC TTCCTCGG CT TTCGCA
 C_ CAC AC
 GAM1252 MGC3101 3' ACACCCTGGGGGCAGCTCTCTG 23475 A A_ ATAG C
 CCA TGGCA AGG GCC AGGG GT
 ||||| ||| ||| ||||
 ACCGT TCT CGG TCCC CA
 C CGA GGG_ A
 GAM1252 PP1057 3' CTCACGGCTCCCTTTGCCA 25310 _ ATA
 TGGCAAAGG AGCC GAG
 ||||| ||| |||
 ACCGTTTCC TCGG CTC
 C CA_
 GAM1252 SLC12A5 3' CCCATGGCTCCTCGCCA 21853 AA AGA
 TGGC AGGAGCCAT GGG
 ||| ||||| |||

	ACCG TCCTCGGTA CCC	
	C_ _	
GAM1252 LOC164584 5'	ACGCCCTCCACGGCGTCGTCGC 40157	AAA GA ATA
TA	TGGC G GCC GAGGGCGT	
	ATCG C CGG CTCCCGCA	
	CTG TG CAC	
GAM1252 LOC253216 3'	CCCATAGCCCCTTTGCCA 45517	A C AGA
	TGGCAAAGG GC AT GGG	
	ACCGTTTCC CG TA CCC	
	C A _	
GAM1252 LOC90120 5'	ACGCCCTCAGCCGCCTTGCCA 30850	A A_ CATA
	TGGCAA GG GC GAGGGCGT	
	ACCGTT CC CG CTCCCGCA	
	_ GC A_	
GAM1252 LOC90288 5'	ACGCCCTTCAGCACCCCCTCCC 31104	CAAA_ A CATA
A	TGG GG GC GAGGGCGT	
	ACC CC CG TTCCCGCA	
	CTCCC A AC_	
GAM1253 FBN2 3'	GCAAACAAATCATGCAATG 7726	GCCC AGC
	CATTGCATGA GT TGC	
	GTAACGTACT CA ACG	
	AAA_ A_	
GAM1253 LDLR 3'	GCTTCGGACAGTGCCCATGCAA 6127	A _ T
TG	CATTGCATG GC CCG AGC	
	GTAACGTAC CG GGC TCG	
	C TGACA T	
GAM1253 STARD5 5'	CGCAGCTCCCGACGCAATG 24948	ATGAGCC T_
	CATTGC CG AGCTGCG	
	GTAACG GC TCGACGC	
	CA_ CC	
GAM1253 FLJ20308 3'	CGCCCTGCAAGCTCATGCAA 33197	CC CT
	TTGCATGAGC GTAG GCG	
	AACGTACTCG CGTC CGC	
	AA C_	
GAM1253 PSIP2 5'	GCGCAGCTACGGCGGCGGCAG 27068	ATGA C
	TTGC GCC GTAGCTGCGC	
	GACG CGG CATCGACGCG	
	GCGG _	
GAM1253 LOC163682 3'	CGCACGCAGCCCATGCAGTG 42091	A CCGTA _
	CATTGCATG GC GC TGCG	

GTGACGTAC CG CG ACGC
 C A____ C
 GAM1254 EHD2 3' CGCGCCACCACGCCAGCT 15964 C A
 AGCT GGCG TGGTGGCGCG
 |||| ||| |||||
 TCGA CCGC ACCACCGCGC
 C _
 GAM1254 EIF2S3 3' TGCGCGCCACCACACTTGGCT 7114 C CGA
 AGCT GG TGGTGGCGCGCA
 |||| || |||||
 TCGG TC ACCACCGCGCGT
 T AC_
 GAM1254 FNTB 3' TGCACGCCACCATTTCAGTC 7783 _ C
 GGC GATGGTGGCG GCA
 ||| ||||| |||
 CTG TTACCACCGC CGT
 AC A
 GAM1254 ST7 5' GCGCGATTTCCCGCCGAGCCCG 22430 A AT TGG_
 TG GCTCGGCG GG CGCGC
 || ||||| || |||||
 GC CGAGCCGC CC GCGCG
 C _ TTTA
 GAM1254 ST7 5' GCGCGATTTCCCGCCGAGCCCG 20454 A AT TGG_
 TG GCTCGGCG GG CGCGC
 || ||||| || |||||
 GC CGAGCCGC CC GCGCG
 C _ TTTA
 GAM1254 BNIP-S 3' GCACGCCACCACGCCAGCT 28690 C A C
 AGCT GGCG TGGTGGCG GC
 |||| ||| ||||| ||
 TCGA CCGC ACCACCGC CG
 C _ A
 GAM1254 FLJ14351 3' CGCCACCATACCCAGCT 24072 C CG
 AGCT GG ATGGTGGCG
 |||| || |||||
 TCGA CC TACCACCGC
 _ CA
 GAM1254 FLJ20154 5' TGCCACCACCGCCGAGCCA 36109 A A
 TG GCTCGGCG TGGTGGCG
 || ||||| |||||
 AC CGAGCCGC ACCACCGT
 _ C
 GAM1254 FLJ22160 3' TGCCACCACCAGACTCA 23820 _ C CGA
 TGAG CT GG TGGTGGCG
 |||| || || |||||
 ACTC GA CC ACCACCGT
 A _ ACC
 GAM1254 GNG4 3' CGCGCCACCACACCCAGCT 10810 C CGA
 AGCT GG TGGTGGCGCG
 |||| || |||||

TCGA CC ACCACCGCGC
C AC_
GAM1254 H2AV 3' GCACGCCACCATGCCAGCT 28911 C G C
AGCT GGC ATGGTGGCG GC
||||| ||| ||||| ||
TCGA CCG TACCACCGC CG
C _ A
GAM1254 KIAA1465 3' GCGCGCCACCACGACCAGCT 30504 C _ A
AGCT GG CG TGGTGGCGCGC
||||| ||| ||||| ||
TCGA CC GC ACCACCGCGCG
_ A _
GAM1254 SLC11A1 3' GCGCGCCACCACGCCCAGCT 29902 C A
AGCT GGCG TGGTGGCGCGC
||||| ||| ||||| ||
TCGA CCGC ACCACCGCGCG
C _
GAM1254 TLE4 5' GCGCGCCTCTGCCGAGCGCA 33720 A GAT T
TG GCTCGGC GG GGCGCGC
|| ||||| || |||||
AC CGAGCCG TC CCGCGCG
G _ T
GAM1254 LOC126353 3' TGCCAAGACCATCGCCAAGC 36832 C _
GCT GGCGATGGT GGCG
||| ||||| |||
CGA CCGCTACCA CCGT
A GAA
GAM1254 LOC145725 3' TGCCACCACCAAGCCCA 37951 A C CGA
TG GCT GG TGGTGGCG
|| ||| || |||||
AC CGA CC ACCACCGT
C A _
GAM1254 LOC145732 3' TGCCACCACCAAGCCCA 37960 A C CGA
TG GCT GG TGGTGGCG
|| ||| || |||||
AC CGA CC ACCACCGT
C A _
GAM1254 LOC146443 5' GCACGCCACCACCCAGCTCA 38149 C CGA C
TGAGCT GG TGGTGGCG GC
||||| || ||||| ||
ACTCGA CC ACCACCGC CG
C _ A
GAM1254 LOC166983 5' CGGGCACCACGAGCTCA 42199 GCGA G G
TGAGCTCG TGGTG C CG
||||| ||| ||| ||
ACTCGAGC ACCAC G GC
_ _ G
GAM1254 LOC196957 3' TGCCACCACCAAGCCCA 42432 A C CGA
TG GCT GG TGGTGGCG
|| ||| || |||||

		AC CGA CC ACCACCGT	
		C A ____	
GAM1254	LOC196961 3'	TGCCACCACCAAGCCCA 42441	A C CGA
		TG GCT GG TGGTGGCG	
		AC CGA CC ACCACCGT	
		C A ____	
GAM1254	LOC197138 3'	TGCCACCACCAAGCCCA 42459	A C CGA
		TG GCT GG TGGTGGCG	
		AC CGA CC ACCACCGT	
		C A ____	
GAM1255	CNTN2 3'	GGACACAGCCAGCCCCT 11525	AGC C T
		AGGGGT GGT GT GTCC	
		TCCCCG CCG CA CAGG	
		A__ A _	
GAM1255	FKRP 3'	GCAGTGACCACCTCCCCT 23593	T C_
		AGGGG AG GGTCGTTGT	
		TCCCC TC CCAGTGACG	
		_ CA	
GAM1255	HR 5'	GGCCACGACGACCGCCACCGCC 11618	_ A CCA
		GG GGT GCGGTCGTTGT CC	
		CC CCA CGCCAGCAGCA GG	
		G C CC_	
GAM1255	ICMT 3'	GCAGCGCACCTGCCACCCCT 14781	A _ _
		AGGGGT GC GGT CGTTGT	
		TCCCCA CG CCA GCGACG	
		C T C	
GAM1255	MN1 3'	TGGGCAACCCACCCCT 8276	AGC TC
		AGGGGT GG GTTGTCCA	
		TCCCCA CC CAACGGGT	
		__ C_	
GAM1255	RET T 3'	GGTACTGAGCAGCCACTACCCC 21960	C C GTCC
		AGGGGTAG GGT GTT ACC	
		TCCCCATC CCG CGA TGG	
		A A GTCA	
GAM1255	RET T 3'	GGTACTGAGCAGCCACTACCCC 21786	C C GTCC
		AGGGGTAG GGT GTT ACC	
		TCCCCATC CCG CGA TGG	
		A A GTCA	
GAM1255	SNTB2 3'	ATATTGTACCGCTACCCCT 28377	_ T
		AGGGGTAGCGGT CG TGT	

			TCCCCATCGCCA GT ATA	
			T T	
GAM1255	UBE2H	3'	TGGCAGTTT	GAGACCGCTACCC 9352
	T		GGGGTAGCGGTC	CCA
			TCCCCATCGCCAG	GGT
			AGTTTGAC	
GAM1255	CENTG1	3'	ACGGAAACCCTACCCCT	16563 C CG
			AGGGGTAG GGT TTGT	
			TCCCCATC CCA	GGCA
			— AA	
GAM1255	FLJ10901	3'	GTGGACAGCAGCCACCCTT	20232 AGC C
			AGGGGT GGT GTTGTCCAC	
			TTCCA	CCG CGACAGGTG
			— A	
GAM1255	FUT10	3'	GTGAGATGTTACCACTTACCCC	26391 _C CGT _
	T		AGGGGTA G GGT TGTC CAC	
			TCCCCAT C CCA	G TAG GTG
			T A TT_ A	
GAM1255	GABBR1	5'	TAACGCTCCCCAACAGCTACCC	22424 _____ T_
	CT		AGGGGTAGC	GG CGTTG
			TCCCCATCG	CC GCAAT
			ACAACC TC	
GAM1255	KIAA1399	3'	TGGCAGGGAGCACTACCCCT	34798 CGG G T
			AGGGGTAG TC TTG CCA	
			TCCCCATC	AG GAC GGT
			ACG G _	
GAM1255	KIAA1924	3'	GGCCTGACCGCCACCCCT	36481 A TT
			AGGGGT GCGGTCG GTC	
			TCCCCA CGCCAGT	CGG
			C C_	
GAM1255	PRPF8	3'	TGATGGACAGCACCACCACCC	30689 AGC C C
			GGGT GGT GTTGTCCA CA	
			CCCA CCA CGACAGGT GT	
			CCA _ A	
GAM1255	LOC221935	3'	GTGGACAGTGCCACCTCCT	44501 _ AGC T
			AGG GGT GG CGTTGTCCAC	
			TCC CCA CC GTGACAGGTG	
			T _ _	
GAM1255	LOC245771	5'	GTGGACAGCAGCCACCCTT	44637 AGC C
			AGGGGT GGT GTTGTCCAC	

			TTCCCA CCG CGACAGGTG			
			___ A			
GAM1256	FACL4	5'	CACCACGCGCGCCCCCGCT 23251	A	TGG	_
			AGC GGGGCGC GCG TGGTG			
			TCG CCCC GCG CGC ACCAC			
			C ___ C			
GAM1256	FACL4	5'	CACCACGCGCGCCCCCGCT 10761	A	TGG	_
			AGC GGGGCGC GCG TGGTG			
			TCG CCCC GCG CGC ACCAC			
			C ___ C			
GAM1256	HTR6	5'	GCGACCCAGCGCCCCCGC 6550	A		_
			GC GGGGCGCTGGG CGT			
			CG CCCC GCGACCC GCG			
			C A			
GAM1256	ITGA4	5'	GCACCACGCCCGGGACCCC 6583	CG		
			GGGG CTGGGCGTGGTGC			
			CCCC GGCCCGCACCACG			
			AG			
GAM1256	MAPRE3	5'	GCCTCTGCCGAGCGCCCCCGC 14714	A	_	T_
			GC GGGGCGCTG GGCG GGT			
			CG CCCC GCGAC CCGT CCG			
			C G CT			
GAM1256	MHC2TA	3'	GCCTGCCAGGCCCTGC 5779	G	T	
			GCAGGGGC CTGGGCG GGT			
			CGTCCCCG GACCCGT CCG			

GAM1256	MMP15	3'	CCACCCAGCGCTCCTGCTA 8263		CG	
			TAGCAGGGGCGCTGGG TGG			
			ATCGTCCTCGCGACCC ACC			

GAM1256	AD-020	3'	CACCACAGCATCTGCCCTGCT 21339		CTGG	_
	A		TAGCAGGGGCG GC GTGGTG			
			ATCGTCCCCGT CG CACCAC			
			CTA_ A			
GAM1256	AD-020	3'	CACCACAGCATCTGCCCTGCT 29869		CTGG	_
	A		TAGCAGGGGCG GC GTGGTG			
			ATCGTCCCCGT CG CACCAC			
			CTA_ A			
GAM1256	DNAJC5	3'	GCCCCCAGCACCCCTGC 30814	C	CGT	
			GCAGGGG GCTGGG GGT			

		CGTCCCC CGACCC CCG	
		A _	
GAM1256 KIAA1808	3'	GCACCTTCGCCAGCGCCCCT 41547	G T_
		AGGGGCGCTGG CG GGTGC	
		TCCCCGCGACC GC CCACG	
		_ CTT	
GAM1256 KIAA1867	3'	GCCTCCCAGCGCCTCTGC 45454	CGT
		GCAGGGGCGCTGGG GGT	
		CGTCTCCGCGACCC CCG	
		T_	
GAM1256 KIAA1904	3'	GCTCTCCCCACGCCCTGC 36382	C CGT T
		GCAGGGGCG TGGG GG GC	
		CGTCCCCGC ACCC TC CG	
		_ C_ T	
GAM1256 MGC4796	3'	CCTCCAGGCCCTGC 30828	G CGT T
		GCAGGGGC CTGGG GG G	
		CGTCCCCG GACCC TC C	
		_ _ T	
GAM1256 TIAM2	3'	GCACCACGCCACGTCC 14823	C
		GGGCG TGGCGTGGTGC	
		CCTGC ACCCGCACCACG	
		-	
GAM1256 TSPEAR	3'	GCAGAGGCCAGAGCCCCTGC 29597	G GTGG
		GCAGGGGC CTGGGC TGC	
		CGTCCCCG GACCCG ACG	
		A GAG_	
GAM1256 LOC158310	5'	CACCACCACACCTGCTA 41943	GCGC GCG
		TAGCAGGG TGG TGGTG	
		ATCGTCCC ACC ACCAC	
		AC_ _	
GAM1256 LOC199990	3'	GCACCACGCCACGCAGGCC 42683	_ _
		GGGC GC TGGGCGTGGTGC	
		CCCG CG ACCCGCACCACG	
		GA C	
GAM1256 LOC220143	5'	GCACCACTTCCTGCCCCC 44954	C T C
		GGGG GC GGG GTGGTGC	
		CCCC CG CCT CACCACG	
		_ T T	
GAM1256 LOC90249	5'	GCACCACCACCACCT 31011	_ CGC GC
		AGG GG TGG GTGGTGC	

			TCC CC ACC CACCACG		
			A _ AC		
GAM1257	ABCD2	3'	AAGGATGAGTCTACATTTTA 11656	ACA	
			TAAAGTGTAGAT GTCCTT		
			ATTTTACATCTG TAGGAA		
			AG_		
GAM1257	ATP1A2	3'	GATTTCTACACTTTA 6369	TAC	
			TAAAGTGTAGA AGTC		
			ATTTCACATCT TTAG		
GAM1257	EDNRA	3'	TTTAAGAACTGTATTTTATTTT 32061	T C	
			AAAGTG AGATACAGT CTAAA		
			TTTTAT TTTATGTCA GAATTT		
			_ A		
GAM1257	MCL1	3'	TAAGGACCTAAAAGCACTTTA 22488	AGATACA	
			TAAAGTGT GTCCTTA		
			ATTCACG CAGGAAT		
			AAAATC_		
GAM1257	TCEA1	3'	TTAAGGACTGTATAATTCATT 39204	TAG_	
			AGTG ATACAGTCCTTAA		
			TTAC TATGTCAGGAATT		
			TTAA		
GAM1257	MGC2376	3'	TTAAGGACTTTCCACT 23413	TA TAC	
			AGTG GA AGTCCTTAA		
			TCAC CT TCAGGAATT		
			_ T_		
GAM1257	MIG2	3'	GACTGTATAAATGCATTTTA 35862	G_	
			TAAAGTGTA ATACAGTC		
			ATTTTACGT TATGTCAG		
			AAA		
GAM1257	ZNF387	3'	TAAGGACTGCACTATAGTT 16179	G ATA	
			AA TGTAG CAGTCCTTA		
			TT ATATC GTCAGGAAT		
			G AC_		
GAM1257	LOC151473	3'	TTAAGGACTACATACATTCTA 39123	A GATAC	
			TA AGTGTA AGTCCTTAA		
			AT TTACAT TCAGGAATT		
			C ACA_		
GAM1257	LOC151521	3'	AAGGACTGCCCCACCTTTA 41365	T AGATA	
			TAAAG GT CAGTCCTT		

		ATTTC CA GTCAGGAA		
		_ CCCC_		
GAM1257	LOC197131 3'	GA CTGTATCTTATTTTG 42448	T	
		TAAAGTG AGATACAGTC		
		GTTTTAT TCTATGTCAG		
GAM1257	LOC254973 5'	TGAGGCTATATCTGCACTT 46078	C T	
		AAGTGTAGATA AG CCTTA		
		TTCACGTCTAT TC GGAGT		
		A _		
GAM1258	PPP3CA 3'	TATAGAGAAAAAATTTT 6644	C	
		AAAGTTTTTT CTCTATA		
		TTTTAAAAAA GAGATAT		
		A		
GAM1258	KIAA0471 3'	TAAGGGAAAAAACTTTTAA 16914	TC	
		TTAAAAGTTTTTTTCC TA		
		AATTTTCAAAAAAGG AT		
		GA		
GAM1258	KIAA1594 3'	AGAAGGAAAAAACATTAA 35673	A _	
		TTAAA GTTTTTTCCT CT		
		AATTT CAAAAAAGGA GA		
		A A		
GAM1258	KLHL4 3'	CAATATAGAAAAAAAAC 21194	CC	
		GTTTTTT TCTATATTG		
		CAAAAAA AGATATAAC		
		AA		
GAM1258	LOC219401 3'	CAACATAGAGGAAACCCTT 44588	TTT A	
		AAG TTTCTCTAT TTG		
		TTC AAAGGAGATA AAC		
		CC_ C		
GAM1258	LOC219686 3'	TGTTAAGGAAAAAATTTTAA 43677	G CT	
		TTAAA TTTTTTCCT ATA		
		AATTTT AAAAAAGGA TGT		
		A AT		
GAM1259	ATP8A2 3'	AGAAAGGTGATGGCCAAGATA 44915	AATGGGC C	
		TGTCTTGG CACCTT CT		
		ATAGAACC GTGGAA GA		
		GGTA_ A		
GAM1259	CPSF6 3'	AGGAAGAGGATCACCTTCCAAG 13869	_ GG AC	
ACA		TGTCTTGGAA TG CC CTCCT		

			ACAGAACCTT AC GG GAAGGA		
			CC TA A_		
GAM1259 HIRA	3'	GGAAAGCTGTTCCAACACA	9325	C	G CACC
		TGT TTGGAATGG C TTCC			
		ACA AACCTTGTC G AAGG			
		C _A__			
GAM1259 LIMD1	3'	AGAAAGGCAGCCCATTTTA	15499		CA C
		TGGAATGGGC CCTT CT			
		ATTTTACCCG GGAA GA			
		AC A			
GAM1259 NKX3A	3'	GGAAAACCATTTCTAAAACA	12829	C	GCCACC
		TGT TTGGAATGG TTCC			
		ACA AATCTTACC AAGG			
		A AA__			
GAM1259 NRG1	5'	GAAAAGTGGCCAGAAACAGCA	15140	CT GAA_ C_	
		TGT TG TGGGCCAC TTC			
		ACG AC ACCCGGTG AAG			
		_ AAAG AA			
GAM1259 P2RY2	3'	AGGAAGGTGGCTTACCAAGAT	8413	AA	
		GTCTTGG TGGGCCACCTTCCT			
		TAGAACC ATTCGGTGGAAGGA			
		—			
GAM1259 PCLO	3'	AGGAAAAGCCATTTCAAGACA	45212		G CACC
		TGTCTTGGGAATGG C TTCCT			
		ACAGAACTTTACC G AAGGA			
		_AA__			
GAM1259 SERPIND1	3'	GAAGCCACCTCAAGACA	5688	AA	GCCAC
		TGTCTTGG TGG CTTC			
		ACAGAACT ACC GAAG			
		CC _____			
GAM1259 TMEPAI	3'	AGGCTGGGCGCATCCCAAGACA	21403	A G	ACCTT
		TGTCTTGG ATG GCC CCT			
		ACAGAACC TAC CGG GGA			
		C G GTC__			
GAM1259 TRPM6	3'	AGGAAGGTGGAAAACCAAGA	19196	AATGGG	
		TCTTGG CCACCTTCCT			
		AGAACC GGTGGAAGGA			
		AAAA__			
GAM1259 CDH26	5'	AGAAAGCAGCTTTTCCAAGA	22369	T CAC C	
		TCTTGGAA GGGC CTT CT			

AGAACCTT TTCG GAA GA
 _ AC_ A
 GAM1259 FLJ12587 3' GAAGGTGACCAAGACA 22851 AATGGGC C
 TGTCTTGG CACCTT C
 ||||| |||||
 ACAGAACC GTGGAA G
 A_____ A
 GAM1259 KIAA0759 3' AGAAAGGTGGCCTTGGACAAAA 33439 C GAAT C
 C GT TTG GGGCCACCTT CT
 || ||| ||||| ||
 CA AAC TCCGGTGGAA GA
 A AGGT A
 GAM1259 MGC4294 5' AGGCCACACCCACTCCAGGACA 23607 A CCA_
 TGTCTTGGGA TGGG CCT
 ||||| ||| ||
 ACAGGACCT ACCC GGA
 C ACACC
 GAM1259 SARM 3' GGAAGGCAGCCTCAGACA 17461 T GAAT CA
 TGTCT G GGGC CCTTCC
 ||||| ||| |||||
 ACAGA C TCCG GGAAGG
 _____ AC
 GAM1259 LOC146481 5' AGGAAAATCGGTTCCAAGGACA 38175 _ G CCACC
 TGTC TTGGAAT GG TTCCT
 ||| ||||| || |||||
 ACAG AACCTTG CT AAGGA
 G G AA_
 GAM1259 LOC152002 3' GGAAGACTCATTCCAA 39196 CCAC
 TTGGAATGGG CTTCC
 ||||| |||||
 AACCTTACTC GAAGG
 A_
 GAM1259 LOC153205 5' AGAAAGATGCTCTTTCTCCAAG 41579 AT_ CAC C
 AC GTCTTGA GGGC CTT CT
 ||||| ||| ||| ||
 CAGAACCT CTCG GAA GA
 CTTT TA_ A
 GAM1259 LOC220565 3' AGAAAGATAACCTTAACCAGGA 43631 AAT CCAC C
 CA TGTCTTGG GGG CTT CT
 ||||| ||| ||| ||
 ACAGGACC TCC GAA GA
 AAT AATA A
 GAM1259 LOC221362 3' AGGAAGGTAAATAACCAAAACA 45019 C AATGGGCC
 TGT TTGG ACCTTCCT
 ||| ||| |||||
 ACA AACC TGGAAGGA
 A AATAA_
 GAM1259 LOC92078 5' GAAAGTGGCTTGCCAAAAC 33745 C AATG C
 GT TTGG GGCCAC TTC
 || ||| ||||| |||

			CA AACC TCGGTG AAG			
			A GT__ A			
GAM1260	BLAME	3'	GTTTCTCTCACCCAGGTG 21311	CGT		CT
			CACC GGTGAGAGG GC			
			GTGG CCACTCTCT TG			
			AC_ T_			
GAM1260	MAPRE3	5'	AGCCGCAGCCTCTGCCGC 14710	G		A
			GTGGT AGAGGCTGCG CT			
			CGCCG TCTCCGACGC GA			
			— C			
GAM1260	DNAL4	3'	AGTGCTCTCACACGAGG 12305	—		—
			CC CGTGGTGAGAG GCT			
			GG GCACCACTCTC TGA			
			A G			
GAM1260	FLJ10922	3'	AGTCCCACCCTCACCAT 20252	A C C		
			GTGGTGAG GG TG GACT			
			TACCACTC CC AC CTGA			
			— _ C			
GAM1260	FLJ11286	3'	AGTCCATGTCCTCTCACCA 20413	— _ C		
			TGGTGAGAGG C TG GACT			
			ACCACTCTCC G AC CTGA			
			T T _			
GAM1260	KIAA0789	5'	AGTCGCAGAGAGGGACCCCGGG 31844	T		GAGAGG
			CCCG GGT CTGCGACT			
			GGGC CCA GACGCTGA			
			C GGGAGA			
GAM1260	KIAA1856	3'	AGCCGCAGCCTCCCGGCGG 44522	_ TGA		A
			CCGT GG GAGGCTGCG CT			
			GGCG CC CTCCGACGC GA			
			G _ C			
GAM1260	MGC3248	3'	GCGCCTCTCACACAGGT 26239	C G		T
			ACC GTG TGAGAGGC GC			
			TGG CAC ACTCTCCG CG			
			A _ _			
GAM1260	ODZ2	3'	TGACAGTCACCACGAGG 35098	_ AGAG		_
			CC CGTGGTG GCTG CG			
			GG GCACCAC TGAC GT			
			A _ A			
GAM1260	PP1665	3'	AGCCGCAGCCTCTCTTGAGGG 25089	GTGGT		A
			CCC GAGAGGCTGCG CT			

GGG CTCTCCGACGC GA
AGTT_ C
GAM1260 LOC163231 5' AGCCACACATTACACCACAGTG 40095 CC A____
CAC GTGGTGAG GGCT
||| ||||| |||
GTG CACCACTT CCGA
A_ ACACA
GAM1260 LOC163231 5' AGCCACTCATTACACCACAGTG 40096 CC A____
CAC GTGGTGAG GGCT
||| ||||| |||
GTG CACCACTT CCGA
A_ ACTCA
GAM1260 LOC221424 5' AGCCGCAGCCTCCGCCAC 44976 A A
GTGGTG GAGGCTGCG CT
||||| ||||| ||
CACCGC CTCCGACGC GA
_ C
GAM1261 FLJ21168 3' CAATATTTTCCAGTAACATTAA 24671 _ CACAC
TTAATGTTA TGGA GTATTG
||||| ||| |||||
AATTACAAT ACCT TATAAC
G TT____
GAM1262 CD28 3' ACGTAGACTTGTTCAAGTCTC 12780 C ____
GTTA TGACGAGACT GAATCA TCTACGT
||||||| ||||| |||||
ATTGCTCTGA CTTGGT AGATGCA
A TC
GAM1262 LOC148371 5' ACGTAGATTCGGGCAAGTC 38525 GAGA ATC
GAC CTCGA ATCTACGT
||| ||||| |||||
CTG GGGCT TAGATGCA
AAC_ ____
GAM1262 LOC221838 5' ACGTAGATTCAGGCAAGTC 44458 GAGA C ATC
GAC CT GA ATCTACGT
||| ||| |||||
CTG GA CT TAGATGCA
AACG _ ____
GAM1263 SLC7A8 3' TACGAAGGATCCCCAAGCCCTT 14552 A A A TTGAG_
CA A GAG GCTTG GG CGTA
| ||| ||||| || |||||
A TTC CGAAC CC GCAT
C C C TAGGAA
GAM1263 ERAP140 3' TACGTTTCACTCAAGTTCTC 37088 GTT
GAGAGCTTGAG GAGCGTA
||||||| |||||
CTCTTGA ACTC TTTGCAT
AC_
GAM1263 KIAA0865 3' TACACTCTGATTTTCAAGCTCC 30711 _ TT__ C
TC GAG AGCTTGAGG GAG GTA
||| ||||| ||| |||

		CTC TCGAACTTT CTC CAT	
		C TAGT A	
GAM1263 KIAA1550	3'	ATGTTCCCACACTCTCTTA 33068	CT A TT
		TAAGAGAG TG GG GAGCGT	
		ATTCTCTC AC CC CTTGTA	
		__ A __	
GAM1263 KIAA1715	3'	CAACCTCAAGCTCTTTTA 33790	
		TAAGAGAGCTTGAGGTTG	
		ATTTTCTCGAACTCCAAC	
GAM1263 NPTXR	3'	ACGCTCAACCCCAAGTCCTTT 15582	AG A
		AGAG CTTG GGTGAGCGT	
		TTTC GAAC CCAACTCGCA	
		CT C	
GAM1263 NPTXR	3'	ACGCTCAACCCCAAGTCCTTT 27730	AG A
		AGAG CTTG GGTGAGCGT	
		TTTC GAAC CCAACTCGCA	
		CT C	
GAM1263 LOC201164	3'	ACGCCAGTGCCAAGCTCTTCA 42527	A AG A
		A GAGAGCTTG GTTG GCGT	
		A TTCTCGAAC TGAC CGCA	
		C CG _	
GAM1263 LOC253891	3'	ACACTCGCTGCTTAAGCTC 45322	GT_ C
		GAGCTTGAG TGAG GT	
		CTCGAATTC GCTC CA	
		GTC A	
GAM1264 CASP8	3'	TTGAGATCAAGCCCCACGATG 27209	_ ATCAA
		CA CG TTTGATCTCAA	
		GT GC GAACTAGAGTT	
		A ACCCC	
GAM1264 IRF1	3'	TGAGACCAGTGTATCAGGTCA 32175	AC _ AT A
		TGACC GAT CA TTG TCTCA	
		ACTGG CTA GT GAC AGAGT	
		A_ T _ C	
GAM1264 MAPK4	3'	TTAAACTTGATCAGGTCA 8623	AC _
		TGACC GATCAA TTTGA	
		ACTGG CTAGTT AAATT	
		A_ C	
GAM1264 NR1I2	5'	TGAGATCAAAGTGTTGGGGTCA 9974	ACG A
		TGACC ATCA TTTGATCTCA	

			ACTGG TGGT AACTAGAGT		
			GG_ G		
GAM1264	TEM6	3'	TTGAATCTGTTTCGTGGTCA 22966	T _ TG	
			TGACCACGA CA ATT A		
			ACTGGTGCT GT TAA T		
			T C GT		
GAM1264	ZNF14	3'	GAGACCAGCGTGGTCA 22017	ATCAAT A	
			TGACCACG TTG TCTC		
			ACTGGTGC GAC AGAG		
			_____ C		
GAM1264	CGB5	5'	TGAGATCACTTCACCGTGGTC 26932	ATCAATT	
			GACCACG TGATCTCA		
			CTGGTGC ACTAGAGT		
			CACTTC_		
GAM1264	DKFZp434M0331	5'	AGAGCAAATTGGCCATGGCCA 19074	A CGA A	
			TG CCA TCAATTTG TCT		
			AC GGT GGTAAAC AGA		
			C ACC G		
GAM1264	DKFZp547I224	5'	TGAGATCAAAGTGGC 21481	A GAT_ A	
	A		TG CCAC CA TTTGATCTCA		
			AC GGTG GT AACTAGAGT		
			_ GAAC C		
GAM1265	B4GALT1	3'	TGGCCCCTTGGCAGGTAAG 7249	TTAA	
			CTTACCTGTTA GGCCA		
			GAATGGACGGT CCGGT		
			TCC_		
GAM1265	RPL15	3'	GCCTTAAGATTGGTAAGCT 8862	T A	
			AGCTTACC GTT TTAAGGC		
			TCGAATGG TAG AATTCCG		
			T _		
GAM1265	SDC4	3'	TTGGCCTTTCTGAAGGCAAGAC 8895	_ A G TT	
	T		AG CTT CCT TTA AAGGCCAA		
			TC GAA GGA AGT TTCCGGTT		
			A C _ CT		
GAM1265	AND-1	3'	TGGCCCTAAACATGTAA 13956	C AT A	
			TTAC TGTT TA GGCCA		
			AATG ACAA AT CCGGT		
			T _ C		
GAM1265	FTHFD	5'	TGGCCTTAACCAGAGCT 14480	TAC TTA	
			AGCT CTG TTAAGGCCA		

TCGA GAC AATTCCGGT
 ____ C__

GAM1265 GALNT6 3' GCCTGGGCAACAGGTAAGACT 14072 _ ATA
 AG CTTACCTGTT T AGGC
 || ||||| | |||
 TC GAATGGACAA G TCCG
 A C GG

GAM1265 KIAA0836 3' TGGCCATAGAAAAGTAAGCTT 32250 CTG A A
 AAGCTTAC TT TTA GGCCA
 ||||| || || |||||
 TTCGAATG AA GAT CCGGT
 AA_ _ A

GAM1265 KIAA1322 3' GCCTGCAGGTGAGCT 36029 TATTA
 AGCTTACCTGT AGGC
 ||||| |||
 TCGAGTGGACG TCCG

GAM1265 OSBPL5 3' TGGCCTTAATGCTAAAGC 35992 ACCT T
 GCTT GT ATTAAGGCCA
 ||| || |||||
 CGAA CG TAATTCCGGT
 AT_ _

GAM1265 p25 3' TTGGCCCCTGGAGGTGAGCT 13894 G TTAA
 AGCTTACCT TTA GGCCAA
 ||||| || |||||
 TCGAGTGGA GGT CCGGTT
 _ CC_

GAM1265 RAGB 5' TTGGCCTTAAAGCTAGCCAGCT 18780 TACCT A
 AGCT GTT TTAAGGCCAA
 ||| || |||||
 TCGA CGA AATTCCGGTT
 CCGAT _

GAM1265 LOC148114 5' TGACCTCAGTGGGCAGGTAGCT 38469 T _ A C
 AGCT ACCTGTT ATT AGG CA
 ||| ||||| || ||| ||
 TCGA TGGACGG TGA TCC GT
 _ G C A

GAM1265 LOC152641 3' GCCTTCTGGAAGGTAGGCTT 39299 GTTATT
 AAGCTTACCT AAGGC
 ||||| |||
 TTCGGATGGA TTCCG
 AGGTC_

GAM1265 LOC51696 3' TGACCTTAATACCCCAAGCTT 18313 ACCTGT C
 AAGCTT TATTAAGG CA
 |||| ||||| ||
 TTCGAA ATAATTCC GT
 CCCC_ A

GAM1266 CAPON 3' CCCCAGAGGACCAGAGC 31988 T A A
 G CT TGGTTTTCT GGG
 | || ||||| |||

			C GA ACCAGGAGA CCC		
			_ G _ C		
GAM1266	EGFR	3'	CCCTAAAAATCCAGACTCTTT 11723	AT	C
			AAAGAGTCT GGTTTT TAGGG		
			TTTCTCAGA CTAAAA ATCCC		
			C_ _		
GAM1266	IL18R1	3'	CAGAATAGCTCTTTA 9949	T	GGTTT A
			TAAAGAG CTAT TCT G		
			ATTTCTC GATA AGA C		
			_ _ _ _ C		
GAM1266	FLJ10081	3'	CCTGGGAACCCCAGACTC 19723	AT	T
			GAGTCT GGTTT CTAGG		
			CTCAGA CCAAG GGTCC		
			CC _		
GAM1266	FLJ10511	3'	CCCTAGAAAAACAACCTCT 19899	CTA	G
			AGAGT TG TTTTCTAGGG		
			TCTCA AC AAAAGATCCC		
			_ A		
GAM1266	KIAA0426	3'	CCCCAGAAAACCTTGTCTCT 16308	TCTAT	A
			AGAG GGTTTTCT GGG		
			TCTC TCAAAAGA CCC		
			TGT_ _ C		
GAM1266	LOC150577	5'	CCCTAAACCTCAGACTCTT 41219	AT	TTC
			AAGAGTCT GGTT TAGGG		
			TTCTCAGA CCAA ATCCC		
			CT _		
GAM1267	COL4A6	3'	CACTTAAATTCTCTAACCG 7582	AC	TTACT
			CG TAGAGAATTTG GTG		
			GC ATCTCTTAAAT CAC		
			CA T_ _		
GAM1267	COL4A6	3'	CACTTAAATTCTCTAACCG 27358	AC	TTACT
			CG TAGAGAATTTG GTG		
			GC ATCTCTTAAAT CAC		
			CA T_ _		
GAM1267	E2F6	3'	ACAGACAAATTCTCTAATC 7674	C	TA
			GA TAGAGAATTTGT CTGT		
			CT ATCTCTTAAACA GACA		
			A _		
GAM1267	LOC148756	3'	ACACACTCAAATTCTTTAATC 40901	C	TTAC
			GA TAGAGAATTTG TGTGT		

		CT ATTTCTTAAAC ACACA		
		A TC__		
GAM1267	LOC151405 5'	ACACAGGTAGCATCCCTCTAGT 41337	AATT	_
	C	GACTAGAG TGTTAC TGTGT		
		CTGATCTC ACGATG ACACA		
		CCT_ G		
GAM1267	LOC221061 3'	ACACAGTGTGCTCTCTAGTT 44770	ATTGT	
		GACTAGAGA TACTGTGT		
		TTGATCTCT GTGACACA		
		CGT__		
GAM1268	RBM3 5'	CGACGAGCAGGCACTGGAAGA 34893	_ AACA	C
		TCT C GCCTGCTCG CG		
		AGA G CGGACGAGC GC		
		A GTCA A		
GAM1268	KIAA0523 3'	GAGCAGGACGTTGAGATA 33643	AG	
		TATCTCAAC CCTGCTC		
		ATAGAGTTG GGACGAG		
		CA		
GAM1268	PSMD10 3'	CGAATAACTGTTGAGAT 8679	CC C	
		ATCTCAACAG TG TCG		
		TAGAGTTGTC AT AGC		
		A_ A		
GAM1268	LOC256107 5'	ATCAGCCAAGCAGGCTGCTGAG 46275	A	C_ C
	A	TCTCA CAGCCTGCT GC GAT		
		AGAGT GTCGGACGA CG CTA		
		C AC A		
GAM1269	DKFZp547J036 5'	CCACGCAGACAGTCACACCA 26040	TC_ CA	
		TGGT AT TCTGCGTGG		
		ACCA TG AGACGCACC		
		CAC AC		
GAM1269	KIAA1337 3'	CCACACAGATGGTGTGGACCAT 35983	_	C
	GCTG	TAGCATGGTTCAT CATCTG GTGG		
		GTCGTACCAGGTG GTAGAC CACC		
		TG A		
GAM1270	TRPS1 3'	GACTATTTGACAACCACA 15354	A AA	
		TGT GT TCAAATAGTC		
		ACA CA AGTTTATCAG		
		C AC		
GAM1270	DKFZp434O0515 5'	GACTACCTACTCAGCATTCCA 32787	_	ATCAAA
		TGGAATGT AGTA TAGTC		

	ACCTTACG TCAT ATCAG	
	AC CC___	
GAM1270 LOC148823 3'	GGATCTTGCCACCACATTCCA 29794	A AAT ATA
	TGGAATGT GT CAA GTCC	
	ACCTTACA CA GTT TAGG	
	C CC_ C__	
GAM1270 LOC152316 3'	GACTGCACCACTGCATTCCA 41452	AATCAAA
	TGGAATGTAGT TAGTC	
	ACCTTACGTCA GTCAG	
	CCAC___	
GAM1270 LOC93444 3'	ACTATTTGAAACATTC 35842	AGTAA
	GAATGT TCAAATAGT	
	CTTACA AGTTTATCA	
	A___	
GAM1271 CCNDBP1 5'	ACCTGCCTCCTCTTCGG 27397	_ T TT
	CCGAAGAG AG G CAGGT	
	GGCTTCTC TC C GTCCA	
	C _ _	
GAM1271 PTER 3'	GTACCTAAAAATATTCTC 24998	C__
	GAGAGTGTT AGGTAC	
	CTCTTATAA TCCATG	
	AAA	
GAM1271 SHOC2 3'	TACCTGAAGTGAGTCTTTGGGT 14306	GAGTG
A	TACCCGAAGA TTCAGGTA	
	ATGGGTTTCT AAGTCCAT	
	GAGTG	
GAM1271 DKFZP434I116 5'	GTACCCTGTTCTCTTT 17764	TGTT _
	GAAGAGAG CAGG TAC	
	TTTCTCTT GTCC ATG	
	___ C	
GAM1271 FLJ13848 3'	ACCTAACAGCTCCCTTTGG 24132	A _ C
	CCGAAG GAG TGTT AGGT	
	GGTTTC CTC ACAA TCCA	
	C G _	
GAM1271 KIAA1257 3'	GTACCCGGCCTACCCTTGGGTA 31436	AGAG T CA
	TACCCGA AG GTT GGTAC	
	ATGGGTT TC CGG CCATG	
	CCCA _ C_	
GAM1271 LOC128989 3'	GTACCTGAATGTGAGCTCCT 36945	A ____
	AG GAGT GTTCAGGTAC	

		TC CTCG TAAGTCCATG		
		_ AGTG		
GAM1271	LOC146894 3'	TACCTGAAGGTGACTCCGAGT 29783	C AA	A_ TG
		AC CG GAG G TTCAGGTA		
		TG GC CTC T AAGTCCAT		
		A _ AG GG		
GAM1271	LOC150155 3'	TACCAGCGTCTCCTTCGGGTA 35090	A _	CA
		TACCCGAAG GAG TGTT GGTA		
		ATGGGCTTC CTC GCGA CCAT		
		_ T _		
GAM1271	LOC150383 3'	TACCCGACGTTCTCCCTGG 38946	AA	CA
		CCG GAGAGTGTT GGTA		
		GGT CTCTTGCA G CCAT		
		CC C_		
GAM1272	DIO1 3'	GCCAAAAGATTTAAACCTGT 6451	T	ATGG
		ACAG GTTTAAGT TTTGGC		
		TGTC CAAATTTA AAACCG		
		_ GA_		
GAM1272	HMGB3 3'	CCTCCTGTACTTAAACAC 11817		TTT
		GTGTTTAAGTATGG GG		
		CACAAATTCATGTC CC		
		CT_		
GAM1272	ITGA6 3'	GCCAAATTTAAACTGTT 5703	G	A
		AACAGT TTTAAGT TGGT		
		TTGTCA AAATTTA ACCG		
		_ A		
GAM1272	LTBP2 3'	CCTCTATTACATAAAACACTG 6005	A _	TTT
		CAGTGTTTA GTA TGG GG		
		GTCACAAAT CAT ATC CC		
		A T T_		
GAM1272	SERPINB9 3'	CCAAGCATGCACCAAACACTG 10361	AA_	G
		CAGTGTTT GTATG TTTGG		
		GTCACAAA CGTAC GAACC		
		CCA _		
GAM1272	C20orf142 3'	CCAAACCATACCTGGGCCTGTT 36929	T	A
		AACAG GTTTA GTATGGTTTGG		
		TTGTC CGGGT CATAACCAAACC		
		_ C		
GAM1272	CDC14B 3'	ATCACATTTAAACACTGTT 27160		A
		AACAGTGTTTAAGT TGGT		

		TTGTCACAAATTTA ACTA	
		C	
GAM1272	CDC14B	3' ATCACATTTAAACACTGTT 9757	A
		AACAGTGTTTAAGT TGGT	
		TTGTCACAAATTTA ACTA	
		C	
GAM1272	DATF1	3' TCACACCTAGAACACTGT 22653	AAGTAT T
		ACAGTGTTT GGT TGG	
		TGTCACAAG CCA ACT	
		AT___ C	
GAM1272	DATF1	3' TCACACCTAGAACACTGT 28064	AAGTAT T
		ACAGTGTTT GGT TGG	
		TGTCACAAG CCA ACT	
		AT___ C	
GAM1272	DKFZp762A227	5' CCAAACAGATATCTAAACACT 15317	AG G_
		AGTGTTTA TAT GTTTGG	
		TCACAAAT ATA CAAACC	
		CT GA	
GAM1272	DNAM-1	3' GCCAAACTGAATAAACTGT 13339	G AGTA
		ACAGT TTTA TGGTTTGGC	
		TGTCA AAAT GTCAAACCG	
		_ AA_	
GAM1272	FLJ11011	3' GCCCTACTGCCTAAACACT 20291	A AT TT
		AGTGTTTA GT GGT GGC	
		TCACAAAT CG TCA CCG	
		C _ TC	
GAM1272	FLJ31153	3' GCCTGCGCACCTAAACACTG 29413	A ATG TT
		CAGTGTTTA GT GT GGC	
		GTCACAAAT CA CG CCG	
		C CG_ T_	
GAM1272	HSA250839	3' GCCAAAGGGGTAAACACT 20438	GTATGG
		AGTGTTTAA TTTGGC	
		TCACAAATT AAACCG	
		GGGG_	
GAM1272	KIAA0377	3' CCAAAGACCAAACACTG 16103	TAAGTA _
		CAGTGTT TGGTT TGG	
		GTCACAA ACCAG ACC	
		_____ AA	
GAM1272	SDCCAG1	3' GCCAAATGAACTAAACATTG 11071	A ATG
		CAGTGTTTA GT GTTTGGC	

		GTTACAAAT CA TAAACCG	
		_ AG_	
GAM1272	LOC122330 5'	GCCAAACCTACTAACAACACTG 37517	TA_ T
		CAGTGTT AGTA GGTTTGGC	
		GTCACAA TCAT CCAAACCG	
		CAA _	
GAM1272	LOC256401 3'	ACCACATTTAAACACTGTT 45944	A
		AACAGTGTTTAAGT TGGT	
		TTGTCACAAATTTA ACCA	
		C	
GAM1272	LOC90719 3'	CCAAACAGATATCTAAACACT 31946	AG G_
		AGTGTTTA TAT GTTTGG	
		TCACAAAT ATA CAAACC	
		CT GA	
GAM1273	CBFA2T2 3'	CAGCACCACAGAGTGCTTG 11547	GCCGAC A
		CAAGCACTT TGGT CTG	
		GTTCGTGAG ACCA GAC	
		AC_ C	
GAM1273	CYP24 3'	TCAGCACCATCTTCAGGTGCTT 6430	CC C A
		AAGCACTTG GA TGGT CTGA	
		TTCGTGGAC CT ACCA GACT	
		TT _ C	
GAM1273	DDX6 3'	CAGTACCAGCTTTGGTAATGTT 10643	C _
		AGCA TTGCCGA CTGGTACTG	
		TTGT AATGGTT GACCATGAC	
		_ TC	
GAM1273	GALNS 3'	CCAGTTGGCCCTGCAAGTGCCT 6121	A _
	G	CA GCACTT GCCGACTGG	
		GT CGTGAA CGGTTGACC	
		C CGTCC	
GAM1273	HNRPD 3'	CAGTATTGTAGAGCAAGTCTTG 7914	C CG_ T
		CAAG ACTTGC AC GGTACTG	
		GTTC TGAACG TG TTATGAC	
		_ AGA _	
GAM1273	HNRPD 3'	CAGTATTGTAGAGCAAGTCTTG 25364	C CG_ T
		CAAG ACTTGC AC GGTACTG	
		GTTC TGAACG TG TTATGAC	
		_ AGA _	
GAM1273	LRP4 3'	CAGTACCCTCAGTGCCTG 32196	A TGCC CT
		CA GCACT GA GGTACTG	

GT CGTGA CT CCATGAC
 C _ _ C_
 GAM1273 STAC 3' CAGTACCAATCAGTCAGTGTCA 9118 A T C C
 A GCACT GC GA TGGTACTG
 | |||| || || |||||
 A TGTGA TG CT ACCATGAC
 C C A A
 GAM1273 TTC3 3' TCAGTCAGCGAGTGCTTG 9316 C
 CAAGCACTTGC GACTGG
 ||||| |||||
 GTTCGTGAGCG CTGACT
 A
 GAM1273 AMOT 3' TCAGTAGGACAAGTGTGCG 28417 A _ G
 A GCACTTG CC ACTGG
 | |||| || ||||
 G TGTGAAC GG TGA CT
 C A A
 GAM1273 B3GNT1 5' TCAGCAGCGGCAACAAGTGC 13343 _ A GTA
 GCACT TGCCG CTG CTGA
 |||| |||| || ||||
 CGTGA ACGGC GAC GACT
 ACA _ _
 GAM1273 DKFZp434E1822 5' CAGTACCAGCATATGCT 33983 CT CGAC
 AGCA TGC TGGTACTG
 |||| || |||||
 TCGT ACG ACCATGAC
 AT _
 GAM1273 FLJ20297 3' CAGTAACATCAAGTGCTCA 19359 A CCGAC G
 C AGCACTTG TG TACTG
 | |||| || |||||
 A TCGTGAAC AC ATGAC
 C T _ A
 GAM1273 FLJ20297 3' CAGTAACATCAAGTGCTCA 19649 A CCGAC G
 C AGCACTTG TG TACTG
 | |||| || |||||
 A TCGTGAAC AC ATGAC
 C T _ A
 GAM1273 FLJ23560 3' AGTATTCAGAAAGTGCTTG 23996 GCCGA _
 CAAGCACTT CTGG TACT
 ||||| |||||
 GTTCGTGAA GACT ATGA
 _ T
 GAM1273 G2 3' TCAGTACCAATGGCTGTGC 33113 TT AC
 GCAC GCCG TGGTACTGA
 |||| || |||||
 CGTG CGGT ACCATGACT
 T _ A _
 GAM1273 KIAA0286 3' CAGAACCAGCAAGTGCTCC 33904 A CGAC A
 C AGCACTTGC TGGT CTG
 | |||| || |||||

C TCGTGAACG ACCA GAC
 C A
 GAM1273 PLA2G12 3' CAATATCAAAAACAAGTGCTTG 25150 CCGAC C
 CAAGCACTTG TGGTA TG
 ||||| |||||
 GTTCGTGAAC ACTAT AC
 AAAA_ A
 GAM1273 SV2B 3' TCAGTATTGGAGAAATGCTT 16883 C GCCGA TG
 AAGCA TT C GTACTGA
 ||||| | |||||
 TTCGT AA G TATGACT
 _ AGA_ GT
 GAM1273 LOC133634 3' TCAGCACTTTGGGCAAGTG GTT 37050 G GACT A
 G CAA CACTTGCC GGT CTGA
 || ||||| || |||||
 GTT GTGAACGG TCA GACT
 G GTT_ C
 GAM1273 LOC146146 5' TCAGCACATAGCAAGTGCTCA 38073 A CGACTG A
 C AGCACTTGC GT CTGA
 | ||||| || |||||
 A TCGTGAACG CA GACT
 C ATA_ C
 GAM1273 LOC146452 3' GCTGTGCGCAGTACTCA 38165 A C T T
 C AG ACT GCCGAC GGT
 | || || ||||| |||||
 A TC TGA CGGCTG TCG
 C A _ _
 GAM1273 LOC150630 3' TCAGTGCTGCAGCAAATGGC 41242 AC_ CGAC
 GC TTGC TGGTACTGA
 || ||||| |||||
 CG AACG GTCGTGACT
 GTA AC_
 GAM1273 LOC150776 3' CAGTAACATCAAGTGCTCA 31676 A CCGAC G
 C AGCACTTG TG TACTG
 | ||||| || |||||
 A TCGTGAAC AC ATGAC
 C T_ A
 GAM1273 LOC164295 5' CCAGTACGGCAAGTGCCTG 40141 A _
 CA GCACTTGCCG ACTGG
 || ||||| |||||
 GT CGTGAACGGC TGACC
 C A
 GAM1273 LOC203429 3' CAGCACCAATGCAAGTGC 43048 CGAC A
 GCACTTGC TGGT CTG
 ||||| |||||
 CGTGAACG ACCA GAC
 TA_ C
 GAM1273 LOC221272 5' TCAGTCATTGCACAAGTGCTTG 44964 _ C_
 CAAGCACT TGC GACTGG
 ||||| || |||||

GTTCGTGA ACG CTGACT
 AC TTA
 GAM1273 LOC91445 3' TCAACACCAGAGTTCAGTGTTT 30372 T_ CGA AC
 AAGCACT GC CTGGT TGA
 ||||| || ||||| ||
 TTTGTGA TG GACCA ACT
 CT A_ CA
 GAM1273 LOC92497 5' TGGAGCCAGCAAGTGCTT 34461 CGAC A
 AAGCACTTGC TGGT CTG
 ||||| ||||| |||||
 TTCGTGAACG ACCG GGT
 _ A
 GAM1273 LOC92689 3' CAGTACCAGTCCGTGGCA 34782 _
 TGCC GACTGGTACTG
 ||| |||||
 ACGG CTGACCATGAC
 TGC
 GAM1274 INPP5B 3' GAGCCAATCTTGACCTACC 45735 AT A
 GGTA TTCAAGATTG CTC
 ||| ||||| ||||| |||||
 CCAT AGGTTCTAAC GAG
 CC C
 GAM1274 FLJ23790 5' AGCCAGTGGAATTGCC 29579 AAG A
 GGTAATTTC ATTG CT
 ||||| ||||| |||||
 CCGTTAAAG TGAC GA
 G_ C
 GAM1274 KIAA0493 5' AGCCAGTGGAATTGCC 32138 AAG A
 GGTAATTTC ATTG CT
 ||||| ||||| |||||
 CCGTTAAAG TGAC GA
 G_ C
 GAM1274 KIAA0596 3' AGCCATTTGAAATTACTG 31460 AT A
 CGGTAATTTCAAG TG CT
 ||||| ||||| ||||| |||||
 GTCATTAAAGTTT AC GA
 _ C
 GAM1275 MYO1C 3' ACACCCCGAAGCCCACCTGCAA 30695 ATG _
 TCTC GAGATTGCAG GGGCT GGTGT
 ||||| ||||| ||||| |||||
 CTCTAACGTC CCCGA CCACA
 CA_ AGCC
 GAM1275 FLJ20209 3' ACACCAGCCCCAAAGGCAATTC 41401 A AGA
 T AGAG TTGC TGGGGCTGGTGT
 ||| ||||| ||||| ||||| |||||
 TCTT AACG ACCCCGACCACA
 _ GAA
 GAM1275 FLJ21919 3' GGCCCTTCCGCAATCTC 23277 A T
 GAGATTGC GA GGGGCT
 ||||| ||||| ||||| |||||

		CTCTAACG CT CCCCCG	
		C T	
GAM1275	FLJ30678	5' CACCCGAGCTACAATCTCT 29479	C ATG C
		AGAGATTG AG GGG TG	
		TCTCTAAC TC CCC AC	
		A GAG _	
GAM1275	FYCO1	3' ACACCAGCAGCCACAACCTC 23706	A CAGA G_
		GAG TTG TGG GCTGGTGT	
		CTC AAC ACC CGACCACA	
		C ____ GA	
GAM1276	AGL	3' CAGAAAACCAGCATATTTAA 5465	A CC_
		TTGAATAT CTGGT CTG	
		AATTTATA GACCA GAC	
		C AAA	
GAM1276	AGL	3' CAGAAAACCAGCATATTTAA 6282	A CC_
		TTGAATAT CTGGT CTG	
		AATTTATA GACCA GAC	
		C AAA	
GAM1276	AGL	3' CAGAAAACCAGCATATTTAA 6287	A CC_
		TTGAATAT CTGGT CTG	
		AATTTATA GACCA GAC	
		C AAA	
GAM1276	AGL	3' CAGAAAACCAGCATATTTAA 6292	A CC_
		TTGAATAT CTGGT CTG	
		AATTTATA GACCA GAC	
		C AAA	
GAM1276	AGL	3' CAGAAAACCAGCATATTTAA 6297	A CC_
		TTGAATAT CTGGT CTG	
		AATTTATA GACCA GAC	
		C AAA	
GAM1276	AGL	3' CAGAAAACCAGCATATTTAA 6304	A CC_
		TTGAATAT CTGGT CTG	
		AATTTATA GACCA GAC	
		C AAA	
GAM1276	ANK2	3' ATGCTCAGATGAACAACATATT 6821	AC G C_
		AATAT TG TC CTGAGCAT	
		TTATA AC AG GACTCGTA	
		CA A TA	
GAM1276	ANK2	3' ATGCTCAGATGAACAACATATT 21965	AC G C_
		AATAT TG TC CTGAGCAT	

		TTATA AC AG GACTCGTA		
		CA A TA		
GAM1276	CXCL13	3' CTCAGGGAAAGCATTTAA 13134	ATA GG	
		TTGAAT CT TCCCTGAG		
		AATTTA GA AGGGA		
		C_ A_		
GAM1276	MASP1	3' CTCAGGGACAGCAATTCA 7607	ATA G	
		TGAAT CTG TCCCTGAG		
		ACTTA GAC AGGGA		
		AC_ _		
GAM1276	PLS1	3' ATGCTCAAAATAGTTATATATT 8540	GTCCC	
	CA	TGAATAT ACTG TGAGCAT		
		ACTTATA TGAT ACTCGTA		
		TAT AAA_		
GAM1276	NAPG	3' ATGCTCAGAATCTAATATTCAA 46250	ACT CC	
		TTGAATAT GGT CTGAGCAT		
		AACTTATA CTA GACTCGTA		
		AT_ A_		
GAM1276	PRO1992	3' TTCAAGACCAGATATTCAA 15335	A CC	
		TTGAATAT CTGGTC TGAG		
		AACTTATA GACCAG ACTT		
		_ A_		
GAM1276	LOC150606	5' CTCAGGGGACAATTCAA 41234	ATAC GT	
		TTGAAT TG CCCTGAG		
		AACTTA AC GGGACTC		
		_ AG		
GAM1276	LOC203286	5' GCTTAGAACCAGTATGCCCAA 43496	AA CC	
		TTG TATACTGGT CTGAGC		
		AAC GTATGACCA GATT		
		CC A_		
GAM1277	ACP1	5' AGGCAGTTCCTCCCGGTGA 13957	AACAGA G	
		TCACCGGGGA A TGCTT		
		AGTGGCCCCT T ACGGA		
		_ G		
GAM1277	ACP1	5' AGGCAGTTCCTCCCGGTGA 10507	AACAGA G	
		TCACCGGGGA A TGCTT		
		AGTGGCCCCT T ACGGA		
		_ G		
GAM1277	NOL3	3' CATTTCCCTGGTGA 10062	AAACA	
		TCACCGGGG GAAGTG		

AGTGGTCCC CTTTAC

GAM1277 ZNF179 3' GGCTCATTTCCTCCCGATGA 14000 C CA AGT
TCA CGGGGAAA GA GCT
||| ||||| || |||
AGT GCCCCTTT CT CGG
A A_ _
GAM1277 FLJ14082 3' CTTCTGCCTCCCCGGTGG 24610 AA
TCACCGGGGA CAGAAG
||||||| |||||
GGTGGCCCCT GTCTTC
CC
GAM1277 KIAA1130 3' CAAGCACTCCTGCCTC 31281 AAA A
GGGG CAG AGTGCTTG
||| ||| |||||
CTCC GTC TCACGAAC
_ C
GAM1277 KIAA1536 3' TTTCTGTTCCCCCATTGA 21925 CC A
TCA GGGG AACAGAAG
||| ||| |||||
AGT CCCC TTGTCTTT
TA C
GAM1277 LOC121457 5' CACGTCCTGCTCCCCCTGGTGA 36661 AAA_ AA_
TCACCGGGG CAG GTG
||||||| ||| |||
AGTGGTCCC GTC CAC
CCTC CTG
GAM1277 LOC146227 3' CATTTCTGTTCTCCAATGA 38087 CC A
TCA GGGG AACAGAAGTG
||| ||| |||||
AGT CCTC TTGTCTTTAC
AA C
GAM1277 LOC256940 5' CAAGCATCATGGTTTCCCCAGT 46153 C AGAA
GG TCAC GGGGAAAC GTGCTTG
||| ||||| |||||
GGTG CCCCTTTG TACGAAC
A GTAC
GAM1278 AP2B1 3' CATGTTGGACTGAGACCTAA 6952 AA C_
TTAG TTTCA CCAACATG
||| ||| |||||
AATC AGAGT GGTTGTAC
C_ CA
GAM1278 CBFB 3' CATGCTGGGTGATGAAAGATTA 7506 AGAATT A
TAATTT TCACCCA CATG
||||| ||||| |||
ATTAGA AGTGGGT GTAC
AAGT_ C
GAM1278 CBFB 3' CATGCTGGGTGATGAAAGATTA 23147 AGAATT A
TAATTT TCACCCA CATG
||||| ||||| |||

		ATTAGA AGTGGGT GTAC	
		AAGT__ C	
GAM1278	KIAA0193	3' CATGCTGGTGGCCTTCTGAAT 16541	TT CAA
		ATTTAGAA TCACC CATG	
		TAAGTCTT GGTGG GTAC	
		CC TC_	
GAM1278	MBLL39	3' GTTGAATCATGTGATTCTAGAT 29573	T CC__
	TA	TAATTTAGAATT CA CAAC	
		ATTAGATCTTAG GT GTTG	
		T ACTAA	
GAM1279	C17orf31	3' CAAGGATCGGGCGGAAGCTG 18996	A ACCATCC
		TAGCTTCC CC CCTTG	
		GTCGAAGG GG GGAAC	
		C GCTA__	
GAM1279	FLJ12960	3' CAAGGGGATGGCCCAGGC 23913	CCACCA
		GCTT CCATCCCCTTG	
		CGGA GGTAGGGGAAC	
		CCC__	
GAM1279	GPS2	5' CAAGGGGACATGGAGAAAGC 10824	CCA CCA
		GCTT CCA TCCCCTTG	
		CGAA GGT AGGGGAAC	
		AGA AC_	
GAM1279	GPS2	3' CAAGGGGACATGGAGAAAGC 42146	CCA CCA
		GCTT CCA TCCCCTTG	
		CGAA GGT AGGGGAAC	
		AGA AC_	
GAM1279	PDZD2	5' CAAGGGGAGCCCTGGAAGCTG 39390	CCACCA
		TAGCTTCCA TCCCCTTG	
		GTCGAAGGT AGGGGAAC	
		CCCG__	
GAM1279	LOC126430	5' CAAGGTATTTGGTGGGAAGC 37276	CCATCC
		GCTTCCACCA CCTTG	
		CGAAGGTGGT GGAAC	
		TTAT__	
GAM1279	LOC144501	3' TCAACTCCCTGGGAGTGGGAAGC 40428	CA TCCCC
		GCTTCCAC CCA TTGA	
		CGAAGGTG GGT AACT	
		AG CCCTC	
GAM1279	LOC148398	5' CAAGGAGATGACGGGGGCTA 38530	ACCAC C
		TAGCTTCC CATC CCTTG	

ATCGGGGG GTAG GGAAC
 CA__ A
 GAM1279 LOC167153 5' TCAAAGGGTGGTGAAGAACTA 40230 C CAC T C
 TAG TTC CACCA CCC TTGA
 ||| ||| |||| ||| ||||
 ATC AAG GTGGT GGG AACT
 _ AA_ _ A
 GAM1279 LOC199221 5' CAAGGGGAGCTGGAAGC 39163 CCACCA
 GCTTCCA TCCCCTTG
 ||||| |||||
 CGAAGGT AGGGGAAC
 CG____
 GAM1279 LOC201911 3' CAAGAGGGCGCGGGAGCTA 43389 ACCACCAT _
 TAGCTTCC CCC CTTG
 ||||| ||| |||
 ATCGAGGG GGG GAAC
 CGC____ A
 GAM1279 LOC220565 3' CATTATGATGGTGGTAGAAGC 43632 C CCCT
 GCTTC ACCACCATC TG
 |||| ||||| ||
 CGAAG TGGTGGTAG AC
 A TATT
 GAM1279 LOC254228 3' AAGGGGCCGTGGAAGCT 45917 CACCAT
 AGCTTCCAC CCCCTT
 ||||| |||||
 TCGAAGGTG GGGGAA
 CC____
 GAM1279 LOC256310 3' CAAGAAGATGGAGGAGGTGGAA 46094 A__ CC
 GC GCTTCCACC CCATC CTTG
 ||||| |||| |||
 CGAAGGTGG GGTAG GAAC
 AGGA AA
 GAM1280 ACVR1 5' GTGACCATAGCCCACTG 6763 _ GCG
 CA TGGGT ATGGTCAC
 || |||| |||||
 GT ACCCG TACCAGTG
 C A_
 GAM1280 AF3P21 3' CCACACCCATGTGTA 18568 CGA
 TACACATGGGTG TGG
 ||||| |||
 ATGTGTACCCAC ACC

 GAM1280 FZD6 3' TGACCACCCATTGATTGTA 9596 C__ GCGAT
 TACA ATGGGT GTCA
 ||| |||| |||
 ATGT TACCCA CCAGT
 TAGT _____
 GAM1280 GAS11 3' GTGACCATCTGGGTCTGTGT 7223 G_
 ACATGGGT C GATGGTCAC
 ||||| | |||||

			TGTGTCTG G CTACCA	GTG		
			G T			
GAM1280	GRIN2B	3'	CACTTGCACCCATGTGTA	6490		—
			TACACATGGGTGCGA TG			
			ATGTGTACCCACGTT AC			
			C			
GAM1280	PCDH7	5'	GATTAGCACCCATTG	8451	C	GA
			CA ATGGGTGC TGGTC			
			GT TACCCACG ATTAG			
			— —			
GAM1280	PCDH7	5'	GATTAGCACCCATTG	26215	C	GA
			CA ATGGGTGC TGGTC			
			GT TACCCACG ATTAG			
			— —			
GAM1280	PCDH7	5'	GATTAGCACCCATTG	26219	C	GA
			CA ATGGGTGC TGGTC			
			GT TACCCACG ATTAG			
			— —			
GAM1280	RET	3'	GTGACCACCAACATTCTGTGT	21787	T	CGA_
			ACACA GGGTG TGGTCAC			
			TGTGT CTTAC ACCAGTG			
			AACC			
			—			
GAM1280	RET	3'	GTGACCACCAACATTCTGTGT	21961	T	CGA_
			ACACA GGGTG TGGTCAC			
			TGTGT CTTAC ACCAGTG			
			AACC			
			—			
GAM1280	RGL	3'	GTGACCACCAAGACATATATGT	17508	G	CGA___
			ACATG GTG TGGTCAC			
			TGTAT TAC ACCAGTG			
			A AGAACC			
			—			
GAM1280	ROCK2	3'	GTGACCATTATACTGTGTA	32842	TGG	CG
			TACACA GTG ATGGTCAC			
			ATGTGT CAT TACCAGTG			
			— AT			
			—			
GAM1280	SH3BP4	3'	TGACCATCCATAGAATATGTG	15855	G___	C
			CACATG GTG GATGGTCA			
			GTGTAT TAC CTACCA			
			AAGA			
			—			
GAM1280	C1orf8	5'	CAACGTCACCCATCTGTA	11299	C	_ A
			TACA ATGGGTG CG TG			

ATGT TACCCAC GC AC
 C T A
 GAM1280 CTNNBIP1 3' GTGAGCACACCCGTGTG 21546 CGA G
 CACATGGGTG TG TCAC
 ||||| || |||
 GTGTGCCAC AC AGTG
 G
 GAM1280 DKFZP434E2135 3' GTGACCAAGGCCCATGTGTG 25117 GCGA
 TACACATGGGT TGGTCAC
 ||||| |||||
 GTGTGTACCCG ACCAGTG
 GA
 GAM1280 DKFZp761N0624 3' ACCATTTACACCATTGTA 26072 C _ C
 TACA ATGG GTG GATGGT
 ||| ||| ||| |||||
 ATGT TACC CAC TTACCA
 _ A T
 GAM1280 DKFZp762E1312 5' GTGACCATCAGTGACCTGT 20452 _ _
 ATGGGT GC GATGGTCAC
 ||||| || |||||
 TGTCCA TG CTACCAGTG
 G A
 GAM1280 FBXO24 3' TGACCATTGTGCACATGCG 14465 A G TG
 C CATG G CGATGGTCA
 | ||| | |||||
 G GTAC C GTTACCAGT
 C A GT
 GAM1280 FLJ20651 3' GTGAACTCTACCCATGT 19576 C TGG
 ACATGGGTG GA TCAC
 ||||| || |||
 TGTACCCAT CT AGTG
 CA
 GAM1280 FLJ21168 3' GTGAATGCACACATGTG 24672 G ATGG
 CACATG GTGCG TCAC
 ||||| ||||| |||
 GTGTAC CACGT AGTG
 A A
 GAM1280 GGA2 3' GTGAACTCACACATGTGTA 28923 G CGATGG
 TACACATG GTG TCAC
 ||||| || |||
 ATGTGTAC CAC AGTG
 A TCA
 GAM1280 GGA2 3' GTGAACTCACACATGTGTA 17402 G CGATGG
 TACACATG GTG TCAC
 ||||| || |||
 ATGTGTAC CAC AGTG
 A TCA
 GAM1280 KIAA0350 3' GACCACCGTGGCCATCTG 30670 C G A
 CA ATGG TGCG TGGTC
 || ||| ||| |||||

			GT TACC GTGC ACCAG		
			C G C		
GAM1280	KIAA1550	3'	TGAGCACGCACGTGTA	33074	ATGG A G
			TACAC GTGCG TG TCA		
			ATGTG CACGC AC AGT		
			_____ _ G		
GAM1280	KIAA1729	5'	TGACCATTGCTACATGTG	42951	GGT
			CACATG GCGATGGTCA		
			GTGTAC CGTTACCAGT		
			AT_		
GAM1280	MGC4663	3'	GACCACCGCTTGTGTGTG	23717	TG CGA
			TACACA GGTG TGGTC		
			GTGTGT TCGC ACCAG		
			GT C_		
GAM1280	RIS1	3'	TGACCAAATCCTGTGTA	39273	T GCGA
			TACACA GGGT TGGTCA		
			ATGTGT CCTA ACCAGT		
			_ A_		
GAM1280	ZNF220	5'	TGACGAGACCCATGTGTG	13632	GCGATG
			TACACATGGGT GTCA		
			GTGTGTACCCA CAGT		
			GAG_		
GAM1280	LOC116064	3'	TGACTCTCACCCATGTCA	36497	C C TG
			A ACATGGGTG GA GTCA		
			A TGTACCCAC CT CAGT		
			C T _		
GAM1280	LOC158293	3'	ACCACACCCATGTGT	39805	CGA
			ACACATGGGTG TGGT		
			TGTGTACCCAC ACCA		

GAM1281	LFG	3'	TGAGGAACTGAGGCCACGTCA	37698	AAAAGACAA
			TGACGT AGTTCCTCA		
			ACTGCA TCAAGGAGT		
			CCGGAG_		
GAM1281	MEN1	5'	GAAC TAATTCTGTTACGTCA	44843	A CAA
			TGACGTAA AGA AGTTC		
			ACTGCATT TCT TCAAG		
			G TAA		
GAM1281	RFX5	3'	TGAAGACCTACTTTGTCCTCTA	6049	AAA _ C
	C		GTA GACAAAGT TC TCA		

			CAT CTGTTTCA AG AGT		
			CTC TCC A		
GAM1281	SNX6	3'	TGAGTGC GTTTTGTCTTCACG 22218	A A	TTC_
	T		ACGT AA GACAAAG CTCA		
			TGCA TT CTGTTTT GAGT		
			C C GCGT		
GAM1281	TARBP2	3'	TGAGGAGCAGGCCTTTCACGTC 28630	A	ACAAA
	A		TGACGT AAAG GTTCCTCA		
			ACTGCA TTTC CGAGGAGT		
			C CGGA_		
GAM1281	TPMT	3'	AACCCTTGTCTTTTACTCA 5937	C	A_
			TGA GTAAAAGACAA GTT		
			ACTCATTTTCTGTT CAA		
			_ CC		
GAM1281	AASDHPPT	3'	TGAAAACTTTGTCTTGTCA 17723	TAAA	CC
			TGACG AGACAAAGTT TCA		
			ACTGT TCTGTTTCAA AGT		
			_____ AA		
GAM1281	B3GALT6	3'	AGGAAAGACTTTTATGTCA 27923	ACAAAG	
			TGACGTAAAAG TTCCT		
			ACTGTATTTTC AAGGA		
			AGA_		
GAM1281	DAPK2	3'	AACTTCTGTCTTTTAAGCCA 15632	ACG	_
			TG TAAAAGACA AAGTT		
			AC ATTTTCTGT TTCAA		
			CGA C		
GAM1281	DKFZP761F241	3'	ACTTGTCTTACGTCA 25475	AA	A
			TGACGTAA GACAA GT		
			ACTGCATT CTGTT CA		
			C_ _		
GAM1281	ENAH	3'	ACTTAATCTTTTACATCA 20122	C	CA
			TGA GTAAAAGA AAGT		
			ACTCATTTTCT TTCA		
			A AA		
GAM1281	FLJ30574	3'	AACTGAAGTCTTTTACATC 29446	C	AA_
			GA GTAAAAGAC AGTT		
			CTCATTTTCTG TCAA		
			A AAG		
GAM1281	OSBPL10	3'	TGAGAAGTTGCTTCTTTTACAT 19416	C	CA_ G C
	CA		TGA GTAAAAGA AA TTC TCA		

ACT CATTTTCT TT AAG AGT
 A TCG G _
 GAM1281 ZF 3' GATTTTGTCAATTTTACATCA 22190 C ____
 TGA GTAAAA GACAAAGTT
 ||| ||||| |||||
 ACT CATTTT CTGTTTtag
 A TTA
 GAM1281 LOC116068 3' TGAAGAACTTTGTTTACATCA 36501 C AAA C
 TGA GTA GACAAAGTTC TCA
 ||| ||| ||||| |||
 ACT CAT TTGTTTCAAG AGT
 A ____ A
 GAM1281 LOC151121 5' GAGGAACTTTCCTACTCA 39052 C AAA CA
 TGA GTA GA AAGTTCCTC
 ||| ||| || |||||
 ACT CAT CT TTCAAGGAG
 _ C_ _
 GAM1281 LOC201411 3' AACCTTGTCTTTTACTCA 31526 C A_
 TGA GTAAAAGACAA GTT
 ||| ||||| |||
 ACT CATTTTCTGTT CAA
 _ CC
 GAM1281 LOC254085 5' GGAGCCGTCTTTTACTCA 45972 C AAA
 TGA GTAAAAGAC GTTCC
 ||| ||||| |||||
 ACT CATTTTCTG CGAGG
 _ C_
 GAM1282 FLJ10726 3' GCTGGATCCAATAGTGACCTG 20058 C GTT
 TAGGTCAC ATTGGAT GC
 ||||| ||||| ||
 GTCCAGTG TAACCTA CG
 A GGT
 GAM1282 FLJ23153 3' CAGCACAATGGTGACC 23908 GA
 GGTCACCATTG TGTG
 ||||| |||||
 CCAGTGGTAAC ACGAC
 _
 GAM1282 KIAA1036 3' GCAGCAACATCTGTGAGCC 17127 _ CATT C
 GG TCAC GGATGTTGC GC
 || ||| ||||| ||
 CC AGTG TCTACAACG CG
 G ____ A
 GAM1282 KIAA1577 5' GCAGCACATTATCAGCAGTGAC 32212 CA _ T C
 CTA TAGGTCAC TTG GATGT GC GC
 ||||| || ||| |||
 ATCCAGTG GAC TTACA CG CG
 AC TA _ A
 GAM1282 LOC91308 3' GCAACATTCACTTA 32657 CACCAT
 TAGGT TGGATGTTGC
 ||||| |||||

			ATTCA ACTTACAACG		
			AT_____		
GAM1283	AHCY	3'	TGCCCAGGCCCCACCTCT 6344	A	AGAAATA
			AGAG TGG CTTGGGCA		
			TCTC ACC GGACCCGT		
			C CC_____		
GAM1283	ARCN1	3'	CCAGTCTGTCCCCATCTCT 7367	A	AAT T
			AGAGATGG GA ACT GG		
			TCTCTACC CT TGA CC		
			C GTC _		
GAM1283	ARCN1	3'	TCAATTCATTCCTTCATCTCT 7369	A	AC_
			AGAGATGGAG AAT TTGG		
			TCTCTACTTC TTA AACT		
			C CTT		
GAM1283	ATRN	3'	TGCCTGTCCCTCTCCTTCTC 29303	T	AAT TT
			GAGA GGAGA AC GGGCA		
			CTCT CCTCT TG TCCGT		
			T CCC _		
GAM1283	CDC42	3'	TTGCCTTTTCTCTCCACCCTT 7542	A_	AATACTT
			GAG TGGAGA GGGCAA		
			TTC ACCTCT TCCGTT		
			CC CTTT_____		
GAM1283	CDH1	3'	TGCCCAGCTCCCCAACTC 10566	A	A AATAC
			GAG TGG GA TTGGGCA		
			CTC ACC CT GACCCGT		
			A C C_____		
GAM1283	CDK5R2	3'	GCCCCCATTTCTCCATTTCT 10043		ACTT
			AGAGATGGAGAAAT GGGC		
			TCTTTACCTCTTTA CCCG		
			CC_____		
GAM1283	DOCK1	3'	TTGCCCAAACATTCTTTCTTT 7052	TG	ATAC
			AGAGA GAGAA TTGGGCAA		
			TTTCT TTCTT AACCCGTT		
			_ ACA_		
GAM1283	GGA3	3'	CCAGTATTTCCCCTTCTC 28902	T	A T
			GAGA GG GAAATACT GG		
			CTCT CC CTTTATGA CC		
			T C _		
GAM1283	GGA3	3'	CCAGTATTTCCCCTTCTC 15199	T	A T
			GAGA GG GAAATACT GG		

			CTCT CC CTTTATGA CC		
			T C _		
GAM1283	GJB3	5'	CTGGTTATTCTCCTCTCT 23439	T	C TG
			AGAGA GGAGAAATA T G		
			TCTCT CCTCTTTAT G C		
			_ T GT		
GAM1283	IL22RA2	5'	TCAAGTTCTCTCCACCTCT 27524	A	AAT
			AGAG TGGAGA ACTTGG		
			TCTC ACCTCT TGAAC		
			C CT_		
GAM1283	KCND2	5'	TGCACATCACCTCCATCTCT 14612		AAATACT G
			AGAGATGGAG TG GCA		
			TCTCTACCTC AC CGT		
			CACT__ A		
GAM1283	KLHL3	3'	CCAATGGCATCTCTCCATCT 42268	A A _	
			AGATGGAGA AT CT TGG		
			TCTACCTCT TA GG ACC		
			C C TA		
GAM1283	LMO1	5'	CCACGAGATTCCCCCATCTCT 8128	A_ ATA _	
			AGAGATGG GAA CTTG GG		
			TCTCTACC CTT GAGC CC		
			CC A__ A		
GAM1283	LOXL2	3'	CCCCATTTCTCCTCCTCT 8132	AT	ACTT
			AGAG GGAGAAAT GGG		
			TCTC CCTCTTTA CCC		
			CT C__		
GAM1283	NR2E1	5'	TGTCCATCTCTCCATCT 9280		AATACT
			AGATGGAGA TGGGCA		
			TCTACCTCT ACCTGT		
			CT__		
GAM1283	PDE4A	3'	TTGCCTAGCCTCTCCCTCTC 12877	T	AATAC
			GAGA GGAGA TTGGGCAA		
			CTCT CCTCT GATCCGTT		
			C CC__		
GAM1283	PDGFB	3'	TGCACACTTCCCCATCTTT 8471	A	ATACT G
			AGAGATGG GAA TG GCA		
			TTTCTACC CTT AC CGT		
			C C__ A		
GAM1283	PPP2R5D	3'	CCAGGTATCTCCCCTCCTCT 12916	AT A A	
			AGAG GG GA ATAATTGG		

			TCTC CC CT TATGGACC		
			CT C C		
GAM1283	PPP3CA	3'	TGTGGATATTTCTCCATCCT 6647	A	_ TGG
			AG GATGGAGAAATA CT GCA		
			TC CTACCTCTTTAT GG TGT		
			_ A _		
GAM1283	PRX	3'	GCCTCAGTTTCCCCATCTCT 21939	A	AT T
			AGAGATGG GAA ACT GGGC		
			TCTCTACC CTT TGA TCCG		
			C _ C		
GAM1283	PTEN	5'	CCAGCAGCTTCTGCCATCTCT 5852	_	ATAC
			AGAGATGG AGAA TTGG		
			TCTCTACC TCTT GACC		
			G CGAC		
GAM1283	PXN	3'	TGCCCCACTCTCCATCCT 8758	A	AATACT
			AG GATGGAGA TGGGCA		
			TC CTACCTCT ACCCGT		
			_ C _		
GAM1283	RGR	3'	TTAAGTTATTTCTCATCCCT 8826	A G	_
			AG GATG AGAAATA CTTGG		
			TC CTAC TCTTTAT GAATT		
			C _ T		
GAM1283	SLC2A1	3'	GCCCCCTTCCCATCTCT 13265	A	ATACTT
			AGAGATGG GAA GGGC		
			TCTCTACC CTT CCCG		
			_ C _		
GAM1283	SLC30A3	3'	GTCTATCTCTCCATCCCT 9528	A	AATACT
			AG GATGGAGA TGGGC		
			TC CTACCTCT ATCTG		
			C CT _		
GAM1283	UCP2	5'	CCAGTTTTTCTCCATCTC 9381	T T	
			GAGATGGAGAAA ACT GG		
			CTCTACCTCTTT TGA CC		
			T _		
GAM1283	ZNF175	3'	TTGCCCCCCCTTTCCATCTC 13999		AATACTT
			GAGATGGAGA GGGCAA		
			CTCTACCTTT CCCGTT		
			CCCC _		
GAM1283	AKAP11	3'	CCCACTCTCTCTCATCTCT 18368	_	AATACT
			AGAGATG GAGA TGGG		

			TCTCTAC CTCT	ACCC		
			T CTC__			
GAM1283	ARP5	5'	TGCCCTCTCCCCGTCTCT	35440	A	AATACTT
			AGAGATGG GA	GGGCA		
			TCTCTGCC CT	CCCGT		
			C CT__			
GAM1283	BCAA	5'	GCCCTTCTTCCCCATCTCT	18512	A	ATACTT
			AGAGATGG GAA	GGGC		
			TCTCTACC CTT	CCCG		
			C CTT__			
GAM1283	C17orf31	5'	TGCCTCTCAGTTTCTCCATCT	19009		ACTT
			AGATGGAGAAAT	GGGCA		
			TCTACCTCTTTG	TCCGT		
			ACTC			
GAM1283	C1orf16	3'	TGCCCCATCTCCATCCCT	16859	A	AATACTT
			AG GATGGAGA	GGGCA		
			TC CTACCTCT	CCCGT		
			C AC__			
GAM1283	C1orf24	3'	TGCCTACTTCACCATCTCT	27537	A	ATACT
			AGAGATGG GAA	TGGGCA		
			TCTCTACC CTT	ATCCGT		
			A C__			
GAM1283	C9orf5	3'	TGTAGTATTTTCCCATCTCT	25718	AG	TGG
			AGAGATGG AAATACT	GCA		
			TCTCTACC TTTATGA	TGT		
			CT _			
GAM1283	CLECSF9	3'	TGCCCAAGCATATATCGTCTCT	15690		AGAAATA
			AGAGATGG CTTGGGCA			
			TCTCTGCT GAACCCGT			
			ATATAC_			
GAM1283	CNNM1	3'	TGCCTTCCCTTCCATCTCT	21611		AAATACTT
			AGAGATGGAG	GGGCA		
			TCTCTACCTT	TCCGT		
			CCCT__			
GAM1283	DKFZP564C103	3'	TGTTCCCTCACCCCTCCATCTCT	17902		AAATACTT
			AGAGATGGAG	GGGCA		
			TCTCTACCTC	CTTGT		
			CCACTC__			
GAM1283	DKFZP586I2223	3'	TGCTACTTCCCCATCTTT	17734	A	ATACTTG
			AGAGATGG GAA	GGCA		

		TTTCTACC CTT	TCGT		
		C CA_____			
GAM1283	DKFZP586I2223	3' TGCTACTTCCCCATCTTT	28018	A	ATACTTG
		AGAGATGG GAA	GGCA		
		TTTCTACC CTT	TCGT		
		C CA_____			
GAM1283	DKFZP586I2223	3' TGCTACTTCCCCATCTTT	28020	A	ATACTTG
		AGAGATGG GAA	GGCA		
		TTTCTACC CTT	TCGT		
		C CA_____			
GAM1283	ELF4	3' TTGCCTGGATCTCCTCCCCTCT	7129	AT__	AATAC TG
		AGAG	GGAGA T GGCAA		
		TCTC	CCTCT G CCGTT		
		CCCT	A____GT		
GAM1283	FIGN	3' CCACAAAGAACCTCTCCATCTC	45776	AATAC_ _	
		GAGATGGAGA	TTG GG		
		CTCTACCTCT	AAC CC		
		CCAAGA	A		
GAM1283	FLJ10139	3' CCTATCTCTCCCATCTCT	19735	_	AATACT
		AGAGATGG AGA	TGGG		
		TCTCTACC TCT	ATCC		
		C CT_____			
GAM1283	FLJ12704	3' CCACCTGTTTCTCATCTCT	24564	G	CT
		AGAGATG AGAAATA	TGG		
		TCTCTAC TCTTTGT	ACC		
		_	CC		
GAM1283	FLJ12704	3' TGCATCATTTTCCATC	24566	ATACT	_
		GATGGAGAA	TGG GCA		
		CTACCTTTT	ACT CGT		
		_____	A		
GAM1283	FLJ13265	3' TGCCTCAGTTTCTCCATCTC	24313	AT	T
		GAGATGGAGAA	ACT GGGCA		
		CTCTACCTCTT	TGA TCCGT		
		_	C		
GAM1283	FLJ14213	3' CCAGGATGAGGACCCCTCCATC	24252	AA_____	A
	TC	GAGATGGAG	AT CTTGG		
		CTCTACCTC	TA GGACC		
		CCCAGGAG	_		
GAM1283	FLJ14213	3' CCCTGGGCCTTTCCATCTC	24253	AATA	T
		GAGATGGAGA	CT GGG		

			CTCTACCTTT	GG CCC		
			CCG_ T			
GAM1283	FLJ14327	3'	TCCATTTCTCATCTCT	24429	G	TACT
			AGAGATG AGAAA	TGGG		
			TCTCTAC TCTTT	ACCT		
			— ———			
GAM1283	FLJ14768	3'	GTCTTTCTCTCCATCTCT	26615		AATACTT
			AGAGATGGAGA	GGGC		
			TCTCTACCTCT	TCTG		
			CTT_____			
GAM1283	FLJ20281	5'	CCCAAGTATCAGCATATTTCT	43725		GAGAA
			AGAGATG	ATACTTGGG		
			TCTTTAT	TATGAACCC		
			ACGAC			
GAM1283	FLJ20802	3'	TGCCTTCTCCTCCATTTCT	19675		AAATACTT
			AGAGATGGAG	GGGCA		
			TCTTTACCTC	TCCGT		
			CTCT_____			
GAM1283	FLJ22215	3'	TGCCTCCCCTCTGCCCATCTCT	46283	—	AATACTT
			AGAGATGG AGA	GGGCA		
			TCTCTACC TCT	TCCGT		
			CG CCCC_____			
GAM1283	GLCCI1	5'	CCCAAGTATGCTTCATCTC	44480		AA
			GAGATGGAG	ATACTTGGG		
			CTCTACTTC	TATGAACCC		
			G_			
GAM1283	GPA33	3'	TTGCCACACACTTTCCATCTC	12407		AATACT
	T		AGAGATGGAGA	TGGGCAA		
			TCTCTACCTTT	ACCCGTT		
			CACAC_			
GAM1283	HPCAL4	3'	TGCCCAAGCCCTTCCTCCCCTC	18388	AT	AAATA_
			GAG GGAG	CTTGGGCA		
			CTC CTC	GAACCCGT		
			C_ CTTCCC			
GAM1283	KIAA0268	3'	CCAAATCACTTTTCCATCTCT	34685		ATAC_
			AGAGATGGAGAA	TTGG		
			TCTCTACCTTTT	AACC		
			CACTA			
GAM1283	KIAA0523	3'	CCACATTCATTCTCCATTTC	33639	A	ACT _
			GAGATGGAG AAT	TG GG		

	CTTTACCTC TTA AC CC	
	C CTT A	
GAM1283 KIAA0939	3' CAAGCACATCTCCATCTCT 31058	AATA
	AGAGATGGAGA CTTG	
	TCTCTACCTCT GAAC	
	ACAC	
GAM1283 KIAA0953	3' TGCTCCACCTCTTCATCTCT 33172	AATACT _
	AGAGATGGAGA TGG GCA	
	TCTCTACTTCT ACC CGT	
	CC____ T	
GAM1283 KIAA1280	5' TGCACACACCATCTCCATCTC 34556	AATACT G
	GAGATGGAGA TG GCA	
	CTCTACCTCT AC CGT	
	ACCAC_ A	
GAM1283 KIAA1301	3' TTGCCCAAACATTTCTTT 32980	AC
	GGAGAAAT TTGGGCAA	
	TTTCTTTA AACCCGTT	
	CA	
GAM1283 KIAA1363	3' TTGCCTAGATCCCCCATCTC 34336	A_ AATAC
	GAGATGG GA TTGGGCAA	
	CTCTACC CT GATCCGTT	
	CC A____	
GAM1283 KIAA1655	3' TTGCCCCCTCTCTCTCCATCT 33093	AATACTT
C	GAGATGGAGA GGGCAA	
	CTCTACCTCT CCCGTT	
	CTCTCCC	
GAM1283 KIAA1879	5' TGGCCACCCCCTCCATCTCT 36417	AAATACT G
	AGAGATGGAG TGG CA	
	TCTCTACCTC ACC GT	
	CCCC____ G	
GAM1283 LASP1	3' CCAGGCATATGTTTCCCCATCT 12791	A ____
CT	AGAGATGG GAAATA CTTGG	
	TCTCTACC CTTTGT GGACC	
	C ATAC	
GAM1283 MGC10960	3' CCATGGTGCTTCCCTCCATCTC 26381	_ A _
	GAGATGGA GAA TACT TGG	
	CTCTACCT CTT GTGG ACC	
	CC C T	
GAM1283 MGC12760	3' CCTGGTCACCCTCCATCTCT 26449	AAAT T
	AGAGATGGAG ACT GG	

			TCTCTACCTC	TGG CC		
			CCAC T			
GAM1283	MGC5139	5'	CCGGCATTTC	CCGCCTC	36675	A A T
			GAG TGGAGAAAT	CT GG		
			CTC GCCTCTTTA	GG CC		
			C C _			
GAM1283	NIBAN	3'	TGCCTACTTC	ACCATCTCT	22632	A ATACT
			AGAGATGG GAA	TGGGCA		
			TCTCTACC CTT	ATCCGT		
			A C _			
GAM1283	NSG-X	3'	TGCAAATCTCT	CCCTCTCT	15755	T A ACTTGG
			AGAGA GGAGA AT	GCA		
			TCTCT CCTCT TA	CGT		
			C C AA _			
GAM1283	NXN	3'	CCCAAGTGTCC	AGCCTCT	22806	A_ GAAA
			AGAG TGGA	TACTTGGG		
			TCTC ACCT	GTGAACCC		
			CG _			
GAM1283	PCBP3	3'	TTGCCTGAGACCC	CTCCTCTCT	21752	T AAATA TG
			AGAGA GGAG CT	GGCAA		
			TCTCT CCTC	GA CCGTT		
			_ CCCA_ GT			
GAM1283	PI4KII	3'	TTGCCAAGCCTC	CTCCATCTC	20484	AAATA G
			GAGATGGAG CTTGG	CAA		
			CTCTACCTC	GAACC GTT		
			CTCC_ _			
GAM1283	PRO0659	3'	CCCGGGATCTC	CCATCTCT	15405	ATA
			AGAGATGGAGA CTTGGG			
			TCTCTACCTCT	GGGCCC		
			A _			
GAM1283	PTPRN2	3'	CCACAGCATT	CCTCCATCTT	28367	A A _
			GAGATGGAG AAT CT	TGG		
			TTCTACCTC TTA	GA ACC		
			C C C			
GAM1283	PTPRN2	3'	CCACAGCATT	CCTCCATCTT	28372	A A _
			GAGATGGAG AAT CT	TGG		
			TTCTACCTC TTA	GA ACC		
			C C C			
GAM1283	SHANK3	3'	TGCCCAGTCTT	CCATCTC	32636	AAAT T
			GAGATGGAG ACT	GGGCA		

		CTCTACCTT TGA CCCGT		
		C___ _		
GAM1283	SIAT9	3' TTGATGTATTTCTCCATCCT 9979	A	_TG
		AG GATGGAGAAATAC T G		
		TC CTACCTCTTTATG A T		
		_ T GT		
GAM1283	TIGD1	5' CCCACAGACCGTTCCCCATCTC 42847	A	ATA_ _
	T	AGAGATGG GAA CT TGGG		
		TCTCTACC CTT GA ACCC		
		C GCCA C		
GAM1283	WDR9	3' CTAAATGTCATTCTCCATCTCT 27390		_ C
		AGAGATGGAGAA ATA TTGG		
		TCTCTACCTCTT TGT AATC		
		AC A		
GAM1283	LOC112616	3' TGTCTCCTCTCCATCTCT 28775		AATACTT
		AGAGATGGAGA GGGCA		
		TCTCTACCTCT TCTGT		
		CC___		
GAM1283	LOC126364	3' TTGCTCCCCACCTCCCATCCCT 37274	A	A AATACTT
		AG GATGG GA GGGCAA		
		TC CTACC CT CTCGTT		
		C _ CCACCC_		
GAM1283	LOC145739	3' TCAAGTTATTTCTCCTTCTCT 37964	T	_
		AGAGA GGAGAAATA CTTGG		
		TCTCT CCTCTTTAT GAACT		
		T T		
GAM1283	LOC145845	3' TGTCTCCATTCTGCCATCTCT 40619		_ A ACTT
		AGAGATGG AG AAT GGGCA		
		TCTCTACC TC TTA TCTGT		
		G C CC_		
GAM1283	LOC146909	3' TGCCATGTTCCCCCATCTTT 38270	A_	ATACTTG
		AGAGATGG GAA GGCA		
		TTTCTACC CTT CCGT		
		CC GTA___		
GAM1283	LOC146957	3' TGCCCAGGCTCTCCTCCTC 38282	AT	AATA
		GAG GGAGA CTTGGGCA		
		CTC CCTCT GGACCCGT		
		CT C___		
GAM1283	LOC147791	3' TGCCCCTGGGCTCCCATCTCT 40859	A	AATA T_
		AGAGATGG GA CT GGGCA		

TCTCTACC CT GG CCCGT
 _ CG_ TC
 GAM1283 LOC148710 3' TGCTTGGCAATGCTCTCCATCT 40895 A_ AC TG
 C GAGATGGAGA AT T GGCA
 ||||| || | |||
 CTCTACCTCT TA G TCGT
 CG AC GT
 GAM1283 LOC149372 3' CCCATTTCTCCTCCCT 38727 A T TACT
 AG GA GGAGAAA TGGG
 || || ||||| |||
 TC CT CCTCTTT ACCC
 C _ _
 GAM1283 LOC150319 3' TGCTGGCACTTCTCCATCCT 38898 A ATA TG
 AG GATGGAGAA CT GGCA
 || ||||| || |||
 TC CTACCTCTT GG TCGT
 _ CAC _
 GAM1283 LOC151154 5' GCCCAAGTGCCCTCCTCT 41304 T AAA
 AGA GGAG TACTTGGGC
 || ||| |||||
 TCT CTC GTGAACCCG
 _ CC_
 GAM1283 LOC152245 5' CCACAGGTTTCTCTCTCCATCC 41450 A AAT_ _
 CT AG GATGGAGA ACTTG GG
 || ||||| |||||
 TC CTACCTCT TGGAC CC
 C CTCTT A
 GAM1283 LOC152271 3' TTGCCCAAGTATTTTGTGCTTT 39241 ATGGA
 AGAG GAAATACTTGGGCAA
 ||| |||||
 TTTC TTTTATGAACCCGTT
 GTG_
 GAM1283 LOC154860 5' CCAGAAGGGTATTTTCTCCA 41734 _
 TGGAGAAATACT TGG
 ||||| |||
 ACCTCTTTATGG ACC
 GAAG
 GAM1283 LOC157681 5' CTATTCTATTTCTCATCTC 39643 GA CT_
 GAGATG GAAATA TGG
 ||||| ||||| |||
 CTCTAC CTTTAT ATC
 TC CTT
 GAM1283 LOC164714 3' CCGATGTACACTTCTCCGTC 42177 A_ _
 GATGGAGAA TAC TTGG
 ||||| ||| |||
 CTGCCTCTT ATG AGCC
 CAC T
 GAM1283 LOC196337 3' TGCCTTCAGTTCCTCCACCTC 42362 A A AAT T_
 GAG TGG GA ACT GGGCA
 ||| ||| || |||||

	CTC ACC CT TGA TCCGT		
	C _ CCT CT		
GAM1283 LOC200982 3'	CCAAGTATTTCTCCATGTC 43373	G	
	GA ATGGAGAAATACTTGG		
	CT TACCTCTTTATGAACC		
	G		
GAM1283 LOC203350 3'	TGCCTCGATTTCTTCATCTCT 43539		ACTT
	AGAGATGGAGAAAT GGGCA		
	TCTCTACTTCTTTA TCCGT		
	GC__		
GAM1283 LOC222128 5'	GTCATTTCTCTCACCTCT 44539	A _ _	
	AGAG TG GAGAAAT AC		
	TCTC AC CTCTTTA TG		
	C T C		
GAM1283 LOC254085 5'	TGCCCACTTCTCATCTCT 45973	G	ATACT
	AGAGATG AGAA TGGGCA		
	TCTCTAC TCTT ACCCGT		
	_ C__		
GAM1283 LOC51107 3'	GCCCTGTATTTCTCCATCTC 18096		TT
	GAGATGGAGAAATAC GGGC		
	CTCTACCTCTTTATG CCCG		
	T_		
GAM1283 LOC51308 3'	TGCCCAGGGTCCCCATCCT 18711	A A AATA	
	AG GATGG GA CTTGGGCA		
	TC CTACC CT GGACCCGT		
	_ C G__		
GAM1283 LOC63928 3'	CCAGTTATTCTCCATCTC 22636	AT T	
	GAGATGGAGAA ACT GG		
	CTCTACCTCTT TGA CC		
	AT _		
GAM1283 LOC85414 3'	CCTGGTTTCCCATCTCT 26950	A	ACTT
	AGAGATGG GAAAT GG		
	TCTCTACC CTTTG CC		
	_ GT__		
GAM1283 LOC90678 3'	TGCCCAGGAGCCCCATCCT 28749	A	AGAAATA
	AG GATGG CTTGGGCA		
	TC CTACC GGACCCGT		
	_ CCCGA__		
GAM1283 LOC91151 5'	TGCTCCATCCCTCCTCTCT 27055	T	AAATACT _
	AGAGA GGAG TGG GCA		

TCTCT CCTC ACC CGT
 _ CCT_ T
 GAM1283 LOC91301 5' TGCCTCAGTTTCCCCATCTCT 32653 A AT T
 AGAGATGG GAA ACT GGGCA
 ||||| ||| ||| |||||
 TCTCTACC CTT TGA TCCGT
 C _ C
 GAM1284 APPBP2 3' CAATGCAAGATGCTCTGATAGC 13080 _ T GACAC
 GC ATCAGAG CG CGTTG
 || ||||| || |||||
 CG TAGTCTC GT GTAAC
 A _ AGAAC
 GAM1284 POU2AF1 3' CAAGGGCCTACCCTGATGCCA 12890 A C ACA G
 TGGCATCAG GT GG CC TTG
 ||||| || || |||||
 ACCGTAGTC CA CC GG AAC
 C T _ G
 GAM1284 LOC149401 5' TGCCCAACTCTGAAGCCA 38739 A C A
 TGGC TCAGAGT GG CA
 ||| ||||| || ||
 ACCG AGTCTCA CC GT
 A A C
 GAM1285 A1BG 3' CTCACTGTGTTGCCCAA 28276 CGCTA
 TTGGGCAACACA TGAG
 ||||| |||||
 AACCCGTTGTGT ACTC
 C_
 GAM1285 PDGFRA 3' CTTCTCATGTATATTACCCAA 12883 CAACACAC T
 TTGGG GC ATGAGAAG
 |||| || |||||
 AACCC TG TACTCTTC
 ATTATA_ _
 GAM1285 CBX6 3' TCCCATGCACTTGCCCAA 15577 CACAC T A
 TTGGGCAA GC ATG GA
 ||||| || ||| ||
 AACCCGTT CG TAC CT
 CA_ _ C
 GAM1285 CENTG2 3' CTCCTGGACCACGTTGCCCAA 17157 ACACG T
 TTGGGCAAC CTA GAG
 ||||| ||| |||
 AACCCGTTG GGT CTC
 CACCA C
 GAM1285 DKFZP434A0131 3' CTCCCAAGACCGTGCTTGCCCA 21062 _ ACG AT_
 A
 TTGGGCAA CAC CT GAG
 ||||| ||| || |||
 AACCCGTT GTG GA CTC
 C CCA ACC
 GAM1285 KCNV1 5' CTTCCGGCGTGTCCCAA 15711 CAAC AT
 TTGGG ACACGCT GAG
 |||| ||||| |||

		AACCC TGTGCGG TTC	
		C__ CC	
GAM1285 MARKL1	3'	CTCACCTGCAGCCTGTTGCCCA 25396	CAC_ TA_
A		TTGGGCAACA GC TGAG	
		AACCCGTTGT CG ACTC	
		CCGA TCC	
GAM1285 LOC148293	3'	CTTCTAGGTATTTGCCCA 38518	CAC G T
		TTGGGCAA AC CTA GAG	
		AACCCGTT TG GAT TTC	
		TA_ _ C	
GAM1285 LOC220018	5'	GTAGCATGAGTTGCCCA 44857	A C
		TTGGGCAAC CA GCTAT	
		AACCCGTTG GT CGATG	
		A A	
GAM1285 LOC86651	5'	CTTCTCATTGCTGTATCATCCC 34099	CAAC_ C T
AA		TTGGG ACA GC ATGAGAAG	
		AACCC TGT CG TACTCTTC	
		TACTA _ T	
GAM1286 C1orf6	3'	CTGTTGGAAATTCCAGGGTA 21328	CA C
		TACCCTG AAT TCCAACAG	
		ATGGGAC TTA AGGTTGTC	
		C_ A	
GAM1286 PEX3	3'	AATCTGTTGGAGACATAGG 9690	CAAA
		CCTG TCTCCAACAGATT	
		GGAT AGAGGTTGTCTAA	
		AC_	
GAM1286 BCMP1	3'	AATCTGTAAAGAGCAGG 25454	AAA CC
		CCTGC TCT AACAGATT	
		GGACG AGA TTGTCTAA	
		_ A_	
GAM1286 DKFZP434F1735	5'	TGGGAAAGATTTGCTAGGTA 17857	CT _
		TACC GCAAATCT CCA	
		ATGG CGTTTAGA GGT	
		AT AAG	
GAM1286 FLJ21106	5'	ATCTGTTATTGCAAGGT 24733	C ATCTCC
		ACC TGCAA AACAGAT	
		TGG ACGTT TTGTCTA	
		A A_	
GAM1286 KIAA0914	3'	AATCTGTTGTTTCTGCCAAAGG 17032	CT_ AATCTC
TA		TACC GCA CAACAGATT	

		ATGG CGT GTTGTCTAA	
		AAAC CTTT__	
GAM1286 KIAA1287	3'	AATCTCAAAGATTTGCAG 38324	CCAAC
		CTGCAAATCT AGATT	
		GACGTTTAGA TCTAA	
		AAC__	
GAM1286 MRPS14	3'	CTATTGAGCTTGCAGGG 22641	AT C C
		CCCTGCAA CTC AA AG	
		GGGACGTT GAG TT TC	
		C_ _ A	
GAM1286 LOC91351	3'	AATCCAAAGAAATTTGCAGG 32695	C CAACA
		CCTGCAAAT TC GATT	
		GGACGTTTA AG CTAA	
		A AAAC_	
GAM1287 ATP7A	3'	CCACATTTGAATCCTCT 5492	A CAA
		AGAG AT TTAAATGTGG	
		TCTC TA AGTTTACACC	
		C _	
GAM1287 CGTHBA	3'	CCACACTGATGATTCTC 14355	A AA
		GAGAATCA TTA TGTGG	
		CTCTTAGT AGT ACACC	
		_ C_	
GAM1287 ESRRG	3'	CCACATTTCTCTTTCTCTTT 32997	TCAATT
		AAAGAGAA AAATGTGG	
		TTTCTCTT TTTACACC	
		TCTC__	
GAM1287 RFX5	3'	CCAAGAAACACTGATTTTCTTT 6045	ATTAAATG
CA		TGAAAGAGAATCA TGG	
		ACTTTCTTTTAGT ACC	
		CACAAAGA	
GAM1287 SUFU	3'	CCACCTCTTAACATCTCTTTCA 18251	ATCAA AT_
		TGAAAGAGA TTAA GTGG	
		ACTTTCTCT AATT CACC	
		AC__ CTC	
GAM1287 DJ971N18.2	3'	CACTTCTGATTTTCCTTCA 22133	A ATTAAAT
		TGAA GAGAATCA GTG	
		ACTT CTTT TAGT CAC	
		C CTT__	
GAM1287 FLJ20079	3'	CCACACTTTGAGGATTCTCTTC 19170	A AA _
A		TGAA GAGAATC TTAAA TGTGG	

		ACTT CTCTTAG AGTTT ACACC	
		— G_ C	
GAM1287 KIAA1949	5'	CCACATTTCTCTCTTCTCCCTC 46667	AA TCAATT
A		TGA GAGAA AAATGTGG	
		ACT CTCTT TTTACACC	
		CC CTCTC_	
GAM1287 KIAA1949	5'	CCACATTTCTCTCTTCTCCCTC 44208	AA TCAATT
A		TGA GAGAA AAATGTGG	
		ACT CTCTT TTTACACC	
		CC CTCTC_	
GAM1287 KIAA1949	5'	CCACATTTCTCTCTTCTCCCTC 46712	AA TCAATT
A		TGA GAGAA AAATGTGG	
		ACT CTCTT TTTACACC	
		CC CTCTC_	
GAM1287 TACTILE	3'	CCACATTTTCAATCCTCCTTCA 12409	A AATCAATT
		TGAA GAG AAATGTGG	
		ACTT CTC TTTACACC	
		C CTAAC_	
GAM1287 TTTY2	5'	CCACATTTGTGTCCTCTTTTA 42070	AAT AT
		TGAAAGAG CA TAAATGTGG	
		ATTTTCTC GT GTTTACACC	
		CT_ _	
GAM1287 LOC159148	5'	CCACATTTGTGTCCTCTTTTA 42077	AAT AT
		TGAAAGAG CA TAAATGTGG	
		ATTTTCTC GT GTTTACACC	
		CT_ _	
GAM1287 LOC199692	3'	CCACACTTTGGTTTTCCCTTCA 29810	A TTA
		TGAA GAGAATCAA TGTGG	
		ACTT CTTTGGTT ACACC	
		C TC_	
GAM1287 LOC91012	3'	CCACATTTCTGTACTGTTCCCTC 32280	_ CA_ T_
TTTCA		TGAAAGAG AAT AT AAATGTGG	
		ACTTTCTC TTG TG TTTACACC	
		C TCA TC	
GAM1288 FUT6	5'	AGCCTTTTCACTTTGTACTCA 5649	C TGATCCA
		TGAG TAC AAAAGGCT	
		ACTC ATG TTTCCGA	
		_ TTTCAC_	
GAM1288 PRKCN	3'	CCTTTTGGAGTTGCTC 12399	T TGA
		GAGC AC TCCAAAAGG	

CTCG TG AGGTTTTTCC
T ____

GAM1288 SMARCD2 3' TAGCCTTTCTAAACCAAAGTTC 9052 AC ATCCAA
GAGCT TG AAAGGCTA
||||| || |||||
CTTGA AC TTTCCGAT
A_ CAAATC

GAM1288 SURF5 3' AGCCTTTTTTTGGGCAGTCA 13605 T A _
C ACTG TCCAAAAA GGCT
| ||| ||||| |||
A TGAC GGGTTTTT CCGA
C _ T

GAM1288 FLJ11142 3' AGCCTTCTTGATTGCCCA 20342 A TACT A
TG GC GATCCAA AAGGCT
|| || ||||| |||||
AC CG TTAGGTT TTCCGA
C _ C

GAM1288 KIAA0256 3' TAGCCTTTTTATGAGACAGGTC 32186 G A_ G CC
A
TGA CT CT AT AAAAAGGCTA
||| || || |||||
ACT GA GA TA TTTTCCGAT
G CA G _

GAM1288 KIAA1450 3' AGCCTTTTTTAAGAGAGGCCA 32748 A A GATCC
TG GCT CT AAAAAGGCT
|| ||| || |||||
AC CGG GA TTTTCCGA
_ A GAA_

GAM1288 KIAA1829 3' GCCTTTTTGCCACTCA 31032 CTAC ATC
TGAG TG CAAAAAGGC
|||| || |||||
ACTC AC GTTTTCCG
_ C_

GAM1288 PRO1580 5' AGCCTTTTTTGCCAGGCCA 20566 A TA ATC
TG GC CTG CAAAAAGGCT
|| || || |||||
AC CG GAC GTTTTCCGA
_ _ C_

GAM1288 LOC149373 3' AGCCGAACAGTAGCTCA 38718 A CAAAAA
TGAGCTACTG TC GGCT
||||||| || |||
ACTCGATGAC AG CCGA
A _

GAM1288 LOC165246 5' AGCCTTCCAGTAGCTCA 40126 ATCCAAA
TGAGCTACTG AAGGCT
||||||| |||||
ACTCGATGAC TTCCGA
CC_

GAM1288 LOC256207 3' TAGCCTTTCCAAAGGAGACAGT 45620 T A_ AA_
CA
C ACTG TCC AAAGGCTA
| ||| || |||||

		A TGAC AGG TTTCCGAT	
		C AG AAACC	
GAM1288	LOC90459 3'	AGCCTCCTGAGTAGCTCA 31489	GATC AAA
		TGAGCTACT CA AGGCT	
		ACTCGATGA GT TCCGA	
		____ CC_	
GAM1289	CCND2 3'	CCTTATATCATGTACCTCA 7513	C T T
		TGAGGTACA TG TAT AGG	
		ACTCCATGT AC ATA TCC	
		_ T T	
GAM1289	EPHA2 3'	GCCAAGTAAACAGGGTACCTCA 10714	A _ A
		TGAGGTAC CTGTT ATT GGT	
		ACTCCATG GACAA TGA CCG	
		G A A	
GAM1289	UBE4A 3'	CTAATATCAACAGTATATCTCA 11197	C ____
		TGAGGTA ACTGT TATTAG	
		ACTCTAT TGACA ATAATC	
		A ACT	
GAM1289	DKFZP434P0721 3'	TTACCTAATAATTACCTCA 31874	CACT
		TGAGGTA GTTATTAGGTAA	
		ACTCCAT TAATAATCCATT	

GAM1289	FLJ10287 3'	TACCTAATCTCTTTGTGCCTCA 21155	CTGTT
		TGAGGTACA ATTAGGTA	
		ACTCCGTGT TAATCCAT	
		TTCTC	
GAM1289	FLJ10607 3'	TACCCCATAGGCAGTGTACCCA 37835	A _ TA
		TG GGTACACTGT TAT GGTA	
		AC CCATGTGACG ATA CCAT	
		_ G CC	
GAM1289	KIAA0182 3'	TCTATAACAGTAAACCCCA 35646	A AC T
		TG GGT ACTGTTAT AGG	
		AC CCA TGACAATA TCT	
		C AA _	
GAM1289	KIAA1908 5'	ACCTAATGGTGAACCCCA 36327	A A GTT
		TG GGT CACT ATTAGGT	
		AC CCA GTGG TAATCCA	
		C A ____	
GAM1290	ARHGAP6 5'	CTCCACACCCAGCACCCC 6844	A A A
		GG GGT CTGGGTGT GAG	

			CC CCA GACCCACA CTC		
			_ C C		
GAM1290	CTSB	3'	CCATCAGTTCCCCCAGTACCTC 32327	TGT	AG
	C		GGAGGTACTGGG AG GATGG		
			CCTCCATGACCC TT CTACC		
			CC_ GA		
GAM1290	DMPK	3'	CATCCTCCACGCACCCCC 10661	TACT	A__
			GG GGGTGT GAGGATG		
			CC CCCACG CTCCTAC		
			_____ CAC		
GAM1290	DNMT3L	5'	CCATCCTCTGAACCCCAATCCC 15017	A TACT	G
	C		GG GG GGGT TAGAGGATGG		
			CC CC CCCA GTCTCCTACC		
			_ TAAC A		
GAM1290	GFAP	3'	CCACCCAGCACCCAGCAACTCC 7812	GTA	AGA A
			GGAG CTGGGTGT GG TGG		
			CCTC GACCCACG CC ACC		
			AAC A__ C		
GAM1290	MUC3B	3'	CCATCCTGCACCCCAAGTCCCC 45252	A T	T AG
			GG GG ACTGGG GT AGGATGG		
			CC CC TGACCC CA TCCTACC		
			__ _ _ CG		
GAM1290	MUC4	3'	CCACCCTCAATCAGTACC 28710	GTGTA	A
			GGTACTGG GAGG TGG		
			CCATGACT CTCC ACC		
			AA__ C		
GAM1290	RHO	3'	CCATCCCCTACACCTTCCCCC 6138	A TACT	A
			GG GG GGGTGTAG GGATGG		
			CC CC TCCACATC CCTACC		
			_ CT__ C		
GAM1290	XRCC3	3'	CCACCCCCCACTCAGTGCCTCC 11907	TAGA	A
			GGAGGTACTGGGTG GG TGG		
			CCTCCGTGACTCAC CC ACC		
			CC__ C		
GAM1290	DOK4	3'	CCATCCTCCATGGCACAGCCCT 19880	TA G GTA_	
	CC		GGAGG CTG GT GAGGATGG		
			CCTCC GAC CG CTCCTACC		
			C_ A GTAC		
GAM1290	FLJ12910	5'	CCACCCCCATTCTCAGCTCCTC 23799	TA	TGTAGA A
	C		GGAGG CTGGG GG TGG		

CCTCC GACTC CC ACC
 TC TTACC_ C
 GAM1290 KIAA1130 3' CCATCCTCCACCCAGGCACTTC 31282 A_ TA
 C GGAGGT CTGGGTG GAGGATGG
 ||||| ||||| |||||
 CCTTCA GACCCAC CTCCTACC
 CG _
 GAM1290 KIAA1297 3' CACCCTACCCAGTACC 35709 GTAG A
 GGTACTGGGT AGG TG
 ||||| |||
 CCATGACCCA TCC AC
 _ C
 GAM1290 NMT1 3' CCACCCTCTGCCACCCAGTCCT 22048 T _ A
 CC GGAGG ACTGGGTG TAGAGG TGG
 ||||| ||||| ||||| |||
 CCTCC TGACCCAC GTCTCC ACC
 _ C C
 GAM1290 phospho1 5' CCATCCTGCGCCCCAATACCTC 40060 C T AG
 GAGGTA TGGG GT AGGATGG
 ||||| ||| || |||||
 CTCCAT ACCC CG TCCTACC
 A _ CG
 GAM1290 LOC149606 3' CCACCCTCACCATCAGTACTCC 38781 AG G TA A
 C GG GTACTGG TG GAGG TGG
 || ||||| || ||| |||
 CC CATGACT AC CTCC ACC
 CT _ CA C
 GAM1290 LOC206426 3' CCATCCTCTCCACAGCATCCC 43117 A A _ TGT
 GG GGT CTG GG AGAGGATGG
 || ||| ||| || |||||
 CC CTA GAC CC TCTCCTACC
 _ C A _
 GAM1290 LOC221486 3' CCACCCCCCAGTCTGTCTCCTCC 43741 T T GT AGA A
 GGAGG AC GG GT GG TGG
 ||||| || || || |||
 CCTCC TG TC CA CC ACC
 _ _ TG CCC C
 GAM1290 LOC91208 5' CCACCCCTCACCAACACCTCT 32522 ACTG T A A
 GGAGGT GGTG AG GG TGG
 ||||| ||| || || |||
 TCTCCA CCAC TC CC ACC
 CAA_ _ _ C
 GAM1290 LOC93589 3' CATCCTCACAACAGCCCC 35977 TA GG A
 GG CTG TGT GAGGATG
 || ||| || |||||
 CC GAC ACA CTCCTAC
 CC A_ _
 GAM1291 IRAK4 3' CCATTATTAGATTATGT 30693 TTATC
 ACATAATCTA AATGG
 ||||| |||

			TGTATTAGAT TTACC		
			TA__		
GAM1291	FLJ20772	3'	CCATTGATAACAGAAAATG 19664	AA	A
			CAT TCT TTATCAATGG		
			GTA AGA AATAGTTACC		
			AA C		
GAM1291	VAV3	3'	CCATTCACCAGATTATTTGATG 12758	C	ATTATC
			CATCA ATAATCT AATGG		
			GTAGT TATTAGA TTACC		
			T CCAC__		
GAM1291	LOC150759	3'	CCATACAACAGGACTATGTGAT 39013	A	ATTATCA
	G		CATCACATA TCT ATGG		
			GTAGTGTAT AGG TACC		
			C ACAACA_		
GAM1291	LOC151323	3'	CCATACAACAGGACTATGTGAT 39102	A	ATTATCA
	G		CATCACATA TCT ATGG		
			GTAGTGTAT AGG TACC		
			C ACAACA_		
GAM1291	LOC200399	3'	CCATACAACAGGACTATGTGAT 42810	A	ATTATCA
	G		CATCACATA TCT ATGG		
			GTAGTGTAT AGG TACC		
			C ACAACA_		
GAM1291	LOC253955	3'	CCATTACCAATAGATTACTGAT 45325	CA	ATC
	G		CATCA TAATCTATT AATGG		
			GTAGT ATTAGATAA TTACC		
			C_ CCA		
GAM1291	LOC91923	5'	CATTGATAGACATGTGTG 33543	ATCTA	
			CACATA TTATCAATG		
			GTGTGT GATAGTTAC		
			ACA__		
GAM1292	GIT2	3'	AACTGTTGAGTTGATCACATA 16596	C	TATCC
			TATGTGATCA CTC GTT		
			ATACACTAGT GAG CAA		
			T TTGT_		
GAM1292	GIT2	3'	AACTGTTGAGTTGATCACATA 27678	C	TATCC
			TATGTGATCA CTC GTT		
			ATACACTAGT GAG CAA		
			T TTGT_		
GAM1292	GIT2	3'	AACTGTTGAGTTGATCACATA 27691	C	TATCC
			TATGTGATCA CTC GTT		

		ATACACTAGT GAG CAA	
		T TTGT_	
GAM1293	TAL1	3' AAAAACTGGCAACATT 9166 TA	
		AATGTT GCTAGTTTTT	
		TTACAA CGGTCAAAAA	
—			
GAM1293	DRCTNNB1A	3' AAAAACTAATTTGGCATTTTTAA 26314	TT C
		TTAAATGT AG TAGTTTTT	
		AATTTTACG TT ATCAAAAA	
		GT A	
GAM1293	HGC6.1.1	3' AATTAATAAACATTTTAAATA 15682	GC
		TATTAATGTTTA TAGTT	
		ATAATTTTACAAAT ATTAA	
		A_	
GAM1293	ZNF387	3' AATTTGCTAAATATTTTAA 16170	T
		TTAAATGTTTAGC AGTT	
		AATTTTATAAATCG TTAA	
		T	
GAM1294	ABCA3	3' CATGCGCATCTCCATGTCTG 6744	A _ C
		CA ACATGGAGA CGC TG	
		GT TGTACCTCT GCG AC	
		C AC T	
GAM1294	BAALC	3' TATCAATAAATTCCATGTTT 24197	ACGCC
		AAACATGGAG TGATA	
		TTTGTACCTT ACTAT	
		AAATA	
GAM1294	CERD4	3' ATCAGGCGCCTTCCTGGCCTGA 14343	AA_ T A
	T	ATCA CA GGAG CGCCTGAT	
		TAGT GT CTTC GCGGACTA	
		CCG C C	
GAM1294	CPSF4	3' ATCAGGCGTCTACACTGTCA 13512	A _ G
		A ACA TG AGACGCCTGAT	
		A TGT AC TCTGCGGACTA	
		C C A	
GAM1294	HYA22	3' ATCAGATCCTGTTTGATA 12385	T GACGC
		TATCAAACA GGA CTGAT	
		ATAGTTTGT CCT GACTA	
		_ A_	
GAM1294	KIAA1078	3' TATCAGGTTTACCTGCTTGATA 32472	A T A C
		TATCAA CA GG GA GCCTGATA	

ATAGTT GT CC CT TGGACTAT
 C _ A _
 GAM1294 LOC145842 5' TATCAGTGAACCCCCATGTTT 37998 AGA__ C
 AAACATGG CGC TGATA
 ||||| |||||
 TTTGTACC GTG ACTAT
 CCCAA _
 GAM1294 LOC203378 3' TTAGCCTCCATGTTT 43561 AC C
 AAACATGGAG GC TGA
 ||||| |||||
 TTTGTACCTC CG ATT
 _ _
 GAM1294 LOC253975 5' TAGCTGTCTCCAGTCTGA 45937 A A C
 TCA AC TGGAGACG CTG
 || || ||||| |||
 AGT TG ACCTCTGT GAT
 C _ C
 GAM1295 CEP1 5' ACTTCCCTTCGTTTGCAT 13874 GAAGT AA
 ATGCA AATGAAG AAGT
 |||| ||||| |||
 TACGT TTGCTTC TTCA
 _ CC
 GAM1295 GALNT7 3' TACTTTTCTCCAATACCTGC 18879 AA A A
 GCAG GTA TG AGAAAAGTA
 |||| || |||||
 CGTC CAT AC TCTTTTCAT
 _ A C
 GAM1295 GJA1 3' ACTTTTCTTCTTGCA 5676 GAA T
 ATGCA GTAA GAAGAAAAGT
 |||| |||||
 TACGT CGTT CTTCTTTTCA
 A _ _
 GAM1295 PMM2 3' ACTCTTTTCATCTTCTGCA 35676 TA AA
 TGCAGAAG ATGAAGA AGT
 ||||| ||||| |||
 ACGTCTTC TACTTTT TCA
 _ C_
 GAM1295 RALBP1 3' ACTCTCCTCTCTCCTTCTGCA 13655 TAAT A AA
 TGCAGAAG GA GA AGT
 ||||| || |||||
 ACGTCTTC CT CT TCA
 CTCT C C_
 GAM1295 UBQLN1 3' TACTGCATGCATCACTTCTGCA 15100 A AAGAAA
 T ATGCAGAAGT ATG AGTA
 ||||| ||||| |||
 TACGTCTTCA TAC TCAT
 C GTACG_
 GAM1295 UBQLN2 3' ACTTCTCTTTATTCTGCAT 15111 AGTA A
 ATGCAGA ATGAAGA AAGT
 ||||| ||||| |||

			TACGTCT	TATTTCT	TTCA	
			_____	C		
GAM1295	AP1S2	3'	ACTTTTCTAAGTACTTATACAT	10001	CAG	ATGA
			ATG AAGTA AGAAAAGT			
			TAC TTCAT TCTTTTCA			
			ATA GAA_			
GAM1295	CLDN1	3'	ACTCTTCTTCATTAGCTT	22080	_	A
			AAGT AATGAAGAA AGT			
			TTCG TTA CTTCTT TCA			
			A C			
GAM1295	dA141H5.1	3'	ACTTTTCTTTTCCCCCTGTA	29747		AAGTAAT
			TGCAG GAAGAAAAGT			
			ATGTC TTTCTTTTCA			
			CCCCT_			
GAM1295	FHX	3'	CTTCAATCCTTACTTCTGC	20460	_____	
			GCAGAAGTAA TGAAG			
			CGTCTTCATT ACTTC			
			CCTA			
GAM1295	FLJ20254	3'	ACTTTTCTGGCCCTACTGCA	19315		A TAATGA
			TGCAG AG AGAAAAGT			
			ACGTC TC TCTTTTCA			
			A CCGG_			
GAM1295	FLJ22690	3'	ACTTTTCTACTCCTGTAT	24036		A AATGA
			ATGCAG AGT AGAAAAGT			
			TATGTC TCA TCTTTTCA			
			C _____			
GAM1295	GDAP1L1	3'	ACTTTCCTGTGCCTTTTGCAT	23465		TAATGA A
			ATGCAGAAG AG AAAGT			
			TACGTTTTTC TC TTTCA			
			CGTG_ C			
GAM1295	GMFB	3'	TACTTTTCTCCAGGGACTTTTT	10330	_	AA_ A
	GCA		TGCAGAA GT TG AGAAAAGTA			
			ACGTTTT CA AC TCTTTTCAT			
			T GGG C			
GAM1295	KIAA0254	3'	ACTTCTCTCCCACTTCTGC	16502		AAT A A
			GCAGAAGT GA GA AAGT			
			CGTCTTCA CT CT TTCA			
			CC_ _ C			
GAM1295	KIAA1524	5'	ACTTTTCTTCATGTCTTC	36359		TA
			GAAG ATGAAGAAAAGT			

CTTC TACTTCTTTTCA
 TG
 GAM1295 MGC13007 3' ACTCTTCTTCATTGTGAGATGC 26119 GAA_ A
 A TGCA GTAATGAAGAA AGT
 ||| ||||| |||
 ACGT TGTTACTTCTT TCA
 AGAG C
 GAM1295 PHCA 3' TACTTTTTCAGTTAGATATACTT 20378 A_ A_
 CTGCAT TGCAGAAAGTA TGA GAAAAGTA
 ||||| || |||||
 ACGTCTTCAT ATT CTTTTCAT
 ATAG GA
 GAM1295 PRO1580 5' ACTTCTCTTCACTTCTGC 20565 AAT A
 GCAGAAAGT GAAGA AAGT
 ||||| |||||
 CGTCTTCA CTTCT TTCA
 _ C
 GAM1295 LOC126661 3' TACCTTTCCTCATCTCCAGCTT 36855 A_ A A
 CTGC GCAGAAAGT ATGA GAAA GTA
 ||||| ||| ||| |||
 CGTCTTCG TACT CTTT CAT
 ACCTC C C
 GAM1295 LOC158364 5' ACTTCTCTCCACCCTCTTTTTG 39813 TAA_ A A
 CAT ATGCAGAAG TG AGA AAGT
 ||||| || ||| |||
 TACGTTTTT AC TCT TTCA
 CTCCC C C
 GAM1295 LOC197319 3' ACTTCTCTTCATTACTGATAGT 42475 AGA_ A
 A TGC AGTAATGAAGA AAGT
 || ||||| |||||
 ATG TCATTACTTCT TTCA
 ATAG C
 GAM1296 BTG1 3' ACTGTCTCAACTGTGGTGTGA 7465 AACA TC
 TAACACCACG TG GCAGT
 ||||| || |||||
 ATTGTGGTGT AC TGTCA
 CA_ TC
 GAM1296 PCDH7 5' TACTGCGACTGAACGGCGG 8452 A_ AA T
 CC CG CA GTCGCAGTA
 || || || |||||
 GG GC GT CAGCGTCAT
 CG AA _
 GAM1296 PCDH7 5' TACTGCGACTGAACGGCGG 26217 A_ AA T
 CC CG CA GTCGCAGTA
 || || || |||||
 GG GC GT CAGCGTCAT
 CG AA _
 GAM1296 PCDH7 5' TACTGCGACTGAACGGCGG 26220 A_ AA T
 CC CG CA GTCGCAGTA
 || || || |||||

GG GC GT CAGCGTCAT
CG AA _
GAM1296 SLC9A5 3' TGGTCATGTTCTGGTGT 10937 _
ACACCACGAACATG TCG
||||||| |||
TGTGGTGCTTGTAC GGT
T
GAM1296 KIAA1950 3' ACTGTCACGTTCTGTGG 44484 _ A TC
CCAC GAAC TG GCAGT
||| ||| || |||||
GGTG CTTG AC TGTCA
T C _
GAM1296 MAC30 3' TGACATGTTTCATGAGTCA 31407 C _ C
A AC CA GAACATGTCG
| || |||||
A TG GT CTTGTACAGT
C A A
GAM1296 LOC147219 3' TATCGTGCATGTTCTGGT 40823 T A
ACCACGAACATG CGC GTA
||||||| ||| |||
TGGTGCTTGTAC GTG TAT
_ C
GAM1296 LOC150174 5' ACTTGACATCCGTGGTGT 38867 AAC C
ACACCACG ATGTCG AGT
||||| ||||| |||
TGTGGTGC TACAGT TCA
C _ _
GAM1297 C8orf6 5' ATTCCTCATTTGCCTTA 43004 TAATTCCA
TAAGGTAA AGGAAAT
||||| |||||
ATTCCGTT TCCTTTA
TAC _ _ _
GAM1297 FLJ10193 3' ATTCCTTGAAATTTTAC 19760 AAT C
GT AATT CAAGGAAAT
|| ||| |||||
CA TTAA GTTCCTTTA
CT_ A
GAM1297 FLJ30532 3' ATTCCTTGGAACCTCCCTT 29548 TAATAA
AAGG TTCCAAGGAAAT
||| |||||
TTCC AAGGTTCTTTA
CTCA _
GAM1297 KIAA0537 3' ATTCCTTAGATGTTACC 16863 AT C
GGTAATA TC AAGGAAAT
||||| || |||||
CCATTGT AG TTCCTTTA
_ A
GAM1297 KIAA0596 3' TTCCTTGGAACCTGCCT 31466 ATAA
AGGTA TTCCAAGGAA
||||| |||||

TCCGT AAGGTTCTT
 CCTC
 GAM1297 KIAA0596 3' TATTTCCCTGACTGTTGCCT 31464 ATTC A
 AGGTAATA CA GGAAATA
 ||||| || |||||
 TCCGTTGT GT CCTTTAT
 CA__ C
 GAM1297 KIAA0819 3' TCCTTGAGTTTACGCTCA 31810 A AAT
 A GGT AATTCCAAGGA
 | || |||||
 A TCG TTGAGGTTCTT
 C CAT
 GAM1297 KIAA1766 3' TTCTCGGAACAATTACCTTA 35353 AA A
 TAAGGTAAT TTCC AGGA
 ||||| ||| |||
 ATTCCATTA AAGG TCTT
 AC C
 GAM1297 LAGY 3' TTCCTTGGAATATAGCT 29234 A A
 GGT ATA TTCCAAGGAA
 ||| || |||||
 TCG TAT AAGGTTCTT
 A _
 GAM1297 LAGY 3' TTCCTTGGAATATAGCT 26246 A A
 GGT ATA TTCCAAGGAA
 ||| || |||||
 TCG TAT AAGGTTCTT
 A _
 GAM1297 LAGY 3' TTCCTTGGAATATAGCT 29232 A A
 GGT ATA TTCCAAGGAA
 ||| || |||||
 TCG TAT AAGGTTCTT
 A _
 GAM1297 PRO1768 3' ATTCCTTCCGATTACCT 15324 AATTCC
 AGGTAAT AAGGAAAT
 ||||| |||||
 TCCATTA TTCCTTTA
 GCC__
 GAM1297 LOC124152 3' TGGGTAAACTTATTACCTTA 36737 T____
 TAAGGTAATAA TCCA
 ||||| |||
 ATTCCATTATT GGGT
 CAAAT
 GAM1297 LOC158835 5' TATTTCTGGCATCACCCCTTA 39895 TAATAATT A
 TAAGG CCA GGAAATA
 |||| ||| |||||
 ATTCC GGT CCTTTAT
 CCACTAC_ _
 GAM1298 LOC158014 5' ATCTTCCAAAAGACTATTACA 39689 C TG TAGT
 TGTAAGTCTTTT AGAT
 |||| ||||| |||

			ACATT TCAGAAAA	TCTA		
			A	CCT___		
GAM1299	POU4F1	3'	CAACCCTACACGCACGA	ACTGA 12898	A	GACTTAA
			TTA TTCGTGCG	GTTG		
			AGT AAGCACGC	CAAC		
			C	ACATCC_		
GAM1300	MAB21L1	3'	AAGTTTACATTTTGTTC	12110	C	
			GAA CAAAATGTAA	ACTT		
			CTT GTTTTACATTTGAA			
			T			
GAM1300	SPG3A	3'	AAGTTTACTCTGGTTCCTAA	18046	AAAT	
			TTAGGAACCA	GTAACTT		
			AATCCTTGGT	CATTTGAA		
			CT__			
GAM1300	C6orf5	3'	TTTACATTTTCTTAACA	17783	CCAA	
			TGTTAGGAA	AATGTAAA		
			ACAATTCTT	TTACATTT		

GAM1300	DKFZP586M0622	5'	TATATTCTGATTCCTAACA	17849	C A	
			TGTTAGGAA	CA AATGTA		
			ACAATCCTT	GT TTATAT		
			A C			
GAM1300	FLJ14281	3'	AAGCTTACATGATTCCTAAC	24450	CCAAA A	
			GTTAGGAA	ATGTAA CTT		
			CAATCCTT	TACATT GAA		
			AG__	C		
GAM1300	KIAA1789	5'	TTTTGGTCCAGTTCTAACA	33315	_____	
			TGTTAGGA	ACCAAAA		
			ACAATCTT	TGGTTTT		
			GACC			
GAM1300	OSBPL8	3'	AAGTTTACATTTCAATTTCTA	21902	CCA	
			TAGGAA	AAATGTAACTT		
			ATCTTT	TTTACATTTGAA		
			AAC			
GAM1300	RGS13	3'	AAGTTGACTTTTAGTTCCTAA	29557	C T A	
			TTAGGAAC	AAAA GT AACTT		
			AATCCTTG	TTTT CA TTGAA		
			A _ G			
GAM1300	RGS13	3'	AAGTTGACTTTTAGTTCCTAA	8831	C T A	
			TTAGGAAC	AAAA GT AACTT		

		AATCCTTG TTTT CA TTGAA	
		A _ G	
GAM1300	XLKD1	3' AAGTCCACCCTTGGTTCCTAAC 13506	AAT AA
		GTTAGGAACCAA GT ACTT	
		CAATCCTTGGTT CA TGAA	
		CC_ CC	
GAM1300	LOC51134	3' AAGTCTAATTTTGGTTCCTAAC 18208	GTAA
	A	TGTTAGGAACCAAAAT ACTT	
		ACAATCCTTGGTTTTA TGAA	
		ATC_	
GAM1301	STAF65(gamma)	3' CTTAACTATGACTAGACATGTT 16925	T _ TG A
	ATA	TATAACAT GTC GT TA TTAAG	
		ATATTGTA CAG CA AT AATTC	
		_ AT GT C	
GAM1302	LOC254528	5' CCGGGCGAGCCTCGGATT 45566	ATAA
		AATCCGAG TTGCCCGG	
		TTAGGCTC AGCGGGCC	
		CG_	
GAM1303	DVL3	3' CCTGATGTCCTCAATTGCTGCT 10696	CCC AC AC
		AGCAGCAA GA GCG CAGG	
		TCGTCGTT CT TGT GTCC	
		AA_ CC A_	
GAM1303	E2F3	3' CCTGGTACCATTGAGTTGCTGC 7667	C ACGCG
	T	AGCAGCAAC CGA ACCAGG	
		TCGTCGTTG GTT TGGTCC	
		A ACCA_	
GAM1303	GNAI1	5' CCTGGTCGTGAGGAACAGCCGC 7839	A AAC_ GAA
		GC GC CC CGCGACCAGG	
		CG CG GG GTGCTGGTCC	
		C ACAA A_	
GAM1303	HPSE	3' CCCAGTTCCGTCCAAGTTGCTG 13476	CCGA C CA
	C	GCAGCAAC ACG GAC GG	
		CGTCGTTG TGC TTG CC	
		AACC C AC	
GAM1303	IL1R1	3' CCTCCAGCTGGAATTGCTGCT 6565	C_ AAC GACC
		AGCAGCAA CCG GC AGG	
		TCGTCGTT GGT CG TCC	
		AA _ ACC_	
GAM1303	MADH4	5' CTGGTCGTGTCGCCGCT 11832	AACC A _
		AGC CGA CG CGACCAG	

		TCG GCT GC GCTGGTC	
		CC__ _ T	
GAM1303	RGS3	5' CCTGAGGGCACCCGGTTGCTGC 22089	CGAAC GAC
	T	AGCAGCAACC GC CAGG	
		TCGTCGTTGG CG GTCC	
		CCCA_ GGA	
GAM1303	DKFZp434G179	3' CCTACTCCTCCAGGTTGTTGCT 39040	CGAACGC CC
		AGCAGCAACC GA AGG	
		TCGTTGTTGG CT TCC	
		ACCTC__ CA	
GAM1303	DKFZP434J037	3' CCTGAGCCTCCTGAAGTTGCTG 25218	CCGAAC__ GAC
	CT	AGCAGCAAC GC CAGG	
		TCGTCGTTG CG GTCC	
		AAGTCCTC A__	
GAM1303	DKFZP564J157	3' CCTGGCCATCTTGTTGCTGCT 20528	CC ACGCGA
		AGCAGCAAC GA CCAGG	
		TCGTCGTTG CT GGTCC	
		TT ACC__	
GAM1303	DQX1	5' CCTGGCTCTGCGGGTTGCTG 28598	AACGC _
		CAGCAACCCG GA CCAGG	
		GTCGTTGGGC CT GGTCC	
		GT__ C	
GAM1303	FLJ10922	3' CCTGATCTTGCTATCAATTGCT 20254	CCC AC C__
	GCT	AGCAGCAA GA GCGA CAGG	
		TCGTCGTT CT CGTT GTCC	
		AA_ AT CTA	
GAM1303	FLJ13769	3' CCTGGGGGATTCCAAGTTGTTG 24593	CC_ CGCGA
	CT	AGCAGCAAC GAA CCAGG	
		TCGTTGTTG CTT GGTCC	
		AAC AGGG_	
GAM1303	KIAA1691	3' GCCTGGCCGCACCCAACCTGTG 44468	C AAC_____ A
	TTGTTGC	AAC CG GCG CCAGG C	
		TTG GT CGC GGTCC G	
		T CCAACCCA C	
GAM1303	LGI2	3' CCTGTTTTGTTGAGTTGCTGCT 20000	C G C C
		AGCAGCAAC C AACG GAC AGG	
		TCGTCGTTG G TTGT TTG TCC	
		A_ T _	
GAM1303	PMX2B	3' TTGGGTTCGGGTCACTGC 10017	CA G
		GCAG ACCCGAAC CGA	

CGTC TGGGCTTG GTT
 AC G
 GAM1303 LOC144438 3' CCAAGTTTCTTGAGTTGCTGCT 37735 C ACGC CA
 AGCAGCAAC CGA GAC GG
 ||||| || ||
 TCGTCGTTG GTT TTG CC
 A CT__ AA
 GAM1303 LOC147804 5' CTGGTCGCAATTGCTTCT 38382 C CCCGAAC
 AG AGCAA GCGACCAG
 || |||| |||||
 TC TCGTT CGCTGGTC
 T AA____
 GAM1303 LOC148759 3' CCTGGCACTATGATCCAGTTGC 40903 CC A CGA__
 TGC GCAGCAAC GA CG CCAGG
 ||||| || || ||||
 CGTCGTTG CT GT GGTCC
 AC A ATCAC
 GAM1303 LOC253219 5' CCAGGGTGCGCTCAGTTGCTGC 46561 CC A A A
 GCAGCAAC GA CGCG CC GG
 ||||| || || || ||
 CGTCGTTG CT GCGT GG CC
 A_ C G A
 GAM1303 LOC257358 3' CCTGCCTTCTCGTATTGCTGCT 46388 CC ACGCGAC
 AGCAGCAA CGA CAGG
 ||||| || ||||
 TCGTCGTT GCT GTCC
 AT CTTCC__
 GAM1303 LOC91759 5' CCTAGGGGGGCTGGGGTTGCTGC 33304 GAAC GA _
 GCAGCAACCC GC CC AGG
 ||||| || || ||
 CGTCGTTGGG CG GG TCC
 GT__ GG A
 GAM1304 DGKI 3' ACAATTCTACTGTAACCTACCCA 11078 C A_ _
 TCA A GTG TAGTTACGGT GATTGT
 | || ||||| |||||
 A TAC ATCAATGTCA TTAACA
 C CC TC
 GAM1304 DKFZp547J036 5' ACAACCACGCAGACAGTCAC 26039 A ACG A
 GTGAT GTT GTG TTGT
 |||| || || ||||
 CACTG CAG CAC AACA
 A ACG C
 GAM1304 KIAA0872 3' ACAATCACCGTGCTGCAGC 17242 GA T
 GT TAGT ACGGTGATTGT
 || |||| |||||
 CG GTCG TGCCACTAACA
 AC _
 GAM1304 KIAA1979 3' CAATCACGTTACCATATCA 42589 CG ATA T G
 TGA TG GT ACG TGATTG
 || | || |||||

			ACT AC CA TGC ACTAAC		
			AT ____ T _		
GAM1305	CHES1	3'	CCAAAAGCCATAAGCCTGAA 11697	AGAAC	C
			TTCAG GTGGCTTT GG		
			AAGTC TACCGAAA CC		
			CGAA_ A		
GAM1305	COCH	3'	CCAAAAGCAACATTCGTTCTCT 10292	TG____	C
			AGAGAACG GCTTT GG		
			TCTCTTGC CGAAA CC		
			TTACAA A		
GAM1305	DACH	3'	CCAAAAGCTTTCACCTGAA 28034	A CGT	C
			TTCAG GAA GGCTTT GG		
			AAGTC CTT TCGAAA CC		
			A ____ A		
GAM1305	INPP5A	3'	CCGAATACGCACTCTTGAA 12066	_ AA	GCT
			TTCA GAG CGTG TTCGG		
			AAGT CTC GCAT AAGCC		
			T AC ____		
GAM1305	NUP98	5'	CCGAACCGCGCTTTCTGAA 18442	A	CT
			TTCAGAGA CGTGG TTCGG		
			AAGTCTTT GCGCC AAGCC		
			C ____		
GAM1305	RAP1GA1	3'	CCGGGCCACCCCTCTGAA 8797	AAC	TT
			TTCAGAG GTGGCT CGG		
			AAGTCTC CACCGG GCC		
			CCC ____		
GAM1305	SOS2	3'	CCAAAAGCCACGTTGTTT 33999	G	C
			AGA AACGTGGCTTT GG		
			TTT TTGCACCGAAA CC		
			G A		
GAM1305	C20orf121	5'	CTGTGGCCTCACTCTCTGAA 23630	ACGT	TT
			TTCAGAGA GGCT CGG		
			AAGTCTCT CCGG GTC		
			CACT T_		
GAM1305	ELF4	5'	CCGTTGTCAGCTCTCTGAA 7121	ACG	TTT
			TTCAGAGA TGGC CGG		
			AAGTCTCT ACTG GCC		
			CG_ TT_		
GAM1305	KIAA0218	3'	CCAAATTCTGTTCTCTG 16516	T GC	C
			CAGAGAACG G TTT GG		

	GTCTCTTGT C AAA CC	
	TT _	
GAM1305 KIAA0889 3'	CCAATTCCACATTTCTGAA 17676	AC CT C
	TTCAGAGA GTGG TT GG	
	AAGTCTTT CACC AA CC	
	A_ TT _	
GAM1305 KIAA0945 3'	CCGAAAAGTAGTCTTCTCTGAG 17294	CGTG _
	TTCAGAGAA GCTTT CGG	
	GAGTCTCTT TGAAA GCC	
	CTGA A	
GAM1305 KIAA1198 3'	CCGAATTCTCCGTTTTCTGAA 31707	TG CT
	TTCAGAGAACG G TTCGG	
	AAGTCTTTTGC C AAGCC	
	CT TT	
GAM1305 MGC2827 3'	CCACTGAGCCACTCTCTGAA 23424	AC TC_
	TTCAGAGA GTGGCTT GG	
	AAGTCTCT CACCGAG CC	
	TCA	
GAM1305 TRIP-Br2 3'	CCAAACTTGTTTCTCTGA 16484	GT C C
	TCAGAGAAC GG TTT GG	
	AGTCTCTTG TC AAA CC	
	GT _ _	
GAM1305 LOC115110 3'	CCGAAGTGCCCCTCTGAA 35507	AACGT _
	TTCAGAG GGC TTTCGG	
	AAGTCTC CCG GAAGCC	
	C_ T	
GAM1305 LOC149506 5'	CCAAAAGCCACCTCTGAA 41005	AAC C
	TTCAGAG GTGGCTTT GG	
	AAGTCTC CACCGAAA CC	
	A	
GAM1305 LOC152317 3'	CCAGTTTCATGTTCCCTGAA 41466	A CT C
	TTCAG GAACGTGG TT GG	
	AAGTC CTTGTACT GA CC	
	C TT _	
GAM1305 LOC163882 3'	CCAGAGCCACTTCCTCTGAA 39971	AAC C
	TTCAGAG GTGGCTTT GG	
	AAGTCTC CACCGAGA CC	
	CTT _	
GAM1305 LOC253148 5'	CCAAGTCCCACTCTCTGGA 46299	AC CT C
	TTCAGAGA GTGG TT GG	

AGGTCTCT CACC GA CC
 _ CT A
 GAM1305 LOC90072 3' CCAATTCCACATTTCTGAA 30727 AC CT C
 TTCAGAGA GTGG TT GG
 ||||| ||| ||
 AAGTCTTT CACC AA CC
 A_ TT _
 GAM1305 LOC90630 5' CCGCTCTGCCACGTTCCCTGAG 31825 A TTT_
 TTCAG GAACGTGGC CGG
 |||| ||||| ||
 GAGTC CTTGCACCG GCC
 C TCTC
 GAM1306 ADH7 3' TTCAACGATTAAGAATCATCAT 6326 C C_ C_
 TACA TG AATGATGA CTTG TGTGAA
 || ||||| ||| |||||
 AC TTACTACT GAAT GCAACTT
 A AA TA
 GAM1306 MEF2D 3' TCAACAGCACACTCAGTGCA 46308 A _ ACCT
 TGCA TGA TG TGCTGTTGA
 ||| ||| || |||||
 ACGT ACT AC ACGACAACT
 G C _
 GAM1306 WHSC1 3' CAACAGCATCATCTGCA 28442 AT CCT
 TGCA GATGA TGCTGTTG
 ||| ||| |||||
 ACGT CTACT ACGACAAC
 _ _
 GAM1306 WHSC1 3' CAACAGCATCATCTGCA 28459 AT CCT
 TGCA GATGA TGCTGTTG
 ||| ||| |||||
 ACGT CTACT ACGACAAC
 _ _
 GAM1306 WHSC1 3' CAACAGCATCATCTGCA 17178 AT CCT
 TGCA GATGA TGCTGTTG
 ||| ||| |||||
 ACGT CTACT ACGACAAC
 _ _
 GAM1306 KIAA0227 3' TCAACAGCATCTTCATTGTA 30456 T CCT
 TGCAATGA GA TGCTGTTGA
 ||||| || |||||
 ATGTTACT CT ACGACAACT
 T _
 GAM1306 KIAA1276 5' TCAACAGCAAAATTAACCCGC 33019 AATGA CC
 GC TGA TTGCTGTTGA
 || ||| |||||
 CG ATT AACGACAACT
 CCCA_ AA
 GAM1306 PRO0800 5' TCAACAATATCATCATTCA 20671 C CCT C
 TG AATGATGA TG TGTGAA
 || ||||| || |||||

			AC TTACTACT AT ACAACT		
			— — A		
GAM1306	LOC148266	5'	CAGAAAGCAAAGCCTCATTGCA 38513	TGACC	G
			TGCAATGA TTGCT TTG		
			ACGTTACT AACGA GAC		
			CCGA_ A		
GAM1306	LOC151009	3'	ATACCAAGGTCATCACTG 41290	A	C
			CA TGATGACCTTG TGT		
			GT ACTACTGGAAC ATA		
			C C		
GAM1306	LOC157660	3'	GGCATAGGTCATCACTGCA 41829	A	—
			TGCA TGATGACCT TGCT		
			ACGT ACTACTGGA ACGG		
			C T		
GAM1306	LOC170409	3'	TTCAACAGCATAAAATCACGCA 40317	AA	GACCT
			TGC TGAT TGCTGTTGAA		
			ACG ACTA ACGACAACCTT		
			C_ AAAT_		
GAM1307	GAS11	3'	ACTGCCTAAATGATGCCCG 7219	A	_ AGA
			CG GGCA CG TAGGCAGT		
			GC CCGT GT ATCCGTCA		
			_ A AA_		
GAM1307	LANCL1	3'	CTACCTTGTGCCTCTCA 12695	C	A
			TGA GAGGCACGAG TAG		
			ACT CTCCGTGTTT ATC		
			— C		
GAM1307	MAPT	3'	ACTGCCTATACCCCTCATCA 18831	C	CACGAG
			TGA GAGG ATAGGCAGT		
			ACT CTCC TATCCGTCA		
			A CCA_		
GAM1307	MAPT	3'	ACTGCCTATACCCCTCATCA 18837	C	CACGAG
			TGA GAGG ATAGGCAGT		
			ACT CTCC TATCCGTCA		
			A CCA_		
GAM1307	MAPT	3'	ACTGCCTATACCCCTCATCA 12537	C	CACGAG
			TGA GAGG ATAGGCAGT		
			ACT CTCC TATCCGTCA		
			A CCA_		
GAM1307	MAPT	3'	ACTGCCTATACCCCTCATCA 18825	C	CACGAG
			TGA GAGG ATAGGCAGT		

			ACT CTCC	TATCCGTCA		
			A	CCA__		
GAM1307	NRXN2	3'	CTGCGCGGCCTCGTCA	28990	A	AGATAG
			TGACGAGGC CG	GCAG		
			ACTGCTCCG GC	CGTC		
			_ G			
GAM1307	NRXN2	3'	CTGCGCGGCCTCGTCA	28984	A	AGATAG
			TGACGAGGC CG	GCAG		
			ACTGCTCCG GC	CGTC		
			_ G			
GAM1307	NRXN2	3'	CTGCGCGGCCTCGTCA	17468	A	AGATAG
			TGACGAGGC CG	GCAG		
			ACTGCTCCG GC	CGTC		
			_ G			
GAM1307	C21orf108	3'	CCATCCAGTGCCTCGTCA	42767	GA	A
			TGACGAGGCAC	GAT GG		
			ACTGCTCCGTG	CTA CC		
			AC	_		
GAM1307	DKFZP566G1424	3'	ACTGCTGTCTCACCCTC	41112	CAC	G
			GAGG	GAGATAG CAGT		
			CTCC	CTCTGTC GTCA		
			CA_	_		
GAM1307	FLJ10829	3'	ACTGCTGTCTTCCCTACCTC	20177	CAC__	G
			GAGG	GAGATAG CAGT		
			CTCC	TTCTGTC GTCA		
			ATCCC	_		
GAM1307	KIAA0923	3'	TACTGCCTACCTTAGCT	15243	AC	A
			GGC	GAG TAGGCAGTA		
			TCG	TTC ATCCGTCAT		
			A_	C		
GAM1308	APTX	3'	TCCAGTCCTTCCATGCCCTTCT	19250	CAATCAT	
			AGAAGGGCA	ACTGGA		
			TCTTCCCGT	TGACCT		
			ACCTTCC			
GAM1308	CERD4	3'	TCTGGGGATGTGCCCTTCCCA	14350	A	A ATA TG
			TG	GAAGGGCACA TC C GA		
			AC	CTTCCCGTGT AG G CT		
			C	_ G_ GT		
GAM1308	GPRK6	3'	CCAAAGCTGTCCCTTCTCA	7877	C	ATCATAC
			TGAGAAGGG	ACA TGG		

		ACTCTTCCC TGT ACC	
		_ CGAA__	
GAM1308	INPP5D	3' CCAATAAATTGTGCCTTTCTCA 40303	CA C
		TGAGAAGGGCACAAT TA TGG	
		ACTCTTTCCGTGTTA AT ACC	
		A_ A	
GAM1308	MAB21L1	3' CCGAAATTATTACCCTTCTCA 12112	CAC C AC
		TGAGAAGGG AAT AT TGG	
		ACTCTTCCC TTA TA GCC	
		A__ T AA	
GAM1308	PRKAR1A	3' TCCAGTATAATCTCCTCTGCTC 8607	A CACA C
	A	TGAG AGGG AT ATACTGGA	
		ACTC TCTC TA TATGACCT	
		G CTC_ A	
GAM1308	SCD	3' TCCACAGTGTTGTGCCCTTC 11495	_ T AC
		GAAGGG CACAA CAT TGG	
		CTTCCC GTGTT GTG ACCT	
		C _ AC	
GAM1308	TGFB1	5' TCCACCACTGCGCCCTTCTC 6320	A ATCATAC
		GAGAAGGGC CA TGG	
		CTCTTCCCG GT ACCT	
		C CACC__	
GAM1308	ZNF236	3' TGTGACCGCGCCTTCTCA 14275	_ ACAA
		TGAGAAGG GC TCATA	
		ACTCTTCC CG AGTGT	
		G CC__	
GAM1308	CNNM4	3' CCATTGATCATCCCTTCTCA 21424	CACA TAC
		TGAGAAGGG ATCA TGG	
		ACTCTTCCC TAGT ACC	
		TAC_ T__	
GAM1308	DDM36	3' CCAGCACCAAGTGCCCTTCTC 21951	AATCATA
		GAGAAGGGCAC CTGG	
		CTCTTCCCGTG GACC	
		ACCAC__	
GAM1308	DKFZp761B0514	3' CCAGGCTTGTGCCCTTTCA 26049	A TCATA
		TGAGA GGGCACAA CTGG	
		ACTTT CCCGTGTT GACC	
		_ CG__	
GAM1308	FGF19	3' TCCAGGGACCATTTGCCCTTCC 11595	A CAATCATA
	CA	TG GAAGGGCA CTGGA	

		AC CTTCCCGT	GACCT		
		C	TTACCAGG		
GAM1308	FLJ12547	3'	CCAGTTCTCATGCCCTTTCA	24546	A CAATCAT
			TGAGA GGGCA	ACTGG	
			ACTTT CCGT	TGACC	
			_	ACTCT__	
GAM1308	KIAA0296	3'	CCAGCCTCATCACCGTGCTCTT	16219	AATCATA__
			CTCA	TGAGAAGGGCAC	CTGG
			ACTCTTCTCGTG	GACC	
			CCACTACTCC		
GAM1308	KIAA0523	3'	CCAGTAGAGCTGCCCTTC	33640	CAA A
			GAAGGGCA	TC TACTGG	
			CTTCCCGT	AG ATGACC	
			CG_ _		
GAM1308	KIAA1297	5'	TCCAGCACGACTGTGTCCTCT	35720	A A ATA
			AGA GGGCACA	TC CTGGA	
			TCT CCTGTGT	AG GACCT	
			_	C CAC	
GAM1308	KREMEN	3'	CCAGTTGCACCTTTCTCA	25759	CA ATCAT
			TGAGAAGGG	CA ACTGG	
			ACTCTTTCC	GT TGACC	
			AC	_____	
GAM1308	MGC5457	5'	TCCTTGACTATGCCCTCTC	26347	A CAA TACT
			GAGA GGGCA	TCA GGA	
			CTCT CCGT	AGT CCT	
			C	ATC T__	
GAM1308	PLAGL2	3'	TCCAAGTACATTATGACCCCCT	34881	AA _ C CA _
			CA	TGAG GGG CA AAT TACT GGA	
			ACTC CCC GT TTA	ATGA CCT	
			C_ A A C_ A		
GAM1308	PRO1430	5'	TCCAGGGGTCATGCTCTTCCCA	20677	A CA ATA
			TG GAAGGGCA	ATC CTGGA	
			AC CTTCTCGT	TGG GACCT	
			C	AC G__	
GAM1308	LOC130951	3'	TCAGAGCCTGTGCCCTTCCCA	29027	A ATCATA
			TG GAAGGGCACA	CTGG	
			AC CTTCCCGTGT	GACT	
			C	CCGA__	
GAM1308	LOC201324	5'	CCAGCACCTTGTGCCCTTGCCA	34013	AG TCATA
			TG AAGGGCACAA	CTGG	

		AC TTCCCGTGTT GACC	
		CG CCAC_	
GAM1308	LOC256021	3' TCCAATACAATGCCTCTTCTC 46166	_ CAATCA C
		GAGAAG GGCA TA TGGA	
		CTCTTC CCGT AT ACCT	
		T AAC__ A	
GAM1309	CDKN2D	3' GTGGGGTTATGTATCAGA 7555	C TAC
		TCTGA AC AACCTCAT	
		AGACT TG TTGGGGTG	
		A TA_	
GAM1309	CDKN2D	3' GTGGGGTTATGTATCAGA 27817	C TAC
		TCTGA AC AACCTCAT	
		AGACT TG TTGGGGTG	
		A TA_	
GAM1309	DPYSL2	3' GTATGAGGCTGCAGAACCGGA 7065	ACA A A
		TCTG CT CA CCTCATAC	
		AGGC GA GT GGAGTATG	
		CAA C C	
GAM1309	NXF2	5' GTGAGACTGTAGTGTGTCAGG 19458	AC
		TCTGACACTACA CTCAT	
		GGACTGTGATGT GAGTG	
		CA	
GAM1309	NXF2	5' GTGAGACTGTAGTGTGTCAGG 22590	AC
		TCTGACACTACA CTCAT	
		GGACTGTGATGT GAGTG	
		CA	
GAM1309	SP100	3' GTATGAGGGAAGTGTGTAGA 9084	A TACAA
		TCTG CAC CCTCATAC	
		AGAT GTG GGAGTATG	
		_ TCAAG	
GAM1309	ZFP93	3' GTATGATTTTTAGTGTGTCAG 10428	C CC
		CTGACACTA AA TCATAC	
		GACTGTGAT TT AGTATG	
		_ TT	
GAM1309	CDC14B	3' ATGAAACTGTGTGTCAGA 27161	T ACC
		TCTGACAC ACA TCAT	
		AGACTGTG TGT AGTA	
		_ CAA	
GAM1309	FLJ12806	3' ATGAGGGGAATGCAGTGTGTCAG 23108	A A__
		CTGACACT CA CCTCAT	

			GACTGTGA GT	GGAGTA		
			C AAGG			
GAM1309	HSPC065	3'	GTATAAGGGTTGTACAGA	15454	ACAC	C_
			TCTG TACAACCT ATAC			
			AGAC ATGTTGGG TATG			
			_____ AA			
GAM1309	HTR3A	5'	GTGAGGCTGCAGCCTCAGA	6538	CA A A	
			TCTGA CT CA CCTCAT			
			AGACT GA GT GGAGTG			
			CC C C			
GAM1309	LANO	3'	ATGAGTGCAGTGTGAGA	20129	A AC	
			TCTGACACT CA CTCAT			
			AGACTGTGA GT GAGTA			
			C _			
GAM1309	PASK	3'	GTATGAGGTTATGTTGAGG	17503	_ CTAC	
			TCT GACA AACCTCATAC			
			GGA TTGT TTGGAGTATG			
			G A__			
GAM1309	LOC145663	3'	GTATGAGGCCCGGTGCAG	40551	A ACA	
			CTG CACT CCTCATAC			
			GAC GTGG GGAGTATG			
			_ GCC_			
GAM1309	LOC157507	5'	GTATGAGGTCAGGAGCAGG	39606	ACA ACA	
			TCTG CT ACCTCATAC			
			GGAC GA TGGAGTATG			
			GAG C__			
GAM1309	LOC221337	5'	ATGAGGCTGTAGTGTAAGA	44235	G A	
			TCT AACTACA CCTCAT			
			AGA TGTGATGT GGAGTA			
			A C			
GAM1309	LOC92340	3'	GTGGGTTGCAGTGTGAGG	34200	A T	
			TCTGACACT CAACC CAT			
			GGACTGTGA GTTGG GTG			
			C _			
GAM1310	BCL7B	3'	TGTAGACTCCCGGACTT	7437	A C A C	
			AGGT CG GGA GTC ACA			
			TTCA GC CCT CAG TGT			
			G _ _ A			
GAM1310	F7	3'	GGCTGCGTCTCCTCCGCACACC	21239	AC	_____
	TGT		GCAGGT GCGGA AGTC			

		TGTCCA CGCCT	TCGG	
		CA CCTCTGCG		
GAM1310 F7	3'	GGCTGCGTCTCCTCCGCACACC	5610	AC _____
	TGT	GCAGGT GCGGA	AGTC	
		TGTCCA CGCCT	TCGG	
		CA CCTCTGCG		
GAM1310 RAD51L3	3'	GGTTGTGGA CTGGTCACTGC	28579	GT G GA
		GCAG AC CG AGTCCACAACC		
		CGTC TG GC TCAGGTGTTGG		
		AC _ _		
GAM1310 RAD51L3	3'	GGTTGTGGA CTGGTCACTGC	28581	GT G GA
		GCAG AC CG AGTCCACAACC		
		CGTC TG GC TCAGGTGTTGG		
		AC _ _		
GAM1310 TRIM8	3'	GTGGA CTTCCTGTTCT	25181	T C
		AGG ACG GGAAGTCCAC		
		TCT TGT CCTTCAGGTG		
		_ _		
GAM1310 CENTG1	3'	GTGACTGCGTACCTGT	16568	AAGTC
		GCAGGTACGCGG	CAC	
		TGTCCATGCGTC	GTG	
		A _ _		
GAM1310 DKFZp434G171	3'	TGGA CTTCCTCGCCCTG	38777	TA C
		CAGG CG GGAAGTCCA		
		GTCC GC CCTTCAGGT		
		C _ C		
GAM1310 FBP17	3'	TGGA CTTCCTCGGTCCCTGC	36050	T G
		GCAGG AC CGGAAGTCCA		
		CGTCC TG GCCTTCAGGT		
		C _		
GAM1310 FLJ00001	3'	GTTACGGA CTTCCTCGGCCGC	39785	A A C AC
		GC GGT CG GGAAGTCC	AAC	
		CG CCG GC CCTTCAGG	TTG	
		_ _ _ CA		
GAM1310 FLJ12056	3'	TTGTGGACCTGGGACCT	24470	ACG AA
		AGGT CGG GTCCACAA		
		TCCA GTC CAGGTGTT		
		GG _ C _		
GAM1310 GIT1	3'	GTGCCCCCGCGTGCCTGC	15257	AAGTC
		GCAGGTACGCGG	CAC	

CGTCCGTGCGCC GTG
CCC__

GAM1310 MAPK11 3' GGTCACAGACTTCTGGCCT 8628 ACG CACA
AGGT CGGAAGTC ACC
|||| ||||| ||
TCCG GTCTTCAG TGG
____ ACAC

GAM1310 TNFRSF19L 5' GGC GCCTTCCGCGCACCGGC 26687 A A T__
GC GGT CGCGGAAG CC
|| ||| ||||| ||
CG CCA GCGCCTTC GG
G C CGC

GAM1310 LOC146475 5' TTGCAGACTTCTGGCCT 40701 ACG CA
AGGT CGGAAGTC CAA
|||| ||||| ||
TCCG GTCTTCAG GTT
____ AC

GAM1310 LOC148753 5' GGTCGCGCGGTACCTGC 40899 _ _ AGT
GCAGGTAC GCG GA CC
||||| ||| || ||
CGTCCATG CGC CT GG
G G ____

GAM1310 LOC220002 3' GGCTGTGGACTTCCTCTACTT 44050 CGC A
AGGTA GGAAGTCCACA CC
|||| ||||| || ||
TTCAT CCTTCAGGTGT GG
CT_ C

GAM1310 LOC255265 5' GTGTGGACTTCACCCTG 45659 TACGCG A
CAGG GAAGTCCACA C
|||| ||||| ||
GTCC CTTTCAGGTGT G
CA_____ C

GAM1311 CPNE7 3' CAAGGCCGAAGGGGTGACAAAAT 15786 CAC TG__ A
ACA TGTA TTGT T TTC GCCTTG
|||| ||| | ||| |||||
ACAT AACA G AAG CGGAAC
AA_ GT GG C

GAM1311 IHPK3 3' CAAGACTGGTGGACAAAGTGTA 27655 GTT C
TACACTTGTT TCAG CTTG
||||||| ||| ||||
ATGTGAACAG GGTC GAAC
GT_ A

GAM1311 KLF8 3' CAAGGCTGTGAACAAACATAC 14121 CACT _ _
GTA TGTT GTTT CAGCCTTG
||| ||| ||| |||||
CAT ACAA CAAG GTCGGAAC
____ A T

GAM1311 MMP19 5' CAAAGCTGAAACGCTCTGAGCA 23073 A CTT T C
TGT CA GT GTTTCAGC TTG
||| || ||| ||||| |||

ACG GT CG CAAAGTCG AAC
 A CT_ _ A
 GAM1311 TCF20 3' CAAGGACCCCATCAAGTGTACA 33247 T TTTCAG
 TGTACACTTG TG CCTTG
 ||||| || ||||
 ACATGTGAAC AC GGAAC
 T CCCA_
 GAM1311 STAF42 3' CAAGGCTGAAGTGTATAGTGTA 27596 TGT GT
 TA TGTACACT T TTCAGCCTTG
 ||||| | |||||
 ATATGTGA G AAGTCGGAAC
 TAT TG
 GAM1311 LOC146520 5' CAAGGAAAACAAACAACAAATA 38185 CAC CAG_
 CA TGTA TTGTTGTTT CCTTG
 ||| ||||| ||||
 ACAT AACAACAAA GGAAC
 A_ CAAAA
 GAM1311 LOC253502 3' CAAGGCCGAAGGGTGACAAAAT 45379 CAC TG_ A
 ACA TGTA TTGT T TTC GCCTTG
 ||| ||| | |||||
 ACAT AACA G AAG CGGAAC
 AA_ GT GG C
 GAM1311 LOC90750 3' TTGAAAACAACAGACGTACA 31973 AC _
 TGTAC TTGTTGTTT CAG
 |||| ||||| |||
 ACATG GACAACAAA GTT
 CA A
 GAM1312 PKIA 5' CAAAGAAGTGACTTTTCT 13700 GCTAT C
 GGAAAAGT TAC TCTTTG
 ||||| || |||||
 TCTTTTCA GTG AGAAAC
 _ A
 GAM1312 SLC1A1 3' TCAAAGAGGCCAGTACTTTGCC 10379 A ATTA
 GG AAAGTGCT CCTCTTTGA
 || ||||| |||||
 CC TTTCATGA GGAGAAACT
 G CC_
 GAM1312 SLC6A12 3' CAAAGAGACAAAGGGACTTTTT 9009 G A AC
 C GGAAAAGT CT TT CTCTTTG
 ||||| || |||||
 CTTTTTCA GG AA GAGAAAC
 G A CA
 GAM1312 TAP2 3' TCAAAGAGGCTCAATGACTTTC 6141 A GCTATTA
 C GGAAA GT CCTCTTTGA
 |||| || |||||
 CCTTT CA GGAGAAACT
 _ GTA ACTC
 GAM1312 C20orf4 3' CAAAGAGGCTGTACCCATCC 17771 AAA TATTA
 GGA GTGC CCTCTTTG
 || ||| |||||

CCT CATG GGAGAAAC
 ACC TC____
 GAM1312 CHST4 3' CAAAGAGCTCACCAGCATTTTC 12335 G ATTAC_
 C GGAAAA TGCT CTCTTTG
 ||||| ||| |||||
 CCTTTT ACGA GAGAAAC
 _ CCACTC
 GAM1312 CTAGE-1 3' CAAAGTTATAGCACTGTTCC 22909 A TACCT
 GGAA AGTGCTAT CTTTG
 ||| ||||| |||||
 CCTT TCACGATA GAAAC
 G TT____
 GAM1312 HSPC129 3' CAAAGAACGGCACTTTTTTC 18534 ATTACC
 GGAAAAGTGCT TCTTTG
 ||||| |||||
 CTTTTTCACGG AGAAAC
 CA____
 GAM1312 KIAA1323 3' TAAAAGGTAATAGCATCTTCC 31569 AA C
 GGAA GTGCTATTACCT TTTG
 ||| ||||| |||||
 CCTT TACGATAATGGA AAAT
 C_ _
 GAM1312 KIAA1462 3' CAAAGAGGGTTCACTTTTGC 43920 G CTATTA
 G AAAAGTG CCTCTTTG
 | ||||| |||||
 C TTTTCAC GGAGAAAC
 G TTG____
 GAM1312 P66 3' TCAAAGAAGGACGAATAGCACC 21848 AAAA A__ _
 CTACC GG GTGCTATT CCT CTTTGA
 || ||||| |||||
 CC CACGATAA GGA GAAACT
 ATCC GCA A
 GAM1312 PRO1635 3' TCATTTATTGTAAATAACACTT 20667 C _ CTCTT_
 TTCC GGAAAAGTG TATT AC TGA
 ||||| ||||| |||
 CCTTTTCAC ATAA TG ACT
 A A TTATTT
 GAM1312 TRIP-Br2 3' AAGGAGGTATAACCTTTCC 16479 A GCTAT
 GGAAA GT TACCTCTTT
 ||||| || |||||
 CCTTT CA ATGGAGGAA
 C AT____
 GAM1312 LOC221178 3' CAAAGAGCCGCACTGCTCC 44926 AA TATTAC
 GGA AGTGC CTCTTTG
 ||| ||||| |||||
 CCT TCACG GAGAAAC
 CG CC____
 GAM1312 LOC221300 3' TCAAAGAGATATCTGCACTCC 44148 AAA TAT C
 GGA GTGC TA CTCTTTGA
 ||| ||| |||||

CCT CACG ATGAGAACT
 ____ TCT A
 GAM1312 LOC221712 5' TCAAAGAGGCAAGGTGCCCC 44975 AAAA TG A A
 GG G CT TT CCTCTTTGA
 || | || |||||
 CC C GG AA GGAGAACT
 C__ GT _ C
 GAM1312 LOC256849 5' GGCTAATAGCACTTCTCC 46313 A _
 GGA AAGTGCTATTA CC
 ||| ||||| ||
 CCT TTCACGATAAT GG
 C C
 GAM1313 AQP6 3' GCTCTGGAGAGGCCCCAC 7359 AAA_ CGG
 GTG CCTC TTCAGAGC
 ||| ||| |||||
 CAC GGAG AGGTCTCG
 CCCC ____
 GAM1313 AQP6 3' GCTCTGGAGAGGCCCCAC 27614 AAA_ CGG
 GTG CCTC TTCAGAGC
 ||| ||| |||||
 CAC GGAG AGGTCTCG
 CCCC ____
 GAM1313 COL6A1 3' GCCCTGAGCTGGCCTCAC 7586 AACCT A
 GTGA CCGGTTTCAG GC
 ||| ||||| ||
 CACT GGTGAGTC CG
 CC__ C
 GAM1313 GAB2 3' GCTCTGAGCCAGATTCCAC 14652 A CC C
 GTG AA TC GGTTTCAGAGC
 ||| || |||||
 CAC TT AG CCGAGTCTCG
 C _ A
 GAM1313 GAB2 3' GCTCTGAGCCAGATTCCAC 27847 A CC C
 GTG AA TC GGTTTCAGAGC
 ||| || |||||
 CAC TT AG CCGAGTCTCG
 C _ A
 GAM1313 GLRX 3' GCTCTGAACCAAGTGTCTCCAC 7830 A__ _ CC
 GTG AAC CT GGTTTCAGAGC
 ||| ||| |||||
 CAC TTG GA CCAAGTCTCG
 CTC T _
 GAM1313 HRMT1L1 3' GCTCTGAGCTGGGCTGTCACTT 32506 AACC
 AAGTGA TCCGGTTTCAGAGC
 ||||| |||||
 TTCACT GGGTCGAGTCTCG
 GTC_
 GAM1313 LETM1 3' CTTCCAGAGGTTTCAGCTT 14697 _ C TTCA
 AAG TGAAACCTC GG GAG
 ||| ||||| || |||

			TTC ACTTTGGAG CC	TTC	
			G A ____		
GAM1313	MAPRE1	3'	CTTTGCAGACGTTTCACTCC	14708	A C CGGTT
			A AGTGAAAC TC CAGAG		
			C TCACTTTG AG GTTTC		
			C C AC__		
GAM1313	MTMR6	3'	CTCTGGGAAAGATTTTCATTTT	44936	C CCGG
			AAAGTGAAA CT TTCAGAG		
			TTTTACTTT GA GGGTCTC		
			A AA__		
GAM1313	NKTR	3'	GCTCTCAGCTGGAGGCCCTCT	11863	T AA__ C
	CT		AG GA CCTCCGGTT AGAGC		
			TC CT GGAGGTCGA TCTCG		
			T CCCC C		
GAM1313	WHSC1	3'	CTCTCCTGTGAGATTTCACTTT	28444	C _ TTC
			AAAGTGAAA CTC CGG AGAG		
			TTTCACTTT GAG GTC TCTC		
			A T C__		
GAM1313	WHSC1	3'	CTCTCCTGTGAGATTTCACTTT	28461	C _ TTC
			AAAGTGAAA CTC CGG AGAG		
			TTTCACTTT GAG GTC TCTC		
			A T C__		
GAM1313	WHSC1	3'	CTCTCCTGTGAGATTTCACTTT	17180	C _ TTC
			AAAGTGAAA CTC CGG AGAG		
			TTTCACTTT GAG GTC TCTC		
			A T C__		
GAM1313	DDM36	3'	GCTCTGAAGGTCAAAAGCCTCA	21952	AACCT____ GG
	TTTT		AAGTGA CC TTCAGAGC		
			TTTACT GG AAGTCTCG		
			CCGAAACT _		
GAM1313	DNAJC6	3'	GCTCTGAGGAACCAGGTCCCAC	16660	AA CC _
			GTG ACCT GGT TCAGAGC		
			CAC TGGA CCA AGTCTCG		
			CC _ AGG		
GAM1313	FLJ10314	3'	GCTCTTGCTGGAGGCCTTAC	19817	AA TC
			GTGA CCTCCGGT AGAGC		
			CATT GGAGGTCG TCTCG		
			CC T_		
GAM1313	FLJ20171	3'	CTCTGTTAAGGAAGCTTCATTT	19261	ACC GGTT
	T		AAAGTGAA TCC CAGAG		

	TTTTACTT AGG GTCTC	
	CGA AATT	
GAM1313 KIAA0229	3' GCTCTGAAGACCCAGGCCTCAC 44403	AA CC _
	GTGA CCT GGT TCAGAGC	
	CACT GGA CCA AGTCTCG	
	CC C_ GA	
GAM1313 KIAA0410	3' CTCTACATGAAGATTTCACTTT 16619	C C GTTC
	AAAGTGAAA CT CG AGAG	
	TTTCACTTT GA GT TCTC	
	A A ACA_	
GAM1313 KIAA0565	3' AACCAAAGGTTTACTTT 33215	A CC
	AAAGTGAA CCT GGTT	
	TTTCATTT GGA CCAA	
	_ AA	
GAM1313 KIAA1462	3' ACCCAAAGAGGGTTCACTTT 43918	A C__
	AAAGTGAA CCTC GGT	
	TTTCACTT GGAG CCA	
	G AAAC	
GAM1313 MIC2L1	3' CCAGGATGATGGTTTCACTT 25490	__ _
	AAGTGAAACC TCC GG	
	TTCACTTTGG AGG CC	
	TAGT A	
GAM1313 NASP	3' GCTCTACTTCAGGTTTCACTCC 33738	A CC TC
	A AGTGAAACCT GGT AGAGC	
	C TCACTTTGGA TCA TCTCG	
	C CT _	
GAM1313 ZFP106	3' CTCTGATTTGGACTTCGCTTT 22830	ACC T
	AAAGTGAA TCCGG TCAGAG	
	TTTCGCTT AGGTT AGTCTC	
	C_ T	
GAM1313 LOC152220	3' CTCTATATAGTTTCACTTT 41443	CTCCG TC
	AAAGTGAAAC GT AGAG	
	TTTCACTTTG TA TCTC	
	A_ TA	
GAM1313 LOC254057	3' GCTCTGAGAATTAGCTTCACTT 46349	AC CCGG
	AAGTGAA CT TTCAGAGC	
	TTCACTT GA GAGTCTCG	
	C_ TTAA	
GAM1313 LOC254302	5' GCTCTGAGGATCCGGCCTCAC 46005	AACCT _
	GTGA CCGG TTCAGAGC	

CACT GGCC GAGTCTCG
 CC___ TAG
 GAM1313 LOC254874 5' GCTCTGAGGATCCGGCCTCAC 46004 AACCT ____
 GTGA CCGG TTCAGAGC
 |||| ||| |||||
 CACT GGCC GAGTCTCG
 CC___ TAG
 GAM1313 LOC256207 3' AACCAAAGGTTTACTTT 45616 A CC
 AAAGTGAA CCT GGTT
 ||||| ||| |||
 TTTCA TTT GGA CCAA
 _ AA
 GAM1313 LOC257407 5' CTCTGAACCAGAAGTCATCA 46335 A AACC C
 A GTGA TC GGTT CAGAG
 | ||| || |||||
 A TACT AG CCAAGTCTC
 C GA_ A
 GAM1313 LOC90170 5' CTGAGCTGAAAAC T TCACTCC 30908 A ACCTC
 A AGTGAA CGGTT CAG
 | |||| |||||
 C TCACTT GTCGAGTC
 C CAAAA
 GAM1313 LOC90268 3' TGAACCGGAGACATCACT 31043 AAC
 AGTG A CTCCGGTTCA
 |||| |||||
 TCACT GAGGCCAAGT
 ACA
 GAM1313 LOC91496 5' GCTCTGAGGCAAGACTTCGACT 32917 _ ACC CG _
 TT AAAGT GAA TC GT TCAGAGC
 |||| ||| || |||||
 TTTCA CTT AG CG AGTCTCG
 G C_ AA G
 GAM1313 LOC91661 3' GCTCTGAACTTCTCCTTCATCC 28752 A ACCTCC
 A GTGAA GGTT CAGAGC
 | |||| |||||
 C TACTT TCAAGTCTCG
 C CCTCT_
 GAM1313 LOC92997 3' CTCTGAACCAGAAGTCATCA 35220 A AACC C
 A GTGA TC GGTT CAGAG
 | |||| || |||||
 A TACT AG CCAAGTCTC
 C GA_ A
 GAM1314 BCL2L2 5' AGCTGGGGGCTCCTTGCCA 10257 ____
 TGGCAAGGA TCAGCT
 ||||| |||||
 ACCGTTCTT GGTCGA
 CGGG
 GAM1314 CARD15 3' CTGGCCTCTGCTGATCCTCCCA 22716 CA TT _
 TGG AGGATCAGC GA CCAG
 || ||||| || |||

			ACC TCCTAGTCG CT GGTC		
			C_ T_ CC		
GAM1314 DIA1	3'	CTGGCACTTACTGGTCCTTACC 14247	C	CT__ A	
A		TGG AAGGATCAG TG CCAG			
		ACC TTCCTGGTC AC GGTC			
		A ATTC _			
GAM1314 FGF7	3'	CTGATCAAGCTGGACTTGT 7750	GA	C	
		GCAAG TCAGCTTGA CAG			
		TGTTC GGTCGAACT GTC			
		A_ A			
GAM1314 GARP	3'	CAGGGCCTGATCTTTACCA 12030	C	__	
		TGG AAGGATCAG CTTG			
		ACC TTTCTAGTC GGAC			
		A CG			
GAM1314 GCNT2	5'	CAGGCTGTGGATCCTTGCCA 7238		__	
		TGGCAAGGATC AGCTTG			
		ACCGTTCCTAG TCGGAC			
		GTG			
GAM1314 GGA3	3'	CTGGTTCCTCCCTGCCCCTTGC 28903	AT	CTT__	
CA		TGGCAAGG CAG GACCAG			
		ACCGTTCC GTC TTGGTC			
		CC CCTCC			
GAM1314 GGA3	3'	CTGGTTCCTCCCTGCCCCTTGC 15200	AT	CTT__	
CA		TGGCAAGG CAG GACCAG			
		ACCGTTCC GTC TTGGTC			
		CC CCTCC			
GAM1314 GNRH1	5'	TCACTGTCCTTGCCA 6484	T	CT	
		TGGCAAGGA CAG TGA			
		ACCGTTCCT GTC ACT			
		- -			
GAM1314 NRF1	3'	GGTGCTGACCTTGCCA 30191	A	TTG	
		TGGCAAGG TCAGC ACC			
		ACCGTTCC AGTCG TGG			
		- -			
GAM1314 NTSR1	3'	CTGGCCATGGGTCCTTGCC 8368	AGCT	A	
		GGCAAGGATC TG CCAG			
		CCGTTCTGG AC GGTC			
		GT__ C			
GAM1314 SYNGR1	3'	CTGATCACTGTCCTTGCC 11065	T	CT C	
		GGCAAGGA CAG TGA CAG			

			CCGTTCTCT GTC ACT GTC		
			— — A		
GAM1314	TCF1	3'	CTGGCCAAGCTGAGGTGCC 6148	AGGA	A
			GGCA TCAGCTTG CCAG		
			CCGT AGTCGAAC GGTC		
			GG— C		
GAM1314	AQP9	3'	GGCTGAGAATCTTTGCCA 21968	—	
			TGGCAAGGA TCAGCT		
			ACCGTTTCT AGTCGG		
			AAG		
GAM1314	C8orf2	3'	CTGTTATGAGCTGACCCCCA 14022	CAA A	AC—
			TGG GG TCAGCTTG CAG		
			ACC CC AGTCGAGT GTC		
			— C ATT		
GAM1314	DKFZP586I2223	3'	GGAGGCTGATGCCTGCCA 17731	A —	GA
			TGGCA GG ATCAGCTT CC		
			ACCGT CC TAGTCGGA GG		
			— G —		
GAM1314	FLJ20275	3'	GTCAGATCCTTGCCA 19322	AGCT	
			TGGCAAGGATC TGAC		
			ACCGTTCCTAG ACTG		
			—		
GAM1314	FLJ21742	3'	CTGGTGCCCACGCCCTTGCCA 25913	ATCA T —	
			TGGCAAGG GC TG ACCAG		
			ACCGTTCC CG AC TGGTC		
			— C CCG		
GAM1314	FYCO1	3'	CTGGCCAAGCTGATGACCT 23709	—	A
			AGG ATCAGCTTG CCAG		
			TCC TAGTCGAAC GGTC		
			AG C		
GAM1314	HIC2	3'	CTGGGTCTGGTCCTTACCA 32529	C	CTTGA
			TGG AAGGATCAG CCAG		
			ACC TTCCTGGTC GGTC		
			A TG—		
GAM1314	KIAA0319	3'	CTGGCCTCTCTGATCCTTCCA 16762	C	CTTGA
			TGG AAGGATCAG CCAG		
			ACC TTCCTAGTC GGTC		
			— TCTCC		
GAM1314	KIAA0672	3'	CTGGGGCACTGACCTTTGCCA 16919	A	CT A—
			TGGCAAGG TCAG TG CCAG		

ACCGTTTC AGTC AC GGTC
 C _ GG
 GAM1314 KIAA1036 3' TGGTCAGTCCCTTGCC 17133 ATCA T
 GGCAAGG GCT GACCA
 ||||| |||||
 CCGTTCC TGA CTGGT
 C _ _
 GAM1314 KIAA1280 5' CTGGCCAAGCTGACCGATAGCT 34551 AA_ A A
 GGC GG TCAGCTTG CCAG
 || || ||||| |||||
 TCG CC AGTCGAAC GGTC
 ATAG _ C
 GAM1314 KIAA1855 3' CTGGGCCTGCTCCTTGCCA 44358 T CTTGA
 TGGCAAGGA CAG CCAG
 ||||| || |||||
 ACCGTTCT GTC GGTC
 C CG_
 GAM1314 LOXL4 3' GTCATCCCTGAATCTTGCCA 25930 A CT_
 TGGCAAGG TCAG TGAC
 ||||| ||||| |||||
 ACCGTTCT AGTC ACTG
 A CCT
 GAM1314 SCMH1 3' CTGGCTCATACTGCCCCACCA 14539 CAA AT CT _
 TGG GG CAG TGA CCAG
 || || || || |||||
 ACC CC GTC ACT GGTC
 AC_ CC AT C
 GAM1314 SNAP29 3' CTGGCCCATGTGACCTTTGCCA 11187 A GT A_
 TGGCAAGG TCA C TG CCAG
 ||||| ||||| || |||||
 ACCGTTTC AGT G AC GGTC
 C _ T CC
 GAM1314 LOC112868 5' GGTCTCCAGCCCTTGCCA 36084 ATCA T____
 TGGCAAGG GCT GACC
 ||||| || |||||
 ACCGTTCC CGA CTGG
 _ CCCTC
 GAM1314 LOC132880 5' CTGGCTCAGCTAATCCTTGCTCA 37031 C T _
 TGGCAAGGAT AGCT GA CCAG
 ||||| ||||| || |||||
 ACTGTTCTTA TCGA CT GGTC
 A _ C
 GAM1314 LOC136015 3' TGATCAAGTCCTTGCTA 37501 ATCA C
 TGGCAAGG GCTTGA CA
 ||||| ||||| ||
 ATCGTTCC TGA ACT GT
 _ A
 GAM1314 LOC142927 5' CTGGCCTCAAGTGATCCTTCCA 37567 C G _
 TGG AAGGATCA CTTGA CCAG
 || ||||| ||||| |||||

ACC TTCCTAGT GAACT GGTC
 _ _ CC
 GAM1314 LOC143425 3' CTGGCAGGCTGACCATTACCA 42355 C _ A A
 TGG AA GG TCAGCTTG CCAG
 ||| || ||||| ||||
 ACC TT CC AGTCGGAC GGTC
 A A _ _
 GAM1314 LOC145566 5' CTGGGGTCCACCCTTGCCA 37897 ATCA TGA
 TGGCAAGG GCT CCAG
 ||||| || ||||
 ACCGTTCC TGG GGTC
 CACC ____
 GAM1314 LOC151391 3' CAAGCTTCTGATCCTCCCA 41335 CA ____
 TGG AGGATCA GCTTG
 || ||||| ||||
 ACC TCCTAGT CGAAC
 C_ CTT
 GAM1314 LOC152200 3' CTGGCCAAGCTGACGTCC 41439 _ A
 GGA TCAGCTTG CCAG
 || ||||| ||||
 CCT AGTCGAAC GGTC
 GC C
 GAM1314 LOC154788 3' TGATCAAGTCCTTGCTA 41726 ATCA C
 TGGCAAGG GCTTGA CA
 ||||| ||||| ||
 ATCGTTCC TGAAGT GT
 ____ A
 GAM1314 LOC219505 5' CAGGATACGATACCTTGCCA 43853 _ AG__
 TGGCAAGG ATC CTTG
 ||||| || ||||
 ACCGTTCC TAG GGAC
 A CATA
 GAM1314 LOC219988 5' CTGCAAAGCACTGATCCCTACC 44043 CAA _ GAC
 GG GGATCA GCTT CAG
 || ||||| |||| ||
 CC CCTAGT CGAA GTC
 ATC CA AC_
 GAM1314 LOC222936 5' CTGGTCAAAGTGGGTCTGC 45309 A AT C
 GCA GG CAG TTGACCAG
 ||| || ||||| |||||
 CGT CT GTC AACTGGTC
 _ GG A
 GAM1314 LOC56965 3' CTGGTCAATGCATCCTACACCA 21452 CA_ CA _
 TGG AGGAT GC TTGACCAG
 || |||| ||||| |||||
 ACC TCCTA CG AACTGGTC
 ACA _ T
 GAM1314 LOC85414 3' CTGGTCATTGGGCTGATCATTG 26951 G ____
 CCA TGGCAA GATCAGCT TGACCAG
 ||||| ||||| |||||

		ACCGTT CTAGTCGG ACTGGTC	
		A GTT	
GAM1315 CADPS	3'	GAGAATACATAGTCTAACCA 32507	CA CAA _
		TGG AG ACT TGTATTCTC	
		ACC TC TGA ACATAAGAG	
		AA _ T	
GAM1315 CCND2	3'	GAGAATATGTATGCCTGC 7515	A A TT
		GCA GCA AC GTATTCTC	
		CGT CGT TG TATAAGAG	
		C A _	
GAM1315 EPHB4	3'	GAGAGTGTGACTCCCTTGCCA 10739	CAAAC TG
		TGGCAAG T TATTCTC	
		ACCGTTC A GTGAGAG	
		CCTC_ GT	
GAM1315 LAMP2	3'	GAGATAATTGCTTGCCA 15185	AC A
		TGGCAAGCAA TTGT TTC	
		ACCGTTTCGTT AATA GAG	
		_ _	
GAM1315 LPP	3'	GAAACACTTGCTTGCCA 12107	ACT A
		TGGCAAGCAA TGT TTC	
		ACCGTTTCGTT ACA AAG	
		C_ _	
GAM1315 LRP4	5'	GAGAATACAGGAAGCCCCCA 32200	CAA AAA
		TGG GC CTTGTATTCTC	
		ACC CG GGACATAAGAG	
		CC_ AA_	
GAM1315 MOX2	3'	AGAATACAGAGAGCTTACC 33236	C AAAC
		GG AAGC TTGTATTCT	
		CC TTCG GACATAAGA	
		A AGA_	
GAM1315 NRAP	3'	GAGAGGAAGTTTGTTCACCA 12833	CA GTA
		TGG AGCAAAC TTCTC	
		ACC TTGTTTGAA GAGAG	
		AC G_	
GAM1315 PNN	3'	AATACAGACTGTTTGTTTACCA 35232	C _
		TGG AAGCAAAC TTGTATT	
		ACC TTTGTTTG GACATAA	
		A TCA	
GAM1315 PPT1	3'	GAATGCAAGTTTAATTACCA 30955	C GC
		TGG AA AAAC TTGTATTC	

		ACC TT TTTGAACGTAAG		
		A AA		
GAM1315	SNX5	3' AATATTATTGCTTGCTA	15784	ACTT
		TGGCAAGCAA GTATT		
		ATCGTTCGTT TATAA		
		AT__		
GAM1315	TRPM6	3' AGAGGCAGAGTTTGCTTGCC	19195	GTA
		GGCAAGCAAACCTT TTCT		
		CCGTTCGTTTGAG GAGA		
		ACG		
GAM1315	VTN	5' GAGACCAGAGCCCAGCTTGCCA	6272	AAA_ GTAT
		TGGCAAGC CTT TCTC		
		ACCGTTCG GAG AGAG		
		ACCC ACC_		
GAM1315	AMOT	3' GAACACAGCTTGCTTGC	28413	A T A
		GCAAGCAA CT GT TTC		
		CGTTCGTT GA CA AAG		
		C _ C		
GAM1315	DDX39	3' GAGTGCGAGCCGCCCGCCA	29096	AA AAA
		TGGC GC CTTGTATTC		
		ACCG CG GAGCGTGAG		
		CC CC_		
GAM1315	DKFZP434K2235	3' AGACATGCAGTTTGCTTGC	40594	T _
		GCAAGCAAACCT GTAT TCT		
		CGTTCGTTTGA CGTA AGA		
		_ C		
GAM1315	DKFZP564O0423	3' AGAACACAAGTTTTTGTC	44063	GCA A
		GGCAA AACTTGT TTCT		
		CTGTT TTGAACA AAGA		
		_ C		
GAM1315	DNAJC6	3' GAGAATACAAAAAGCATGC	16659	A AAAC
		GCA GC TTGTATTCTC		
		CGT CG AACATAAGAG		
		A AAA_		
GAM1315	DYRK4	5' AGAATACGGTAAGCTTCCCA	32122	C AA T
		TGG AAGC ACT GTATTCT		
		ACC TTCG TGG CATAAGA		
		C AA _		
GAM1315	EFA6R	3' GAGAGGCAGGGCCTGCTTGTC	17624	AA_ A
		TGGCAAGCA CTTGT TTCTC		

ACTGTTCGT GGACG GAGAG
 CCG _
 GAM1315 FBP17 5' AGAATACAAGTATACGTCA 36046 AAGCAA
 TGGC ACTTGATTCT
 ||| |||||
 ACTG TGAACATAAGA
 CATA_
 GAM1315 FLJ10420 3' AGAGGTTGAGTTTGCTGCCA 19855 A GTA
 TGGCA GCAAACCTT TTCT
 ||||| ||||| |||
 ACCGT CGTTTGAG GAGA
 _ TTG
 GAM1315 FLJ13409 3' GAAAACAAGTAGTCCTGTTTGC 23878 A____ A
 CA TGGCAAGCA ACTTGT TTC
 ||||| ||||| |||
 ACCGTTTGT TGAACA AAG
 CCTGA A
 GAM1315 FLJ13782 3' GAAACTGTTTGTTTGCCA 24437 TT A
 TGGCAAGCAAAC GT TTC
 ||||| || |||
 ACCGTTTGTTTG CA AAG
 T_ _
 GAM1315 FLJ20343 3' AATATCTTAGTTTGCTACCA 19399 CA T_
 TGG AGCAAACCT GTATT
 || ||||| |||||
 ACC TCGTTTGA TATAA
 A_ TTC
 GAM1315 FLJ21125 3' GATGCAAGCCCCTTGCCA 23891 CAAA
 TGGCAAG CTTGTATT
 ||||| |||||
 ACCGTTT GAACGTAG
 CCC_
 GAM1315 FLJ22009 3' AGAATCACTGCTGCCA 30243 A AACT T
 TGGCA GCA TG ATTCT
 ||||| || |||||
 ACCGT CGT AC TAAGA
 _ C_ _
 GAM1315 KIAA0987 5' GAACAGGAGTTTGCTGCCA 14676 A GTA
 TGGCA GCAAACCTT TTC
 ||||| ||||| |||
 ACCGT CGTTTGAG AAG
 _ GAC
 GAM1315 MGC19556 3' AGAGTATCTGCTTTCCA 27312 C AACTT
 TGG AAGCA GTATTCT
 || ||||| |||||
 ACC TTCGT TATGAGA
 T C_
 GAM1315 VIT1 5' AATAAGGGCTTGCTTGCC 20764 A TG
 GGCAAGCAA CT TATT
 ||||| || |||

CCGTTCGTT GG ATAA
 C GA
 GAM1315 YME1L1 3' AGAATACAAGTAGCATTGC 15535 _ AA
 GCAA GC ACTTGTATTCT
 ||||| || |||||
 CGTT CG TGAACATAAGA
 A A_
 GAM1315 LOC145483 3' AGAATACAAGTAATTGCCA 37880 GCAA
 TGGCAA ACTTGTATTCT
 ||||| |||||
 ACCGTT TGAACATAAGA
 AA_
 GAM1315 LOC147649 3' GAGAGGTTAAGTTGCTTGCCA 38356 A TA
 TGGCAAGCAA CTTG TTCTC
 ||||| ||||| |||||
 ACCGTTTCGTT GAAT GAGAG
 _ TG
 GAM1315 LOC151443 5' GAGAACACGAGGCTTGCCA 39115 AAA A
 TGGCAAGC CTTGT TTCTC
 ||||| ||||| |||||
 ACCGTTTCG GAGCA AAGAG
 _ C
 GAM1315 LOC167153 5' AGAATACATGTTCACTTCCA 40229 C CA T
 TGG AAG AAC TGTATTCT
 ||| ||| ||| |||||
 ACC TTC TTG ACATAAGA
 _ AC T
 GAM1315 LOC220930 5' GAGGCTAGAAGTTCCGCTTGCC 44735 A_ G TT
 A
 TGGCAAGC AACTT TA CTC
 ||||| ||||| ||| |||
 ACCGTTTCG TTGAA AT GAG
 CC G CG
 GAM1315 LOC220965 3' AGAATACAACAGGTAGCCA 43946 AA AAAC
 TGGC GC TTGTATTCT
 ||||| ||| |||||
 ACCG TG AACATAAGA
 A_ GAC_
 GAM1315 LOC91286 3' AGTAAGGGTATGCTTACCA 32621 C A TG
 TGG AAGCA ACT TATT
 ||| ||||| ||| |||||
 ACC TTCGT TGG ATGA
 A A GA
 GAM1316 CLDN14 5' ACCCCGAGGGGCCAGGGA 29309 A _ T
 TC CC GGGCCCTTG GGT
 || || ||||| ||| |||
 AG GG CCCGGGAGC CCA
 _ A C
 GAM1316 CLN6 3' GCCCAGGCTCAGGCCCATGA 19551 CC _ T
 TCA GGGCC CTTG GGT
 ||| ||||| ||||| |||

		AGT CCCGG GGAC CCG		
		A_ ACTC _		
GAM1316 CTBP1	3'	GCCTGGGCAGAGGGCCCGG 33729	GTGG	
		CCGGGCCCTT TAGGC		
		GGCCCGGGAG GTCCG		
		ACGG		
GAM1316 CXorf6	3'	GCCTCAGGCAGAGCCCGGT 11993	CC GGT	
		ACCGGGC TTGT AGGC		
		TGGCCCG GACG TCCG		
		A_ GAC		
GAM1316 CXorf6	3'	GCCCGGTACAGGGCCCGGTG 11992	T GTA	
		CACCGGGCCCT GTG GGC		
		GTGGCCCGGGA CAT CCG		
		_ GGC		
GAM1316 CYP46	3'	GCCCACCCAGGGCCCGG 13484	T T A	
		CCGGGCCCT G GGT GGC		
		GGCCCGGGA C CCA CCG		
		_ _ C		
GAM1316 DHFR	5'	GCCCGGCGGCAGGGCCCGGCGA 6449	A T G A_	
		TC CCGGGCCCT GT GT GGC		
		AG GGCCCGGGA CG CG CCG		
		C _ G GC		
GAM1316 FPGS	3'	GCCCAGAGCCCGGTGG 11402	CC T	
		TCACCGGGC TTG GGT		
		GGTGGCCCG GAC CCG		
		A_ _		
GAM1316 GPC1	3'	GCCCACCTTGGACCCTGGTGA 7873	_ C TTGT A	
		TCACC GGG CC GGT GGC		
		AGTGG CCC GG CCA CCG		
		T A TT_ C		
GAM1316 HCN4	5'	CCCAGCCGGGCCCCGGGA 11978	A TTGT A_	
		TC CCGGGCCC GGT GG		
		AG GGCCCGGG CCG CC		
		_ _ _ AC		
GAM1316 LTBR	3'	GCCTGAGTAGGGCCCGGGGA 8141	A TGTGG	
		TC CCGGGCCCT TAGGC		
		AG GGCCCGGGA GTCCG		
		G TGA_		
GAM1316 NDUFV3	5'	GCCCACTGAAAGCCTGGTGA 22045	CCTTG A	
		TCACCGGGC TGGT GGC		

AGTGGTCCG GTCA CCG
 AAA__ C
 GAM1316 PFKFB4 3' GCCCAGCATGGACCTGGTGA 10909 C T GGTA
 TCACCGGG CC TGT GGC
 ||||| || ||| |||
 AGTGGTCC GG ACG CCG
 A T AC__
 GAM1316 SIL 3' GCCTACCACAAGGCTCCTG 8985 C_
 CGGG CCTTGTGGTAGGC
 ||| |||||
 GTCC GGAACACCATCCG
 TC
 GAM1316 SOX4 5' ACCGGGAGGGCCCGGCGA 9072 A G
 TC CCGGGCCCTT TGGT
 || ||||| |||
 AG GGCCCGGGAG GCCA
 C G
 GAM1316 SYNGR1 3' GCCCACCACAAGAGGCTGTGA 11067 CG _ A
 TCAC GGCC CTTGTGGT GGC
 ||| ||| ||||| |||
 AGTG TCGG GAACACCA CCG
 _ A C
 GAM1316 TAF7 5' CCGGACGGAGGGCCCGGCGA 12176 A G G GTA
 TC CCGG CCCTT TG GG
 || ||| |||| || ||
 AG GGCC GGGAG GC CC
 C _ _ AGG
 GAM1316 THBS1 3' CCTACCATCTCAGTGA 9255 C CCCTT
 TCAC GGG GTGGTAGG
 ||| ||| |||||
 AGTG CTC TACCATCC
 A ____
 GAM1316 TUFT1 3' CCTGGCAAGGCCTGGTGA 21316 C GG
 TCACCGGGCC TTGT TAGG
 ||||| ||| |||
 AGTGGTCCGG AACG GTCC
 _ _
 GAM1316 ADAMTS10 5' GCCCCAAAAGGAGCCCGGTGA 25231 _ G TA
 TCACCGGGC CCTT TGG GGC
 ||||| ||| ||| |||
 AGTGGCCCG GGAA ACC CCG
 A A C_
 GAM1316 BRAG 5' GCCCACCACATGGCTCGGT 16942 CT T A
 ACCGGGCC TG GGT GGC
 ||||| || ||| |||
 TGGCTCGG AC CCA CCG
 T_ _ C
 GAM1316 DKFZP762D096 5' CCCAAGCCAGGGCCCCCGGTGA 32665 _ T GGTA
 TCACCGGG CCCT GT GG
 ||||| ||| || ||

AGTGGCCC GGGA CG CC
 C C AAC_
 GAM1316 FASTK 5' CCTGCGCAGGGCCCGGGGA 24729 A T G
 TC CCGGGCCCT GTG TAGG
 || ||||| || ||||
 AG GGCCCGGGA CGC GTCC
 G _ _
 GAM1316 FLJ10898 5' GCCATCCACAAGGGCCCACT 29894 C TA
 AC GGGCCCTTGTGG GGC
 || ||||| ||||
 TG CCCGGGAACACC CCG
 A TA
 GAM1316 FLJ12800 3' GCCTCTCTAGGGCCCTGGTGA 23192 _ TGT T
 TCACC GGGCCCT GG AGGC
 |||| |||| || ||||
 AGTGG CCCGGGA TC TCCG
 T TC_ _
 GAM1316 FLJ21709 3' CCTACCACGGCTCCGG 38168 _ CTT
 CCGG GCC GTGGTAGG
 |||| || |||||
 GGCC CGG CACCATCC
 T _
 GAM1316 HSPB7 5' GCCTGGGCAGGGCCCGG 15782 T GG
 CCGGGCCCT GT TAGGC
 ||||| || ||||
 GGCCCGGGA CG GTCCG
 _ G_
 GAM1316 KIAA0087 3' CCAATCATTAAGCCCTGTGA 16556 C CCTT A
 TCAC GGGC GTGGT GG
 |||| || |||| ||
 AGTG CCG TACTA CC
 T AAT_ A
 GAM1316 KIAA0318 5' GCCTTCCCACAAGGGCCCGG 34188 T_
 CCGGGCCCTTGTGG AGGC
 ||||| ||||
 GGCCCGGGAACACC TCCG
 CT
 GAM1316 KIAA0545 3' GCCCAGCTGTGGTCCCGGTGA 31636 C TT TG A_
 TCACCGGG CC G GT GGC
 ||||| || | || ||
 AGTGGCCC GG T CG CCG
 T _ GT AC
 GAM1316 KIAA1322 5' GCCTACCGCGTGCCCGG 36028 CCT
 CCGGGC TGTGGTAGGC
 |||| |||||
 GGCCCG GCGCCATCCG
 T_
 GAM1316 KIAA1719 5' CCTACGTGCGGCCCGGTGG 33818 CTT _
 TCACCGGGCC GTG GTAGG
 ||||| || ||||

GGTGGCCCGG CGT CATCC
___ G
GAM1316 KIAA1924 3' GCCTCACGGAAGGGCCCGGTGG 36477 G GT
TCACCGGGCCCTT TG AGGC
||||||| || |||
GGTGGCCCGGGAA GC TCCG
G AC
GAM1316 KPNA6 3' GCCTCAGGGCCTGGTGA 14688 T T
TCACCGGGCCCT G GGT
||||||| |||
AGTGGTCCGGGA C CCG
_T
GAM1316 MGC10812 3' GCCTGGCTGAGGGCCGGG 25413 G GT _
CC GGCCCTT GGT AGGC
|| ||||| ||| |||
GG CCGGGAG TCG TCCG
G _ G
GAM1316 MGC15827 3' GCCCACCACCACCTTCCCGGTG 26702 CCCTT_ A
A TCACCGGG GTGGT GGC
||||| ||||| |||
AGTGGCCC CACCA CCG
TTCCAC C
GAM1316 MR 5' CCTATGGAGGCCCATGA 25255 CC _ TGTG
TCA GGGCC CT GTAGG
||| ||||| || |||||
AGT CCCGG GG TATCC
A_ A ____
GAM1316 TRIM2 3' CCTAGGTCACAAGACCCAGGGA 17600 A _ CC _
TC CC GGG CTTGTGG TAGG
|| ||| ||||| |||
AG GG CCC GAACACT ATCC
_ A A_ GG
GAM1316 LOC199964 5' GCCCTGGGAGGGGCCAGG 43267 _ G TA
CC GGGCCCTT TGG GGC
|| ||||| ||| |||
GG CCCGGGAG GTC CCG
A G _
GAM1316 LOC199986 5' GCCCAGGGGAAGACCCAGGGA 43273 A _ ____ T
TC CC GGG CCCTTG GGT
|| ||| ||||| |||
AG GG CCC GGGGAC CCG
_ A AGAA _
GAM1316 LOC220549 5' GCCTACCATGGTCACCCATGA 44651 CC CCC TG
TCA GGG T TGGTAGGC
||| ||| | |||||
AGT CCC G ACCATCCG
A_ ACT GT
GAM1316 LOC254532 3' GCCATGGGAAGGGCCCAGG 46211 _ _
CC GGGCCCTT GTGGT
|| ||||| |||||

GG CCCGGGAA TACCG
A GGG
GAM1316 LOC90917 3' GCCTTTGTCAGGACCCTGTGA 32169 C C T TG T
TCAC GGG CCT G G AGGC
||||| ||| ||| | ||||
AGTG CCC GGA T T TCCG
T A C GT _
GAM1316 LOC91409 3' ACCCTAAGGGCCCCATGA 32801 CC T
TCA GGGCCCTTG GGT
||| ||||||| |||
AGT CCCGGGAAT CCA
AC C
GAM1316 LOC91948 5' ACAGCAACAGGCCCAAGTGA 33572 C C_ G
TCAC GGGCC TTGT GT
||||| ||||| ||| ||
AGTG CCCGG AACG CA
A AC A
GAM1317 UCP3 3' GAATTCACACCTTAGGTG 9384 GTTG A
CACC TAA GTGTGAATTC
||||| ||| |||||||||
GTGG ATT CACACTTAAG
_ C
GAM1317 CDC10 3' AATTCACATAATAAACGATG 43792 C GTAAA
CA CGTT GTGTGAATT
|| ||||| |||||||||
GT GCAA TACACTTAA
A ATAA_
GAM1317 FLJ10716 3' GAATTCGTTCTACAACATGA 20045 CC AA TG
TCA GTTGT AG TGAATTC
||| ||||| || |||||||
AGT CAACA TC GCTTAAG
A_ _ TT
GAM1317 KIAA0976 3' GAATTCACACGTAGACGAC 17165 AAA_
GTTGT GTGTGAATTC
||||| |||||||||
CAGCA CACACTTAAG
GATG
GAM1317 KIAA1136 3' GAATTAAATGCTTTACAACATG 43882 CC G_
A TCA GTTGTAAGTGT AATTC
||| ||||||||| |||||
AGT CAACATTTTCGTA TTAAG
A_ AA
GAM1317 UBE2V2 3' GAATTCAGGTTTACAAGATGA 9375 CCG G G
TCA TTGTAAA T TGAATTC
||| ||||||| | |||||||
AGT AACATTT G ACTTAAG
AG_ _ G
GAM1317 LOC121274 5' GAACCCACACTGCAGTGG 36655 AA AA
CCGTTGT AGTGTG TTC
||||||| ||||||| |||

GGTGACG TCACAC AAG
— CC
GAM1317 LOC121536 3' AGTTTTCACCTTACTACAGTGA 36662 C T T
TCAC GT GTAAAGTG GAATT
|||| || ||||| ||||
AGTG CA CATTTCAC TTTGA
A T T
GAM1317 LOC151201 3' AATTCACACAACTTACATG 41319 T A—
CGT GTAA GTGTGAATT
||| ||| ||||| ||||
GTA CATT CACACTTAA
— CAAA
GAM1317 LOC152282 5' CAAGCTTTGCAACAATGA 39254 CC G
TCA GTTGTAAGT TG
||| ||||| ||
AGT CAACGTTTCG AC
AA A
GAM1317 LOC254312 5' GAATTCAACACAACACG 46114 T AAA _
CGT GT GTGT GAATTC
||| || ||| |||||
GCA CA CACA CTTAAG
— A_ A
GAM1317 LOC254413 5' GAAGTTAACTTTACAAAATGA 46401 CCG G A
TCA TTGTAAAGT TGA TTC
||| ||||| ||| |||
AGT AACATTTCA ATT AAG
AA_ A G
GAM1317 LOC90288 3' GAATTTACTCTACAAC 31107 AA T
GTTGT AG GTGAATTC
|||| || ||||| ||||
CAACA TC CATTTAAG
— T
GAM1318 ZFP103 5' GCCGCGGAGTCCG GCCCCA 12220 AAT A _
TGG CCG ACTCCGTG C
||| ||| ||||| ||
ACC GGC TGAGGCGC G
CCC C C
GAM1318 FLJ11850 3' TTCAGTGGAGTTTCAGGTTCCA 22953 C TGCG
TGGAATC GAACTCCG GAA
||||| ||||| |||
ACCTTGG CTTGAGGT CTT
A GA_
GAM1318 FLJ20507 3' GTTCCGCACGATCCGGAACCCA 19515 AA AACTC
TGG TCCG CGTGCGGAAC
||| ||| ||||| ||||
ACC AGGC GCACGCCTTG
CA CTA_
GAM1318 FLJ20507 3' GTTCCGCACGATCCGGAACCCA 30223 AA AACTC
TGG TCCG CGTGCGGAAC
||| ||| ||||| ||||

ACC AGGC GCACGCCTTG
 CA CTA__
 GAM1318 RGS7 3' TTCCGCACAGAAAGTTTCA 8829 CCGAAC C
 TGAAT TC GTGCGGAA
 ||||| || |||||
 ACTTTG AG CACGCCTT
 AA__ A
 GAM1318 LOC126302 3' CTGCATGGGTTCAAATCCCA 36820 A CC T
 TGG AT GAAC CCGTGCGG
 ||| || |||| |||||
 ACC TA CTTG GGTACGTC
 C AA _
 GAM1318 LOC126302 3' CTGCATGGGTTCAAATCCCA 36821 A CC T
 TGG AT GAAC CCGTGCGG
 ||| || |||| |||||
 ACC TA CTTG GGTACGTC
 C AA _
 GAM1318 LOC126302 3' CTGCATGGGTTCAAATCCCA 36822 A CC T
 TGG AT GAAC CCGTGCGG
 ||| || |||| |||||
 ACC TA CTTG GGTACGTC
 C AA _
 GAM1318 LOC143677 5' TTCTGCACTCAAATTCCA 40374 CC ACTCC
 TGAAT GA GTGCGGAA
 ||||| || |||||
 ACCTTA CT CACGTCTT
 AA ____
 GAM1318 LOC149703 3' CCCGAGGTCTGCTGGATTCCA 41063 AACT_ G C
 TGAATCCG CC TG GG
 ||||| || |||
 ACCTTAGGT GG GC CC
 CGTCT A _
 GAM1319 ANKTM1 3' ACTGTACCATGCCTGTCA 14254 G CGA AG
 TGAC AGGCA GGT GCAGT
 |||| |||| || |||||
 ACTG TCCGT CCA TGTCA
 _ A__ _
 GAM1319 GAS11 3' CACTGCCTAAATGATGCCCG 7221 A _ AGG
 CG GGCA CG TAGGCAGTG
 || |||| || |||||
 GC CCGT GT ATCCGTCAC
 _ A AA_
 GAM1319 LANCL1 3' CTACCTTGTGCCTCTCA 12695 C
 TGA GAGGCACGAGGTAG
 ||| |||||
 ACT CTCCGTGTTCCATC
 _
 GAM1319 MAPT 3' CACTGCCTATACCCCTCATCA 12539 C CACGAG
 TGA GAGG GTAGGCAGTG
 ||| |||| |||||

		ACT CTCC	TATCCGTCAC		
		A CCA__			
GAM1319	MAPT	3' CACTGCCTATACCCCTCATCA	18827	C	CACGAG
		TGA GAGG	GTAGGCAGTG		
		ACT CTCC	TATCCGTCAC		
		A CCA__			
GAM1319	MAPT	3' CACTGCCTATACCCCTCATCA	18833	C	CACGAG
		TGA GAGG	GTAGGCAGTG		
		ACT CTCC	TATCCGTCAC		
		A CCA__			
GAM1319	MAPT	3' CACTGCCTATACCCCTCATCA	18839	C	CACGAG
		TGA GAGG	GTAGGCAGTG		
		ACT CTCC	TATCCGTCAC		
		A CCA__			
GAM1319	NRXN2	3' CTGCGCGGCCTCGTCA	28984	A	AGGTAG
		TGACGAGGC CG	GCAG		
		ACTGCTCCG GC	CGTC		
		_ G__			
GAM1319	NRXN2	3' CTGCGCGGCCTCGTCA	28990	A	AGGTAG
		TGACGAGGC CG	GCAG		
		ACTGCTCCG GC	CGTC		
		_ G__			
GAM1319	NRXN2	3' CTGCGCGGCCTCGTCA	17468	A	AGGTAG
		TGACGAGGC CG	GCAG		
		ACTGCTCCG GC	CGTC		
		_ G__			
GAM1319	PSD	5' CACTGCCTACCCACCTGCC	8667	CGA_	
		GGCA	GGTAGGCAGTG		
		CCGT	CCATCCGTCAC		
		CCAC			
GAM1319	FLJ10829	3' CACTGCTGTCTTCCCTACCTC	20178	CAC_	TA
		GAGG	GAGG GGCAGTG		
		CTCC	CTTC TCGTCAC		
		ATCC	TG		
GAM1319	FLJ20584	3' CACTGCCTCACTGCACCTGCC	19558	CGA_	_
		GGCA	GGT AGGCAGTG		
		CCGT	TCA TCCGTCAC		
		CCACG	C		
GAM1319	FLJ20699	3' CACTGCCTGTCCCCGTCCC	19616	C	A _
		GG	ACG GG TAGGCAGTG		

				CC TGC CC GTCCGTCAC					
			C C T						
GAM1319	KIAA0603	3'	GTGGACCTCGTGCTCATCA	16830	C G		AG		
			TGA GAG CACGAGGT GC						
			ACT CTC GTGCTCCA TG						
			A _ GG						
GAM1319	KIAA1399	5'	CCAGCCTTGCCTCATCA	34797	C CG		A		
			TGA GAGGCA AGGT GG						
			ACT CTCCGT TCCG CC						
			A _ A						
GAM1319	KIAA1404	3'	CACTGCCTTTTGCCCTCGCCA	31049	A CA		GT		
			TG CGAGG CGAG AGGCAGTG						
			AC GCTCC GTTT TCCGTCAC						
			C C_ _						
GAM1319	WIT-1	5'	CACCACCCCCTCTACCTCTTCA	17988	C CAC		TA CA		
			TGA GAGG GAGG GG GTG						
			ACT CTCC CTCC CC CAC						
			T AT_ _ AC						
GAM1319	LOC197342	3'	CACTGCCTACCTCCTGCC	42486	C				
			GGCA GAGGTAGGCAGTG						
			CCGT CTCCATCCGTCAC						
			C						
GAM1320	HAL	3'	AAATTTGGAAACAGATTG	7886	AA				
			TAATT TGTTTTCAAATTT						
			GTTAG ACAAGGTTTAAA						
			_						
GAM1320	TSG	3'	AAATTTGGACCGTTATTTATA	21809	T TT				
			TATAA TAATG TCCAAATTT						
			ATATT ATTGC AGGTTTAAA						
			T C_						
GAM1320	BCMP1	3'	AAATTTGGATAGCTTAATTATA	25453	T _				
			TATAATTAA GTT TCCAAATTT						
			ATATTAATT CGA AGGTTTAAA						
			_ T						
GAM1321	CCND2	3'	ATGGAAAAAATACATTGA	7511	A				
			TCAATGTATTTTT CAT						
			AGTTACATAAAAA GTA						
			G						
GAM1321	CLCA2	3'	AAACTGTATTAATAATGCATTG	13289	T_ T				
	A		TCAATGTATTTT TACA GTTTT						

AGTTACGTAAAA ATGT CAAAA
 TT _
 GAM1321 MPHOSPH1 3' AAAACATGTATATACATT 18286 TTTT
 AATGTAT TACATGTTTT
 ||||| |||||
 TTACATA ATGTACAAAA
 T__
 GAM1321 BLR1 3' GGGAAGTGTGAAGAAACACACTG 7446 A A G
 A TCA TGT TTTTTTACAT TTTT
 ||| ||| ||||| |||
 AGT ACA AAAGAATGTG AGGG
 C C A
 GAM1321 BLR1 3' GGGAAGTGTGAAGAAACACACTG 26776 A A G
 A TCA TGT TTTTTTACAT TTTT
 ||| ||| ||||| |||
 AGT ACA AAAGAATGTG AGGG
 C C A
 GAM1321 C21orf25 3' AAAACATGTGAATACTAC 31793 TTT
 GTA TTTACATGTTTT
 ||| |||||
 CAT AAGTGTACAAAA
 CAT
 GAM1321 DNCLI1 3' TAAAACATGTAAAAGGATTTGG 29928 TGTA
 TCAA TTTTTTACATGTTTTA
 ||| |||||
 GGTT GGAAAATGTACAAAAT
 TA__
 GAM1321 KIAA0644 3' AAATGTGAAAAAAATACA 16781 A
 TGTATTTTTT CATGTTT
 ||||| |||||
 ACATAAAAAA GTGTAA
 A
 GAM1321 M96 3' GTGTAAAAAATATATTGA 14288 _
 TCAATGTATTTTTT ACAT
 ||||| |||||
 AGTTATATAAAAAA TGTG
 A
 GAM1321 MIG-6 3' TAAAACATGCTTAAGAAAAATG 21018 A A__
 CACTGA CA TGTATTTTTT CATGTTTAA
 || ||||| |||||
 GT ACGTAAAAAG GTACAAAAT
 C AATTC
 GAM1321 MRPL56 3' TAAAACATGTTTATAAAGTACA 26658 TT__
 TGTATTTT ACATGTTTAA
 ||||| |||||
 ACATGAAA TGTACAAAAT
 TATT
 GAM1321 OSBPL8 3' AAGATTGGTAAATAAATACATT 21901 _ AT
 GA TCAATGTATTT TTTAC GTTTT
 ||||| ||||| |||||

		AGTTACATAAAA AAATG TAGAA	
		T GT	
GAM1321	LOC116068	3' AAAACTTTTAAAAAATACATT 36499	CAT
		AATGTATTTTTTA GTTTT	
		TTACATAAAAAAT CAAAA	
		TTT	
GAM1321	LOC51141	3' TAAAACATGCCATACATTG 34050	TTTTTA
		CAATGTAT CATGTTT	
		GTTACATA GTACAAAAT	
		CC__	
GAM1321	LOC92249	3' AAGCATGCAAAAACACATTGA 34017	AT A
		TCAATGT TTTT CATGTTT	
		AGTTACA AAAAA GTACGAA	
		C_ C	
GAM1322	A1BG	3' ATCTTGGCTCACAGCAACCTCT 28275	AT__ GGT A
		AGAG CTG AG CCAAGAT	
		TCTC GAC TC GGTTCTA	
		CAAC AC_ _	
GAM1322	AHR	3' ATCTTGGCTCACTGCAACCTCT 7331	ATC _ _ A
		AGAG TG GGT AG CCAAGAT	
		TCTC AC TCA TC GGTTCTA	
		CA_ G C _	
GAM1322	ATP7A	3' ATCTTGGCTCACTGCAACCTCT 5490	ATC _ _ A
		AGAG TG GGT AG CCAAGAT	
		TCTC AC TCA TC GGTTCTA	
		CA_ G C _	
GAM1322	CAPN10	3' ATCCCAGAGCTTCCCAGGATCC 23346	A _ T ACCAA_
	CT	AG GATC TGGG AG GAT	
		TC CTAG ACCC TC CTA	
		C G T GAGACC	
GAM1322	CAPN10	3' ATCCCAGAGCTTCCCAGGATCC 23348	A _ T ACCAA_
	CT	AG GATC TGGG AG GAT	
		TC CTAG ACCC TC CTA	
		C G T GAGACC	
GAM1322	CAPN10	3' ATCCCAGAGCTTCCCAGGATCC 23350	A _ T ACCAA_
	CT	AG GATC TGGG AG GAT	
		TC CTAG ACCC TC CTA	
		C G T GAGACC	
GAM1322	CAPN10	3' ATCCCAGAGCTTCCCAGGATCC 23352	A _ T ACCAA_
	CT	AG GATC TGGG AG GAT	

		TC CTAG ACCC TC CTA	
		C G T GAGACC	
GAM1322 CIAS1	5'	ATCTTGGCTCACTGCAGCCTC 11320	AT _ _ A
		GAG CTG GGT AG CCAAGAT	
		CTC GAC TCA TC GGTTCTA	
		C _ G C _	
GAM1322 CYP8B1	3'	ATCTTGGCTCACTACAACCTCT 10621	ATCTG _ A
		AGAG GGT AG CCAAGAT	
		TCTC TCA TC GGTTCTA	
		CAACA C _	
GAM1322 DFFB	3'	ATCTTGGCTCACTGCAACCTC 42239	ATC _ _ A
		GAG TG GGT AG CCAAGAT	
		CTC AC TCA TC GGTTCTA	
		CA _ G C _	
GAM1322 FZD4	3'	ATCTTGGCTCACTGCAACCTCT 14482	ATC _ _ A
		AGAG TG GGT AG CCAAGAT	
		TCTC AC TCA TC GGTTCTA	
		CA _ G C _	
GAM1322 MAK	3'	ATCTTGGCTTACTGCAACCTC 12527	ATC _ GA
		GAG TG GGTA CCAAGAT	
		CTC AC TCAT GGTTCTA	
		CA _ G TC	
GAM1322 MEFV	3'	ATCTTGGCTCACTGCAACCTC 5767	ATC _ _ A
		GAG TG GGT AG CCAAGAT	
		CTC AC TCA TC GGTTCTA	
		CA _ G C _	
GAM1322 MLANA	3'	ATCTTGGCTCACCATAACCTC 12027	ATCTG _ A
		GAG GGT AG CCAAGAT	
		CTC CCA TC GGTTCTA	
		CAATA C _	
GAM1322 MS4A1	3'	TGGTTTACCAGGACCTCT 5634	A G
		AGAG TCT GGTAGACCA	
		TCTC AGG CCATTTGGT	
		C A	
GAM1322 NONO	3'	ATCTCGGCTCACTGCAATCTCT 39898	C _ _ A A
		AGAGAT TG GGT AG CC AGAT	
		TCTCTA AC TCA TC GG TCTA	
		_ G C _ C	
GAM1322 PER2	3'	ATCTTGGCTCACTGCAACCTCT 23087	ATC _ _ A
		AGAG TG GGT AG CCAAGAT	

		TCTC AC TCA TC GGTTCCTA	
		CA_ G C _	
GAM1322 RHD	3'	ATCTTGGCTCACTGCAACCTCT 18216	ATC _ _ A
		AGAG TG GGT AG CCAAGAT	
		TCTC AC TCA TC GGTTCCTA	
		CA_ G C _	
GAM1322 RHD	3'	ATCTTGGCTCACTGCAACCTCT 18336	ATC _ _ A
		AGAG TG GGT AG CCAAGAT	
		TCTC AC TCA TC GGTTCCTA	
		CA_ G C _	
GAM1322 SEDL	3'	ATCTTGGCTCACTGCAACCTC 15905	ATC _ _ A
		GAG TG GGT AG CCAAGAT	
		CTC AC TCA TC GGTTCCTA	
		CA_ G C _	
GAM1322 SEDL	3'	ATCTTGGCTCACTGCAACCTC 15906	ATC _ _ A
		GAG TG GGT AG CCAAGAT	
		CTC AC TCA TC GGTTCCTA	
		CA_ G C _	
GAM1322 SEPN1	3'	ATCTTGGCTCACTGCAACCTC 32987	ATC _ _ A
		GAG TG GGT AG CCAAGAT	
		CTC AC TCA TC GGTTCCTA	
		CA_ G C _	
GAM1322 SLC14A2	5'	ATCTTGGCTCACTGCAACCTC 14007	ATC _ _ A
		GAG TG GGT AG CCAAGAT	
		CTC AC TCA TC GGTTCCTA	
		CA_ G C _	
GAM1322 TAPBP	3'	ATCTTGGCTTACTGCAACCTC 9177	ATC _ GA
		GAG TG GGTA CCAAGAT	
		CTC AC TCAT GGTTCCTA	
		CA_ G TC	
GAM1322 TDGF1	3'	ATCTTGGTTCACTGCAACCTC 9208	ATC _ AG
		GAG TG GGT ACCAAGAT	
		CTC AC TCA TGGTTCTA	
		CA_ G CT	
GAM1322 TNFRSF10B	3'	ATCTTGGCTCAGTGCAACCTC 9935	AT_____ TAGA
		GAG CTGGG CCAAGAT	
		CTC GACTC GGTTCCTA	
		CAACGT _____	
GAM1322 TRPV1	3'	ATCTTGGCTCACTGCAACCTCT 20810	ATC _ _ A
		AGAG TG GGT AG CCAAGAT	

			TCTC AC TCA TC GGTCTA		
			CA_ G C _		
GAM1322	TRPV1	3'	ATCTTGGCTCACTGCAACCTCT 27990	ATC _ _ A	
			AGAG TG GGT AG CCAAGAT		
			TCTC AC TCA TC GGTCTA		
			CA_ G C _		
GAM1322	TRPV1	3'	ATCTTGGCTCACTGCAACCTCT 27998	ATC _ _ A	
			AGAG TG GGT AG CCAAGAT		
			TCTC AC TCA TC GGTCTA		
			CA_ G C _		
GAM1322	TRPV1	3'	ATCTTGGCTCACTGCAACCTCT 28006	ATC _ _ A	
			AGAG TG GGT AG CCAAGAT		
			TCTC AC TCA TC GGTCTA		
			CA_ G C _		
GAM1322	WNT8B	3'	ATCCTGGTCTGCACCTCT 29983	TCT _ A	
			AGA GG GTAGACCA GAT		
			TCT CC CGTCTGGT CTA		
			___ A C		
GAM1322	ZNF264	3'	ATCTTGGCTCACTGCAACCTC 9453	ATC _ _ A	
			GAG TG GGT AG CCAAGAT		
			CTC AC TCA TC GGTCTA		
			CA_ G C _		
GAM1322	ARPP-19	3'	ATCTTGGCTCACTGCAACCTCT 13418	ATC _ _ A	
			AGAG TG GGT AG CCAAGAT		
			TCTC AC TCA TC GGTCTA		
			CA_ G C _		
GAM1322	ASE-1	3'	ATCTTGGCTCACTGCAACCTC 14403	ATC _ _ A	
			GAG TG GGT AG CCAAGAT		
			CTC AC TCA TC GGTCTA		
			CA_ G C _		
GAM1322	BA108L7.2	3'	ATCTTGGCTCACTGCAACCTCT 25235	ATC _ _ A	
			AGAG TG GGT AG CCAAGAT		
			TCTC AC TCA TC GGTCTA		
			CA_ G C _		
GAM1322	BICD2	3'	ATCCTGGGCCCAGATC 34850	AGA A	
			GATCTGGGT CCA GAT		
			CTAGACCCG GGT CTA		
			___ C		
GAM1322	C13orf1	3'	ATCTTGGCTCACTGCAACCTCT 21689	ATC _ _ A	
			AGAG TG GGT AG CCAAGAT		

		TCTC AC TCA TC GGTCTA		
		CA_ G C _		
GAM1322	C9orf9	3' ATCTTGGCTCACTGCAACCTC	21023	ATC _ _ A
		GAG TG GGT AG CCAAGAT		
		CTC AC TCA TC GGTCTA		
		CA_ G C _		
GAM1322	CLDN15	3' ATCTGTACTCCCCAGATCTC	28791	T ACCA
		GAGATCTGGG AG AGAT		
		CTCTAGACCC TC TCTA		
		C ATG_		
GAM1322	DCOHM	3' ATCTTGGCTCACTGCAGTCTC	25841	T _ _ A
		GAGA CTG GGT AG CCAAGAT		
		CTCT GAC TCA TC GGTCTA		
		_ G C _		
GAM1322	FLJ10232	3' ATCTTGGCTCACTGCAACCTC	19772	ATC _ _ A
		GAG TG GGT AG CCAAGAT		
		CTC AC TCA TC GGTCTA		
		CA_ G C _		
GAM1322	FLJ10535	3' ATCTTGGCTCACTGCAACCTCT	19916	ATC _ _ A
		AGAG TG GGT AG CCAAGAT		
		TCTC AC TCA TC GGTCTA		
		CA_ G C _		
GAM1322	FLJ10922	3' ATCTTGGCTCACTGCAACCTC	20253	ATC _ _ A
		GAG TG GGT AG CCAAGAT		
		CTC AC TCA TC GGTCTA		
		CA_ G C _		
GAM1322	FLJ12572	5' ATCTTGGCTCACTGCAACCTCT	23196	ATC _ _ A
		AGAG TG GGT AG CCAAGAT		
		TCTC AC TCA TC GGTCTA		
		CA_ G C _		
GAM1322	FLJ14642	3' ATCCTAGTCTATCTAGCTC	26593	AT CAA
		GAG CTGGGTAGAC GAT		
		CTC GATCTATCTG CTA		
		_ ATC		
GAM1322	FLJ20136	3' ATCTTGGCTCACTGCAATCTCT	19227	C _ _ A
		AGAGAT TG GGT AG CCAAGAT		
		TCTCTA AC TCA TC GGTCTA		
		_ G C _		
GAM1322	FLJ20344	3' ATCTTGGCTCACTGCAACCTC	19403	ATC _ _ A
		GAG TG GGT AG CCAAGAT		

		CTC AC TCA TC GGTTCTA	
		CA_ G C _	
GAM1322	FLJ20452	3' TCTGGCCTCCCAGATC 19490	T A A
		GATCTGGG AG CCA GA	
		CTAGACCC TC GGT CT	
		_ C _	
GAM1322	FLJ23356	3' ATCTTGGCTCACTGCAGCCTCT 25957	AT _ _ A
		AGAG CTG GGT AG CCAAGAT	
		TCTC GAC TCA TC GGTTCTA	
		C_ G C _	
GAM1322	FLJ23563	3' ATCTCGGTTCACTGCAACCTCT 33559	ATC _ AG A
		AGAG TG GGT ACC AGAT	
		TCTC AC TCA TGG TCTA	
		CA_ G CT C	
GAM1322	FLJ30532	3' ATCTTGGCTCACTGCAGCCTCT 29547	AT _ _ A
		AGAG CTG GGT AG CCAAGAT	
		TCTC GAC TCA TC GGTTCTA	
		C_ G C _	
GAM1322	FLJ31153	3' ATCTCGGCTCACTGCAATCTCT 29412	C _ _ A A
		AGAGAT TG GGT AG CC AGAT	
		TCTCTA AC TCA TC GG TCTA	
		_ G C _ C	
GAM1322	GRWD	3' ATCTTGGCTCACTGCAACCTC 25576	ATC _ _ A
		GAG TG GGT AG CCAAGAT	
		CTC AC TCA TC GGTTCTA	
		CA_ G C _	
GAM1322	H2AV	3' ATCTTGGCTCACTGCAACCCTC 28908	ATC _ _ A
		GAG TG GGT AG CCAAGAT	
		CTC AC TCA TC GGTTCTA	
		CCA G C _	
GAM1322	HCA4	3' ATCTTGGCTCAGTGCAATCTCT 38020	C G TA _
		AGAGAT TG G GA CCAAGAT	
		TCTCTA AC T CT GGTTCTA	
		_ G GA C	
GAM1322	KIAA0022	3' ATCTTGGCTCTCTCCAATCTC 17025	C GT _
		GAGAT TGG AGA CCAAGAT	
		CTCTA ACC TCT GGTTCTA	
		_ TC C	
GAM1322	KIAA0186	3' ATCTTGGCTCACTGCAATCTCT 22036	C _ _ A
		AGAGAT TG GGT AG CCAAGAT	

			TCTCTA AC TCA TC GGTCTA		
			_ G C _		
GAM1322	KIAA0453	3'	ATCCAAAGCTACCCAGTCCCT 34228	A T	ACCAA
			AG GA CTGGGTAG GAT		
			TC CT GACCCATC CTA		
			C _ GAAAC		
GAM1322	KIAA0475	3'	ATCTTGGCTCACTGCAACCTC 16947	ATC _ _ A	
			GAG TG GGT AG CCAAGAT		
			CTC AC TCA TC GGTCTA		
			CA_ G C _		
GAM1322	KIAA0514	3'	ATCTGTTAAGATCCAGATCTCT 16204		AGACCA
			AGAGATCTGGGT AGAT		
			TCTCTAGACCTA TCTA		
			GAATTG		
GAM1322	KIAA0557	3'	ATCTTGGCTCACCACAACCTC 38203	ATC _ _ A	
			GAG TG GGT AG CCAAGAT		
			CTC AC CCA TC GGTCTA		
			CA_ A C _		
GAM1322	KIAA0599	3'	ATCTTGGCTTACTGCAACCTC 37854	ATC _ GA	
			GAG TG GGTA CCAAGAT		
			CTC AC TCAT GGTCTA		
			CA_ G TC		
GAM1322	KIAA0945	3'	ATCCTGGTTTCCAGATCT 17290	T A	
			AGATCTGGG AGACCA GAT		
			TCTAGACCC TTTGGT CTA		
			_ C		
GAM1322	KIAA1028	3'	ATCTTGGCTCACTCCAACCTC 44154	ATC _ _ A	
			GAG TGG GT AG CCAAGAT		
			CTC ACC CA TC GGTCTA		
			CA_ T C _		
GAM1322	KIAA1040	3'	ATCTTGGCTCACTGCAACCTCT 35739	ATC _ _ A	
			AGAG TG GGT AG CCAAGAT		
			TCTC AC TCA TC GGTCTA		
			CA_ G C _		
GAM1322	KIAA1198	3'	ATCTCGGCTCACTGCAATCTCT 31703	C _ _ A A	
			AGAGAT TG GGT AG CC AGAT		
			TCTCTA AC TCA TC GG TCTA		
			_ G C _ C		
GAM1322	KIAA1198	3'	ATCTTGGCTCACTGCAACCTC 31704	ATC _ _ A	
			GAG TG GGT AG CCAAGAT		

		CTC AC TCA TC GGTTCTA	
		CA_ G C _	
GAM1322 KIAA1257	3'	ATCTCGGCTCACTACAGCCTCT 31429	AT _ _ A A
		AGAG CTG GGT AG CC AGAT	
		TCTC GAC TCA TC GG TCTA	
		C_ A C _ C	
GAM1322 KIAA1497	5'	ATCTTGGCTCACTGCAACCTCT 33524	ATC _ _ A
		AGAG TG GGT AG CCAAGAT	
		TCTC AC TCA TC GGTTCTA	
		CA_ G C _	
GAM1322 KIAA1582	5'	ATCTTGACCCAAGAGTTCT 32581	A _ AGAC
		AGAG TCT GGGT CAAGAT	
		TCTT AGA CCA GTTCTA	
		G A _ _ _	
GAM1322 KIAA1829	3'	ATCTTGGCTCACTGCAGCCTCT 31028	AT _ _ A
		AGAG CTG GGT AG CCAAGAT	
		TCTC GAC TCA TC GGTTCTA	
		C_ G C _	
GAM1322 KIAA1915	3'	ATCTTGACACAGTAGATCTT 36268	G_ AGAC
		GAGATCTG GT CAAGAT	
		TTCTAGAT CA GTTCTA	
		GA CA_ _	
GAM1322 KIAA1918	3'	ATCTTGGTCTCCACAACTCT 36212	ATC _ T
		AGAG TG GG AGACCAAGAT	
		TCTC AC CC TCTGGTTCTA	
		AA_ A _	
GAM1322 KIAA1971	3'	ATCTTGGCTTACTGCAACCTC 36728	ATC _ GA
		GAG TG GGTA CCAAGAT	
		CTC AC TCAT GGTTCTA	
		CA_ G TC	
GAM1322 KIAA1987	5'	ATCTCGGCTCACTGCAATCTC 42494	C _ _ A A
		GAGAT TG GGT AG CC AGAT	
		CTCTA AC TCA TC GG TCTA	
		_ G C _ C	
GAM1322 KLK7	3'	ATCTTGGCTCACTGCAACCTC 29273	ATC _ _ A
		GAG TG GGT AG CCAAGAT	
		CTC AC TCA TC GGTTCTA	
		CA_ G C _	
GAM1322 KLK7	3'	ATCTTGGCTCACTGCAACCTC 11476	ATC _ _ A
		GAG TG GGT AG CCAAGAT	

		CTC AC TCA TC GGTTCTA	
		CA_ G C _	
GAM1322 LY75	3'	ATCTCGGCTCACTGCAAATCTC 8149	C _ _ A A
		GAGAT TG GGT AG CC AGAT	
		CTCTA AC TCA TC GG TCTA	
		A G C _ C	
GAM1322 MGC3771	5'	ATCTCGGCTCACCCCAACCTC 25233	ATC TA _ A
		GAG TGGG GA CC AGAT	
		CTC ACCC CT GG TCTA	
		CA_ CA C C	
GAM1322 MGC4638	3'	ATCTTGGCTCACTGCAACCTC 25557	ATC _ _ A
		GAG TG GGT AG CCAAGAT	
		CTC AC TCA TC GGTTCTA	
		CA_ G C _	
GAM1322 MKRN4	3'	ATCTTGGCTCACTGCAACCTC 25041	ATC _ _ A
		GAG TG GGT AG CCAAGAT	
		CTC AC TCA TC GGTTCTA	
		CA_ G C _	
GAM1322 MRPL44	3'	ATCTTGGTTTGATCAAATCTTT 23226	C GG
		AGAGAT TG TAGACCAAGAT	
		TTTCTA AC GTTTGGTTCTA	
		A TA	
GAM1322 MRPS27	3'	ATCTTGGCTCACTGCAACCTC 17473	ATC _ _ A
		GAG TG GGT AG CCAAGAT	
		CTC AC TCA TC GGTTCTA	
		CA_ G C _	
GAM1322 PAK6	3'	CTTGACAGCCCAGGTCCCT 21390	A AGAC
		AG GATCTGGGT CAAG	
		TC CTGGACCCG GTTC	
		C ACA_	
GAM1322 PRO0365	5'	ATCTTGGCTCACTGCAACCTCT 15385	ATC _ _ A
		AGAG TG GGT AG CCAAGAT	
		TCTC AC TCA TC GGTTCTA	
		CA_ G C _	
GAM1322 SLC2A10	3'	ATCTTGGCTCACTGCAACCTC 25062	ATC _ _ A
		GAG TG GGT AG CCAAGAT	
		CTC AC TCA TC GGTTCTA	
		CA_ G C _	
GAM1322 SSH2	3'	ATCTTAGTCTCTTCAGGATCTT 31177	_ T C
T		AGAGATC TGGG AGAC AAGAT	

TTTCTAG ACTT TCTG TTCTA
 G C A
 GAM1322 TU12B1-TY 3' ATCTTGGCTCACTCCAACCTC 18643 ATC _ _ A
 GAG TGG GT AG CCAAGAT
 ||| ||| ||| ||| ||| |||
 CTC ACC CA TC GGTTCTA
 CA_ T C _
 GAM1322 LOC115704 3' ATCTTGGTCTGTACCCCTC 36401 ATCT _
 GAG GGGT AGACCAAGAT
 ||| ||| ||| ||| ||| |||
 CTC CCCA TCTGGTTCTA
 _ _ TG
 GAM1322 LOC116236 3' TCTTGCCCCAGATTCT 36544 A TAGAC
 AGAG TCTGGG CAAGA
 ||| ||| ||| ||| ||| |||
 TCTT AGACCC GTTCT
 _ C _
 GAM1322 LOC120526 3' TCTTGGTCCGTATTTC 36623 C GTAG
 GAGAT TGG ACCAAGA
 ||| ||| ||| ||| ||| |||
 CTTTA GCC TGGTTCT
 T _
 GAM1322 LOC121506 5' ATCTTACTTACCCAGAACTCT 36667 A ACC
 AGAG TCTGGGTAG AAGAT
 ||| ||| ||| ||| ||| |||
 TCTC AGACCCATT TTCTA
 A CA_
 GAM1322 LOC128387 3' ATCTTGGCTCACTGCAACCTC 36928 ATC _ _ A
 GAG TG GGT AG CCAAGAT
 ||| ||| ||| ||| ||| |||
 CTC AC TCA TC GGTTCTA
 CA_ G C _
 GAM1322 LOC132625 3' ATCTTGGCTCACTGCAACCTC 37372 ATC _ _ A
 GAG TG GGT AG CCAAGAT
 ||| ||| ||| ||| ||| |||
 CTC AC TCA TC GGTTCTA
 CA_ G C _
 GAM1322 LOC135763 3' ATCTTGGCTCACTGCAACCTC 28880 ATC _ _ A
 GAG TG GGT AG CCAAGAT
 ||| ||| ||| ||| ||| |||
 CTC AC TCA TC GGTTCTA
 CA_ G C _
 GAM1322 LOC143187 3' ATCTTGGCTCACTGCAACCTC 29743 ATC _ _ A
 GAG TG GGT AG CCAAGAT
 ||| ||| ||| ||| ||| |||
 CTC AC TCA TC GGTTCTA
 CA_ G C _
 GAM1322 LOC145226 3' TGGCCTATTTAGATTTCCT 37810 AG A
 AG ATCTGGGTAG CCA
 || ||| ||| ||| ||| |||

	TC TAGATTTATC GGT	
	CT C	
GAM1322 LOC145955 3'	ATCTCTGTCCCCAGCCTCT 40643	AT TA CA
	AGAG CTGGG GAC AGAT	
	TCTC GACCC CTG TCTA	
	C_ _ TC	
GAM1322 LOC146455 3'	ATCTCGGCTCACTGCAATCTCT 38156	C _ _ A A
	AGAGAT TG GGT AG CC AGAT	
	TCTCTA AC TCA TC GG TCTA	
	_ G C _ C	
GAM1322 LOC146909 3'	ATCTTGGCTCACTGCAACCTC 38264	ATC _ _ A
	GAG TG GGT AG CCAAGAT	
	CTC AC TCA TC GGTTCTA	
	CA_ G C _	
GAM1322 LOC147429 5'	ATCCTGGCTCACTGCAATCTC 38336	C _ _ A A
	GAGAT TG GGT AG CCA GAT	
	CTCTA AC TCA TC GGT CTA	
	_ G C _ C	
GAM1322 LOC149117 5'	ATCTCGGCTCACTGCGACCTCT 40953	A TG _ A A
	AGAG TC GGT AG CC AGAT	
	TCTC AG TCA TC GG TCTA	
	C CG C _ C	
GAM1322 LOC149461 3'	ATCTGAGACCCAGATCCT 38760	A AGACCA
	AG GATCTGGGT AGAT	
	TC CTAGACCCA TCTA	
	_ GAG_	
GAM1322 LOC149836 5'	ATCCTGGGTACTCAGGCCTCT 38824	AT GA A
	AGAG CTGGGTA CCA GAT	
	TCTC GACTCAT GGT CTA	
	CG G_ C	
GAM1322 LOC150054 5'	ATCTTGGTGACAAAGAGCCCT 41124	AGA GG AG
	AG TCT GT ACCAAGAT	
	TC AGA CA TGGTTCTA	
	CCG AA G_	
GAM1322 LOC150960 3'	ATCTTGGCTCGCTGCAACCTC 39029	ATC _ _ A
	GAG TG GGT AG CCAAGAT	
	CTC AC TCG TC GGTTCTA	
	CA_ G C _	
GAM1322 LOC152925 3'	ATCTCGGCTTACTCCAACCTCT 39329	ATC _ GA A
	AGAG TGG GTA CC AGAT	

	TCTC ACC CAT GG TCTA	
	CA_ T TC C	
GAM1322 LOC154739 5'	ATCCTGGTGGTAGGTCTCT 41715	GGTAG A
	AGAGATCTG ACCA GAT	
	TCTCTGGAT TGGT CTA	
	GG___ C	
GAM1322 LOC157798 5'	ATCTCGATCTCTTGATCTC 41846	T T CCA
	GAGATC GGG AGA AGAT	
	CTCTAG TTC TCT TCTA	
	_ _ AGC	
GAM1322 LOC158237 5'	ATCTTGAATGAGCTGATCTCT 30326	TGGG GAC
	AGAGATC TA CAAGAT	
	TCTCTAG GT GTTCTA	
	TCGA AA_	
GAM1322 LOC165229 5'	TCCTGGCCCAGGTTCTC 40124	_ TAGA A
	GAGA TCTGGG CCA GA	
	CTCT GGACCC GGT CT	
	T ____ C	
GAM1322 LOC170082 5'	ATCTTGGCTCACTGCAAACCTC 40168	ATC _ _ A
	GAG TG GGT AG CCAAGAT	
	CTC AC TCA TC GGTTCTA	
	AA_ G C _	
GAM1322 LOC196264 3'	ATCTTGGCTCACTGCAACCTCT 42333	ATC _ _ A
	AGAG TG GGT AG CCAAGAT	
	TCTC AC TCA TC GGTTCTA	
	CA_ G C _	
GAM1322 LOC200169 5'	ATCTTGGCTCACTGCAACCTCT 43283	ATC _ _ A
	AGAG TG GGT AG CCAAGAT	
	TCTC AC TCA TC GGTTCTA	
	CA_ G C _	
GAM1322 LOC200314 3'	ATCTTGGCTCACTGCAACCTC 43292	ATC _ _ A
	GAG TG GGT AG CCAAGAT	
	CTC AC TCA TC GGTTCTA	
	CA_ G C _	
GAM1322 LOC200339 3'	ATCTTGGCTCACTGCAACCTCT 43296	ATC _ _ A
	AGAG TG GGT AG CCAAGAT	
	TCTC AC TCA TC GGTTCTA	
	CA_ G C _	
GAM1322 LOC200860 3'	ATCTTGGTTCACTGCAACCTC 43352	ATC _ AG
	GAG TG GGT ACCAAGAT	

	CTC AC TCA TGGTTCTA	
	CA_ G CT	
GAM1322 LOC201292 5'	ATCTTGGCCTCCTGGGTCTC 42562	TG T A
	GAGATC GG AG CCAAGAT	
	CTCTGG CC TC GGTCTA	
	GT _ C	
GAM1322 LOC201294 3'	ATCTTGGCTCACTGCAACCTC 42565	ATC _ _ A
	GAG TG GGT AG CCAAGAT	
	CTC AC TCA TC GGTCTA	
	CA_ G C _	
GAM1322 LOC203276 3'	ATCCTGGTGGTAGGTCTCT 43482	GGTAG A
	AGAGATCTG ACCA GAT	
	TCTCTGGAT TGGT CTA	
	GG_ C	
GAM1322 LOC203305 3'	ATCCTGGTGGTAGGTCTCT 43506	GGTAG A
	AGAGATCTG ACCA GAT	
	TCTCTGGAT TGGT CTA	
	GG_ C	
GAM1322 LOC220662 3'	ATCTTGGTTCACTGCAACCTC 43821	ATC _ AG
	GAG TG GGT ACCAAGAT	
	CTC AC TCA TGGTTCTA	
	CA_ G CT	
GAM1322 LOC222070 5'	ATCTTGGCTCACTGCAACCTCT 45177	ATC _ _ A
	AGAG TG GGT AG CCAAGAT	
	TCTC AC TCA TC GGTCTA	
	CA_ G C _	
GAM1322 LOC254243 3'	ATCCTGGTGGTAGGTCTCT 46508	GGTAG A
	AGAGATCTG ACCA GAT	
	TCTCTGGAT TGGT CTA	
	GG_ C	
GAM1322 LOC51193 5'	ATCTCGGGTCACCACAACCTC 18453	ATC _ A A_
	GAG TG GGT GACC AGAT	
	CTC AC CCA CTGG TCTA	
	CA_ A _ GC	
GAM1322 LOC51200 3'	ATCTTGGCTCACCACAACCTCT 18480	ATC _ _ A
	AGAG TG GGT AG CCAAGAT	
	TCTC AC CCA TC GGTCTA	
	CA_ A C _	
GAM1322 LOC89932 3'	ATCTTGGCTCACTGCAACCTC 30487	ATC _ _ A
	GAG TG GGT AG CCAAGAT	

		CTC AC TCA TC GGTTCTA	
		CA_ G C _	
GAM1322	LOC90038	3' ATCCTGGTGGTAGGTCTCT 30645	GGTAG A
		AGAGATCTG ACCA GAT	
		TCTCTGGAT TGGT CTA	
		GG__ C	
GAM1322	LOC90371	5' ATCTTGGCTCACTGCAACCTC 31319	ATC _ _ A
		GAG TG GGT AG CCAAGAT	
		CTC AC TCA TC GGTTCTA	
		CA_ G C _	
GAM1322	LOC90408	5' ATCTTGGCTCACTGCAACCTCT 31394	ATC _ _ A
		AGAG TG GGT AG CCAAGAT	
		TCTC AC TCA TC GGTTCTA	
		CA_ G C _	
GAM1322	LOC92249	5' CTTGTCTCAGATCTCT 34023	TAGAC
		AGAGATCTGGG CAAG	
		TCTCTAGACTC GTTC	
		T__	
GAM1322	LOC92283	3' ATCTTGGCTCACTGCAACCTC 34091	ATC _ _ A
		GAG TG GGT AG CCAAGAT	
		CTC AC TCA TC GGTTCTA	
		CA_ G C _	
GAM1323	ELMO1	3' AAGTTCCACAGGATGGTCA 28201	_AG CA
		TG C ATCC TGGAACCT	
		AC G TAGG ACCTTGAA	
		T G_ AC	
GAM1323	FMN2	3' TAAGAGGCAGTATCTGCACT 38742	CCCA GAA
		AGTGCAGAT TG CTTA	
		TCACGTCTA AC GAAT	
		TG__ GGA	
GAM1323	GYS1	3' TCCAGATCTGCACTGG 42625	CCA
		TCAGTGCAGATC TGGA	
		GGTCACGTCTAG ACCT	

GAM1323	SIM1	3' AAGGACCAGGATTGCACTGA 11508	A CA AA
		TCAGTGCAG TCC TGG CTT	
		AGTCACGTT AGG ACC GAA	
		_ _ AG	
GAM1323	FLJ11383	3' TAAGTTCCAATTCTACAC 24479	C TCCCA
		GTG AGA TGGAACCTTA	

		CAC TCT ACCTTGAAT		
		A TA__		
GAM1323	KIAA0268	3' GAGTTTTCAGATCCCACT	34686	CA CCA
		AGTG GATC TGGAACCT		
		TCAC CTAG ACTTTGAG		
		AC ____		
GAM1323	KIAA0416	3' TAAGCCAAAAATCTGTACT	17838	CCCA AA
		AGTGCAGAT TGG CTTA		
		TCATGTCTA ACC GAAT		
		AAA_ ____		
GAM1323	KIAA0836	3' AAGATACAGATCTGCACTGA	32244	CCA GAA
		TCAGTGCAGATC TG CTT		
		AGTCACGTCTAG AC GAA		
		____ ATA		
GAM1323	KIAA0884	5' AGAGTCACGGAATCTGTACTGA	34774	C A AA
		TCAGTGCAGAT CC TGG CT		
		AGTCATGTCTA GG ACT GA		
		A C GA		
GAM1323	SMOC1	3' TAAGTTTTTGGATCTGCTACTG	22699	_ CAT
	A	TCAGT GCAGATCC GGAACCTTA		
		AGTCA CGTCTAGG TTTTGAAT		
		T T__		
GAM1323	LOC115399	3' AAGTCCTCTGTGGGAACCCAC	36343	CAGA ____
		GTG TCCCATGGA ACTT		
		CAC AGGGTGTCT TGAA		
		CCCA CC		
GAM1323	LOC116236	3' TCCAAGAATCTGCACTGA	36543	CCCA
		TCAGTGCAGAT TGGA		
		AGTCACGTCTA ACCT		
		AGA_		
GAM1324	CCR9	3' TGAGGAATACAGTGAGCAG	13433	TTTTT
		TTGCTCACT TTCCTCA		
		GACGAGTGA AAGGAGT		
		CAT__		
GAM1324	CCR9	3' TGAGGAATACAGTGAGCAG	25250	TTTTT
		TTGCTCACT TTCCTCA		
		GACGAGTGA AAGGAGT		
		CAT__		
GAM1324	COL17A1	5' GATAAAAAAAAAAGTGAGCA	28269	CC
		TGCTCACTTTTTTTT TC		

		ACGAGTGAAAAAAAA AG	
		AT	
GAM1324 COL17A1	5'	GATAAAAAAAAAAGTGAGCA 6107	CC
		TGCTCACTTTTTTTT TC	
		ACGAGTGAAAAAAAA AG	
		AT	
GAM1324 CSPG3	3'	AGGAAAGAAAAATAAGCAA 10613	CAC
		TTGCT TTTTTTTCCT	
		AACGA AAAAGAAAGGA	
		ATA	
GAM1324 DBN1	5'	TTGAGGAACTGAGGCAA 28126	CACT TT
		TTGCT TT TTCCTCAA	
		AACGG AG AAAGGAGTT	
		TC	
GAM1324 DGKI	3'	GGAAAAAAAAAACAGCAA 11080	CAC
		TTGCT TTTTTTTTCC	
		AACGA AAAAAAAGG	
		CAA	
GAM1324 HPS1	3'	TGAGAAGGTGGCAGTGAGGAA 5695	G T TT C
		TT CTCCT T TTT CTCA	
		AA GAGTGA G GGA GAGT	
		G C GT A	
GAM1324 HS2ST1	3'	TGAGGAGAAAAGCAA 14579	CACTTT
		TTGCT TTTTCCTCA	
		AACGA AAAGAGGAGT	
GAM1324 MAP3K7IP2	3'	GGAAAAAAAAACAAGCAA 17485	CAC
		TTGCT TTTTTTTTCC	
		AACGA AAAAAAAGG	
		ACA	
GAM1324 MGAT5	5'	TGAGGATTCAGTGAGCAA 8241	TTTTTT
		TTGCTCACT TCCTCA	
		AACGAGTGA AGGAGT	
		CTT	
GAM1324 OGG1	5'	GAGGAAAGCATGAGCAG 8391	CTTTT
		TTGCTCA TTTTCCTC	
		GACGAGT GAAAGGAG	
		AC	
GAM1324 OGG1	5'	GAGGAAAGCATGAGCAG 18808	CTTTT
		TTGCTCA TTTTCCTC	

			GACGAGT	GAAAGGAG		
			AC__			
GAM1324	OGG1	5'	GAGGAAAGCATGAGCAG	18813	CTTTT	
			TTGCTCA	TTTTCTC		
			GACGAGT	GAAAGGAG		
			AC__			
GAM1324	PAPPA	5'	TTGAGGAGGAAAGCGAG	8443	A	TT
			CTC	CTTTT	TTCCTCAA	
			GAG	GAAAG	GAGGAGTT	
			C	__		
GAM1324	PPP1R12A	3'	TTTAAAGGAAAAAAGCGCAA	8306	TCA	C
			TTGC	CTTTTTTTCCT	AAAA	
			AACG	GAAAAAAGGA	TTTT	
			C__	A		
GAM1324	PRKG2	3'	GAAAAAAGTAAAGCAA	12941	C_	
			TTGCT	ACTTTTTTTC		
			AACGA	TGAAAAAAG		
			AA			
GAM1324	TEM6	3'	TGAGGAACCAAAGGAAGCAA	22965	CA	TTT
			TTGCT	CTTT	TTCCTCA	
			AACGA	GAAA	AAGGAGT	
			AG	CC_		
GAM1324	BCoR	3'	TTTAAAGGAGAAAAAATGA	19339	C_	C
	GTAA		TTGCTCA	TTTTTTTCCT	AAAA	
			AATGAGT	AAAAAAGAGGA	TTTT	
			AAA	A		
GAM1324	CLGN	3'	GAGGAAAAAGAAGCAA	10568	CACT	
			TTGCT	TTTTTTCCTC		
			AACGA	AGAAAAAGGAG		
			__			
GAM1324	DKFZP564F013	3'	TTTGTAGAAAAAAGTACGGCA	45206	C_	TC
			TGCT	ACTTTTTTT	CTCAAAA	
			ACGG	TGAAAAAAG	GAGTTTT	
			CA	__		
GAM1324	DKFZp761F2014	3'	TTTGTAGGAAGAGGGAAAGTGA	21465	C	__
	CAA		TTG	TCACTTTT	TTTCTCAAAA	
			AAC	AGTGAAAG	AGAAGGAGTTTT	
			_	GG		
GAM1324	FLJ10738	3'	AGGCTGGAGAAGTGAACAA	20069	C	TT
			TTG	TCACTTTTTT	CCT	

AAC AGTGAAGAGG GGA
A TC
GAM1324 FLJ13962 3' GAGGAAAGCAGCTGTGAG 24297 TT _
CTCAC TT TTTTCCTC
||||| || |||||
GAGTG GA GAAAGGAG
TC C
GAM1324 FLJ14621 5' TTGAGGAAAAATTTCTTAAAGC 26584 CACTTT__
AA TTGCT TTTTCCTCAA
||||| |||||
AACGA AAAAAGGAGTT
AATTCTTT
GAM1324 FLJ20275 3' TGAGGAAATGGGCAA 19324 CTTTTT
TTGCTCA TTTCTCA
||||| |||||
AACGGGT AAAGGAGT

GAM1324 KIAA1013 3' GGAAAAAAGACAAGCAA 42858 CAC
TTGCT TTTTTTTTCC
||||| |||||
AACGA AGAAAAAAGG
AC_
GAM1324 KIAA1028 3' TGAAGAAAAAGGTGACAA 44165 C CC
TTG TCACTTTTTTTT TCA
||| ||||| |||
AAC AGTGAAAAAGA AGT

GAM1324 KIAA1254 3' TTGAGGAGACAAGTGA 34700 TTT
TCACTT TTTCTCAA
||||| |||||
AGTGAA AGAGGAGTT
C_
GAM1324 MGC16175 5' GAGGAAGAAGAGCAA 26512 ACTTT
TTGCTC TTTTCCTC
||||| |||||
AACGAG AAGAAGGAG

GAM1324 NXPH3 3' TGAGGAAAGATAGCAA 32722 CACTTT
TTGCT TTTTCCTCA
||||| |||||
AACGA AGAAAGGAGT
T____
GAM1324 RNF38 3' GAAAAAAAAGTGTAACAA 23061 CT_
TTG CACTTTTTTTTC
||| |||||
AAC GTGAAAAAAAAG
AAT
GAM1324 SP329 5' GAGGAAAGCAGCTGTGAG 25098 TT _
CTCAC TT TTTTCCTC
||||| || |||||

		GAGTG GA GAAAGGAG		
		TC C		
GAM1324	LOC145195 3'	TGAAGGAGGAAAACAAGGCAA	40517	CACT _
		TTGCT TTTTTTCCT CA		
		AACGG AAAAGGAGGA GT		
		AAC_ A		
GAM1324	LOC145900 5'	AGGAAAAGAAAGCAA	38011	CACT
		TTGCT TTTTTTCCT		
		AACGA AAGAAAAGGA		

GAM1324	LOC149372 5'	TTTTGAGGGATCAGAAAAGTGA	38733	__
		TCACTTTTTT TTCCTCAAAA		
		AGTGAAAAGA AGGGAGTTTT		
		CT		
GAM1324	LOC153146 3'	AGGGAAAAAAGCAA	41576	CACT
		TTGCT TTTTTTCCT		
		AACGA AAAAAAGGGA		

GAM1324	LOC203378 3'	AGGAGATGGGAAGAAGCAA	43547	CA _
		TTGCT CTTTTT TTCCT		
		AACGA GAAGGG AGAGGA		
		A_ T		
GAM1324	LOC254778 3'	AGGAAGGAAAAAAGCAA	45976	CAC
		TTGCT TTTTTTTCCT		
		AACGA AAAAGGAAGGA		
		A_		
GAM1324	LOC254936 5'	AGGAAAAGAAAGCAA	45526	CACT
		TTGCT TTTTTTCCT		
		AACGA AAGAAAAGGA		

GAM1324	LOC51580 3'	AGGAAAAAAAAAATGAACAG	18012	C C
		TTG TCA TTTTTTTCCT		
		GAC AGT AAAAAAAGGA		
		A A		
GAM1324	LOC90639 5'	TTTGAAAAAAAAAAAAAGTGG	31833	CC__
		TCACTTTTTTTT TCAAA		
		GGTGAAAAAAAA AGTTT		
		AAAA		
GAM1324	LOC90777 3'	AAAAAGATACAGTGAGTAA	31990	__
		TTGCTCACT TTTTTT		

AATGAGTGA AGAAAAA
 CAT
 GAM1325 GARP 3' CTCAAGGTCACACAGTGA 12032 GAGTG CCC
 TCACTGTG GATC GAG
 ||||| ||| |||
 AGTGACAC CTGG CTC
 A__ AA_
 GAM1325 GFAP 3' CTCTCCACCCCATAGTGA 7814 A TCCCC
 TCACTGTGG GTGGA GAG
 ||||| ||| |||
 AGTGATACC CACCT CTC
 C ____
 GAM1325 LOC91252 3' ACTCAGCTGGCCCACTCCACAG 32551 AT CCC_
 CTGTGGAGTGG C GAGT
 ||||| | |||
 GACACCTCACC G CTCA
 CG TCGA
 GAM1326 ALDH1B1 3' AGTCTCACTCTGTGCCCCAG 6347 CT A A A
 CTG GC ACA AGTGA ACT
 || ||| ||||| |||
 GAC CG TGT TCACT TGA
 C_ C C C
 GAM1326 C7 3' AGTCTCACTTTGTTGCCCAG 6187 CT A
 CTG GCAACAAAGTGA ACT
 || ||||| |||
 GAC CGTTGTTTCACT TGA
 C_ C
 GAM1326 CLASP2 3' AGTTTGCCATTGTTGCAGAGTT 32266 G A_ G
 A TAACT CTGCAACAA GT AAAC
 |||| ||||| || |||||
 ATTGA GACGTTGTT CG TTTGA
 _ AC _
 GAM1326 CYP8B1 3' AGTCTCACTCTGTTGCCCAG 10620 CT A A
 CTG GCAACA AGTGA ACT
 || ||||| ||||| |||
 GAC CGTTGT TCACT TGA
 C_ C C
 GAM1326 DCN 3' TTCATTGAGCAGTTA 28574 G ACAA
 TAACTGCT CA GTGAA
 ||||| || |||||
 ATTGACGA GT TACTT
 _ ____
 GAM1326 DEK 3' CACATTTGTTGCACCAATTA 9536 C C _
 TAA TG TGCAACAAA GTG
 || || ||||| |||
 ATT AC ACGTTGTTT CAC
 A C A
 GAM1326 EGFL5 5' TTTATTTGTACAGCAGTTA 41887 CA G
 TAACTGCTG ACAA TGAA
 ||||| ||||| |||

			ATTGACGAC TGTTT ATTT	
			A _ _	
GAM1326	MADD	3'	AGTTTCACTCTGTGAGGAGT 28234	G G A A
			ACT CT CA CA AGTGAAACT	
			TGA GA GT GT TCACTTTGA	
			G _ _ C	
GAM1326	MADD	3'	AGTTTCACTCTGTGAGGAGT 28250	G G A A
			ACT CT CA CA AGTGAAACT	
			TGA GA GT GT TCACTTTGA	
			G _ _ C	
GAM1326	MADD	3'	AGTTTCACTCTGTGAGGAGT 28245	G G A A
			ACT CT CA CA AGTGAAACT	
			TGA GA GT GT TCACTTTGA	
			G _ _ C	
GAM1326	MADD	3'	AGTTTCACTCTGTGAGGAGT 28240	G G A A
			ACT CT CA CA AGTGAAACT	
			TGA GA GT GT TCACTTTGA	
			G _ _ C	
GAM1326	MADD	3'	AGTTTCACTCTGTGAGGAGT 28255	G G A A
			ACT CT CA CA AGTGAAACT	
			TGA GA GT GT TCACTTTGA	
			G _ _ C	
GAM1326	MADD	3'	AGTTTCACTCTGTGAGGAGT 9785	G G A A
			ACT CT CA CA AGTGAAACT	
			TGA GA GT GT TCACTTTGA	
			G _ _ C	
GAM1326	MRPL49	3'	GTCTCACTCTGTTGCCCAG 34478	CT A A
			CTG GCAACA AGTGA AC	
			GAC CGTTGT TCACT TG	
			C _ C C	
GAM1326	NKX3A	3'	TTCCTTTTTGCAGCAATTA 12831	C C T
			TAA TGCTGCAA AAAG GAA	
			ATT ACGACGTT TTTC CTT	
			A _ _	
GAM1326	SEDL	3'	AGTCTCACTCTGTTGCCAGGC 15903	_ A A
			GCT GCAACA AGTGA ACT	
			CGG CGTTGT TCACT TGA	
			AC C C	
GAM1326	SFRS2IP	5'	AGTTTCACTCTGTTGCAG 11085	A
			CTGCAACA AGTGAAACT	

				GACGTTGT TCACTTTGA			
				C			
GAM1326	TSN	3'	TTCTGCTATTGCAGCAATTA	10988	C	CAA	_
			TAA TGCTGCAA AGT GAA				
			ATT ACGACGTT TCG CTT				
			A A__ T				
GAM1326	VSNL1	3'	TTTTAAAATTGCAGCAGTTG	9419		CAAAG	
			TAAGTCTGCTGCAA TGAAA				
			GTTGACGACGTT ATTTT				
			AAA__				
GAM1326	VTN	5'	GTGACCTTTTGCTGCAGCAG	6274	A	TGAA	
			CTGCTGCA CAAAG AC				
			GACGACGT GTTTC TG				
			C CAG_				
GAM1326	ALTE	3'	TTTCACTTTGCGGAGTTG	11108	G	CAA	
			TAAGT CTGCAA AGTGAAA				
			GTTGA GGCGTT TCACTTT				
			— —				
GAM1326	ASB16	3'	AGTCTCACTCTGTTGCCCAG	28107	CT	A	A
			CTG GCAACA AGTGA ACT				
			GAC CGTTGT TCACT TGA				
			C_ C C				
GAM1326	C11orf17	3'	AGTCTCACTCTGTTGCCCAG	21805	CT	A	A
			CTG GCAACA AGTGA ACT				
			GAC CGTTGT TCACT TGA				
			C_ C C				
GAM1326	C21orf25	3'	AGTTTCACTCTGTTGCCCAG	31797	CT	A	
			CTG GCAACA AGTGAAACT				
			GAC CGTTGT TCACTTTGA				
			C_ C				
GAM1326	C21orf25	3'	TTTCACTTTAAAATGCGCA	31803	T	AC__	
			TGC GCA AAAGTGAAA				
			ACG CGT TTTCACTTT				
			_ AAAA				
GAM1326	CCR1	3'	GCTTTATTGCAGCGATTA	6975	C	C	
			TAA TGCTGCAA AAAGT				
			ATT GCGACGTT TTTCG				
			A A				
GAM1326	CHSY1	3'	AGTCTCACTCTGTTACCCAGGC	17171	GC__	A	A
			GCT AACAA AGTGA ACT				

CGG TTGT TCACT TGA
ACCCA C C

GAM1326 DKFZP434B044 3' AGTTTCACTCTGTTGCCCAAGG 25552 GCT_ A
T ACT GCAACA AGTGAACT
||| ||||| |||||
TGG CGTTGT TCACTTTGA
AACC C

GAM1326 DKFZp761F2014 3' TCACTTTGTTAGCGTTG 21462 T CA
TAAC GCTG ACAAAGTGA
||| ||| |||||
GTTG CGAT TGTTTCACT

— —
GAM1326 DKFZp761N1114 3' AGTCTCACTCTGTTGCCAGGC 38604 _ A A
GCT GCAACA AGTGA ACT
||| ||||| ||||| |||
CGG CGTTGT TCACT TGA
AC C C

GAM1326 FLJ10640 5' AGTCTCACTCTGCTGCCTAGGC 21111 _ A A A
GCT GCA CA AGTGA ACT
||| ||| ||||| |||
CGG CGT GT TCACT TGA
ATC C C C

GAM1326 FLJ13114 3' AGTCTCACTCTGTGCGCCAG 23748 CT A A A
CTG GC ACA AGTGA ACT
||| || ||||| |||
GAC CG TGT TCACT TGA
C_ C C C

GAM1326 FLJ13197 3' AGTCTCACTCTGTTGCCAG 23871 CT A A
CTG GCAACA AGTGA ACT
||| ||||| ||||| |||
GAC CGTTGT TCACT TGA
C_ C C

GAM1326 FLJ13456 3' AGTTTCACTCTGTGCGCCCAAGC 32796 _ A A
GCT GC ACA AGTGAACT
||| || ||||| |||||
CGA CG TGT TCACTTTGA
ACC C C

GAM1326 FLJ14442 3' AGTCTCACTCTGTTACCCAGGC 26533 GC_ A A
GCT AACAA AGTGA ACT
||| ||||| ||||| |||
CGG TTGT TCACT TGA
ACCCA C C

GAM1326 FLJ20004 3' GTCTCACTCTGTGCGCCAG 45645 CT A A A
CTG GC ACA AGTGA AC
||| || ||||| |||
GAC CG TGT TCACT TG
C_ C C C

GAM1326 FLJ22531 5' AGTCTCACTCTGTTACCCAG 23943 CTGC A A
CTG AACAA AGTGA ACT
||| ||||| ||||| |||

		GAC TTGT TCACT TGA		
		CCA_ C C		
GAM1326	FLJ23263	5' AGTCTCACTCTGTGCGCCAG	24765	CT A A A
		CTG GC ACA AGTGA ACT		
		GAC CG TGT TCACT TGA		
		C_ C C C		
GAM1326	FLJ31101	3' AGTCTCACTCTGTGCGCCAG	19682	CT A A A
		CTG GC ACA AGTGA ACT		
		GAC CG TGT TCACT TGA		
		C_ C C C		
GAM1326	GBTS1	3' TCATGTGGTTGTTGCAGCA	29732	A__
		TGCTGCAACAA GTGA		
		ACGACGTTGTT TACT		
		GGTG		
GAM1326	GL004	3' TTTCTAACATTGCAGCAGTT	32830	CAAAGT
		AACTGCTGCAA GAAA		
		TTGACGACGTT CTTT		
		ACAAT_		
GAM1326	KIAA0417	3' TTCACAGAACTTTGCAGCAGTT	35294	CAAA__
		AACTGCTGCAA GTGAA		
		TTGACGACGTT CACTT		
		TCAAGA		
GAM1326	KIAA0475	3' AGTCTCACTCTGTTGCCAG	16946	CT A A
		CTG GCAACA AGTGA ACT		
		GAC CGTTGT TCACT TGA		
		C_ C C		
GAM1326	KIAA0561	3' AGTCTCACTCTGTTGCCCGG	32763	CT A A
		CTG GCAACA AGTGA ACT		
		GGC CGTTGT TCACT TGA		
		C_ C C		
GAM1326	KIAA0594	3' AGTCTCACTCTGTTGCCAG	32385	CT A A
		CTG GCAACA AGTGA ACT		
		GAC CGTTGT TCACT TGA		
		C_ C C		
GAM1326	KIAA0720	3' AGTCTCACTCTGTACCTAGGT	31230	GCTGCA A A
	TG	TAACT ACA AGTGA ACT		
		GTTGG TGT TCACT TGA		
		ATCCAC C C		
GAM1326	KIAA1054	3' AGTTTCACTCTGTTGCCAG	33952	CT A
		CTG GCAACA AGTGAACT		

		GAC CGTTGT TCACTTTGA		
		C_ C		
GAM1326	KIAA1143	3' CACCTGTTTCAGCAGTTA	34071	C AA
		TAAGTCTG AACA GTG		
		ATTGACGAC TTGT CAC		
		T C_		
GAM1326	KIAA1373	3' AGTCTCACTCTGTGCGCCAG	35122	CT A A A
		CTG GC ACA AGTGA ACT		
		GAC CG TGT TCACT TGA		
		C_ C C C		
GAM1326	KIAA1649	3' AGTCTCACTCTGTTGCCAAGGC	26102	___ A A
		GCT GCAACA AGTGA ACT		
		CGG CGTTGT TCACT TGA		
		AAC C C		
GAM1326	KIAA1655	3' AGTCTCACTCTGTGCGCCAG	33081	CT A A A
		CTG GC ACA AGTGA ACT		
		GAC CG TGT TCACT TGA		
		C_ C C C		
GAM1326	KIAA1971	3' AGTCTCACTCTGTGCGCCAG	36727	CT A A A
		CTG GC ACA AGTGA ACT		
		GAC CG TGT TCACT TGA		
		C_ C C C		
GAM1326	MGC2477	5' AGTCTCACTCTGTTGCCCAGC	23540	___ A A
		GCT GCAACA AGTGA ACT		
		CGA CGTTGT TCACT TGA		
		CC C C		
GAM1326	MGC5149	3' AGTCTCACTCTGTCAACCAG	35782	C CA A A
		CTG TG ACA AGTGA ACT		
		GAC AC TGT TCACT TGA		
		C _ C C		
GAM1326	PEG10	3' AGTTTCACTTTTCATCAGCA	17423	CAAC
		TGCTG AAAGTGAAACT		
		ACGAC TTTCACCTTTGA		
		TACT		
GAM1326	PELI1	5' AGTCTCACTCTGTGCGCCAG	21814	CT A A A
		CTG GC ACA AGTGA ACT		
		GAC CG TGT TCACT TGA		
		C_ C C C		
GAM1326	SCAMP-4	3' AGTTTCACTCTGTGCGCCAG	27818	CT A A
		CTG GC ACA AGTGAAACT		

			GAC CG TGT TCACTTTGA		
			C_ C C		
GAM1326	SERF1B	3'	AGTCTCACTCTGTCACCAG	23256	C CA A A
			CTG TG ACA AGTGA ACT		
			GAC AC TGT TCACT TGA		
			C _ C C		
GAM1326	SS-56	3'	AGTCTCACTCTGTTGCCAG	29988	CT A A
			CTG GCAACA AGTGA ACT		
			GAC CGTTGT TCACT TGA		
			C_ C C		
GAM1326	STK33	5'	AGTTGCTTTTGTGTCAGAGTTA	31495	G TGA
			TAACT CTGCAACAAAG AACT		
			ATTGA GACGTTGTTTT TTGA		
			_ CG_		
GAM1326	SUN1	3'	AGTCTCACTCTGTTGCCAG	24792	CT A A
			CTG GCAACA AGTGA ACT		
			GAC CGTTGT TCACT TGA		
			C_ C C		
GAM1326	LOC112724	5'	TTTCACTCTGTCGCCAGGC	28778	_ A A
			GCT GC ACA AGTGAAA		
			CGG CG TGT TCACTTT		
			AC C C		
GAM1326	LOC112817	3'	AGTTTCACTCTGTACCCAGGC	28780	GCA_ A
			GCT ACA AGTGAAACT		
			CGG TGT TCACTTTGA		
			ACCCAC C		
GAM1326	LOC135398	3'	AGTCTCACTCTGTACCCAGC	37385	CA_ A A
			GCTG ACA AGTGA ACT		
			CGAC TGT TCACT TGA		
			CCAC C C		
GAM1326	LOC146050	3'	AGTCTCACTCTGTCGTCCAG	38053	CT A A A
			CTG GC ACA AGTGA ACT		
			GAC TG TGT TCACT TGA		
			C_ C C C		
GAM1326	LOC152220	3'	AGTTTCACTTTGTATAAAAGTT	41440	GCTGCA
	A		TAACT ACAAAGTGAAACT		
			ATTGA TGTTTCACTTTGA		
			AAATA_		
GAM1326	LOC152300	3'	AGTCTCACTTTGTACCCAGGC	39249	GCA_ A
			GCT ACAAAGTGA ACT		

	CGG TGTTCCTACT TGA	
	ACCCAC C	
GAM1326 LOC158293 3'	TTCACCTTTCAGCAGTT 39807	CAAC
	AACTGCTG AAAGTGAA	
	TTGACGAC TTTCACCT	
GAM1326 LOC196264 3'	AGTCTCACTCTGTGCGCCAGGC 42331	__ A A A
	GCT GC ACA AGTGA ACT	
	CGG CG TGT TCACT TGA	
	AC C C C	
GAM1326 LOC200316 3'	AGTTTCACTCTGTGCGCCAG 42795	CT A A
	CTG GC ACA AGTGAACT	
	GAC CG TGT TCACTTTGA	
	C_ C C	
GAM1326 LOC200471 5'	TCATGCTGTTGCAGCAGT 43304	AA
	ACTGCTGCAACA GTGA	
	TGACGACGTTGT TACT	
	CG	
GAM1326 LOC202908 5'	AGTTGACCACTGCAGCAGT 42994	ACAAA A__
	ACTGCTGCA GTG AACT	
	TGACGACGT CAC TTGA	
	____ CAG	
GAM1326 LOC203350 3'	AGTCTCACTCTGTTGCCAG 43529	CT A A
	CTG GCAACA AGTGA ACT	
	GAC CGTTGT TCACT TGA	
	C_ C C	
GAM1326 LOC220074 3'	AGTCTCACTCTGTACACAG 29822	C CA A A
	CTG TG ACA AGTGA ACT	
	GAC AC TGT TCACT TGA	
	_ AC C C	
GAM1326 LOC221477 3'	TCATGTTGTTAAGCAGTTA 44259	GC A
	TAAGTCT AACA GTGA	
	ATTGACGA TTGTT TACT	
	A_ G	
GAM1326 LOC254249 5'	GTTTCTGTTGCAGAGTTA 45712	G AAGT
	TAAGT CTGCAACA GAAAC	
	ATTGA GACGTTGT CTTTG	
GAM1326 LOC50999 3'	TTCATTATTACCAGCAGTTA 18119	CAACAA
	TAAGTCTG AGTGAA	

ATTGACGAC TTACTT
 CATTA_
 GAM1326 LOC90141 3' AGTCTCACTTTGTCACCTAAGC 30879 GCA___ A
 GCT ACAAAGTGA ACT
 ||| ||||| |||
 CGA TGTTTCACT TGA
 ATCCAC C
 GAM1326 LOC93276 5' AGTTGACCACTGCAGCAGT 35589 ACAA A_
 ACTGCTGCA GTG AACT
 ||||| ||| |||
 TGACGACGT CAC TTGA
 _____ CAG
 GAM1327 CORO2B 3' CGCACAAAGAGTTTAT 32256 C CC
 ATAAACTC TTGT GCG
 ||||| ||| |||
 TATTTGAG AACA CGC
 A _
 GAM1327 LEF1 3' CCAGTGAGGAGTTCATGGA 18391 G A TTG _
 TC AT AACTCC TCCGC GG
 || ||||| ||||| |||
 AG TA TTGAGG AGGTG CC
 G C _ A
 GAM1328 ITPR2 3' GGTA AAAAGTACACTTTA 7994 G ACA
 TAAAGTGTAC TTT TACC
 ||||| ||| |||
 ATTTACATG AAA ATGG
 A _
 GAM1328 SLC19A2 3' TGGTGTGTGTA TACTT 34195 TTTAC
 AAGTGTACG ATACCG
 ||||| |||||
 TTCATATGT TGTGGT

 GAM1328 C1orf24 3' GGCAACATGTGCCTTCACACTT 27534 ACGTT ACC
 TA TAAAGTGT TACAT GCC
 ||||| ||||| |||
 ATTTACACA GTGTA CGG
 CTTCC CAA
 GAM1328 C20orf82 3' ATGTAAACGCCCACCTTA 41084 A TA
 TAA GTG CGTTTACAT
 ||| ||| |||||
 ATT CAC GCAAATGTA
 C CC
 GAM1328 KIAA0217 3' ATGTAACCATACACTTTA 33277 CGT
 TAAAGTGTA TTACAT
 ||||| |||||
 ATTTACAT AATGTA
 ACC
 GAM1328 KIAA0729 3' GGCAGTATATAAATGGTGCTTT 45806 TG A C C
 A TAAAG T CGTTTA ATAC GCC
 |||| | ||||| ||||| |||

	ATTTC G GTAAAT TATG CGG	
	GT _ A A	
GAM1328 LOC253017 5'	GGCAAATGTTAAAACACACTTT 45870	AC _ ACC
A	TAAAGTGT GTTT ACAT GCC	
	ATTTTACA CAAA TGTA CGG	
	_ AT AA_	
GAM1329 C20orf4 3'	AACCAGAAAGGTTTCTGCCCAG 17770	CGTGGC_
	CTGGGCAGA CTGGTT	
	GACCCGTCT GACCAA	
	TTGGAAA	
GAM1329 C9orf7 3'	GCCAGGCCTACCCAGGGA 19034	CAGACGT
	TCCCTGGG GGCCTGGT	
	AGGGACCC CCGGACCG	
	AT_____	
GAM1329 DKFZP762D096 3'	ACCGTCCCCTACCCAGGGA 32663	C ACGT CC
	TCCCTGGG AG GG TGGT	
	AGGGACCC TC CC GCCA	
	A _ CT	
GAM1329 FLJ10829 3'	AACCAGGTTGATCTGCCACAG 20176	_ CG
	CTG GGCAGA TGGCCTGGTT	
	GAC CCGTCT GTTGGACCAA	
	A A_	
GAM1329 KIAA0255 3'	AGACCACATCCACCCAGGGA 16412	CA C C
	TCCCTGGG GA GTGG CT	
	AGGGACCC CT CACC GA	
	AC A A	
GAM1329 LOC143909 5'	AGCCCACGCCTCCCAGGGA 40386	C A C
	TCCCTGGG AG CGTGG CT	
	AGGGACCC TC GCACC GA	
	_ C C	
GAM1329 LOC151996 5'	AGGTCTCCACGTCTGCCCAGG 41411	_____
	CCTGGGCAGACGTGG CCT	
	GGACCCGTCTGCACC GGA	
	TCT	
GAM1329 LOC254042 3'	AACTTTGCACGTCTGCC 45790	G CT
	GGCAGACGTG C GGTT	
	CCGTCTGCAC G TCAA	
	_ TT	
GAM1329 LOC256158 5'	AACCAGGCCGGCCACTCAGAGA 46614	C CAGACG
	TC CTGGG TGGCCTGGTT	

AG GACTC GCCGGACCAA
 A ACCG_
 GAM1329 LOC256158 5' AACCAGGCTGGCACCGCCCAGA 46615 _ AGACGT
 GG CC CTGGGC GGCCTGGTT
 || ||||| |||||
 GG GACCCG TCGGACCAA
 A CCACGG
 GAM1329 LOC92689 3' AACCAGGCCACACAGCAGGGG 34779 GG AGAC
 CCCT GC GTGGCCTGGTT
 ||| || |||||
 GGGG CG CACCGGACCAA
 A ACA_
 GAM1330 SMARCA3 3' TTAAGAGTACTATTTTTTCCA 9039 TTT C
 TGGAAAAA GTA TACTCTTAA
 ||||| || |||||
 ACCTTTTT TAT ATGAGAATT
 _ C
 GAM1330 TBXA2R 5' GGTATACAAATTCCTCCA 6726 AA C
 TGG AATTTGTA TACT
 ||| ||||| |||
 ACCT TTAAACAT ATGG
 CC _
 GAM1330 FLJ22843 3' AAGGCTGTGCAAATCCTCCA 24820 AAA TA T
 TGG AATTTGTAC C CTT
 ||| ||||| | |||
 ACCT TAAACGTG G GAA
 CC_ TC_
 GAM1330 KIAA1465 5' AAGAGTAGCGGACGTTTTGCCA 30499 A TTGTA
 TGG AAAAT CTACTCTT
 ||| ||||| |||||
 ACC TTTTG GATGAGAA
 G CAGGC
 GAM1330 KIAA1958 3' TTAAGAGTAACAATAATTTCTA 39833 AAT AC
 TGGAAA TTGT TACTCTTAA
 ||||| ||| |||||
 ATCTTT AACA ATGAGAATT
 AAT _
 GAM1330 PRO1770 3' TTAAGAGTAATATATTTAATTT 15327 _ _ C
 TATCCA GGA AAAATT TGTA TACTCTTAA
 ||| ||||| ||| |||||
 CCT TTTTAA ATAT ATGAGAATT
 A TTT A
 GAM1330 PTD012 5' AAGAGTAGCTCTATTTGTCCA 15268 A TTGTA
 TGG AAAAT CTACTCTT
 ||| ||||| |||||
 ACCT TTTA GATGAGAA
 G TCTC_
 GAM1330 SNX10 3' TTAAGAGTATTTAACCTTTTCCA 14969 AAT TAC
 TGGAAA TTG TACTCTTAA
 ||||| ||| |||||

		ACCTTT AAT ATGAGAATT	
		CC_ TT_	
GAM1330	STRN3	3' AAGAGTAGCTTTTTTTCA 15934	TTTGTA
		TGGAAAAA CTACTCTT	
		ACTTTTTT GATGAGAA	
		TC____	
GAM1330	LOC221931	3' TTAAGAGTACATAATGTTCC 45120	AAAT AC
		GGAA TTGT TACTCTTAA	
		CCTT AATA ATGAGAATT	
		GT_ C_	
GAM1331	C21orf108	3' GCCCAGCAAGTCAATACATACT 42770	___ GT AC C
		AGTAT TTG T GC GGGC	
		TCATA AAC A CG CCCG	
		CAT TG A_ A	
GAM1331	LOC168391	5' CCCAGCACAACCAGGTATCTGC 40243	_ AC C
	T	AGCAG TATTTGGTT GC GGG	
		TCGTC ATGGACCAA CG CCC	
		T CA A	
GAM1332	CLCN3	3' AAAAAGAAAGGAAATAT 7563	GA
		GTATTTCTT TCTTTT	
		TATAAAGGAA AGAAAAA	

GAM1332	IRF2	3' GGAAAAAGTATCATGGAAATAT 7956	T _
	TA	TAGTATTTCC TGAT CTTTTTCC	
		ATTATAAAGG ACTA GAAAAAGG	
		T T	
GAM1332	LPP	3' GAAAAAGATAAGAAATACTA 12106	CTTG
		TAGTATTTT ATCTTTTTC	
		ATCATAAAG TAGAAAAAG	
		AA_	
GAM1332	MME	3' AAAAAGTTACAGAAATACTA 14152	CT T
		TAGTATTTT TGA CTTTTT	
		ATCATAAAG ATT GAAAAA	
		AC _	
GAM1332	MME	3' AAAAAGTTACAGAAATACTA 6600	CT T
		TAGTATTTT TGA CTTTTT	
		ATCATAAAG ATT GAAAAA	
		AC _	
GAM1332	MME	3' AAAAAGTTACAGAAATACTA 14148	CT T
		TAGTATTTT TGA CTTTTT	

		ATCATAAAG ATT GAAAAA	
		AC _	
GAM1332 MME	3'	AAAAAGTTACAGAAATACTA 14156	CT T
		TAGTATTTTCTGA CTTTTT	
		ATCATAAAG ATT GAAAAA	
		AC _	
GAM1332 PBP	3'	GGAAAAAGACCAGGTCTAC 8416	TTT T A
		GTA CCT G TCTTTTCC	
		CAT GGA C AGAAAAAGG	
		CT_ _ C	
GAM1332 RBBP8	5'	GAAAAGGTCAGAAAATATTA 8801	CC
		TAGTATTT TTGATCTTTT	
		ATTATAAA GACTGGAAAAG	
		A_	
GAM1332 BM-002	3'	AAAAAGCTCAAGGAAATAC 18723	T
		GTATTTCTTGA CTTTTT	
		CATAAAGGAACT GAAAAA	
		C	
GAM1332 KIAA0855	3'	GGAAAAGTAGAGAAAGAAATGC 17375	C GA _
		GTATTTCTT TCT TTTTCC	
		CGTAAAG AA AGA AAAAGG	
		_ AG TG	
GAM1332 KIAA0871	3'	GGAAAGGACAAGAAAAAACTA 17331	A C A
		TAGT TTT CTTG TCTTTTCT	
		ATCA AAA GAAC AGGAAAGG	
		A A _	
GAM1332 KIAA1843	3'	GGAAAATATAAGGAAATACTG 31162	ATCT
		TAGTATTTCTTG TTTTCC	
		GTCATAAAGGAAT AAAAGG	
		AT_	
GAM1332 KLHL4	3'	AAAAAGGTCATGAAACAC 21191	A CT
		GT TTTC TGATCTTTT	
		CA AAAG ACTGGAAAAA	
		C T_	
GAM1332 OCT11	3'	AAAAAGGGGGGGAATAC 15679	GA
		GTATTTCTT TCTTTT	
		CATAAAGGGG GAAAAA	
		G_	
GAM1332 SPRY2	5'	GAAAAAAGAGGAAATACT 12454	GATC
		AGTATTTCTT TTTTCT	

		TCATAAAGGAG	AAAAAG		
		A__			
GAM1332	STRBP	5'	GGAAAAAGAAGCTAAAATACTA	20420	CCTTGA
			TAGTATTT TCTTTTTC		
			ATCATAAA AGAAAAAGG		
			ATCGA_		
GAM1332	TIP47	3'	AAAAAATCAGGGATATA	12416	T C
			TAT TCCTTGAT TTTT		
			ATA AGGGACTA AAAAA		
			T A		
GAM1332	LOC200268	3'	GAAAATTTAAGGAAATAT	42763	TCT
			GTATTCCTTGA TTTTC		
			TATAAGGAATT AAAAG		
			T__		
GAM1332	LOC91818	5'	GAAAAAGAGTTAAGGGAAATCT	33404	T GA__
	A		TAG ATTCCTT TCTTTTTC		
			ATC TAAAGGGA AGAAAAAG		
			_ ATTG		
GAM1332	LOC92573	5'	GAAAAAGATTTAGACATACTA	34598	T CTT
			TAGTAT TC GATCTTTTTC		
			ATCATA AG TTAGAAAAAG		
			C AT_		
GAM1333	B4GALT4	3'	CTGATTCTTTGTTTGCAATA	9859	C _
			TATTGCAAAC AAAGAA CGG		
			ATAACGTTTG TTTCTT GTC		
			_ A		
GAM1333	DMPK	3'	CCCACCTATCGTTGGTTCGCAA	10664	A A AC
			TTGC AACCAA GA GGTGGG		
			AACG TTGGTT CT CCACCC		
			C G AT		
GAM1333	NET1	3'	TTTGCCTTGGTTTGCAATA	12476	AGAAC TG
			TATTGCAAACCAA GG GG		
			ATAACGTTTGTT CC TT		
			_____ GT		
GAM1333	RS1	3'	CCACCCTCTGCCTTGCAATA	5875	ACCAA AC
			TATTGCAA AGA GGTGG		
			ATAACGTT TCT CCACC		
			CCG_ C_		
GAM1333	C20orf110	3'	CCCACTGTCTCAATCTGCAA	38835	AACCAA A
			TTGCA AGA CGGTGGG		

AACGT TCT GTCACCC
CTAAC_ _
GAM1333 DKFZP586C1619 3' CCATCTCAGTTTGCAA 31018 CAAA AC
TTGCAAAC GA GGTGG
||||| || ||||
AACGTTTG CT CTACC
A_ _ _
GAM1333 FLJ13593 3' CCCACCGTGATGACTTGAAATA 24149 G AC AAGA
TATT CAA CA ACGGTGGG
||| ||| || |||||
ATAA GTT GT TGCCACCC
A CA AG_ _
GAM1333 My015 3' CCCAGATTTTGGTTTCCAATA 33106 C AACGG
TATTG AAACCAAAG TGGG
|||| ||||| |||
ATAAC TTTGGTTTT ACCC
C AG_ _
GAM1333 PIP3-E 3' CCTATTTTCTTTGGTTTGCAA 33176 CG
TTGCAAACCAAAGAA GTGGG
||||||| ||||
AACGTTTGGTTTCTT TATCC
TT
GAM1333 LOC129011 5' CCCAGATAAGTTTGGTTTTCAA 36964 C GAACGG
TTG AAACCAA TGGG
|| ||||| |||
AAC TTTGGTTT ACCC
T GAATAG
GAM1333 LOC204301 3' CTGTTCTCTTTGGTTTGGAATA 43092 G _
TATT CAAACCAAAGA ACGG
|||| ||||| |||
ATAA GTTTGGTTTCT TGTC
G CT
GAM1333 LOC253805 3' CAGTGCTCTCTGGTTTGC 46133 A A G
GCAAACCA AGA CG TG
||||| ||| |||
CGTTTGGT TCT GT AC
C C G
GAM1333 LOC254358 3' CTGTTCTCTTTGGTTTGGAATA 45530 G _
TATT CAAACCAAAGA ACGG
|||| ||||| |||
ATAA GTTTGGTTTCT TGTC
G CT
GAM1334 F3 3' AAACCTACAGAGTTTATG 33295 CCAGCCTA
CATAAAC TGTAGTTT
||||| |||||
GTATTTG ACATCAAA
AG_ _ _ _
GAM1334 USP14 3' ACATAGGTGGGTTTATG 11626 G
CATAAACCCA CCTATGT
||||||| |||||

GTATTTGGGT GGATACA

GAM1334 C17orf26 3' ACCTTGGGCTGGGTCTATG 29184 A T_
CATA ACCCAGCCTA GT
||||| ||||| ||
GTAT TGGGTCGGGT CA
C TC

GAM1334 MO25 3' ACATGGCTGGGTTTCATG 18413 A T
CAT AACCCAGCC ATGT
||| ||||| ||||
GTA TTGGGTCGG TACA
C

GAM1334 SLC11A2 3' TGCACAGACTGTGTTTATG 6227 C C A
CATAAAC CAG CT TGTA
||||| ||| || ||||
GTATTTG GTC GA ACGT
T A C

GAM1335 CHST6 3' CAGGTTTAGAAGCTT 22244 TAAT
AAGCTTTTAG ACCTG
||||| ||||
TTCGAAGATT TGGAC

GAM1335 RB1 3' TCAGATATTATTGCTTTA 43705 TTTT C
TAAAGC AGTAATA CTGA
||||| ||||| ||||
ATTTG TATTAT GACT
A

GAM1335 ZNF2 3' CAGGTATCACTGCACTTTAA 22068 CTTT A
TTAAAG TAGT ATACCTG
||||| ||| |||||
AATTTC GTCA TATGGAC
AC_ C

GAM1335 C1orf22 3' TTCAGGTATTTTCAAGTTTTAA 24843 TTAGT
TTAAAGCTT AATACCTGAA
||||| |||||
AATTTTGAA TTATGGACTT
CTT_

GAM1335 CNNM1 3' TTCAGGTAAAAAAAAGTTT 21612 AGTAAT
AAGCTTTT ACCTGAA
||||| |||||
TTTGAAAA TGGACTT
AAAAAT

GAM1335 FLJ10619 3' TTCAGATATTGTCAGCTTTGA 19970 TT ATAC
TTAAAGCT TAGTA CTGAA
||||| |||| ||||
AGTTTCGA GTTAT GACTT
CT A_

GAM1335 FLJ20986 5' TTCAAGTGGTATTTAAAAGCTT 23729 GT _
TAA TTAAAGCTTTTA AATACC TGAA
||||| ||||| ||||

		AATTCGAAAA	TTATGG	ACTT	
		—	TGA		
GAM1335	KIAA0748	3'	CAGGTGATTA	AAAAAGCTTTA	16702 AG _
			TAAAGCTTTT	TAAT ACCTG	
			AATTCGAAAA	ATTA TGGAC	
			—	G	
GAM1335	MDS028	3'	TTCAGGTATTAGT	CAGCTT	20537 TTTAG
			AAGCT	TAATACCTGAA	
			TTCGA	ATTATGGACTT	
			CTG	—	
GAM1335	PLAGL2	3'	TTCAGGTATTATTTACTTT	34883 CTTTT	
			AAAG	AGTAATACCTGAA	
			TTTC	TTATTATGGACTT	
			AT	—	
GAM1335	SCYB5	3'	TTCAGAATTTCTAAAAGTTT	8885 T AC	
			AAGCTTTTAG	AAT CTGAA	
			TTTGAAAATC	TTA GACTT	
			T	A_	
GAM1335	TP53INP1	3'	TTCAGGTACATTAAGCTTTAG	27113 TTAGTAA	
			TTAAAGCTT	TACCTGAA	
			GATTTCGAA	ATGGACTT	
			TTAC	—	
GAM1335	TP53INP1	3'	TTCAGGTACATTAAGCTTTAG	36122 TTAGTAA	
			TTAAAGCTT	TACCTGAA	
			GATTTCGAA	ATGGACTT	
			TTAC	—	
GAM1335	LOC153205	3'	CAGAATATATACTAGAAGCT	41581 _ C_	
			AGCTTTTAGTA	ATA CTG	
			TCGAAGATCAT	TAT GAC	
			A	AA	
GAM1335	LOC158798	5'	TCAGACACTGAAGGCTT	39893 AATAC	
			AAGCTTTTAGT	CTGA	
			TTCGGAAGTCA	GACT	
			CA	—	
GAM1335	LOC196411	3'	GTATACTAAAAGCCTTAA	42364 A A	
			TTAA GCTTTTAGTA	TAC	
			AATT	CGAAAATCAT ATG	
			C	—	
GAM1335	LOC90233	3'	TTCAGGTATGTGGGAAGCTCTG	28745 A AGTA	
	A		TTA AGCTTTT	ATACCTGAA	

		AGT TCGAAGG TATGGACTT	
		C GTG_	
GAM1336	NCKAP1	3' AACATTTGCCAAACTAAAT 15095	AATC
		GTTTA TGGCAAATGTT	
		TAAAT ACCGTTTACAA	
		CAA_	
GAM1336	ATP10D	3' AACATTTGCCAAATCCAAC 36200	TAA C
		AGTT AT TGGCAAATGTT	
		TCAA TA ACCGTTTACAA	
		CC_ A	
GAM1336	FLJ12085	3' AACATTCACCTTTGTTTAAGCTT 23032	CT CA
	A	TAAGTTTAAAT GG AATGTT	
		ATTCGAATTTG TC TTACAA	
		TT AC	
GAM1336	MACF1	3' GAACATTTGGGGTTTTAAACT 14379	T GG
		AGTTTAAA CT CAAATGTTC	
		TCAAATTT GG GTTTACAAG	
		T G_	
GAM1336	SCLY	3' AACACTTGCCAGAACTAAATT 18588	AA_ A
		AGTTTA TCTGGCAA TGTT	
		TTAAAT AGACCGTT ACAA	
		CAA C	
GAM1336	LOC143879	3' AACATTTTCAGGATTTAAATT 37658	GGC
		AGTTTAAATCT AAATGTT	
		TTAAATTTAGG TTTACAA	
		AC_	
GAM1336	LOC197131	3' GAACAATCAGATTTAAAC 42447	CAAA
		GTTTAAATCTGG TGTTT	
		CAAATTTAGACT ACAAG	
		A_	
GAM1337	RANBP2	3' GTTAAAGATTTGCTTTAT 12948	TA
		GTAAA AAATCTTTAAC	
		TATTT TTTAGAAATTG	
		CG	
GAM1337	DKFZp761D0614	3' TTGTTAAAGATTTATTTTAC 42313	TA_
		GTAAA AAATCTTTAACAA	
		CATTT TTTAGAAATTGTT	
		TTA	
GAM1337	FLJ10546	3' AAAGATTTTATTTAGTAA 29910	G
		TTAC TAAATAAAATCTTT	

AATG ATTTATTTTAGAAA

GAM1337 FLJ23074 3' TTGTTAAAGATCTACTTATTTA 24651 A___
C GTAAATAA ATCTTTAACAA

||||||| |||||
CATTTATT TAGAAATTGTT
CATC

GAM1337 LOC123628 5' TGTTGTGGATTTATTTAC 37254 A T
GTAAATAAA TCT TAACA

||||||| ||| |||||
CATTTATTT AGG GTTGT

GAM1338 FLJ13769 3' GGACATGTAAGCAAGTAA 24595 ATATC A
TTACTTGTTTA TAT TCC

||||||| ||| |||
AATGAACGAAT GTA AGG
C

GAM1338 KIAA1958 3' GATATAAGCAAAAACAAGTGA 39830 AATATC
TTACTTGTTT TATATC

||||||| |||||
AGTGAACAAA ATATAG
AACGA_

GAM1338 MGC26651 3' GATATAGATACCATAGTCAAG 29470 T A___
CTTG TTA TATCTATATC

||| ||| |||||
GAAC GAT ATAGATATAG
T ACC

GAM1339 LOC199725 3' CCATTAGTAAGAATTACTAATA 43242 _ T_ C
TGTT GT TTCTTACTAA GG

||| || ||||| |||
ATAA CA AAGAATGATT CC
T TT A

GAM1340 GRIN2C 5' GAACTTCACAGCCCGAGTGA 6493 _ _ CGCGA
TCACT GGG TGTGA AGTTC

||||| ||| |||||
AGTGA CCC ACACT TCAAG
G G _

GAM1340 PER2 3' GACTGCCACCACACCCAG 23092 AC_ GA
CTGGGTGTG GC AGTT

||||||| || |||
GACCCACAC CG TCAG
CAC _

GAM1340 TAPBP 3' TGCCACCACACCCAGTGA 9184 AC_
TCACTGGGTGTG GCG

||||||| |||
AGTGACCCACAC CGT
CAC

GAM1340 C20orf21 3' AACTCCCGGGACACCCAGGA 19440 A GA C A
TC CTGGGTGT CG GA GTT

|| ||||| || |||

AG GACCCACA GC CT CAA
 _ GG C _
 GAM1340 FLJ10535 3' GAGCCACCACACCCAGCGA 19920 A ACGCGAA
 TC CTGGGTGTG GTTC
 || ||||| ||||
 AG GACCCACAC CGAG
 C CAC____
 GAM1340 FLJ10687 3' TGAACCCACACACACCCAATGA 20010 C ACGCGAA
 TCA TGGGTGTG GTTCA
 ||| ||||| ||||
 AGT ACCCACAC CAAGT
 A ACACC____
 GAM1340 KIAA0350 3' GGACACGCCACACCCAG 30672 AC AA
 CTGGGTGTG GCG GTTC
 ||||| ||| ||||
 GACCCACAC CGC CAGG
 _ A_
 GAM1340 LEAP-2 5' AACTTTGCCCCCATCTCACCCA 27543 T C____
 GT ACTGGGTG GA GCGAAGTT
 ||||| || |||||
 TGACCCAC CT CGTTTCAA
 T ACCCC
 GAM1340 LOC148534 3' AACTTCATTACTACCCAG 38547 _ CGC
 CTGGGT GTGA GAAGTT
 ||||| ||| |||||
 GACCCA CATT CTTCAA
 T A____
 GAM1341 AHR 3' TAAATCCAACCAATTTTC 7333 GG A
 G AGTTG TTGGATTTA
 | |||| |||||
 C TTAAC AACCTAAAT
 TT C
 GAM1341 CA12 3' CCAAATCCAACCTCCTGTCA 6879 GA A____
 TGACGGG GTTG TTGG
 ||||| ||| ||||
 ACTGTCC CAAC AACC
 TC CTA
 GAM1341 CHL1 3' TAAATCCAAAGTCCCC 13394 G GAT
 GGGGA TT TGGATTTA
 ||||| || |||||
 CCCCT AA ACCTAAAT
 G ____
 GAM1341 KIAA1190 3' TTAAACCCCCACCACTCCCCG 35226 TGATT A
 CGGGGAGT GG TTAA
 ||||| || |||||
 GCCCCTCA CC AAATT
 CCACC C
 GAM1341 PRO1386 5' AAATCCAAGGTCTCCCCATC 25286 C TTGA
 GA GGGGAG TTGGATT
 || ||||| |||||

CT CCCCTC AACCTAAA
 A TGG_
 GAM1342 CDH5 3' GCCCATTCCCAAGGGGAGACTGA 7548 GTATGG A A
 TCAGT TG GAA TGGGC
 |||| | ||| ||||
 AGTCA AC CTT ACCCG
 GAGGGA C _
 GAM1342 PKHD1 3' GGCCCATTTCTTTTCAAACCTGA 28942 GTA T
 TCAGT TGG GAGAAATGGGCC
 |||| ||| ||||| |||||
 AGTCA ACT TTCTTTACCCGG
 A__ T
 GAM1342 RAB5A 3' GCCCATTCTCCACACTGG 10371 ATGGT
 TCAGTGT GAGAAATGGGC
 ||||| ||||| |||||
 GGTCACA CTCTTTACCCG
 C____
 GAM1342 DKFZp761K1423 3' CCCATTTCTAAATGTACACT 20471 GTG
 AGTGTATG AGAAATGGG
 ||||| |||||
 TCACATGT TCTTTACCC
 AAA
 GAM1342 HEYL 3' CCCATCTCTCCTTCTCACTG 15929 TAT T A
 CAGTG GG GAGA ATGGG
 |||| | ||| ||||
 GTCAC TC CTCT TACCC
 TCT _ C
 GAM1342 KIAA0418 3' GCCCCTGTCCCTCGCCATACAC 15997 AA _
 TGA TCAGTGTATGGTGAG AT GGGC
 ||||| ||||| ||| ||||
 AGTCACATACCGCTC TG CCCG
 CC TC
 GAM1342 KIAA1247 3' CCCATTTCTCATTTAACA 30989 AT
 TGT GGTGAGAAATGGG
 ||| ||||| |||||
 ACA TTA CTCTTTACCC
 AT
 GAM1342 KIAA1701 3' CCCATCTCACCACACTG 33684 AT AA
 CAGTGT GGTGAGA TGGG
 |||| | ||||| ||||
 GTCACA CCACTCT ACCC
 _ _
 GAM1342 MAB21L2 5' CACTCACCTACACTGA 13149 T AAATGG
 TCAGTGTA GGTGAG G
 ||||| ||||| |
 AGTCACAT CCACTC C
 _ A____
 GAM1342 MDS028 3' CCCACTCCCCACTGTCACTG 20534 T A_ AA
 CAGTG ATGGTG GA TGGG
 |||| | |||| | ||||

GTCAC TGTCAC CT ACCC
 _ CC C_
 GAM1342 PRO2012 3' GCCCATTTCCCATTATACAT 20681 A
 GTGTATGGTG GAAATGGGC
 ||||| |||||
 TACATATTAC CTTTACCCG
 C
 GAM1343 CD22 3' CAAACCTCCAAAACCTCCTGC 7531 CGA C
 GT AGTTT GGAGGTTTG
 || |||| |||||
 CG TCAAA CCTCCAAAC
 TCC A
 GAM1343 DACH 5' CAAACCTCCTCCTTTTCACCTT 28033 TC TTTC
 CA TGAAG GAAG GGAGGTTTG
 |||| || |||||
 ACTTC CTTT CCTCCAAAC
 CA TCCT
 GAM1343 HMOX1 3' AAACCTCCAAAAGCCCTGA 7908 AA C_
 TCG GTTT GGAGGTTT
 || |||| |||||
 AGT CGAA CCTCCAAA
 CC AA
 GAM1343 PCCX2 3' CAAATTTTAAAATTTGACTTC 32821 CG
 A TGAAGTCGAAGTTT GAGGTTTG
 ||||| |||||
 ACTTCAGCTTTAAA TTTTAAAC
 A_
 GAM1344 MOT8 5' GACCGGCGCCGCGGGA 20825 A ATATTG
 TC CCGCGGCGC GGTC
 || ||||| ||||
 AG GGCGCCGCG CCAG
 _ G_
 GAM1344 TLR10 5' AGACCCAATATACAGGGTTTTG 25229 CC GGCGC
 A TCA GC ATATTGGGTCT
 ||| || |||||
 AGT TG TATAACCCAGA
 TT GGACA
 GAM1344 YAP 5' GAGCCGCAGCGCCGCGGCGA 29153 A ATAT G
 TC CCGCGGCGC TGG TC
 || ||||| |||
 AG GGCGCCGCG GCC AG
 C AC_ G
 GAM1345 ABL1 3' TGTCCACATCCCCAGAGCCCA 14228 A GAGGA _
 TG GCTC TGGGGA TGGACA
 || ||| |||| |||||
 AC CGAG ACCCCT ACCTGT
 C _ AC
 GAM1345 ABL1 3' TGTCCACATCCCCAGAGCCCA 11640 A GAGGA _
 TG GCTC TGGGGA TGGACA
 || ||| |||| |||||

AC CGAG ACCCCT ACCTGT
 C _____ AC
 GAM1345 ASGR1 5' CCACCCCCATTCTCCAAGCTT 7385 C_ A
 GAGCT GAGGATGGGG TGG
 |||| ||||||| ||
 TTCGA CTCTTACCCC ACC
 AC C
 GAM1345 EMS1 3' CCATCCCCTGATGCCCA 28866 A _ AGGAT
 TG GC TCG GGGGATGG
 || ||| |||||||
 AC CG AGT CCCCTACC
 C T _____
 GAM1345 EMS1 3' CCATCCCCTGATGCCCA 11735 A _ AGGAT
 TG GC TCG GGGGATGG
 || ||| |||||||
 AC CG AGT CCCCTACC
 C T _____
 GAM1345 MKI67 3' CATCCAGTCCTGAGCTCA 8252 G GG
 TGAGCTC AGGAT GGATG
 ||||| |||| ||||
 ACTCGAG TCCTG CCTAC
 _ A_
 GAM1345 PACE 3' CATCCTACCCTCGGGCCCA 8423 A ATG
 TG GCTCGAGG GGGATG
 || |||||| |||||
 AC CGGGCTCC TCCTAC
 C CA_
 GAM1345 PACE 3' GCCACCCCCTCAAGCCA 8425 A C ATG A A
 TG GCT GAGG GGG TGG C
 || ||| |||| ||| ||| |
 AC CGA CTCC CCC ACC G
 _ A _ _ C
 GAM1345 RARA 3' CCCCATCCTCAGAACTCA 6687 C _
 TGAG TC GAGGATGGGG
 |||| || |||||||
 ACTC AG CTCCTACCCC
 A A
 GAM1345 STXBP1 3' TGTCTCGCCATCCTCAAGACTC 9144 _ C G TG
 A TGAG CT GAGGATGG GA GACA
 |||| || ||||||| || ||||
 ACTC GA CTCCTACC CT CTGT
 A A G _
 GAM1345 C8orf13 3' TGCCATAAACATCCTTGA 39658 GGG A
 TCGAGGATG ATGG CA
 ||||||| |||| ||
 AGTTCCTAC TACC GT
 AAA _
 GAM1345 FLJ12442 5' CACCGCCACACTCGAGCCCA 23209 A GA _ A
 TG GCTCGAG TGG GG TG
 || |||||| ||| || ||

AC CGAGCTC ACC CC AC
 C AC G _
 GAM1345 FLJ21032 5' CGCCCCCACCCTCGAGCTC 24396 A A
 GAGCTCGAGG TGGGG TG
 ||||| ||||| ||
 CTCGAGCTCC ACCCC GC
 C C
 GAM1345 FLJ21432 3' TGTCCAGGTTTCTCCTGAGCTC 23770 G T GG A_
 A TGAGCTC AGGA G G TGGACA
 ||||| ||||| | |||||
 ACTCGAG TCCT C T ACCTGT
 _ _ TT GG
 GAM1345 JM4 3' CATCCACCCTTCTCCATGCTCA 14078 TC_ T _
 TGAGC GAGGA GG GGATG
 |||| ||||| |||||
 ACTCG CTCTT CC CCTAC
 TAC C A
 GAM1345 KIAA0984 5' CCCAGCTCCGCGAGCTCA 32643 A _
 TGAGCTCG GGA TGGG
 ||||| ||| ||||
 ACTCGAGC CCT ACCC
 G CG
 GAM1345 KIAA1463 3' CACCTCATCCTCAAACCTC 35769 CTC A
 GAG GAGGATGGGG TG
 ||| ||||| ||||| ||
 CTC CTCCTACTCC AC
 AAA _
 GAM1345 KIAA1706 3' CATCTGCATCCCCGAGCCCA 44575 A A G
 TG GCTCG GGATG GGATG
 || ||||| ||||| |||||
 AC CGAGC CCTAC TCTAC
 C C G
 GAM1345 LASP1 3' CCATTTTCATCCTGAGCCCA 12792 A G GG
 TG GCTC AGGATG GATGG
 || ||||| ||||| |||||
 AC CGAG TCCTAC TTACC
 C _ TT
 GAM1345 MGC16063 3' CCCTCCCCATCCCCAGCCCA 27591 A CGA T
 TG GCT GGATGGGGA GG
 || ||| ||||| ||||| ||
 AC CGA CCTACCCCT CC
 C CC_ C
 GAM1345 MGC2474 3' TGCCCACCCCCCTGTCCCCCGA 23421 A_ _ A A
 GCT AGCTCG GGAT GGGG TGG CA
 ||||| ||||| ||||| ||||| ||
 TCGAGC CCTG CCCC ACC GT
 CC TC C C
 GAM1345 OMD 3' TCCATCCCCCTAGCTCA 11456 CG ATG
 TGAGCT AGG GGGATGGA
 ||||| ||| ||||| |||||

ACTCGA TCC CCCTACCT

GAM1345 P37NB 5' TCCATTCCCCAAGTTCA 12435 CGAGGA _
TGAGCT TGGGGA TGGA
||||| ||||| |||||
ACTTGA ACCCCT ACCT

_____ T
GAM1345 PER3 3' TCCATGATGACCATCCTCATAG 18822 C_ GG____
CTCA TGAGCT GAGGATGG ATGGA
||||| ||||| |||||
ACTCGA CTCCTACC TACCT

TA AGTAG
GAM1345 T2BP 5' TGTCCACCCCATCCTGCGCCC 34683 A T G A
A TG GC C AGGATGGGG TGGACA
|| || | ||||| |||||
AC CG G TCCTACCCC ACCTGT
C C _ C

GAM1345 TOB2 3' CCAGCTATCCTCGCACTCA 45766 CT GGA
TGAG CGAGGATGG TGG
||| ||||| |||
ACTC GCTCCTATC ACC
AC G_

GAM1345 LOC120939 5' TGCCTTTGACCATCCTCAAAGC 37516 A C_ GGAT_ A
CA TG GCT GAGGATGG GG CA
|| || | ||||| || ||
AC CGA CTCCTACC CC GT
_ AA AGTTT _

GAM1345 LOC128989 3' CCATCTGTGTCCCCATGCCCA 36941 A TCGA G
TG GC GGATG GGATGG
|| || ||||| |||||
AC CG CCTGT TCTACC
C TACC G

GAM1345 LOC148085 5' TGCCCATGGTGTCTCAAGC 40868 C GGG A
GCT GAGGATG ATGG CA
||| ||||| ||||| ||
CGA CTCCTGT TACC GT
A GG_ C

GAM1345 LOC220776 3' CACCCACCATCCCTCCAGCCCA 33930 A C _ _ A
TG GCT GAGG ATGG GG TG
|| ||| ||||| || ||
AC CGA CTCC TACC CC AC
C C C A C

GAM1345 LOC221042 5' CATCCAATGCCTCGAGCCCA 44752 A ATGG
TG GCTCGAGG GGATG
|| ||||| |||||
AC CGAGCTCC CCTAC
C GTAA

GAM1345 LOC256905 3' CATCCATTCCTGAGCTCA 46296 G TGG
TGAGCTC AGGA GGATG
||||| ||| |||||

		ACTCGAG TCCT CCTAC		
		_ TA_		
GAM1345	LOC93380	3' TGCCCACCCCATCCCCGAGC 35728	A	A A
		GCTCG GGATGGGG TGG CA		
		CGAGC CCTACCCC ACC GT		
		C _ C		
GAM1346	ATP2A2	3' TGAGGCTCTGTAACCTTATCTA 7402	ATTCTT	A_
	A	TTAGATAAG GA CTCA		
		AATCTATTC CT GAGT		
		CAATGT CG		
GAM1346	KIAA1674	3' AGTGAGTTTCCTCATTTTCATC 34102	A	TCCT
		GAT AGAT GAACTCACT		
		CTA TTTA TTTGAGTGA		
		C CTCC		
GAM1347	IDS	5' GCCAAGTCTCTAACGTGACA 5698	A	ATC
		TGTCACGT TAGAGGC GGC		
		ACAGTGCA ATCTCTG CCG		
		_ AA_		
GAM1347	LOC200269	3' CCGTGGCTTTCTGACACGTGAC 42759	A_	_ AT
	A	TGTCACGT TAGAG GC CGG		
		ACAGTGCA GTCTT CG GCC		
		CA T GT		
GAM1348	IRF1	3' GCTCCCTGCTTTGGCTG 32174	T A T	
		CAGCCAAA GCA GGG GT		
		GTCGGTTT CGT CCC CG		
		_ _ T		
GAM1348	MPP2	3' ATCCTTAGCCCCCATATCTGGC 30079	A CAA	GTTT
	TG	CAGCCA ATG GGGT GAT		
		GTCGGT TAT CCCG CTA		
		C ACC ATTG		
GAM1348	RHD	3' AGGCACCCACCACATCTGGCT 18335	A CAA_	
		AGCCA ATG GGGTGTTT		
		TCGGT TAC CCCACGGA		
		C ACCA		
GAM1348	RHD	3' AGGCACCCACCACATCTGGCT 18215	A CAA_	
		AGCCA ATG GGGTGTTT		
		TCGGT TAC CCCACGGA		
		C ACCA		
GAM1348	TCTA	3' CAAACACCCACATACCTGGC 22730	A_	CAA
		GCCA ATG GGGTGTTTG		

			CGGT TAC CCCACAAAC		
			CCA A__		
GAM1348	FLJ10620	3'	ATGCCCTTGCTTTGGCT	19971	T
			AGCCAAA GCAAGGGTGT		
			TCGGTTT CGTTCCCGTA		
			—		
GAM1348	FLJ11753	3'	AACGCTCACACTTGGCTG	23962	A CAA
			CAGCCAA TG GGGTGTT		
			GTCGGTT AC CTCGCAA		
			C A__		
GAM1348	KIAA1100	3'	TAAGCCCCTGCATTTG	17086	A T
			CAAATGCA GGG GTTTG		
			GTTTACGT CCC CGAAT		
			— —		
GAM1348	KIAA1199	3'	CAAACATCTTTCAGCTG	35897	CAAA C
			CAGC TG AAGGGTGT TTG		
			GTCG AC TTTCTACAAAC		
			— —		
GAM1348	NCX	5'	GGCGCCCTGCCTTGGC	18261	AT A
			GCCAA GCA GGGTGTT		
			CGGTT CGT CCCGCGG		
			C_ _		
GAM1348	OLIG1	3'	CAACCGCCTTGCATCCAGT	45752	CAA G T
			GC ATGCAAGG TG TTG		
			TG TACGTTCC GC AAC		
			ACC _ C		
GAM1348	PP3501	3'	CAAACACCATGTAACCTG	22329	CCAAA AG
			CAG TGCA GGTGTTTG		
			GTC ATGT CCACAAAC		
			CA__ A_		
GAM1348	STIP-1	3'	CAAACAACCTTGGCTG	34527	AATGCA G
			CAGCCA AGG TGTTTG		
			GTCGGT TCC ACAAAC		
			— A		
GAM1348	YKT6	3'	ATCAAACACAGGTGCACTCAGC	13318	CAAA AGG
	TG		CAGC TGCA GTGTTTGAT		
			GTCG ACGT CACAAACTA		
			ACTC GGA		
GAM1348	LOC145216	3'	GGGCACCTCCACATCTGGCTG	40507	A CAA
			CAGCCA ATG GGGTGTTT		

		GTCGGT TAC TCCACGGG		
		C ACC		
GAM1348	LOC146513 5'	ATCAAACACCCTGCATT	40708	A
		AATGCA GGGTGTGTTGAT		
		TTACGT CCCACAACTA		
		—		
GAM1348	LOC147081 5'	CAAGCTCCTGCATTTGGC	38288	A T
		GCCAAATGCA GGG GTTTG		
		CGGTTTACGT CCT CGAAC		
		— —		
GAM1348	LOC257464 5'	CAAACAGCATATTGGC	43162	_ AAGGG
		GCCAA ATGC TGTTTG		
		CGGTT TACG ACAAAC		
		A ———		
GAM1348	LOC51194 3'	CAAATTCATTAAATTTGGCTG	18459	GCAAG TG
		CAGCCAAAT GG TTTG		
		GTCGGTTTA CT AAAC		
		AATTA TA		
GAM1348	LOC90190 3'	TTTGGTCCCCTCACATTTGGC	30948	CA TG TT
		GCCAAATG AGGG T GA		
		CGGTTTAC TCCC G TT		
		AC CT GT		
GAM1349	DKFZP586D0623 5'	AGCCTAAAACGACACACCCA	35626	TA A_
		TGG GTGTT TTTAGGCT		
		ACC CACAG AAATCCGA		
		CA CA		
GAM1349	MAPKAPK3 3'	GCCCCACCCCACCATGGTA	11010	A_ TTATTTA
		TACCATGGT GTG GGC		
		ATGGTACCA CAC CCG		
		CCC C_———		
GAM1349	MGC10955 5'	CCTCCCCTGCCATGGTA	26398	TTATTT
		TACCATGGTAGTG AGG		
		ATGGTACCGTCAC TCC		
		CC_———		
GAM1349	MRPL10 3'	CCTGCCACTGCCACAGTA	29768	CA TTATT
		TAC TGGTAGTG TAGG		
		ATG ACCGTCAC GTCC		
		AC C_———		
GAM1349	LOC149578 5'	AGCCTAAACGCCACCACCA	38780	A TTA
		TGGT GTG TTTAGGCT		

		ACCA CAC AAATCCGA	
		C CGC	
GAM1350	CLCN3	3' TAAAACTACTACTATGATATA 7568	GG A
		TATA ATAGTA TAGTTTTA	
		ATAT TATCAT ATCAAAAT	
		AG C	
GAM1350	TRIM14	3' AAAACTATAGTCCTATA 16664	AGTA
		TATAGGAT ATAGTTTT	
		ATATCCTG TATCAAAA	
		A__	
GAM1350	TRPS1	3' AAAACTATTACTAGGCTGATAA 15346	A A_
		TTAT GG TAGTAATAGTTTT	
		AATA TC ATCATTATCAAAA	
		G GG	
GAM1350	KIAA1431	3' AAAACTTGATTCTATAATG 31549	AGTAAT
		CATTATAGGAT AGTTTT	
		GTAATATCTTA TCAAAA	
		GT__	
GAM1351	ARPP-19	3' TACCTAACTTCTAGTGTAGTA 13421	CATAATCTA
		TACTATAC TTAGGTA	
		ATGATGTG AATCCAT	
		ATCTTC__	
GAM1351	LOC113523	3' ACCTAGGCTATATGGTATAGT 36149	ATCTA
		ACTATACCATA TTAGGT	
		TGATATGGTAT GATCCA	
		ATCG_	
GAM1352	HOXA7	3' AATATTGTATAAATTGTTTTCA 13768	AGC
		TGAAAATAATTTATA TATT	
		ACTTTTGTAAATAT ATAA	
		GTT	
GAM1352	SCN1A	3' TTAACAGCTTTTTGGTTATTTT 42838	TAT A
	TA	TGAAAATAATT AAGCT TTAA	
		ATTTTTATTGG TTCGA AATT	
		TTT C	
GAM1352	DKFZp761N1114	3' AATAGCTTATCTATATTCTCA 38603	A ATTT
		TGA AATA ATAAGCTATT	
		ACT TTAT TATTCGATAA	
		C ATC_	
GAM1352	FLJ11040	3' GCTTATAAAGCATTTTCA 20297	AA
		TGAAAAT TTTATAAGC	

		ACTTTTA AAATATTCG		
		CG		
GAM1352	LOC199678	3' AGCTTTTAAATTATTTTCA	43226	T_
		TGAAAATAATTTA AAGCT		
		ACTTTTATTAAAT TTCGA		
		TT		
GAM1353	EGLN2	5' TTCTTAACATTGCTGCATGGTA	18993	TA A
		TACCGTGT TAAT TTAAGAA		
		ATGGTACG GTTA AATTCTT		
		TC C		
GAM1353	BAG4	5' TCTTAAGGAACACGGTG	11310	ATAATA
		TACCGTGTT TTAAGA		
		GTGGCACAA AATTCT		
		GG__		
GAM1353	DKFZp761H079	3' TCTTAATATCAGCAAGGTG	29600	G ATA
		TACC TGTT ATATTAAGA		
		GTGG ACGA TATAATTCT		
		A C__		
GAM1353	KIAA0232	3' TTCTTAATTGATAACAC	36040	AAT
		GTGTTAT ATTAAGAA		
		CACAATA TAATTCTT		
		GT_		
GAM1353	KIAA1116	3' TTCTTAATATGAACATGGTA	17042	ATA
		TACCGTGTT ATATTAAGAA		
		ATGGTACAA TATAATTCTT		
		G__		
GAM1353	KIAA1557	3' TTCTTAATACTGTACCAC	30642	T A
		GTG TATA TATTAAGAA		
		CAC ATGT ATAATTCTT		
		C C		
GAM1353	LOC158549	3' TTCTTAATATTAGTCAC	42013	TTA
		GTG TAATATTAAGAA		
		CAC ATTATAATTCTT		
		TG_		
GAM1353	LOC51212	5' TTAATACATAACACGGTA	18519	AA
		TACCGTGTTAT TATTAA		
		ATGGCACAAATA ATAATT		
		C_		
GAM1354	GARP	3' GGTCTCCAAATTACAGCCCA	12034	AAA CT
		TG TGTAATTTGGA CT		

		AC ACATTAAACCT GG	
		CCG CT	
GAM1354	GDF8	3' AGGAGATCAAATTACATTT 11765	A
		AAATGTAATTTGG CTCTT	
		TTTACATTAAACT GAGGA	
		A	
GAM1354	LPP	3' AAGTTGTTACCAAATACACATT 12104	A_ _ T_
	TCA	TGAAATGT ATTTGG AC CTT	
		ACTTTACA TAAACC TG GAA	
		CA AT TT	
GAM1354	RAP1A	3' AAGAGCATGGATGCATTTCA 8793	A TT GA
		TGAAATGTA T G CTCTT	
		ACTTTACGT A T GAGAA	
		_ GG AC	
GAM1354	FLJ10052	3' GAATGTGTTCAAATACATCTCA 19713	A A TC_
		TGA ATGTA TTTGGAC TTC	
		ACT TACAT AAAC TTG AAG	
		C _ TGT	
GAM1354	FLJ11730	3' AGAACACAAGTCACATTTCA 22994	A GAC
		TGAAATGT ATTTG TCT	
		ACTTTACA TGAAC AGA	
		C ACA	
GAM1354	FLJ21939	3' TGGAAGAGATTCACGATTTCA 22803	GTAATT _
		TGAAAT TGGA CTCTTCCA	
		ACTTTA ACTT GAGAAGGT	
		GC_ A	
GAM1354	FLJ23537	3' GAAGAGACATTCAAATACATTT 24363	A _
	CA	TGAAATGTA TTTGGA CTCTTC	
		ACTTTACAT AAAC TT GAGAAG	
		_ ACA	
GAM1354	KIAA0367	3' GAAAGCCCAAATTACACCTC 33421	AA A C
		GA TGTAATTTGG CT TTC	
		CT ACATTAAACC GA AAG	
		CC C _	
GAM1354	KIAA0555	3' TGGAAGAAGATAAATTACTCTC 16685	AAT GAC
	A	TGA GTAATTTG TCTTCCA	
		ACT CATTAAAT AGAAGGT	
		CT_ AGA	
GAM1354	KIAA0594	3' GGTCAATTACATTTCA 32388	TG
		TGAAATGTAATT GACT	

ACTTTACATTAA CTGG

GAM1354 KIAA1691 3' AGGGGTTCAAACCCACCTCA 44461 AA TAA
TGA TG TTTGGACTCTT
||| || |||||
ACT AC AAACCTGGGGA
CC CCC

GAM1354 MGC13159 3' AGAATAAATTATATTCA 26750 GA
TGAAATGTAATTTG CT
||||||| ||
ACTTTATATTAAAT GA
AA

GAM1354 SCDGF-B 3' TGGCCGTACAAATTACATTTCA 26985 G TCTT
TGAAATGTAATTTG AC CCA
||||||| || |||
ACTTTACATTAAAC TG GGT
A CC__

GAM1354 SCDGF-B 3' TGGCCGTACAAATTACATTTCA 24883 G TCTT
TGAAATGTAATTTG AC CCA
||||||| || |||
ACTTTACATTAAAC TG GGT
A CC__

GAM1354 ZNF297 3' TGGAAGGGGAACCACAGTTTCA 11936 GTAATT A__
TGAAAT TGG CTCTTCCA
||||| || |||||
ACTTTG ACC GGGAAGGT
AC__ AAG

GAM1354 LOC152742 3' GAAGACACCACATTTCA 41545 AATTT AC
TGAAATGT GG TCTTC
||||| || ||||
ACTTTACA CC AGAAG
____ AC

GAM1354 LOC153163 3' TGGCTCTCCAACCTTACATTTCA 39363 T CTCTT
TGAAATGTAA TTGGA CCA
||||||| |||| |||
ACTTTACATT AACCT GGT
C CTC__

GAM1354 LOC196453 5' GAAGAGGCAAATGACATTTCA 43577 A GA
TGAAATGT ATTTG CTCTTC
||||| |||| |||||
ACTTTACA TAAAC GAGAAG
G G_

GAM1355 B3GALT2 3' ATGACGTGGTAAATGTGAA 9870 AG
TTCACATTTTACCAC GTCGT
||||||| ||||
AAGTGTAATGGTG CAGTA

GAM1355 B4GALT4 3' TCTGTAGTAAAATGTGAA 9860 C
TTCACATTTTAC ACAGG
||||||| ||||

		AAGTGTA [—] AAATG TGTCT	
		A	
GAM1355	DISC1	3' GAGCTGGTAA [—] ATGTGAA 20738	CA G
		TTCACATTTTACCA G TC	
		AAGTGTA [—] AAATGGT C AG	
		— G	
GAM1355	EGFL5	5' CGAACTGCAATA [—] ATGTGAA 41882	TACCA G
		TTCACATTT CAG TCG	
		AAGTGTA [—] AA GTC AGC	
		TAAC_ A	
GAM1355	HOXB6	3' CAACAACAATA [—] ATAAGATGTG 30087	ACCACAG C
	AA	TTCACATTTT GT GTTG	
		AAGTGTA [—] GAA CA CAAC	
		ATAATAA A	
GAM1355	DKFZP434G1415	3' ACTTGATGGTAA [—] ATATG 25314	C _
		CA ATTTTACCA CAGGT	
		GT TAA [—] AATGGT GTTCA	
		A A	
GAM1355	KIAA1958	3' ATCTGTGATCAA [—] AATGTGAA 39828	AC_
		TTCACATTTT CACAGGT	
		AAGTGTA [—] AAA GTGTCTA	
		CTA	
GAM1355	LOC153163	3' GACGGTAA [—] AATGTGAA 39362	ACAG
		TTCACATTTTACC GTC	
		AAGTGTA [—] AAATGG CAG	
		—	
GAM1355	LOC200609	5' ATGTTTTTGTGGTAA [—] AAT 43325	T_
		ATTTTACCACAGG CGT	
		TAA [—] AATGGTGTTT GTA	
		TT	
GAM1355	LOC202266	3' CAGTGTCTGTGGCAATATG 43419	T A T
		CAT TT CCACAGG CGTTG	
		GTA AA GGTGTCT GTGAC	
		T C _	
GAM1356	KIAA1348	3' TATTGTCTGAAAGAATCTT 34030	C_
		AAGATTCTTTCA CAATA	
		TTCTAAGAAAGT GTTAT	
		CT	
GAM1356	RAB39	3' GAATGATGCAATGAAAGAATTT 37645	CCA_ A
		AGATTCTTTCA AT CATTC	

TTTAAGAAAGT TA GTAAG
 AACG _
 GAM1356 LOC150630 5' AATGCACAATGGGAAGAATCTT 41237 ACCAATA
 A TAAGATTCTTTC CATT
 ||||| |||
 ATTCTAAGAAGG GTAA
 GTAACAC
 GAM1357 OAS3 3' TAAAAACACCCACATATGCTTT 12863 ATTA__ A
 TC GAAAAGTA GGT TTTTAA
 ||||| ||| |||||
 CTTTTCGT CCA AAAAAT
 ATACAC C
 GAM1357 C1orf9 3' TTAAACTTGCCTAATACCTTTC 18341 A A TT
 T AGAAA GTA TTAGGTA TTTAA
 ||||| ||| ||||| |||||
 TCTTT CAT AATCCGT AAATT
 C _ TC
 GAM1357 ENDOFIN 3' TTAAATGAAC TAATTACTTTT 16369 GTATT
 AAAAGTAATTAG TTTAA
 ||||| ||| |||||
 TTTTCATTAATC AAATT
 AAGT_
 GAM1357 FLJ10607 3' AAATGCTTTATTACCTTTCT 37831 A T
 AGAAA GTAAT AGGTATTT
 ||||| ||||| |||||
 TCTTT CATTA TTCGTAAA
 C T
 GAM1357 KIAA0332 3' TTAAAAATAAATAGTACCACTT 31424 A__ GG
 TTCT AGAAAAGT ATTA TATTTTAA
 ||||| ||| |||||
 TCTTTTCA TGAT ATAAAAATT
 CCA AA
 GAM1357 NBR2 3' AAAAATACCTAACTATGGTT 12422 AA A
 AA GTA TTAGGTATTTT
 || ||| |||||
 TT TAT AATCCATAAAAA
 GG C
 GAM1357 ZDHHC2 3' TAAAAATACCTAAAGTGC 18491 A_
 GTA TTAGGTATTTTAA
 ||| |||||
 CGT AATCCATAAAAAT
 GA
 GAM1357 LOC128338 3' ATGCCTATACTTTTTT 36926 AT
 AGAAAAGTA TAGGTAT
 ||||| |||||
 TTTTTCAT ATCCGTA
 _
 GAM1357 LOC253981 3' TTTAAACACTCCAGTTACTTTT 45869 A TAT_
 C GAAAAGTAATT GG TTTTAA
 ||||| ||| |||||

CTTTTCATTGA CC AAAATT
 _ TCAC
 GAM1358 DVL3 3' ATAAC TTTCTCTTTAAGCCTCT 10688 ATCCCGT__
 GCTA TAGCAGAGG AAAGTTAT
 ||||| |||||
 ATCGTCTCC TTTCAATA
 GAATTTCTC
 GAM1358 FLJ10244 3' ATAAC TTTGTCTGTCTC 19778 CCCG
 GAGGAT TAAAGTTAT
 |||| | |||||
 CTCCTG GTTTCAATA
 TCCT
 GAM1359 MAPRE1 3' GCAAAAAGTACCTCTTCTTA 14709 T_ T _
 TAAGA AG GTACTTTT GC
 |||| || ||||| ||
 ATTCT TC CATGAAAA CG
 TC _ A
 GAM1359 MBL2 3' TGTGTCAAACAGTACACTATCT 5765 _ CC
 TA TAAGATAGTGTACT TTTG CACA
 ||||| |||| ||||
 ATTCTATCACATGA AAAC GTGT
 C T_
 GAM1359 PKD2 3' GTAACAAGCACACTATTT 30178 A _
 AGATAGTGT CTT TTGC
 ||||| || ||||
 TTTATCACA GAA AATG
 C C
 GAM1359 DDX33 3' GTGGGCAAAGAAGATCT 21377 AGTGTA
 AGAT CTTTGTCCAC
 |||| | |||||
 TCTA GAAAACGGGTG
 GAA__
 GAM1359 FLJ13491 3' TGGGCAAAGATGCTGCCTTA 23889 A A T
 TAAG TAGTGT CTTT GCCCA
 |||| |||| |||| ||||
 ATTC GTCGTA GAAA CGGGT
 C _ _
 GAM1359 KIAA1915 5' GTGACAGGGGTACACTCTC 36271 T CC
 GA AGTGTACTTTTG CAC
 || ||||| |||| ||||
 CT TCACATGGGGAC GTG
 C A_
 GAM1359 NXP-2 3' TGGACACATTATCTTA 35231 ACTTTT C
 TAAGATAGTGT G CCA
 ||||| || ||||
 ATTCTATTACA C GGT
 _ _ A
 GAM1359 ZNF33A 3' TGTGAAGATTGTACACTAT 43902 TT GCC
 ATAGTGTAC TT CACA
 ||||| || ||||

		TATCACATG AG GTGT		
		TT AA_		
GAM1359	LOC157226 5'	GGCAAAGGTTCCCACCTTA 31977	ATA T__	
		TAAG GTG ACTTTTGCC		
		ATTC CAC TGGAAACGG		
		__ CCT		
GAM1360	PART1 3'	AAATACTAATGCACCACGTCA 18665	ATAA CA	
		TGAC GTGCAT GGTAATT		
		ACTG CACGTA TCATTAAA		
		CAC_ A_		
GAM1360	GRIN3A 3'	GTTACTCACACTTATGTC 28537	CATCA	
		GACATAAGTG GGTAAT		
		CTGTATTCAC TCATTG		
		AC__		
GAM1360	KIAA0218 3'	TACCTGCTAGTCTTGTGTCA 16518	TGCAT	
		TGACATAAG CAGGTA		
		ACTGTGTTT GTCCAT		
		TGATC		
GAM1361	BUB3 3'	TGTTTCTATCTCTAAATGA 11096	C C T_	
		TCAT TGGAGA AGA CA		
		AGTA ATCTCT TCT GT		
		A A TT		
GAM1361	NXF2 5'	CTAGATGATCTCTAAAGG 19457	GG CA	
		TCT AGA GATCATCTAG		
		GGA TCT CTAGTAGATC		
		AA _		
GAM1361	RPS6KA5 3'	ATTGGAATCTGCCTCCTAATGA 11141	CT A CA	
		TCAT GGAG CAGAT TCTAGT		
		AGTA CCTC GTCTA AGGTTA		
		AT C _		
GAM1361	ZNF2 3'	ATCTGCATCTCCAGATGA 22066	_	
		TCATCTGGAGA CAGAT		
		AGTAGACCTCT GTCTA		
		AC		
GAM1361	FLJ11004 5'	GGTTTTTGCCTCCAGATGA 20287	A TC	
		TCATCTGGAG CAGA ATC		
		AGTAGACCTC GTTT TGG		
		C T_		
GAM1361	MOST2 3'	TGATCTGCTCCAGATGA 21555	A	
		TCATCTGGAG CAGATCA		

AGTAGACCTC GTCTAGT

GAM1361 RASGRF2 3' ACTGGAATTCTGTCTCCAGAGA 30596 A TCA
TC TCTGGAGACAGA TCTAGT
|| ||||| |||||
AG AGACCTCTGTCT AGGTCA
_ TA_
GAM1361 LOC219688 5' ACCAGATGAAACCTCTCCAGG 44696 CAGA A
TCTGGAGA TCATCT GT
||||| |||||
GGACCTCT AGTAGA CA
CCAA C
GAM1361 LOC221663 5' ACTAATCTCTATCCCAGATGA 45037 A C TCATC
TCATCTGG GA AGA TAGT
||||| || ||| |||||
AGTAGACC CT TCT ATCA
_ A CTA_
GAM1361 LOC51336 5' ACTGCCATCCATCTCCAGA 18752 CA CATC
TCTGGAGA GAT TAGT
||||| ||| |||||
AGACCTCT CTA GTCA
AC CC_
GAM1361 LOC90670 3' TGCCCTGTCTCAGATGA 31885 G AT
TCATCTG AGACAG CA
||||| ||||| ||
AGTAGAC TCTGTC GT
_ CC
GAM1362 BS69 3' CTGTTCAAAGGCATTATCTGT 13406 A C C_
ACAGGTAAT CCT TG CGG
||||| ||| || |||||
TGTCTATTA GGA AC GTC
C A TT
GAM1362 FLJ23590 3' ATATCAATCTTAGACATTACCT 23939 ACC CCG_
GT ACAGGTAAT TCTG GATAT
||||| ||| |||||
TGTCCATTA AGAT CTATA
C_ TCTAA
GAM1362 KIAA0993 3' ATCCCCAAAGACATTATCTGT 32075 AC C CC
ACAGGTAAT CT TG GGAT
||||| || || |||||
TGTCTATTA GA AC CCTA
CA A C_
GAM1362 LOC222001 5' TTGCCAGAATCATTACCTGT 44642 ACC C
ACAGGTAAT TCTG CGG
||||| ||| |||||
TGTCCATTA AGAC GTT
CTA C
GAM1363 TCF7 3' GACAGAGGACCATTACAATA 9193 T AAA
TGGTT G GATGGTCCTCTGTC
||||| ||||| ||||| |||||

		ATCAA C TTACCAGGAGACAG		
		_ A _		
GAM1363	ARHU	3' ACAAAAGATTAATCTTTAAACC 22179	A _	CTC
	A	TGGTTTGAA GAT GGTC TGT		
		ACCAAATTT CTA TTAG ACA		
		_ A AAA		
GAM1363	KIAA0194	3' GACTACACCATCTCTCAAGCCA 32826	A	CCTCT
		TGGTTTGA AGATGGT GTC		
		ACCGAACT TCTACCA CAG		
		C CAT_		
GAM1363	KIAA0222	3' ACAAAGGATCTTAAACCA 16044	AAGAT	C
		TGGTTTGA GGCCT TGT		
		ACCAAATT CTAGGA ACA		
		_ A		
GAM1363	PGRMC2	3' ACAGAAAGATCATTGAAACCA 13011	G AA	C_
		TGGTTT A GATGGTC TCTGT		
		ACCAAA T TTAGTAG AGACA		
		G_ AA		
GAM1363	SAMHD1	3' GACAGAGGAATCCCCCAAATA 30734	AAA	GG
		TGGTTTG GAT TCCTCTGTC		
		ATCAAAC CTA AGGAGACAG		
		CCC _		
GAM1363	TSPEAR	3' GACAGAGGACCACCTCCCCATA 29596	T AA_ A	
	C	GT TG AG TGGTCCTCTGTC		
		CA AC TC ACCAGGAGACAG		
		T CCC C		
GAM1363	LOC148529	5' GACAAAGAGGCCTCTTCCAACC 40890	T A T T _	
	CA	TGG TTG AAGA GG CCTCT GTC		
		ACC AAC TTCT CC GGAGA CAG		
		C C _ _ AA		
GAM1363	LOC148823	3' GACAAAGCTTAACTCTTTCAAC 29792	T	TGGTC_ C
	CA	TGGTT GAAAGA CT TGTC		
		ACCAA CTTTCT GA ACAG		
		_ CAATTC A		
GAM1363	LOC220963	3' ACAGAAGACTTCAAGCCA 43955	AAGAT	C
		TGGTTTGA GGC TCTGT		
		ACCGAACT TCAG AGACA		
		_ A		
GAM1363	LOC221337	3' ACAGAAATATTTTCAAACC 44234	A	GTCC
		GGTTTGAA GATG TCTGT		

CCAAAC TTAT AGACA
 _ AA_
 GAM1363 LOC255671 3' ACAGAGGGCTCCAGACCA 46438 AAAGAT
 TGGTTTG GGTCTCTGT
 ||||| |||||
 ACCAGAC TCGGGAGACA
 C____
 GAM1364 SLC25A15 3' CACTGACCAACCAACCAAACTC 15526 A TTG ACC
 CA TG AGTTT TG GGTCA GTG
 || ||||| || |||||
 AC TCAA AC CCAGTCAC
 C CCA CAA
 GAM1364 XRCC3 3' CACTGTGCCCCACAAAAC TTCA 11906 T ACC _
 TGAAGTTTT GTG GGT CAGTG
 ||||| || || |||||
 ACTTCAAAA CAC CCG GTCAC
 _ C_ T
 GAM1364 FLJ00060 5' CACTGACCAATCACCCCAAC 30627 TTT CC
 GTT GTGA GGTCA GTG
 || |||||
 CAA CACT CCAGTCAC
 CCC AA
 GAM1364 FLJ12969 5' CACCAACCGGGACAAAAC TTCA 23124 T GA CA
 TGAAGTTTT GT CCGT GTG
 ||||| || |||||
 ACTTCAAAA CA GGCCA CAC
 _ G_ AC
 GAM1364 FLJ13189 3' CACTTGTTCTCACA AAAAC 24328 CC T_ _
 GTTTTTGTGA GG CA GTG
 ||||| || |||||
 CAAAACACT CC GT CAC
 _ TT T
 GAM1364 FOXP1 3' CACCAACCCAGTATCACA AAAA 26403 A CC_ CA
 CTCA TGA GTTTTTGTGA GGT GTG
 || ||||| || |||||
 ACT CAAAACACT CCA CAC
 _ ATGAC AC
 GAM1364 MRPS27 3' ACCTGTCTCACAAGAACTTCA 17471 _ C
 TGAAGTTTTTGT GAC GGT
 ||||| || |||||
 ACTTCAAGAACA CTG CCA
 CT T
 GAM1364 LOC157773 5' CACCAACCAGACACCAAACTTC 39669 TT ACC CA
 GAAGTTT GTG GGT GTG
 ||||| || || |||||
 CTTCAA CAC CCA CAC
 C_ AGA AC
 GAM1364 LOC162333 5' ACAGTCACAAAAC TTTC 42122 CG
 GAAGTTTTTGTGAC GT
 ||||| ||

CTTCAAAAACACTG CA
A_
GAM1365 DLG5 5' CCATCTTTGACCCTAACACTTT 40334 AA TGTA
AAAGTGTTAG TT ATGG
||||||| || |||
TTTCACAATC AG TACC
CC TTTC_
GAM1365 MBL2 3' CCATTTACAACAAACAC 5760 AGAAT
GTGTT TTGTAAATGG
|||| | |||||
CACAA AACATTTACC
AC_
GAM1365 DKFZp566H0824 5' CCATTCAACCATCTCTAACATT 18975 ATTT A
AGTGTTAGA GT AATGG
|||||| | |||||
TTACAATCT CA TTACC
CTAC C
GAM1365 DKFZP566J091 3' CCATTTTGCTTCCCAGCACTTT 25185 A_ TTT _
T AAAAGTGTT GAA GTAAA TGG
||||||| || | |||||
TTTTCACGA CTT CGTTT ACC
CC _ T
GAM1365 FLJ10901 3' CCACTGCTCCTTCTAACATTTT 20228 TTT AA
AAAGTGTTAGAA GTA TGG
||||||| || | |||
TTTTACAATCTT CGT ACC
CCT C_
GAM1365 GW112 3' CCATCTGCTTCTAACGC 13132 TTT A
GTGTTAGAA GTA ATGG
||||||| || | |||||
CGCAATCTT CGT TACC
_ C
GAM1365 KIAA0993 3' CATGTATTCTAACATTT 32080 TTGTAA
AAGTGTTAGAA ATG
||||||| |||
TTTACAATCTTA TAC
TG_
GAM1365 KIAA1822 3' CATTATTTCTAACACTT 33550 TTTGTA
AAGTGTTAGAA AATG
||||||| |||
TTCACAATCTT TTAC
TA_
GAM1365 PAK6 3' CCATGCTAAGTCTAACACT 21388 A TAA
AGTGTTAGA TTTG ATGG
||||||| ||| |||
TCACAATCT GAAT TACC
_ CG_
GAM1365 TNFRSF21 3' CCATTTACAAATGTACCTT 15802 T TAGA
AAG GT ATTTGTAAATGG
||| || | |||||

TTC CA TAAACATTTACC
 _ TG_
 GAM1365 LOC120892 3' CCATGAGGATAAATATCTAACA 36648 _ AA_
 CTTTT AAAAGTGTTAGA ATTTGT ATGG
 ||||| |||| ||||
 TTTTCACAATCT TAAATA TACC
 A GGAG
 GAM1365 LOC157653 5' CCATCTACAAATTCAGACTCTT 39633 T A A
 AAG GTT GAATTTGTA ATGG
 ||| ||| ||||| ||||
 TTC CAG CTAAACAT TACC
 T A C
 GAM1365 LOC245771 5' CCACTGCTCCTTCTAACATTTT 44633 TTT AA
 AAAGTGTTAGAA GTA TGG
 ||||| ||| |||
 TTTTACAATCTT CGT ACC
 CCT C_
 GAM1366 ERBB2 3' CTGAAACCTAGTACTGCCCCCC 10745 T AAA TC_
 A TG GG CAGTACTG TTCAG
 || || ||||| ||||
 AC CC GTCATGAT AAGTC
 _ CCC CCA
 GAM1366 FOXD2 5' AGACAAATGCCGTTTCCACA 10787 A C_
 TGTGGAAAC GTA TGTCT
 ||||| ||| ||||
 ACACCTTTG CGT ACAGA
 C AA
 GAM1366 ACAA2 5' TCTGAAGATGCATGTTTCCA 44096 _ ACT
 TGGAACA GT GTCTTCAGA
 ||||| || |||||
 ACCTTTGT CG TAGAAGTCT
 A _
 GAM1366 CHUK 3' TCTGAAAACAAGGTTTCCATA 6947 AGTAC C
 TGTGGAAAC TGT TTCAGA
 ||||| ||| |||||
 ATACCTTTG ACA AAGTCT
 GA_ A
 GAM1366 DDX28 5' CTGAAGACCTTATCTCCCA 20409 T AACA CT
 TG GGA GTA GTCTTCAG
 || ||| ||| |||||
 AC CCT TAT CAGAAGTC
 _ C_ TC
 GAM1366 DIS3 3' TCCAAAGATAGTATTTCCA 17303 ACA CA
 TGGAA GTACTGTCTT GA
 |||| ||||| ||
 ACCTT TATGATAGAA CT
 _ AC
 GAM1366 DJ328E19.C1.1 3' TCTGAAGACAATGGACCCAC 17683 AAA GTAC
 GTGG CA TGTCTTCAGA
 |||| || |||||

			CACC GT ACAGAAGTCT		
			CAG A__		
GAM1366	FLJ21032	3'	CTGAGATTCTATTTCCACA 24398	C TACT	T
			TGTGGAAA AG GTCT CAG		
			ACACCTTT TC TAGA GTC		
			A T__ _		
GAM1366	FLJ21817	3'	CTGGATACACTTTTCCACA 22783	C ACT	C
			TGTGGAAA AGT GT TTCAG		
			ACACCTTT TCA CA AGGTC		
			_ _ _ T		
GAM1366	GPR88	3'	TCTATTTTAGGTACCGTTTCAC 22573	G A	GTCTTC
	A		TGTG AAAC GTACT AGA		
			ACAC TTTG CATGG TCT		
			_ C ATTTTA		
GAM1366	GPS2	5'	CTGAAGACCTGGAATTCCTCA 10825	T A__	TACT
			TG GGAA CAG GTCTTCAG		
			AC CCTT GTC CAGAAGTC		
			C AAG _		
GAM1366	KIAA0295	3'	TCTGAAGACAGCACAGCAGCCA 33786	AAACA	A
	TA		TGTGG GT CTGTCTTCAGA		
			ATACC CA GACAGAAGTCT		
			GACGA C		
GAM1366	KIAA0561	3'	TGAAGGCCACTTCCCA 32766	T AAC	ACT
			TG GGA AGT GTCTTCA		
			AC CCT TCA CGGAAGT		
			_ _ _ C_		
GAM1366	KIAA1826	3'	TCTGAAGGTGCTTTTCCACA 33378	C	TGT
			TGTGGAAA AGTAC CTTCAGA		
			ACACCTTT TCGTG GAAGTCT		
			T _		
GAM1366	MGC3184	3'	TCTGAAGAGCACATCTCCAC 25232	AACA TAC	_
			GTGGA G TG TCTTCAGA		
			CACCT C AC AGAAGTCT		
			_ TAC G		
GAM1366	MGC5139	5'	GAAGACAACATCTACA 36679	AACA	AC
			TGTGGA GT TGTCTTC		
			ACATCT CA ACAGAAG		
			A__ _		
GAM1366	NXPH3	3'	TCTGAAGAAACCTGTCCCCAC 32720	AA	TACTG
			GTGG ACAG TCTTCAGA		

		CACC TGTC AGAAGTCT	
		CC CAA__	
GAM1366 P11	5'	TCTGGAGACACCAGCTCCACA 12642	AACA AC_
		TGTGGA GT TGTCTTCAGA	
		ACACCT CG ACAGAGGTCT	
		__ ACC	
GAM1366 LOC127262	3'	CTGAAGTGACACTTTTCCACA 37459	C ACTGT
		TGTGGAAA AGT CTTCAG	
		ACACCTTT TCA GAAGTC	
		T CAGT_	
GAM1366 LOC149013	3'	TCTGAAGACAATGGACCCAC 38633	AAA GTAC
		GTGG CA TGTCTTCAGA	
		CACC GT ACAGAAGTCT	
		CAG A__	
GAM1366 LOC149317	3'	TCTGAAGACAATGGACCCAC 38709	AAA GTAC
		GTGG CA TGTCTTCAGA	
		CACC GT ACAGAAGTCT	
		CAG A__	
GAM1366 LOC220638	3'	TCTGAAGACAATGGACCCAC 36589	AAA GTAC
		GTGG CA TGTCTTCAGA	
		CACC GT ACAGAAGTCT	
		CAG A__	
GAM1366 LOC221975	3'	CTGAAGACATGCTCTCACA 44496	AAAC C
		TGTGG AGTA TGTCTTCAG	
		ACACT TCGT ACAGAAAGTC	
		C__ _	
GAM1366 LOC257031	3'	TCTGAAGACAATGGACCCAC 45390	AAA GTAC
		GTGG CA TGTCTTCAGA	
		CACC GT ACAGAAGTCT	
		CAG A__	
GAM1367 BCAT1	3'	CCATATAACATGGGATTTTCCT 32896	AT _
C		GA GAAAGTTT TGTTATATGG	
		CT CTTTtagg ACAATATACC	
		C_ GT	
GAM1367 TIRAP	3'	CCATATAAATTGTTTATTC 27475	AGTTTTG
		GAATGAA TTATATGG	
		CTTATTT AATATACC	
		GTTA__	
GAM1367 BCL2L12	5'	CCAACACAGAACTTCCATTC 28914	A TATA
		GAATG AAGTTTTGT TGG	

CTTAC TTCAAGACA ACC
 C CA__
 GAM1367 KIAA1798 5' CCATATAACAAAAATGGATTTC 30402 GAAAG
 GAAT TTTTGTATATGG
 ||| |||||
 CTTA AAAACAATATACC
 GGTA_
 GAM1368 MMP19 3' AAACAGAAACCCAACTACCCC 8266 A TATACGC
 GG GGTAGTTGG GTTT
 || ||||| |||
 CC CCATCAACC CAAA
 _ CAAAGA_
 GAM1368 MMP19 3' AAACAGAAACCCAACTACCCC 23071 A TATACGC
 GG GGTAGTTGG GTTT
 || ||||| |||
 CC CCATCAACC CAAA
 _ CAAAGA_
 GAM1368 PCTK3 3' TGCATACCAACCCCTCC 36127 TA AC
 GGAGG GTTGGTAT GCG
 |||| ||||| ||
 CCTCC CAACCATA CGT
 C_ _
 GAM1369 ATP10C 3' TCCTCAGAACCATTTC 23689 TGC GC
 GAATG GT TCTGAGGA
 |||| || |||||
 CTTAC CA AGACTCCT
 _ _
 GAM1369 PTPRF 3' TGTCCTCAGAGCAGGGGCCA 28199 T G_
 TG GC TGCTCTGAGGACA
 || || |||||
 AC CG ACGAGACTCCTGT
 _ GGG
 GAM1369 PTPRF 3' TGTCCTCAGAGCAGGGGCCA 8725 T G_
 TG GC TGCTCTGAGGACA
 || || |||||
 AC CG ACGAGACTCCTGT
 _ GGG
 GAM1369 C20orf36 3' TCCTCAGAGCAGGTCTGA 20223 AATGT G
 TCG GC TGCTCTGAGGA
 || || |||||
 AGC TG ACGAGACTCCT
 _ G
 GAM1369 CNM3 3' TGTCCTCAGAACTAGACATC 19125 A GCGTGC
 GA TGT TCTGAGGACA
 || || |||||
 CT ACA AGACTCCTGT
 _ GATCA_
 GAM1369 KIAA1786 3' TCCTCAAATACATGGCACATTTC 32847 _ CTC_
 GAATGTGC GTG TGAGGA
 ||||| || |||||

CTTACACG TAC ACTCCT
 G ATAA
 GAM1369 NY-REN-41 3' TGGATCACACACATTCGA 27943 C C
 TCGAATGTG GTG TCTG
 ||||| ||| |||
 AGCTTACAC CAC AGGT
 A T
 GAM1369 PALM 3' GTCCCCAGAGGCACATTCG 8440 GTG A
 CGAATGTGC CTCTG GGAC
 ||||| ||| |||
 GCTTACACG GAGAC CCTG
 C
 GAM1369 PCQAP 3' TGTCTCAGAGCACACACACT 18034 AA_ C
 GA TCG TGTG GTGCTCTGAGGACA
 || ||| |||||
 AGT ACAC CACGAGACTCCTGT
 CAC _
 GAM1369 LOC57019 3' TCCCCAACACATTTGA 21569 C GCTC A
 TCGAATGTG GT TG GGA
 ||||| || |||
 AGTTTACAC CA AC CCT
 _ C
 GAM1369 LOC90485 3' CAGCGCACGCACACCGG 31553 AA T
 TCG TGTGCGTGC CTG
 || ||||| |||
 GGC ACACGCACG GAC
 C_ C
 GAM1370 M17S2 5' CCAAAAAAAGATACCT 25608 CATAAG
 AGGTATCTTT TTTGG
 ||||| |||
 TCCATAGAAA AAACC
 A
 GAM1370 PIK3R3 3' GCCAAGATGATAAAAAAACCT 30603 ATC C AAG
 TC GAAGGT TTT AT TTTGGC
 |||| ||| || |||||
 CTTCCA AAA TA GAACCG
 AAA A GTA
 GAM1370 ZNF10 3' GCCAACTTACTGATATCCTC 17695 A TTTCA
 GA GGTATC TAAGTTTGGC
 || |||| |||||
 CT CTATAG ATTCAAACCG
 C TC_
 GAM1370 DKFZP564I052 3' CCAAACCTTATATATACTCC 33136 A CTTTC
 A GGTAT ATAAGTTTGG
 |||| |||||
 C TCATA TATTCAAACC
 C TATA_
 GAM1370 FEM-2 3' GCCAACTCTTGAAGCACC 16008 ATC TA
 GGT TTTCA AGTTTGGC
 || |||| |||||

CCA GAAGT TCAAACCG
 C__ TC
 GAM1370 MYH10 5' GCCAACATTGAAACATACCTTC 34263 C TAA T
 GAAGGTAT TTTCA GTT GGC
 ||||| |||| ||||
 CTTCCATA AAAGT CAA CCG
 C TA__
 GAM1370 LOC201283 3' CTTACAGAAAGATACCCTC 30304 A A_
 GA GGTATCTTTC TAAG
 || ||||| ||||
 CT CCATAGAAAG ATTC
 C AC
 GAM1370 LOC51321 5' CTTACAGAAAGATACCCTC 18742 A A_
 GA GGTATCTTTC TAAG
 || ||||| ||||
 CT CCATAGAAAG ATTC
 C AC
 GAM1370 LOC91768 3' ACTTTTAAAAGATACCCTC 33321 A CAT
 GA GGTATCTTT AAGT
 || ||||| ||||
 CT CCATAGAAA TTCA
 C ATT
 GAM1371 KIAA0092 3' AATCATAATTTCAACTAGAT 16153 C _
 GTC AGTTGAAATTA GATT
 ||| ||||| ||||
 TAG TCAACTTTAAT CTAA
 A A
 GAM1371 LOC221979 3' AATGAAATTATCAACTGGC 44512 T AATTA
 G CCAGTTGA GATTTTCATT
 | ||||| |||||
 C GGTCAACT TTAAAGTAA
 _ A__
 GAM1372 ATP6V1A1 3' TGCTTCCAAAGTGGCCTACTCA 7411 GC GCACTT
 TGAG AGGCCACTT GCA
 ||| ||||| ||||
 ACTC TCCGGTGAA CGT
 A_ ACCTT_
 GAM1372 BTG2 3' TGCTTGGAAGTGGCCTCCCCA 13631 A C G CTT
 TG GG AGGCCACTT CA GCA
 || || ||||| || ||||
 AC CC TCCGGTGAA GT CGT
 _ C G T__
 GAM1372 CAT 3' TGCAAATGCAAGCTAGTGGCTT 7488 AG CA_ C
 CA TGAGGC GC CTTGCA TTGCA
 ||||| || ||||| ||||
 ACTTCG TG GAACGT AACGT
 G_ ATC A
 GAM1372 CBFA2T3 3' GCATTCAAGTGCACCTGCCTCA 11690 CCACT _
 TGAGGCAGG TGCACT TGC
 ||||| ||||| ||||

			ACTCCGTCC	ACGTGA	ACG	
			_____	CTT		
GAM1372	GM2A	3'	CAAGGCTGCCTGCCTCA	33657	CACTT	A
			TGAGGCAGGC	GC CTTG		
			ACTCCGTCCG	CG GAAC		
			T_____			
GAM1372	MAPK8IP1	3'	TGCAAGTGCCCGCCCTGCC	11941	CCACTT	
			GGCAGG	GCACTTGCA		
			CCGTCC	CGTGAACGT		
			CGCC_____			
GAM1372	PYCR1	3'	GCAAGTGCTTCCCAGCCCA	34731	A A	CCACTT
			TG GGC GG	GCACTTGC		
			AC CCG CC	CGTGAACG		
			_____ A CTT_____			
GAM1372	SALL2	3'	GTCAAATGGCCTGCCCA	31937	A	C C
			TG GGCAGGCCA	TTG AC		
			AC CCGTCCGGT	AAC TG		
			_____ A _____			
GAM1372	SEPX1	3'	GCGGAAGTAGCTTGCCTCA	18458	C	GCAC
			TGAGGCAGGC	ACTT TTGC		
			ACTCCGTTCG	TGAA GGCG		
			A _____			
GAM1372	FLJ11186	3'	CAAGTGATCCGCCTGTCTCA	20368	CACTTG	
			TGAGGCAGGC	CACTTG		
			ACTCTGTCCG	GTGAAC		
			CCTA_____			
GAM1372	KIAA0367	3'	TGCAAGGTGGCCTACTCA	33428	GC	_____
			TGAG	AGGCCAC TTGCA		
			ACTC	TCCGGTG AACGT		
			A_ G			
GAM1372	KIAA0924	3'	TGGGTTCAAGCAACCCTGCCTC	17069	CCA_	C
	A		TGAGGCAGG	CTTG ACTTG		
			ACTCCGTCC	GAAC TGGGT		
			CAAC T			
GAM1372	KIAA1503	5'	CAAGTTCTTGGCCTGCCT	33915	CTTGC	
			AGGCAGGCCA	ACTTG		
			TCCGTCCGGT	TGAAC		
			TCT_____			
GAM1372	STRBP	5'	GCAAGTGATCCGCCTGCCTCA	20419	CACTTG	
			TGAGGCAGGC	CACTTG		

		ACTCCGTCCG	GTGAACG		
		CCTA__			
GAM1372	LOC134266 3'	GCCCAAGCAATCCTGCCTCA	37069	CCAC	ACTT
		TGAGGCAGG TTGC GC			
		ACTCCGTCC AACG CG			
		T__ AACG			
GAM1372	LOC149506 3'	CGGGTTCAAGCGATCCTGCCTC	41007	CCA_	C
	A	TGAGGCAGG CTTG ACTTG			
		ACTCCGTCC GAAC TGGGC			
		TAGC T			
GAM1372	LOC158364 5'	CGAGAGGCATAGTGACCTGCCT	39815	C _	A_
	CA	TGAGGCAGG CACT TGC CTTG			
		ACTCCGTCC GTGA ACG GAGC			
		A T GA			
GAM1372	LOC200470 5'	TGCAGAGCGGCCTGCTCA	43310	G	A _
		TGAG CAGGCC CT TGCA			
		ACTC GTCCGG GA ACGT			
		_ C G			
GAM1372	LOC201627 3'	TGCAAGTGATTGTCCTGCCTCA	42899	C	CTTG
		TGAGGCAGG CA CACTTGCA			
		ACTCCGTCC GT GTGAACGT			
		T TA__			
GAM1372	LOC221042 5'	GCAAGTGCCCCTGCTTCA	44755	CCACTT	
		TGAGGCAGG GCACTTGC			
		ACTTCGTCC CGTGAACG			
		C_____			
GAM1373	DISC1 3'	TGTATTTGAAAATTCTGC	20741	T__	
		GC ATTTTCAAATACA			
		CG TAAAAGTTTATGT			
		TCT			
GAM1373	EVA1 3'	TGTATGGACAGTTTTTCCG	12380	ATT	AA
		CGGAAAAGCT TTCA TACA			
		GCCTTTTGA AGGT ATGT			
		C__ _			
GAM1373	F13A1 3'	TATTTCAAAAACATGCTTTTCC	43773	TA__	C
		GGAAAAGC TTTT AAATA			
		CCTTTTCG AAAA TTTAT			
		TACA C			
GAM1373	GPM6A 3'	TATTTGAAAAGGCTTCC	11780	AA	A
		GGA AGCT TTTTCAAATA			

CCT TCGG AAAAGTTTAT

GAM1373 KIF5C 3' ATGTATCTGTACAGTAGCTTTC 10851 A TT_ A
GAAA GCTATT CA ATACAT
||||| |||
CTTT CGATGA GT TATGTA
_ CAT C

GAM1373 MAP7 3' ATGTATTTATAAAGTTTTTCC 10117 AT TC
GGAAAAGCT TT AAATACAT
||||| |||
CCTTTTGA AA TTTATGTA
_ TA

GAM1373 RAG1 3' TGTATTTGGTGCTTCTTC 6043 A TATTT
GGA AAGC TCAAATACA
||| |||
CTT TTCG GGTATGT
C T_

GAM1373 TFDP2 3' ATGCATTTATATAGCTTTTTC 12974 TTTC A
GGAAAAGCTAT AAAT CAT
||||| |||
CTTTTCGATA TTTA GTA
TAC_ C

GAM1373 KIAA1819 3' TGTGTAAAATAGCCTTCC 34537 AA CAA
GGAA GCTATTTT ATACA
||| |||
CCTT CGATAAAA TGTGT
C_ _

GAM1373 MGC15619 5' ATTTGAGATCTTTTCC 26157 CTAT
GGAAAAG TTTCAAAT
||||| |||
CCTTTTC AGAGTTTA
T_

GAM1373 LOC115294 3' TATTTGAAGATTGGCTTTTCC 36146 _
GGAAAAGCTA TTTCAAATA
||||| |||
CCTTTTCGGT AGAAGTTTAT
T

GAM1373 LOC158357 3' TGCAAGATAGCTTTTCCG 39820 _
CGGAAAAGCTATTTT CA
||||| |||
GCCTTTTCGATAGAA GT
C

GAM1373 LOC256905 3' ATGTATTTTGTGAGTTTCTCC 46295 A ATTTTC
GGA AAGCT AAATACAT
||| |||
CCT TTTGA TTTATGTA
C GTGT_

GAM1374 CNR1 3' AAAACATTCTATCTACTGA 18160 TAA CCC
TCAGT AG GGAATGTTTT
||||| |||

AGTCA TC TCTTACAAAA
 ____ TA_
 GAM1374 KLRG1 3' AAAACCCGGTCTTAACTGA 12391 A C AAT
 TCAGTTAA G CCGG GTTTT
 ||||| | ||| ||||
 AGTCAATT C GGCC CAAAA
 _ T ____
 GAM1374 FLJ25416 3' AAAAACAAGGAGCTTTAGCT 29623 _ GGAA
 AGTTAAAGC CC TGTTTTT
 ||||| || |||||
 TCGATTTCG GG ACAAAAA
 A A ____
 GAM1374 PFTK1 3' AAAAACATTCCAAGCCAATTGG 14749 AAA CC
 TCAGTT GC GGAATGTTTTT
 |||| | |||||
 GGTTAA CG CCTTACAAAAA
 C _ AA
 GAM1375 SLC17A5 3' CTGGACTGAGGGGAGTGTGCCC 14813 A A GCC_
 A TG GCA CACTCCCT CCAG
 || || ||||| ||||
 AC CGT GTGAGGGG GGTC
 C _ AGTCA
 GAM1375 SPTBN1 5' AGCTGAAGCAGGGCAGGGCATC 9095 CAACACT ____
 AACTCA AG CCCTGCCC CAGCT
 || ||||| ||||
 TC GGGACGGG GTCGA
 AACTAC_ ACGAA
 GAM1375 TK2 3' AGCTGGGGCAAGGGGCAGCCA 10957 A AACA C
 TG GC CTCC TGCCCCAGCT
 || || |||| |||||
 AC CG GGGG ACGGGGTCGA
 _ AC_ A
 GAM1375 CBCIP2 3' AGCCAGGGCAGGGTTTTGCGTT 26605 AACACT CA
 CA TGAGC CCCTGCCC GCT
 |||| ||||| |||
 ACTTG GGGACGGG CGA
 CGTTTT AC
 GAM1375 DCAMKL1 3' GCTAGGGGGTGTCTTCTCA 11116 C _
 TGAG AACACTCCCT GC
 |||| ||||| ||
 ACTC TTGTGGGGGA CG
 T T
 GAM1375 DKFZp761F2014 3' GGCCCAGGGAGTTCTGCTCA 21460 AC CC
 TGAGCA ACTCCCTG CC
 |||| ||||| ||
 ACTCGT TGAGGGAC GG
 CT CC
 GAM1375 ELAC1 3' GCTGGGGTGACACTGCTC 43722 ACAC CCT
 GAGCA TC GCCCCAGC
 |||| || |||||

			CTCGT AG TGGGGTCG	
			CAC_ _	
GAM1375	FLJ00007	3'	AGCTGGGGGGCAGTGCTGTCCA 35306	AG A C TG
			TG CA CACT CC CCCAGCT	
			AC GT GTGA GG GGGGTCGA	
			CT C C _	
GAM1375	FLJ14768	3'	AGCTGGGGCAGGGGAGCCCA 26614	A AACAC
			TG GC TCCCTGCCCCAGCT	
			AC CG GGGGACGGGGTCGA	
			C A _	
GAM1375	GFR	3'	AGCCAAAGCAGGGAGCCTTTCT 14632	C CA CCCA
			AG AA CTCCCTGC GCT	
			TC TT GAGGGACG CGA	
			T CC AAAC	
GAM1375	KIAA0346	5'	AGCTGGGGCAGGGGGCCGTGCC 33919	A ACA
	CA		TG GCA CTCCCTGCCCCAGCT	
			AC CGT GGGGGACGGGGTCGA	
			C GCC	
GAM1375	KIAA1327	5'	AGCTGCTGAAGAACATGTTGCT 35762	CTCC GCCC
	CA		TGAGCAACA CT CAGCT	
			ACTCGTTGT GA GTCGA	
			ACAA AGTC	
GAM1375	P17.3	5'	CTGGAAGCAAAGAGGGTTGCTC 21139	A CC C_
	A		TGAGCAAC CTC TGC CCAG	
			ACTCGTTG GAG ACG GGTC	
			G AA AA	
GAM1375	RASSF2	3'	AGCTGGGGTAGAGGCACTGCCC 16390	A AACT _
	A		TG GCA CC CTGCCCCAGCT	
			AC CGT GG GATGGGGTCGA	
			C CAC_ A	
GAM1375	TEX27	3'	AGCTGGGGAAGCTGCCGCCCA 22458	A AA CTCC G
			TG GC CA CT CCCAGCT	
			AC CG GT GA GGGGTCGA	
			C CC C_ A	
GAM1375	VI	3'	AGCTGGGAACCTTGGTGTTCG 15106	CCCTGC
			GCAACACT CCCAGCT	
			CGTTGTGG GGGTCGA	
			TTCAA_	
GAM1375	LOC150935	5'	AGCAGGGGGCTGGGGCTCA 39017	AACACT T A
			TGAGC CCC GCCCC GCT	

ACTCG GGG CGGGG CGA
 _____ T A
 GAM1375 LOC196955 5' AGCCAAGGTGCTGGTGTGCCA 37928 A CCCT _ CA_
 TG GCAACACT GC CC GCT
 || ||||| || ||
 AC CGTTGTGG CG GG CGA
 _ T__ T AAC
 GAM1375 LOC222008 3' AGCTGGGGCAGTCCAGTCACTC 45122 CA ACTCC
 A TGAG AC CTGCCCCAGCT
 ||| || |||||
 ACTC TG GACGGGGTCGA
 AC ACCT_
 GAM1375 LOC57805 3' AGCCAGGGCAGGGGTGGCT 22149 AA T CA
 AGC CAC CCCTGCCC GCT
 ||| || ||||| ||
 TCG GTG GGGACGGG CGA
 _ _ AC
 GAM1376 TCN2 5' CCAGCTGTGGTCAGGAGAGCCT 5915 A G T CC
 AG CTC CCTGACCAC AGC GG
 || || ||||| || ||
 TC GAG GGA CTGGTG TCG CC
 C A _ A_
 GAM1376 TRPC6 5' CGGGCCAGTGGGCGAG 10974 TGAC A
 CTCGCC CACT GCCCG
 |||| || ||||
 GAGCGG GTGA CGGGC
 _ C
 GAM1376 DKFZP434F091 5' CGGACTTCAGGCGGATCT 17738 CT CCACT C
 AGA CGCCTGA AG CCG
 || ||||| || ||
 TCT GCGGACT TC GGC
 AG _ A
 GAM1376 FLJ23132 5' CGAAGTGTGTCAGGCGCGTCT 45981 T C AGCC
 AGAC CGCCTGAC ACT CG
 ||| ||||| || ||
 TCTG GCGGACTG TGA GC
 C _ A_
 GAM1376 NTN4 5' CCGGGCTAGCGGCAGACGAG 31512 C A A
 CTCG CTG CC CTAGCCCGG
 ||| || || |||||
 GAGC GAC GG GATCGGGCC
 A _ C
 GAM1376 SEC61A1 5' CCGGGCTAGCACTGACGTGTCT 14984 T CCTGACCA
 AGAC CG CTAGCCCGG
 ||| || |||||
 TCTG GC GATCGGGCC
 T AGTCAC_
 GAM1376 TGIF2 3' CCATCTGCTGGTCAGGAAGTC 22365 CG C CCC
 GACT CCTGACCA TAG GG
 ||| ||||| || ||

	CTGA GGA	CTGGT GTC	CC		
	A_	C	TA_		
GAM1376	LOC145098	5'	CGGCTAGTGGACTGAGTT	37796	CCTGA C
			GACTCG CCACTAGCC	G	
			TTGAGT GGTGATCGG	C	
			CA_	A	
GAM1376	LOC145719	5'	CCAGCTGATCGGGTCAGGCAAG	40572	C AC_ CC
		TC	GACT GCCTGACC TAGC	GG	
			CTGA CGGACTGG	GTCG CC	
			A	GCTA A_	
GAM1376	LOC145720	5'	CCAGCTGATCGGGTCAGGCAAG	40562	C AC_ CC
		TC	GACT GCCTGACC TAGC	GG	
			CTGA CGGACTGG	GTCG CC	
			A	GCTA A_	
GAM1376	LOC155382	5'	CGAGCCAGCAGCCGAGCT	41764	A C ACCA A C
			AG CTCG CTG	CT GC CG	
			TC GAGC GAC	GA CG GC	
			_ C _	C A	
GAM1376	LOC197114	5'	CCAGCTGATTGGGTCAGGCAAG	43186	C AC_ CC
		TC	GACT GCCTGACC TAGC	GG	
			CTGA CGGACTGG	GTCG CC	
			A	GTTA A_	
GAM1376	LOC254013	5'	CCAGGGCGAGTGACAGGCGAG	45479	AC A _
			CTCGCCTG CACT	GCCC GG	
			GAGCGGAC	GTGA CGGG CC	
			A_	G A	
GAM1377	CORO2A	5'	AGGCCAGCCTGGACAAA	9426	A A_
			TTTGTCCAG	CT GCCT	
			AAACAGGTC	GA CGGA	
			C	CC	
GAM1377	FAM8A1	3'	TGTTTGCCTGGATAAA	18383	ACTA CT
			TTTGTCCAG	GC AACA	
			AAATAGGTC	CG TTGT	
			_	T_	
GAM1377	FLJ22843	3'	TCGCGTTAAGAAGCCTGGACAA	24821	A AGCC A
		G	TTTGTCCAG	CT TAAC CGA	
			GAACAGGTC	GA ATTG GCT	
			C	AGA_ C	
GAM1377	LOC200310	3'	CGTCTTCTCGCCCTGGACAAA	32707	ACTA CT_ C
			TTTGTCCAG	GC AA ACG	

			AAACAGGTC	CG	TT	TGC	
			C__	CTC	C		
GAM1377	LOC90625	3'	GTTAGGCTGGGACAA	31820		AGAC	
			TTGTCC	TAGCCTAAC			
			AACAGG	GTCGGATTG			
GAM1378	AXIN1	3'	CTGTCCTGCCCCCAAGGA	30517	CC	AAAA	
			TCC	GGGGG	CAGGATAG		
			AGG	CCCCC	GTCCTGTC		
			AA				
GAM1378	CALB1	3'	AGCTATAATGTTTCCCTC	11368	A	GG	
			GGGGGAAA	CA	ATAGCT		
			CTCCCTTT	GT	TATCGA		
				AA			
GAM1378	CLTCL1	3'	AGCCATCCCAGAGCCTGGGGA	31834		GGAAAACA	A
			TCCCCGGG	GGAT	GCT		
			AGGGGTCC	CCTA	CGA		
			GAGAC__	C			
GAM1378	EGFL4	5'	AGCTGTCCCGTCCCCCAGGA	30961	CC	AAACA	
			TCC	GGGGGA	GGATAGCT		
			AGG	CCCCCT	CCTGTCGA		
			A_	GC__			
GAM1378	EXTL3	3'	GCCTTCTTCCCTCGGGGA	7169		AAACA	TA
			TCCCCGGGGGA	GGA	GC		
			AGGGGCTCCCT	TCT	CG		
				TC			
GAM1378	LRP1	3'	GCCTCCCCTCCCCTGGGGA	8138		AAACA	TA
			TCCCCGGGGGA	GGA	GC		
			AGGGGTCCCCT	CCT	CG		
			CC__	C_			
GAM1378	PACSIN1	5'	AGCCCCCTCCTCCCCCGGG	44312		AAAC	ATA
			CCCGGGGGA	AGG	GCT		
			GGGCCCCCT	TCC	CGA		
			CC__	CC_			
GAM1378	PACSIN1	3'	AGTTTTCCA	CTCTGCCCGGGG	44313		GAAAACA
			TCCCCGGGG	GGA	AGCT		T
			AGGGGCCCC	CCT	TTGA		
			GTCTCA_	T			
GAM1378	CRA	3'	AGCTATCCCATCTTCAGG	13515	G	AAACA	
			CC	GGGGA	GGATAGCT		

		GG CTTCT CCTATCGA		
		A AC__		
GAM1378	FLJ14124	3' AGACGTCCCTCCCTCGGGGA 24303	AAACA	AG
		TCCCCGGGGGA GGAT CT		
		AGGGGCTCCCT CCTG GA		
		C__ CA		
GAM1378	FLJ20413	3' AGCCTCCTTCCTCCCCGGGGA 19451	AAAAC	TA
		TCCCCGGGGG AGGA GCT		
		AGGGGCCCCCT TCCT CGA		
		CCT__ C_		
GAM1378	IL-17RC	3' AGCTACTTCCATCCCCCGGGGA 26455	AAACA	_
		TCCCCGGGGGA GGA TAGCT		
		AGGGGCCCCCT CCT ATCGA		
		A__ TC		
GAM1378	KIAA0876	3' AGCTGTCTCCTGCCCCAGGGA 32293	C	GAAAA _
		TCCC GGGG CAGGA TAGCT		
		AGGG CCCC GTCCT GTCGA		
		A _ CT		
GAM1378	KIAA1576	3' GGCTCTCCTTCCCCCGGGGA 32774	AAAC	T
		TCCCCGGGGGA AGGA AGCT		
		AGGGGCCCCCT TCCT TCGG		
		_ C		
GAM1378	PP1201	3' AGCTATTTCTTCCCCC 22711	AACA	
		GGGGGAA GGATAGCT		
		CCCCCTT TTTATCGA		
		C__		
GAM1378	WDR7	3' AGCTTACCCCTTTCCCCCGG 17608	ACA	AT
		CCGGGGGAAA GG AGCT		
		GGCCCCCTT CC TCGA		
		CC_ AT		
GAM1378	LOC149076	3' AGCCCCCTACATCCCCCGGGGA 38637	C	AAAC ATA
		TCCC GGGGGA AGG GCT		
		AGGG CCCCCT TCC CGA		
		C ACA_ CC_		
GAM1378	LOC199920	5' CTGTTTCTCCCCCCTAGGA 42661	CC_	_
		TCC GGGGGA AAACAG		
		AGG CCCCCT TTTGTC		
		ATC C		
GAM1378	LOC200470	5' GCCGCTCTGCCCCCGGGGA 43307	AAAA	ATA
		TCCCCGGGGG CAGG GC		

	AGGGGCCCCC GTCT CG		
	_____ CGC		
GAM1378 LOC220097 5'	AGCCATCCTGTCTTCTGCTTG 44896	_ A A	
	CGGG GGAA ACAGGAT GCT		
	GTTC TCTT TGTCTA CGA		
	G C C		
GAM1378 LOC222031 3'	GTTTCATTTTCCCCGAGGA 45135	C ACA	
	TCC CGGGGGAAA GGAT		
	AGG GCCCCTTT CTTG		
	A A_		
GAM1378 LOC90979 3'	ATTCAGTTTCCCCCAAGGA 32231	CC ACA	
	TCC GGGGGAAA GGAT		
	AGG CCCCTTT CTTA		
	AA GA_		
GAM1379 KIAA1322 3'	CGATGGGCAGTGGCTCACCCCC 36025	C C ATTGA	
A	TGG GG GAG TGCCCATCG		
	ACC CC CTC ACGGGTAGC		
	C A GGTG_		
GAM1379 TIP120B 3'	ATGGGCATCTTCCATGCCACCA 35859	C A_ TT	
	TGG GGCG GA GATGCCCAT		
	ACC CCGT CT CTACGGGTA		
	A AC T_		
GAM1379 LOC120448 5'	GGGCATCAACCTCACCCCA 37222	C C A	
	TGG GG GAG TTGATGCCC		
	ACC CC CTC AACTACGGG		
	_ A C		
GAM1379 LOC256158 5'	GATGGGCAGCCGCCGCC 46627	AGATTGA	
	GGCGGCG TGCCCATC		
	CCGCCGC ACGGGTAG		
	CG_____		
GAM1380 FENS-1 3'	TAAATCTCTTTACTATGT 21894	T TC	
	ACATAGTA AAG GATTTA		
	TGTATCAT TTC CTAAAT		
	_ T_		
GAM1380 PRO0902 5'	AATTGATTCTTACTATG 27604	_____	
	CATAGTATA AGTCGATT		
	GTATCATAT TTAGTTAA		
	CC		
GAM1381 RAB1A 3'	AATTTAGAAATTATCCCTAA 34786	TTCGATG	
	TTAGGGATATA AGATT		

AATCCCTATAT TTAA
 TAAAGA_
 GAM1381 KIAA0367 3' GAATCCTAGAAAAATAATCCCT 33422 A CGA_ A
 AA TTAGGGAT TATT TG GATTC
 ||||| ||| || ||||
 AATCCCTA ATAA AT CTAAG
 _ AAAG C
 GAM1381 KIAA1030 3' AATCTCATTTCATTCCTAA 44816 ATATTC
 TTAGGGAT GATGAGATT
 ||||| |||||
 AATCCTTA TTA CTCTAA
 C_____
 GAM1381 LOC162239 3' GAATCTCCTGGGAATCTATCCC 40050 T GAT_
 TAA TTAGGGATA ATT C GAGATTC
 ||||| ||| |||||
 AATCCCTAT TAAG CTCTAAG
 C GGTC
 GAM1382 ABR 3' TGCTTTGCCTTGCTGC 6751 AAA GAT
 GCAGCAAG GT GAGGCA
 ||||| || |||||
 CGTCGTTC CG TTTCGT

 GAM1382 ABR 3' TGCTTTGCCTTGCTGC 22496 AAA GAT
 GCAGCAAG GT GAGGCA
 ||||| || |||||
 CGTCGTTC CG TTTCGT

 GAM1382 BN51T 3' GCACATCCTTGCTGCT 42283 AAAGT AG
 AGCAGCAAG GATG GC
 ||||| ||| ||
 TCGTCGTTC CTAC CG
 _____ A_
 GAM1382 CMAR 3' TGCCTTGGTTTTTACTGCT 11699 C AGTGAT
 AGCAG AAGAA GAGGCA
 |||| |||| |||||
 TCGTC TTTT TTCCGT
 A GG_____
 GAM1382 CNR1 3' ATGCCAAGGACCTTTTGCTGC 18163 AA GATGA
 GCAGCAAGA GT GGCAT
 ||||| || |||||
 CGTCGTTTT CA CCGTA
 C_ GGAA_
 GAM1382 CRIM1 3' TTACACTTTTTGCTGCT 18562 A A
 AGCAGCAAGAA GTG TGA
 ||||| ||| |||
 TCGTCGTTTTT CAC ATT

 GAM1382 PCDHA1 3' CCTCACCTTTCGCTGTT 25384 AA TGA
 AGCAGC GAAAG TGAGG
 ||||| |||| |||||

			TTGTCG CTTTC ACTCC		
			— C—		
GAM1382	PCDHA1	3'	CCTCACCTTTCGCTGTT	20865	AA TGA
			AGCAGC GAAAG TGAGG		
			TTGTCG CTTTC ACTCC		
			— C—		
GAM1382	PCDHA10	3'	CCTCACCTTTCGCTGTT	20875	AA TGA
			AGCAGC GAAAG TGAGG		
			TTGTCG CTTTC ACTCC		
			— C—		
GAM1382	PCDHA10	3'	CCTCACCTTTCGCTGTT	25616	AA TGA
			AGCAGC GAAAG TGAGG		
			TTGTCG CTTTC ACTCC		
			— C—		
GAM1382	PCDHA11	3'	CCTCACCTTTCGCTGTT	20885	AA TGA
			AGCAGC GAAAG TGAGG		
			TTGTCG CTTTC ACTCC		
			— C—		
GAM1382	PCDHA12	3'	CCTCACCTTTCGCTGTT	20896	AA TGA
			AGCAGC GAAAG TGAGG		
			TTGTCG CTTTC ACTCC		
			— C—		
GAM1382	PCDHA13	3'	CCTCACCTTTCGCTGTT	20906	AA TGA
			AGCAGC GAAAG TGAGG		
			TTGTCG CTTTC ACTCC		
			— C—		
GAM1382	PCDHA2	3'	CCTCACCTTTCGCTGTT	20916	AA TGA
			AGCAGC GAAAG TGAGG		
			TTGTCG CTTTC ACTCC		
			— C—		
GAM1382	PCDHA3	3'	CCTCACCTTTCGCTGTT	20926	AA TGA
			AGCAGC GAAAG TGAGG		
			TTGTCG CTTTC ACTCC		
			— C—		
GAM1382	PCDHA4	3'	CCTCACCTTTCGCTGTT	20936	AA TGA
			AGCAGC GAAAG TGAGG		
			TTGTCG CTTTC ACTCC		
			— C—		
GAM1382	PCDHA5	3'	CCTCACCTTTCGCTGTT	20946	AA TGA
			AGCAGC GAAAG TGAGG		

			TTGTCG CTTTC ACTCC		
			— C—		
GAM1382	PCDHA6	3'	CCTCACCTTTCGCTGTT 20956	AA	TGA
			AGCAGC GAAAG TGAGG		
			TTGTCG CTTTC ACTCC		
			— C—		
GAM1382	PCDHA6	3'	CCTCACCTTTCGCTGTT 25588	AA	TGA
			AGCAGC GAAAG TGAGG		
			TTGTCG CTTTC ACTCC		
			— C—		
GAM1382	PCDHA7	3'	CCTCACCTTTCGCTGTT 20966	AA	TGA
			AGCAGC GAAAG TGAGG		
			TTGTCG CTTTC ACTCC		
			— C—		
GAM1382	PCDHA8	3'	CCTCACCTTTCGCTGTT 20976	AA	TGA
			AGCAGC GAAAG TGAGG		
			TTGTCG CTTTC ACTCC		
			— C—		
GAM1382	PCDHA9	3'	CCTCACCTTTCGCTGTT 25601	AA	TGA
			AGCAGC GAAAG TGAGG		
			TTGTCG CTTTC ACTCC		
			— C—		
GAM1382	PCDHAC1	3'	CCTCACCTTTCGCTGTT 20845	AA	TGA
			AGCAGC GAAAG TGAGG		
			TTGTCG CTTTC ACTCC		
			— C—		
GAM1382	PCDHAC2	3'	CCTCACCTTTCGCTGTT 20855	AA	TGA
			AGCAGC GAAAG TGAGG		
			TTGTCG CTTTC ACTCC		
			— C—		
GAM1382	PYGM	5'	ATGCCTCAGTTTCTCCCAACCGC 12128	AGCA—	GTGA
			GC AGAAA TGAGGCAT		
			CG TCTTT ACTCCGTA		
			CCACCC G—		
GAM1382	SPG7	3'	TGCCTTGTTTTTACTGCT 9090	C	AGTGAT
			AGCAG AAGAA GAGGCA		
			TCGTC TTTTT TTCCGT		
			A GG—		
GAM1382	CCR6	5'	ATGCCTCTCTTTTCTT 25368	T T	
			AAGAAAG GA GAGGCAT		

TTCTTTT CT CTCCGTA
 T _
 GAM1382 COAS3 3' ATGCCCCAAAGTTTCTTGT 29118 G GA A
 GCAAGAAA T TG GGCAT
 ||||| | |||||
 TGTTCTTT G AC CCGTA
 _AA C
 GAM1382 CPLX1 3' GCCCCTTTCTCTTGCTGTT 13452 AAGT TGA_
 AGCAGCAAGA GA GGC
 ||||| || |||
 TTGTCGTTCT CT CCG
 ____ TTCC
 GAM1382 DKFZP434L1435 5' ATGCCTCATTTGCCTCTCGCTT 44266 C A AAGT
 CT AG AGC AGA GATGAGGCAT
 || ||| |||||
 TC TCG TCT TTA CTCCGTA
 T C CCGT
 GAM1382 DNAJC5 3' GCCCCCAGCACCCCTGCCTGCT 30815 CA AAA A A_
 AGCAG AG GTG TG GGC
 |||| || ||| |||
 TCGTC TC CAC AC CCG
 CG CC_ G CC
 GAM1382 FLJ12875 3' ATGCCTCATCACTTAAGC 23754 AAGA
 GC AAGTGATGAGGCAT
 || |||||
 CG TTA CTACTCCGTA
 AA_
 GAM1382 FLJ13181 5' GCCTCGTCTTCCCGTCTGC 24829 _AA AGT
 GCAG C GAA GATGAGGC
 ||| | ||| |||||
 CGTC G CTT CTGCTCCG
 T CC _
 GAM1382 FLJ14564 3' CCTCCACTCCCTTGTTGCT 37596 AA AT
 AGCAGCAAG AGTG GAGG
 ||||| ||| |||
 TCGTTGTTT TCAC CTCC
 CC _
 GAM1382 FLJ14800 3' GCCTCAGCTTGCTGCT 26623 AAAGTGA
 AGCAGCAAG TGAGGC
 ||||| |||||
 TCGTCGTTT ACTCCG
 G____
 GAM1382 JAM1 3' ATGCCTCAAAGCCTTGCT 29327 AAA GA
 AGCAAG GT TGAGGCAT
 |||| || |||||
 TCGTTC CG ACTCCGTA
 ____ AA
 GAM1382 JAM1 3' ATGCCTCAAAGCCTTGCT 29336 AAA GA
 AGCAAG GT TGAGGCAT
 |||| || |||||

		TCGTTC CG ACTCCGTA	
		___ AA	
GAM1382 JAM1	3'	ATGCCTCAAAGCCTTGCT 29347	AAA GA
		AGCAAG GT TGAGGCAT	
		TCGTTC CG ACTCCGTA	
		___ AA	
GAM1382 JAM1	3'	ATGCCTCAAAGCCTTGCT 18860	AAA GA
		AGCAAG GT TGAGGCAT	
		TCGTTC CG ACTCCGTA	
		___ AA	
GAM1382 KCNB2	5'	ATGCCTTAGCTTCCTCCCGCCG 45963	A A__ A GA
C		GC GC AG AAGT TGAGGCAT	
		CG CG TC TTCG ATTCCGTA	
		C CCC C _	
GAM1382 KIAA0275	3'	ATGCCTCGCTCCTTCCTGC 16549	C AA GAT
		GCAG AAG AGT GAGGCAT	
		CGTC TTC TCG CTCCGTA	
		C C_ _	
GAM1382 KIAA0494	5'	GCGTTCCTCACTTTCTTACTCT 16591	C C AT G
		AG AG AAGAAAGTG GA GC	
		TC TC TTCTTTCAC TT CG	
		_ A CC G	
GAM1382 KIAA1184	3'	CCTCATCATCCTTCTCATCGCT 22896	AGCA A_
		AGC AGAA GTGATGAGG	
		TCG TCTT TACTACTCC	
		CTAC CC	
GAM1382 OBTP	5'	GCCCCCTCCTTTCTTGCTGC 19078	T TGA
		GCAGCAAGAAAG GA GGC	
		CGTCGTTCTTTC CT CCG	
		_ CCC	
GAM1382 RP4-622L5	3'	GTCCTCCCTCCTTGCTGC 21203	AA TGAT _
		GCAGCAAG AG GAGG C	
		CGTCGTTTC TC CTCC G	
		C_ C_ T	
GAM1382 LOC126302	3'	CCTCATTCTTGCTGCT 36819	AAGTG
		AGCAGCAAGA ATGAGG	
		TCGTCGTTCT TACTCC	

GAM1382 LOC127602	5'	GCCTTTCTTGCTGCT 36905	AAGTGAT
		AGCAGCAAGA GAGGC	

TCGTCGTTCT TTCCG

GAM1382 LOC128954 5' TCGCCACTTTCTTGCTGCT 37322 A
AGCAGCAAGAAAGTG TGA
||||| |||
TCGTCGTTCTTTTAC GCT
C
GAM1382 LOC136069 5' CCCACTCACCGTCCTTGCTGCT 37390 _AA _A
AGCAGCAAG A GTGA TG GG
||||| | ||| ||
TCGTCGTTT T CACT AC CC
C GC C _
GAM1382 LOC148490 5' ATGCCTCAGGCTTGCTCCTGCT 38545 A _ GA
GT GCAGCA GA AAGT TGAGGCAT
||||| || ||| |||||
TGTCGT CT TTCG ACTCCGTA
C CG G_
GAM1382 LOC149401 3' ATGGCTCGCTCTCTCACTGCT 38737 CA A GAT G
AGCAG AGA AGT GAG CAT
||||| ||| ||| ||| |||
TCGTC TCT TCG CTC GTA
AC C _ G
GAM1382 LOC157273 3' GCCTCTCCCTTGCTGT 41785 AAAGT T
GCAGCAAG GA GAGGC
||||| || |||||
TGTCGTTT CT CTCCG
C _ _
GAM1382 LOC160156 5' ATGCCTCCAGCCTTTGCTGCT 39991 AAA GAT
AGCAGCAAG GT GAGGCAT
||||| || |||||
TCGTCGTTT CG CTCCGTA
C _ AC_
GAM1382 LOC161247 5' CCTGCTCACCTTTTGCTGC 40015 AA TG
GCAGCAAGA GTGA AGG
||||| ||| |||
CGTCGTTTT CACT TCC
C _ CG
GAM1382 LOC255779 3' CCTCCCTACTTGCTGCT 45942 AGAA AT
AGCAGCA AGTG GAGG
||||| ||| |||
TCGTCGT TCAT CTCC
_ CC
GAM1383 DMPK 5' CATGCATTCCCCCTACTCT 10662 ATA
AGAGTAGGGGGAG TATG
||||| ||| |||
TCTCATCCCCCTT GTAC
AC_
GAM1383 CLDN15 3' CATGCTCACCTCCCCTACCCTG 28792 A _ ATA
CAG GTAGGGG GAG TATG
||| ||||| ||| |||

GTC CATCCCC CTC GTAC
 C TCCA ____
 GAM1383 HIC2 3' TACCAGGACCCCCTCCCCCTAC 32532 _ ATATA__
 CTC GAG TAGGGGGAG TGGTA
 ||| ||||| |||||
 CTC ATCCCCCTC ACCAT
 C CCCCAGG
 GAM1383 KIAA1189 3' TACCATCTCTCTCTCCCCCTAC 35651 A TAT__
 CT AG GTAGGGGGGAGA ATGGTA
 || ||||| |||||
 TC CATCCCCCTCT TACCAT
 _ CTCTC
 GAM1383 KIAA1500 3' ACCACACTTTCCTCCTACTC 32062 TATA
 GAGTAGGGGGGAGA TGGT
 ||||| |||||
 CTCATCCTCCTTT ACCA
 CAC_
 GAM1383 NIR3 3' ACCACACAGTGCTCCCTGCCCT 32923 A AGATATA
 G CAG GTAGGGGG TGGT
 ||| ||||| |||||
 GTC CGTCCCTC ACCA
 C GTGACAC
 GAM1383 SPBPBP 5' ACCACATACCCTCACTTCCCCC 13508 AGT ____ _ A
 TTCCCT G AGGGGGA GA TAT TGGT
 | ||||| || |||||
 C TCCCCCT CT ATA ACCA
 CCT TCA CCC C
 GAM1383 STAT2 3' TACCAGTCTCCTCCCCTACTCT 11890 _ ATA
 G CAGAGTAGGGG GAGAT TGGTA
 ||||| ||||| |||||
 GTCTCATCCCC CTCTG ACCAT
 TC ____
 GAM1383 LOC119392 3' ACCACATATTTCCATCTG 29757 GG A
 TAG GGAGATAT TGGT
 ||| ||||| |||||
 GTC CCTTTATA ACCA
 TA C
 GAM1383 LOC123242 5' ACCATATTTCTCCCCACTCTG 37238 AG T
 CAGAGT GGGGAGA ATATGGT
 ||||| ||||| |||||
 GTCTCA CCCCTCT TATACCA
 _ T
 GAM1383 LOC221688 3' CATTTATCTTCCCCCACCCT 44990 A A T
 AG GT GGGGGGAGATA ATG
 || || ||||| |||||
 TC CA CCCCTTCTAT TAC
 C C T
 GAM1383 LOC253001 5' ACCATATTTCTCCCCACTCTG 46055 AG T
 CAGAGT GGGGAGA ATATGGT
 ||||| ||||| |||||

			GTCTCA CCCCTCT TATACCA		
			___ T		
GAM1384	HOXD3	3'	TCCAATCTGGTAATGGTGT 13775	TATCC	
			ACACCATTACC TGGA		
			TGTGGTAATGG ACCT		
			TCTA_		
GAM1384	JRK	3'	TCCATGACGATGGTGT 41838	ACCTA C	
			AACACCATT TC TGGA		
			TTGTGGTAG AG ACCT		
			C___ T		
GAM1384	OXCT	3'	GTTTTTATAATAGGTAAT 6020	CC	
			ATTACCTAT TGGAAAC		
			TAATGGATA ATTTTGT		
			AT		
GAM1384	PCDH7	3'	GTTTCCAGAATAAATATGTGTG 26216	_ TACC C	
	T		ACAC CAT TAT CTGGAAAC		
			TGTG GTA ATA GACCTTTG		
			T TAA_ A		
GAM1384	PRKAB1	3'	TCATAATAGGTGACAGTGTT 12932	CA CC	
			AACAC TTACCTAT TGG		
			TTGTG AGTGGATA ACT		
			AC AT		
GAM1384	PROX1	5'	CCAGGAGAAAATGGTGT 8649	ACCTA	
			AACACCATT TCCTGG		
			TTGTGGTAA AGGACC		
			AAG_		
GAM1384	SMT3H1	3'	TTTCTCATTTGGTAATGGTGT 30128	TATCCT	
			AACACCATTACC GGAAA		
			TTGTGGTAATGG TCTTT		
			TTTAC_		
GAM1384	TRPC1	3'	TTCCAAAATAAGCTGTTAATGG 9309	_ C___ CC	
	TGT		ACACCATTA C TAT TGGAA		
			TGTGGTAAT G ATA ACCTT		
			T TCGA AA		
GAM1384	BTN1A1	3'	GTTTCCAGGATAGATGTTG 7468	C TAC	
			CA CAT CTATCCTGGAAAC		
			GT GTA GATAGGACCTTTG		
			T _		
GAM1384	CRA	3'	GTTTCTGCTGCAGATAGTGGTG 13517	C ATCCT	
	TT		AACACCATTA CT GGAAAC		

		TTGTGGTGAT GA	TCTTTG	
		A CGTCG		
GAM1384	DKFZP434A043	5' TTTCCAGGATCATGCTGTT	17706	C TACCT
		AACA CAT ATCCTGGAAA		
		TTGT GTA TAGGACCTTT		
		C C____		
GAM1384	FLJ10853	5' CCGGGATCATGGTGTT	20215	TACCT
		AACACCAT ATCCTGG		
		TTGTGGTA TAGGGCC		
		C____		
GAM1384	FLJ23462	3' TTTCTTTTTAGGTAAGTGGT	24269	_ TCCT
		ACCA TTACCTA GAAA		
		TGGT AATGGAT TCTTT		
		C TTT_		
GAM1384	HSPC019	3' TTTCCAGGCATAGCAATG	15253	AC _
		CATT CTAT CCTGGAAA		
		GTAA GATA GGACCTTT		
		C_ C		
GAM1384	KIAA0057	3' TCCAGAAAGGTAATGGTG	14625	ATC
		CACCATTACCT CTGGA		
		GTGGTAATGGA GACCT		
		AA_		
GAM1384	KIAA0429	5' GTTTCCAGTTGTCTAACGGGT	16474	A A CC TC
		AAC CC TTA TA CTGGAAAC		
		TTG GG AAT GT GACCTTTG		
		_ C CT T_		
GAM1384	KIAA0523	5' CTGGAGATAAGTAATGGTG	33641	C _TG
		CACCATTAC TATC C G		
		GTGGTAATG ATAG G C		
		A A GT		
GAM1384	KIAA1538	3' TTCCAGAAATGTGGTGGT	35436	CT C
		ACCATTAC AT CTGGAA		
		TGGTGGTG TA GACCTT		
		_ A		
GAM1384	KIAA1644	3' GTTCCCAGGGTGAGTGG	41202	ACC A
		CCATT TATCCTGG AAC		
		GGTGA GTGGGACC TTG		
		_ C		
GAM1384	S164	3' TTTCCCAGAGCATGGTGTT	30484	TACCTA CT
		AACACCAT TC GAAA		

	TTGTGGTA	AG CCTTT		
	CG____	AC		
GAM1384 STK33	5'	TTTCCAGGATGGTAATAGGT	31496	_ T
		ACC ATTACC ATCCTGGAAA		
		TGG TAATGG TAGGACCTTT		
		A _		
GAM1384 LOC118611	5'	CAGGAAGACAATGGTGTT	37186	AC A
		AACACCATT CT TCCTG		
		TTGTGGTAA GA AGGAC		
		CA _		
GAM1384 LOC124044	3'	TCCAGTGGTAATGGTG	37434	TATC
		CACCATTACC CTGGA		
		GTGGTAATGG GACCT		
		T____		
GAM1384 LOC144110	3'	CCTGGAAGGTGATGGTG	37678	A T
		CACCATTACCT TCC GG		
		GTGGTAGTGGA AGG CC		
		_ T		
GAM1384 LOC149832	5'	CTTTGAAGGAATGGTGTT	41080	A A CT
		AACACCATT CCT TC GG		
		TTGTGGTAA GGA AG TC		
		_ _ TT		
GAM1384 LOC155038	3'	TTTCAAGACAGTGGTGTT	39534	ACCTA C
		AACACCATT TC TGGAA		
		TTGTGGTGA AG ACTTT		
		C____ A		
GAM1384 LOC220020	5'	TTTCCAGGATGTTTGTGT	44868	CATT CT
		ACAC AC ATCCTGGAAA		
		TGTG TG TAGGACCTTT		
		TT__ _		
GAM1384 LOC253842	3'	TCTTGTAATAGGTGATAATGTT	46505	CC CCT_
		AACA ATTACCTAT GGA		
		TTGT TAGTGGATA TCT		
		AA ATGT		
GAM1384 LOC255475	5'	TTCCCTTGGGAATGGTGTT	46605	A TATCCT
		AACACCATT CC GGAA		
		TTGTGGTAA GG CCTT		
		_ TTC__		
GAM1384 LOC91263	3'	TCCAGCGTGATGGTGTT	32595	CTATC
		AACACCATTAC CTGGA		

TTGTGGTAGTG GACCT
 C____
 GAM1384 LOC91818 3' GTTCCAGTGGACACAAGGTG 33406 ATTAC_ TC
 CACC CTA CTGGAAAC
 |||| ||| |||||
 GTGG GGT GACCTTTG
 AACACA ____
 GAM1384 LOC91923 5' TTTCCCTAATTAATGGTGTT 33546 CC TCCT
 AACACCATTA TA GGAAA
 ||||| || ||||
 TTGTGGTAAT AT CCTTT
 TA C____
 GAM1385 ADORA1 3' GAGGAGCCTGGAGTGTA 6328 G CA A
 TACG CT CCA GCTCCTC
 ||| || ||| |||||
 ATGT GA GGT CGAGGAG
 _ _ C
 GAM1385 ALK 5' GAAGAGCTTGGAGGAGCC 36321 A_ C
 GGCTC CCAAGCTC TC
 |||| ||||| ||
 CCGAG GGTTCGAG AG
 GA A
 GAM1385 FRAT2 3' GGAGGAGCTTAGTAAGTGGTG 14372 G C C
 TAC GCT AC AAGCTCCTCC
 ||| ||| || |||||
 GTG TGA TG TTCGAGGAGG
 G A A
 GAM1385 FLJ10726 3' AGGAGCTTTGGCCATATA 20056 C T CC
 TATA GGC CA AAGCTCCT
 |||| ||| || |||||
 ATAT CCG GT TTCGAGGA
 A _ _
 GAM1385 LOC219848 3' GGAGGAGCCCGGTGTCTCTATA 43987 C CT AA
 TATA GG CACC GCTCCTCC
 |||| || ||| |||||
 ATAT TC GTGG CGAGGAGG
 C T_ CC
 GAM1385 LOC255031 5' GGAAGAGCTTGGGCGACATG 46432 GC A_ C
 CG TC CCAAGCTC TCC
 || || ||||| |||
 GT AG GGTTCGAG AGG
 AC CG A
 GAM1386 ATP11A 3' CACATGTACGCACCACA 37803 A TACGT
 TGTG TGC GTGCA TGTG
 ||| ||||| |||
 ACAC ACGCATGT ACAC
 C _____
 GAM1386 ITGAM 3' ACGTGTGCACACACCACA 6247 A C
 TGTG TG GTGCATACGT
 |||| || |||||

ACAC AC CACGTGTGCA
 C A
 GAM1386 CSR1 3' CATACATATGCACGCACACA 18357 A C T
 TGTG TCGTGCATA GT GTG
 |||| ||||| || |||
 ACAC ACGCACGTAT CA TAC
 _ A _
 GAM1386 CSR1 3' CGCACATGCACACATACACA 18358 _ C ACGT
 TGTG ATG GTGCAT TGTG
 |||| || ||||| ||||
 ACAC TAC CACGTA ACGC
 A A C__
 GAM1386 DNAJC6 3' CACACATGCACGCACACA 16658 A ACGT
 TGTG TCGTGCAT TGTG
 |||| ||||| ||||
 ACAC ACGCACGTA ACAC
 _ C__
 GAM1386 FLJ11618 3' CCCACAAGACCAAGCATCACA 22792 G CATACG
 TGTGATGC TG TTGTGGG
 ||||| || |||||
 ACACTACG AC AACACCC
 A CAG__
 GAM1386 KIAA0914 3' GCGCATGCACGCACACA 17036 A A
 TGTG TCGTGCAT CGT
 |||| ||||| |||
 ACAC ACGCACGTA GCG
 _ C
 GAM1386 MGC20255 3' CCCACAACCCACACACACCAC 27427 A C CATAC
 GTG TG GTG GTTGTGGG
 ||| || |||||
 CAC AC CAC CAACACCC
 C A ACC__
 GAM1386 LOC162461 3' CCCACAACACATGATAAACACA 40057 ATG__ CATAC
 TGTG CGTG GTTGTGGG
 |||| |||| |||||
 ACAC GTAC CAACACCC
 AAATA A__
 GAM1387 BCL11B 3' TAGAGGATATGAAATGCCAT 23169 A CC A
 ATG CATTTTCT ATCTT CTA
 || ||||| |||| |||
 TAC GTAAAGTA TAGGA GAT
 C _ _
 GAM1387 SCD 3' GTAATAAGATGGCTGTGGCAT 11493 A TTCAT C
 ATG CAT CCATCTTA TAC
 ||| || ||||| |||
 TAC GTG GGTAAGAAT ATG
 G TC__ A
 GAM1387 TCFL4 3' AAGTGAATGAGATGTCA 31768 C T
 TGACATTTCT CA CTT
 ||||| || |||

		ACTGTAGAGTA GT GAA		
		A _		
GAM1387 WNT5A	3'	GGAAGGACAAGAATGTCAT 9430	CA_ A	
		ATGACATTT TCC TCT		
		TACTGTAAG AGG AGG		
		AAC A		
GAM1387 ZNF161	3'	GTAGTTGGCAAGATGAAATGCC 13997	A CAT T	
A		TG CATTTTCATC CT ACTAC		
		AC GTAAAGTAG GG TGATG		
		C AAC T		
GAM1387 BZW1	3'	GAGTTGTAGATAAAATGTCAT 16128	C _ T	
		ATGACATTT ATC CA CTT		
		TACTGTAAA TAG GT GAG		
		A AT T		
GAM1387 CHORDC1	3'	AAGCAAGATGAAATGTCA 14436	CAT	
		TGACATTTTCATC CTT		
		ACTGTAAAGTAG GAA		
		AAC		
GAM1387 DKFZP434A043	3'	AGTTTGAATGAAATGTTAT 17699	CCA TT	
		ATGACATTTTCAT TC ACT		
		TATTGTAAAGTA AG TGA		
		_ TT		
GAM1387 DKFZP434L0718	3'	GTAGAGGCCAGGCTGAAATGTC 25821	T AT_ A	
AT		ATGACATTTTCA CC CTT CTAC		
		TACTGTAAAGT GG GGA GATG		
		C ACC _		
GAM1387 FLJ11827	3'	AGATGGGATGAAATTTCA 24721	C _	
		TGA ATTTTCATCC ATCT		
		ACT TAAAGTAGG TAGA		
		T G		
GAM1387 FLJ22944	3'	AGGGTAATGAAATGTCA 24781	CC	
		TGACATTTTCAT ATCTT		
		ACTGTAAAGTA TGGGA		
		A_		
GAM1387 KIAA1371	3'	GTGGCAATGAAATGCCAT 42908	A _	
		ATG CATTTTCAT CCAT		
		TAC GTAAAGTA GGTG		
		C AC		
GAM1387 KIAA1755	3'	AGAAATGAAATGTCAT 30747	CCA	
		ATGACATTTTCAT TCT		

			TACTGTAAAGTA AGA		
			A__		
GAM1387 KIAA1795	3'	AGAGATGAAATGTGCAT	35699	_	CA
		ATG ACATTTTCATC TCT			
		TAC TGTAAGTAG AGA			
		G			
GAM1387 RNAHP	3'	AGCAAGATGGACAAGGTG	14299	CA	A
		CATTT TCCATCTT CT			
		GTGGA AGGTAGAA GA			
		AC C			
GAM1387 SLC26A7	3'	AGTAAGATGTGAAATTCA	27411	C	TC
		TGA ATTTCA CATCTTACT			
		ACT TAAAGT GTAGAATGA			
		- -			
GAM1387 ZDHC5	5'	AGTAACTTTTGAAGTGTGCAT	44008		TCCATC
		ATGACATTTCA TTACT			
		TACTGTGAAGT AATGA			
		TTTCA_			
GAM1387 LOC145098	5'	AGGAGCAGATGAAATGTGCAT	37795		CA_
		ATGACATTTTCATC TCTT			
		TACTGTAAAGTAG AGGA			
		ACG			
GAM1387 LOC146795	5'	AGTTGTGAATGAAATGTC	38242	C	CTT
		GACATTTTCAT CAT ACT			
		CTGTAAAGTA GTG TGA			
		A T_			
GAM1387 LOC148266	3'	GTAGTAAGATAGTGAGCATTCA	38514	CAT	CC
	T	ATGA TTCAT ATCTTACTAC			
		TACT GAGTG TAGAATGATG			
		TAC A_			
GAM1387 LOC151579	3'	GAGTTGTAGATAAAATGTGCAT	34422	C	_ T
		ATGACATTT ATC CA CTT			
		TACTGTAAA TAG GT GAG			
		A AT T			
GAM1387 LOC152620	3'	AGCTGGACAAATGTGCAT	30174	CA	T
		ATGACATTT TCCA CT			
		TACTGTAAA AGGT GA			
		C_ C			
GAM1387 LOC199907	3'	AGCTGGATAAAAATGTCA	42657	C_	T
		TGACATTT ATCCA CT			

		ACTGTAAA TAGGT GA	
		AA C	
GAM1387	LOC255565 3'	GAGCCAGGATGAAATGTCA 45591	AT_
		TTGACATTTTCATCC CTT	
		ACTGTAAAGTAGG GAG	
		ACC	
GAM1388	DXS1283E 3'	CAAAATACACAACTTTTAGCA 35060	G _
		TGC AAGAGT TGTATTTTG	
		ACG TTTTCA ACATAAAAC	
		A AC	
GAM1388	TOPBP1 3'	CAAAATACAACTCCTCAGC 13885	_ A
		GC GA GAGTTGTATTTTG	
		CG CT CTCAACATAAAAC	
		A C	
GAM1389	DSCR3 3'	AGAATATATTTAAATGCAA 12683	GATCCAA
		TTGCATTTAAA GTTCT	
		AACGTAAATTT TAAGA	
		ATA__	
GAM1389	MGAT5 5'	CAGAACTTATTCCTCCTAAATG 8236	A_ ATCC
	TAA	TTGCATTTA AG AAGTTCTG	
		AATGTAAAT TC TTCAAGAC	
		CC CTTA	
GAM1389	PIK3CG 3'	GAAGTTGGATTTCAAATGCAA 8511	AA
		TTGCATTT AGATCCAAGTTC	
		AACGTAAA TTTAGGTTCAAG	
		C_	
GAM1389	FLJ13449 3'	CAGAACTTGGATTTCCTTAAAT 23759	_
		ATTTAA AGATCCAAGTTCTG	
		TAAATT TTTAGGTTCAAGAC	
		C	
GAM1389	KIAA1025 3'	CAGAACCTTTTTTAAATGTAA 31995	TCCAA
		TTGCATTTAAAGA GTTCTG	
		AATGTAAATTTTT CAAGAC	
		TC__	
GAM1389	PCDH17 5'	AGATTAGATCTCTAAATGCAG 15811	A CAAGT
		TTGCATTTA AGATC TCT	
		GACGTAAAT TCTAG AGA	
		C ATT__	
GAM1389	ZNF384 3'	AGAAAAGGGAGCCCCAAATGCA 28542	AAAGA AAG
	A	TTGCATTT TCC TTCT	

			AACGTAAA AGG AAGA		
			CCCCG GAA		
GAM1389	LOC166042	5'	CTTAGATCTCCAAATGCAG 40199	AA	C
			TTGCATTT AGATC AAG		
			GACGTAAA TCTAG TTC		
			CC A		
GAM1389	LOC222662	3'	CAGAACTTGAATCCTTTAA 44601	_	C
			TTAAAG AT CAAGTTCTG		
			AATTTC TA GTTCAAGAC		
			C A		
GAM1390	CALU	3'	TAGGGGCCACATATTACA 6886	ATAT	G
			TGTAATAT GCC TCTA		
			ACATTATA CGG GGAT		
			CAC_ _		
GAM1390	EIF2AK3	3'	TGGATCATATATATTACA 11245	CC	
			TGTAATATATATG GTCTA		
			ACATTATATATAC TAGGT		
			—		
GAM1390	PEX3	3'	AGTTTTTGTGGGCATATATATA 9691	_	GTCT_
			TACA TGTA ATATATATGCC AAAC		
			ACAT TATATATACGG TTTGA		
			A GTGTT		
GAM1390	SIM1	3'	AGTGTGCATATATACTACA 11509	A	_ T
			TGTA TATATATGC CG CT		
			ACAT ATATATACG GT GA		
			C T _		
GAM1391	ABCD2	5'	GGAAGCTGCGAGGATTCCA 11659	CA_	A
			TGGAATCC CA CTTTT		
			ACCTTAGG GT GAAGG		
			AGC C		
GAM1391	RAD51L1	3'	GCTTAAGTCATGGAATTCTA 28576	C CA	TT
			TGGAAT CCA ACT TAGGT		
			ATCTTA GGT TGA ATTCG		
			A AC _		
GAM1391	RAD51L1	3'	GCTTAAGTCATGGAATTCTA 8787	C CA	TT
			TGGAAT CCA ACT TAGGT		
			ATCTTA GGT TGA ATTCG		
			A AC _		
GAM1391	C1orf16	3'	GACTGCTGTAGGATTTC A 16857	C	ACTTTTA
			TGGAATCC ACA GGTC		

	ACTTTAGG TGT TCAG	
	A CG_____	
GAM1391 DKFZP434C212 3'	GACCTAGATGAGAGTCCA 34170	A C CAACT
	TGGA TC CA TTTAGGTC	
	ACCT AG GT AGATCCAG	
	G A _____	
GAM1391 DKFZP566J091 3'	AGGCAGTGGTGGGATTCCA 25184	A TTTAG
	TGGAATCCCAC ACT GTCT	
	ACCTTAGGGTG TGA CGGA	
	G _____	
GAM1391 FLJ22419 5'	AGACACCGCGGTGGGATTCCA 24006	AACTTTTAG
	TGGAATCCCAC GTCT	
	ACCTTAGGGTG CAGA	
	GCGCCA_____	
GAM1391 HSPC055 5'	ATTTGAAAGCTGTGTA ACTCCA 15436	ATCC A
	TGGA CACA CTTTTAGGT	
	ACCT GTGT GAAAGTTTA	
	CAAT C	
GAM1391 IL-17RE 3'	AGACCTAGGTTGAGCAGAGCTC 29464	A_ CCA_ TT
CA	TGGA TC CAACT TAGGTCT	
	ACCT AG GTTGG ATCCAGA	
	CG ACGA _____	
GAM1391 KIAA0057 3'	GACCTGATATGGGATCCC 14619	A CAACTT
	GG ATCCCA TTAGGTC	
	CC TAGGGT AGTCCAG	
	C AT_____	
GAM1391 KIAA0447 3'	ACTCAA ACTGGGGATTCCA 35493	A ACT AG
	TGGAATCCC CA TTT GT	
	ACCTTAGGG GT AAA CA	
	_ C_ CT	
GAM1391 KIAA1855 3'	ACCCAGTCTGCCCTTGGGATTC 44350	_____ _ TTTA
CA	TGGAATCCCA CA ACT GGT	
	ACCTTAGGGT GT TGA CCA	
	TCCC C C_____	
GAM1391 KIAA1871 3'	AGACCTAGGTACTAAAATTCCA 30703	CCCACA TT
	TGGAAT ACT TAGGTCT	
	ACCTTA TGG ATCCAGA	
	AAATCA _____	
GAM1391 MGC32104 3'	ACCTAAAAGTATTAAATTCC 29503	CCCACA
	GGAAT ACTTTTAGGT	

CCTTA TGAAAATCCA
 AATTA_
 GAM1391 RPH3A 3' GGCCCAAACCTGAGATTCCA 17308 C CAACT A
 TGGAATC CA TTT GGTC
 ||||| || ||| ||||
 ACCTTAG GT AAA CCGG
 A CC__ C
 GAM1391 LOC121838 5' ACCTAAAAATGCAAATTCCA 37416 CCCA AC
 TGGAAT CA TTTTAGGT
 ||||| || |||||
 ACCTTA GT AAAATCCA
 AAC_ AA
 GAM1391 LOC145980 3' CCAAAGCTGTGGGATCACA 40648 GA A TA
 TG ATCCCACA CTTT GG
 || ||||| ||| ||
 AC TAGGGTGT GAAA CC
 AC C _
 GAM1391 LOC149703 3' AGACCCCGAGGTCTGCTGGATT 41062 CA _ TA
 CCA TGGAATCC CA ACTTT GGTCT
 ||||| || ||| ||||
 ACCTTAGG GT TGGAG CCAGA
 TC C CC
 GAM1391 LOC170395 3' GCCTATTGTGGGACTTCA 37545 A CTTT
 TGGA TCCCACAA TAGGT
 ||| ||||| ||||
 ACTT AGGGTGTT ATCCG
 C _
 GAM1392 AKAP1 3' GAATACAGCACTGCTTGC 29266 AAC TT T
 GCA AGC GT CTGTATTC
 ||| ||| || |||||
 CGT TCG CA GACATAAG
 _ T_ C
 GAM1392 HLF 3' GAACACAGAGTGTGTTTTTGCA 7904 C TGT A
 TGCAAA AGC T TCTGT TTC
 ||||| ||| ||||| |||
 ACGTTT TTG G AGACA AAG
 _ TTG C
 GAM1392 NEO1 3' GAACACAGAATGAGCCAGCA 8317 AAACA TG A
 TGC GCT TTCTGT TTC
 ||| ||| ||||| |||
 ACG CGA AAGACA AAG
 AC__ GT C
 GAM1392 PMM2 3' GAAACCAGGACAGGCCATCTGC 35680 AACA TA
 A TGCA GCTTGTTCTG TTC
 ||| ||||| |||
 ACGT CGGACAGGAC AAG
 CTAC CA
 GAM1392 TTN 3' ATAAAGCAAGCTATCTGCA 28502 AAC C
 TGCA AGCTTGTT TGT
 ||| ||||| |||

			ACGT TCGAACGA ATA		
			CTA A		
GAM1392	TTN	3'	ATAAAGCAAGCTATCTGCA 28507	AAC	C
			TGCA AGCTTGTT TGT		
			ACGT TCGAACGA ATA		
			CTA A		
GAM1392	TTN	3'	ATAAAGCAAGCTATCTGCA 28517	AAC	C
			TGCA AGCTTGTT TGT		
			ACGT TCGAACGA ATA		
			CTA A		
GAM1392	BIA2	3'	GAATATGAAATATTTGCA 35318	CAGCT	CT
			TGCAAA TGTT GTATTC		
			ACGTTT ATAA TATAAG		
			_____ AG		
GAM1392	CDC14B	3'	GGAACACAGAGTGCTTCTCCCG 9761	AAAC__	TTG A
	CA		TGC AGC TTCTGT TTCC		
			ACG TCG GAGACA AAGG		
			CCCTCT T__ C		
GAM1392	FLJ13441	3'	GAAACAGAGCACAGGCTGTCTG 23392	A	__ A
	CA		TGCA ACAGCT TGTTCTGT TTC		
			ACGT TGTCGG ACGAGACA AAG		
			C AC _		
GAM1392	FLJ22529	3'	GGAATACAGGCATGAGCCACCG 24171	AAACA	TG_
	CA		TGC GCT T TCTGTATTCC		
			ACG CGA A GGACATAAGG		
			CCAC_ GT C		
GAM1392	KIAA0738	3'	GGAATTGAACAGGCTGCTTGCA 16279	A	TGT
			TGCAA CAGCTTGTTT ATTCC		
			ACGTT GTCGGACAAG TAAGG		
			C T__		
GAM1392	KIAA1764	5'	GAATTTGGGCAAGCTATTT 34354	C	TGT
			AAA AGCTTGTTT ATTCT		
			TTT TCGAACGGG TAAG		
			A TT_		
GAM1392	LAGY	3'	AATACAGAAGGGGTGTTTG 29231	G	G
			CAAACA CTT TTCTGTATT		
			GTTTGT GGG AAGACATAA		
			_ G		
GAM1392	LAGY	3'	AATACAGAAGGGGTGTTTG 29233	G	G
			CAAACA CTT TTCTGTATT		

			GTTTGT GGG AAGACATAA		
			— G		
GAM1392	LAGY	3'	AATACAGAAAGGGGTGTTTG 26245	G G	
			CAAACA CTT TTCTGTATT		
			GTTTGT GGG AAGACATAA		
			— G		
GAM1392	MRPS11	5'	GGAAGTGTCTAGAACGAACCATT 23127	AAACAGC	— —
	CGCA		TGC TTGTTCT GTA TTCC		
			ACG AGCAAGA CGT AAGG		
			CTTACCA T C		
GAM1392	MRPS11	5'	GGAAGTGTCTAGAACGAACCATT 45377	AAACAGC	— —
	CGCA		TGC TTGTTCT GTA TTCC		
			ACG AGCAAGA CGT AAGG		
			CTTACCA T C		
GAM1392	TNRC3	5'	CAGAACAAAGCTGTTCTCA 12493	CA	
			TG AACAGCTTGTCTG		
			AC TTGTCGAACAAGAC		
			TC		
GAM1392	LOC146958	3'	AATACAAAAAGTATGTTTGTA 40770	— GTTC	
			TGCAAACA GCTT TGTATT		
			ATGTTTGT TGAA ACATAA		
			A AA__		
GAM1392	LOC150622	5'	GAAAGTGAACAAGCCACCTGC 38996	AACA T A	
			GCA GCTTGTTT GT TTC		
			CGT CGAACAAG CA AAG		
			CCAC T _		
GAM1392	LOC196540	3'	GAATACAGAACAGCTCCTGGCA 43150	AAAC T	
			TGC AGCT GTTCTGTATTC		
			ACG TCGA CAAGACATAAG		
			GTCC _		
GAM1392	LOC200047	5'	GAATACTTGGAAGTTGTTTAC 42698	C G T_	
	A		TG AAACAGCTT TTC GTATTC		
			AC TTTGTTGAA AGG CATAAG		
			A _ TT		
GAM1392	LOC92597	3'	AATACAAAAATGAGTTTGTGCA 34671	CA TG C_	
			TGCAAA GCT TT TGTATT		
			ACGTTT TGA AA ACATAA		
			_ GT AA		
GAM1393	CLCA3	3'	GGGACATCAAGTAACA 11354	A AGCTTG	
			TGTTA CTTGATG CCC		

			ACAAT GA	ACTAC	GGG	
			—	A	—	
GAM1393	EPM2A	3'	AGGGCAAGCTGGAGTTAATA	12224		GATG
			TGTTAACTT AGCTTGCCCT			
			ATAATTGAG TCGAACGGGA			
			G	—		
GAM1393	MAGEA10	5'	AGGGTGACTCAAGTCAACA	22034	A TGA	CTG
			TGTTACT TGAGTCCCT			
			ACAA TGA ACTC A GGGA			
			C — — GT			
GAM1393	MBD3	3'	GAGGGCAGGTTCCAAGCCACA	10020	TAA	AT
			TGT CTTG GAGCTTGCCCTC			
			ACA GAAC CTTGGACGGGAG			
			CC_ —			
GAM1393	PCDH11X	3'	AAGCAGTTCAAGTTGACA	26799		TGA
			TGTTAACTTGA GCTT			
			ACAGTTGAACT CGAA			
			TGA			
GAM1393	PCDH11X	3'	AAGCAGTTCAAGTTGACA	26784		TGA
			TGTTAACTTGA GCTT			
			ACAGTTGAACT CGAA			
			TGA			
GAM1393	PCDH11Y	3'	AAGCAGTTCAAGTTGACA	26818		TGA
			TGTTAACTTGA GCTT			
			ACAGTTGAACT CGAA			
			TGA			
GAM1393	SMG1	3'	GCAAGCTCACCGCCTGAACA	17477	AACT	A
			TGTT TG TGAGCTTGC			
			ACAA GC ACTCGAACG			
			GTCC C			
GAM1393	AD-020	3'	AAGTCATCAAGTAAACA	21337	A	G
			TGTT ACTTGATGA CTT			
			ACAA TGA	ACTACT GAA		
			A	—		
GAM1393	AD-020	3'	AAGTCATCAAGTAAACA	29867	A	G
			TGTT ACTTGATGA CTT			
			ACAA TGA	ACTACT GAA		
			A	—		
GAM1393	CHST4	3'	AGAGCAAGCTCTTAAGTTCACA	12334	T	T C
			TGT AACTTGA GAGCTTGC CT			

ACA TTGAATT CTCGAACG GA
 C _ A
 GAM1393 FLJ00024 5' GAGGGCAAGATCCAAG 31893 AT G
 CTTG GA CTTGCCCTC
 |||| || |||||
 GAAC CT GAACGGGAG
 _ A
 GAM1393 LOC203297 5' GAGGGCAAGATCCAAG 37137 AT G
 CTTG GA CTTGCCCTC
 |||| || |||||
 GAAC CT GAACGGGAG
 _ A
 GAM1394 PIK3R3 3' CATGTGCTTCCATACAGTG 30602 CA TGTT
 TAC TATGG GGCACGTG
 || |||| |||||
 GTG ATACC TCGTGTAC
 AC T__
 GAM1394 SGCB 3' GCTCAACATCATATAGTA 5743 C _
 TAC ATATGGTGTTG GC
 || ||||| ||
 ATG TATACTACAAC CG
 A T
 GAM1394 DCAMKL1 3' CACATGACCAATCATATGGTA 11112 GT _ C
 TACCATATGGT TGG CA GTG
 ||||| || || ||
 ATGGTATACTA ACC GT CAC
 _ A A
 GAM1394 FLJ12517 3' GCACGTGCCATGGCTATGT 23269 GT
 ATATGGT TGGCACGTGC
 |||| |||||
 TGTATCG ACCGTGCACG
 GT
 GAM1394 FLJ14936 3' GCACACAACAGAACCATAGG 26669 A G GCAC
 CC TATGGT TTG GTGC
 || |||| || ||
 GG ATACCA GAC CACG
 _ A AACA
 GAM1394 HH114 5' CACATGCCAAACATCATA 26249 _ C
 TATGGTGTT GGCA GTG
 |||| || || ||
 ATACTACAA CCGT CAC
 A A
 GAM1394 TTY7 3' CACACGCTCACATTGGTA 25672 TATG T AC
 TACCA GTGT GGC GTG
 |||| || || ||
 ATGGT TACA TCG CAC
 _ C CA
 GAM1394 LOC147054 5' GCACGTGCGCACACACACA 40793 _ _ _
 TG GTGT TG GCACGTGC
 || || || || || ||

			AC CACA AC CGTGCACG		
			A C G		
GAM1394	LOC147929	5'	CGCGTGTGCACCACAGG	38420	ATA TG
			CC TGGTGT GCACGTG		
			GG ACCACG TGTGCGC		
			AC_ _		
GAM1394	LOC90591	3'	GCATTGAAACCCACATGGTA	31759	A T GG C
			TACCAT TGG GTT CA GTGC		
			ATGGTA ACC CAA GT TACG		
			C _ A_ _		
GAM1395	CHAC	3'	TGCTATTGATTTCTCTCT	27141	CCC
			AGAGAGAAATTG AGCA		
			TCTCTCTTTAGT TCGT		
			TA_		
GAM1395	EPHA3	3'	AGTGCCAAATGCTCTCTCA	11739	AAA CCCA
			TGAGAGAG TTG GCACT		
			ACTCTCTC AAC CGTGA		
			GTA _		
GAM1395	EPHB2	3'	AAGTGTGTGATTTCTCTCCCA	10729	A TG CCA
			TG GAGAGAAAT C GCACTT		
			AC CTCTCTTTA G TGTGAA		
			C GT _		
GAM1395	RORB	3'	TGTAAACATTTTCTCTCTCA	13788	T CCCA
			TGAGAGAGAAA TG GCA		
			ACTCTCTCTTT AC TGT		
			T AAA_		
GAM1395	CHST3	3'	AAGTGCTGGCCGTTCTT	10473	ATT C
			GAGAA GCC AGCACTT		
			TTCTT CGG TCGTGAA		
			GC_ _		
GAM1395	CHST3	3'	CTGGACAATTTCTCTGTCA	10481	G C
			TGA AGAGAAATTG CCAG		
			ACT TCTCTTTAAC GGTC		
			G A		
GAM1395	FLJ20069	3'	TGGAATTTCTCTTCA	19159	G GC
			TGA AGAGAAATT CCA		
			ACT TCTCTTTAA GGT		
			_ _		
GAM1395	FLJ23042	3'	TTGGGCAACCCCTCCCTCA	24798	A AAA_
			TGAG GAG TTGCCAG		

		ACTC CTC AACGGGTT		
		C CCCC		
GAM1395 KIAA0232	3'	CTGTGTTTTCTCTCTTA 36036	TT C	
		TGAGAGAGAAA GC CAG		
		ATTCTCTCTTT TG GTC		
		— T		
GAM1395 KIAA0478	3'	AAGCACTGAGAAATTCTTTCTC 16973	A GCC CA	
A		TGAGAGAGAA TT CAG CTT		
		ACTCTTTCTT AA GTC GAA		
		— AGA AC		
GAM1395 KIAA1319	3'	AAGTGCCGACACCTCCCTCA 21865	A AAA CCCA	
		TGAG GAG TTG GCACTT		
		ACTC CTC AGC CGTGAA		
		C CAC —		
GAM1395 LOC139673	3'	TTGGGCATTTTCTCTCTCA 37406	T	
		TGAGAGAGAAA TGCCCAG		
		ACTCTCTCTTT ACGGGTT		
		T		
GAM1395 LOC145317	5'	AGTGCTGAAGGACTCCTCA 40529	A AAATTG —	
		TGAG GAG CC CAGCACT		
		ACTC CTC GG GTCGTGA		
		— A — AA		
GAM1396 FKRP	3'	CGCCCAGGGCCTGTGTTCCA 23592	A T TC AA	
		TG GA CA CAGGCCCTG CG		
		AC CT GT GTCCGGGAC GC		
		— T — CC		
GAM1396 PCTP	3'	CACAGCCTTGATGATCTCA 22193	C CC	
		TGAGATCATC AGGC TG		
		ACTCTAGTAG TCCG AC		
		T AC		
GAM1396 RAGE	5'	GCGTTCAGGGCCTGACGGTT 15495	ATC	
		GATC CAGGCCCTGAACGC		
		TTGG GTCCGGGACTTGCG		
		CA_		
GAM1396 STK31	5'	TCCGGCCTGAATGATCTC 26761	C CT	
		GAGATCAT CAGGCC GA		
		CTCTAGTA GTCCGG CT		
		A C_		
GAM1396 KIAA0293	5'	GCGCTCAGGGCCCGGGCGG 30396	AT A A	
		TC CC GGCCCTGA CGC		

		GG GG CCGGGACT GCG		
		CG C C		
GAM1396 KIAA1023	3'	CAGGTCCCCAAATGATCTTA	19088	CCA_ C
		TGAGATCAT GG CCTG		
		ATTCTAGTA CC GGAC		
		AACC T		
GAM1396 MGC16384	3'	AGGGTAACCAGATGATCTCA	27593	CAG__
		TGAGATCATC GCCCT		
		ACTCTAGTAG TGGGA		
		ACCAA		
GAM1396 MGC16386	3'	CACTGCCTGGATGCATCTCA	27958	_ CC
		TGAGAT CATCCAGGC TG		
		ACTCTA GTAGGTCCG AC		
		C TC		
GAM1396 MGC4549	3'	GGGGCCTGAACTGATCTCA	26171	TC_
		TGAGATCA CAGGCCCT		
		ACTCTAGT GTCCGGGG		
		CAA		
GAM1396 SYNPO2	3'	TCATTTCTGAGTGATCTCA	35593	TC CCC
		TGAGATCA CAGG TGA		
		ACTCTAGT GTCT ACT		
		GA TT_		
GAM1396 LOC146229	3'	CAGCTGGATGACCTCA	38108	A GCC
		TGAG TCATCCAG CTG		
		ACTC AGTAGGTC GAC		
		C _		
GAM1396 LOC151816	5'	TCAGGCCTGGACAGCCTCA	41390	ATCA C
		TGAG TCCAGGCC TGA		
		ACTC AGGTCCGG ACT		
		CGAC _		
GAM1396 LOC154449	5'	GGTGGCCTGGACAATCCA	39476	A CA _
		TG GAT TCCAGGCC CT		
		AC CTA AGGTCCGG GG		
		_ AC T		
GAM1396 LOC155179	3'	CAGGTCCCCAAATGATCTTA	39555	CCA_ C
		TGAGATCAT GG CCTG		
		ATTCTAGTA CC GGAC		
		AACC T		
GAM1396 LOC158056	5'	GCGTCGTGGGTCTGGACGACCT	39716	A A _ A
CA		TGAG TC TCCAGGCC TGA CGC		

ACTC AG AGGTCTGGG GCT GCG
 C C T _
 GAM1396 LOC158525 5' TTCACCCAAATGGTCTCA 39859 CCA CCC
 TGAGATCAT GG TGAA
 ||||| || |||
 ACTCTGGTA CC ACTT
 AA_ C_
 GAM1396 LOC197196 5' AGGCTGCTTGGATGACCTCA 43198 A _
 TGAG TCATCCAGGC CCT
 ||| ||||| |||
 ACTC AGTAGGTTCTG GGA
 C TC
 GAM1396 LOC221486 5' GCGTTCAGACCCAGACGATGCC 43745 AG A CA CC
 A TG ATC TC GG CTGAACGC
 || ||| || || |||||
 AC TAG AG CC GACTTGCG
 CG C AC A_
 GAM1396 LOC51200 3' TCTGGCCTGGATAATCTCA 18483 C CT
 TGAGAT ATCCAGGCC GA
 ||||| ||||| ||
 ACTCTA TAGGTCCGG CT
 A T_
 GAM1396 LOC90381 3' CAGGGCCTCGATGGCCTCA 31343 AT C
 TGAG CATC AGGCCCTG
 ||| ||| |||||
 ACTC GTAG TCCGGGAC
 CG C
 GAM1397 DPH2L2 5' ACTCAGGCCCCGAAGCTGTCC 7057 CAACA AA
 GGACAGTT GT TGAGT
 ||||| || |||||
 CCTGTCTGA CG ACTCA
 AGCCC G_
 GAM1397 LRP4 3' CTCCTGTGTAACCTCCTA 32199 C TAAT
 TAGGA AGTTCAACAG GAG
 ||||| ||||| |||
 ATCCT TCAAGTTGTC TTC
 _ C_
 GAM1397 PSEN1 3' ACTCATTACCGTCTGTGATTGC 5454 A _ _ A
 C GG CAGTT CA AC GTAATGAGT
 || |||| || || |||||
 CC GTTAG GT TG CATTACTCA
 _ T C C
 GAM1397 PSEN1 3' ACTCATTACCGTCTGTGATTGC 14232 A _ _ A
 C GG CAGTT CA AC GTAATGAGT
 || |||| || || |||||
 CC GTTAG GT TG CATTACTCA
 _ T C C
 GAM1397 SOX10 3' TCATTACTGTCTCCTG 13825 CAGTTCA
 TAGGA ACAGTAATGA
 |||| |||||

GTCCT TGTCATTACT
 C_____
 GAM1397 EIF5 3' ACTTTGCTCTATTGAACTGTCT 7697 C TAAT
 TA TAGGACAGTTCAA AG GAGT
 ||||| || ||||
 ATTCTGTCAAGTT TC TTCA
 A TCGT
 GAM1397 KIAA0179 3' ACTCATTACCGTATTCGCC 32365 AC TCA A
 GG AGT AC GTAATGAGT
 || || || |||||
 CC TTA TG CATTACTCA
 GC ____ C
 GAM1397 KIAA0215 3' CTCACTACTGTCTTCCT 16382 C TTCA A
 AGGA AG ACAGTA TGAG
 ||| || ||||| ||||
 TCCT TC TGTCAT ACTC
 _ ____ C
 GAM1397 KIAA0459 3' TTCAGCGCTGAACTGTACTA 30582 G ACA AA
 TAG ACAGTTCA GT TGAG
 || ||||| || ||||
 ATC TGTCAAGT CG ACTT
 A ____ CG
 GAM1397 KIAA1814 3' ACTCCAGACACTGAACTGTCCT 34836 ACA AAT
 AGGACAGTTCA GT GAGT
 ||||| || ||||
 TCCTGTCAAGT CA CTCA
 CA_ GAC
 GAM1397 TRAF3 3' ACTCGGAGATGCTAACTGTCT 30038 CAA GTAA
 TA TAGGACAGTT CA TGAGT
 ||||| || ||||
 ATTCTGTCAA GT GCTCA
 ATC AGAG
 GAM1398 ATP1B2 3' ACCCCAAAGGTATTTTGA 7387 AGGAA C____
 TCAAAAGT GCT GGGGT
 ||||| || ||||
 AGTTTTTA TGG CCCA
 ____ AAA
 GAM1398 CNTNAP2 3' ACCCTGCTTCATACTCTTGA 15412 A G TC
 TCAA AGTA GAAGC GGGGT
 ||| ||| |||| ||||
 AGTT TCAT CTTCG TCCA
 C A ____
 GAM1398 CTSL 5' ACCCCGAACTCTGCTGGCCTTG 7628 A____ GA C
 A TCAA AGTAG AG TCGGGGT
 ||| |||| || |||||
 AGTT TCGTC TC AGCCCCA
 CCGG ____ A
 GAM1398 GATA2 3' ACCCCCTCGCCTCCTACTCTGA 7801 AA A TC_
 TCA AGTAGGA GC GGGGT
 || ||||| || ||||

AGT TCATCCT CG CCCCA
 C_ C CTC
 GAM1398 IL1A 3' CTGTTTGCCTTCTACTTTT 31307 A T_
 AAAAGTAGGA GC CGG
 ||||| || ||
 TTTTCATCTT CG GTC
 C TTT
 GAM1398 IMPDH1 3' ACCCCAGTGTCCACTTTTGG 6577 A A C
 TCAAAAGT GGA GCT GGGGT
 ||||| || || ||||
 GGTTTCA CCT TGA CCCCA
 _ G _
 GAM1398 PCSK1 3' ACCTTCTGGCTTCCTTCT 6023 T C_
 AG AGGAAGCT GGGGT
 || ||||| ||||
 TC TCCTTCGG TTCCA
 T TC
 GAM1398 BICD2 3' CCTGCCTTCCCACATTCTGA 34851 A _ A CT
 TCA AA GT GGAAG CGGG
 || || |||| ||||
 AGT TT CA CCTTC GTCC
 C A C C_
 GAM1398 FLJ31709 3' CCTGTGGCCGCCACTTTTGA 29456 A AA _
 TCAAAAGT GG GCT CGGG
 ||||| || || ||||
 AGTTTCA CC CGG GTCC
 _ GC T
 GAM1398 KIAA0285 3' ACCCCAGCCCCCAGCTCTGA 16745 AA A AA C
 TCA AGT GG GCT GGGGT
 || || || ||||
 AGT TCG CC CGA CCCCA
 C_ A CC _
 GAM1398 KIAA0367 3' GCCCACCTCCACTTTTGA 33423 A AGCTCG
 TCAAAAGT GGA GGGT
 ||||| || ||||
 AGTTTCA CCT CCG
 _ CCA_
 GAM1398 KIAA1649 3' TTTGTTATTCTACCTTTGA 26114 A GCT
 TCAAA GTAGGAA CGGG
 |||| |||| ||||
 AGTTT CATCCTT GTTT
 C ATT
 GAM1398 MGC2306 3' ACCCCCTCGCCTCCTACTCTGA 26350 AA A TC_
 TCA AGTAGGA GC GGGGT
 || ||||| || ||||
 AGT TCATCCT CG CCCCA
 C_ C CTC
 GAM1398 POMT2 5' ACCCCGAGCTGCCCTCTT 15034 T A_
 AAG AGG AGCTCGGGGT
 || || |||||

TTC TCC TCGAGCCCCA
 _ CG
 GAM1398 PRO2032 3' ACCCTTTAATCCAACTTTTGA 20684 A AGCTC
 TCAAAAAGT GGA GGGGT
 ||||| || ||||
 AGTTTTCA CCT TCCCA
 A AATT_

GAM1398 RAB20 5' CGCGCTTCCTCTCTTGA 19464 A T T
 TCAA AG AGGAAGC CG
 ||| || ||||| ||
 AGTT TC TCCTTCG GC
 C _ C

GAM1398 TPD52 3' CCTGTCTCCTACTTTGA 11531 A A CT
 TCAAA GTAGGA G CGGG
 |||| ||||| | ||||
 AGTTT CATCCT C GTCC
 _ _ T_

GAM1398 LOC115399 3' ACCCCGAGCTGTCCCTGCCTGA 36344 AAA A__
 TCA GTAGG AGCTCGGGGT
 || |||| ||||| ||||
 AGT CGTCC TCGAGCCCCA
 C__ CTG

GAM1398 LOC146243 3' ACCCCCACTCCTATCCTGA 40674 AAA A CTC
 TCA GTAGGA G GGGGT
 || ||||| | ||||
 AGT TATCCT C CCCC
 CC_ _ AC_

GAM1398 LOC148293 3' CCCGATCCTTCTTCTGA 38517 A T AGC
 TCA AAG AGGA TCGGG
 ||| ||| |||| ||||
 AGT TTC TCCT AGCCC
 C T _

GAM1398 LOC256073 5' ACCCCTTCTCTCCTACCTCTGA 46227 AAA _ CTC
 TCA GTAGGA AG GGGGT
 || ||||| || ||||
 AGT CATCCT TC CCCC
 CTC C TT_

GAM1399 MPP6 5' AACTACGAGCCACGAGTTTGCA 18566 T GCATAA
 G CTGCAG CT CTCGTAGTT
 ||||| || ||||| ||||
 GACGTT GA GAGCATCAA
 T GCACC_

GAM1399 FLJ10326 3' AACCACGAGAGATGACTGCAG 19829 TGCATAA A
 CTGCAGTC CTCGT GTT
 ||||| ||||| ||||
 GACGTCAG GAGCA CAA
 TAGA__ C

GAM1399 KIAA1111 3' AGCTACCATGCAGGCCACAG 46018 CA AACTC
 CTG GTCTGCAT GTAGTT
 || ||||| |||||

			GAC CGGACGTA	CATCGA		
			AC	C_____		
GAM1399	MGC32104	3'	GCTATTTG	CAGACTACAG	29507	C TAACTC
			CTG AGTCTGCA	GTAGT		
			GAC TCAGACGT	TATCG		
			A	T_____		
GAM1400	KIAA0379	3'	CTCATTTG	ACACACTATTAGA	33811	ACA C
			TTTAATGGTGTG	TCAAA GAG		
			AGATTATCACAC	AGTTT CTC		
			_____	A		
GAM1400	KIAA1610	3'	CTCATTTG	ATGTATTAATCAT	33340	GTG_ C
			ATGGT	ACATCAAA GAG		
			TACTA	TGTAGTTT CTC		
			ATTA	A		
GAM1401	HIF1A	3'	TGGGTAAAGCC	ATTTAC	7269	TC A
			GT AAT GCTTT	ACCCA		
			CA TTA CGAAATGGGT			
			T_	C		
GAM1401	KCNS2	3'	AGGCTGTC	CAGACTGACCTGTAA	33897	T _____
			TTACAGGT CA	ATAGCTT		
			AATGTCCA GT	TGTCGGA		
			_	CAGAC		
GAM1401	RB1CC1	3'	TAAAGATTG	AACCTGTAA	16632	TAG
			TTACAGGTTCAA	CTTTA		
			AATGTCCAAGTT	GAAAT		
			TA_			
GAM1401	SC5DL	3'	TGAAGTTACAA	ACCTGTAA	43697	CAA
			TTACAGGTT	TAGCTTTA		
			AATGTCCAA	ATTGAAGT		
			AC_			
GAM1401	SFRP4	3'	TAAAACTAGGA	ACCTGTA	8939	AA C
			TACAGGTTT	TAG TTTA		
			ATGTCCAAG	ATC AAAT		
			G_	A		
GAM1401	SHOX	3'	TAGAGTCT	ATTGAACTG	6057	G _
			CAG TTCAATAG	CTTTA		
			GTC AAGTTATC	GAGAT		
			A	T		
GAM1401	SUDD	3'	GGCACGATGGCT	CAAACCTGTA	9923	CAAT TTAC_
	A		TTACAGGTT	AGCT CC		

			AATGTCCAA TCGG GG	
			AC__ TAGCAC	
GAM1401	SUV39H2	3'	TGAGTGTATGTCTGAACCTGTA 23976	_ GCTT C
	A		TTACAGGTTCA ATA TAC CA	
			AATGTCCAAGT TGT GTG GT	
			C AT__ A	
GAM1401	UBL3	3'	GAGCTACTTTTCATCTAAACCTG 13967	CAA_____
	TAA		TTACAGGTT TAGCTT	
			AATGTCCAA ATCGAG	
			ATCTACTTTC	
GAM1401	FLJ23074	3'	TGGGTAAATGTTAGAACTGTA 24650	G _ GC
	A		TTACAG TTC AATA TTTACCCA	
			AATGTC AAG TTGT AAATGGGT	
			_ A A_	
GAM1401	SRPK1	3'	AAGTTTTAATAGAACCTGTAA 9107	AAT_____
			TTACAGGTTC AGCTT	
			AATGTCCAAG TTGAA	
			ATAATT	
GAM1401	LOC158130	3'	AAAGCTATGCTTCTGTGA 34302	TTCA
			TTACAGG ATAGCTTT	
			AGTGTCT TATCGAAA	
			TCG_	
GAM1401	LOC202781	3'	AAGGTTACTCAACCTGTAA 43442	CAA
			TTACAGGTT TAGCTTT	
			AATGTCCAA ATTGGAA	
			CTC	
GAM1401	LOC221962	3'	TGGATAGAGTGAATCACACCTG 44530	TCAATA_ C
	TAA		TTACAGGT GCTTTA CCA	
			AATGTCCA TGAGAT GGT	
			CACTAAG A	
GAM1402	LOC90342	5'	AACACTGGAAATCATTTTACCA 31248	A GA _
	CA		TGTGGTAAAGT ATT CCA TGTT	
			ACACCATTTTA TAA GGT ACAA	
			C A_ C	
GAM1403	ALS2	3'	CTCAAAAGTATTGTGGCACCTC 21928	G CGAAA
	A		TGAGGTGCCA AA TTTGAG	
			ACTCCACGGT TT AAACCTC	
			G ATGA_	
GAM1403	AQP6	3'	CAAATTTAGCACCTTA 27611	CAGAACG
			TGAGGTGC AAATTTG	

			ATTCCACG	TTTAAAC		
			A_____			
GAM1403	CDH1	3'	CTCAAGCTATCCTTGACCTCA	10563	C	AACGAAA
			TGAGGTGC AG	TTTGAG		
			ACTCCACG TC	GAACTC		
			T CTATC__			
GAM1403	CYP8B1	5'	CAAAGCTCTCTGGCACCCA	10623	A	AC AA
			TG GGTGCCAGA GA	TTTG		
			AC CCACGGTCT CT	AAAC		
			— — CG			
GAM1403	EIF4G1	5'	CTCAAGGGGTTTCTGGCACCT	11396		CGAAA
			AGGTGCCAGAA	TTTGAG		
			TCCACGGTCTT	GAACTC		
			TGGG_			
GAM1403	SLC1A5	5'	CAGATTCTGGCATCCCA	12141	A	ACGAA
			TG GGTGCCAGA	ATTTG		
			AC CTACGGTCT	TAGAC		
			C			
GAM1403	SLC1A5	5'	CAGATTCTGGCATCCCA	38401	A	ACGAA
			TG GGTGCCAGA	ATTTG		
			AC CTACGGTCT	TAGAC		
			C			
GAM1403	FLJ14950	5'	CAAATTCCCCCAGCATCTCA	26670		CAGAAC A
			TGAGGTGC	GAA TTTG		
			ACTCTACG	CTT AAAC		
			ACCCC_			
GAM1403	FLJ20033	3'	CTCAACCAATTTGGCACCCCA	19126	A	ACGAAAT
			TG GGTGCCAGA	TTGAG		
			AC CCACGGTTT	AACTC		
			C	AACC_		
GAM1404	APXL	3'	TCATAGAAAATCAATCTGGTG	7355	T	CC_ T
			CACCAGATT AT	CTAT GA		
			GTGGTCTAA TA	GATA CT		
			C AAA			
GAM1404	KIAA0193	3'	TCAATAATATAAGACCTGGTGT	16546	A_	CCC
	TA		TAACACCAG TTTAT	TATTGA		
			ATTGTGGTC GAATA	ATAACT		
			CA	TA_		
GAM1404	LOC151414	3'	TCAATGGCCTTCAAATTGGTGT	39112		ATTTATCC
	TA		TAACACCAG	CTATTGA		

		ATTGTGGTT	GGTAACT		
		AAACTTCC			
GAM1404	LOC254532	5' TCAATAGGGATGATGACGG	46213	AGAT	
		CC TTATCCCTATTGA			
		GG AGTAGGGATAACT			
		CAGT			
GAM1405	FZD10	3' TGATATTTTTCATGCTCC	14053	CA	CG
		GG CATGAAAAA GTCA			
		CC GTACTTTTT TAGT			
		TC A_			
GAM1405	MAPK4	3' AATGTACACCACTCCTCATGTG	8619	AAAAC	C_
	CC	GGCACATGA GGT ACATT			
		CCGTGTACT CCA TGTA			
		CCTCA CA			
GAM1405	TIA1	3' AATGTGATAAGTTCTTATGCC	22558	CAT	AAACG
		GGCA GAA GTCACATT			
		CCGT CTT TAGTGTA			
		ATT GAA__			
GAM1405	TIA1	3' AATGTGATAAGTTCTTATGCC	22733	CAT	AAACG
		GGCA GAA GTCACATT			
		CCGT CTT TAGTGTA			
		ATT GAA__			
GAM1405	TOB1	3' TGCATCATTTTTCATTTGCC	12309	C	C _
		GGCA ATGAAAAA GGT CA			
		CCGT TACTTTTT CTA GT			
		T A C			
GAM1405	ZNF216	3' ATGTAGTTCCCATGTGCC	12619	AAA	GGTC
		GGCACATG AAC ACAT			
		CCGTGTAC TTG TGTA			
		CC_ A__			
GAM1405	DKFZP566M114	3' TGTTGAATCTTTTCATGTGCC	25815	ACGG	_
		GGCACATGAAAA TCA CA			
		CCGTGTACTTTT AGT GT			
		CTA_ T			
GAM1405	EFA6R	3' ATGAGGCAGCTTCATGTGC	17622	AAACG	A
		GCACATGAA GTC CAT			
		CGTGTACTT CGG GTA			
		CGA__ A			
GAM1405	FLJ23816	5' AATGTGACCACCGTCAGCC	29477	ACA	AAAAC
		GGC TGA GGTACATT			

CCG ACT CCAGTGTA
 ____ GCCA_
 GAM1405 KIAA0478 5' TGGCTCATGTTTCCATGTGCC 16991 _ AAC_
 GGCACATG AAA GGTCA
 ||||| || ||||
 CCGTGTAC TTT TCGGT
 C GTAC
 GAM1405 KIAA1871 3' AATGTGGGAACTCTTCATGTG 30701 AAACGG_
 CACATGAA TCACATT
 ||||| |||||
 GTGTACTT GGTGTAA
 CTCAAAG
 GAM1405 MGC22014 3' AATGTGACCGTCTGTATGACCC 32214 CA AAAA
 G CGG CATG ACGGTCACATT
 || ||| |||||
 GCC GTAT TGCCAGTGTA
 CA GTC_
 GAM1405 PRKWNK2 3' AATGTGACAATATTTTCATCAC 43516 CAC ACG_
 CG CGG ATGAAAA GTCACATT
 || ||||| |||||
 GCC TACTTTT CAGTGTA
 AC_ ATAA
 GAM1405 SPRY2 3' GCTTTTTGTCCATGTGCCG 12455 AA_ C
 CGGCACATG AAA GGT
 ||||| || |||
 GCCGTGTAC TTT TCG
 CTG T
 GAM1405 LOC122786 3' TGA CTGTTTCTCATGTGCC 36701 _
 GGCACATGA AAAACGGTCA
 ||||| |||||
 CCGTGTACT TTTTGTCA GT
 C
 GAM1405 LOC203275 3' GCTGTTTTCATGACCG 43026 CA A
 CGG CATG AAAACGGT
 || ||| |||||
 GCC GTAC TTTTGTCTG
 A_ C
 GAM1405 LOC257319 3' AATGTTAGACTTTTTCATCTGC 45828 C AC _
 C GGCA ATGAAAA GGTC ACATT
 ||| ||||| ||| |||||
 CCGT TACTTTT TCAG TGTA
 C _ AT
 GAM1406 DDX3 3' AAGACAGTACAAAAACAC 7032 A G TCC
 GTGT TTTG TGCT GTCTT
 ||| ||| ||| |||||
 CACA AAAC ATGA CAGAA
 A _ _
 GAM1406 ARG99 3' GAAGACGAAAACAGCAAA 25669 G C C
 TTTG TG TT CGTCTTC
 ||| || || |||||

			AAAC AC AA GCAGAAG		
			G A A		
GAM1406	FLJ23462	3'	AGAAACTCTACACCAAATACAC 24260	CTTCC	C
			GTGTATTTGGTG GT TTCT		
			CACATAAACCAC CA AAGA		
			ATCT_ _		
GAM1406	GOLGA1	3'	AAGACCCTTAGTACCAAATACA 7857	TCC_	
	C		GTGTATTTGGTGCT GTCTT		
			CACATAAACCATGA CAGAA		
			TTCC		
GAM1407	DHCR24	3'	AATGTGGGATTTGGAGTCAGAC 16521	ACAA	TC
	A		TGTCTGA CAG CCCACATT		
			ACAGACT GTT GGGTGTA		
			GAG_ TA		
GAM1407	GTF2H1	3'	GGGAGACTGTTGCTCAACCA 11792	TC A	_
			TG TGA CAACAGTC CCC		
			AC ACT GTTGTGAG GGG		
			CA C A		
GAM1407	C1orf24	3'	AATGTGGGAAGTGGACACCCAG 27527	AACAA_	C
	A		TCTG CAGT CCCACATT		
			AGAC GTCA GGGTGTA		
			CCACAG A		
GAM1407	FLJ10891	3'	AATGTGGCAAGTTTTTCAGACA 20226	C	AGTCC
			TGTCTGAA AAC CCACATT		
			ACAGACTT TTG GGTGTAA		
			T AAC_		
GAM1407	FLJ12666	3'	GGGACTGTTTCCAGGCA 23831	AAC	
			TGTCTG AACAGTCCC		
			ACGGAC TTGTCAGGG		
			CT_		
GAM1407	FLJ14011	5'	AATGTGGGGAAAGCTTCAATCA 22649	TC	CAACAG
			TG TGAA TCCCCACATT		
			AC ACTT AGGGGTGTAA		
			TA CGAA_		
GAM1407	HARS2	3'	AATGTGGGGCCCCTTGTTC 28077	CAGT	
			TGAACAA CCCCACATT		
			ACTTGTT GGGGTGTAA		
			CCCC		
GAM1407	KIAA0426	3'	AATGTGGGAAAGTTTTTCAGCCA 16304	T C	AG C
			TG CTGAA AAC TCCC ACATT		

	AC GACTT TTG AGGG TGTA	
	C _ AA _	
GAM1407 KIAA1871	3' AATGTGGGAAAACCTTTCAATCA 30700	TC CAAC C__
	TG TGAA AGT CCCACATT	
	AC ACTT TCA GGGTGTA	
	TA ____ AAA	
GAM1407 LOC147660	3' AATGTGGCAAATTTTTTCAGACA 38349	CAACAGTCC
	TGTCTGAA CCACATT	
	ACAGACTT GGTGTAA	
	TTTAAAC__	
GAM1407 LOC157657	3' TGCAGACTGCACATTCGGACA 39627	CAA_ CC
	TGTCTGAA CAGTC CA	
	ACAGGCTT GTCAG GT	
	ACAC AC	
GAM1407 LOC90333	3' AATGTGGCAAATTTTTTCAGACA 31217	CAACAGTCC
	TGTCTGAA CCACATT	
	ACAGACTT GGTGTAA	
	TTTAAAC__	
GAM1407 LOC91664	3' AATGTGGCAAATTTTTTCAGACA 33212	CAACAGTCC
	TGTCTGAA CCACATT	
	ACAGACTT GGTGTAA	
	TTTAAAC__	
GAM1407 LOC92283	3' AATGTGGGAAGACTTTTAGACA 34090	CAAC _
	TGTCTGAA AGTC CCCACATT	
	ACAGATTT TCAG GGGTGTA	
	____ AA	
GAM1408 ENPP3	3' CCACTGGAGATGCTGGG 11461	AACA
	TCCA ATCTCCAGTGG	
	GGGT TAGAGGTCACC	
	CG__	
GAM1408 SLC1A4	3' CCATTTCACTTCTTGGATATCA 8994	ACAATCTCC
	TGATATCCAA AGTGG	
	ACTATAGGTT TTACC	
	CTTCACT__	
GAM1408 LOC120856	3' CCACTGGAAATTATTTTG 36636	C_ C
	CAAA AAT TCCAGTGG	
	GTTT TTA AGGTCACC	
	TA A	
GAM1408 LOC158263	3' CCACTGGGGTGCCTGGAT 39798	AA AT
	ATCCA CA CTCCAGTGG	

		TAGGT GT GGGGTCACC	
		CC _	
GAM1409	FLJ10718 3'	GCTTAGAGAGAATAAGCTTCTT 20049	AA A_
		AAGAAGCTTAT TT TAAGC	
		TTCTTCGAATA AG ATTCG	
		AG AG	
GAM1409	FLJ14281 5'	GCTTATAGAAAGCTTGCTT 24452	_ ATAA
		AAG AAGCTT TTATAAGC	
		TTC TCGAA GATATTCG	
		G A_	
GAM1409	FLJ20139 3'	GGCTTACACTAAGCTTTT 19236	TAATTA
		AGAAGCTTA TAAGCC	
		TTTTCGAAT ATTCGG	
		CAC_	
GAM1409	FLJ31101 3'	GGCTTTAAATAGGCTTC 19685	AA T
		GAAGCTTAT TTA AAGCC	
		CTTCGGATA AAT TTCGG	
		_ _	
GAM1409	KIAA0964 3'	AGGGCTCACAATTTGGCTTTTT 17087	TAT ATA
		AAGAAGCT AATT AGCCCT	
		TTTTTCGG TTAA TCGGA	
		T_ CAC	
GAM1409	STX12 3'	AGGGCCCAAATGCATAAGTTTC 32982	A_ ATAA
	TT	AAGAAGCTTAT ATT GCCCT	
		TTCTTTGAATA TAA CGGGA	
		CG ACC_	
GAM1409	LOC139231 3'	GGCTTATAATCATGTGTTTT 37142	T A
		GAAGC TAT ATTATAAGCC	
		TTTTG GTA TAATATTCGG	
		T C	
GAM1409	LOC146669 5'	GGGCTTGAGAAGCTCCTT 38226	A ATAATTA
		AAG AGCTT TAAGCCC	
		TTC TCGAA GTTCGGG	
		C GA_	
GAM1409	LOC149650 3'	GGGCTCATAATTGTTGC 38794	TT A
		GC ATAATTAT AGCCC	
		CG TGTTAATA TCGGG	
		T_ C	
GAM1410	B29 3'	TCCTCTACTAAGCCCAGTTA 25685	A CA CC
		TAACTG GT AGT GGGGA	

		ATTGAC CG TCA CTCCT		
		C AA T_		
GAM1410 FANCC	3'	TCCCTCAGCCCAGACTCAGT 34907	AA_ CC	
		ACTGAGTC GT GGGGA		
		TGACTCAG CG TCCCT		
		ACC AC		
GAM1410 GNA15	3'	CCCTTGCTTGACTCAGTT 30104	CC	
		AACTGAGTCAAGT GGGG		
		TTGACTCAGTTCG TCCC		
		T_		
GAM1410 HS3ST4	3'	TCCCATCAGTTTGATTCAATTA 36371	C TCCG_	
		TAA TGAGTCAAG GGA		
		ATT ACTTAGTTT CCCT		
		A GACTA		
GAM1410 MAN2A1	5'	TCCTGCCGACTCAGTTG 8180	AAGTC	
		TAAGTGAAGT CGGGG		
		GTTGACTCAG GTCCT		
		CC_		
GAM1410 NAGA	3'	CCTGGACTTGACCAATTA 5800	C A	
		TAA TG GTCAAGTCCGGG		
		ATT AC CAGTTCAGGTCC		
		A _		
GAM1410 P4HA1	3'	TCCATGATTGATTGAGT 6626	G CGG	
		ACTGAGTCAA TC GGA		
		TGACTTAGTT AG CCT		
		_ TA_		
GAM1410 PDGFRB	3'	CCCCAGGGAAGTCAAGT 32814	CAAG _	
		AACTGAGT TCC GGGG		
		TTGACTCA GGG CCCC		
		A_ A		
GAM1410 PTGS1	3'	TCCTGGTTTGACTCAGTT 27900	T	
		AACTGAGTCAAG CCGGGG		
		TTGACTCAGTTT GGTCT		
		-		
GAM1410 PTGS1	3'	TCCTGGTTTGACTCAGTT 6679	T	
		AACTGAGTCAAG CCGGGG		
		TTGACTCAGTTT GGTCT		
		-		
GAM1410 RUNX1	3'	TCCCTCCACAAGTCAAGT 7503	CAA CC	
		AACTGAGT GT GGGGA		

		TTGACTCA CA TCCCT	
		A__ CC	
GAM1410	C20orf20 3'	TCCCTGTGTGACTCAGTT 20248	AGTC
		AACTGAGTCA CGGGGA	
		TTGACTCAGT GTCCCT	
		GT__	
GAM1410	CLIC2 5'	TCCAGGTCTGACTCAGT 6968	A T GG
		ACTGAGTCA G CC GGA	
		TGACTCAGT C GG CCT	
		T A	
GAM1410	CTDP1 3'	TCCCCGGACCAGCCCTCAGT 11073	TCAA_
		ACTGAG GTCCGGGGA	
		TGACTC CAGGCCCCCT	
		CCGAC	
GAM1410	DCTN4 3'	CCTCTTTAACTCAGTTA 33665	C TCC
		TAAGT AAG GGGG	
		ATTGACTCA TTT CTCC	
		A ____	
GAM1410	DKFZP586C1619 3'	CCAGCTTGCTCAGTTA 31017	T CC
		TAAGT CAAGT GG	
		ATTGACTC GTTCG CC	
		_ A_	
GAM1410	FLJ20574 3'	TCTTTTCTTGACTTAG 19556	TCC
		CTGAGTCAAG GGGGA	
		GATTCAGTTC TTTCT	
		T__	
GAM1410	KIAA0121 3'	TCCTTACTTCCTGCCTCAGTTA 35972	T ____ CC
		TAAGT CA AGT GGGGA	
		ATTGACTC GT TCA TTCCT	
		C CCT ____	
GAM1410	KIAA0417 3'	TCCCCTTGGACTCAACTTA 35291	CA ____
		TGAGT AGTCC GGGGA	
		ATTCA TCAGG CCCCT	
		AC TT	
GAM1410	KIAA1538 3'	CCCCATCTTTGACTCAGTT 35422	TCC
		AACTGAGTCAAG GGGG	
		TTGACTCAGTTT CCCC	
		CTA	
GAM1410	KIAA1881 5'	CCCCGGATGTGCTCAGT 45655	T A
		ACTGAG CA GTCCGGGG	

		TGACTC GT TAGGCCCC		
		_ G		
GAM1410 MYOZ2	3'	TCCCATTTC AATTCAGTTA	18693	CA TCCG
		TAAGT GAGT AG GGA		
		ATTGACTTA TT CCCT		
		AC TA__		
GAM1410 NDST4	5'	TCCAGCTTTAACTCAGTTG	22892	C_ CC
		TAAGT GAGT AAGT GGG		
		GTTGACTCA TTCG CCT		
		AT A_		
GAM1410 NPAS3	3'	CCCTGTTTGACTAAGT	22666	G TC
		ACT AGTCAAG CGGGG		
		TGA TCAGTTT GTCCC		
		A _		
GAM1410 SSB-4	3'	TCCCCAGGACACTCAGTT	28104	CAA _
		AACTGAGT GTCC GGGGA		
		TTGACTCA CAGG CCCCT		
		_ A		
GAM1410 SYNE-1	3'	TCCCCGGACTCATGAATTC	17615	_ _
		GAGT CA AGTCCGGGGA		
		CTTA GT TCAGGCCCT		
		A AC		
GAM1410 WNT10A	5'	TCCCCGGACCCCTGTGCCAG	24896	A _ A__
		CTG GT CA GTCCGGGGA		
		GAC CG GT CAGGCCCT		
		_ T CCC		
GAM1410 LOC148753	5'	TCCCCGGACTCCGGCCAG	40900	A A_
		CTG GTC AGTCCGGGGA		
		GAC CGG TCAGGCCCT		
		_ CC		
GAM1410 LOC152559	3'	CCCCAGGAGGCTCAGT	39283	AAG _
		ACTGAGTC TCC GGGG		
		TGACTCGG AGG CCCC		
		_ A		
GAM1410 LOC155032	3'	TCCCCGACGTTCTAGTTA	41748	G TCAA C
		TAAGT AG GTC GGGGA		
		ATTGA TC CAG CCCCT		
		_ TTG_ _		
GAM1410 LOC90155	3'	CCCCATGATTCAGTTA	30900	AGTCC
		TAAGT GAGTCA GGGG		

ATTGACTTAGT CCCC
 A____
 GAM1411 PVR 3' CATCATTAGCATGAACCACCCA 13253 CTA AA
 TGG GTTT ATGCTAATGATG
 ||| ||| |||||
 ACC CAAG TACGATTACTAC
 CAC ____
 GAM1411 KIAA0635 5' CATCTCAATTTACTAGCCA 16055 T GCTAAT
 TGGCTAGT TAAAT GATG
 ||||| ||| |||
 ACCGATCA ATTTA CTAC
 C ACT____
 GAM1411 KIAA0894 3' CATGTCATTTAGACTAACCA 17055 C CTA
 TGG TAGTTTAAATG ATG
 ||| ||||| |||
 ACC ATCAGATTTAC TAC
 A TG_
 GAM1411 LOC54505 5' CATCCAGTATTTAACCCAGCCA 33694 AGT AAT
 TGGCT TTAAATGCT GATG
 |||| ||||| |||
 ACCGA AATTTATGA CTAC
 CCC C_
 GAM1412 PDGFRA 3' ATGAGGCCGGATGAAACTTCTC 12880 _C _A
 A TGAGAAGTT C TTCG CC CAT
 ||||| | ||| |||
 ACTCTTCAA G AGGC GG GTA
 A T C A
 GAM1412 STK38 3' TTATGTGGAAAACCCTCA 14134 AA CCTTCG
 TGAG GTT CCACATAA
 ||| ||| |||||
 ACTC CAA GGTGTATT
 C_ AA____
 GAM1412 DKFZp434K2435 3' TGAGCAAGGGAACCTCCTCA 26001 A C_
 TGAG AGTTCCTT GC CA
 ||| ||||| |||
 ACTC TCAAGGGA CG GT
 C A A
 GAM1412 FLJ20051 3' ATTATGTGACTGGGACTCCA 21162 A A TTCGC
 TG GA GTTCC CACATAAT
 || ||||| |||||
 AC CT CAGGG GTGTATTA
 _ _ TCA____
 GAM1412 LOC221687 3' ATGGAGGAGAAGGAACTTCTCA 44302 G A_
 TGAGAAGTTCCTTC CC CAT
 ||||| ||| |||
 ACTCTTCAAGGAAG GG GTA
 A AG
 GAM1413 DKC1 3' ATGAAAGAGGCAGAGTTTATC 7043 C ATA
 GA AAATT CTCTTTCAT
 || ||||| |||||

		CT TTTGAG GAGAAAGTA	
		A ACG	
GAM1413 IL16	3'	ATGAAAAATACAGTTTGTCA 10839	TATACTC
		TGACAAACT TTTCAT	
		ACTGTTTGA AAAGTA	
		CATAA__	
GAM1413 CCNB3	3'	ATGAAAGAAAAAATATTGTCAT 27396	ACTTATAC
A		TATGACAA TCTTTCAT	
		ATACTGTT AGAAAGTA	
		ATAAAAA_	
GAM1413 DKFZP586M1120	3'	AAGGACAAGTTTGTGCAT 25317	ATAC
		ATGACAAACTT TCTTT	
		TACTGTTTGAA AGGAA	
		C__	
GAM1413 PB1	3'	ATGAAATGTGAAGTTTGTGTC 19978	A TC
		GACAAACTT TAC TTTCAT	
		CTGTTTGAA GTG AAAGTA	
		_ T_	
GAM1413 SRP9	3'	ATGTTTTGTATAAATTTGTCAT 38649	C TCTTT
G		TATGACAAA TTATAC CAT	
		GTACTGTTT AATATG GTA	
		A TTTT_	
GAM1413 LOC145268	5'	AGAGAATAAATTTGTCATA 37812	C A
		TATGACAAA TTAT CTCT	
		ATACTGTTT AATA GAGA	
		A A	
GAM1413 LOC153205	3'	ATGAAAGAGTAACCTGTC 41580	AACTTA
		GACA TACTCTTTCAT	
		CTGT ATGAGAAAGTA	
		CCA__	
GAM1414 ATP1A2	3'	GACAATATTAATTTGGAT 6366	CG GG
		ATCCAAATTAA T GTC	
		TAGGTTTAATT A CAG	
		AT A_	
GAM1414 PRG4	3'	ATCTTAATTTGGATTAA 12383	C
		TTAAATCCAAATTAA GT	
		AATTTAGGTTTAATT TA	
		C	
GAM1414 TAPBP	3'	GACCCACGGGGTAACGGGTCTA 9181	A AAATTAA
A		TTA ATCC CGTGGGTC	

		AAT TGGG GCACCCAG		
		C CAATGGG		
GAM1414	CEPT1	3' GACCTTGAATTTGGATT 12737	AACGT	
		AATCCAAATT GGGTC		
		TTAGGTTTAA TCCAG		
		GT__		
GAM1414	FLJ20086	3' ACTTAATTTTGGATTTAA 19190	TTAACG	
		TTAAATCCAAA TGGGT		
		AATTTAGGTTT ATTCA		
		TA__		
GAM1415	DEK	3' CAATAAAATAAATCTAAATCA 9535	C GGTC	
		TGATTTAGGT TGTT TATTG		
		ACTAAATCTA ATAA ATAAC		
		A AA__		
GAM1415	FLJ31300	3' CAACAGACCAACAGATAACTCA 29461	TTTAG A	
		TGA GTCTGTTGGTCT TTG		
		ACT TAGACAACCAGA AAC		
		CAA__ C		
GAM1416	DMP1	3' GGCTATGAACACGATATCA 10660	ACG ACTT	
		TGATATCGT TCG GCT		
		ACTATAGCA AGT CGG		
		CA_ AT__		
GAM1416	ELF2	3' AGCAGCTCACTACGATATCA 13742	C C C	
		TGATATCGTA GT GA TTGCT		
		ACTATAGCAT CA CT GACGA		
		_ _ C		
GAM1416	KIAA1586	5' AGCAAGTCATATTGATATTA 44347	TAC C	
		TGATATCG GT GACTTGCT		
		ATTATAGT TA CTGAACGA		
		TA_ _		
GAM1416	MAB21L2	5' CAAGCCGGCTACGGTATCA 13148	C A	
		TGATATCGTA GTCG CTTG		
		ACTATGGCAT CGGC GAAC		
		_ C		
GAM1416	MAP2K6	3' AGCAAGTTCACTACAGCATCA 25700	ATC C C	
		TGAT GTA GT GACTTGCT		
		ACTA CAT CA TTGAACGA		
		CGA _ C		
GAM1416	MAP2K6	3' AGCAAGTTCACTACAGCATCA 8640	ATC C C	
		TGAT GTA GT GACTTGCT		

ACTA CAT CA TTGAACGA
 CGA _ C
 GAM1417 FLJ20055 3' GACTCAACAACAATATCACA 19146 C CTA
 TG GATGTTGTTG AGTC
 || ||||| ||||
 AC CTATAACAAC TCAG
 A AAC
 GAM1417 KIAA0907 3' GTCGACTTATTTTATACATAGC 17278 G TGTTGC
 A TGC ATGT TAAGTCGAC
 ||| ||| |||||
 ACG TACA ATTCAGCTG
 A TATTTT
 GAM1417 LOC219722 5' GGCCACGACAACATCACA 44711 C CTAA
 TG GATGTTGTTG GTC
 || ||||| |||
 AC CTACAACAGC CGG
 A AC__
 GAM1417 LOC256113 5' GGCCAAGACAACAACATC 46261 _ AA
 GATGTTGTTG CT GTC
 ||||| || |||
 CTACAACAAC GA CGG
 A AC
 GAM1418 FLJ12409 3' AATTTGAGGAACTGGATGTGAC 24751 GT AA_
 GTC ACATC TTCCTCAAATT
 ||| ||| |||||
 CAG TG TAG AAGGAGTTTAA
 _ GTC
 GAM1418 LOC115442 5' AGGAATTGAAATACAACA 35981 C CA
 TGT GTA TCAATTCCT
 ||| ||| |||||
 ACA CAT AGTTAAGGA
 A AA
 GAM1418 LOC196074 3' TGTGGGAATTGATACACA 42322 C CA _
 TGT GTA TCAATTCCT CA
 ||| ||| ||||| ||
 ACA CAT AGTTAAGGG GT
 _ _ T
 GAM1419 ACRC 3' GTTGATGGTATTGATTGAAA 27518 TA C _
 TTTCA GTT GT CCATCAAC
 |||| ||| || |||||
 AAAGT TAG TA GGTAGTTG
 _ T T
 GAM1419 CASP8 3' TGAAGTGAACATATGAAG 27207 TCCA
 TTTCATAGTTCTG TCA
 ||||| |||
 GAAGTATCAAGT AGT
 GA__
 GAM1419 NR2E1 3' TTGATGGACAAAATGAGA 9281 AG C
 TTTTCAT TT GTCCATCAA
 ||||| || |||||

		AGAGTA AA CAGGTAGTT	
		A_ _	
GAM1419 VNN1	3'	TGATGGATTGATAGTGAAA 11041	A C
		TTTCAT GTT GTCCATCA	
		AAAGTG TAG TAGGTAGT	
		A T	
GAM1419 C6orf37	3'	GTTGATGGAAAATGGACTA 33514	___
		TAGTTCG TCCATCAAC	
		ATCAGGT AGGTAGTTG	
		AAA	
GAM1419 CCR6	3'	TGATGTGATCTATGAAG 10580	TTC _
		TTTCATAG GTC CATCA	
		GAAGTATC TAG GTAGT	
		___ T	
GAM1419 CCR6	3'	TGATGTGATCTATGAAG 25374	TTC _
		TTTCATAG GTC CATCA	
		GAAGTATC TAG GTAGT	
		___ T	
GAM1419 FLJ20208	3'	GTTGATGGGTTTCTGTGAAA 19294	TTCG
		TTTCATAG TCCATCAAC	
		AAAGTGTC GGGTAGTTG	
		TTT_	
GAM1419 OR2C3	5'	TGATGGACTGAGTGAAG 37177	AGT _
		TTTCAT TC GTCCATCA	
		GAAGTG AG CAGGTAGT	
		___ T	
GAM1419 RI58	3'	TGATGGACATGTGAAA 14798	GTTC
		TTTCATA GTCCATCA	
		AAAGTGT CAGGTAGT	
		A___	
GAM1419 TEX27	3'	TTGATGGTGGTTGAAA 22462	TAGT T
		TTTCA TCG CCATCAA	
		AAAGT GGT GGTAGTT	
		T___ _	
GAM1419 LOC123036	3'	GTTGAAAGAATTATGAAA 36718	GTCCA
		TTTCATAGTTC TCAAC	
		AAAGTATTAAG AGTTG	
		AA___	
GAM1419 LOC221773	3'	TTGATGATCACTGTGAAA 43768	TC C
		TTTCATAGT GTC ATCAA	

			AAAGTGTCA TAG TAGTT		
			C_ _		
GAM1419	LOC253584	5'	GATGGACTTAACTGTGAAA 46322	C_	
			TTTCATAGTT GTCCATC		
			AAAGTGTCAA CAGGTAG		
			TT		
GAM1419	LOC253912	3'	TGACTTTGAACTATGAAG 46484	TCCA	
			TTTCATAGTTTCG TCA		
			GAAGTATCAAGT AGT		
			TTC_		
GAM1419	LOC51185	3'	TTGATGGGACATGAAG 18425	A CGT	
			TTTCAT GTT CCATCAA		
			GAAGTA CAG GGTAGTT		
			- - -		
GAM1420	CASP7	3'	AAACAGAAACCATTCTAGGTG 6895	G	___
			CG CTGGAAT TTCTGTTT		
			GT GATCTTA AAGACAAA		
			G CCA		
GAM1420	CASP7	3'	AAACAGAAACCATTCTAGGTG 27191	G	___
			CG CTGGAAT TTCTGTTT		
			GT GATCTTA AAGACAAA		
			G CCA		
GAM1420	CASP7	3'	AAACAGAAACCATTCTAGGTG 27192	G	___
			CG CTGGAAT TTCTGTTT		
			GT GATCTTA AAGACAAA		
			G CCA		
GAM1420	CASP7	3'	AAACAGAAACCATTCTAGGTG 27193	G	___
			CG CTGGAAT TTCTGTTT		
			GT GATCTTA AAGACAAA		
			G CCA		
GAM1420	DAPP1	3'	AAACAGAAAGTTACAAATG 15729	GC G	
			CG TG AATTTCTGTTT		
			GT AC TTGAAGACAAA		
			AA A		
GAM1420	GPR81	3'	AAACAGAAACCGGGCTCAGTC 26277	_ AA_	
			GGCTG G TTTCTGTTT		
			CTGAC C AAAGACAAA		
			T GGGCC		
GAM1420	HSPD1	3'	GAACACTCAAAATTCCAGCAAT 30207	CCG	C_
	GA		TCA GCTGGAATTT TGTTT		

AGT CGACCTTAAA ACAAG
 AA_ ACTC
 GAM1420 OSBP 5' GGAAACAGCAGCCAATCGGCGA 8407 A GC AATTT
 TC CCG TGG CTGTTTCC
 || ||| ||| |||||
 AG GGC ACC GACAAAGG
 C TA GAC__
 GAM1420 PGF 3' GAAACAGCTCAGCCAGTGG 8491 C AATTT
 TCAC GGCTGG CTGTTTC
 |||| ||||| |||||
 GGTG CCGACT GACAAAG
 A C____
 GAM1420 VLDLR 3' AAGCCATATTCCAGCAGTGA 34448 CG TTCT
 TCAC GCTGGAAT GTTT
 |||| ||||| ||||
 AGTG CGACCTTA CGAA
 A_ TAC_
 GAM1420 acmsd 5' AAACAGGGCAGCCAGTGA 28727 C GAAT
 TCAC GGCTG TTCTGTTT
 |||| ||||| |||||
 AGTG CCGAC GGGACAAA
 A ____
 GAM1420 ADAM9 3' AAACAGAACTGAGTGTGA 9904 CG _ AA
 TCAC GCT GG TTTCTGTTT
 |||| ||| || |||||
 AGTG TGA TC AAAGACAAA
 _ G _
 GAM1420 B3GALT6 3' AAACAGGACCAGCCGG 27922 AAT
 CCGGCTGG TTCTGTTT
 ||||| |||||
 GGCCGACC AGGACAAA

 GAM1420 BC008967 5' GGAAACAGAACTCGCAG 30477 _ A
 CTG GA TTTCTGTTTCC
 ||| || |||||
 GAC CT AAAGACAAAGG
 G C
 GAM1420 CL683 3' AACATGAATTTCCAGCCGATGA 17923 C T _
 TCA CGGCTGGAA TTC TGTT
 ||| ||||| ||| ||||
 AGT GCCGACCTT AAG ACAA
 A T T
 GAM1420 FLJ14596 5' GAAAGGATACTCCAGCCGGAGA 26571 A ATT G
 TC CCGGCTGGA TCT TTTC
 || ||||| ||| ||||
 AG GGCCGACCT AGG AAAG
 A CAT _
 GAM1420 GPT2 3' GGAAACAGAACTCCCAACTG 28525 CT_ A
 CGG GGA TTTCTGTTTCC
 ||| ||| |||||

		GTC CCT AAAGACAAAGG	
		AAC C	
GAM1420 KIAA0020	5'	GAACAAATTCCAGCCGG 17020	TC
		CCGGCTGGAATT TGTTT	
		GGCCGACCTTAA ACAAG	
		—	
GAM1420 KIAA0766	3'	AAACAGAAAAATCTACCGGT 16739	C A_
		ACCGG TGGA TTTCTGTTT	
		TGGCC ATCT AAAGACAAA	
		— AA	
GAM1420 KIAA0864	3'	GGAAACGGGGCCCAGCC 31685	AAT
		GGCTGG TTCTGTTTCC	
		CCGACC GGGGCAAAGG	
		C_	
GAM1420 KIAA1344	5'	GGAAACAGAACACAGCAGTGA 35871	CG GAAT
		TCAC GCTG TTCTGTTTCC	
		AGTG CGAC AAGACAAAGG	
		A_ AC_	
GAM1420 LASP1	3'	GAAACAGAAATGACCACGTGA 12798	CGGC A_
		TCAC TGG ATTTCTGTTTC	
		AGTG ACC TAAAGACAAAG	
		C_ AG	
GAM1420 MRPL35	3'	GGAAACAGAAATTTAGAATGG 18737	GCTG
		CCG GAATTTCTGTTTCC	
		GGT TTAAAGACAAAGG	
		AAGA	
GAM1420 PURG	3'	GAAACAGAAATTGACCTCCGGT 15006	CT _
		ACCGG GG AATTTCTGTTTC	
		TGGCC CC TTAAAGACAAAG	
		T_ AG	
GAM1420 RHOBTB1	3'	AAACAGAAACCAATCGGT 43949	GC AA
		ACCG TGG TTTCTGTTT	
		TGGC ACC AAAGACAAA	
		TA _	
GAM1420 VPS4B	3'	AAACAGAAATTACCCAGT 11292	_
		GCTGG AATTTCTGTTT	
		TGACC TTAAAGACAAA	
		CA	
GAM1420 LOC150397	3'	AAACAGAAACCCAGAATGG 38956	G_ AA
		CCG CTGG TTTCTGTTT	

GGT GACC AAAGACAAA
AA C_
GAM1420 LOC199221 5' GAAACAGGAACAGCCAGTGG 39164 C GAA
TCAC GGCTG TTTCTGTTTC
|||| |||| |||||
GGTG CCGAC AAGGACAAAG
A ____
GAM1420 LOC221688 3' AAACAGAAACCCTGAGCCG 44989 _ AA
CGGCT GG TTTCTGTTT
|||| || |||||
GCCGA TC AAAGACAAA
G CC
GAM1421 CD28 3' AGCAAAGTGTGGTATCCA 12781 C _ AA
TG GATACCAC CT GCT
|| ||||| || |||
AC CTATGGTG GA CGA
_ T AA
GAM1421 DSG1 3' GGTGAGGTTGAGGAATATCACA 7656 C CCA A
TG GATA CCT AGCTTCACC
|| ||| || |||||
AC CTAT GGA TTGGAGTGG
A AA_ G
GAM1421 HNRPA1 3' TGAAGCTTGTGTATCCA 25247 C C CT
TG GATAC AC AAGCTTCA
|| |||| || |||||
AC CTATG TG TTCGAAGT
_ _ _
GAM1421 MYCL2 3' GGCTGACAGATGGTATGCA 11856 G C A_
TGC ATACCA CT AGCT
|| ||||| || |||
ACG TATGGT GA TCGG
_ A CAG
GAM1421 PCK3 3' GGCAGGTGGTACCGTA 36125 A AA
TGCG TACCACCT GCT
|||| ||||| |||
ATGC ATGGTGGA CGG
C ____
GAM1421 SRGAP2 3' TGAAGCCCTTGGTATCGC 36880 CCTAA
GCGATACCA GCTTCA
|||||| |||||
CGCTATGGT CGAAGT
TCC_
GAM1421 C11orf9 3' AGCCCCCAGATGGTATTGCA 14943 C AA_
TGCGATACCA CT GCT
||||||| || |||
ACGTTATGGT GA CGA
A CCCC
GAM1421 GGA2 3' GTGAAGCTGCAGCCGGCATCCA 28924 C A AC A_
TG GAT CC CT AGCTTCAC
|| ||| || |||||

		AC CTA GG GA TCGAAGTG	
		_ C CC CG	
GAM1421 KIAA1856	3'	GACGTGCAGACGGTGTGCGCA 44524	AC AA T
		TGCGATACC CT GC TC	
		ACGCTGTGG GA TG AG	
		CA CG C	
GAM1421 MGC10870	5'	GTGAAGCTCTGGGACATGGCA 26083	G ACCA TA
		TGC AT CC AGCTTCAC	
		ACG TA GG TCGAAGTG	
		G CAG_ TC	
GAM1421 MGC20460	5'	TGAAGTTTTGGTATCGC 27589	CCT
		GCGATACCA AAGCTTCA	
		CGCTATGGT TTTGAAGT	

GAM1421 TOR1B	3'	GCCTTACGTGGTATCACA 15842	C C _
		TG GATACCAC TAAG C	
		AC CTATGGTG ATT C G	
		A C C	
GAM1421 ZNF17	3'	TGAAGCTTACAGTACTGCA 40068	A CACC
		TGCG TAC TAAGCTTCA	
		ACGT ATG ATTCGAAGT	
		C AC__	
GAM1421 LOC146237	5'	GGTGAAGCTGTGACATC 40671	AC CTA
		GAT CAC AGCTTCACC	
		CTA GTG TCGAAGTGG	
		CA _____	
GAM1421 LOC146733	5'	GTGAAGCTCAGTGCAGCTGCA 40731	ATAC CTA
		TGCG CAC AGCTTCAC	
		ACGT GTG TCGAAGTG	
		CGAC AC_	
GAM1421 LOC222183	3'	GAGGAGGTGGTACAGCA 45185	GA AAG
		TGC TACCACCT CTTC	
		ACG ATGGTGGA GGAG	
		AC _____	
GAM1422 CLK2	3'	GTGAGGTAACCAGGTGGCATC 6972	CTG_
		GATGCCACC TGCCTCGC	
		CTACGGTGG ATGGAGTG	
		ACCA	
GAM1422 DNM2	3'	GTGGGCCCGAGGGCGGCCTC 11388	T A T T
		GA GCC CCCTG GCC CGC	

		CT CGG GGGAC CGG GTG	
		C C C _	
GAM1422 FLNB	3'	GTGGGCGAACATCTGGTCAGCA 31147	C_ CT CC
TC		GATGC ACC GTG TCGCCAC	
		CTACG TGG TAC AGCGGGTG	
		AC TC A_	
GAM1422 HR	3'	GTGAGGAGAGGGTGGCATC 11619	GTG
		GATGCCACCCT CCTCGC	
		CTACGGTGGGA GGAGTG	
		GA_	
GAM1422 MN1	3'	GCAGACAAAGCAGGTGGCAT 8274	C GCC_ _
		ATGCCACC TGT TC GC	
		TACGGTGG ACG AG CG	
		_ AAAC A	
GAM1422 NGFR	3'	TGGGGAACAAGGTGGCATC 8335	_ G
		GATGCCACCCT GT CCTCG	
		CTACGGTGGGA CA GGGGT	
		A A	
GAM1422 RAI2	5'	GCAGGCCAAGTGGCATC 22349	CC T C
		GATGCCAC TG GCCT GC	
		CTACGGTG AC CGGA CG	
		A_ _ _	
GAM1422 Apg4B	3'	GCAGACACCACAGGTGGCATC 14975	CC_ _
		GATGCCACCCTGTG TC GC	
		CTACGGTGGGACAC AG CG	
		CAC A	
GAM1422 D15Wsu75e	5'	GCGAGCAGCGCAGGGCGGCCTC 33102	T A _
		GA GCC CCCTGTGC CTCGC	
		CT CGG GGGACGCG GAGCG	
		C C AC	
GAM1422 DLAD	5'	CGAAATGGACAAAGTGGCATC 27779	CC G _
		GATGCCAC TGT CC TCG	
		CTACGGTG ACA GG AGC	
		AA _ TAA	
GAM1422 DNAJC8	3'	GTGAGCACACAGAGCAGCATC 15559	CACC C_
		GATGC CTGTG CTCGC	
		CTACG GACAC GAGTG	
		ACGA AC	
GAM1422 FLJ14751	3'	TGAGAAACAAAGTGGCATT 26612	CC GC
		GATGCCAC TGT CTCG	

		TTACGGTG ACA GAGT		
		AA AA		
GAM1422	FLJ23548	3' TGGAAAGTTACAGGGTAGCAT	23827	C C CGC
		ATGC ACCCTGTG CT CCA		
		TACG TGGGACAT GA GGT		
		A T A__		
GAM1422	KIAA1193	3' GGGCGAGGGGGTGCA	33585	C TGTG
		TGC ACCC CCTCGCCC		
		ACG TGGG GGAGCGGG		
		— —		
GAM1422	KIAA1323	5' GCAGTTTCCAAGGTGGCATC	31565	C TGC_ C
		GATGCCACC TG CT GC		
		CTACGGTGG AC GA CG		
		A CTTT _		
GAM1422	KIAA1337	3' GTGGATGTTACAGGGTGGC	35986	CCT C
		GCCACCCTGTG CG CCAC		
		CGGTGGGACAT GT GGTG		
		T__ A		
GAM1422	KIAA1705	3' TGAAGATCACAAGGTGGTATC	35861	C CC GCC
		GATGCCACC TGTG TC CA		
		CTATGGTGG ACAC AG GT		
		A T_ AA_		
GAM1422	MGC10715	3' TGGACACTCAGGCACAGAGTGG	23616	C CGC__
	C	GCCAC CTGTGCCT CCA		
		CGGTG GACACGGA GGT		
		A CTCACA		
GAM1422	MGC20253	3' GTGGGCATAGGTGGCA	29397	C T
		TGCCACC TGTGCC CGC		
		ACGGTGG ATACGG GTG		
		— —		
GAM1422	PDE2A	3' GTGAGCAGAGTGTGGCATC	8463	C G C
		GATGCCAC CT TGC TCGC		
		CTACGGTG GA ACG AGTG		
		T G _		
GAM1422	LOC123242	5' GCAGCACAGGGCTGCATC	37242	CA CTC
		GATGC CCCTGTGC GC		
		CTACG GGGACACG CG		
		TC A__		
GAM1422	LOC148114	5' GGCAGGGTCAGGGTGGC	38468	T TC
		GCCACCCTG GCC GCC		

			CGGTGGGAC TGG CGG		
			_ GA		
GAM1422	LOC149086	3'	GTGGGCCAGGATGGCA 40946	C T T	
			TGCCA CCTG GCC CGC		
			ACGGT GGAC CGG GTG		
			A _ _		
GAM1422	LOC151996	5'	GCAGGCGACACGGGGGTA 41414	A _ _ C	
			TGCC CCC TGT GCCT GC		
			ATGG GGG ACA CGGA CG		
			_ C G _		
GAM1422	LOC253001	5'	GCAGCACAGGGCTGCATC 46058	CA CTC	
			GATGC CCCTGTGC GC		
			CTACG GGGACACG CG		
			TC A_		
GAM1422	LOC253256	5'	GTGGAAGGAGCCAGGGTGGCA 46048	T CT GC	
			TGCCACCCTG GC C CCAC		
			ACGGTGGGAC CG G GGTG		
			_ AG AA		
GAM1422	LOC253847	5'	GCTCTGGCCCAGGGTGGCA 45941	T TC_	
			TGCCACCCTG GCC GC		
			ACGGTGGGAC CGG CG		
			C TCT		
GAM1422	LOC92840	3'	GCGTCGGGCACAGGGCAGCTC 28761	T CA _	
			GA GC CCCTGTGCCT CGC		
			CT CG GGGACACGGG GCG		
			_ AC CT		
GAM1423	FGF9	3'	GGGCCACTTGCTTGATT 7752	A AT	
			AATCAA GCAAGTGGC CC		
			TTAGTT CGTTCACCG GG		
			_ _		
GAM1423	GPC4	3'	CTGCAGACTACTGCTTTGA 7176	A CA CA	
			TCAAAGCA GTGG TC CAG		
			AGTTTCGT CATC AG GTC		
			_ _ AC		
GAM1423	MEN1	5'	CTGTGGATGTGAGCATTGCTTT 44842	_ G_	
G			CAAAGCAA GT GCATCCACAG		
			GTTTCGTT CG TGTAGGTGTC		
			A AG		
GAM1423	MOCS2	5'	CTGTGGATTTCTACACCCTTGA 10874	AGCAA C_	
T			ATCAA GTGG ATCCACAG		

			TAGTT CATC TAGGTGTC	
			CCCA_ TT	
GAM1423	PKIB	3'	GATGCTACTCACTTTGATT 26230	CA
			AATCAAAG AGTGGCATC	
			TTAGTTTC TCATCGTAG	
			AC	
GAM1423	PSEN1	3'	TGGATGTTTCTTCTTTGA 14235	C TG
			TCAAAG AAG GCATCCA	
			AGTTTC TTC TGTAGGT	
			_ TT	
GAM1423	PSEN1	3'	TGGATGTTTCTTCTTTGA 5457	C TG
			TCAAAG AAG GCATCCA	
			AGTTTC TTC TGTAGGT	
			_ TT	
GAM1423	RNMT	3'	CTGTGGTAACTCATTTTGATT 9887	CA GGCAT
			AATCAAAG AGT CCACAG	
			TTAGTTTT TCA GGTGTC	
			AC AT__	
GAM1423	UBE2V1	3'	ATGACACTTCCTTGCTTTGG 9368	___ G
			TCAAAGCA AGTG CAT	
			GGTTTCGT TCAC GTA	
			TCCT A	
GAM1423	UBE2V1	3'	ATGACACTTCCTTGCTTTGG 22520	___ G
			TCAAAGCA AGTG CAT	
			GGTTTCGT TCAC GTA	
			TCCT A	
GAM1423	UBE2V1	3'	ATGACACTTCCTTGCTTTGG 22767	___ G
			TCAAAGCA AGTG CAT	
			GGTTTCGT TCAC GTA	
			TCCT A	
GAM1423	BMF	3'	CTGTGGATGGGGGCCGTGAT 27279	AA AAGTGG
			ATCA GC CATCCACAG	
			TAGT CG GTAGGTGTC	
			GC GGG__	
GAM1423	FLJ12668	3'	CTGTGGAACTGCTGCTTCT 24559	C TG _
			AG AAG GCA TCCACAG	
			TC TTC CGT AGGTGTC	
			_ GT CA	
GAM1423	FLJ21916	3'	TGTGGATGTTACCTTGCTT 23386	_
			AAGCAAG TGGCATCCACA	

TTCGTTC ATTGTAGGTGT
 C
 GAM1423 FLJ22127 3' TGTGAATAGTCATTTGACT 23043 _ _ C
 AG CAAGTGGC AT CACA
 || ||||| || |||
 TC GTTTACTG TA GTGT
 A A A
 GAM1423 FLJ22794 5' GGGTTACGCCACCTGCTTTG 44033 A ____
 CAAAGCA GTGGC ATCC
 ||||| |||| |||
 GTTTCGT CACCG TGGG
 C CAT
 GAM1423 KIAA0493 3' CTGCGGAGCAATTCTTGCTTT 32140 TG__ A A
 AAAGCAAG GC TCC CAG
 ||||| || ||| |||
 TTTCGTTC CG AGG GTC
 TTAA _ C
 GAM1423 KIAA0515 3' GTGGATATATGGCATTGA 31929 A AA GC
 TCAA GC GTG ATCCAC
 ||| || ||| |||||
 AGTT CG TAT TAGGTG
 A G_ A_
 GAM1423 KIAA0795 3' GTGGATCAGTTTGATT 24587 AAGC G GC
 AATCA AA TG ATCCAC
 |||| || || |||||
 TTAGT TT AC TAGGTG
 ____ G ____
 GAM1423 KIAA0863 3' CTGTGGATGTAAACCTCGTTT 45635 A ____
 AAGC AG TGGCATCCACAG
 ||| || |||||
 TTTG TC ATTGTAGGTGTC
 C CAA
 GAM1423 KIAA1068 3' CTGTGGCGACCTTGCTTTGGTT 17644 TGGCAT
 AATCAAAGCAAG CCACAG
 ||||| || |||||
 TTGGTTTCGTTT GGTGTC
 CAGC__
 GAM1423 KIAA1332 3' GTGGATTGATTTGATT 35259 G AGTGGC
 AATCAAA CA ATCCAC
 ||||| || |||||
 TTAGTTT GT TAGGTG
 A ____
 GAM1423 KIAA1545 3' GTCGAGCCACTTGCTTTG 30442 A C
 CAAAGCAAGTGGC TC AC
 ||||| || |||
 GTTTCGTTACCG AG TG
 _ C
 GAM1423 MGC16386 3' GTGGGTTTCCCCTTTGATT 27959 CAAGT C_
 AATCAAAG GG ATCCAC
 ||||| || |||||

		TTAGTTTC	CC	TGGGTG	
		C		TT	
GAM1423	MGC2560	3'	CTGTGGATTATATTGCTTGA	25467	A GTGGC
			TCAA GCAA ATCCACAG		
			AGTT CGTT TAGGTGTC		
			_ ATAT_		
GAM1423	LOC127602	5'	CTGTGGATGCCCTCACCTT	36904	CA_ T
			AAG AG GGCATCCACAG		
			TTC TC CCGTAGGTGTC		
			CAC _		
GAM1423	LOC149606	3'	TGTGGATGCCACCGGCTT	38786	AA
			AAGC GTGGCATCCACA		
			TTCG CACCGTAGGTGT		
			GC		
GAM1423	LOC149837	3'	CTGTGAATGTATAATTTTGATT	41099	CAAGTG C
			AATCAAAG GCAT CACAG		
			TTAGTTTT TGTA GTGTC		
			AATA_ A		
GAM1423	LOC199692	3'	CTGTATGGACACTTGCTT	29811	GCA _
			AAGCAAGTG TCC ACAG		
			TTCGTTTAC AGG TGTC		
			_ TA		
GAM1423	LOC202934	3'	CTGCAGAAGCTCTATCTTTGAT	43458	CA T A CA
		T	AATCAAAG AG GGC TC CAG		
			TTAGTTTC TC TCG AG GTC		
			TA _ A AC		
GAM1423	LOC255465	3'	CTGCAGAAGCTCTATCTTTGAT	46451	CA T A CA
		T	AATCAAAG AG GGC TC CAG		
			TTAGTTTC TC TCG AG GTC		
			TA _ A AC		
GAM1423	LOC257286	3'	GAGCCACTCACTTTTATT	45373	C CA A
			AAT AAAG AGTGGC TC		
			TTA TTTC TCACCG AG		
			T AC _		
GAM1423	LOC90979	3'	TGGAGACCACTTACTTTG	32233	C CA
			CAAAG AAGTGG TCCA		
			GTTTC TTCACC AGGT		
			A AG		
GAM1424	SDC2	3'	ATCACTTACAGAACCA	33326	AGTC
			TGG TCTGTAAGTGAT		

ACC AGACATTCACTA
 A____
 GAM1424 KIAA0171 3' ATCAACTGAAGAGTCCATTAA 16121 GT GTA _
 TTAAATGGA CTCT AGT GAT
 ||||| ||| ||| |||
 AATTACCT GAGA TCA CTA
 _ AG_ A
 GAM1424 MOST2 5' CACAGCAAGACTCCGTCTAA 21548 A C AA
 TTA ATGGAGTCT TGT GTG
 || ||||| ||| |||
 AAT TGCCTCAGA ACG CAC
 C _ A_
 GAM1424 USP8 3' ATCACTTACAGGTACCATTAA 11629 AGT T
 TAAATGG C CTGTAAGTGAT
 ||||| | |||||
 ATTTACC G GACATTCACTA
 AT__
 GAM1424 ZDHC2 3' ATCACATAGAACTCCATT 18486 C AA
 AATGGAGT TCTGT GTGAT
 ||||| |||| ||||
 TTACCTCA AGATA CACTA
 A _
 GAM1424 LOC220071 5' CACTGAAAAGAATCCATTAA 44877 G CTGTA
 TTAAATGGA TCT AGTG
 ||||| || |||
 AATTACCT AGA TCAC
 A AAAG_
 GAM1425 DISC1 3' CAACCTTCTCAGGACAAGCCCA 20734 A CATA A
 TG GC TTTTGAGAA GTTG
 || || ||||| ||||
 AC CG AGGACTCTT CAAC
 C AAC_ C
 GAM1425 VCAM1 3' CAACTTTCCCAATGTGGC 6737 TT A
 GCCATAT TG GAAAGTTG
 ||||| || |||||
 CGGTGTA AC CTTTCAAC
 _ C
 GAM1425 VCAM1 3' CAACTTTCCCAATGTGGC 27983 TT A
 GCCATAT TG GAAAGTTG
 ||||| || |||||
 CGGTGTA AC CTTTCAAC
 _ C
 GAM1425 DKFZp434F1719 3' CAACTTTCTTATCAGGCTCAA 25988 ATATTT
 TTGAGCC TGAGAAAGTTG
 ||||| |||||
 AACTCGG ATTCTTTCAAC
 ACT__
 GAM1425 FLJ10852 3' CAACTTTCCATTCTCATGGTC 21117 G ATTT_ A
 AA TTGA CCAT TG GAAAGTTG
 ||| ||| || |||||

AACT GGTA AC CTTTCAAC
 _ CTCTTT _
 GAM1425 MGC4643 3' CTGTCTCAAAATATTGCCCAA 26438 A C A
 TTG GC ATATTTTGAGA AG
 ||| || ||||| ||
 AAC CG TATAAACTCT TC
 C T G
 GAM1425 p25 3' CAACTCTCCCAAATGGCTCAG 13890 AT A A
 TTGAGCCAT TTTG GA AGTTG
 ||||| ||| || |||||
 GACTCGGTA AAAC CT TCAAC
 _ C C
 GAM1426 FGFR3 3' ATTTATGGGCCCTGGCAC 5643 T TCAAGAA
 GTGCT GG CCCATAAAT
 |||| || |||||
 CACGG CC GGGTATTTA
 T CC_____
 GAM1426 CNM4 3' ATGGGTTCTCAACTGTA 21422 TT CA
 TGC GGT AGAACCCAT
 ||| || |||||
 ATG TCA TCTTGGGTA
 _ AC
 GAM1426 DKFZp434N035 3' ATTTATGGGTTCTTTTCCA 26006 TC
 TGG AAGAACCATAAAT
 ||| |||||
 ACC TTCTTGGGTATTTA
 TT
 GAM1426 MGC13138 3' GTGGGCTCCTGACCAAGCAC 27232 A A
 GTGCTTGGTCA GA CCCAT
 ||||| || |||||
 CACGAACCACT CT GGGTG
 C C
 GAM1426 MIDORI 3' TATGTTTGACCAAGGCAC 36530 _ AACC
 GTGC TTGGTCAAG CATA
 |||| ||||| |||||
 CACG AACCACTTT GTAT
 G _____
 GAM1426 STK29 3' TTTATGGATTCTCCGCAC 42319 TT TCA C
 GTGC GG AGAA CCATAAA
 |||| || |||||
 CACG CC TCTT GGTATTT
 _ _ A
 GAM1427 DLG5 5' TCATGAGTGAGCGTGACCAG 40341 TAGATAC
 TTGGTC CACTCATGA
 |||| |||||
 GACCAG GTGAGTACT
 TGCGA_____
 GAM1427 FLRT2 3' CATGATATTTAGACCAA 14880 CCAC
 TTGGTCTAGATA TCATG
 ||||| |||||

AACCAGATTTAT AGTAC

GAM1427 Nrap 3' CAGGAGTTCTAGACCAA 29237 TACC A
TTGGTCTAGA ACTC TG
||||||| ||| ||
AACCAGATCT TGAG AC

_____ G
GAM1427 CDC14B 3' TCATGAGCAACATTAGGCTA 27173 ATACCA
TGGTCTAG CTCATGA
||||||| |||||
ATCGGATT GAGTACT

ACAAC_
GAM1427 DKFZP434C1715 3' TCATAAGTCCATGGACCAA 41677 GATACC C
TTGGTCTA ACT ATGA
||||||| ||| |||||
AACCAGGT TGA TACT
ACC____ A

GAM1427 KIAA0171 3' GTGGGTGGTGAGACCA 16123 AGA
TGGTCT TACCACTCAT
||||| |||||
ACCAGA GTGGTGGGTG

GAM1427 KIAA0420 3' TCATGCCCAATCTGGACCAA 31729 ACCACT
TTGGTCTAGAT CATGA
||||||| |||||
AACCAGGTCTA GTACT
ACCC__

GAM1427 MGC4655 3' TCACAAGTTGCTAGACCAA 27148 ATACC CA
TTGGTCTAG ACT TGA
||||||| ||| |||
AACCAGATC TGA ACT
GT____ AC

GAM1427 PDE10A 3' TCATGAATTTAGTTAGACTAA 13465 ATACCAC
TTGGTCTAG TCATGA
||||||| |||||
AATCAGATT AGTACT
GATTTA_

GAM1427 PPI5PIV 3' TCACACGGGTATCCAGAGCAA 21278 G A ACTCA
TTG TCT GATACC TGA
||| ||| ||||| |||
AAC AGA CTATGG ACT
G C GCAC_

GAM1427 RDH-E2 3' TCATAGGCAGTGATCCTAGACC 29080 A__ CA TC
AA TTGGTCTAG TAC C ATGA
||||||| ||| | |||||
AACCAGATC GTG G TACT
CTA AC GA

GAM1427 LOC147632 5' TCATGAGTGACAAGTGTAGC 28828 T G AC__
G CTA AT CACTCATGA
||| ||| |||||

C GAT TG GTGAGTACT
 _ G AACA
 GAM1427 LOC155061 3' CATGAGTGGGGAAGAGCAA 39535 G AGATA
 TTG TCT CCACTCATG
 ||| ||| |||||
 AAC AGA GGTGAGTAC
 G AGG_

GAM1427 LOC255252 3' TCATGAGTAGGGCAATAGAC 45547 GATA _
 GTCTA CC ACTCATGA
 |||| | |||||
 CAGAT GG TGAGTACT
 AACG A

GAM1427 LOC257354 3' TCATGCCCAATCTGGACCAA 45582 ACCACT
 TTGGTCTAGAT CATGA
 ||||| ||||
 AACCAGGTCTA GTACT
 ACCC_

GAM1428 ANKH 3' GAAATAACGCATTCTGA 27637 ACCTA A
 TCGAATGT GT ATTTC
 ||||| || ||||
 AGCTTACG CA TAAAG
 _ A

GAM1428 CALCR 3' AAATGAGGAGGTACATTGA 7476 G AGTA
 TC AATGTACCT ATTT
 || ||||| ||||
 AG TTACATGGA TAAA
 _ GGAG

GAM1428 TFRC 3' TGAAATTACTACAAAATTTGA 9227 GTACC
 TCGAAT TAGTAATTTCA
 |||| | |||||
 AGTTTA ATCATTAAAGT
 AAAC_

GAM1428 BM-002 3' TGAAATTACCAGATATTC 18726 AC A
 GAATGT CT GTAATTTCA
 |||| | |||||
 CTTATA GA CATTAAAGT
 _ C

GAM1428 SEC15L 3' TGAAATTGATTACAAATACATT 35766 CC_ _
 TGA TCGAATGTA TAGT AATTTCA
 ||||| ||| |||||
 AGTTTACAT ATTA TTAAAGT
 AAAC G

GAM1428 LOC51667 3' TGAGTGCCAGGTGCAT 18199 A AT
 ATGTACCT GTA TTCA
 ||||| ||| ||||
 TACGTGGA CGT GAGT
 C _

GAM1429 AKAP13 3' AAACATGCAAAGTCCCACTTT 43173 GAAC
 AAAGTGGCAGTTTG TGTTT
 ||||| ||||

TTTACCGTCAAAC ACAA
 GT__
 GAM1429 CYP19 3' TTCCAAACACCACTTTA 5563 CA
 TAAAGTGG GTTTGGAA
 ||||| |||||
 ATTCACC CAAACCTT
 A_
 GAM1429 CYP19 3' TTCCAAACACCACTTTA 25273 CA
 TAAAGTGG GTTTGGAA
 ||||| |||||
 ATTCACC CAAACCTT
 A_
 GAM1429 FLJ13639 3' AGTTCCCAAACCTGCACTTTA 24022 G _
 TAAAGTG CAGTTTGG AACT
 ||||| ||||| |||
 ATTCAC GTCAAACC TTGA
 _ C
 GAM1429 KIAA1676 3' AAACAGTTCCAGCAGGCTCTCT 44724 T_ AGT
 AG GGC TTGGAACGTGTT
 || ||| |||||
 TC TCG GACCTTGACAAA
 TC GAC
 GAM1429 KIAA1796 3' AAACAAACAACCTACCACTTT 43961 C T GAAC
 AAAGTGG AGTT G TGT
 ||||| ||| | |||
 TTTACC TCAA C ACAA
 A _AA_
 GAM1430 BCL7B 3' TGACAACAGTACCCATCCCCCA 7436 A T AA T
 TG GG AT GTGCTGTT GTCA
 || ||| ||||| |||
 AC CC TA CATGACAA CAGT
 C C CC _
 GAM1430 FOXO1A 3' TGTCAACACTCATACTTCA 7759 A CTGT T
 TGAGGTAT AGTG TTG CA
 ||||| ||| |||
 ACTTCATA TCAC AAC GT
 C _ T
 GAM1430 KLF7 5' TGACAAACAAACAGCCCCA 9810 A ATAA GC
 TG GGT GT TGTGTGCA
 || ||| || |||||
 AC CCG CA ACAAACAGT
 C A_ A_
 GAM1430 MAPK4 3' TTGACAAACAGCAGACCCTACA 8624 _ TATAAG
 TG AGG TGCTGTTGTCAA
 || ||| |||||
 AC TCC ACGACAAACAGTT
 A CAG_
 GAM1430 FLJ12221 3' GGCCTCAGCCTCATACCTCA 31345 A T TTT
 TGAGGTAT AG GCTG GTC
 ||||| || ||| |||

ACTCCATA TC CGAC CGG
 C _ TC_
 GAM1430 FLJ13110 3' ACAAACAGTGTACACTC 23218 _ AAGT
 GAG GTAT GCTGTTTGT
 ||| ||| |||||
 CTC CATG TGACAAACA
 A ____
 GAM1430 KIAA0350 3' GACACAGCACTCACAGCCCA 30669 A ATA_ TT
 TG GGT AGTGCTGT GTC
 || ||| ||||| |||
 AC CCG TCACGACA CAG
 _ ACAC _
 GAM1430 KIAA1209 3' TGACAATAGTGCCCACACCTTA 30473 ATAA TG T
 TGAGGT G CTGTT GTCA
 ||||| | |||| |||
 ATTCCA C GATAA CAGT
 CACC GT _
 GAM1430 MRPL48 5' TGACAAACATGGAGAAACCTCA 18128 ATAAGTGC
 TGAGGT TGTTTGTCA
 ||||| |||||
 ACTCCA ACAACAGT
 AAGAGGT_
 GAM1430 LOC204084 5' TGACAAACCTCTCTACACCCCA 43089 A ATA TGCT
 TG GGT AG GTTTGTCA
 || ||| || |||||
 AC CCA TC CAAACAGT
 C CA_ TCTC
 GAM1430 LOC221964 3' ACAAACAGCATTAAACGTCA 45110 G ATA
 TGA GT AGTGCTGTTTGT
 ||| || |||||
 ACT CA TTACGACAAACA
 G A_
 GAM1430 LOC51107 3' TTGAATCTGCACTTATCCCCA 18099 A T TGTTTG
 TG GG ATAAGTGC TCAA
 || || ||||| |||
 AC CC TATTCACG AGTT
 _ C TCTA_
 GAM1431 CDC7L1 3' AGGGAAGCTGCAGGACCAA 9592 _ A CGAA
 TTGGTCCT CA CT TCTCT
 ||||| || |||
 AACCAGGA GT GA AGGGA
 C C ____
 GAM1431 C20orf30 3' AGAAACTATAGCTGAGGACTAA 15429 A CGAATC
 TTGGTCCTCA CT TCT
 ||||| || |||
 AATCAGGAGT GA AGA
 C TATCAA
 GAM1431 MGC12335 3' AGAGAAGGATGCTGAGGACC 26475 AC_ GAA
 GGTCCTCA TC TCTCT
 ||||| || |||

		CCAGGAGT AG AGAGA		
		CGT GA_		
GAM1431	LOC92305	3' GTTTGAGTTGAGGACCAA 28760		
		TTGGTCCTCAACTCGAAT		
		AACCAGGAGTTGAGTTTG		
GAM1432	CDC42	3' CAGCTGGTGTGCGCATCATA 7541	GA	T
		TATGATG TG TACCAGCTG		
		ATACTAC GC GTGGTCGAC		
		G_ T		
GAM1432	INPP5A	3' CAGCTGTGTGTCCATCA 12065	GTT	_
		TGATGGAT AC CAGCTG		
		ACTACCTG TG GTCGAC		
		___ T		
GAM1432	KIF5C	3' TTGTTAATATCCATCATA 10860	C	
		TATGATGGATGTTA CAG		
		ATACTACCTATAAT GTT		
		T		
GAM1432	MBNL	3' CAGCCACAAGACATCCACATA 22025	A	ACCA_
		TATG TGGATGTT GCTG		
		ATAC ACCTACAG CGAC		
		_ AACAC		
GAM1432	REQ	3' CAGCTGGTAAGGTCTTCA 12949	T	G
		TGA GGAT TTACCAGCTG		
		ACT TCTG AATGGTCGAC		
		_ G		
GAM1432	SH3BP4	3' CAGCTAGGCTACACCCATCATG 15851	A	TA _
		TATGATGG TGT CC AGCTG		
		GTACTACC ACA GG TCGAC		
		C TC A		
GAM1432	TBL1X	3' CAGCTAGCACCCCTTCATA 12179	T	A ACC
		TATGA GG TGTT AGCTG		
		ATACT CC ACGA TCGAC		
		T C _		
GAM1432	EML4	3' CAGCTAAGCCTTCATCATA 21142	T	ACC
		TATGATGGA GTT AGCTG		
		ATACTACTT CGA TCGAC		
		C A_		
GAM1432	FLJ00007	3' CAGCTGGTAGTCCATCA 35307	GT	
		TGATGGAT TACCAGCTG		

ACTACCTG ATGGTCGAC

GAM1432 FLJ21302 3' CAGCTGGCAGGCATTCAT 23182 A_
ATGGATGTT CCAGCTG
||||||| |||||
TACTTACGG GGTTCGAC
AC
GAM1432 FLJ22596 5' CAGCTGGTGCAGCCTCA 24702 T A T
TGA GG TGT ACCAGCTG
||| || ||| |||||
ACT CC ACG TGGTCGAC
_ G _
GAM1432 FLJ22625 3' CAGCTAATTACCTCATCATA 24041 AT TACC
TATGATGG GT AGCTG
||||||| || |||||
ATACTACT CA TCGAC
C_ TTAA
GAM1432 FLJ23462 3' AGCCACACTCCATCATA 24261 _ TACCA
TATGATGGA TGT GCT
||||||| ||| |||
ATACTACCT ACA CGA
C C____
GAM1432 KIAA1879 5' CAGCTGGTATTTGGACAACA 36411 A GA T_
TG TG TG TACCAGCTG
|| || || |||||
AC AC GT ATGGTCGAC
A AG TT
GAM1432 KOC1 5' CAGCTGGATCCATCCATCA 43778 TTA
TGATGGATG CCAGCTG
||||||| |||||
ACTACCTAC GGTTCGAC
CTA
GAM1432 MYLE 3' CAGCTGGTTGGGGGCACCATC 15234 A ____
GATGG TGTT ACCAGCTG
|||| |||| |||||
CTACC ACGG TGGTCGAC
_ GGGT
GAM1432 RAB40B 3' CAGCTGGTGGATGCATC 13694 G G
GATG AT TTACCAGCTG
|||| || |||||
CTAC TA GGTGGTCGAC
G _
GAM1432 YKT6 3' CAGCTGGGAGTGTCCATCAT 13319 TG A
ATGATGGA TT CCAGCTG
||||||| || |||||
TACTACCT GA GGTTCGAC
GT G
GAM1432 LOC122970 3' CAGCTGACCTTTTCATTATA 36714 TGTTAC
TATGATGGA CAGCTG
||||||| |||||

		ATATTACTT	GTCGAC		
		TTCCA_			
GAM1432	LOC149992 5'	CAGCTGGTCTACACCAACA	38842	A A T_	
		TG TGG TGT ACCAGCTG			
		AC ACC ACA TGGTCGAC			
		A _ TC			
GAM1432	LOC153339 5'	CAGCTATTAATTCATCATA	41613	GTTACC	
		TATGATGGAT AGCTG			
		ATACTACTTA TCGAC			
		ATTA__			
GAM1432	LOC153910 3'	CAGCTGGCACCAGCATCTA	39438	A__	
		TGGATGTT CCAGCTG			
		ATCTACGA GGTTCGAC			
		CCAC			
GAM1432	LOC196955 3'	CAGCTGGTGCTGACCCACA	37932	A AT__ T	
		TG TGG GT ACCAGCTG			
		AC ACC CG TGGTCGAC			
		_ CAGT _			
GAM1432	LOC202347 3'	CAGCCAAGGTCCATCAT	43430	G ACCA	
		ATGATGGAT TT GCTG			
		TACTACCTG AA CGAC			
		G C__			
GAM1432	LOC219401 3'	CAGCCACAGTTCATCTATCATA	44590	TTACCA_	
		TATGATGGATG GCTG			
		ATACTATCTAC CGAC			
		TTGACAC			
GAM1432	LOC255012 5'	CAGCAGACCCCATCATA	46043	AT ACCA	
		TATGATGG GTT GCTG			
		ATACTACC CAG CGAC			
		CC A__			
GAM1432	LOC255096 5'	CAGCTGGTGTCCACCATCAT	46606	A T_	
		ATGATGG TG TACCAGCTG			
		TACTACC AC GTGGTCGAC			
		_ CT			
GAM1432	LOC90309 5'	CAGCTAGATGATCATCATA	31150	A ACC	
		TATGATGG TGTT AGCTG			
		ATACTACT GTAG TCGAC			
		A A__			
GAM1433	BCL2 3'	TTCAGTTAAAAATCCAGATGGC	6264	A C GA	
	A	TGTCATCT GA TTT AACTGAA			

		ACGGTAGA CT AAA TTGACTT		
		C A A_		
GAM1433	NDP	3' CGATTTCAAAGTCCAGATACCA 5806	TC A	C
		TG ATCT GACTTTGAAA TG		
		AC TAGA CTGAAACTTT GC		
		CA C A		
GAM1433	RFX5	3' TTCAGTCTCATTTAGATGATA 6050	CTT A	
		TGTCATCTAGA TGA ACTGAA		
		ATAGTAGATTT ACT TGA		
		_____ C		
GAM1433	FLJ21148	3' AGTTCAGTCTAGATGGCA 24293	TT A	
		TGTCATCTAGACT GAA CT		
		ACGGTAGATCTGA CTT GA		
		_____ -		
GAM1433	KIAA1671	3' CAGAGTAGCCTAGATGACA 32691	_____	
		TGTCATCTAG ACTTTG		
		ACAGTAGATC TGAGAC		
		CGA		
GAM1433	KIAA1678	5' TTCAGAGTCCAGATGGCA 35789	A	
		TGTCATCT GACTTTGAA		
		ACGGTAGA CTGAGACTT		
		C		
GAM1433	MGC2562	3' TTCAAGATCAGTCTGGACAACA 26165	CA _____	
		TGT TCTAGACT TTGAA		
		ACA AGGTCTGA AACTT		
		AC CTAG		
GAM1433	NYD-SP25	3' TCAGTCTCAAAGTCACCTTGA 27293	TCTA A	
		TCA GACTTTGA ACTGA		
		AGT CTGAAACT TGA		
		TCCA C		
GAM1433	OSBPL3	3' CAACTTCTGTCCAGATGACA 17814	A TTT AC	
		TGTCATCT GAC GAA TG		
		ACAGTAGA CTG CTT AC		
		C T_ CA		
GAM1433	PRO2958	3' TCAGTTATTATAGATGACA 20627	GACTTTGA	
		TGTCATCTA AACTGA		
		ACAGTAGAT TTGACT		
		ATTA_____		
GAM1433	RAI17	3' CAGTCACTGTCCCAGACGGCA 43858	A A_ TT AA	
		TGTC TCT GAC TGA CTG		

		ACGG AGA CTG ACT GAC		
		C CC TC _		
GAM1433	LOC145508 3'	TTCAGCATCACCAAGATGACA 37888	AGACTT	AA
		TGTCATCT TGA CTGAA		
		ACAGTAGA ACT GACTT		
		ACC_ AC		
GAM1433	LOC149566 5'	TCAGTTCATTGACCAGATGACA 41017	AGACTT	A
		TGTCATCT TGAA CTGA		
		ACAGTAGA ACTT GACT		
		CCAGTT _		
GAM1433	LOC253639 3'	TTCAAAGTCAGATGACA 45856	A	
		TGTCATCT GACTTTGAA		
		ACAGTAGA CTGAAACTT		
		_		
GAM1434	CLECSF5 3'	AGATCAGCAGAGCCACCCTA 14916	A C	
		TAGGGT GC CTGTTGATTT		
		ATCCCA CG GACGACTAGA		
		C A		
GAM1434	USH3A 5'	GGA CTCCCAACAGGGGTACCC 27563	G	ATTG
		GGGTA CCCTGTTG CC		
		CCCAT GGGACAAC GG		
		G CCTCA		
GAM1434	FLJ10846 5'	CAGAGAACAGGGCTCCCC 20197	T	GA
		GGG AGCCCTGTT TTTG		
		CCC TCGGGACAA AGAC		
		C G_		
GAM1434	MRPS35 3'	TGACAAAATAAGAACTACCCTG 22400	CC GTTGA	C
		TAGGGTAG CT TTTG CA		
		GTCCCATC GA AAAC GT		
		AA ATA_ A		
GAM1434	SEMA4F 3'	GCAAATCAGGGCTTCCCCCTA 10459	T_	GTT
		TAGGG AGCCCT GATTTGC		
		ATCCC TCGGGA CTAAACG		
		CCT _		
GAM1434	LOC90120 3'	CAACAGGCAGAGGCTACCCTA 30851	_	GAT
		TAGGGTAGCC CTGTT TTG		
		ATCCCATCGG GACGG AAC		
		A AC_		
GAM1435	DFFB 3'	ACAAGGACATTCACTGCTG 42237	T	GA
		CAGC GTGAATGTTC GT		

GTCG CACTTACAGG CA
 T AA
 GAM1435 EDN3 5' CTCGAACCCCCACAGCTG 5581 AAT
 CAGCTGTG GTTCGAG
 ||||| |||||
 GTCGACAC CAAGCTC
 CCC
 GAM1435 BTN1A1 3' TACAAAACTCAAAAGTTGTTTG 7469 AATG_____ C C III
 CACAGCTG TG TT GAGT TTGT A
 || || |||| ||| I
 AC AA CTCA AACA T
 GTTTGTTGA A A III
 GAM1435 KIAA0121 3' ACAGGAAAACCCACCCACAGCTG 35965 AA TTCGAG
 CAGCTGTG TG TCTTGT
 ||||| || |||||
 GTCGACAC AC AGGACA
 CC CAAA____
 GAM1435 MGC3265 3' ACAAGAAAACATTTACA 23457 CGAG
 TGTGAATGTT TCTTGT
 ||||| |||||
 ACATTTACAA AGAACA
 A____
 GAM1435 UBN1 3' ACAAACTCAGGCCAGAGCCAC 18852 AA__ TT_ C
 AGCTG CAGCTGTG TG C GAGT TTGT
 ||||| || | |||| ||||
 GTCGACAC AC G CTCA AACA
 CGAG CG A A
 GAM1435 LOC146723 3' ACAAAATAATGGCATTACAGC 38227 CGA C
 GCTGTGAATGTT GT TTGT
 ||||| |||||
 CGACACTTACGG TA AACA
 TAA A
 GAM1435 LOC158158 3' ACAAGACTATATCCCACACCTG 39732 C A_ TCG
 CAG TGTG ATGT AGTCTTGT
 || ||| ||| |||||
 GTC ACAC TATA TCAGAACA
 C CC ____
 GAM1436 HIVEP2 3' TATGGGAAAACATTCCA 13586 CTGACA
 TGGGATGTTT CCATA
 ||||| |||||
 ACCTTACAAA GGTAT
 AG____
 GAM1436 SYT1 3' AGTATCGTCTGCATTCCA 12167 TTCT ACC
 TGGGATGT GAC ATACT
 ||||| || |||||
 ACCTTACG CTG TATGA
 T__ C__
 GAM1436 ZNF278 3' GGAAGCCAGAAGCATCCCA 15626 ACA_
 TGGGATGTTTCTG CC
 ||||| ||||| ||

ACCCTACGAAGAC GG
 CGAA
 GAM1436 ZNF278 3' GGAAGCCAGAAGCATCCCA 25775 ACA_
 TGGGATGTTTCTG CC
 ||||| ||
 ACCCTACGAAGAC GG
 CGAA
 GAM1436 ZNF278 3' GGAAGCCAGAAGCATCCCA 25785 ACA_
 TGGGATGTTTCTG CC
 ||||| ||
 ACCCTACGAAGAC GG
 CGAA
 GAM1436 SEC15B 3' TATAGTGTCAAAAGTGTCT 33128 TG C C
 GGA TTT TGACAC ATA
 ||| ||||| |||
 TCT GAA ACTGTG TAT
 GT A A
 GAM1436 SS18L1 3' AAGTATGGTCAAAGGAAAAAAA 32556 G__ GAC_
 TCCCA TGGGAT TTTCT ACCATACTT
 ||||| ||||| |||||
 ACCCTA AAAGG TGGTATGAA
 AAA AAAC
 GAM1436 LOC145815 5' ATGCTTCAGAAACACCTCA 40602 A CAC
 TGGG TGTTTCTGA CAT
 ||| ||||| |||
 ACTC ACAAAGACT GTA
 C TC_
 GAM1437 DNASE1L1 5' TCAAACACCCCTAACTCAG 13568 A T_
 CTGA TT GGGTGTGTTGA
 |||| || |||||
 GACT AA CCCACAACT
 C TC
 GAM1437 SLC6A6 3' ACTTCCAAGCTCAGTCTAAA 9002 A A T
 TTTA ACTGA TTTGGG GT
 |||| ||||| |||
 AAAT TGACT GAACCT CA
 C C T
 GAM1438 CKN1 3' TGGCTTAAACATGAAA 5532 CAA
 TTTCATGTT TGAGTCA
 ||||| |||||
 AAAGTACAA ATTCGGT
 —
 GAM1438 GCN1L1 3' ATCTCCACCCATTAAACATGAA 34567 C A CAT
 G TTTCATGTT AATG GT AGAT
 ||||| ||||| |||
 GAAGTACAA TTAC CA TCTA
 A C CC_
 GAM1438 TNFRSF10B 3' ATCCATGACCAAATTAAATATG 9934 C GA_ A
 AAA TTTCATGTT AAT GTCAT GAT
 ||||| ||| ||||| |||

		AAAGTATAA TTA CAGTA CTA	
		A AAC C	
GAM1438 ENAH	3'	ATCTATGACTTCTACAT 20123	TCAAT
		ATGT GAGTCATAGAT	
		TACA TTCAGTATCTA	
		TC__	
GAM1438 SLC5A7	3'	ATCTTTATCATTAAACATGAA 22388	C GTCAT
		TTCATGTT AATGA AGAT	
		AAGTACAA TTACT TCTA	
		A ATT__	
GAM1439 ARHI	3'	CTCTCACTAAAGATGTTA 11043	C CA
		TAACATTTT AG AGAG	
		ATTGTAGAA TC TCTC	
		A AC	
GAM1439 F8	3'	ATTCCTGCTGAAAAT 5614	AGA C
		ATTTTCAGCA GGA GT	
		TAAAAGTCGT CCT TA	
		__ T	
GAM1439 GALR1	3'	TCCTCTAAAAATGTTA 7218	CAGCA
		TAACATTTT AGAGGA	
		ATTGTAAAA TCTCCT	
		A__	
GAM1439 CAPN13	3'	CGAATCTTCCTGAAAATG 29379	C GGA
		CATTTTCAG AAGA CG	
		GTAAAAGTC TTCT GC	
		C AA_	
GAM1439 FLJ22794	3'	CACGTTTTGCCAAAAATG 44026	CA GAG
		CATTTT GCAA GACGTG	
		GTAAAA CGTT TTGCAC	
		AC __	
GAM1439 KIAA0212	3'	CACTGACTCATTGAAAATGTTA 16142	CAA GAC
		TAACATTTTCAG GAG GTG	
		ATTGTAAAAGTT CTC CAC	
		A__ AGT	
GAM1439 KIAA1317	3'	CACAGTTATCTTACTGAAAATG 41624	C G _
		CATTTTCAG AAGA GAC GTG	
		GTAAAAGTC TTCT TTG CAC	
		A A A	
GAM1439 KIAA1596	5'	CATGTACTATTAATGAAAATGT 35120	GCAAG G
TA		TAACATTTTCA AG ACGTG	

		ATTGTAAAAGT TC TGTAC		
		AATTA A		
GAM1439	MGC21854 3'	CTCCTGCTGAAAAATGTTA 27448	_	A
		TAACATTTT CAGCA GAG		
		ATTGTAAAA GTCGT CTC		
		A C		
GAM1439	STK17A 3'	TTCTACACTGAAAATGTTA 11153		CAAG
		TAACATTTTCAG AGGA		
		ATTGTAAAAGTC TCTT		
		ACA_		
GAM1439	LOC148545 3'	CATGTTCTTGCTGAAAA 38553		GG
		TTTTCAGCAAGA ACGTG		
		AAAAGTCGTTCT TGTAC		
		—		
GAM1439	LOC219347 5'	TGCCTCGCTGAAAAGT 44679	A	AA A
		AC TTTTCAGC GAGG CG		
		TG AAAAGTCG CTCC GT		
		— — —		
GAM1439	LOC51696 3'	CTCTTACTAAAATGTTA 18311		C C
		TAACATTTT AG AAGAG		
		ATTGTAAAA TC TTCTC		
		_ A		
GAM1440	MYEOV 5'	CATATTAGCTCCCACTCA 28999	A	T
		TGAGTG GGAGCTAAT GTG		
		ACTCAC CCTCGATTA TAC		
		— —		
GAM1440	SLC9A1 5'	CAGAGTCCCAGCTCCTCAGTCA 34855	G	A__ G
		TGA TGAGGAGCT ATT TG		
		ACT ACTCCTCGA TGA AC		
		G CCC G		
GAM1440	DKFZP434B205 3'	GGTGCCGCTCCTCACTCA 37127		TAATT TG
		TGAGTGAGGAGC G TC		
		ACTCACTCCTCG C GG		
		C__ GT		
GAM1440	DKFZp434F142 3'	ACAGGCCTAGCTCCTCCCTCA 25992	T	A__
		TGAG GAGGAGCTA TTGT		
		ACTC CTCCTCGAT GACA		
		C CCG		
GAM1440	FLJ14437 5'	TAAGGTAACTCCTCACTC 26310		C TG
		GAGTGAGGAG TAAT TG		

	CTCACTCCTC ATTG AT	
	A GA	
GAM1440 KIAA0522 3'	GCATATCCAGTCCTCACTCA 35624	AAT
	TGAGTGAGGAGCT TGTGT	
	ACTCACTCCTCGA ATACG	
	CCT	
GAM1440 MGC11287 3'	GACCAGACCCCTCACTCA 25500	AGCTAA T
	TGAGTGAGG TTG GTC	
	ACTCACTCC GAC CAG	
	CCA__ _	
GAM1440 NPC1L1 3'	TGACACACGCCCTCCTCA 15039	T A TAAT
	TGAG GAGG GC TGTGTCA	
	ACTC CTCC CG ACACAGT	
	_ _ C__	
GAM1440 PP3501 3'	CACCCCAGCTCCTCACTC 22330	AATT
	GAGTGAGGAGCT GTG	
	CTCACTCCTCGA CAC	
	CCC_	
GAM1440 LOC129676 5'	CAGGGTCCAGCTCCTCCTCA 37282	T A_ G
	TGAG GAGGAGCT ATT TG	
	ACTC CTCCTCGA TGG AC	
	_ CC G	
GAM1440 LOC145624 5'	TTGACACAACCCCTTCCCATTG 40549	A CTAA
A	TGAGTG GGAG TTGTGTCAA	
	ACTTAC CCTT AACACAGTT	
	_ CCCC	
GAM1440 LOC146988 3'	CGCTTCTAGCCCCTCTCTCA 40778	T A ATT
	TGAG GAGG GCTA GTG	
	ACTC CTCC CGAT CGC	
	T C CTT	
GAM1440 LOC147004 3'	TTGAATGTAACCTCCTCACTCA 40781	CTAATTGTG
	TGAGTGAGGAG TCAA	
	ACTCACTCCTT AGTT	
	CAATGTA__	
GAM1440 LOC148181 5'	GGCACAGTCCTCCCTCA 38481	T AATT
	TGAG GAGGAGCT GTGTC	
	ACTC CTCCTCGA CACGG	
	C ____	
GAM1440 LOC148930 3'	TTGGTGTCTTAACCTCCACCACT 38622	A_ C TT TG
CA	TGAGTG GGAG TAA G TCAA	

ACTCAC CCTC ATT T GGTT
 CA A C_ GT
 GAM1440 LOC150630 3' CAGTCCAGCCCCTTACTCA 41238 A A_
 TGAGTGAGG GCT ATTG
 ||||| ||| |||
 ACTCATTCC CGA TGAC
 C CC
 GAM1440 LOC151445 3' TGACACAGATATCCCCACCA 34420 A A GCTAA
 TG GTG GGA TTGTGTCA
 || ||| ||| |||||
 AC CAC CCT GACACAGT
 _ C ATA_
 GAM1440 LOC152313 5' TGA CTCAGAGCTTCTCACCCA 41481 A AA T
 TG GTGAGGAGCT TTG GTCA
 || ||||| ||| |||
 AC CACTCTTCGA GAC CAGT
 C _ T
 GAM1440 LOC154990 5' GGCACAGCTCCTCCCTCA 39521 T AATT
 TGAG GAGGAGCT GTGTC
 ||| ||||| |||
 ACTC CTCCTCGA CACGG
 C _
 GAM1440 LOC158476 5' TTGAGGGGTCCAGCTCCTCATC 42002 G AATTGTG
 A TGA TGAGGAGCT TCAA
 ||| ||||| |||
 ACT ACTCCTCGA AGTT
 _ CCTGGGG
 GAM1440 LOC158835 3' CACTAGCCCTCACTCA 39894 A ATT
 TGAGTGAGG GCTA GTG
 ||||| ||| |||
 ACTCACTCC CGAT CAC
 _ _
 GAM1440 LOC196872 5' GACCCGAGTCCTCACTCA 42417 G AAT T
 TGAGTGAGGA CT TG GTC
 ||||| || |||
 ACTCACTCCT GA GC CAG
 _ _ C
 GAM1440 LOC200261 3' TGCAAGCCCAGTCCTCACTCA 42753 G AA_
 TGAGTGAGGA CT TTGTG
 ||||| || |||
 ACTCACTCCT GA AACGT
 _ CCCG
 GAM1440 LOC222134 5' TTGACACAATCAGCTTTACTTA 45173 _ A
 TTCA TGAGTGAG GAGCT ATTGTGTCAA
 ||||| ||| |||||
 ACTTATTC TTCGA TAACACAGTT
 AT C
 GAM1440 LOC254173 3' ACAACAAGCTCCTCACCA 46286 A AA
 TG GTGAGGAGCT TTGT
 || ||||| |||

			AC CACTCCTCGA AACA		
			— AC		
GAM1440	LOC255975	5'	GGCACAGCTCCTCCCTCA 45891	T	AATT
			— TGAG GAGGAGCT GTGTC		
			ACTC CTCCTCGA CACGG		
			C —		
GAM1440	LOC256529	5'	GGGGCAGCTCCTCACCA 46589	A	AATT G
			— TG GTGAGGAGCT GT TC		
			AC CACTCCTCGA CG GG		
			— — G		
GAM1441	TPMT	3'	GCAACTCCTTGCTCACAGTGA 5938		ATTAAATT
			TTACT CAAGGAGTTGC		
			AGTGA GTTCCTCAACG		
			CACTC—		
GAM1441	HNRPA3	3'	GCATTTGTGAATTTAATAG 12323	AG	T
			CTATTAAATTCA GAGT GC		
			GATAATTTAAGT TTTA CG		
			G_ _		
GAM1441	LOC201564	3'	GCTGCTGAATTTAAATAGTAA 39200	_	A G
			TTACTATT AAATTCA G AGT		
			AATGATAA TTTAAGT C TCG		
			A _ G		
GAM1441	LOC220988	3'	GCATTTGTGAATTTAATAG 43682	AG	T
			CTATTAAATTCA GAGT GC		
			GATAATTTAAGT TTTA CG		
			G_ _		
GAM1442	GABRE	5'	CTTGGCAGATGGCCTTTAA 22530	A	TC TG
			TTAAA GCC TTTGT AG		
			AATTT CGG AGACG TC		
			C T_ GT		
GAM1442	ICOS	3'	CTTATCAAAGAGATTTTAA 14389	GC	T
			TTAAAA CTCTTTG TGAG		
			AATTTT GAGAAAC ATTC		
			A_ T		
GAM1442	NEBL	3'	GCCCATGGAGGAGGCTCTTGA 13101	A	GT A
			TTAA AGCCTCTTT TG GC		
			AGTT TCGGAGGAG AC CG		
			C GT C		
GAM1442	RAG1	3'	GCAGGGGTAAGCGGCTTTTAA 6038	—	
			TTAAAAGCC TCTTTGT		

		AATTTTCGG GGGGACG	
		CGAAT	
GAM1442 RBL2	3'	GCTCTGGCAAAGCTTTTAG 12132	CTC _
		TTAAAAGC TTTGTT GAGC	
		GATTTTCG AACCGG CTCG	
		____ T	
GAM1442 SH3BP2	3'	CAGGGAAGAAGCTTTTGA 8944	C G
		TTAAAAGC TCTTT TTG	
		AGTTTTCG AGAAG GAC	
		A G	
GAM1442 TAZ	3'	GCTCAAACGTGGCTTTTAG 5587	TCTTTG
		TTAAAAGCC TTGAGC	
		GATTTTCGG AACTCG	
		TGCA__	
GAM1442 TIM3	3'	GCTCAAACGGGCTTTTA 26525	CTTTG
		TAAAAGCCT TTGAGC	
		ATTTTCGGG AACTCG	
		CA__	
GAM1442 ZNF10	3'	CATCAAAGAAGCTTTTGA 17694	C T
		TTAAAAGC TCTTTG TG	
		AGTTTTCG AGAAAC AC	
		A T	
GAM1442 ZNF35	5'	CTCAAGAAGAAGCTTTTGA 9465	C G
		TTAAAAGC TCTTT TTGAG	
		AGTTTTCG AGAAG AACTC	
		A _	
GAM1442 C1orf22	3'	CTCTCTCAAGAAGCTTTTAA 24838	C TGTT
		TTAAAAGC TCTT GAG	
		AATTTTCG AGAA CTC	
		A CTCT	
GAM1442 C20orf180	3'	CAATAAAATGGCTTTTAA 20495	TC
		TTAAAAGCC TTTGTTG	
		AATTTTCGG AAATAAC	
		TA	
GAM1442 FLJ10751	3'	GCTCCCTGGAGGTTTTTAA 20094	TTGTT
		TTAAAAGCCTCT GAGC	
		AATTTTGGAGG CTCG	
		TCC__	
GAM1442 FLJ10751	3'	GCTCCCTGGAGGTTTTTAA 20193	TTGTT
		TTAAAAGCCTCT GAGC	

		AATTTTGGAGG	CTCG		
		TCC__			
GAM1442	FLJ22029	3'	GCCAGCATCAAGGCTTTTAA	24506	CTT A
			TTAAAAGCCT TGTTG GC		
			AATTTTCGGA ACGAC CG		
			ACT _		
GAM1442	GOLGA1	3'	CTCTATGGGAGTGGCTTTTAA	7860	T GTT_
			TTAAAAGCC CTTT GAG		
			AATTTTCGG GAGG CTC		
			T GTAT		
GAM1442	GS3955	5'	GCCCATTGTTGGGGCTTCTAA	22303	A TTGT A
			TTA AAGCCTCT TG GC		
			AAT TTCGGGGG AC CG		
			C TTT_ C		
GAM1442	KIAA0261	3'	GCTTAGCAAAATACTTTTAA	33833	CCTC
			TTAAAAG TTTGTTGAGC		
			AATTTTC AAACGATTCTG		
			ATA_		
GAM1442	NDRG4	3'	GCCCAAGGCAGCGAGGCTT	23214	T _ A
			AAGCCTC TTGT TG GC		
			TTCGGAG GACG AC CG		
			C GA C		
GAM1442	NDRG4	3'	GCCCAAGGCAGCGAGGCTT	21699	T _ A
			AAGCCTC TTGT TG GC		
			TTCGGAG GACG AC CG		
			C GA C		
GAM1442	NFX1	3'	CATTCAAAGAGGCTCTTTA	8325	_ T_
			TAAA AGCCTCTTTG TG		
			ATTT TCGGAGAAAC AC		
			C TT		
GAM1442	RNAHP	3'	CAGGAAAGAAGCTTTTAA	14300	C G
			TTAAAAGC TCTTT TTG		
			AATTTTCG AGAAA GAC		
			A G		
GAM1442	SEC15B	3'	GCTCTGCAGAGCTTTTAA	33124	CTC T
			TTAAAAGC TTTGT GAGC		
			AATTTTCG AGACG CTCG		
			_ T		
GAM1442	SLC26A10	5'	CAACAGTGGCTTTTAA	28559	TCT
			TTAAAAGCC TTGTTG		

			AATTTTCGG GACAAC		
			T__		
GAM1442	TU3A	3'	GCTCCAAGAGGCTCCTGA 14033	AA	TGTT
			TTA AGCCTCTT GAGC		
			AGT TCGGAGAA CTCG		
			CC C__		
GAM1442	ZFP91	3'	GCTCTCCAGTGGCTTTTAA 27576		TCT TT
			TTAAAAGCC TTG GAGC		
			AATTTTCGG GAC CTCG		
			T__ CT		
GAM1442	LOC130612	3'	GCTCCCAAGAGGCTCCTGA 36999	AA	TGTT
			TTA AGCCTCTT GAGC		
			AGT TCGGAGAA CTCG		
			CC CC__		
GAM1442	LOC151195	5'	CTTAGAAAGGCTTTTAA 39076		CTTTG
			TTAAAAGCCT TTGAG		
			AATTTTCGGA GATTC		
			AA__		
GAM1442	LOC152220	3'	CTCAACAAAGGGCTTTT 41442	T	
			AAAAGCC CTTTGTTGAG		
			TTTTCGG GAAACAAC		
			-		
GAM1442	LOC196527	3'	CTCAGATTTTAGAGGCTTTT 42399		TTG__
			AAAAGCCTCT TTGAG		
			TTTTCGGAGA GACTC		
			TTTTA		
GAM1442	LOC197358	3'	GCTCAGCTGGAAGCTTTTGA 42510	C	TT
			TTAAAAGC TCT GTTGAGC		
			AGTTTTTCG AGG CGACTCG		
			A T_		
GAM1442	LOC200734	3'	GCCACGGAGGAGGCTTCTAA 42840	A	GT A
			TTA AAGCCTCTTT TG GC		
			AAT TCGGAGGAG AC CG		
			C GC _		
GAM1442	LOC201164	3'	GCCCGGCCGGGCTTTTAA 42530		CTTT A
			TTAAAAGCCT GTTG GC		
			AATTTTCGGG CGGC CG		
			C__ C		
GAM1442	LOC254085	5'	CTCACAGTTAGGCTTTTA 45971	CT	T
			TAAAAGCCT TTGT GAG		

		ATTTTCGGA GACA CTC		
		TT _		
GAM1442	LOC257117 5'	GCCTATTAAGAGGCTTTT 46026	TGT A	
		AAAAGCCTCTT TG GC		
		TTTTCGGAGAA AT CG		
		TT_ C		
GAM1442	LOC257336 5'	CTCAACAATGGTCTTTT 46003	_ TCT	
		AAAAG CC TTGTTGAG		
		TTTTC GG AACAACTC		
		T T__		
GAM1443	NOLA1 5'	AAATTAGTGGTTAAGGTTATCT 21053	CT C	
	A	TAGG ATCTT AACCACTAATT		
		ATCT TGGAA TTGGTGATTAAA		
		AT _		
GAM1443	SRRM1 3'	AGTGAAGCTGAAGATAACCT 12449	C AC__	
		AGG TATCTTCA CACT		
		TCC ATAGAAGT GTGA		
		A CGAA		
GAM1443	CSL4 3'	GTGATATTGGAAATAGCCTA 18125	C C__	
		TAGGCTAT TTCAA CAC		
		ATCCGATA AGGTT GTG		
		A ATA		
GAM1443	PRMT6 3'	TGGTGTCTGAAATAGCCTA 19935	C AC_	
		TAGGCTAT TTCA CACTA		
		ATCCGATA AAGT GTGGT		
		_ CTT		
GAM1444	APG5L 3'	GCCTCTGGGATTTTACCAGTCA 11263	_ G C__	
		TGACTGGTAAA TT TA GC		
		ACTGACCATT AG GT CG		
		T G CTC		
GAM1444	SOCS5 3'	GCTCTACATCTTATCAGTCA 15226	AT C_	
		TGACTGGTAA TGTA GC		
		ACTGACTATT ACAT CG		
		CT CT		
GAM1444	XRCC2 3'	CTTTGTATTAATTTACCA 11902	TAC	
		TGGTAAATTG GCAAAG		
		ACCATTTAAT TGTTTC		
		TA_		
GAM1444	C21orf6 3'	GCTCCAATTTGCCAGCCA 18856	A TAC	
		TG CTGGTAAATTG GC		

AC GACCGTTTAAC CG
 C CT_
 GAM1444 FLJ11259 3' TTGCTTTACCAGTTA 20389 TTGTAC A
 TGACTGGTAAA GCA A
 ||||| |||
 ATTGACCATT CGT T
 C
 GAM1444 KIAA0514 5' GCCTTGCATATGGTTCTGACCA 16210 A__ TG C A
 GTCA TGACTGGT AAT TA GCAA GC
 ||||| || |||||
 ACTGACCA TTG AT CGTT CG
 GTC GT A C
 GAM1444 KIAA1317 3' GCTTTGTTTGTAACTTACCAG 41627 ATTG __
 T ACTGGTAA TAC GCAAAGC
 ||||| || |||||
 TGACCATT ATG TGTTTCG
 CAA_ TT
 GAM1444 ZNF300 5' TGAGGAAAATTTACCAGTCA 27441 GTACG
 TGACTGGTAAATT CA
 ||||| ||
 ACTGACCATTAA GT
 AAGGA
 GAM1444 LOC255018 5' CTTACGCCATATTCTTACCAG 46546 AT_ A_ CA
 TC GACTGGTAA TGT CG AAG
 ||||| || ||
 CTGACCATT ATA GC TTC
 CTT CC AC
 GAM1445 HGF 3' TAAATCACTTGTCATGAT 45225 C ACAA
 ATCG GA TGAGTGATTTA
 ||| || |||||
 TAGT CT GTTCACTAAAT
 A ____
 GAM1445 KIAA0218 3' CACTCATTGTCCATGATG 16515 CGA
 CATCG ACAATGAGTG
 |||| |||||
 GTAGT TGTTACTCAC
 ACC
 GAM1445 LOC153688 3' CATTCAATATCACGATG 41657 C AC
 CATCG GA AATGAGTG
 |||| || |||||
 GTAGC CT TTA CTAC
 A A_
 GAM1446 FBLN5 3' GACACAGACGTTAGGCATTTC 13024 CA ACC C
 GAAATGCC AAC TTG GTC
 ||||| || |||
 CTTTACGG TTG GAC CAG
 A_ CA_ A
 GAM1446 GNAI3 3' ATGCATTTTGAGCATTTC 13238 C CACCT
 TGAAATGC CAAA TCGT
 ||||| ||| ||||

			ACTTTACG GTTT	ACGTA		
			A T_____			
GAM1446	ILF1	3'	GGGGTCTTGGGCATTTC	10843	_ A	
			TGAAATGCCCAA AC CCT			
			ACTTTACGGGTT TG GGG			
			C _			
GAM1446	MPP2	3'	ATGTACTTGGGCATCTCA	30080	A	ACACCT
			TGA ATGCCCAA TGCGT			
			ACT TACGGGTT ATGTA			
			C C_____			
GAM1446	MTM1	3'	GTATTGTGTTTATGCATTTC	5790	CC	CT
			TGAAATGC AAACAC TGC			
			ACTTTACG TTTGTG ATG			
			TA TT			
GAM1446	DNCLI1	3'	ATGCAGTTTGGGCATTT	29927		ACCT
			AAATGCCCAAAC TGCGT			
			TTTACGGGTTTG ACGTA			

GAM1446	FBXO21	3'	GTTGGTATTTGGGCACTTTA	27325	A	C TT
			TGAA TGCCCAAA ACC GC			
			ATTT ACGGGTTT TGG TG			
			C A T_			
GAM1446	KIAA1615	3'	GACTTACTAGTTTGGGCATTT	34086		ACCTTGC
	CA		TGAAATGCCCAAAC GTC			
			ACTTTACGGGTTTG CAG			
			GATCATT			
GAM1446	PEG10	3'	TGCATCTGGGCATTTC	17432		AACACCT
			TGAAATGCCCA TGCG			
			ACTTTACGGGT ACGT			
			CT_____			
GAM1446	LOC155435	3'	ACGGATCCTGTTTGGGCCTTCA	39568	AT	CCTTG
			TGAA GCCCAAACA CGT			
			ACTT CGGGTTTGT GCA			
			C_ CCTAG			
GAM1446	LOC160717	5'	GAGGTGTTTGGCATCCCA	40008	AA	C
			TG ATGCC AAACACCTT			
			AC TACGG TTTGTGGAG			
			CC _			
GAM1446	LOC222865	3'	ATGCGTCACATGGGCATTTC	44621		AACACCT
			TGAAATGCCCA TGCGT			

		ACTTTACGGGT GCGTA	
		ACACT__	
GAM1447	ADAMTS1	5' TCTGCGCGCCCTTCCAACGAA 13853	AA_ T
		TTTGTTGGAAG GT CAGG	
		AAGCAACCTTC CG GTCT	
		CCG C	
GAM1447	AQP6	3' TCCTGAACCACTGGCCCCAAC 27618	A__ AA
		GTTGG AG GTTCAGGA	
		CAACC TC CAAGTCCT	
		CCGG AC	
GAM1447	DMD	5' CCTGAACAATGTCAACAAG 10160	AAGAA
		TTTGTTGG GTTCAGG	
		GAACAACCT CAAGTCC	
		GTAA_	
GAM1447	DMD	5' CCTGAACAATGTCAACAAG 10174	AAGAA
		TTTGTTGG GTTCAGG	
		GAACAACCT CAAGTCC	
		GTAA_	
GAM1447	ED1	3' CCCAAGCTTCCCAACAGA 7096	AA CA
		TTTGTTGG GAAGTT GG	
		AGACAACC CTTCGA CC	
		__ AC	
GAM1447	EGFR	3' TGGGCTCTTCCAACAAG 11727	A
		TTTGTTGGAAGA GTTCA	
		GAACAACCTTCT CGGGT	
		__	
GAM1447	FACL5	3' TCCTGAACCTGGGAACAAA 32108	GGAAGA
		TTTGTT AGTTCAGGA	
		AAACAA TCAAGTCCT	
		GGG__	
GAM1447	GAB2	3' CCACTACCTCCTCCAACAAA 27843	A A TCA
		TTTGTTGGA GA GT GG	
		AAACAACCT CT CA CC	
		C C TCA	
GAM1447	GAB2	3' CCACTACCTCCTCCAACAAA 14647	A A TCA
		TTTGTTGGA GA GT GG	
		AAACAACCT CT CA CC	
		C C TCA	
GAM1447	HOXB9	3' CCTCTCCTTCCAACAAA 23446	A TTC
		TTTGTTGGAAG AG AGG	

		AAACAACCTTC TC TCC	
		C _	
GAM1447 IMPDH1	3'	CCTAGCCTCCCAGCAAA 6578	AA A C
		TTTGTTGG GA GTT AGG	
		AAACGACC CT CGA TCC	
		_ C _	
GAM1447 KCNJ16	3'	TCCTGGGAGACTCCAACAAA 20730	AGAAG
		TTTGTTGGA TTCAGGA	
		AAACAACCT GGGTCCT	
		CAGA_	
GAM1447 NAGA	3'	CCTTCATTCTTTCAACAAA 5801	GTTC
		TTTGTTGGAAGAA AGG	
		AAACAACCTTTCTT TCC	
		ACT_	
GAM1447 NRIP1	3'	TCCTAAGAACAATGCCAACAAA 30120	AAGAA _
		TTTGTTGG GTTC AGGA	
		AAACAACC CAAG TCCT	
		GTAA_ AA	
GAM1447 POU4F1	3'	TCCTGGTAGAACCTTTCAACAA 12901	AAGT_
A		TTTGTTGGAAG TCAGGA	
		AAACAACCTTC GGTCT	
		CAAGAT	
GAM1447 SPON1	3'	CCAATGCATTCTTCAACAAA 31299	A _ TCA
		TTTGTTGGA GAA GT GG	
		AAACAACCTT CTT CG CC	
		C A TAA	
GAM1447 BMF	3'	CCTTCTTCCCCACCAACAAA 27277	AA_ TTC
		TTTGTTGG GAAG AGG	
		AAACAACC CTTC TCC	
		ACCC T_	
GAM1447 CASP9	3'	TCCTGAGTGGTGCCAAACAAA 6901	_ AAGAA
		TTTGTT GG GTTCAGGA	
		AAACAA CC TGAGTCCT	
		A GTGG_	
GAM1447 CECR7	5'	TCCCAGGCACCTCCAACAGA 38881	A AA CA
		TTTGTTGGA G GTT GGA	
		AGACAACCT C CGG CCT	
		_ CA AC	
GAM1447 CLECSF9	5'	CCTGAATCTTACCAACAAA 15688	_ AG
		TTTGTTGG AAGA TTCAGG	

		AAACAACC TTCT AAGTCC		
		A _		
GAM1447 CNOT8	3'	ACTTTTCCTTCCAGCAAA 11177		___
		TTTGTTGGAAG AAGT		
		AAACGACCTTC TTCA		
		CTT		
GAM1447 DCOHM	3'	TCCTGAACTCCTGGGCTCAAG 25850	TTGGA A	
		TTTG AG AGTTCAGGA		
		GAAC TC TCAAGTCCT		
		TCGGG C		
GAM1447 DDX17	5'	CCAGGCTTCTCCCAACAGA 25155	A CA	
		TTTGTTGG AGAAGTT GG		
		AGACAACC TCTTCGG CC		
		C A_		
GAM1447 FLJ10242	5'	TCCTGAAGCAGATCAACAAA 19777	AAGAAG	
		TTTGTTGG TTCAGGA		
		AAACAAC T AAGTCCT		
		AGACG_		
GAM1447 FLJ10936	3'	TCCTGAACTTCTCCCATTA 20271	T A	
		TTG TGG AGAAGTTCAGGA		
		AAT ACC TCTTCAAGTCCT		
		T C		
GAM1447 FLJ13614	3'	TCTGTTTCTTCCCACAAA 29149	T TT	
		TTTGT GGAAGAAG CAGG		
		AAACA CCTTCTTT GTCT		
		C _		
GAM1447 FLJ13881	3'	CCTGAACTCCTGAGCGACAGA 24067	GA_ A	
		TTTGTTG AG AGTTCAGG		
		AGACAGC TC TCAAGTCC		
		GAG C		
GAM1447 FLJ14082	5'	CCTGAGCTCCCACAAA 24609	T AGAA	
		TTTGT GGA GTTCAGG		
		AAACA CCT CGAGTCC		
		C _		
GAM1447 FLJ14117	3'	CTTGATTACCCCAACAAA 23049	AA GT	
		TTTGTTGG GAA TCAGG		
		AAACAACC CTT AGTTC		
		CA _		
GAM1447 FLJ21106	5'	CCGGAGACTTCTCCTAACAAA 24734	A CA_	
		TTTGTTGG AGAAGTT GG		

		AAACAATC TCTTCAG CC	
		C AGG	
GAM1447	FLJ32389	3' TCCCAGGCTTACTCTCCCAATA 29435	A ____ CA
	AA	TTTGTGTTGG AGA AGTT GGA	
		AAATAACC TCT TCGG CCT	
		C CAT AC	
GAM1447	GALNT12	3' CCAGGACTCTGCCCAACAAA 23927	A_ A A
		TTTGTGTTGG AGA GTTC GG	
		AAACAACC TCT CAGG CC	
		CG _ A	
GAM1447	HPIP	3' CCTTGCCCTTCCAACAAA 21736	AA TC
		TTTGTGTTGGAAG GT AGG	
		AAACAACCTTC CG TCC	
		C_ T_	
GAM1447	HRIHFB2122	3' CCTGAACCTCTTAACCTTAATAA 13899	____ A
	A	TTTGTGTTGG AAGA GTTCAGG	
		AAATAATT TTCT CAAGTCC	
		CAA C	
GAM1447	KIAA0057	3' TCCTCTTATTCTTCCACAAA 14626	T GTTC
		TTTGT GGAAGAA AGGA	
		AAACA CCTTCTT TCCT	
		_ ATTC	
GAM1447	KIAA0194	3' CCTCTTCCCCCAACAAG 32823	AA TTC
		TTTGTGTTGG GAAG AGG	
		GAACAACC CTTC TCC	
		CC ____	
GAM1447	KIAA0444	3' TCCTGAACTCCTCAAGCA 31246	G A A
		TGTT GA GA GTTCAGGA	
		ACGA CT CT CAAGTCCT	
		A C _	
GAM1447	KIAA0470	3' TCCTAAAATTTTCCAACA 16777	AG C
		TGTTGGAAGA TT AGGA	
		ACAACCTTTT AA TCCT	
		AA _	
GAM1447	KIAA0663	3' TCTAACTCTCCCAACAAA 16815	A A C
		TTTGTGTTGG AGA GTT AGG	
		AAACAACC TCT CAA TCT	
		C _ _	
GAM1447	KIAA1155	3' TCCTGAACCCCATTC AAGAAA 31200	G AGAA
		TTT TTGGA GTTCAGGA	

	AAA AACTT CAAGTCCT	
	G ACCC	
GAM1447 KIAA1416	5' CCCGAATCCTCCCCAACAAG 41803	AA A_ A
	TTTGTTGG GA GTTC GG	
	GAACAACC CT TAAG CC	
	C_ CC C	
GAM1447 KIAA1656	3' CCTGGGTTCTTCCACACAAA 32729	_ G
	TTTGT TGGAAGAA TTCAGG	
	AAACA ACCTTCTT GGGTCC	
	C _	
GAM1447 MGC20253	3' TCCTTTGAATGTTCCAACAAA 29398	GAA _
	TTTGTGGA GTTCA GGA	
	AAACAACCTT TAAGT CCT	
	G_ TT	
GAM1447 MGC4655	3' TCCTGAACTCACACAACAA 27149	GAA A
	TTGTTG GA GTTCAGGA	
	AACAAC CT CAAGTCCT	
	ACA _	
GAM1447 SLC39A3	3' CCTGTTCTTCTCCCAACGAA 29358	AA_ TT
	TTTGTTGG GAAG CAGG	
	AAGCAACC CTTC GTCC	
	CTC TT	
GAM1447 SNAP29	3' CCAAGTTCTTCCAGCAAA 11186	G CA
	TTTGTTGGAAGAA TT GG	
	AAACGACCTTCTT AA CC	
	G _	
GAM1447 SRF	3' TCCTCTCCTTCCCACAAA 9105	T A TTC
	TTTGT GGAAG AG AGGA	
	AAACA CCTTC TC TCCT	
	C C _	
GAM1447 SS18L1	3' CCTGACATCCAGCAAA 32561	AGAA T
	TTTGTTGGA GT CAGG	
	AAACGACCT CA GTCC	
	A_ _	
GAM1447 SYNE-1	3' TCCCAAACCTACCAACAAG 17614	AAGA CA
	TTTGTTGG AGTT GGA	
	GAACAACC TCAA CCT	
	A_ AC	
GAM1447 TED	3' CCAAAAGCAGCTCCAACAGA 17913	A AA CA_
	TTTGTTGGA G GTT GG	

		AGACAACCT C CGA CC	
		_GA AAA	
GAM1447 UNC5D	3'	TCCTGAACTACAAGCAAA 28115	GGAAGA
		TTTGTT AGTTCAGGA	
		AAACGA TCAAGTCCT	
		ACA__	
GAM1447 ZFP91	3'	TCCTATACCGCTCTCCCAACAA 27579	A A__ TC
A		TTTGTTGG AGA GT AGGA	
		AAACAACC TCT CA TCCT	
		C CGC TA	
GAM1447 LOC116437	3'	TCCTGAACTTCCTGTACCACA 36579	T AA__
		TGT GG GAAGTTCAGGA	
		ACA CC CTTCAAGTCCT	
		_ ATGTC	
GAM1447 LOC118987	3'	TCCCAAACGTGTTCCAACAA 36608	GAA CA
		TTGTTGGAA GTT GGA	
		AACAACCTT CAA CCT	
		GTG AC	
GAM1447 LOC121219	5'	TCCTAGCTGGTTCCAGCAAA 36652	GA C
		TTTGTTGGAA AGTT AGGA	
		AAACGACCTT TCGA TCCT	
		GG _	
GAM1447 LOC121506	3'	CCTGAACTCAGCAGA 36668	GAAGA
		TTTGTTG AGTTCAGG	
		AGACGAC TCAAGTCC	

GAM1447 LOC145225	3'	CCCAAACCTCCTCCAGCAAG 40524	A A CA
		TTTGTTGG AG AGTT GG	
		GAACGACC TC TCAA CC	
		C C AC	
GAM1447 LOC150054	5'	CCTAAAATTTCCAACAA 41125	AAG C
		TTGTTGGAAG TT AGG	
		AACAACCTTT AA TCC	
		AA_ _	
GAM1447 LOC151521	3'	CCTAAACTCTTCTCTCCCCAG 41368	A__ ____ C
CAAA		TTTGTTGG AGA AGTT AGG	
		AAACGACC TCT TCAA TCC	
		CCC CTTC A	
GAM1447 LOC219673	5'	TCCTAATTTAGGCCCTCCCAAC 44694	A ____ C
GAA		TTTGTTGG AG AAGTT AGGA	

	AAGCAACC TC	TTTAA TCCT	
	C CCGGA	_	
GAM1447 LOC220766 3'	TCCTAAAATTTTCCAACA	43656	AG C
	TGTTGGAAGA TT AGGA		
	ACAACCTTTT AA TCCT		
	AA _		
GAM1447 LOC253350 5'	CCTGCATTTGCTCTTCTAACAA	46586	___ T
A	TTTGTTGGAAGA AGT CAGG		
	AAACAATCTTCT TTA GTCC		
	CGT C		
GAM1447 LOC257336 5'	CCTGGGAGCTCCACACAAA	46002	_ A AAG
	TTTGT TGA G TTCAGG		
	AAACA ACCT C GGGTCC		
	C _ GA_		
GAM1447 LOC257358 3'	TCCTGAACCTCAAATCAACA	46390	AA_ A
	TGTTGG GA GTTCAGGA		
	ACAAC CT CAAGTCCT		
	AAA C		
GAM1447 LOC51634 3'	TCCTGAACTTTGGTTCATAAA	18102	T A_
	TTTGT GGA GAAGTTCAGGA		
	AAATA CTT TTTCAAGTCCT		
	_ GG		
GAM1447 LOC91133 3'	CCTGAACTTCCTCTGGCA	32430	TG A
	TGT GA GAAGTTCAGG		
	ACG CT CTTCAAGTCC		
	GT C		
GAM1447 LOC92344 3'	CCTGACCTCCAATAAA	34209	AGAA T
	TTTGTTGGA G TCAGG		
	AAATAACCT C AGTCC		
	___ C		
GAM1447 LOC93070 3'	TCCTGAACTTCTCCCATTA	35326	T A
	TTG TGG AGAAGTTCAGGA		
	AAT ACC TCTTCAAGTCCT		
	T C		
GAM1447 LOC93259 5'	TCCTGAACCTGGAACAA	35561	GGA AA
	TTGTT AG GTTCAGGA		
	AACAA TC CAAGTCCT		
	GG_ _		
GAM1448 MPHOSPH9 3'	CTGGGAGAAGAATAAATCA	23065	C G G
	TGATTTATTC TC TCC AG		

		ACTAAATAAG AG AGG TC	
		A _ G	
GAM1448	DKFZP566J2046 3'	CATCTCGGACTTGCTGAATCA 25251	TTCCTC
		TGATTTA GTCCGAGATG	
		ACTAAGT CAGGCTCTAC	
		CGTT__	
GAM1448	NY-REN-60 3'	CATCTAAGAAGAAATAGATCA 33317	CC G CG
		TGATTTATT TC TC AGATG	
		ACTAGATAA AG AG TCTAC	
		__ A AA	
GAM1448	ZDHC5 5'	CATCAAGAGAGAAATAAATTA 44009	C G CGA
		TGATTTATT CTC TC GATG	
		ATTAAATAA GAG AG CTAC	
		A _ AA_	
GAM1448	LOC196549 5'	TCATCTCAAATGATTATAAAT 29808	TCC CC_
	CA	TGATTTAT TCGT GAGATGA	
		ACTAAATA AGTA CTCTACT	
		TT_ AAA	
GAM1448	LOC205327 3'	CATCAAGGAAATAAATCA 43104	CCTCG GA
		TGATTTATT TCC GATG	
		ACTAAATAA AGG CTAC	
		____ AA	
GAM1449	ALEX2 5'	GCAGAACTTGTAAGCCTAAACT 16634	ACT A
	G	TAGTTTAGGC TGA TTCTGC	
		GTCAAATCCG GTT AAGACG	
		AAT C	
GAM1449	FOX1 5'	CAGTAATCCTAAACTA 10780	CACTTGA _
		TAGTTTAGG ATT CTG	
		ATCAAATCC TAA GAC	
		____ T	
GAM1449	LRP4 3'	GCAAAATCTCTGTCCCTAAAC 32201	C TT_ _ C
	TA	TAGTTTAGG AC GA ATT TGC	
		ATCAAATCC TG CT TAA ACG	
		_ TCT C A	
GAM1449	SNX5 3'	GGCAGAATCCAAATACTGGGTT 15785	TT GCAC A
		AG TAG TTG ATTCTGCC	
		TT GTC AAC TAAGACGG	
		GG ATA_ C	
GAM1449	TFDP1 3'	GCAGAATTCAACTTTTAAAC 13976	CAC
		GTTTAGG TTGAATTCTGC	

CAAATTT AACTTAAGACG
 TTC
 GAM1449 C5orf5 3' GCAAAATATTATGCCTAAAGTA 18698 G CTTGA C
 TA TTTAGGCA ATT TGC
 || ||||| ||| |||
 AT AAATCCGT TAA ACG
 G ATTA_ A
 GAM1449 FLJ20552 3' GCAAAATTCAAGAACAACAACTG 19548 AGGCA C
 TAGTTT CTTGAATT TGC
 ||||| ||||| |||
 GTCAAA GAACTTAA ACG
 ACAA_ A
 GAM1449 P114-RHO-GEF 3' GGCAGAATCCACTTCCCAAAC 17640 A CACT A
 GTTT GG TG ATTCTGCC
 ||| || || |||||
 CAAA CC AC TAAGACGG
 C TTC_ C
 GAM1449 LOC118851 3' GCAGAATTCCTGCCAAAGC 37201 A CTT
 GTTT GGCA GAATTCTGC
 ||| ||| |||||
 CGAA CCGT CTTAAGACG
 A C_
 GAM1450 KIAA1128 3' GCATCCCAAGGCCACTAACACA 33969 A A_ G
 TGTGTTAGT GCCT GA GC
 ||||| ||| |||
 ACACAATCA CGGA CT CG
 C ACC A
 GAM1450 LOC150225 3' AAACACCCCTAGGCTGTGGAAG 41184 G AG A C
 CA TGT TT TAGCCTAG GG GTTT
 ||| || ||||| || |||
 ACG AG GTCGGATC CC CAAA
 A GT C A
 GAM1451 CCNT2 3' ATAAGGTGGTTGTGCTACTGTA 27769 C TCGG
 TACAG AGCGCA CGCCTTAT
 |||| ||||| |||||
 ATGTC TCGTGT GTGGAATA
 A TG_
 GAM1451 KIAA1161 5' AAGACGCCGGTGCTGCTCA 39744 C AT C
 A AGCAGCGC CGGCG CTT
 | ||||| ||||| |||
 A TCGTCGTG GCCGC GAA
 C _ A
 GAM1451 KIAA1274 3' AAGGTGCACACTGCTGTG 43907 CGCATCG
 TACAGCAG GCGCCTT
 ||||| |||||
 GTGTCGTC CGTGGAA
 ACA_
 GAM1452 CYFIP2 5' TGGACCCGCCGCAGAGCCA 36440 A AAC
 TGGCTCTGC GCG TCTA
 ||||| ||| |||

		ACCGAGACG CGC AGGT		
		C CC_		
GAM1452 ELL	3'	AGACAGCTGCTCAGAGCCA 13279	___	GAAC
		TGGCTCT GCAGC TCT		
		ACCGAGA CGTCG AGA		
		CT AC_		
GAM1452 GNAS	5'	GGAGCCGCTCTCTGCAGAGCCA 18680		C A_
		TGGCTCTGCAG GA CTCT		
		ACCGAGACGTC CT GAGG		
		T CGCC		
GAM1452 GRB10	5'	AGACAGTGCTACAGAGCCA 11784	C	AAC
		TGGCTCTG AGCG TCT		
		ACCGAGAC TCGT AGA		
		A GAC		
GAM1452 SBF1	5'	AGAGCCACTGCAGAGTCA 32625		CGAA
		TGGCTCTGCAG CTCT		
		ACTGAGACGTC GAGA		
		ACC_		
GAM1452 TRIM14	3'	AGAATCTCACTATCAGAGCCA 16665	C_ C	AC_
		TGGCTCTG AG GA TCT		
		ACCGAGAC TC CT AGA		
		TA A CTA		
GAM1452 C11orf9	3'	TGGAGCCCGCTGCAGGCCA 14947	T	AA
		TGGC CTGCAGCG CTCTA		
		ACCG GACGTCGC GAGGT		
		_ CC		
GAM1452 C5orf7	3'	AGAGGCCCTTCACCCAGAGCCA 31940	CAGC	___
		TGGCTCTG GAA CTCT		
		ACCGAGAC CTT GAGA		
		CCA_ CCCG		
GAM1452 CXYorf1	5'	GGTAGAGCAGAGCCGGAGCCA 39911	CA	GAA_
		TGGCTCTG GC CTCTACC		
		ACCGAGGC CG GAGATGG		
		_ AGAC		
GAM1452 FLJ10743	3'	GGGAGGTCCCCACAGAGCCA 20080	CAGC	A T A
		TGGCTCTG GA C CT CCC		
		ACCGAGAC CT G GA GGG		
		ACCC _ _ _		
GAM1452 FLJ22593	5'	AGACAACGCTGCAGAGCC 24017		AAC
		GGCTCTGCAGCG TCT		

	CCGAGACGTCGC AGA	
	AAC	
GAM1452 FLJ22944 3'	GGTAGTTGGGCTGCAGAGTCA 24782	GAACT
	TGGCTCTGCAGC CTACC	
	ACTGAGACGTCG GATGG	
	GGTT_	
GAM1452 KIAA0620 3'	AGAAGTCTCACCGGCAGAGCCA 31119	AGC_ _ _
	TGGCTCTGC GA ACT CT	
	ACCGAGACG CT TGA GA	
	GCCA C A	
GAM1452 KIAA0864 5'	AGGCATTGCTGCAGAACC 31683 C	AC
	GG TCTGCAGCGA TCT	
	CC AGACGTCGTT GGA	
	A AC	
GAM1452 KIAA1432 5'	GTAGATTTACTGCAGAGC 33151	CG C
	GCTCTGCAG AA TCTAC	
	CGAGACGTC TT AGATG	
	AT _	
GAM1452 KIAA1719 3'	GGTAGAATCAGTAGAGCCA 33822	AGC AC
	TGGCTCTGC GA TCTACC	
	ACCGAGATG CT AGATGG	
	A_ A_	
GAM1452 LOC129607 3'	GGACACTCCTGCAGAGCCA 36974	C AC_
	TGGCTCTGCAG GA TCT	
	ACCGAGACGTC CT AGG	
	_ CAC	
GAM1452 LOC154089 3'	GGCAGAAACAACCTCCAGAGCCA 39463	C CGAAC A
	TGGCTCTG AG TCT CC	
	ACCGAGAC TC AGA GG	
	C AACAA C	
GAM1452 LOC200093 5'	GGTAGAGCAGAGCCGGAGCCA 31603	CA GAA_
	TGGCTCTG GC CTCTACC	
	ACCGAGGC CG GAGATGG	
	_ AGAC	
GAM1452 LOC221876 5'	CGGGCGGTGCGCTGCAGGCCA 45076	T AACT TA
	TGGC CTGCAGCG C CCCG	
	ACCG GACGTCGC G GGGC	
	_ GT_ GC	
GAM1452 LOC91040 5'	GGTAGAGCAGAGCCGGAGCCA 32320	CA GAA_
	TGGCTCTG GC CTCTACC	

		ACCGAGGC CG GAGATGG	
		___ AGAC	
GAM1453 CERD4	3'	ACATGGCATTGTGGGAAAGC 14341	___ CA C
		GCTT CCCAAA CT TGT	
		CGAA GGGTTT GG ACA	
		A AC T	
GAM1453 CHAC	3'	CCAAAACCTGTTTGGGAAGC 27139	CTCTG
		GCTTCCCAAACA TTTGG	
		CGAAGGGTTTGT AAACC	
		CCA___	
GAM1453 CRH	5'	CCTGCGAAGCGCCTGGGAAGC 6409	AACA C TT
		GCTTCCCA CT TGT GG	
		CGAAGGGT GA GCG CC	
		CCGC A T_	
GAM1453 DDEF1	3'	CCAAACAGAGCATGAGGAACCA 29963	C _ AACA
		TGG TTCC CA CTCTGTTTGG	
		ACC AAGG GT GAGACAAACC	
		_ A AC___	
GAM1453 DNASE2	3'	CAGCACTTTGGGAAGCCA 7048	CACT
		TGGCTTCCCAA CTG	
		ACCGAAGGGTTT GAC	
		CAC_	
GAM1453 SLC9A5	3'	CAAACAGAGAAGGAACCCA 30062	C CAAACA
		TGG TTCC CTCTGTTTG	
		ACC AAGG GAGACAAAC	
		C AA___	
GAM1453 VHL	3'	CAGTACTTTGGGAAGCCA 6159	CACT
		TGGCTTCCCAA CTG	
		ACCGAAGGGTTT GAC	
		CAT_	
GAM1453 ARFGAP1	3'	CCAGCACAAAGGGCCCAGGAAG 20107	CAAACA C _
	CCA	TGGCTTCC CT TGT TTGG	
		ACCGAAGG GA ACA GACC	
		ACCCGG A C	
GAM1453 CNM2	3'	CCAAACAGGGATTGAGAAACCA 19153	C CCAAACA
		TGG TTC CTCTGTTTGG	
		ACC AAG GGGACAAACC	
		A ACTTA___	
GAM1453 DKFZp547D155	3'	CCAGGCAGCGCCCCAGGAAGCC 34868	CAAACACT
	A	TGGCTTCC CTGTTTGG	

			ACCGAAGG	GACGGACC		
			ACCCCGC_			
GAM1453	DKFZP564B1023	3'	CAAAGCTTTGGGAAGCCA	25341		CACTCTG
			TGGCTTCCCAA	TTTG		
			ACCGAAGGGTTT	AAAC		
			CG_____			
GAM1453	FLJ12428	3'	AAACATTTGGGAAACCA	23066	C	CACTC
			TGG TTCCCAA	TGTTT		
			ACC AAGGGTTT	ACAAA		
			A _____			
GAM1453	FLJ20694	3'	CAGCACTTTGGGAAGCCA	19607		CACT
			TGGCTTCCCAA	CTG		
			ACCGAAGGGTTT	GAC		
			CAC_			
GAM1453	FLJ22693	5'	TCAAACATCCAGGGAAGCCA	22974		AAACACTC
			TGGCTTCCC	TGTTTGG		
			ACCGAAGGG	ACAAACT		
			ACCT_____			
GAM1453	KIAA0972	5'	CCAAACAGATGCAGAAGAACCC	17226	C	CCAAA C
	A		TGG TTC	CA TCTGTTTGG		
			ACC AAG	GT AGACAAACC		
			C AAGAC _			
GAM1453	KIAA1056	3'	CAGCACTTTGGGAAGCCA	17047		CACT
			TGGCTTCCCAA	CTG		
			ACCGAAGGGTTT	GAC		
			CAC_			
GAM1453	KIAA1871	3'	CAGCACTTTGGGAAGCCA	30704		CACT
			TGGCTTCCCAA	CTG		
			ACCGAAGGGTTT	GAC		
			CAC_			
GAM1453	MAN1	3'	CCAAGAAGTGTTTGGATAACCA	15616	CTTC	CTG
			TGG CCAAACACT	TTTGG		
			ACC GGTTTGTGA	GAACC		
			AATA	A_		
GAM1453	MRPS18B	3'	CAGCACTTTGGGAAGCCA	15274		CACT
			TGGCTTCCCAA	CTG		
			ACCGAAGGGTTT	GAC		
			CAC_			
GAM1453	ZAK	3'	CAGATACTTGGGAGGCCA	28605		AACTC
			TGGCTTCCCAA	TGTTTG		

	ACCGGAGGGTT	ATAGAC	
	C_____		
GAM1453 LOC142779 3'	CAAACAGAAGGGAAAACA	37559	GC AAACAC
	TG TTCCC TCTGTTTG		
	AC AAGGG AGACAAAC		
	AA A_____		
GAM1453 LOC143381 3'	CCTCTGAGCACTTGGGCAGCCA	37613	T ACA TGTTT
	TGGCT CCCAA CTC GG		
	ACCGA GGGTT GAG CC		
	C CAC TCT__		
GAM1453 LOC148823 3'	GAGTACTTTGGGAAGCCA	29793	C_
	TGGCTTCCCAA ACTC		
	ACCGAAGGGTTT TGAG		
	CA		
GAM1453 LOC159036 3'	CAGCACTTTGGGAAGCCA	42052	CACT
	TGGCTTCCCAA CTG		
	ACCGAAGGGTTT GAC		
	CAC_		
GAM1453 LOC161823 3'	CAGCACTTTGGGAAGCCA	40033	CACT
	TGGCTTCCCAA CTG		
	ACCGAAGGGTTT GAC		
	CAC_		
GAM1453 LOC203350 3'	CAGCACTTTGGGAAGCCA	43532	CACT
	TGGCTTCCCAA CTG		
	ACCGAAGGGTTT GAC		
	CAC_		
GAM1453 LOC257464 3'	CCAGGACACAATCTGGGAAGCC	43165	AACACTC _
A	TGGCTTCCCA TGTT TGG		
	ACCGAAGGGT ACAG ACC		
	CTAAC__ G		
GAM1453 LOC257482 3'	CCAAACAGGATCTGGAAAACC	45235	C C AACAC
	GG TT CCA TCTGTTTG		
	CC AA GGT GGACAAACC		
	A A CTA__		
GAM1453 LOC90288 3'	TAAATGCTGTGGGAAGCCA	31113	AACACTCT
	TGGCTTCCCA GTTTG		
	ACCGAAGGGT TAAAT		
	GTCG__		
GAM1453 LOC92228 3'	CCAGGCATACACAGGAAGCCA	34003	CAAACACTC
	TGGCTTCC TGTTTG		

ACCGAAGG ACGGACC
 ACACAT____
 GAM1454 CD244 3' CCAGAGCACATGCTGACCTGA 18524 AC C TCG
 TCAG TC GC GTGCTCTGG
 |||| ||| |||||
 AGTC AG CG CACGAGACC
 C_ T TA_
 GAM1454 HS3ST3A1 5' TCCTTGCCGAGAGAACCTGA 12679 AC CG GCTCT
 TCAG TC CTCGGT GGA
 |||| || ||||| |||
 AGTC AG GAGCCG CCT
 CA A_ GTT_
 GAM1454 PRX 3' CCAGAACATCCAGAGTCTG 21933 CGCTC C
 CAGACTC GGTG TCTGG
 ||||| ||| |||||
 GTCTGAG CTAC AGACC
 AC____ A
 GAM1454 RASD1 5' CCAGCCCCGAGCGGAGCCGGA 18168 AGA T CT
 TC CTCCGCTCGG GCT GG
 || ||||| ||| ||
 AG GAGGCGAGCC CGA CC
 GCC _ _
 GAM1454 SLC4A10 3' CCAAAGCATTGAAAGCCGA 22594 C _ C
 TC GC TCGGTGCT TGG
 || || ||||| |||
 AG CG AGTTACGA ACC
 C AA A
 GAM1454 SPHK2 3' CCAATGGGGCGGAGCCTGA 21312 A G GCTC
 TCAG CTCCGCTC GT TGG
 |||| ||||| || |||
 AGTC GAGGCGGG TA ACC
 C G ____
 GAM1454 TGM2 3' CAGAGCAGAGTCTGG 10952 CGCTCGG _
 TCAGACTC TGCTCT G
 ||||| ||||| |
 GGTCTGAG ACGAGA C
 A
 GAM1454 ZNF278 3' CCAAAAACAAAATGGAGTCTGA 25783 CTCG GCTC
 TCAGACTCCG GT TGG
 ||||||| || |||
 AGTCTGAGGT CA ACC
 AAAA AAA_
 GAM1454 APCL 3' CCAAGCGCTCCGGCGGAG 12497 T T T _
 CTCCGC CGG GC CT GG
 ||||| ||| || |||
 GAGGCG GCC CG GA CC
 _ T C A
 GAM1454 CGRP-RCP 3' CCAGAGCACTGTTGGAAGTCTG 15822 _ CT
 G TCAGACT CCG CGGTGCTCTGG
 ||||| ||| |||||

GGTCTGA GGT GTCACGAGACC
A T_

GAM1454 DKFZP564M182 3' CCAAAGCTGCAGAGTCTGA 38218 C TC GCTC
TCAGACTC GC GGT TGG
||||||| || ||| |||
AGTCTGAG CG TCG ACC
A _ AAA_

GAM1454 KIAA1171 3' TCCAGGGCTCCAAGCTGAGTCT 42482 C C T
GA TCAGACTC GCT GG GCTCTGGA
||||||| ||| || |||||||
AGTCTGAG CGA CC CGGGACCT
T A T

GAM1454 LIPG 3' CCAGAGCACCAAGTCCAG 12654 CC C
CT GCT GGTGCTCTGG
|| ||| |||||||
GA TGA CCACGAGACC
CC A

GAM1454 MGC10715 5' TCCAGAGCAGAGGAATCT 23615 C GCTCGG
AGA TCC TGCTCTGGA
||| ||| |||||||
TCT AGG ACGAGACCT
A AG_

GAM1454 MGC4504 3' CCAGAGCAGAGCTGGAGCTGA 23560 A _ GG
TCAG CTCC GCTC TGCTCTGG
|||| ||| ||| |||||||
AGTC GAGG CGAG ACGAGACC
_ T _

GAM1454 LOC142955 5' CCAGAGCAAGAAAAGCTGA 37572 A CCGC GG
TCAG CT TC TGCTCTGG
|||| || || |||||||
AGTC GA AG ACGAGACC
_ AA_ A_

GAM1454 LOC165257 5' CCAGCGGAGCGGAGCCTGG 40128 A G TGCT
TCAG CTCCGCTC G CTGG
|||| ||||||| | |||
GGTC GAGGCGAG C GACC
C G_

GAM1454 LOC91266 5' CCCTGCACCCGAGCGGCACCT 32601 ACT _ TCT
AG CCGCTCGG TGC GG
|| ||||||| ||| ||
TC GGCGAGCC ACG CC
CAC C TC_

GAM1455 VDR 3' CGGGGAACCTCCTGAAATAT 5946 C A _
ATA TTCAG AGT CTCCG
||| ||||| ||| |||||
TAT AAGTC TCA GGGGC
A C A

GAM1455 FLJ20281 5' CTGAAGACTTCTAAGATATTA 43726 _ C C
TAATA CTT AGAAGTCT CGG
||||| ||| ||||||| |||

		ATTAT GAA TCTTCAGA GTC	
		A _ A	
GAM1455	SLC26A7	3' TCCATTTCTGAAGTATT 27416	CTCC
		AATACTTCAGAAGT GGA	
		TTATGAAGTCTTTA CCT	

GAM1455	LOC134266	3' CCTTTCTGCTTCTGAAGTAT 37067	CTCC_
		ATACTTCAGAAGT GG	
		TATGAAGTCTTCG CC	
		TCTTT	
GAM1455	LOC144438	3' CGGTCTTCTGAAGTAT 37736	TCT
		ATACTTCAGAAG CCG	
		TATGAAGTCTTC GGC	
		T_	
GAM1456	FACL2	3' AGTTCCACAATCTCTTCT 22096	_
		AGAAGAGATTG GGAAGT	
		TCTTCTCTAAC CCTTGA	
		A	
GAM1456	PKHD1	3' ACAGAACTTCAAGTCTCTTC 28936	GG C
		GAAGAGATT GAA TTCTGT	
		CTTCTCTGA CTT AAGACA	
		A_ C	
GAM1456	ARL8	3' ACAGAAATTTTAGCTCTTTTCT 44760	TTG C
		AGAAGAGA GGAA TTCTGT	
		TCTTTTCT TTTT AAGACA	
		CGA A	
GAM1456	DKFZp547H025	3' CGACAGAAAGAAGTCTCTTCT 21370	GGGAAC
		AGAAGAGATT TTCTGTCTG	
		TCTTCTCTGA AAGACAGC	
		AGA_	
GAM1456	DKFZP761F241	3' CAGCCATTCCAATCTCTTCT 25476	ACTT
		AGAAGAGATTGGGA CTG	
		TCTTCTCTAACCTT GAC	
		ACC_	
GAM1456	FLJ13881	3' CGACAGAAGCCCCAGGCCTC 24068	A_ AA
		GAG TTGGG CTTCTGTCTG	
		CTC GACCC GAAGACAGC	
		CG C_	
GAM1456	FLJ22644	3' CAGATTCCCAACTCTTCT 24740	A CT
		AGAAGAG TTGGGAA TCTG	

TCTTCTC AACCCTT AGAC

GAM1456 KIAA0258 3' CAGGTGGTCCCCAGATCTCTTC 16644 _ A _
GAAGAGAT TGGG ACT TCTG
||||||| ||| ||| |||
CTTCTCTA ACCC TGG GGAC
G C T

GAM1456 KIAA0296 3' CAGTGTTGCTCCCATCTCTTCT 16217 T _ TT
AGAAGAGAT GGGA AC CTG
||||||| ||| ||| |||
TCTTCTCTA CCCT TG GAC
_ CGT T_

GAM1456 KIAA1100 3' CAGACCCGTGCCCAATCTCCTC 17083 A A T_
T AGA GAGATTGGG AC TCTG
||| ||||||| ||| |||
TCT CTCTAACCC TG AGAC
C G CCC

GAM1456 SLC25A21 3' AGGTATTCCAAATCTCTTCT 24966 G CT
AGAAGAGATT GGAA TCT
||||||| ||| ||| |||
TCTTCTCTAA CCTT GGA
A AT

GAM1456 LOC149372 3' CGACAGAAGTCCAATTTTCTT 38729 TTG A
AAGAGA GGA CTTCTGTCTG
||||| ||| |||||||
TTCTTT CCT GAAGACAGC
TAA _

GAM1456 LOC154860 5' CGACAGAAGCTGGGCGCTTT 41735 AGA TG GAA
GAAG T G CTTCTGTCTG
|||| | | |||||||
TTTC G C GAAGACAGC
GCG GT _

GAM1456 LOC197358 5' ACAGAAGTCTGACCTCTCT 42505 A A TG GA
AG AGAG T G ACTTCTGT
|| ||| | | |||||||
TC TCTC A C TGAAGACA
_ C GT _

GAM1456 LOC257177 5' ACAAAGAGAGCATCTCTTCT 45675 TGGGAA C
AGAAGAGAT CTT TGT
||||||| ||| |||
TCTTCTCTA GAA ACA
CGAGA_ A

GAM1457 ZNF146 5' CATTTCTCTCAAACCTTA 13993 AC C
TAAGGTTT GAGGAA GTG
||||||| ||||||| |||
ATTCCAAA CTCCTT TAC
CT _

GAM1457 KIAA0063 3' AACCATGTCCAAAACC 17015 ACGA A
GGTTT GGA CGTGGTT
||||| ||| |||||||

		CCAAA CCT GTACCAA		
		A__ _		
GAM1457	KIAA0676	3' AAACCACAGATAATAACAAACC 17391	ACGAGGAAC_	
		TTA TAAGGTTT GTGGTTT		
		ATTCCAAA CACCAAA		
		CAATAATAGA		
GAM1457	NXPH3	3' AACAGATTTCCTCCCAAACCTT 32711	AC CGTG	
		A TAAGGTTT GAGGAA GTT		
		ATTCCAAA CTCCTT CAA		
		CC TAGA		
GAM1458	CALCRL	3' ACAAAACACCTTGTCAACCTC 12375	ATC T _	
		GAG TTG GCA GTGTTTGT		
		CTC AAC TGT CACAAAACA		
		C_ _ TC		
GAM1458	CDK10	3' ACAACCTGAAGCACAAGTTCCC 27553	A T AG TT	
		A TG GA CTTGTGC TG TTGT		
		AC CT GAACACG GT AACA		
		C T AA CC		
GAM1458	ADAM9	3' ACAAAACACCACAAAACAGACT 9905	A _ _ CA	
		TCA TGAG TCT TGTG GTGTTTGT		
		ACTT AGA ACAC CACAAAACA		
		C CAAA _		
GAM1458	KIAA1164	3' ACAAAACAAAACAAAACACTCA 34439	ATC GCAG	
		TGAG TTGT TGTTTTGT		
		ACTC AACA ACAAAACA		
		AA_ AA_		
GAM1458	KIAA1211	3' ACAAAACAGGCGAAATACCTCA 34158	ATCTTG AG	
		TGAG TGC TGTTTTGT		
		ACTC GCG ACAAAACA		
		CATAAA G_		
GAM1458	KIAA1458	3' ACAAAACAGAACAAGTCTCA 34202	T GCAG	
		TGAGA CTTGT TGTTTTGT		
		ACTCT GAACA ACAAAACA		
		_ AG_		
GAM1458	MGC5566	3' ACAATGTTGGCACAAGACTCA 23485	A AGTGTT	
		TGAG TCTTGTGC TTGT		
		ACTC AGAACACG AACA		
		_ GTTGT_		
GAM1458	PANK	3' ACAAAGTTAAGCACAAGATCT 28714	AGTG	
		AGATCTTGTGC TTTTGT		

TCTAGAACACG GAAACA
 AATT
 GAM1458 LOC146667 5' ACATGTGTACACAGATCTCA 40710 _ _
 TGAGATCT TGTGCA GTGT
 ||||| ||||| ||||
 ACTCTAGA ACATGT TACA
 C G
 GAM1458 LOC147184 5' AACGGTGAACACAAGATTCA 29786 A _ G
 TGAG TCTTGTG CA TGTT
 ||| ||||| || ||||
 ACTT AGAACAC GT GCAA
 _ AA G
 GAM1458 LOC149448 3' ACAAACAAAACAAAACCCTCA 40989 ATC_ GCAG
 TGAG TTGT TGTTTTGT
 ||| ||| |||||
 ACTC AACA ACAAACA
 CCAA AA_
 GAM1458 LOC200531 5' ACAAACACCATGTGGAGACTC 42817 A G _
 A TGAG TCTT TGCA GTGTTTTGT
 ||| ||| ||| |||||
 ACTC AGAG GTGT CACAAAACA
 _ _ AC
 GAM1458 LOC257443 3' ACAAACAGAACAAGTCTCA 45871 T GCAG
 TGAGA CTTGT TGTTTTGT
 |||| ||| |||||
 ACTCT GAACA ACAAACA
 _ AG_
 GAM1458 LOC51301 5' ACAAACACTGTAGGGAACCTC 18669 A_ G
 GAG TCTT TGCAGTGTTTTGT
 || ||| |||||
 CTC AGGG ATGTCACAAAACA
 CA _
 GAM1458 LOC90110 5' ACATACACAAGATCCA 30840 A CA
 TG GATCTTGTG GTGT
 || ||||| |||
 AC CTAGAACAC TACA
 _ A_
 GAM1459 CYP1A1 3' ACACAACAATCCTTCTATTCTA 6111 AG A GCTA
 TA ATAGAA GGGTTG TGT
 || ||||| ||||| |||
 AT TATCTT CCTAAC ACA
 CT _ AAC_
 GAM1459 LAD1 3' ACAGCAGCACCTTTCCTCTC 12084 TA_ TG A_
 GA GAAAGGGT GCT TGT
 || ||||| ||| |||
 CT CTTTCCCA CGA ACA
 CTC _ CG
 GAM1459 LIPE 5' ACATAGTCCCCTCCTATT 11825 AA TT
 GATAG AGGG GGCTATGT
 |||| ||| |||||

TTATC TCCC CTGATACA
 C_ _
 GAM1459 SVIL 3' TCAACCTTTCTACCTTA 9149 A G
 TAAG TAGAAAGG TTGG
 ||| ||||| |||
 ATTC ATCTTTCC AACT
 C _
 GAM1459 SVIL 3' TCAACCTTTCTACCTTA 22346 A G
 TAAG TAGAAAGG TTGG
 ||| ||||| |||
 ATTC ATCTTTCC AACT
 C _
 GAM1459 KIAA0189 3' CATAACAGCCCCTTTCTCA 16317 T _ GC
 A AGAAAGGG TTG TATG
 | ||||| || |||
 A TCTTTCCC GAC ATAC
 C C A_
 GAM1459 NUDT11 3' ACACAGCTAGCTCCTCATC 30136 A AA A
 GAT GA GGGTTGGCT TGT
 ||| || ||||| |||
 CTA CT CTCGATCGA ACA
 _ C_ C
 GAM1459 PLAGL2 3' AGCAACCCTTCTCACCTTA 34873 AT_ A G
 TAAG AGAA GGGTTG CT
 ||| ||| ||||| ||
 ATTC TCTT CCCAAC GA
 CAC _ _
 GAM1459 PRO2958 3' CTAACCCTTTCTACCTTA 20625 A
 TAAG TAGAAAGGGTTGG
 ||| ||||| |||||
 ATTC ATCTTTCCCAATC
 C
 GAM1459 LOC154790 5' ACATAGCCGCCAGACCTCTTC 39489 AG ____
 GAA GGTT GGCTATGT
 ||| ||| |||||
 CTT CCAG CCGATACA
 CT ACCG
 GAM1459 LOC203197 3' ACACAGCCAACCCTGCTGCTCT 43008 T AA__ A
 CT AGA AG AGGGTTGGCT TGT
 ||| || ||||| |||
 TCT TC TCCCAACCGA ACA
 C GTCG C
 GAM1459 LOC254249 5' ACATACCTACCCTTTTCTACCT 45711 A _ T C
 AG TAGAAA GGGT GG TATGT
 || ||||| ||| || |||||
 TC ATCTTT CCCA CC ATACA
 C T T _
 GAM1460 KIAA0237 3' CAGCCCTCCTAATACCTCA 16441 A AAC
 TGAG TATTAGGG CTG
 ||| ||||| |||

		ACTC ATAATCCT GAC	
		C CCC	
GAM1460 KIAA0453	3'	CGGCCCCCTTCCCCAAATCCCA 34229	A A A CCT A
		TG GAT TT GGGAA GG CCG	
		AC CTA AA CCCTT CC GGC	
		C _ C CC _ _	
GAM1460 MGC10812	3'	CTGGGGGCTCCTCTAACATCTC 25411	A _ A__ TG
A		TGAGAT TTAG GGA CC G	
		ACTCTA AATC CCT GG C	
		C T CGG GT	
GAM1460 LOC219397	3'	CGGCCCAGGTTCCCCGACCTC 44899	ATATTA A
		GAG GGGAACCTGG CCG	
		CTC CCCTTGGACC GGC	
		CACGC_ C	
GAM1461 MS4A3	3'	ATCAGCATTATAAAAAGTGT 12777	A _ C
		ACGCTTTTTG AA GC GAT	
		TGTGAAAAAT TT CG CTA	
		A A A	
GAM1462 PDE4D	3'	TGATGGGATGGTGTGATATA 36437	T _ C
		TAT TCAACACCA CCC TCG	
		ATA AGTTGTGGT GGG AGT	
		T A T	
GAM1462 PPP1R8	3'	GGGGGTGGGGTTGAAATA 28855	A
		TATTTCAAC CCACCCCT	
		ATAAAGTTG GGTGGGGG	
		G	
GAM1462 PPP1R8	3'	GGGGGTGGGGTTGAAATA 8569	A
		TATTTCAAC CCACCCCT	
		ATAAAGTTG GGTGGGGG	
		G	
GAM1462 PPP1R8	3'	GGGGGTGGGGTTGAAATA 15339	A
		TATTTCAAC CCACCCCT	
		ATAAAGTTG GGTGGGGG	
		G	
GAM1462 SUDD	3'	TGAAGTTATGGGTGACTTGAAA 9924	CAC CTCG_
TA		TATTTCAA CACCC TTCA	
		ATAAAGTT GTGGG AAGT	
		CA_ TATTG	
GAM1462 KIAA0603	3'	GACAAGCTGTGTTGAAATA 16828	CACCC C
		TATTTCAACAC CT GTT	

		ATAAAGTTGTG	GA CAG	
		TC__ A		
GAM1462	MEGF10	3' AATGCTTTCAGTGTTGAAATA	26208	CACCCCT
		TATTTCAACAC	CGTT	
		ATAAAGTTGTG	GTAA	
		ACTTTC_		
GAM1462	MGC13008	5' AGGAAGTAGGGTTGAAATA	26406	A _ C_
		TATTTCAAC	CC AC CCT	
		ATAAAGTTG	GG TG GGA	
		_ A AA		
GAM1462	MGC14156	3' AGGAGTGATGTTGGAATA	26727	C C
		TATTTCAACA	CAC CCT	
		ATAAGGTTGT	GTG GGA	
		A A		
GAM1462	PCDH10	5' CGAGGACAGTCTTGAAATA	26768	C CACC
		TATTTCAA	AC CCTCG	
		ATAAAGTT	TG GGAGC	
		C ACA_		
GAM1462	PCDH10	5' CGAGGACAGTCTTGAAATA	21883	C CACC
		TATTTCAA	AC CCTCG	
		ATAAAGTT	TG GGAGC	
		C ACA_		
GAM1462	TRIM2	3' TGAATCTTTGGTGTATTGAAAT	17604	__ CCCCTC
	A	TATTTCA	ACACCA GTTCA	
		ATAAAGT	TGTGGT TAAGT	
		TA	TTC__	
GAM1462	LOC142893	5' TGAACCACTAGGGTGTTGAAA	40321	ACCCCTC
		TTTCAACACC	GTTCA	
		AAAGTTGTGG	CAAGT	
		GATCAC_		
GAM1462	LOC148545	3' GGAAAGTGGTTTGAAATA	38554	C C__
		TATTTCAA	ACCAC CC	
		ATAAAGTT	TGGTG GG	
		_ AAA		
GAM1462	LOC150170	5' GATGATGGTGTTGAAG	38862	CCCC
		TTTCAACACCA	TCGTT	
		GAAGTTGTGGT	AGTAG	

GAM1462	LOC150175	5' GATGATGGTGTTGAAG	38884	CCCC
		TTTCAACACCA	TCGTT	

GAAGTTGTGGT AGTAG

GAM1462 LOC150215 5' GATGATGGTGTTGAAG 38888 CCCC
TTTCAACACCA TCGTT
||||||| ||||
GAAGTTGTGGT AGTAG

GAM1462 LOC150218 5' GATGATGGTGTTGAAG 38915 CCCC
TTTCAACACCA TCGTT
||||||| ||||
GAAGTTGTGGT AGTAG

GAM1463 DATF1 3' ACGCTACACACCCACATGA 22650 GTAC A
TCA GG TGTGTGGTGT
||| || |||||
AGT CC ACACATCGCA
ACA_ C

GAM1463 DATF1 3' ACGCTACACACCCACATGA 28061 GTAC A
TCA GG TGTGTGGTGT
||| || |||||
AGT CC ACACATCGCA
ACA_ C

GAM1463 DDX28 5' GCTCCACACACCGTACTGA 20411 A T
TCAGTACGG TGTGTGG GT
||||||| ||||| ||
AGTCATGCC ACACACC CG
_ T

GAM1463 KIAA0014 3' ATAGACATCTCACCAGCACTGA 16112 ACGGAT T
TCAGT GTG GGTGTCTAT
||||| ||| |||||
AGTCA CAC CTACAGATA
CGAC_ T

GAM1463 LOC158156 3' AGAGTGGCACATCCTACTGA 39736 C GG G
TCAGTA GGATGTGT T TCT
||||| ||||| |||
AGTCAT CCTACACG G AGA
_ GT_

GAM1464 CIT 3' TTTCAGCAAACCAACCTC 34566 A ATC
GAGGT GTG TGCTGAAG
||||| ||| |||||
CTCCA CAC ACGACTTT
C CAA

GAM1464 DEDD 3' GCCCTCAGCAGAACTTC 26880 AGTGA A
GAGGT TCTGCTGA GGC
||||| ||||| |||
CTTCA AGACGACT CCG
_ C

GAM1464 NUMA1 3' GCCTTCAGCAGCAGCTCA 44882 T GAT
G AGT CTGCTGAAGGC
||| |||||

A TCG GACGACTTCCG
 C AC_
 GAM1464 FLJ10916 5' AGCCTTCAGCAGATTCCGTC 20249 _ TAGT
 GA GG GATCTGCTGAAGGCT
 || || |||||
 CT CC TTAGACGACTTCCGA
 G ____
 GAM1464 FLJ20584 3' CCCCCACAAGTCACTGCCTC 19559 TC C AA
 GAGGTAGTGA TG TG GG
 ||||| || ||
 CTCCGTCAC T AC AC CC
 GA _ CC
 GAM1464 KIAA1508 3' GCCTTTTCATCACTACCCG 30995 A CTGCT
 CG GGTAGTGAT GAAGGC
 || ||||| ||||
 GC CCATCACTA TTTCCG
 _ CT____
 GAM1464 MGC2705 5' AGCCTCGTCCTGGACCCCTACC 26414 TGA C__ A
 TCG CGAGGTAG TCTG TGA GGCT
 ||||| ||| || ||||
 GCTCCATC AGGT GCT CCGA
 CCC CCT _
 GAM1464 PLAC3 5' AGCCTTCAACAACCAACAACC 34364 A GATC C
 GGT GT TG TGAAGGCT
 ||| || || |||||
 CCA CA AC ACTTCCGA
 A ACCA A
 GAM1464 LOC149837 3' AGCCTTCAACAATGGCACCATC 41098 _ A G C C
 GA GGT GT AT TG TGAAGGCT
 || ||| || || |||||
 CT CCA CG TA AC ACTTCCGA
 A _ G _ A
 GAM1464 LOC51292 5' AGCCCTCAGATTCATCGCTACC 18652 A CTG_ A
 CCG CG GGTAGTGAT CTGA GGCT
 || ||||| ||| ||||
 GC CCATCGCTA GACT CCGA
 C CTTA C
 GAM1465 EGR2 3' TGGATGTCAGAGTTGATCTA 5973 C G G
 TGGATCAAC CTGAC AT CA
 ||||| |||| || ||
 ATCTAGTTG GACTG TA GT
 A _ G
 GAM1465 INHBB 3' TGCAATTAAAGGGTTGACCCA 7948 A GACGA_
 TGG TCAACCCT TGCA
 || ||||| ||||
 ACC AGTTGGGA ACGT
 C AATTA
 GAM1465 PACE4 3' TGCATTGTTAATCATCCA 8432 CAACCC
 TGGAT TGACGATGCA
 |||| |||||

		ACCTA ATTGTTACGT	
		CTA____	
GAM1465	PACE4	3' TGCATTGTTAATCATCCA 28721	CAACCC
		TGGAT TGACGATGCA	
		ACCTA ATTGTTACGT	
		CTA____	
GAM1465	FLJ21615	3' CTGTCTTCTCAGCAGTTGATCC 25911	C_ C TGC
	A	TGGATCAAC CTGA GA ACAG	
		ACCTAGTTG GACT CT TGTC	
		AC _ TC_	
GAM1465	KCNS1	3' TGGATCCCCAGAGTTGATCCA 8048	C AC G
		TGGATCAAC CTG GAT CA	
		ACCTAGTTG GAC CTA GT	
		A CC G	
GAM1465	KIAA1045	3' CGTCCCCCAGGATTGATCCA 35195	C AC_
		TGGATCAA CCTG GATG	
		ACCTAGTT GGAC CTGC	
		A CCC	
GAM1465	LOC152195	3' TGTCATCTAGGTTAATCCA 41434	C CTGAC C
		TGGAT AACC GATG ACA	
		ACCTA TTGG CTAC TGT	
		A AT____ _	
GAM1465	LOC199990	3' TGTGTGTCAAAGTTGTCCA 42685	T CC GAT
		TGGA CAAC TGAC GCACA	
		ACCT GTTG ACTG TGTGT	
		_ AA _	
GAM1466	ADCY6	5' TGGCCAGGCTGGTCTTGAAC 17593	C _ A A
		GTTCA AGACT CTT GG CCA	
		CAAGT TCTGG GGA CC GGT	
		_ TC _ _	
GAM1466	BCL10	3' TGGCCAGGCTGGTCTTGAAC 10010	C _ A A
		GTTCA AGACT CTT GG CCA	
		CAAGT TCTGG GGA CC GGT	
		_ TC _ _	
GAM1466	CARD15	3' TGGTTGATGCCTGTGAAC 22720	AC_ TTAG
		GTTCACAG TC GACCA	
		CAAGTGTC AG TTGGT	
		CGT ____	
GAM1466	CDC6	3' TGGCCAGGCTGGTCTTGAAC 6924	C _ A A
		GTTCA AGACT CTT GG CCA	

			CAAGT TCTGG GGA CC GGT		
			— TC — —		
GAM1466	CDH17	3'	TGGCCAGGCTGGTCTTGAAC 10271	C	— A A
			GTTCA AGACT CTT GG CCA		
			CAAGT TCTGG GGA CC GGT		
			— TC — —		
GAM1466	CHRM1	3'	GTGCTGAGTCTGTGAAT 45442	TT	G
			G TTCACAGACTC AG AC		
			TAAGTGTCTGAG TC TG		
			— G		
GAM1466	COX15	3'	TGGCCGGGCTGGTCTTGAAC 27792	C	CTTA_ A
			GTTCA AGACT GG CCA		
			CAAGT TCTGG CC GGT		
			— TCGGG —		
GAM1466	DSCR3	3'	TGGCCAGGCTGGTCTTGAAC 12689	C	— A A
			GTTCA AGACT CTT GG CCA		
			CAAGT TCTGG GGA CC GGT		
			— TC — —		
GAM1466	FBLN5	3'	GTTCAAAGACTGTGAAC 13025	AC	A
			G TTCACAG TCTT GGAC		
			CAAGTGTC AGAA CTTG		
			— A		
GAM1466	FLRT2	3'	GGGAAAAGAGTCTGTGAA 14883	AGGA	
			TTCACAGACTCTT CC		
			AAGTGTCTGAGAA GG		
			AAG_		
GAM1466	GNE	3'	TGGCCAGGCTGGTCTTGAAC 11977	C	— A A
			GTTCA AGACT CTT GG CCA		
			CAAGT TCTGG GGA CC GGT		
			— TC — —		
GAM1466	GRAF	3'	GGTTAGATCTGTGAAC 17444	C	TAG
			G TTCACAGA TCT GACC		
			CAAGTGTCT AGA TTGG		
			— — —		
GAM1466	GRIK3	3'	TGGTCCTAATCTTCTGAAC 6487	C_	CTC
			GTTCA AGA TTAGGACCA		
			CAAGT TCT AATCCTGGT		
			CT — —		
GAM1466	KIF2	3'	GGA ACTAAAGTCTGTGA 10849	C	GA
			TACACAGACT TTAG CC		

AGTGTCTGA AATC GG
 _ AA
 GAM1466 LENG4 3' TGGTCCCGGGAATTCTGTGAAC 23588 C_ TA
 GTTCACAGA TCT GGACCA
 ||||| ||| |||||
 CAAGTGTCT AGG CCTGGT
 TA GC
 GAM1466 MYB 3' TGGTCTTAGCCTGTAGAC 29944 TC ACTC
 GT ACAG TTAGGACCA
 || ||| |||||
 CA TGTC GATTCTGGT
 GA C__
 GAM1466 NCALD 3' TTCTAAGCTGTGAAC 25747 ACT
 GTTCACAG CTTAGGA
 ||||| |||||
 CAAGTGTC GAATCTT

 GAM1466 PCDHA9 3' TGGATGGAGACTGTGAAC 15213 A TAGGA
 GTTCACAG CTCT CCA
 ||||| ||| |||
 CAAGTGTC GAGG GGT
 A TA__
 GAM1466 PDGFRA 3' TGGTCCTATTTTGTGAA 12886 CTCT
 TTCACAGA TAGGACCA
 ||||| |||||
 AAGTGTTT ATCCTGGT
 TT__
 GAM1466 PEA15 3' TGGCCCCCTGGGCTTGTGAAC 9853 GA TTA A
 GTTCACA CTC GG CCA
 ||||| ||| |||
 CAAGTGT GGG CC GGT
 TC TCC C
 GAM1466 PIK3R1 3' GTCTGATCTGTGAAT 34038 C TTA
 GTTCACAGA TC GGAC
 ||||| || |||
 TAAGTGTCT AG TCTG

 GAM1466 PPEF2 3' TGGTCAGGCTGGTCTTGAAC 12905 C CTTAG
 GTTCA AGACT GACCA
 |||| |||| ||||
 CAAGT TCTGG CTGGT
 _ TCGGA
 GAM1466 RPH3AL 3' TGGCCAGGCTGGTCTTGAAC 13849 C _ A A
 GTTCA AGACT CTT GG CCA
 |||| |||| ||| |||
 CAAGT TCTGG GGA CC GGT
 _ TC _ _
 GAM1466 SEDL 3' TGGTCAGGCTGGTCTTGAAC 15915 C CTTAG
 GTTCA AGACT GACCA
 |||| |||| ||||

		CAAGT TCTGG CTGGT		
		_ TCGGA		
GAM1466	SEDL	3' TGGTCAGGCTGGTCTTGAAC 15916	C	CTTAG
		GTTCA AGACT GACCA		
		CAAGT TCTGG CTGGT		
		_ TCGGA		
GAM1466	SH3BP2	3' TGGCCAGGCTGGTCTTGAAC 8952	C	_ A A
		GTTCA AGACT CTT GG CCA		
		CAAGT TCTGG GGA CC GGT		
		_ TC _ _		
GAM1466	SLC22A12	5' GGCCCCGAGTCTGTGAA 29405		TTA A
		TTCACAGACTC GG CC		
		AAGTGTCTGAG CC GG		
		CC_ _		
GAM1466	TBXA2R	3' TGGCCAGGCTGGTCTTGAAC 6731	C	_ A A
		GTTCA AGACT CTT GG CCA		
		CAAGT TCTGG GGA CC GGT		
		_ TC _ _		
GAM1466	TEC	3' GTCTAGAGTCTGTGCAC 9219 T		TA
		GT CACAGACTCT GGAC		
		CA GTGTCTGAGA TCTG		
		C _		
GAM1466	TRPS1	3' GGTCTTGAGACCTGTGAAC 15357		AC
		GTTCACAG TCTTAGGACC		
		CAAGTGTC AGAGTTCTGG		
		C_		
GAM1466	USP9Y	3' TGGTCCTAATCTGTAAAT 32018	C	CTC
		GTT ACAGA TTAGGACCA		
		TAA TGTCT AATCCTGGT		
		A _		
GAM1466	WHSC1	3' GGTCCTACTGCTGTGAGC 17185		ACTCT
		GTTCACAG TAGGACC		
		CGAGTGTC ATCCTGG		
		GTC_		
GAM1466	WHSC1	3' GGTCCTACTGCTGTGAGC 28449		ACTCT
		GTTCACAG TAGGACC		
		CGAGTGTC ATCCTGG		
		GTC_		
GAM1466	WHSC1	3' GGTCCTACTGCTGTGAGC 28466		ACTCT
		GTTCACAG TAGGACC		

			CGAGTGTC ATCCTGG			
			GTC__			
GAM1466	ZNF264	3'	TGGCCAGGTTGGTCTTGAAC 9463	C	__	A A
			GTTCA AGACT CTT GG CCA			
			CAAGT TCTGG GGA CC GGT			
			__ TT __			
GAM1466	ARHF	3'	TGGCCAGGCTGGTCTTGAAC 21122	C	__	A A
			GTTCA AGACT CTT GG CCA			
			CAAGT TCTGG GGA CC GGT			
			__ TC __			
GAM1466	ARPP-19	3'	TGGCCAGGCTGGTCTTGAAC 13425	C	__	A A
			GTTCA AGACT CTT GG CCA			
			CAAGT TCTGG GGA CC GGT			
			__ TC __			
GAM1466	C11orf25	3'	GTCTGAGTCTGTGCAC 25401 T			TTA
			GT CACAGACTC GGAC			
			CA GTGTCTGAG TCTG			
			C __			
GAM1466	C1QTNF6	3'	TGGCCAGGCTGGTCTTGAAC 25660	C	__	A A
			GTTCA AGACT CTT GG CCA			
			CAAGT TCTGG GGA CC GGT			
			__ TC __			
GAM1466	C9orf9	3'	TGGCCAGGCTGGTCTTGAAC 21030	C	__	A A
			GTTCA AGACT CTT GG CCA			
			CAAGT TCTGG GGA CC GGT			
			__ TC __			
GAM1466	CALN1	3'	TGGAGCTAAGAGTCCGTAAC 25520	C A		GA
			GTT AC GACTCTTAG CCA			
			CAA TG CTGAGAATC GGT			
			__ C GA			
GAM1466	CARD6	3'	TGGTCAGGCTGGTCTTGAAC 26323	C		CTTAG
			GTTCA AGACT GACCA			
			CAAGT TCTGG CTGGT			
			__ TCGGA			
GAM1466	CBX6	3'	TGGTCCTAAGAATGGGA 15579	A		GAC
			TTC CA TCTTAGGACCA			
			AGG GT AGAATCCTGGT			
			__ A__			
GAM1466	CDC14A	3'	GTTTTAGTTCTGTGAAC 9766			CTC
			GTTACAGA TTAGGAC			

CAAGTGTCT GATTTTG
T__
GAM1466 CHRAC1 3' GTCTAGTCTGTGAAT 18906 CTTA
GTTACAGACT GGAC
||||||| |||
TAAGTGTCTGA TCTG

GAM1466 DKFZP434F0318 3' TGGCCAGGCTGGTCTTGAAC 25144 C _ A A
GTTCA AGACT CTT GG CCA
|||| ||| || |||
CAAGT TCTGG GGA CC GGT
_ TC _ _

GAM1466 DKFZP564G092 5' TGGCCAGGCTGGTCTTGAAC 17878 C _ A A
GTTCA AGACT CTT GG CCA
|||| ||| || |||
CAAGT TCTGG GGA CC GGT
_ TC _ _

GAM1466 DKFZP564O0463 3' TGGCAAAGTCTGTGAGC 15446 CTT GA_
GTTACAGACT AG CCA
||||||| || |||
CGAGTGTCTGA TC GGT
_ AAAC

GAM1466 DKFZp761O0113 5' TGGTCAGGCTGGTCTTGAAC 20449 C CTTAG
GTTCA AGACT GACCA
|||| ||| |||
CAAGT TCTGG CTGGT
_ TCGGA

GAM1466 EIF2C2 3' TGGTTTTAAAGCCTTGAAC 35614 C A C
GTTCA AG CT TTAGGACCA
|||| || ||| |||
CAAGT TC GA AATTTTGGT
_ C _

GAM1466 FLJ12903 3' TGGTCAGGCTGGTCTTGAAC 22984 C CTTAG
GTTCA AGACT GACCA
|||| ||| |||
CAAGT TCTGG CTGGT
_ TCGGA

GAM1466 FLJ13188 3' TGGTCAGGCTGGTCTTGAAC 22607 C CTTAG
GTTCA AGACT GACCA
|||| ||| |||
CAAGT TCTGG CTGGT
_ TCGGA

GAM1466 FLJ13197 3' TGGCCAGGCTGGTCTTGAAC 23875 C _ A A
GTTCA AGACT CTT GG CCA
|||| ||| || |||
CAAGT TCTGG GGA CC GGT
_ TC _ _

GAM1466 FLJ14084 3' CCTGTTAGAAGTCTGTGAGC 22285 _ _
GTTACAGACT CT TAGG
||||||| || |||

		CGAGTGTCTGA GA GTCC	
		A TT	
GAM1466	FLJ14950	3' TGGCCAGGCTGGTCTTGAAC 26678	C _ A A
		GTTCA AGACT CTT GG CCA	
		CAAGT TCTGG GGA CC GGT	
		_ TC _ _	
GAM1466	FLJ14957	3' TGGTCAGGCTGGTCTTGAAC 26685	C CTTAG
		GTTCA AGACT GACCA	
		CAAGT TCTGG CTGGT	
		_ TCGGA	
GAM1466	FLJ20010	3' TGGCCCTCACTTAGCTTGTGAA 21110	GA CTT_ A
	C	GTTCACTA CT AGG CCA	
		CAAGTGT GA TCC GGT	
		TC TTCAC C	
GAM1466	FLJ20695	3' TGGTCTTGTAATTGTGAAC 19615	ACTCT
		GTTCAACAG TAGGACCA	
		CAAGTGTT GTTCTGGT	
		AAT_	
GAM1466	FLJ22944	3' TGGCCCTGCCACTGTGGAC 24784	ACTCT A
		GTTCAACAG TAGG CCA	
		CAGGTGTC GTCC GGT	
		ACC_ C	
GAM1466	FLJ23519	3' TGGTCCTGTGTACCTGCGGAC 25978	A ACTCT
		GTTCA CAG TAGGACCA	
		CAGG GTC GTCCTGGT	
		C CATGT	
GAM1466	FLJ31101	3' TGGCCAGGCTGGTCTTGAAC 19687	C _ A A
		GTTCA AGACT CTT GG CCA	
		CAAGT TCTGG GGA CC GGT	
		_ TC _ _	
GAM1466	FLJ31153	3' TGGCCAGGCTGGTCTTGAAC 29415	C _ A A
		GTTCA AGACT CTT GG CCA	
		CAAGT TCTGG GGA CC GGT	
		_ TC _ _	
GAM1466	GREB1	3' TGGCCAGGCTGGTCTTGTGAAC 16126	_ _ A A
		GTTCACTA GACT CTT GG CCA	
		CAAGTGT CTGG GGA CC GGT	
		T TC _ _	
GAM1466	GRP3	3' TGGGACTGAGCCTGTGAAT 17674	ACT GA
		GTTCAACAG CTTAG CCA	

		TAAGTGTC GAGTC GGT		
		C__ AG		
GAM1466 HSMPP8	3'	TGGTCAGGCTGGTCTTGAAC 44905	C	CTTAG
		GTTCA AGACT GACCA		
		CAAGT TCTGG CTGGT		
		_ TCGGA		
GAM1466 JM11	3'	TGGCCAGGCTGGTCTTGAAC 27333	C	_ A A
		GTTCA AGACT CTT GG CCA		
		CAAGT TCTGG GGA CC GGT		
		_ TC _ _		
GAM1466 KIAA0087	3'	TGGCCAGGCTGGTCTTGAAC 16561	C	_ A A
		GTTCA AGACT CTT GG CCA		
		CAAGT TCTGG GGA CC GGT		
		_ TC _ _		
GAM1466 KIAA0352	3'	TGGTCCTAAATTTTATGA 16826	C	CTC
		TCA AGA TTAGGACCA		
		AGT TTT AATCCTGGT		
		A TA_		
GAM1466 KIAA0449	3'	GTTCAGTCCTGTGAAC 19054	_	CTTA
		GTTCACAG ACT GGAC		
		CAAGTGTC TGA CTTG		
		C _ _ _		
GAM1466 KIAA0472	5'	TGGCCAGGCTGGTCTTGAAC 35584	C	_ A A
		GTTCA AGACT CTT GG CCA		
		CAAGT TCTGG GGA CC GGT		
		_ TC _ _		
GAM1466 KIAA0513	5'	TGGCCAGGCTGGTCTTGAAC 16364	C	_ A A
		GTTCA AGACT CTT GG CCA		
		CAAGT TCTGG GGA CC GGT		
		_ TC _ _		
GAM1466 KIAA0557	3'	TGGTCAGGCTGGTCTTGAAC 38213	C	CTTAG
		GTTCA AGACT GACCA		
		CAAGT TCTGG CTGGT		
		_ TCGGA		
GAM1466 KIAA0828	3'	GTCTGATCTGTGGAC 39516	C	TTA
		GTTCACAGA TC GGAC		
		CAGGTGTCT AG TCTG		
		_ _ _		
GAM1466 KIAA0831	3'	TGGCCAGGCTGGTCTTGAAC 17210	C	_ A A
		GTTCA AGACT CTT GG CCA		

	CAAGT TCTGG GGA CC GGT	
	TC _ _	
GAM1466 KIAA1198 3'	TGGCCAGGCTGGTCTTGAAC 31719	C _ A A
	GTTCA AGACT CTT GG CCA	
	CAAGT TCTGG GGA CC GGT	
	TC _ _	
GAM1466 KIAA1257 3'	TGGCCAGGCTGGTCTTGAAC 31443	C _ A A
	GTTCA AGACT CTT GG CCA	
	CAAGT TCTGG GGA CC GGT	
	TC _ _	
GAM1466 KIAA1430 3'	GGATCAGGCCTGTGAAC 39358	ACT A A
	G TTCACAG CTT GG CC	
	CAAGTGTC GGA CT GG	
	C _ _ A	
GAM1466 KIAA1500 3'	TGGTCCTAAGGAAGCATGAGC 32070	CAGAC
	GTTCA TCTTAGGACCA	
	CGAGT GGAATCCTGGT	
	ACGAA	
GAM1466 KIAA1655 3'	TGGCCAGGCTGGTCTTGAAC 33092	C _ A A
	GTTCA AGACT CTT GG CCA	
	CAAGT TCTGG GGA CC GGT	
	TC _ _	
GAM1466 KIAA1727 3'	GTCCAGGAGGCCTGTGGAC 32037	A _ A
	G TTCACAG CTCTT GGAC	
	CAGGTGTC GAGGA CCTG	
	CG _	
GAM1466 KIAA1971 3'	TGGCCAGGCTGGTCTTGAAC 36732	C _ A A
	GTTCA AGACT CTT GG CCA	
	CAAGT TCTGG GGA CC GGT	
	TC _ _	
GAM1466 KLK7 3'	TGGCCAGCGTGGTCTTGAAC 29275	C CTTA _ A
	GTTCA AGACT GG CCA	
	CAAGT TCTGG CC GGT	
	TGCGA _	
GAM1466 KLK7 3'	TGGCCAGCGTGGTCTTGAAC 11478	C CTTA _ A
	GTTCA AGACT GG CCA	
	CAAGT TCTGG CC GGT	
	TGCGA _	
GAM1466 MGC16153 5'	GGTGAGGCAATCTGTGAGC 26510	C _ AGG
	G TTCACAGA TCTT ACC	

			CGAGTGTCT GGAG TGG		
			AAC ____		
GAM1466	MGC21675	3'	TGGTCAGGCTGGTCTTGAAC 27446	C	CTTAG
			GTTCA AGACT GACCA		
			CAAGT TCTGG CTGGT		
			_ TCGGA		
GAM1466	MGC4707	3'	TGGCCCTATCAGCCTGTGAAC 23565	A CT	A
			GTTCACAG CT TAGG CCA		
			CAAGTGTC GA ATCC GGT		
			C CT C		
GAM1466	NINJ2	3'	TGGTCAGGCTGGTCTTGAAC 18606	C	CTTAG
			GTTCA AGACT GACCA		
			CAAGT TCTGG CTGGT		
			_ TCGGA		
GAM1466	Nup43	3'	TGGCCAGGCTGGTCTTGAAC 23938	C	__ A A
			GTTCA AGACT CTT GG CCA		
			CAAGT TCTGG GGA CC GGT		
			_ TC _ _		
GAM1466	OCT11	3'	TGGTCAGGCTGGTCTTGAAC 15680	C	CTTAG
			GTTCA AGACT GACCA		
			CAAGT TCTGG CTGGT		
			_ TCGGA		
GAM1466	PAI-RBP1	3'	TGGTTCCTTTGTGAAC 17894	CTCTTA	
			GTTCACAGA GGACCA		
			CAAGTGTTT CTGGT		
			C ____		
GAM1466	PEL1	5'	TGGCCAGGCTGGTCTTGAAC 21818	C	__ A A
			GTTCA AGACT CTT GG CCA		
			CAAGT TCTGG GGA CC GGT		
			_ TC _ _		
GAM1466	PIP3-E	3'	GTCCTGCAGTGTCTGTGAGC 33181	T _	
			GTTCACAGAC CT TAGGAC		
			CGAGTGTCTG GA GTCCTG		
			T C		
GAM1466	PPP1R3B	3'	CCACGAGAGTCTGTGCAC 23858	T	A_
			GT CACAGACTCTT GG		
			CA GTGTCTGAGAG CC		
			C CA		
GAM1466	PRO2198	3'	GGAGGGGAATCTGTGAAC 20695	C	AGGA
			GTTCACAGA TCTT CC		

			CAAGTGTCT AGGG GG		
			A GA__		
GAM1466	RASSF2	3'	TGGCCAGGCTGGTCTTGAAC 16398	C __ A A	
			GTTCA AGACT CTT GG CCA		
			CAAGT TCTGG GGA CC GGT		
			_ TC _ _		
GAM1466	RGPR	3'	TGGTCCTAGTTTTGTGCAC 26971	T CTC	
			GT CACAGA TTAGGACCA		
			CA GTGTTT GATCCTGGT		
			C T__		
GAM1466	SCYA22	3'	TGGCCAGGCTGGTCTTGAAC 43717	C __ A A	
			GTTCA AGACT CTT GG CCA		
			CAAGT TCTGG GGA CC GGT		
			_ TC _ _		
GAM1466	SEMA4F	3'	TGGTCTTGGCCTGTGAAT 10461	A CTT	
			GTTCA CAG CT AGGACCA		
			TAAGTGTC GG TTCTGGT		
			C __		
GAM1466	SLC6A14	3'	TGGCCAGGCTGGTCTTGAAC 14105	C __ A A	
			GTTCA AGACT CTT GG CCA		
			CAAGT TCTGG GGA CC GGT		
			_ TC _ _		
GAM1466	TCL6	5'	TGGCCAGGCTGGTCTTGAAC 15771	C __ A A	
			GTTCA AGACT CTT GG CCA		
			CAAGT TCTGG GGA CC GGT		
			_ TC _ _		
GAM1466	TCL6	5'	TGGCCAGGCTGGTCTTGAAC 21764	C __ A A	
			GTTCA AGACT CTT GG CCA		
			CAAGT TCTGG GGA CC GGT		
			_ TC _ _		
GAM1466	TCL6	5'	TGGCCAGGCTGGTCTTGAAC 21773	C __ A A	
			GTTCA AGACT CTT GG CCA		
			CAAGT TCTGG GGA CC GGT		
			_ TC _ _		
GAM1466	TCL6	5'	TGGCCAGGCTGGTCTTGAAC 14847	C __ A A	
			GTTCA AGACT CTT GG CCA		
			CAAGT TCTGG GGA CC GGT		
			_ TC _ _		
GAM1466	TRIM2	3'	GTTTTACATCTGTGAAC 17601	CTCT	
			GTTCA CAGA TAGGAC		

		CAAGTGTCT	ATTTTG		
		AC__			
GAM1466	TUSP	3'	TGGCCAGGCTGGTCTTGAAC	21537	C __ A A
			GTTCA AGACT CTT GG CCA		
			CAAGT TCTGG GGA CC GGT		
			__ TC __		
GAM1466	WNT10A	5'	GTCCCACTGGGCTGTGAGC	24895	A TTA_
			G TTCACAG CTC GGAC		
			CGAGTGTC GGG CCTG		
			__ TCAC		
GAM1466	ZF5128	3'	TGGCCTTCTGTGAAT	15672	CTCTT A
			G TTCACAGA AGG CCA		
			TAAGTGTCT TCC GGT		

GAM1466	ZFP106	3'	TGGTATAAAGCTGTGAAC	22837	A C GG
			G TTCACAG CT TTA ACCA		
			CAAGTGTC GA AAT TGGT		
			__ _ A_		
GAM1466	LOC112817	3'	TGGCCAGGCTGGTCTTGAAC	28783	C __ A A
			GTTCA AGACT CTT GG CCA		
			CAAGT TCTGG GGA CC GGT		
			__ TC __		
GAM1466	LOC121504	3'	TGGCCAGGCTGGTCTTGAAC	36671	C __ A A
			GTTCA AGACT CTT GG CCA		
			CAAGT TCTGG GGA CC GGT		
			__ TC __		
GAM1466	LOC128989	3'	TGGTCAGGCTGGTCTTGAAC	36947	C CTTAG
			GTTCA AGACT GACCA		
			CAAGT TCTGG CTGGT		
			__ TCGGA		
GAM1466	LOC135818	3'	TGGTCAGGCTGGTCTTGAAC	37097	C CTTAG
			GTTCA AGACT GACCA		
			CAAGT TCTGG CTGGT		
			__ TCGGA		
GAM1466	LOC145371	3'	TGGCTCCAATCTGTGGAC	37850	CTC A _
			G TTCACAGA TT GGA CCA		
			CAGGTGTCT AA CCT GGT		
			_____ C		
GAM1466	LOC145678	3'	TGGTCCTAAGAGTGAAGGAA	40556	ACAG
			TTC ACTCTTAGGACCA		

		AAG TGAGAATCCTGGT	
		GAAG	
GAM1466	LOC145813 5'	TGGCCCACGCTGGTCTTGAAC 40599	C CTTA_ A
		GTTCA AGACT GG CCA	
		CAAGT TCTGG CC GGT	
		_ TCGCA C	
GAM1466	LOC146894 3'	TGGCCAGGCTGGTCTTGAAC 29785	C _ A A
		GTTCA AGACT CTT GG CCA	
		CAAGT TCTGG GGA CC GGT	
		_ TC _ _	
GAM1466	LOC146909 3'	TGGCCAGGCTGGTCTTGAAC 38271	C _ A A
		GTTCA AGACT CTT GG CCA	
		CAAGT TCTGG GGA CC GGT	
		_ TC _ _	
GAM1466	LOC148887 5'	TGGTCAGGCTGGTCTTGAAC 40913	C CTTAG
		GTTCA AGACT GACCA	
		CAAGT TCTGG CTGGT	
		_ TCGGA	
GAM1466	LOC152018 5'	TGGTGAGAGCTTGTGAAC 41424	GA AGG
		GTTCACTA CTCTT ACCA	
		CAAGTGT GAGAG TGGT	
		TC _ _ _	
GAM1466	LOC153077 3'	TGGCCAGGCTGGTCTTGAAC 41571	C _ A A
		GTTCA AGACT CTT GG CCA	
		CAAGT TCTGG GGA CC GGT	
		_ TC _ _	
GAM1466	LOC153454 5'	TGGCTGAAAGCCTGTGGAC 39377	A C GA
		GTTACACAG CT TTAG CCA	
		CAGGTGTC GA AGTC GGT	
		C A _ _	
GAM1466	LOC154877 5'	TGGCCAGGCTGGTCTTGAAC 41747	C _ A A
		GTTCA AGACT CTT GG CCA	
		CAAGT TCTGG GGA CC GGT	
		_ TC _ _	
GAM1466	LOC158476 3'	TGGCCAGGCTGGTCTTGAAC 42001	C _ A A
		GTTCA AGACT CTT GG CCA	
		CAAGT TCTGG GGA CC GGT	
		_ TC _ _	
GAM1466	LOC158865 5'	TGGCCAGGCTGGTCTTGAAC 42039	C _ A A
		GTTCA AGACT CTT GG CCA	

	CAAGT TCTGG GGA CC GGT	
	— TC — —	
GAM1466 LOC162333 5'	TGGAGTGAAGTCTGTGA 42138	C GGA
	TCACAGACT TTA CCA	
	AGTGTCTGA AGT GGT	
	— GA_	
GAM1466 LOC164955 3'	GTCTGGGCTGTGAAC 40113	A TTA
	G TTCACAG CTC GGAC	
	CAAGTGTC GGG TCTG	
	— ———	
GAM1466 LOC169225 5'	TGGTCCTCGTCATCTGTGGAC 42205	CTCTT
	G TTCACAGA AGGACCA	
	CAGGTGTCT TCCTGGT	
	ACTGC	
GAM1466 LOC196529 3'	TGGCCAGGCTGGTCTTGAAC 42412	C — A A
	G TTCA AGACT CTT GG CCA	
	CAAGT TCTGG GGA CC GGT	
	— TC — —	
GAM1466 LOC199786 3'	TGGTCAGGCTGGTCTTGAAC 42623	C CTTAG
	G TTCA AGACT GACCA	
	CAAGT TCTGG CTGGT	
	— TCGGA	
GAM1466 LOC200316 3'	TGGCCAGGCTGGTCTTGAAC 42796	C — A A
	G TTCA AGACT CTT GG CCA	
	CAAGT TCTGG GGA CC GGT	
	— TC — —	
GAM1466 LOC200982 3'	TGGCATGAAATCTGTGAAT 43379	CTC GGA
	G TTCACAGA TTA CCA	
	TAAGTGTCT AGT GGT	
	AA_ AC_	
GAM1466 LOC201626 3'	TGGCCAGGCTGGTCTTGAAC 42892	C — A A
	G TTCA AGACT CTT GG CCA	
	CAAGT TCTGG GGA CC GGT	
	— TC — —	
GAM1466 LOC203197 3'	TGGCCAAGCTGGTCTTGAAC 43013	C — A A
	G TTCA AGACT CTT GG CCA	
	CAAGT TCTGG GAA CC GGT	
	— TC — —	
GAM1466 LOC220064 3'	TGGCCAGGCTGGTCTTGAAC 44870	C — A A
	G TTCA AGACT CTT GG CCA	

	CAAGT TCTGG GGA CC GGT		
	TC		
GAM1466 LOC220074 3'	TGGCCAGGCTGGTCTTGAAC 29825	C	___ A A
	GTTCA AGACT CTT GG CCA		
	CAAGT TCTGG GGA CC GGT		
	TC		
GAM1466 LOC221964 3'	TGGCCAGGCTGGTCTTGAAC 45114	C	___ A A
	GTTCA AGACT CTT GG CCA		
	CAAGT TCTGG GGA CC GGT		
	TC		
GAM1466 LOC222031 3'	TGGCCAGGCTGGTCTTGAAC 45138	C	___ A A
	GTTCA AGACT CTT GG CCA		
	CAAGT TCTGG GGA CC GGT		
	TC		
GAM1466 LOC222224 5'	TGGCCAGGCTGGTCTTGAAC 45198	C	___ A A
	GTTCA AGACT CTT GG CCA		
	CAAGT TCTGG GGA CC GGT		
	TC		
GAM1466 LOC253981 3'	TGGTCAGGCTGGTCTTGAAC 45868	C	CTTAG
	GTTCA AGACT GACCA		
	CAAGT TCTGG CTGGT		
	TCGGA		
GAM1466 LOC254057 5'	TGGCCGCTGGGCTGTGAAC 46351	A	TTA A
	GTTACACAG CTC GG CCA		
	CAAGTGTC GGG CC GGT		
	TCG		
GAM1466 LOC256306 3'	TGGCCAGGCTGGTCTTGAAC 46240	C	___ A A
	GTTCA AGACT CTT GG CCA		
	CAAGT TCTGG GGA CC GGT		
	TC		
GAM1466 LOC257127 5'	TGGCCAGGCTGGTCTTGAAC 46232	C	___ A A
	GTTCA AGACT CTT GG CCA		
	CAAGT TCTGG GGA CC GGT		
	TC		
GAM1466 LOC51008 5'	TGGTCAGGCTGGTCTTGAAC 18065	C	CTTAG
	GTTCA AGACT GACCA		
	CAAGT TCTGG CTGGT		
	TCGGA		
GAM1466 LOC90288 3'	TGGTCAGGCTGGTCTTGAAC 31117	C	CTTAG
	GTTCA AGACT GACCA		

		CAAGT TCTGG CTGGT		
		_ TCGGA		
GAM1466	LOC90459	3' TGGTCAGGCTGGTCTTGAAC 31494	C	CTTAG
		GTTCA AGACT GACCA		
		CAAGT TCTGG CTGGT		
		_ TCGGA		
GAM1466	LOC96597	3' GGCCAACAGCTGTGAAC 33231	A C A A	
		GTTCACAG CT TT GG CC		
		CAAGTGTC GA AA CC GG		
		_ C _ _		
GAM1467	BCL2L2	3' CAACCCCTCCTTTCCCCT 10259	A	AC
		AG GGAGAGGAGG TTG		
		TC CCTTCTCCTCC AAC		
		C CC		
GAM1467	CDK2	3' AATCTCACCCCTCTCCTC 7551	AG	CTTGC
		GAGGAGAGG GA GATT		
		CTCCTCTCC CT CTAA		
		CA _ _ _		
GAM1467	CYP8B1	3' TGTACCCTCCTCCCCTCT 10628	A	ACT
		AGAGG GAGGAGG TGCG		
		TCTCC CTCCTCC ATGT		
		C C _		
GAM1467	GAN	3' TAATCTTTTCTCCTTCCCTC 22563	AG	CTTGC
		GAGG AGGAGGA GATTA		
		CTCC TCCTCCT CTAAT		
		CT TTT _		
GAM1467	KIFC3	3' AATGGCAGCCCTCCCCGCCCT 12080	A AGA	A T G
		AG GG GGAGG CT GC ATT		
		TC CC CCTCC GA CG TAA		
		C GCC C _ G		
GAM1467	NYX	3' CAATCCTCCTCCTCCTCT 22887	_	C
		AGAGGAG AGGAGGA TTG		
		TCTCCTC TCCTCCT AAC		
		C _		
GAM1467	NYX	3' CAATCCTCCTCCTCCTCT 22888	_	C
		AGAGGAG AGGAGGA TTG		
		TCTCCTC TCCTCCT AAC		
		C _		
GAM1467	PIM2	3' CAAGTGTGCCCTCCTCTCTTCT 30133		
		AGAGGAGAGGAGG ACTTG		

			TCTTCTCTCCTCC	TGAAC		
			CGTG			
GAM1467	PML	3'	TTGCCCTCCCCTTCTC	27082	A	ACTT
			GAGGAG GGAGG GCGA			
			CTCTTC CCTCC CGTT			
			C	_____		
GAM1467	PML	3'	TTGCCCTCCCCTTCTC	27086	A	ACTT
			GAGGAG GGAGG GCGA			
			CTCTTC CCTCC CGTT			
			C	_____		
GAM1467	PMX1	5'	CAAGACATCACCTCTCCTC	22913		AG ____
			GAGGAGAGG GA CTTG			
			CTCCTCTCC CT GAAC			
			CA ACA			
GAM1467	PMX1	5'	CAAGACATCACCTCTCCTC	13778		AG ____
			GAGGAGAGG GA CTTG			
			CTCCTCTCC CT GAAC			
			CA ACA			
GAM1467	PPP2R5A	3'	AATTCATTCTCCTCTTCCTCT	12907		CT C
			AGAGGA GAGGAGGA TG GATT			
			TCTCCT CTCCTCCT AC TTAA			
			T T_ _			
GAM1467	ALS2CR3	3'	GAGTCCTTCCTCTCCCCT	17411	A	__
			AG GGAGAGGA GGA CT			
			TC CCTCTCCT CCTGAG			
			C T			
GAM1467	FLJ13189	5'	CGCTCCTCTTCTCCCCT	24330	A	CTT
			AG GGAGAGGAGGA GCG			
			TC CCTCTTCTCCT CGC			
			C	_____		
GAM1467	GP5	3'	CAACCCCTCCTCTCTCT	10815	G	AC
			AGAG AGAGGAGG TTG			
			TCTC TCTCCTCC AAC			
			CC			
GAM1467	IL1F10	5'	TGCCCTTCTCTCCTC	26283		ACTT
			GAGGAGAGGAGG GCG			
			CTCCTCTCTTCC CGT			

GAM1467	KIAA0935	3'	CAAGCCAGCCCTCTCCTCT	36009		A__ A
			AGAGGAGAGG GG CTTG			

			TCTCCTCTCC	CC GAAC		
			CGA _			
GAM1467	KIAA1388	5'	GCAGCCGCTCCTCTCCTC	44951	GAC	
			GAGGAGAGGAG	TTGC		
			CTCCTCTCCTC	GACG		
			GCC			
GAM1467	KIAA1674	3'	CAAGCCCTCCTTTCCCCT	34103	A	A
			AG GGAGAGGAGG	CTTG		
			TC CCTTTCCTCC	GAAC		
			C	C		
GAM1467	NBL1	3'	CAACTCTTCCTCCCCTCT	29837	A	C
			AGAGG GAGGAGGA	TTG		
			TCTCC CTCCTTCT	AAC		
			C	C		
GAM1467	NEIL2	5'	CAACCCCTCCTCTTCCCT	29672	A	AC
			AG GGAGAGGAGG	TTG		
			TC CTTCTCCTCC	AAC		
			C	CC		
GAM1467	PTK6	5'	CGGGAGGTCCTCCTCCCCCTCT	12600	A_	_ G
			AGAGG GAGGAGGAC	TT CG		
			TCTCC CTCCTCCTG	AG GC		
			CC	G G		
GAM1467	RAB3IL1	3'	CAAGACCCCCCTCTCTTC	15061	A A_	
			GAGGAGAGG GG	CTTG		
			CTTCTCTCC CC	GAAC		
			C CA			
GAM1467	SEC24A	5'	TAATGCGCCCCCCCCCTCTTCTC	40234	A ACTT	_
			GAGGAGAGG GG	GCG ATTA		
			CTCTTCTCC CC	CGC TAAT		
			_ CCC_	G		
GAM1467	SLC1A7	3'	CAAGCCCCGCTCTCCTCT	13488	A A_	
			AGAGGAGAGG GG	CTTG		
			TCTCCTCTCC CC	GAAC		
			G CC			
GAM1467	STRAIT11499	5'	AATCCCTCCTCCTCTGCTCT	22208	G	CTTGC
			AGAG AGAGGAGGA	GATT		
			TCTC TCTCCTCCT	CTAA		
			G	CC__		
GAM1467	LOC145988	5'	CAAGTCCTCCTCCGCCTC	38035	A_	
			GAGG GAGGAGGACTTG			

	CTCC CTCCTCCTGAAC		
	GC		
GAM1467 LOC148529 5'	AATCACATCCTCTCTCCT 40889	G	CT C
	AGGAGAG AGGA TG GATT		
	TCCTCTC TCCT AC CTAA		
	— — A		
GAM1467 LOC150407 3'	GTAATCCTCCTCCCTCT 38951	A	C
	AGAGG GAGGAGGA TTGC		
	TCTCC CTCCTCCT AATG		
	— —		
GAM1467 LOC157567 5'	TAATCGCAAACCTCCTCCCTT 39613	A	AC
	GAGG GAGGAGG TTGCGATTA		
	TTCC CTCCTTC AACGCTAAT		
	— A—		
GAM1467 LOC159121 3'	TAAGAACCTCCTCTCCTC 42064	A—	
	GAGGAGAGGAGG CTTG		
	CTCCTCTCCTCC GAAT		
	AA		
GAM1467 LOC196812 3'	TAATCCATGCCCTCCTCTCT 43137	ACT	C
	GGAGAGGAGG TG GATTA		
	TCTCTCCTCC AC CTAAT		
	CGT —		
GAM1467 LOC199923 5'	CAACGTCCCTCCTCTCCCT 42666	A	—
	AG GGAGAGGAGGAC TTG		
	TC CCTCTCCTCCTG AAC		
	— C		
GAM1467 LOC92465 5'	AATCACCATTCTCCTTCCTCT 34391	G	CTTGC
	AGAGGA AGGAGGA GATT		
	TCTCCT TCCTCTT CTAA		
	— ACCA—		
GAM1468 ANKRD6 3'	ACGTAATCCCGTCTGAA 17251	AAA	TA
	TTCA GCG GGATTACGT		
	AAGT TGC CCTAATGCA		
	C— —		
GAM1468 FLJ10853 3'	ATGTAGATAGCGCTTTTGAA 20212		AGGA
	TTCAAAAGCGT TTACGT		
	AAGTTTTCGCG GATGTA		
	ATA—		
GAM1468 FLJ22625 3'	ACGTAATCCAGTATTTGGA 24040	A	GTA
	TTCAAA GC GGATTACGT		

	AGGTTT TG CCTAATGCA	
	A A__	
GAM1468 KIAA0446	5' GTGACCACCTTTTGAA 34152	C A A
	TTCAAAAG GT GG TTAC	
	AAGTTTTC CA CC AGTG	
	— — —	
GAM1468 LOC126964	3' ACGTAATCCCCACATTTGA 36881	AGC A_
	TCAA GT GGATTACGT	
	AGTT CA CCTAATGCA	
	A__ CC	
GAM1468 LOC158476	3' ACATAATCCTGAATGTTGAA 41994	AAGCG C
	TTCAA TAGGATTA GT	
	AAGTT GTCCTAAT CA	
	GTAA_ A	
GAM1469 VPS41	3' ACCAGTGACCCTGAAAAGTGA 15735	TAA T AAAC
	TCAGTTTTCA G GT GGT	
	AGTCAAAGT C CA CCA	
	__ C GTGA	
GAM1469 DKFZp547I224	3' ACCGCTCAACTACATGGAAACT 21472	A_ GTAAA
GA	TCAGTTTTTCAT AGT CGGT	
	AGTCAAAGGTA TCA GCCA	
	CA ACTC_	
GAM1469 KIAA0916	3' ACCATTTTTACATCCATGAAAA 17415	AA C__
T	GTTTTTCAT GTGTAAA GGT	
	TAAAAGTA TACATT CCA	
	CC TTA	
GAM1469 PAI-RBP1	3' ACCATTACACCTAAAGACTGA 17892	CA A A C
	TCAGTTTT TA GTGT AA GGT	
	AGTCAGAA AT CACA TT CCA	
	__ C C A	
GAM1469 PRO1992	3' CACTTACAGGAAGACTGA 15332	A__
	TCAGTTTTC TAAGTG	
	AGTCAGAAG ATTCAC	
	GAC	
GAM1469 LOC112476	3' ACCGTTTACTCTGCAAAACTGA 29750	CATA T
	TCAGTTTT AG GTAAACGGT	
	AGTCAAAA TC CATTTGCCA	
	CG__ T	
GAM1469 LOC147219	3' CCTGTATCATGAAAAGTGA 40822	AAGT AAC
	TCAGTTTTTCAT GTA GG	

AGTCAAAAGTA TAT CC
 C__ GT_
 GAM1469 LOC150139 3' ACCGTTTAGGCTAAAAC 38856 CATA G
 GTTTT AGT TAAACGGT
 |||| ||| |||||
 CAAAA TCG ATTTGCCA
 ____ G
 GAM1469 LOC150157 3' ACCGCTCAACTACATGGAAACC 41139 A A_ GTAAA
 GA TC GTTTTCAT AGT CGGT
 || ||||| ||| |||
 AG CAAAGGTA TCA GCCA
 C CA ACTC_
 GAM1469 LOC152502 3' ACCATTACACCTAAAGACTGA 29834 CA A A C
 TCAGTTTT TA GTGT AA GGT
 ||||| || ||| |||
 AGTCAGAA AT CACA TT CCA
 __ C C A
 GAM1469 LOC196890 3' ACCGCTCAACTACATGGAAACC 43154 A A_ GTAAA
 GA TC GTTTTCAT AGT CGGT
 || ||||| ||| |||
 AG CAAAGGTA TCA GCCA
 C CA ACTC_
 GAM1470 FLT1 3' AGCAAATAGTGATAACA 7764 ACC
 TGTTATCA ATTTGTT
 ||||| |||||
 ACAATAGT TAAACGA
 GA_
 GAM1470 TIF1 3' ACAAACATGGGTGGTAACA 30275 A _
 TGTTATCA CCAT TTGT
 ||||| ||| |||
 ACAATGGT GGTA AACA
 G CA
 GAM1470 FLJ14600 3' GTGAACAATGGATAACA 26575 AACCAT
 TGTTATC TTGTTCGC
 ||||| |||||
 ACAATAG AACAAAGTG
 GT____
 GAM1471 NFATC1 3' CCTGGTACCACTCAGAACCTCC 12814 A C ACGA
 A TG AG GTTCTGAGTG CAGG
 || || ||||| |||
 AC TC CAAGACTCAC GTCC
 C _ CATG
 GAM1471 BTBD3 3' CCGCCGCCACCCAGAGTGTGGT 17337 A_ A A ACA
 C GA GCGTTCTG GTG CG GG
 || ||||| ||| |||
 CT TGTGAGAC CAC GC CC
 GG C C CG_
 GAM1471 DKFZp761N0624 3' CCTAAATGTACTCAGAACACTT 26074 C ACGAC
 AAG GTTCTGAGTG AGG
 ||| ||||| |||

TTC CAAGACTCAT TCC
 A GTAAA
 GAM1471 FLJ21709 3' CTACCGTCAGGATGCTTCA 38169 GAGT AC
 TGAAGCGTTCT GACG AG
 ||||| ||| ||
 ACTTCGTAGGA CTGC TC
 CA
 GAM1471 GTPBP5 3' CCTGTCCTTCAGAACACTTC 32574 C TGAC
 GAAG GTTCTGAG GACAGG
 ||| ||||| |||||
 CTTT CAAGACTT CTGTCC
 A C____
 GAM1471 MGC21675 5' CCCATCGTCACTCTCCATGGCC 27444 A GTTCT_ CA
 TC GA GC GAGTGACGA GG
 || || ||||| ||
 CT CG CTCACTGCT CC
 C GTACCT AC
 GAM1471 U5-100K 3' CTGTTTTTCAGAACCCTCA 30011 A C TGAC
 TGA G GTTCTGAG GACAG
 ||| ||||| |||||
 ACT C CAAGACTT TTGTC
 _C T____
 GAM1471 LOC150407 3' TGTTACTCAGAACACTTCA 38954 C
 TGAAG GTTCTGAGTGACG
 |||| |||||
 ACTTC CAAGACTCATTGT
 A
 GAM1472 PRKACB 3' CGCATGTAAATGCTGATA 8602 G _____
 TATCAGCA TTTAC CG
 ||||| |||| ||
 ATAGTCGT AAATG GC
 TAC|||
 GAM1472 SEDL 3' CGCAGTAAACTGTTGATA 15909 _____
 TATCAGCAGTTTAC CG
 ||||| ||||| ||
 ATAGTTGTCAAATG GC
 AC|||
 GAM1472 SLC35A1 3' CTGAGTGAAGTCTAATA 13127 C CG
 TAT AGCAGTTTAC AG
 ||| ||||| ||
 ATA TCGTCAAGTG TC
 A AG
 GAM1472 SRD5A1 3' CTGGGTAATAACTGCTGATA 6716 _ G
 TATCAGCAGTT TACC AG
 ||||| |||| ||
 ATAGTCGTCAA ATGG TC
 TA G
 GAM1472 ADMP 3' GGGGCGCTAGTAAACTGATGAT 29657 G _____ AGGG
 A TATCA CAGTTTAC CG C
 ||||| ||||| || |

	ATAGT GTCAAATG GC G	
	A ATCIII GGA	
GAM1472 KIAA0872 3'	CGCCCTCAATGCTGGCTGCTG 17246	TACC__
	CAGCAGTT GAGGGCG	
	GTCGTCGG CTCCCGC	
	TCGTAA	
GAM1472 LOC148137 3'	CGCCCCCGCCCGCTGCTGA 29516	TTAC A
	TCAGCAGT CG GGGCG	
	AGTCGTCG GC CCCGC	
	CCC_ C	
GAM1472 LOC162333 5'	CGCCCTCGAGGTGCACTG 42127	T _
	CAGT TACC GAGGGCG	
	GTCA GTGG CTCCCGC	
	C AG	
GAM1473 FLJ20345 3'	TTAAAAATGGAGCCTTTCA 19407	CC
	TGAAAGGCTCCATT TAA	
	ACTTTCCGAGGTAA ATT	
	AA	
GAM1473 FYCO1 3'	GGGAATAGAACCTTTCAA 23711	C C
	TTGAAAGG TC ATTCT	
	AACTTTCC AG TAAGGG	
	A A	
GAM1473 KIAA1061 3'	GCCATTAAGGAATGAACTCTTT 35268	CTC _ A
CAA	TTGAAAGG CATTCT AAT GC	
	AACTTTCT GTAAGGA TTA CG	
	CAA A C	
GAM1473 KIAA1300 5'	TAGGGAAGGAGCCTTTCAA 31482	A
	TTGAAAGGCTCC TTCCTA	
	AACTTTCCGAGG AGGGAT	
	A	
GAM1473 PRO1386 3'	GCTATTAGGAATATTTACCT 25291	CTCC_
	AGG ATTCCTAATAGC	
	TCC TAAGGATTATCG	
	ATTTA	
GAM1473 TOMM70A 3'	CTATTAGAAATGACTCCCTTTC 16790	CTC_ C
AA	TTGAAAGG CATT CTAATAG	
	AACTTTCC GTAA GATTATC	
	CTCA A	
GAM1473 LOC157931 5'	GCCATTTTCATCTGGAGCTTTCA 41903	G TTCCT A
A	TTGAAAG CTCCA AAT GC	

		AACTTTC GAGGT TTA CG	
		_ CTACT C	
GAM1473	LOC222166 3'	CTATTAAAGAGCCTTTCAA 45154	CATTCC
		TTGAAAGGCTC TAATAG	
		AACTTTCCGAG ATTATC	
		AA_____	
GAM1474	CSPG3 3'	GTGTTAAAACTGAAACAC 10615	ACC A
		GTGTTTCA TT AACAC	
		CACAAAGT AA TTGTG	
		CA_ A	
GAM1474	PCDHA1 3'	TAAGGATAAAACACGTCA 20867	CAA
		TGACGTGTTT CCTTA	
		ACTGCACAAA GGAAT	
		ATA	
GAM1474	PCDHA1 3'	TAAGGATAAAACACGTCA 25386	CAA
		TGACGTGTTT CCTTA	
		ACTGCACAAA GGAAT	
		ATA	
GAM1474	PCDHA10 3'	TAAGGATAAAACACGTCA 25618	CAA
		TGACGTGTTT CCTTA	
		ACTGCACAAA GGAAT	
		ATA	
GAM1474	PCDHA10 3'	TAAGGATAAAACACGTCA 20877	CAA
		TGACGTGTTT CCTTA	
		ACTGCACAAA GGAAT	
		ATA	
GAM1474	PCDHA11 3'	TAAGGATAAAACACGTCA 20888	CAA
		TGACGTGTTT CCTTA	
		ACTGCACAAA GGAAT	
		ATA	
GAM1474	PCDHA12 3'	TAAGGATAAAACACGTCA 20898	CAA
		TGACGTGTTT CCTTA	
		ACTGCACAAA GGAAT	
		ATA	
GAM1474	PCDHA13 3'	TAAGGATAAAACACGTCA 20908	CAA
		TGACGTGTTT CCTTA	
		ACTGCACAAA GGAAT	
		ATA	
GAM1474	PCDHA2 3'	TAAGGATAAAACACGTCA 20918	CAA
		TGACGTGTTT CCTTA	

			ACTGCACAAA GGAAT	
			ATA	
GAM1474	PCDHA3	3'	TAAGGATAAAACACGTCA 20928	CAA
			TGACGTGTTT CCTTA	
			ACTGCACAAA GGAAT	
			ATA	
GAM1474	PCDHA4	3'	TAAGGATAAAACACGTCA 20938	CAA
			TGACGTGTTT CCTTA	
			ACTGCACAAA GGAAT	
			ATA	
GAM1474	PCDHA5	3'	TAAGGATAAAACACGTCA 20948	CAA
			TGACGTGTTT CCTTA	
			ACTGCACAAA GGAAT	
			ATA	
GAM1474	PCDHA6	3'	TAAGGATAAAACACGTCA 20958	CAA
			TGACGTGTTT CCTTA	
			ACTGCACAAA GGAAT	
			ATA	
GAM1474	PCDHA6	3'	TAAGGATAAAACACGTCA 25590	CAA
			TGACGTGTTT CCTTA	
			ACTGCACAAA GGAAT	
			ATA	
GAM1474	PCDHA7	3'	TAAGGATAAAACACGTCA 20968	CAA
			TGACGTGTTT CCTTA	
			ACTGCACAAA GGAAT	
			ATA	
GAM1474	PCDHA8	3'	TAAGGATAAAACACGTCA 20978	CAA
			TGACGTGTTT CCTTA	
			ACTGCACAAA GGAAT	
			ATA	
GAM1474	PCDHA9	3'	TAAGGATAAAACACGTCA 25604	CAA
			TGACGTGTTT CCTTA	
			ACTGCACAAA GGAAT	
			ATA	
GAM1474	PCDHAC1	3'	TAAGGATAAAACACGTCA 20847	CAA
			TGACGTGTTT CCTTA	
			ACTGCACAAA GGAAT	
			ATA	
GAM1474	PCDHAC2	3'	TAAGGATAAAACACGTCA 20857	CAA
			TGACGTGTTT CCTTA	

			ACTGCACAAA	GGAAT		
			ATA			
GAM1474	CUGBP2	3'	GTGTAGTTGAAACAGTCA	13332	G	CTTAA
			TGAC TGTTTCAAC	ACAC		
			ACTG ACAAAGTTG	TGTG		
			— A —			
GAM1474	PRO2831	3'	TGTTTAAGGTTTCTGACAC	20611	TC_	
			GTGTT AACCTTAAACA			
			CACAG TTGGAATTTGT			
			TCT			
GAM1474	LOC150577	3'	CGTGTTCACTTTGAAAACACGT	41220	_	CCTTA
			CA TGACGTGTTT CAA	AACACG		
			ACTGCACAAA GTT	TTGTGC		
			A TCAC_			
GAM1475	TXNIP	3'	CGCTTAAATCATGTGA	13197	GT	
			TCGCA TGATTTAAGCG			
			AGTGT ACTAAATTCGC			
			—			
GAM1475	ZNF215	3'	GTTATCAACTGCAATG	14913	C	TTA
			CAT GCAGTTGAT	AGC		
			GTA CGTCAACTA	TTG		
			A —			
GAM1475	ARNTL2	5'	GCGCCTACGGGCTGCGGTG	21415	GATT	A
			CATCGCAGTT	TA GCGC		
			GTGGCGTCGG	AT CGCG		
			GC_ C			
GAM1475	BNIP-S	3'	GCTAATAAACTGCGATG	28691	G	TA
			CATCGCAGTT	ATT AGC		
			GTAGCGTCAA	TAA TCG		
			A —			
GAM1475	DKFZP564D0764	3'	GCGCTTAAATCCAAGACT	42575	—	
			AGTT	GATTTAAGCGC		
			TCAG	CTAAATTCGCG		
			AAC			
GAM1475	FLJ10352	3'	CTTAAAGTCAATCTGCGA	25825	—	—
			TCGCAG	TTGATTT AAG		
			AGCGTC	AACTGAA TTC		
			T A			
GAM1475	LOC120772	5'	GCGCCTAGGGCTGCGG	36629	GAT	A
			TCGCAGTT	TTA GCGC		

			GGCGTCGG	GAT CGCG		
			— C			
GAM1475	LOC139767	5'	GCGCTTAAACATTGTGA	37346	T A	
			TCGCAGT G TTTAAGCGC			
			AGTGTTA C AAATTCGCG			
			_ A			
GAM1475	LOC154007	3'	GCAAGTCAACTGCCATG	39454	C	AA
			CAT GCAGTTGATTT GC			
			GTA CGTCAACTGAA CG			
			C —			
GAM1475	LOC256867	5'	GCGCCTAGGGCTGCGG	45475	GAT	A
			TCGCAGTT TTA GCGC			
			GGCGTCGG GAT CGCG			
			— C			
GAM1476	C8orf14	5'	CTGTGGAGAAGTCTCCT	27640	AAC	T
			AGGA CTTCTCCA CGG			
			TCCT GAAGAGGT GTC			
			CT_ _			
GAM1476	CXYorf1	5'	TTGGAGAGAAGGTCTCCTTG	39916	A	CA G
			TAAGGA ACCTTCTC TC GA			
			GTTTCCT TGGAAGAG AG TT			
			C _ G			
GAM1476	FLJ31709	3'	TCCAAGAAAGTTTCCTT	29458	C	CCATC
			AAGGAAAC TTCT GGA			
			TTCCTTTG AAGA CCT			
			A A_			
GAM1476	HARSL	3'	TTTGTAGAAAAGGTTTCCT	14510	C	CAT
			AGGAAACCTT TC CGGA			
			TCCTTTGGAA AG GTTT			
			A AT_			
GAM1476	KIAA0513	3'	CTGACAGAGAAGGTCTCCT	16356	A	CA
			AGGA ACCTTCTC TCGG			
			TCCT TGGAAGAG AGTC			
			C AC			
GAM1476	LOC166042	5'	CGCTCCAGGAGAAGGCACCCTT	40198	AAA	ATC _
	A		TAAGG CCTTCTCC GGA CG			
			ATTCC GGAAGAGG CCT GC			
			CAC A_ C			
GAM1476	LOC200093	5'	TTGGAGAGAAGGTCTCCTTG	31607	A	CA G
			TAAGGA ACCTTCTC TC GA			

			G TTCCT TGGAAGAG AG TT		
			C _ G		
GAM1476	LOC91040	5'	TTGGAGAGAAGGTCTCCTTG 32326	A	CA G
			TAAGGA ACCTTCTC TC GA		
			G TTCCT TGGAAGAG AG TT		
			C _ G		
GAM1477	LASS2	3'	AGGCTAACCTTTCTAAGCT 33621	A__	
			AGCTTAGAAG AGTTT		
			TCGAATCTTT TCGGA		
			CCAA		
GAM1477	HEMK	3'	ATCCACTTCTTCAAGCT 18263	A	TT
			AGCTT GAAGAAGT GAT		
			TCGAA CTTCTTCA CTA		
			_ C_		
GAM1477	LOC145623	3'	CAACACTGCTGTCTTTAAGCTT 40543	A _	TTGA
			AAGCTTAGA GA AGT TGTTG		
			TTCGAATTT CT TCG ACAAC		
			_ G TC__		
GAM1478	FLJ12704	3'	ATGGAGCACCATCACTGA 24563	ATC	CTC
			TCAGTGAT GT GCTCCAT		
			AGTCACTA CA CGAGGTA		
			C__ __		
GAM1478	MEGF10	3'	CATGAAAGTGGAATCACTGA 26212	ATCG	C_
			TCAGTGAT TCTCGCT CATG		
			AGTCACTA AGGGTGA GTAC		
			__ AA		
GAM1478	LOC90133	3'	CATGGACAGCATCATCACTGA 30867	ATC T	CGC
			TCAGTGAT G CT TCCATG		
			AGTCACTA C GA AGGTAC		
			CTA_ C__		
GAM1479	FIBL-6	3'	GAAAGCCAAACCAAACGAA 36100	CC	AA
			TTCGTTGT TGGTT GTTTTT		
			AAGCAACA ACCAA CGAAAG		
			A_ AC		
GAM1479	KIAA1795	3'	AAAACTAAGAAGAACAATGAA 35697	C GG	A
			TTCGTTGT CT TTA GTTTTT		
			AAGTAACA GA AAT CAAAAA		
			A AG _		
GAM1479	LOC91263	5'	GAAAAATTGCCAAAACAAAGAA 32594	G	CC TA
			TTC TTGT TGGT AGTTTTTC		

AAG AACA ACCG TTA AAAAG
 A AA _
 GAM1479 LOC92391 3' AAAA ACTTCCAATGACAAGAA 34270 G C_ TT
 TTC TTGTC TGG AAGTTTT
 ||| |||| | |||||
 AAG AACAG ACC TTCAAAAA
 _ TA _
 GAM1480 DUSP4 5' AGGGCGCGCGGCATTTCC 27666 A G AAACA
 A AAGTG CG CGCGCCCT
 | |||| || |||||
 C TTTAC GC GCGCGGGA
 C G _
 GAM1480 NRXN2 3' CAGGGCACGTGCTCACAGCCCT 28982 T GAAA_ C
 AG GGC CACG GCCCTG
 || ||| |||| |||||
 TC CCG GTGC CGGGAC
 _ AACTC A
 GAM1480 NRXN2 3' CAGGGCACGTGCTCACAGCCCT 28988 T GAAA_ C
 AG GGC CACG GCCCTG
 || ||| |||| |||||
 TC CCG GTGC CGGGAC
 _ AACTC A
 GAM1480 NRXN2 3' CAGGGCACGTGCTCACAGCCCT 17466 T GAAA_ C
 AG GGC CACG GCCCTG
 || ||| |||| |||||
 TC CCG GTGC CGGGAC
 _ AACTC A
 GAM1480 NUP62 3' CAGGGCGCAGTGGCTCACCCCT 18627 T C AA _
 AG GG GA CAC GCGCCCTG
 || ||| || |||||
 TC CC CT GTG CGCGGGAC
 C A CG A
 GAM1480 POMZP3 5' CGCGTTTCACTTTT 14528 C AAC
 AAAAGTGG GA ACGCG
 ||||| || |||||
 TTTTCACC CT TGCGC
 A _
 GAM1480 DKFZp434I099 5' CAGAGCGCGTGTTTCTGGTCGC 26016 _ C
 GTGGC GAAACACGCGC CTG
 |||| ||||| |||||
 CGCTG CTTTGTGCGCG GAC
 GT A
 GAM1480 KIAA0828 3' CAGGTTTGTGTTTGTTCCTT 39511 C C C_
 TT AAAAGTGG GAAACA GCG CCTG
 ||||| ||||| || |||||
 TTTTCACC CTTTGT TGT GGAC
 _ T TT
 GAM1480 MGC2452 3' CAGGAGGTTTGTCTCAACTT 26365 A GC A C GC
 CC A AAGTG GA ACA GC CCTG
 | |||| || ||| || ||||

C TTCAC CT TGT TG GGAC
 C AA C T GA
 GAM1480 MGC4655 5' CAGGGCGTCCGGGGCTGCGCCA 27147 A AAACA_ ____
 CTTCC A AAGTGGCG CG CGCCCTG
 | ||||| || |||||
 C TTCACCGC GC GCGGGAC
 C GTCGGG CT
 GAM1480 LOC145945 5' CAGGGCACGTGTTTTGAGCCT 40630 T ____ C
 CT AG GGC GAAACACG GCCCTG
 || ||| ||||| |||||
 TC CCG TTTTGTGC CGGGAC
 T AGT A
 GAM1480 LOC219513 3' CAGAGCACGTGTTTCGCGGC 45290 G C C
 GT GCGAAACACG GC CTG
 || ||||| || |||
 CG CGCTTTGTGC CG GAC
 G A A
 GAM1480 LOC220021 3' CAGCCTGCCGTTTGCCACT 44849 ACAC CC
 AGTGGCGAA GCG CTG
 ||||| ||| |||
 TCACCGTTT CGT GAC
 GC__ CC
 GAM1480 LOC90918 5' AGGAAGTCATGTCTCACTACTT 32176 C A C_ GC
 TT AAAAGTGG GA ACA GC CCT
 ||||| || ||| |||
 TTTTCATC CT TGT TG GGA
 A C AC AA
 GAM1480 LOC92340 3' CAGGGTGTGTTTCCCCAC 34197 C_ GC
 GTGG GAAACAC GCCCTG
 ||| ||||| |||||
 CACC CTTTGTG TGGGAC
 CC ____
 GAM1480 LOC93166 5' CAGGGCGCACACTCTCGCGCAC 35461 _ AACAC_
 GTG GCGA GCGCCCTG
 ||| ||| |||||
 CAC CGCT CGCGGGAC
 G CTCACA
 GAM1481 MAGEA10 5' ACACAGTGGGTCGCAGGATCTG 22033 GTA_ TT
 A TCAGATC GAT CCACTGTGT
 ||||| || |||||
 AGTCTAG CTG GGTGACACA
 GACG ____
 GAM1481 PRPS2 3' ACACAATGGAAATTCAGACCTT 8654 A_ GTA C
 GA TCAG TC GATTTCCA TGTGT
 ||| || ||||| |||||
 AGTT AG TTAAAGGT ACACA
 CC AC_ A
 GAM1481 DKK2 3' CACAGTGGAAATTACTGA 15774 ATCGTA
 TCAG GATTTCCACTGTG
 ||| |||||

AGTC TTAAAGGTGACAC
 A_____
 GAM1481 FLJ12838 5' TGGAAATCCACAATTTGA 23925 C A
 TCAGAT GT GATTTC
 ||||| || |||||
 AGTTTA CA CTAAAGGT
 A C
 GAM1481 KIAA0781 3' ACACAGTGAAAATCCAGGA 33498 GTA C
 TC GATTT CACTGTGT
 || ||||| |||||
 AG CTAAA GTGACACA
 GAC A
 GAM1481 SEC8 3' ACACAGTGATGCCTCACACCCT 22358 ATC A TTTC_
 GA TCAG GT GA CACTGTGT
 ||| || || |||||
 AGTC CA CT GTGACACA
 CCA _ CCGTA
 GAM1481 SOX30 3' CACAGTGAAAATTCTCGG 13873 TA C
 TCG GATTT CACTGTG
 ||| ||||| |||||
 GGC TAAA GTGACAC
 TC A
 GAM1481 LOC144455 3' ACACAGTGTCTGTCACCAACCT 37750 ATC A_ TTC
 GA TCAG GT GAT CACTGTGT
 ||| || || |||||
 AGTC CA CTG GTGACACA
 CAA AC CT_
 GAM1481 LOC145644 5' AGTGGAACCCACGATCTGA 32290 AGA_
 TCAGATCGT TTTCCACT
 ||||| |||||
 AGTCTAGCA AAAGGTGA
 CCCA
 GAM1481 LOC200953 5' CACAGTGGACACGAGCTGA 43367 A AGATT
 TCAG TCGT TCCACTGTG
 ||| ||| |||||
 AGTC AGCA AGGTGACAC
 G C____
 GAM1482 CENTG1 3' CACAACTCACCTCCCTCT 16565 A CTTTGT
 AGA GG GTGAGTTTGTG
 ||| || |||||
 TCT CC CACTCAAACAC
 C TC____
 GAM1482 FLJ11726 3' CACTGAGAACACAAAGGCCTCT 24524 A _ GAGTTT
 A TAGA GGC TTTGTGT GTG
 ||| ||| ||||| |||
 ATCT CCG AAACACA CAC
 _ G AGAGT_
 GAM1482 LOC219731 5' AGTTCAACAAAGCCTTCTA 44716 G GT
 TAGAAGGCTTTGT TGA T
 ||||| ||||| ||| |

ATCTTCCGAAACA ACT A
 _ TG
 GAM1483 TNFSF15 3' ACAAGACAGACTCCACTCA 11598 T AAT T C
 TGA GTG GT CT GTCTTGT
 ||| ||| ||| ||| ||| |||
 ACT CAC CA GA CAGAACA
 _ CT_ _ _
 GAM1483 VHL 3' AAGAAAAACATTACATC 6156 CTCG
 GATGTGAATGTT TCTT
 ||| ||| ||| ||| ||| |||
 CTACACTTACAA AGAA
 AA_
 GAM1483 FLJ00060 3' AACAAAACGATAATATTTTCA 30625 _ C C
 TCA TGATGTGAA TGTT TCGT TTGTT
 ||| ||| ||| ||| ||| |||
 ACTACACTT ATAA AGCA AACAA
 T T A
 GAM1483 KIAA1678 3' AACATTCTCAAAACATCACATC 35786 A CTCGTCT
 A TGATGTGA TGTT TGTT
 ||| ||| ||| ||| ||| |||
 ACTACACT ACAA ACAA
 _ AACTCTT
 GAM1483 LOC148508 3' AACATATGAATATTCACACCA 40884 A TCGTCT
 TG TGTGAATGTT TGTT
 || ||| ||| ||| ||| |||
 AC ACACTTATAAG ACAA
 C TAT_
 GAM1483 LOC222681 3' ATGAGAACACCACACCA 44608 A AA
 TG TGTG TGTTCTCGT
 || ||| ||| ||| ||| |||
 AC ACAC ACAAGAGTA
 C C_
 GAM1483 LOC222681 3' ATGAGAACACCACACCA 44609 A AA
 TG TGTG TGTTCTCGT
 || ||| ||| ||| ||| |||
 AC ACAC ACAAGAGTA
 C C_
 GAM1483 LOC222681 3' ATGAGAACACCACACCA 44610 A AA
 TG TGTG TGTTCTCGT
 || ||| ||| ||| ||| |||
 AC ACAC ACAAGAGTA
 C C_
 GAM1483 LOC222681 3' ATGAGAACACCACACCA 44611 A AA
 TG TGTG TGTTCTCGT
 || ||| ||| ||| ||| |||
 AC ACAC ACAAGAGTA
 C C_
 GAM1483 LOC222681 3' ATGAGAACACCACACCA 44612 A AA
 TG TGTG TGTTCTCGT
 || ||| ||| ||| ||| |||

			AC ACAC ACAAGAGTA		
			C C_		
GAM1483	LOC222681	3'	ATGAGAACACCACATCA	44613	AA
			TGATGTG TGTTCTCGT		
			ACTACAC ACAAGAGTA		
			C_		
GAM1483	LOC257507	3'	ATGAGAACACCACACCA	46674	A AA
			TG TGTG TGTTCTCGT		
			AC ACAC ACAAGAGTA		
			C C_		
GAM1483	LOC257507	3'	ATGAGAACACCACACCA	46675	A AA
			TG TGTG TGTTCTCGT		
			AC ACAC ACAAGAGTA		
			C C_		
GAM1483	LOC257507	3'	ATGAGAACACCACACCA	46676	A AA
			TG TGTG TGTTCTCGT		
			AC ACAC ACAAGAGTA		
			C C_		
GAM1483	LOC257507	3'	ATGAGAACACCACACCA	46677	A AA
			TG TGTG TGTTCTCGT		
			AC ACAC ACAAGAGTA		
			C C_		
GAM1483	LOC257507	3'	ATGAGAACACCACACCA	46678	A AA
			TG TGTG TGTTCTCGT		
			AC ACAC ACAAGAGTA		
			C C_		
GAM1483	LOC257507	3'	ATGAGAACACCACATCA	46679	AA
			TGATGTG TGTTCTCGT		
			ACTACAC ACAAGAGTA		
			C_		
GAM1483	LOC257625	3'	ATGAGAACACCACACCA	46730	A AA
			TG TGTG TGTTCTCGT		
			AC ACAC ACAAGAGTA		
			C C_		
GAM1483	LOC257625	3'	ATGAGAACACCACACCA	46731	A AA
			TG TGTG TGTTCTCGT		
			AC ACAC ACAAGAGTA		
			C C_		
GAM1483	LOC257625	3'	ATGAGAACACCACACCA	46732	A AA
			TG TGTG TGTTCTCGT		

AC ACAC ACAAGAGTA
 C C_
 GAM1483 LOC257625 3' ATGAGAACACCACACCA 46733 A AA
 TG TGTG TGTTCTCGT
 || ||| |||||
 AC ACAC ACAAGAGTA
 C C_
 GAM1483 LOC257625 3' ATGAGAACACCACACCA 46734 A AA
 TG TGTG TGTTCTCGT
 || ||| |||||
 AC ACAC ACAAGAGTA
 C C_
 GAM1483 LOC257625 3' ATGAGAACACCACATCA 46735 AA
 TGATGTG TGTTCTCGT
 ||||| |||||
 ACTACAC ACAAGAGTA
 C_
 GAM1484 SIAT4A 3' CTTCCCAAAGCTCATTTA 8980 C AA
 TAGAT GAGCTTTG AAG
 |||| ||||| ||
 ATTTA CTCGAAAC TTC
 _ CC
 GAM1485 ANKH 3' TGGGTATAAACTGTTGA 21253 CGAG
 TCAACAGTTTG TCCA
 ||||| |||
 AGTTGTCAAAT GGGT
 AT_
 GAM1485 ANXA9 5' GAGTCAGACAACTGCTGG 9623 A TGCGA CA
 TCA CAGTT GTC ACTC
 || ||| || |||
 GGT GTCAA CAG TGAG
 C _ AC
 GAM1485 DGCR2 3' AGAGCTGGACTCGCTCATCTGT 11611 TTT_ A
 ACAG GCGAGTCCA CTCT
 ||| ||||| |||
 TGTC CGCTCAGGT GAGA
 TACT C
 GAM1485 GLS 3' GAGCTGGATTAGCTGTTGA 17107 TGCG A
 TCAACAGTT AGTCCA CTC
 ||||| |||| |||
 AGTTGTCTGA TTAGGT GAG
 _ C
 GAM1485 INMT 3' AGAGCTAGTGTAAGCTGTTGA 13647 AGTCCAA
 TCAACAGTTTGCG CTCT
 ||||| |||
 AGTTGTCTGAATGT GAGA
 GATC_
 GAM1485 PPP1R12B 3' AGAGTCATCAGCAAAGTGT 25795 _ GTCCA
 ACAGTTTGC GA ACTCT
 ||||| || |||

		TGTCAAACG CT TGAGA		
		A AC___		
GAM1485 STAM	3'	AGTCAAACCTTACAAAACTGTT 9540	___ CG	CCA
G		CAACAGTT TG AGT ACT		
		GTTGTCAA AC TCA TGA		
		AA AT AAC		
GAM1485 WTAP	3'	AGTTGGACTCATTGATGG 11343	A	TTGC
		TCA CAGT GAGTCCAACT		
		GGT GTTA CTCAGGTTGA		
		A _____		
GAM1485 KIAA0121	3'	ACTCTGAGGGCAAACCTGCTGA 35966	A	_____
		TCA CAGTTTGC GAGT		
		AGT GTCAAACG CTCA		
		C GGAGT		
GAM1485 KIAA0546	3'	AGTTGATAAAAATTGTTGA 35328	GCGA	C
		TCAACAGTTT GTC AACT		
		AGTTGTAAA TAG TTGA		
		AA___ _		
GAM1485 KIAA0903	3'	AGTCAGACTCATTGTTGA 35368	TTGC	CA
		TCAACAGT GAGTC ACT		
		AGTTGTTA CTCAG TGA		
		_____ AC		
GAM1485 KIAA1580	5'	AGAGTTAGACCCGCGGGGGTTG 34406	AG	A C
G		TCAAC TTTGCG GTC AACTCT		
		GGTTG GGGCGC CAG TTGAGA		
		G_ C A		
GAM1485 LOC131000	5'	AGTTATAACGGCAAATTGCTGA 37348	A	GA CC_
		TCA CAGTTTGC GT AACT		
		AGT GTTAAACG CA TTGA		
		C G_ ATA		
GAM1485 LOC158434	5'	AGTTGGACTCGTAGGTA CTG 41982	___	
		CAGT TTGCGAGTCCAACT		
		GTCA GATGCTCAGGTTGA		
		TG		
GAM1485 LOC90643	3'	AGAATTGGAGAGAACTGTT 31851	GCGAG	C
		AACAGTTT TCCAA TCT		
		TTGTCAAG AGGTT AGA		
		AG___ A		
GAM1485 LOC91813	5'	AGCTGGACTTGCCGCTGT 33395	TT	A
		ACAGT GCGAGTCCA CT		

		TGTCG CGTTCAGGT GA	
		C_ C	
GAM1486 PML	3'	CTCTAGTGTCCCCATCTGTAAA 27077	AATT A
		TTTACAGATGG ATA TAGAG	
		AAATGTCTACC TGT ATCTC	
		CC_ G	
GAM1486 ZNF192	3'	CTCTGGTGCACCTCCATCTGTAA 12987	ATTATAA
		TTACAGATGGA TAGAG	
		AATGTCTACCT GTCTC	
		CACGTG_	
GAM1486 MGC14161	5'	CTCTACCATGGCCGACTCCTCT 26721	T A____ AA
		GTAAA TTACAGA GGA TTAT TAGAG	
		AATGTCT CCT GGTA ATCTC	
		_ CAGCC CC	
GAM1487 DDEF2	3'	ACTACTGATGGTTTATGACA 9965	CT AAA
		TGTCATAA TCAT TAGT	
		ACAGTATT GGTA ATCA	
		T_ GTC	
GAM1487 PTPRO	3'	ATTTATGAAGTTATGGCA 8738	
		TGTCATAACTTCATAAAT	
		ACGGTATTGAAGTATTTA	
GAM1487 PTPRO	3'	ATTTATGAAGTTATGGCA 25018	
		TGTCATAACTTCATAAAT	
		ACGGTATTGAAGTATTTA	
GAM1487 PTPRO	3'	ATTTATGAAGTTATGGCA 25027	
		TGTCATAACTTCATAAAT	
		ACGGTATTGAAGTATTTA	
GAM1487 PTPRO	3'	ATTTATGAAGTTATGGCA 25003	
		TGTCATAACTTCATAAAT	
		ACGGTATTGAAGTATTTA	
GAM1487 PTPRO	3'	ATTTATGAAGTTATGGCA 25009	
		TGTCATAACTTCATAAAT	
		ACGGTATTGAAGTATTTA	
GAM1487 TACC1	3'	AGACTATTTGCCATGAC 12960	AACTTCA
		GTCAT TAAATAGTCT	

CAGTA GTTTATCAGA
 CC____
 GAM1487 DKFZp762K2015 3' AGATATGGAAGTTATGACA 35883 ATAAATA
 TGTCACTAATTC GTCT
 ||||| |||
 ACAGTATTGAAG TAGA
 GTA____
 GAM1487 FLJ21290 3' AAGACTATCTGTTTCCCTTGAC 24631 TAACTTC A
 A TGTCA ATA ATAGTCTT
 ||| || |||||
 ACAGT TGT TATCAGAA
 TCCCTT_ C
 GAM1487 IPLA2(GAMMA) 5' AGACCATGAATTATGGCA 30443 C AAATA
 TGTCAATA TTCAT GTCT
 ||||| ||| |||
 ACGGTATT AAGTA CAGA
 _ C____
 GAM1487 MGC11349 5' AAGACCATTATTTGTGACTCT 24759 TAACT ____
 GACA GTCA TCATAAATA GTCTT
 ||| ||||| |||
 CAGT AGTGTTTAT CAGAA
 CTC__ TTAC
 GAM1487 LOC219686 3' AGGATGTTTTATGAAGTCACA 43672 CATA TA
 TGT ACTTCATAAA GTCTT
 || ||||| |||
 ACA TGAAGTATTT TAGGA
 C__ TG
 GAM1488 AKAP1 3' TTGATGATATTTAACCAGTTTT 29267 A TTGAA
 AAAACTG TTA GTCATCAA
 ||||| || |||||
 TTTTGAC AAT TAGTAGTT
 C TTA__
 GAM1488 AKAP1 3' TTGATGATATTTAACCAGTTTT 9581 A TTGAA
 AAAACTG TTA GTCATCAA
 ||||| || |||||
 TTTTGAC AAT TAGTAGTT
 C TTA__
 GAM1488 APPBP2 3' TGATGAGGTAATAATCA 13084 AAG
 TGATTATTG TCATCA
 ||||| |||
 ACTAATAAT AGTAGT
 GG_
 GAM1488 CYR61 3' GATGACTTTCTGTTTT 7277 T TTATTG
 AAAAC GA AAGTCATC
 |||| || |||||
 TTTTG CT TTCAGTAG
 T ____
 GAM1488 FBXL3A 3' TGACAGTACATAATCAGTT 14457 _ AA
 AACTGATTAT TG GTCA
 ||||| || |||

			TTGACTAATA AT CAGT		
			C GA		
GAM1488	ROBO1	3'	ATGATTTCAAATCAGTTTT 8847	A	
			AAAAGTCACTT TGAAGTCAT		
			TTTGACTAA AACTTTAGTA		
			—		
GAM1488	ROBO1	3'	ATGATTTCAAATCAGTTTT 28582	A	
			AAAAGTCACTT TGAAGTCAT		
			TTTGACTAA AACTTTAGTA		
			—		
GAM1488	SFRP4	3'	ATGACTTCAGTTTCTGTTTT 8936	T TT	
			AAAAC GA ATTGAAGTCAT		
			TTTG CT TGAAGTCAT		
			T T_		
GAM1488	TCTE1L	3'	TGAAAACAAAATCAGTTTT 35144	A AAG	
			AAAAGTCACTT TTG TCA		
			TTTGACTAA AAC AGT		
			_ AAA		
GAM1488	AP1S2	3'	TTGATGACTTCTGTGGCA 10004	A T_	
			TG TTAT GAAGTCATCAA		
			AC GGTG CTTAGTAGTT		
			_ TT		
GAM1488	API5	3'	TGATAAAGATCATCAGTTTT 13364	T GAA	
			AAAAGTCACTT ATT GTCA		
			TTTGACTA TAG TAGT		
			C AAA		
GAM1488	CGI-57	3'	TGAGGTTTCAATAAACAGTTT 36575	A GT A	
			AAAGTCACTT TATTGAA C TCA		
			TTTGAC AATAACTT G AGT		
			A TG_		
GAM1488	DKFZp434A2417	3'	TGATACTTGAATAATCA 32864	G C	
			TGATTATT AAGT ATCA		
			ACTAATAA TTCA TAGT		
			G _		
GAM1488	FLJ12488	3'	ATGACTCAGTTTCAGTT 25265	TT A	
			AAAGTCACTT ATTGA GTCAT		
			TTGACT TGAAGTCAT		
			T_ _		
GAM1488	KIAA0633	3'	TGATGACTTCACTGGGAG 45142	GA T	
			CT TTA TGAAGTCATCA		

	GA GGT ACTTCAGTAGT	
	G_ C	
GAM1488 KIAA0794	3' TTGATCTCTCCTATAATCAGT 39188	TGA TC
	ACTGATTAT AG ATCAA	
	TGACTAATA TC TAGTT	
	TCC TC	
GAM1488 KIAA0924	3' TGATGACTTTTATAAGTTT 17068	GAT T
	AAACT TAT GAAGTCATCA	
	TTTGA ATA TTTCAGTAGT	
	___ T	
GAM1488 KIAA1430	3' GTGAATTAATCAGTTTT 39359	TTGAAG
	AAACTGATTA TCAT	
	TTTTGACTAAT AGTG	
	TA___	
GAM1488 KIAA1495	3' TTGATGACTCTTACATAGTC 36226	- -
	GATTAT TGA AGTCATCAA	
	CTGATA ATT TCAGTAGTT	
	C C	
GAM1488 PGR1	3' TTGATGACCTCAATATGAGTTT 27125	G T A
	AAACT AT ATTGA GTCATCAA	
	TTTGA TA TAACT CAGTAGTT	
	G _ C	
GAM1488 PRO1635	3' TGATTCAGTAACCAGTTT 20668	A G
	AAACTG TTATTGAA TCA	
	TTTGAC AATGACTT AGT	
	C _	
GAM1488 SMAP1	3' ACTTGCAAAATCAGTTTT 22456	A _
	AAACTGATT TTG AAGT	
	TTTTGACTAA AAC TTCA	
	_ G	
GAM1488 LOC158427	3' GAATGATAATCAGTTTT 29245	GAAG
	AAACTGATTATT TC	
	TTTTGACTAATAG AG	
	TA___	
GAM1488 LOC163231	5' ATGACTCAGTTTCAGTT 40097	TT A
	AACTGA ATTGA GTCAT	
	TTGACT TGACT CAGTA	
	T_ _	
GAM1488 LOC205251	5' ATGATGTAATCAGTT 43588	TGAA
	AACTGATTAT GTCAT	

TTGACTAATG TAGTA

GAM1488 LOC220018 5' TTGATGACCTCCAATAGCTC 44858 _ AA_
GA TTATTG GTCATCAA
|| ||||| |||||
CT GATAAC CAGTAGTT
C CTC

GAM1488 LOC51336 3' TGACCAAAAATCAGTTTT 18759 A AA
AAAAGTATT TTG GTCA
||||||| ||| |||
TTTTGACTAA AAC CAGT
A _

GAM1488 LOC91266 5' GTGTTTTTCATCAATCAGTTTT 32603 AT T_
AAAAGTATT TGAAG CAT
||||||| |||| |||
TTTTGACTAA ACTTT GTG
CT TT

GAM1489 ITK 3' GCTTATCCAAAATTATCTCT 12077 CG____
AGAGATAGTTT AAGT
||||||| |||
TCTCTATTAAC TTCG
ACCTA

GAM1489 KRTHA8 3' CAATGACTTCATTTTTTCT 13645 TAGTTTC
AGAGA GAAGTCATTG
||||| |||||
TCTTT CTTCAGTAAC
TTTTA_

GAM1489 TEM8 3' GCCTATTCAAAATTATCTCT 25918 C GTCATT
AGAGATAGTTT GAA GC
||||||| ||| ||
TCTCTATTAAC CTT CG
A ATC_

GAM1489 BC022889 3' GCAATTCAAAATTATCTC 40684 C AGTC
GAGATAGTTT GA ATTGC
||||||| || |||||
CTCTATTAAC CT TAACG
A _

GAM1489 FLJ20546 3' GGCAACGAGCGAAACTACATCT 19544 GA AAG A
AGA TAGTTTCG TC TTGCC
||| ||||| || |||||
TCT ATCAAAGC AG AACGG
AC G_ C

GAM1489 FLJ20671 3' GGCAACATGGTGAAACTGTCTC 19592 AA CA
T AGAGATAGTTTCG GT TTGCC
||||||| || |||||
TCTCTGTCAAAGT TA AACGG
GG C_

GAM1489 FLJ23121 3' CAATTTTGGAACATCTC 24002 A G TC
GAGAT GTTTC AAG ATTG
||||| ||||| ||| |||

CTCTA CAAAG TTT TAAC
 _ G _
 GAM1489 KIAA1877 3' GCAATGACAATTCAACCATATC 32882 GTTTC _
 T AGATA GAA GTCATTGC
 ||||| ||| |||||
 TCTAT CTT CAGTAACG
 ACCAA AA
 GAM1489 MGC20470 5' GCAACAAGGAAACTATCCT 29686 A GAAGTCA
 AG GATAGTTTC TTGC
 || ||||| |||
 TC CTATCAAAG AACG
 _ GAAC _
 GAM1489 MGC4400 3' GGCAACATAGCGAGACTACCTC 26400 A AAGTCA
 T AGAG TAGTTTCG TTGCC
 ||| ||||| |||
 TCTC ATCAGAGC AACGG
 C GATAC _
 GAM1489 NLI-IF 3' GCAATGACCTCAGACTTCT 22174 T C A
 AGA AGTTT GA GTCATTGC
 ||| ||||| ||| |||||
 TCT TCAGA CT CAGTAACG
 _ _ C
 GAM1489 Spir-2 3' GGCGCACTTCAAAACCCTC 34964 ATA C CAT
 GAG GTTT GAAGT TGCC
 ||| ||| ||||| |||
 CTC CAAA CTTCA GCGG
 C _ A C _
 GAM1489 LOC120856 3' GACCTCAGAACTATCTCT 36640 TC A
 AGAGATAGTT GA GTC
 ||||| ||| |||
 TCTCTATCAA CT CAG
 GA C
 GAM1489 LOC143916 3' GCAATGATTGAACCACTTCT 37651 T TTCGA
 AGA AGT AGTCATTGC
 ||| ||| |||||
 TCT TCA TTAGTAACG
 _ CCAAG
 GAM1489 LOC146506 3' GGCAATGACAGATACTACCTGC 38180 _ A T GAA
 T AG AG TAGT TC GTCATTGCC
 || || ||| || |||||
 TC TC ATCA AG CAGTAACGG
 G C T A _
 GAM1489 LOC152316 3' GGCAATGACCCAAGACCATCAT 41453 _ A CGAA
 CT AGA GAT GTTT GTCATTGCC
 ||| ||| ||| |||||
 TCT CTA CAGA CAGTAACGG
 A C ACC _
 GAM1489 LOC169026 3' GGCAATGACTCTGAGGCTATAT 40266 G A
 CT AGA ATAGTTTCG AGTCATTGCC
 ||| ||||| |||||

			TCT TATCGGAGT TCAGTAACGG		
			A C		
GAM1489	LOC221876	5'	GGTCTTCGAAACCCTCTC 45078	TA	_
			GAGA GTTTCGAAG TC		
			CTCT CAAAGCTTC GG		
			CC T		
GAM1490	FLJ13187	3'	AACAAAAACACATGATTTGGAA 23869	A	TGC C
			TTC CAAATT GTGTTTT GTT		
			AAG GTTTAG CACAAAA CAA		
			_ TA_ A		
GAM1490	PLU-1	3'	AACAAAAACAGCAGTTTGTGA 13400	T G	C
			TCACAAATT GC TGTTTT GTT		
			AGTGTTTGA CG ACAAAA CAA		
			_ _ A		
GAM1490	PLU-1	3'	AACAAAAACAGCAGTTTGTGA 42249	T G	C
			TCACAAATT GC TGTTTT GTT		
			AGTGTTTGA CG ACAAAA CAA		
			_ _ A		
GAM1490	LOC197336	5'	GACACGCAAATTCGTGAA 29809	A	
			TTCAC AATTTGCGTGTT		
			AAGTG TTAAACGCACAG		
			C		
GAM1491	ISLR	3'	GAAGCCTCAGTGGTGAATTC 12072	G A	A
			GAATTCTA CA CTGAG CTTC		
			CTTAAGGT GT GACTC GAAG		
			G _ C		
GAM1491	SON	3'	AAGTCTGACTAGAATTC 27743	_	ACTGA
			GAATTCTAG CA GACTT		
			CTTAAGATC GT CTGAA		
			A _____		
GAM1491	SON	3'	AAGTCTGACTAGAATTC 29039	_	ACTGA
			GAATTCTAG CA GACTT		
			CTTAAGATC GT CTGAA		
			A _____		
GAM1491	SON	3'	AAGTCTGACTAGAATTC 29044	_	ACTGA
			GAATTCTAG CA GACTT		
			CTTAAGATC GT CTGAA		
			A _____		
GAM1491	C20orf38	3'	AAGTCTCAGCAATAGAATTGAA 20321	G	GCAA
			TT AATTCTA CTGAGACTT		

AA TTAAGAT GACTCTGAA
 G AAC_
 GAM1491 DKFZP572C163 5' AAGCTTTCTGTCAGAAATTCAA 30655 AG ACT A
 TTGAATTCT CA GAG CTT
 ||||| || ||| ||
 AACTTAAGA GT TTC GAA
 CT CT_ _
 GAM1491 KIAA0416 3' AAGTCTCAGCCCAGTTCAATTC 17829 CT AA_
 AG TTGAATT AGC CTGAGACTT
 ||||| ||| |||||
 GACTTAA TTG GACTCTGAA
 C_ ACCC
 GAM1491 MASA 3' GAAGTCTCAGTTCAGTGAACAC 32372 AA TAGC
 AA TTG TTC AACTGAGACTTC
 ||| ||| |||||
 AAC AAG TTGACTCTGAAG
 AC TGAC
 GAM1491 LOC152065 5' TCACTGCCAGAATTCAA 41430 A AC
 TTGAATTCT GCA TGA
 ||||| ||| |||
 AACTTAAGA CGT ACT
 C C_
 GAM1491 LOC220766 5' GAAGTCTTCTCCTGGAAC TCA 43652 A CAACT
 TTGA TTCTAG GAGACTTC
 ||| ||||| |||||
 AACT AAGGTC TTCTGAAG
 C CTC_
 GAM1492 CDC23 3' AGTTAGAAGTACTTCTGTCTCA 11031 C A _ _
 CTTA TAAGTGAG CA AAGTG TC AACT
 ||||| || ||||| || |||||
 ATTCACTC GT TTCAT AG TTGA
 T C GA A
 GAM1492 EGLN3 3' AGTCTTTCTTCAGCTCACTTG 22617 CAA TGTCA
 TAAGTGAGC AAG ACT
 ||||| ||| |||
 GTTCACTCG TTC TGA
 AC_ TTTC_
 GAM1492 PXF 3' AGCTGGCTGTCTGCTGTTCACT 8749 AAAGT A
 AGTGAGCCA GTCA CT
 ||||| ||| ||
 TCACTTGGT CGGT GA
 CCTGT C
 GAM1492 SCN1A 5' ATACTTTTGAATCACTTA 42829 GC
 TAAGTGA CAAAAGTGT
 ||||| |||||
 ATTCACT GTTTTCATA
 AA
 GAM1492 KIAA1260 3' AGCTGACACTTCTGAAACTCA 30156 C_ A A
 TGAG CA AAGTGTCA CT
 ||| || ||||| ||

		ACTC GT TTCACAGT GA	
		AAA C C	
GAM1492	LASP1	3' GAGGTCTTTCAGCTCATTTA 12799	CA _ G
		TAAGTGAGC AAAG T TC	
		ATTTACTCG TTTC G AG	
		AC T G	
GAM1492	NCOA2	3' AGCTGACCGGGGCTCACTTG 13293	AAAAGT A
		TAAGTGAGCC GTCA CT	
		GTTCACTCGG CAGT GA	
		GC _ C	
GAM1492	SNRK	3' AGTTATATCCTTTGGCTCAGCT 19306	_ A_ C
		AG TGAGCCAAA GTGT AACT	
		TC ACTCGGTTT TATA TTGA	
		G CC _	
GAM1492	LOC145662	3' ACACTTTTAGCTCAGTTA 37917	G C
		TAA TGAGC AAAAGTGT	
		ATT ACTCG TTTTCACA	
		G A	
GAM1492	LOC203350	3' AGTTTGACATGGGCTCACT 43530	AAAG _
		AGTGAGCCA TGTCAA CT	
		TCACTCGGT ACAGTT GA	
		_ T	
GAM1493	LIMK1	3' CAGCCCCTGCAGTCATCTCA 8123	CTG AA_
		TGAGATGATT GTAG CTG	
		ACTCTACTGA CGTC GAC	
		_ CCC	
GAM1493	LIMK1	3' CAGCCCCTGCAGTCATCTCA 18794	CTG AA_
		TGAGATGATT GTAG CTG	
		ACTCTACTGA CGTC GAC	
		_ CCC	
GAM1493	MKI67	3' CAGCCCCACCAAGATCATTTCA 8251	TC AGAA
		TGAGATGAT TGGT CTG	
		ACTTTACTA ACCA GAC	
		GA CCCC	
GAM1493	NID	3' CAGTTCCTCACCATCATC 8339	TTC A_
		GATGA TGGT GAACTG	
		CTACT ACCA CTTGAC	
		_ CTC	
GAM1493	PDAP1	3' CAGCCCTACCCATTGATCATTT 44421	CT_ AA
	CA	TGAGATGATT GGTAG CTG	

		ACTTTACTAG CCATC GAC		
		TTAC CC		
GAM1493	RPL17	5' CAGCTGTTCTGAATCATCT 6695	TG	AA
		AGATGATTC GTAG CTG		
		TCTACTAAG TGTC GAC		
		CT _		
GAM1493	TEM8	3' CAGGGGCCAGAATATCTCA 25916	A	AGAA
		TGAGATG TTCTGGT CTG		
		ACTCTAT AAGACCG GAC		
		_ GG_		
GAM1493	ZNF264	3' CAGTTGGGCAAAATCATCT 9454	CTG	AG
		AGATGATT GT AACTG		
		TCTACTAA CG TTGAC		
		AA_ GG		
GAM1493	ARHGEF16	5' CAGCTCTACCAGGAGATCCA 15799	A	GA A
		TG GAT TTCTGGTAGA CTG		
		AC CTA AGGACCATCT GAC		
		_ G_ C		
GAM1493	DKFZp761J139	5' CAGCTCCATTATAATCATCT 26033	C	A A
		AGATGATT TGGT GA CTG		
		TCTACTAA ATTA CT GAC		
		T C C		
GAM1493	DKFZp761N0624	3' CAGTTGGGCAGAATCATCT 26073	G	AG
		AGATGATTCTG T AACTG		
		TCTACTAAGAC G TTGAC		
		_ GG		
GAM1493	DKFZp762E1511	3' CAGCCCCACCAGGCCTCATTTTC 29932	T_	AGAA
	A	TGAGATGA TCTGGT CTG		
		ACTTTACT GGACCA GAC		
		CC CCCC		
GAM1493	FLJ14917	3' CAGTTCTACCTTTTATCT 26666	TTCT	
		AGATGA GGTAGAACTG		
		TCTATT CCATCTTGAC		
		TT_		
GAM1493	KIAA1237	3' CAGCTGACAAATCATCTC 39219	C	G AA
		GAGATGATT TG TAG CTG		
		CTCTACTAA AC GTC GAC		
		_ A _		
GAM1493	NETO2	3' AGTAAAGAATCATTTCA 19861	GGTAGA	
		TGAGATGATTCT ACT		

ACTTTACTAAGA TGA
 AA____
 GAM1493 TRPM3 3' CAGTTCTACCTAACGTCCCA 32391 A ATTCT
 TG GATG GGTAGAACTG
 || ||| |||||
 AC CTGC CCATCTTGAC
 C AAT__
 GAM1493 LOC142820 3' CAGTTCTTTGGAATCACCCCT 37561 A_ TG T
 AG TGATTG G AGAACTG
 || ||||| | |||||
 TC ACTAAG T TCTTGAC
 CC GT_
 GAM1493 LOC163682 5' CAGTCCCACCAGAGTGGCTCA 42088 ATG AGA
 TGAG ATTCTGGT ACTG
 ||| ||||| |||
 ACTC TGAGACCA TGAC
 GG_ CCC
 GAM1493 LOC51312 3' AGTCCCACATCATCTCA 20658 TC TAGA
 TGAGATGAT TGG ACT
 ||||| ||| |||
 ACTCTACTA ACC TGA
 C_ C____
 GAM1494 CACNA2D3 5' GTAAAGAAGCTGGCAAAGA 20434 GAGGA
 TCTT CCAGCTTCTTTAC
 ||| |||||
 AGAA GGTGGAAGAAATG
 AC____
 GAM1494 FOLR1 5' AAGCTAAGCCTCAAGATA 18781 ACC
 TATCTTGAGG AGCTT
 ||||| |||
 ATAGAACTCC TCGAA
 GAA
 GAM1494 SP3 3' TAAAAAAGCTGGTGGGTGAAAG 40135 GAGG__ C
 A TCTT ACCAGCTT TTTA
 ||| ||||| |||
 AGAA TGGTCGAA AAAT
 AGTGGG A
 GAM1494 COP9 3' AAAGAAGCTATGAAGATA 13533 GAGGACC
 TATCTT AGCTTCTTT
 ||||| |||||
 ATAGAA TCGAAGAAA
 GTA____
 GAM1494 KIAA0303 5' AGGAAATAGCCCTCAAGATA 34423 ACCA ____
 TATCTTGAGG GCT TCTT
 ||||| ||| |||
 ATAGAACTCC CGA AGGA
 ____ TAA
 GAM1494 KIAA1007 5' TAAAGAAGAACTGAAGATA 44947 G GACCAG
 TATCTT AG CTTCTTTA
 ||||| || |||||

			ATAGAA TC	GAAGAAAT		
			G AA_____			
GAM1494	KIAA1336	3'	AAAGAAGTCTGTCTAAGA	35798	GA	CA
			TCTT GGAC GCTTCTTT			
			AGAA TCTG TGAAGAAA			
			___ TC			
GAM1494	NY-REN-60	3'	TAAAGAACTTTTCCTCAGGA	33318	CC	C
			TCTTGAGGA AG TTCTTTA			
			AGGACTCCT TC AAGAAAT			
			T_ _			
GAM1494	LOC152190	5'	AAGCTGGTCCTCAAAGTA	34523	TC	
			TA TTGAGGACCAGCTT			
			AT AACTCCTGGTCGAA			
			GA			
GAM1494	LOC257471	3'	TAAAAAAGCTGGTGGGTGAAAG	45787	GAGG_	C
	A		TCTT ACCAGCTT TTTA			
			AGAA TGGTCGAA AAAT			
			AGTGGG A			
GAM1495	GPRK7	3'	GTCCCCAAAGCATGTCA	29229	AAAT	
			TGATATGCTTTGG GAC			
			ACTGTACGAAACC CTG			
			C_			
GAM1495	CAGE	5'	CATAGCCACTCTGGATGCATAT	40245	_ TG	AA A
	CA		TGATATGC TT GA TG CTATG			
			ACTATACG AG CT AC GATAC			
			T GT C_ C			
GAM1495	FLJ20079	3'	CATAGCCATCACGAGCATGTCA	19169	T GAA	A
			TGATATGCTT G ATG CTATG			
			ACTGTACGAG C TAC GATAC			
			_ AC_ C			
GAM1495	HSA250839	3'	CATTCCCCAAAGCAATCA	20437	A	A_
			TGAT TGCTTTGG AATG			
			ACTA ACGAAACC TTAC			
			_ CC			
GAM1495	KIAA0376	3'	CATGCCACAAAGCATATCA	32672	GAA_	
			TGATATGCTTTG ATG			
			ACTATACGAAAC TAC			
			ACCG			
GAM1495	pcnp	3'	CATAGTCACAGACAAAAGCATA	21626	A	GGAAA_
	CA		TG TATGCTTT TGACTATG			

		AC ATACGAAA	ACTGATAC	
		— ACAGAC		
GAM1495	LOC145854 3'	CATAATACAAAGCATATTA	38006	GAA_
		TGATATGCTTTG	ATG	
		ATTATACGAAAC	TAC	
		ATAA		
GAM1495	LOC152271 5'	AGTCATTTCCACAGCCTCA	39238	TAT T
		TGA GCT TGGAAATGACT		
		ACT CGA ACCTTTACTGA		
		C_ C		
GAM1495	LOC152315 5'	CATAACCATGAGTATATCA	39256	_ AA
		TGATATGCTT TGG	ATG	
		ACTATATGAG ACC	TAC	
		T AA		
GAM1495	LOC219919 5'	AGTCATTTCCACAGCCTCA	44799	TAT T
		TGA GCT TGGAAATGACT		
		ACT CGA ACCTTTACTGA		
		C_ C		
GAM1496	CDKN2B 3'	CAAACCTAAAGGTGCACT	27807	G AAT
		AGTGCAT TT	TAGTTTG	
		TCACGTG AA	ATCAAAC	
		G _		
GAM1496	ATIP1 3'	CAAACCTAACTAAGTGTGT	21860	TG T A
		G CA GTTA TTAGTTTG		
		T GT CAAT AATCAAAC		
		GT _ C		
GAM1496	DKFZp761D221 3'	ACAAACCAATATCTGCACTTG	26054	T TA A
		CAAGTGCA GT	ATT GTTTGT	
		G TTCACGT TA	TAA CAAACA	
		C _ C		
GAM1496	FLJ00026 3'	ATTAATTTAACATGCATTT	32425	_
		AAGTGCATGT TAA	TTAGT	
		TTTACGTACAATT	AATTA	
		T		
GAM1496	HCA127 3'	ACAAATCCTTTTAAACATGCATT	20755	TTA_
		AGTGCATGT TAA	GTTTGT	
		TTACGTACAATT	TAAACA	
		TTCC		
GAM1496	TPD52 3'	ACATCTTGTCAACATGCATT	11529	A T TT
		AGTGCATGTT	AT AG TGT	

		TTACGTACAA TG TC ACA	
		C T T_	
GAM1496	LOC115073 3'	ACAAACCAATTAAGTGTACTT 36235	G A
		AAGTGCAT TTAATT GTTTGT	
		TTCATGTG AATTAA CAAACA	
		_ C	
GAM1496	LOC221641 5'	ACAAAAAGCCCAACATGCATT 45007	AATTAG
		AGTGCATGTT TTTGT	
		TTACGTACAA AAACA	
		CCCGAA	
GAM1496	LOC91250 5'	ATTAATCAACATGCCTTGT 32545	T A
		ACAAG GCATGTT ATTAGT	
		TGTTC CGTACAA TAATTA	
		_ C	
GAM1497	BCL7B 3'	ATCTGTGACCTCCAGGCAGC 7434	GA AC
		GCT GCC GAGGTCACAGAT	
		CGA CGG CTCCAGTGTCTA	
		_ AC	
GAM1497	TCF12 3'	ATCTGTGACCATAGCCTAGCTA 9200	A CACGA
		TAGCTG GC GGTACACAGAT	
		ATCGAT CG CCAGTGTCTA	
		C ATA_	
GAM1497	DKFZP564O043 3'	CTTTGCCATAGTTCAGCTA 44429	CACGA T C
		TAGCTGAGC GG CA AG	
		ATCGACTTG CC GT TC	
		ATA_ _ T	
GAM1497	HYA22 3'	ATCTGCAATTGTGTGGCTCA 12386	AG CA
		TGAGCCACG GT CAGAT	
		ACTCGGTGT TA GTCTA	
		GT AC	
GAM1497	KIAA0652 3'	ATCTGTGAAGAGTCTCAGC 16407	CC GAGG
		GCTGAG AC TCACAGAT	
		CGACTC TG AGTGTCTA	
		_ AGA_	
GAM1497	KIAA0836 3'	ATCTGTGACCTATATCAAGT 32245	_ GCCACG
		GCT GA AGGTCACAGAT	
		TGA CT TCCAGTGTCTA	
		A ATA_	
GAM1497	RCD-8 3'	TGACCTCAAGCTCAGCTA 15642	CAC
		TAGCTGAGC GAGGTCA	

ATCGACTCG CTCCAGT
 AA_
 GAM1497 STX3A 3' TTGGACCTGACTCAGCTA 10389 C CGA A
 TAGCTGAG CA GGTC CAG
 ||||| || ||| |||
 ATCGACTC GT CCAG GTT
 A ____ _
 GAM1497 LOC149134 5' CTGTGACCATGAGGCCAGCTG 40958 A A A
 TAGCTG GCC CG GGTCACAG
 ||||| ||| || |||||
 GTCGAC CGG GT CCAGTGTC
 C A A
 GAM1497 LOC197335 5' CTATGACCTCGTGTCTC 42480 C_ C
 GAG CACGAGGTCA AG
 || ||||| ||
 CTC GTGCTCCAGT TC
 CT A
 GAM1497 LOC220522 3' ATCTACAACCTCTGGTTCGGCT 30352 C CAC
 A TAGCTGAGCCA GAGGT AGAT
 ||||| ||| |||
 ATCGGCTTGGT CTCCA TCTA
 _ ACA
 GAM1497 LOC92573 5' ATCTAAGATTCATAGCTCAGCT 34593 CAC G AC
 AGCTGAGC GAG TC AGAT
 ||||| ||| |||
 TCGACTCG CTT AG TCTA
 ATA _ AA
 GAM1498 CARP 3' ACACTTTCAGAGCCTTCCCACC 15720 A A CT_
 CA TG GT GGAGGGCTC GTGT
 || ||||| |||
 AC CA CCTTCCGAG CACA
 C C ACTTT
 GAM1498 CGTHBA 3' GCACCCCTGGCCCTCCCAGCCA 14359 A A_ CCT_
 TG GT GGAGGGCT GTGT
 || ||||| |||
 AC CG CCTCCCGG CACG
 _ AC TCCC
 GAM1498 CNN2 3' GCACAGGGACCCCCACCCA 10584 A A A CT
 TG GT GG GGG CCTGTGT
 || || ||| |||||
 AC CA CC CCC GGACACG
 C C _ AG
 GAM1498 COL15A1 3' GTACACAGAAACAGGACTGCTC 7589 GAGGGCTC
 A TGAGTAG CTGTGTAC
 ||||| |||||
 ACTCGTC GACACATG
 AGGACAAA
 GAM1498 EXTL1 5' GCAGACAGCCCTCCTCTCA 10755 T C_
 TGAG AGGAGGGCT CTGT
 ||| ||||| |||

			ACTC TCCTCCCGA GACG		
			— CA		
GAM1498	LAMC1	3'	ACACCCCTTCCTCCTACCA 8073	A	CTCCT
			TG GTAGGAGGG GTGT		
			AC CATCCTCCT CACA		
			— TCCCC		
GAM1498	OAS2	3'	ACACCTCTCCAAGCCCTCCTAC 8373		CCT_____
			GTAGGAGGGCT GTGT		
			CATCCTCCCGA CACA		
			ACCTCTC		
GAM1498	PKNOX1	3'	CAGAGCCCTCCTGCTCA 10912		C
			TGAGTAGGAGGGCTC TG		
			ACTCGTCCTCCCGAG AC		
			—		
GAM1498	PSME3	3'	ACACAGACTCCTACTC 12370		GGCTC
			GAGTAGGAG CTGTGT		
			CTCATCCTC GACACA		
			A_____		
GAM1498	SLC31A1	3'	ACACACACCCCTGCTCA 7601	A	GCTCC
			TGAGTAGG GG TGTGT		
			ACTCGTCC CC ACACA		
			— AC_____		
GAM1498	C16orf5	3'	GCTGGAGCCCTCCTACCCG 15054	A	T
			TG GTAGGAGGGCTCC GT		
			GC CATCCTCCCGAGG CG		
			C T		
GAM1498	DKFZP586G1122	3'	ACCCAGGCCCCCCACCCA 30725	A A A	TC T
			TG GT GG GGGC CTG GT		
			AC CA CC CCG GAC CA		
			C C _ _ C		
GAM1498	DPYSL4	3'	GCAGAGCCCTCCTGCTCA 13142		C
			TGAGTAGGAGGGCTC TGT		
			ACTCGTCCTCCCGAG ACG		
			—		
GAM1498	FLJ13848	3'	GTACACAGGGCCTCCCTCACCC 24134	A _	AG T
	A		TG GT AGG GGC CCTGTGTAC		
			AC CA TCC CCG GGACACATG		
			C C CT _		
GAM1498	FLJ14775	3'	GCCTGAGCCCTCCTGCCCA 26617	A	CT
			TG GTAGGAGGGCTC GT		

AC CGTCCTCCCGAG CG
 C TC
 GAM1498 FLJ20254 3' GCATCTCAGCCTCCTACCCA 19316 A G CCT
 TG GTAGGAGG CT GTGT
 || ||||| || ||||
 AC CATCCTCC GA TACG
 C _ CTC
 GAM1498 FLJ32752 5' GTGGGAACCCTCCTATCA 29483 G C TG
 TGA TAGGAGGG TCC T
 ||| ||||| ||| |
 ACT ATCCTCCC AGG G
 _ A GT
 GAM1498 KIAA0738 3' ACAGCTGAGACCTCCTACTCA 16276 G _
 TGAGTAGGAGG CTC CTGT
 ||||| ||| ||||
 ACTCATCCTCC GAG GACA
 A TC
 GAM1498 KIAA0953 3' GCACAGCCTCCCCTCCTATCCA 33169 AG CTC_
 TG TAGGAGGG CTGTGT
 || ||||| |||||
 AC ATCCTCCC GACACG
 CT CTCC
 GAM1498 KIAA1867 3' ACACCTCAACCCTCCTAGTCA 45452 G CTCCT
 TGA TAGGAGGG GTGT
 ||| ||||| ||||
 ACT ATCCTCCC CACA
 G AACTC
 GAM1498 KPNB3 3' GTACAAAGAAGCCTCCTACCCA 8063 A G C G
 TG GTAGGAGG CT CT TGTAC
 || ||||| || |||||
 AC CATCCTCC GA GA ACATG
 C _ A A
 GAM1498 PJA1 5' GCAGGAGCCCTCCTACCCG 22756 A
 TG GTAGGAGGGCTCCTGT
 || ||||| |||||
 GC CATCCTCCCGAGGACG
 C
 GAM1498 RAB3IL1 3' ACCTGGGCCCTCCCACCCA 15060 A A CT
 TG GT GGAGGGCTC GT
 || || ||||| ||
 AC CA CCTCCCGGG CA
 C C TC
 GAM1498 SEC61A1 3' ACCTGATGCCCTCCTACCCA 14982 A _ CT
 TG GTAGGAGGGC TC GT
 || ||||| || ||
 AC CATCCTCCCG AG CA
 C T TC
 GAM1498 SKIP 3' GCACAACCTTCCTCCCTACTCA 18599 _ CTCC
 TGAGTAGG AGGG TGTGT
 ||||| ||| ||||

		ACTCATCC TCCT ACACG		
		C TCCA		
GAM1498	SKIP	3' GCACAACCTTCCTCCCTACTCA 28262	_	CTCC
		TGAGTAGG AGGG TGTGT		
		ACTCATCC TCCT ACACG		
		C TCCA		
GAM1498	ZNF317	3' ACACAGGAGCCCCCAC 35633	A	A
		GT GG GGGCTCCTGTGT		
		CA CC CCGAGGACACA		
		C _		
GAM1498	LOC146890	5' TACACAGGAGGGCTGCTAATCA 40765	G	G GG
		TGA TAG AG CTCCTGTGTA		
		ACT ATC TC GAGGACACAT		
		A G GG		
GAM1498	LOC148758	3' ACACAGGGGTCCCCACGCA 38586	A	A A
		TG GT GG GGGCTCCTGTGT		
		AC CA CC CCTGGGGACACA		
		G _ _		
GAM1498	LOC149113	3' ATGGGAGCCCCCATACCCA 38640	A	_ A
		TG GTA GG GGGCTCCTGT		
		AC CAT CC CCGAGGGTA		
		C A _		
GAM1498	LOC154403	3' ATGGGAGCCCCCATACCCA 39468	A	_ A
		TG GTA GG GGGCTCCTGT		
		AC CAT CC CCGAGGGTA		
		C A _		
GAM1498	LOC154992	3' ATGGGAGCCCCCATACCCA 39518	A	_ A
		TG GTA GG GGGCTCCTGT		
		AC CAT CC CCGAGGGTA		
		C A _		
GAM1498	LOC201868	3' ATGGGAGCCCCCATACCCA 42921	A	_ A
		TG GTA GG GGGCTCCTGT		
		AC CAT CC CCGAGGGTA		
		C A _		
GAM1498	LOC222068	3' GCACTCTTACCCTCCTTCTCA 44537	T	CTCCT
		TGAG AGGAGGG GTGT		
		ACTC TCCTCCC CACG		
		T ATTCT		
GAM1498	LOC93052	5' ACACAGCGGCCCCACCTCA 35300	T	A_ C
		G AGG GGGCT CTGTGT		

			A TCC CCCGG GACACA		
			C AC C		
GAM1499	CDKN1B	3'	AAACAACAACACAATAACA 10272	TTTG	GA
			TGTTATTGT GTTG GTTT		
			ACAATAACA CAAC CAAA		
			____ AA		
GAM1499	EMX2	3'	AAACCCTACAAAACAAAACA 42314	A	GTT A
			TGTT TTGTTTTG GG GTTT		
			ACAA AACAAAAC CC CAAA		
			A AT_ _		
GAM1499	LAMP2	3'	GAAACTCCATCTTCAAAACAAA 15183	A	T_
	ACA		TGTT TTGTTTTGG TGGAGTTTC		
			ACAA AACAAAAC ACCTCAAAG		
			_ TCT		
GAM1499	PAX6	5'	AAACCCCAACCAACAAAAC 5825	A T A	
			GTT TTGTTT GGTTGG GTTT		
			CAA AACAAA CCAACC CAAA		
			_ _ C		
GAM1499	PAX6	5'	AAACCCCAACCAACAAAAC 7309	A T A	
			GTT TTGTTT GGTTGG GTTT		
			CAA AACAAA CCAACC CAAA		
			_ _ C		
GAM1499	C1orf22	3'	AAACTCCAACGTTGTAATTACA 24834	T	TTTTG
			TGT ATTG GTTGGAGTTT		
			ACA TAAT CAACCTCAA		
			T GTTG_		
GAM1499	DSCR1L1	3'	AAACACACAAGAACAATAACA 12427	GGT	GA
			TGTTATTGTTTT TG GTTT		
			ACAATAACAAGA AC CAAA		
			AC_ A_		
GAM1499	FLJ14906	3'	TCCAACAACAACAACA 26663	A	TTG
			TGTT TTGTT GTTGGA		
			ACAA AACAA CAACCT		
			C _		
GAM1499	FLJ22794	5'	GAAACTCATTGAAAACAATGAC 44029		GGTTG
	A		TGTTATTGTTTT GAGTTTC		
			ACAGTAACAAAA CTCAAAG		
			GTTA_		
GAM1499	KIAA0471	3'	CCAACGGAAAACAATACA 16911	T	_ G
			TGT ATTGTTT T GTTGG		

			ACA TAACAAA G CAACC		
			— A G		
GAM1499	KIAA1456	3'	GAAACTCCATCTCCAACAAAAC 33263	A	TT T
	A		TGTT TTGTT GG TGGAGTTTC		
			ACAA AACAA TC ACCTCAAAG		
			— CC T		
GAM1499	PRO1768	5'	AAACCCAAAACAAAACAAAACA 15322	A	G_ A
			TGTT TTGTTTTG TTGG GTTT		
			ACAA AACAAAAC AACC CAAA		
			— AA —		
GAM1499	S164	3'	AAACCCCTTTAAAACAAAACA 30481	A	TT A
			TGTT TTGTTTTGG GG GTTT		
			ACAA AACAAAATT CC CAAA		
			— TC C		
GAM1499	SP329	5'	GAAACTCCAGCTCACACAA 25097	TTT	
			TTGT GGTGGAGTTTC		
			AACA TCGACCTCAAAG		
			CAC		
GAM1499	LOC123443	5'	AAACCCAAACAAAACAAAACA 36725	A	G A
			TGTT TTGTTTTG TTGG GTTT		
			ACAA AACAAAAC AACC CAAA		
			— A —		
GAM1499	LOC130535	3'	GAAACTCCGTCTCAAAACAAAA 37476	A	_T
	CA		TGTT TTGTTTTG G TGGAGTTTC		
			ACAA AACAAAAC C GCCTCAAAG		
			— T T		
GAM1499	LOC130813	3'	CTGGCCAAAACAAAAACA 37311	A	TG
			TGTT TTGTTTTGGT G		
			ACAA AACAAAACCG C		
			A GT		
GAM1499	LOC149301	3'	AAACCCAAAAAAACAAAAACA 38686	A	GG A
			TGTT TTGTTTT TTGG GTTT		
			ACAA AACAAAA AACC CAAA		
			A AA —		
GAM1499	LOC164382	3'	AAGCAAAACAAAACAATAACA 42159		GTTGGA
			TGTTATTGTTTTG GTTT		
			ACAATAACAAAAC CGAA		
			AAAA_		
GAM1499	LOC203523	3'	GAAACTATGCAAAACAAAACA 43053	A	GTTGG
			TGTT TTGTTTTG AGTTTC		

ACAA AACAAAAC TCAAAG
 _ GTA_
 GAM1499 LOC85479 5' GAAACTATAGAACCAAAAAATA 26958 G GG_
 ACA TGTATT TTTTGGTT AGTTTC
 ||||| ||||| |||||
 ACAATAA AAAACCAA TCAAAG
 _ GATA
 GAM1500 CHC1L 3' TTAAAACAGCCTGTAATTAT 6932 AG C
 ATAA AT GGCTGTTTTAA
 ||| || |||||
 TATT TG CCGACAAAATT
 AA T
 GAM1500 DAG1 3' GATTTAAAATGGTGATGCTT 10632 _ G
 AAG ATCG CTGTTTTAAATC
 ||| ||| |||||
 TTC TAGT GGTAATAATTTAG
 G _
 GAM1500 FBXL11 3' GATTCAACAGGAAACCGATCTT 14681 ____ TTA
 AAGATCGG CTGTT AATC
 ||||| ||||| |||||
 TTCTAGCC GACAA TTAG
 AAAG C_
 GAM1500 VPS26 3' GATTTAAAACATGGCATCTC 11327 TCG _
 GA GCT GTTTTAAATC
 || ||| |||||
 CT CGG CAAAATTTAG
 CTA TA
 GAM1500 KIAA0555 3' GATTCAAAACCAGGATCTTTA 16684 GG _ A
 TAAAGATC CTG TTTT AATC
 ||||| ||| ||||| |||||
 ATTTCTAG GAC AAAA TTAG
 _ C C
 GAM1500 ZNF185 3' GATCCAAAACAGCCTCTCT 14003 TC AA
 AGA GGCTGTTTT ATC
 ||| ||||| |||
 TCT CCGACAAAA TAG
 CT CC
 GAM1500 LOC115265 3' GATACTACAAAGCCAATCTTTA 36309 C GTTTTAA
 T ATAAAGAT GGCT ATC
 ||||| ||||| |||
 TATTTCTA CCGA TAG
 A AACATCA
 GAM1500 LOC257407 5' GGACCTAAAACAGTGTCT 46337 CG AA
 AGAT GCTGTTTTA TCC
 ||||| ||||| |||
 TCTG TGACAAAAT AGG
 _ CC
 GAM1501 C20orf12 5' AATACGCTTTTGGAATGAA 19955 AA T
 TTTATT TA AAAGCGTATT
 ||||| || |||||

			AAGTAA GT TTTCGCATAA		
			AG _		
GAM1502	DSC1	3'	TTTGCAAAC TGATGTTA	23660	CAAATC
			TAGCATTAGT TGCAAA		
			ATTGTAGTCA ACGTTT		
			A_____		
GAM1502	DSC1	3'	TTTGCAAAC TGATGTTA	11390	CAAATC
			TAGCATTAGT TGCAAA		
			ATTGTAGTCA ACGTTT		
			A_____		
GAM1502	RDX	3'	TTTGTTGGTAACTAATGTTA	8812	CAA T
			TAGCATTAGT ATC GCAAA		
			ATTGTAATCA TGG TGTTT		
			A_ T		
GAM1502	RPA1	3'	TGTTTTTTTTGACTAAAGCTA	8856	A TCT_
			TAGC TTAGTCAAA GCA		
			ATCG AATCAGTTT TGT		
			A TTTT		
GAM1502	TNFSF8	3'	TGCAGATGGCCTAATGCT	6916	TCAA
			AGCATTAG ATCTGCA		
			TCGTAATC TAGACGT		
			CGG_		
GAM1502	BRAL1	5'	TGTTTGCAAAGGCAATGC	22395	A AAATC
			GCATT GTC TGCAAACA		
			CGTAA CGG ACGTTTGT		
			_ AA_		
GAM1502	FLJ12838	3'	TTTGCA GATTTGTGGTTA	23926	ATTAGT
			TAGC CAAATCTGCAAA		
			ATTG GTTTAGACGTTT		
			GT_		
GAM1502	HSPC067	5'	TGCTTTGATCCACTAATGCTA	15459	CAA T_
			TAGCATTAGT ATC GCA		
			ATCGTAATCA TAG CGT		
			CC_ TTT		
GAM1502	KIAA1210	3'	TGCCATTTTGATAATGCTA	46089	G TCT
			TAGCATTATCAAA GCA		
			ATCGTAATAGTTT CGT		
			_ TAC		
GAM1502	KIAA1676	3'	TGTTTTGAGCTTTTGACTAAT	44730	T_ GC
			ATTAGTCAAA CT AAACA		

			TAATCAGTTT GA TTTGT		
			TC GT		
GAM1502	MEIS3	3'	TAGTGTTTGACTACTGCTA 38310	T	_
			TAGCA TAGTCAAAT CTG		
			ATCGT ATCAGTTTG GAT		
			C T		
GAM1502	PCBP4	3'	TGCAGATTTCTTGCTGCT 21679	T TC	
			AGCA TAG AAATCTGCA		
			TCGT GTT TTTAGACGT		
			C C_		
GAM1502	PCBP4	3'	TGCAGATTTCTTGCTGCT 26894	T TC	
			AGCA TAG AAATCTGCA		
			TCGT GTT TTTAGACGT		
			C C_		
GAM1502	PCBP4	3'	TGCAGATTTCTTGCTGCT 26896	T TC	
			AGCA TAG AAATCTGCA		
			TCGT GTT TTTAGACGT		
			C C_		
GAM1502	PRO2032	3'	TGTTTCTTTTTTAACTAATGCT 20685	C TCTGC	
	A		TAGCATTAGT AAA AAACA		
			ATCGTAATCA TTT TTTGT		
			A TTTC_		
GAM1502	SLC1A7	3'	TGTTTGCAAATTCAGTGTTA 13492	AGTCA C	
			TAGCATT AAT TGCAAACA		
			ATTGTGA TTA ACGTTTGT		
			C_ A		
GAM1502	ZDHHC3	3'	GTCTGGCATGACTAATGT 18690	AATC AA_	
			GCATTAGTCA TGC AC		
			TGTAATCAGT ACG TG		
			_ GTC		
GAM1502	LOC157918	3'	TGTTTACAAGATGACTAATTCT 41901	C AA GC_	
	A		TAG ATTAGTCA TCT AAACA		
			ATC TAATCAGT AGA TTTGT		
			T _ ACA		
GAM1502	LOC257468	3'	TAGTGTTTGACTACTGCTA 45625	T	_
			TAGCA TAGTCAAAT CTG		
			ATCGT ATCAGTTTG GAT		
			C T		
GAM1502	LOC257486	3'	TGCCATTTTGATAATGCTA 34327	G TCT	
			TAGCATT TCAAA GCA		

		ATCGTAAT AGTTT CGT		
		— TAC		
GAM1503	PKHD1	3' AGAACTGTTGATTTC	28937	TCGCCC C
		TGAAATCA ACAG TCT		
		ACTTTAGT TGTC AGA		
		— A		
GAM1503	SOCS5	3' TAGAGCTACAGGTGTTCA	15231	ATCAT CAC
		TGAA CGCC AGCTCTA		
		ACTT GTGG TCGAGAT		
		— ACA		
GAM1503	ATP9A	3' AGCTGTGGCTGCTTGTTTCA	31075	CAT C
		TGAAAT CG CCACAGCT		
		ACTTTG GT GGTGTCGA		
		TTC C		
GAM1503	DKFZP434P0721	3' ATAGAGCTGTGCAGATCTTCA	31869	ATC GCC
		TGAA ATC CACAGCTCTAT		
		ACTT TAG GTGTCGAGATA		
		C_ AC_		
GAM1503	KIAA1255	3' ATAGAGCTGCATTGTCGGTGAT	33347	A _CCA_
	TCCA	TG AATCATCG C CAGCTCTAT		
		AC TTAGTGGC G GTCGAGATA		
		C T TTAC		
GAM1503	RAB22A	3' ATAGGACTGATGGAAATGATTT	30110	CG CA CT
	CA	TGAAATCAT CC CAG CTAT		
		ACTTTAGTA GG GTC GATA		
		AA TA AG		
GAM1503	LOC129607	3' TAGAGCTGTGTGACTTTA	36975	A TCGCC
		TGAA TCA CACAGCTCTA		
		ATTT AGT GTGTCGAGAT		
		C _		
GAM1503	LOC157918	3' AGCTGTGGGCAAGAGGTCA	41893	AA ATC
		TGA TC GCCCACAGCT		
		ACT AG CGGGTGTCGA		
		GG AA_		
GAM1503	LOC157919	5' AGCTGTGGGCAAGAGGTCA	39680	AA ATC
		TGA TC GCCCACAGCT		
		ACT AG CGGGTGTCGA		
		GG AA_		
GAM1503	LOC219623	5' GTAGAGCTGATGATCTCA	43947	A GCCCAC
		TGA ATCATC AGCTCTAT		

			ACT TAGTAG	TCGAGATG		
			C	_____		
GAM1504	GATA2	3'	GTTGATTGTACGTAGCCA	7805	AG	CCTAC
			TG TACGTACAA	CAAC		
			AC ATGCATGTT	GTTG		
			CG	A_____		
GAM1504	MGC2306	3'	GTTGATTGTACGTAGCCA	26355	AG	CCTAC
			TG TACGTACAA	CAAC		
			AC ATGCATGTT	GTTG		
			CG	A_____		
GAM1504	SPTLC2	3'	CTGTTGGTAAATCCTCTGCTCA	11278		CGTACAACC
			TGAGTA	TACCAACAG		
			ACTCGT	ATGGTTGTC		
			CTCCTAA	_____		
GAM1504	LOC51014	3'	GTGAGTTACACGTA	32752	AC	C
			TGAGTACGT	AAC TAC		
			ACTCATGCA	TTG GTG		
			CA	A		
GAM1504	LOC51213	3'	TGGAAGAGCCGTATGTACTCA	18527		AAC_ A
			TGAGTACGTAC	CT CCA		
			ACTCATGTATG	GA GGT		
			CCGA	A		
GAM1504	LOC92399	3'	CTGCTGGCAAAGGCCTGTACT	29011		TACAA A_____ A
	CA		TGAGTACG	CCT CCA CAG		
			ACTCATGT	GGA GGT GTC		
			CC_____	AAAC C		
GAM1505	B3GALT3	3'	ATTTTACCTGTTTTTGGT	27017	AA	
			ACCAGGAACA	TAAAT		
			TGGTTTTTGT	ATTTTA		
			CC			
GAM1505	B3GALT3	3'	ATTTTACCTGTTTTTGGT	27020	AA	
			ACCAGGAACA	TAAAT		
			TGGTTTTTGT	ATTTTA		
			CC			
GAM1505	FCAR	3'	TAGGATTCCACCTTGTCTGGT	28433	G	ATAA_
	G		CACCAG ACAA	AATCCTA		
			GTGGTC TTGTT	TTAGGAT		
			_	CCACC		
GAM1505	FCMD	3'	AGGATTTTACAGCCTTCTGATG	13572	C	ACAAA
	A		TCA CAGGA	TAAATCCT		

		AGT GTCTT ATTTTAGGA	
		A CCGAC	
GAM1505	MAFK	5' GGGAGCTCTGTCCTGGTGA 8173	A AATAAAA
		TCACCAGGA CA TCCT	
		AGTGGTCCT GT AGGG	
		_ CTCG__	
GAM1505	PKNOX1	3' TAGGACTTCTGTTTCCTGGT 10914	_ AATA A
		ACCAGGAA CA AA TCCTA	
		TGGTCCTT GT TT AGGAT	
		T C__ C	
GAM1505	RAP1GA1	3' AGGATTTTCTTCCCAGGGA 8795	A A_ CAAAT
		TC CC GGAA AAAATCCT	
		AG GG CCTT TTTTAGGA	
		_ AC C__	
GAM1505	RDS	3' TAGGATATGCCCTCCTGGTGA 5865	ACAA AAA
		TCACCAGGA ATA TCCTA	
		AGTGGTCCT TAT AGGAT	
		CCCG __	
GAM1505	SCN1A	3' ATTTTATTTATATTTCTGGT 42831	C__
		ACCAGGAA AAATAAAAT	
		TGGTCTTT TTTATTTTA	
		ATA	
GAM1505	TLX1	5' TAGGATTTTACTTCTTG 12046	CAAA
		CAGGAA TAAAATCCTA	
		GTTCTT ATTTTAGGAT	
		C__	
GAM1505	CENTG2	3' AGGACCCCTTGTCTGCTGGTGG 17155	A ATAAAA
		TCACCAGGA CAA TCCT	
		GGTGGTCCT GTT AGGA	
		_ CCC__	
GAM1505	DC-TM4F2	3' AGGCATTTTGTCTGCTGGTGA 25196	TAAAAT
		TCACCAGGAACAAA CCT	
		AGTGGTCTTTGTTT GGA	
		TAC__	
GAM1505	DKFZP566K0524	3' GATTTTATTTGGAAAGGTGG 34372	AGGAA
		TCACC CAAATAAAATC	
		GGTGG GTTTATTTTAG	
		AAAG_	
GAM1505	KIAA0062	3' AGGATGCTCACTTGTTCTACT 34792	CC ATAAA_
	GA	TCA AGGAACAA ATCCT	

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AGT TCCTTGTT TAGGA
CA CACTCG
GAM1505 KIAA0153 3' AGGGCTTTGTTCTG 17496 TAAAA
CCAGGAACAAA TCCT
||||||| |||
GGTCCTTGTTT GGA
C____
GAM1505 KIAA0825 3' AGGATTTGTGCTCCTATGA 30589 CC A AATA
TCA AGGA CA AAATCCT
||| ||| || |||||
AGT TCCT GT TTTAGGA
A_ C G____
GAM1505 KIAA1036 3' TAGGATTTTTAAATGCTGGTGA 17131 GAACAAAT
TCACCAG AAAATCCTA
||||| |||||
AGTGGTC TTTTAGGAT
GTAAAT____
GAM1505 KIAA1437 3' AGGAGTTCTATTTGTTCTG 30382 A AAA_
GA TC CCAGGAACAAATA TCCT
|| ||||| |||
AG GGTCTTGTTTAT AGGA
G CTTG
GAM1505 KIAA1854 3' AGGCTGATTTGTTCTAGT 35523 C AAAAT
AC AGGAACAAAT CCT
|| ||||| |||
TG TCCTTGTTTA GGA
A GTC____
GAM1505 MGC11352 5' AGGCATTTTGTCTG 32354 TAAAAT
TCACCAGGAACAAA CCT
||||||| |||
AGTGGTCTTTGTTT GGA
TAC____
GAM1505 MGC26954 3' TAGGATTTTATTTGTACT 29639 A
GG ACAAATAAAATCCTA
|| ||||| |||
TC TGTTTATTTAGGAT
A
GAM1505 PPP1R16B 3' AGGCAATTCGTTCTG 30763 _ AAAAT
CCAGGAAC AAAT CCT
||||| ||| |||
GGTCCTTG TTTA GGA
C AC____
GAM1505 RAB17 3' AGGATTTCCACATCTTGGTGA 22785 ACAAATA
TCACCAGGA AAATCCT
||||| |||||
AGTGGTTCT TTTAGGA
ACACC____
GAM1505 RNF38 3' TAGGATATCCCTCACCTGTTCC 23063 C AATAAA____
TGATGA CA CAGGAACA ATCCTA
|| ||||| |||||

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		GT GTCCTTGT	TAGGAT		
		A	CCACTCCCTA		
GAM1505	SEC22C	3'	AGGATTCTATTTTGTTTAATGG	10403	G_ _ A
			CCA GAACAAA TA AATCCT		
			GGT TTTGTTT AT TTAGGA		
			AA T C		
GAM1505	LOC146520	3'	TGGGCTATTTCAATTCCTGGT	38190	C_ AAAT
			ACCAGGAA AAATA CCTA		
			TGGTCCTT TTTAT GGGT		
			AC C_		
GAM1505	LOC154930	3'	AGGATTTTACTGTGTTGG	39503	GA AA
			CCAG ACA TAAAATCCT		
			GGTT TGT ATTTTAGGA		
			G_ C_		
GAM1505	LOC197285	3'	AGGATTTGGGTCCTGGTGA	42414	ACAAATA
			TCACCAGGA AAATCCT		
			AGTGGTCCT TTTAGGA		
			GGG_		
GAM1505	LOC221584	5'	AGGATGTGTGGTCCTGGTGA	45041	A AATAAA
			TCACCAGGA CA ATCCT		
			AGTGGTCCT GT TAGGA		
			G GTG_		
GAM1505	LOC253782	3'	AGTGAACACTATTTGTTCTGG	45796	AAA _
			CCAGGAACAAATA TC CT		
			GGTCCTTGTTTAT AG GA		
			CA_ T		
GAM1506	CLCN3	5'	GTCACGGGCGAAGCTAGAACACT	7567	C C A_ A
			AG TGTTCTAGT TC TCG TGAC		
			TC ACAAGATCA AG GGC ACTG		
			_ CG _		
GAM1506	CREBL2	3'	TCACTGATTAACAGCT	6995	C TCATCGA
			AGCTGTT TAGTC TGA		
			TCGACAA ATTAG ACT		
			A TC_		
GAM1506	CRIP1	3'	GTCATGAAAACAGAACAGT	36539	A C_ C
			GCTGTTCT GT TCAT GAT		
			TGACAAGA CA AGTA CTG		
			C AA _		
GAM1506	FLJ10989	3'	GTCAGAAGATCTAGAACAGC	20282	TCTC GA_
			GCTGTTCTAG ATC TGAC		

		CGACAAGATC TAG ACTG	
		_____ AAG	
GAM1506	FLJ22794 5'	ATCAATGTAAGTACAACAGCT 44025	CT C
		AGCTGTTCTAGT CAT GAT	
		TCGACAAGATCA GTA CTA	
		AT A	
GAM1506	KIAA0445 5'	CATAGACAAGTACAGCAGCT 16145	CTCA G
		AGCTGTTCTAGT TC ATG	
		TCGACGAGATCA AG TAC	
		AC__ A	
GAM1506	MGC12760 5'	CATAGACAAGTACAGCAGCT 26447	CTCA G
		AGCTGTTCTAGT TC ATG	
		TCGACGAGATCA AG TAC	
		AC__ A	
GAM1506	POMT1 3'	TCATCGACAACGAAAAGC 14019	G TA CTCA
		GCT TTC GT TCGATGA	
		CGA AAG CA AGCTACT	
		A __ AC__	
GAM1506	LOC144266 5'	TCATCTTTGAGGCCAGAACAGC 37711	A TC
		GCTGTTCT GTCTCA GATGA	
		CGACAAGA CGGAGT CTA CT	
		C TT	
GAM1506	LOC149579 5'	CATAGACAAGTACAGCAGCT 35241	CTCA G
		AGCTGTTCTAGT TC ATG	
		TCGACGAGATCA AG TAC	
		AC__ A	
GAM1507	CLECSF5 3'	GTAAGTAATACCTATCTCA 14921	C_
		TGAGATAG ATTACTAC	
		ACTCTATCTAATGATG	
		CA	
GAM1507	FBXL5 3'	AGAATGTTGGTAATGCCATGTC 27302	G A CA
	A	TGA AT GCATTACTA ATTCT	
		ACT TA CGTAATGGT TAAGA	
		G C TG	
GAM1507	FBXL5 3'	AGAATGTTGGTAATGCCATGTC 14460	G A CA
	A	TGA AT GCATTACTA ATTCT	
		ACT TA CGTAATGGT TAAGA	
		G C TG	
GAM1507	GDF8 3'	AGAATAAAGTATGCTATCTCA 11764	CTACA
		TGAGATAGCATTATTCT	

			ACTCTATCGTAGT	TAAGA		
			CAA_			
GAM1507	DIO2	3'	AGAATTGTAGTTCTTAGTCCCA	6453	A	AGCATT
			TG GAT	ACTACAATTCT		
			AC CTG	TGATGTTAAGA		
			C ATTCT_			
GAM1507	DIO2	3'	AGAATTGTAGTTCTTAGTCCCA	15163	A	AGCATT
			TG GAT	ACTACAATTCT		
			AC CTG	TGATGTTAAGA		
			C ATTCT_			
GAM1507	KIAA0444	3'	GAAACCTAGTAATGCCATC	31242	A	CAA
			GAT GCATTACTA	TTC		
			CTA CGTAATGAT	AAG		
			C	CCA		
GAM1507	RAB40A	5'	AGATTTGAGCAATGCTATTTCA	39926	A	ACAAT
			TGAGATAGCATT CT	TCT		
			ACTTTATCGTAA GA	AGA		
			C CTTT_			
GAM1508	BACE	5'	CGGATCTCCCCTGACCGCTCTC	14419	A	T AACT
	C		A AGAGC GTCG	GAGATCCG		
			C TCTCG CAGT	CTCTAGGC		
			C C CCC_			
GAM1508	BACE	5'	CGGATCTCCCCTGACCGCTCTC	29087	A	T AACT
	C		A AGAGC GTCG	GAGATCCG		
			C TCTCG CAGT	CTCTAGGC		
			C C CCC_			
GAM1508	CA11	5'	CGGATCTCAGTCCCTGGCTGCT	6876	T	A__
	TT		AGAGC GTCG	ACTGAGATCCG		
			TTTCG CGGT	TGACTCTAGGC		
			T CCC			
GAM1508	DNMT3B	3'	CAGTGCCGACAGCTCTCC	13762	A	A_
			A AGAGCTGTCG	ACTG		
			C TCTCGACAGC	TGAC		
			C	CG		
GAM1508	FMOD	3'	CAGCACTTGACAGCTCTCC	7770	A	A__
			A AGAGCTGTCGA	CTG		
			C TCTCGACAGTT	GAC		
			C	CAC		
GAM1508	GAS1	5'	GATCTCGACAGCTGTT	7799	G	GAAC
			AA AGCTGTC	GAGATC		

TT TCGACAG CTCTAG
 G _____
 GAM1508 GNAZ 3' GACCTCCAGCCACTCACAGCTC 7846 C A____ _ A
 TTT AAAGAGCTGT GA CTG AG TC
 ||||| || ||| ||
 TTTCTCGACA CT GAC TC AG
 _ CACC C C
 GAM1508 ACAA2 5' GGTATTCAAACAGCTCTT 44095 CGAAC AT
 AAGAGCTGT TGAG CC
 ||||| ||| ||
 TTCTCGACA ACTT GG
 A_____ AT
 GAM1508 CCR6 3' GATTTTAACAGCTCT 25369 CGAAC
 AGAGCTGT TGAGATC
 ||||| |||||
 TCTCGACA ATTTTAG

 GAM1508 CCR6 3' GATTTTAACAGCTCT 10576 CGAAC
 AGAGCTGT TGAGATC
 ||||| |||||
 TCTCGACA ATTTTAG

 GAM1508 FLJ14356 5' CTTGGGCAACTCGAGCAGCTCT 25152 A _ A_____ TG
 CC A AGAGCTG TCGA C AG
 | ||||| ||| | ||
 C TCTCGAC AGCT G TC
 C G CAACG GT
 GAM1508 FLJ20034 3' CGGATCTCAGCTGGATCCCT 19133 CT GAA
 AG GTC CTGAGATCCG
 || ||| |||||
 TC TAG GACTCTAGGC
 CC GTC
 GAM1508 MAP2K4 3' ATCTCAGTTGTTTGCTTCTT 8915 _ TGT G
 AAGA GC C AACTGAGAT
 ||| || | |||||
 TTCT CG G TTGACTCTA
 T TTT _
 GAM1508 MGC35558 3' GGATCTCAGAACAGTCTTT 29616 G CGAA
 AAAGA CTGT CTGAGATCC
 |||| ||| |||||
 TTTCT GACA GACTCTAGG
 _ A____
 GAM1508 SGKL 3' GGTATTTCAAAGCTCTTT 14926 GTCGAAC _
 AAAGAGCT TGAGAT CC
 ||||| ||||| ||
 TTTCTCGA ACTTTA GG
 A_____ T
 GAM1508 SYT13 3' GATCTCAGGTGATCTACCCTC 44890 CT____ AA
 GAG GTCG CTGAGATC
 || ||| |||||

CTC TAGT GACTCTAG
 CCATC G_
 GAM1508 LOC197358 3' TGGACATCAACAGCTTT 42512 CGAAC GA
 AGAGCTGT TGA TCCG
 ||||| ||| |||
 TTTCGACA ACT AGGT
 _____ AC
 GAM1508 LOC256230 5' CGGATCTCTCCAACAGCTGCTC 46540 A _ CGAACT
 C A AG AGCTGT GAGATCCG
 || ||||| |||||
 C TC TCGACA CTCTAGGC
 C G ACCT_
 GAM1508 LOC256231 5' CGGATCTCTCCAACAGCTGCTC 46542 A _ CGAACT
 C A AG AGCTGT GAGATCCG
 || ||||| |||||
 C TC TCGACA CTCTAGGC
 C G ACCT_
 GAM1508 LOC92539 5' ATCTCAGCTCTGGCTCTTT 34501 GTC A
 AAAGAGCT GA CTGAGAT
 ||||| || |||||
 TTTCTCGG CT GACTCTA
 T_ C
 GAM1509 PRKACB 3' ACATCTGAGCTCACACT 8601 CA TA
 AGTG AGCTCAG ATGT
 ||| ||||| |||
 TCAC TCGAGTC TACA
 AC _
 GAM1510 CACNB1 3' TGGAACACTCTGGTCCGCCTCA 6387 AT C T
 TGAG CG ACTA GAGTGTTC
 ||| || ||| |||||
 ACTC GC TGGT CTCACAAGGT
 C_ C _
 GAM1510 IMPA1 3' AGCCTCATAGTCAATCCCA 12055 A CGC T
 TG GAT ACTATGAG GTT
 || ||| ||||| |||
 AC CTA TGATACTC CGA
 C AC_ _
 GAM1510 TUFT1 3' TGGAGTGCAGTAGCGCGATCTC 21319 A GA TG
 A TGAGATCGC CTAT G TTCCA
 ||||| ||| | |||||
 ACTCTAGCG GATG C GAGGT
 C A_ GT
 GAM1510 MGC13138 3' TGGAGTGCAATAGCGCAATCTC 27233 C A GA TG
 A TGAGAT GC CTAT G TTCCA
 ||||| || ||| | |||||
 ACTCTA CG GATA C GAGGT
 A C A_ GT
 GAM1510 RAB3IL1 3' TGGAAATGTAACGCGATCTC 15065 AC GAGT
 GAGATCGC TAT GTTCCA
 ||||| ||| |||||

CTCTAGCG ATG TAAGGT
 CA ____
 GAM1510 RNF8 3' TGGAGTACAGTAGTGCAATCTC 10099 C GA
 A TGAGAT GCACTAT GTGTTCCA
 ||||| ||||| |||||
 ACTCTA CGTGATG CATGAGGT
 A A_
 GAM1510 ZNF323 5' GGAACAGTACGATCTTA 25170 C ATGAGT
 TGAGATCG ACT GTTCC
 ||||| || |||||
 ATTCTAGC TGA CAAGG
 A ____
 GAM1510 LOC201965 3' TACTCCATAGTGCAATCCA 42935 A C _
 TG GAT GCACTATG AGTG
 || ||| ||||| |||||
 AC CTA CGTGATAC TCAT
 _ A C
 GAM1510 LOC51696 3' TGGAGTGCAGTAGTGCGATCTC 18315 GA TG
 A TGAGATCGCACTAT G TTCCA
 ||||| ||||| | |||||
 ACTCTAGCGTGATG C GAGGT
 A_ GT
 GAM1510 LOC93349 3' TGGAATGCAATGGCGCGATCTC 28771 A GA
 A TGAGATCGC CTAT GTGTTCCA
 ||||| ||| |||||
 ACTCTAGCG GGTA CGTAAGGT
 C A_
 GAM1511 NKTR 3' GGTCATCATACATCCCACA 11864 T C TATCA
 TGTGG ATG ATG GACT
 ||||| ||| |||||
 ACACC TAC TAC CTGG
 C A TA_
 GAM1511 OXTR 3' GAAGTACTCACACATGCCACA 6621 CA ATCAG
 TGTGGTATG TGT ACTTC
 ||||| ||| |||||
 ACACCGTAC ACA TGAAG
 _ CTCA_
 GAM1511 CBLN1 3' AAATCTGATATATTACACA 10554 GTATGC C
 TGTG ATGTATCAGA TT
 ||| ||||| ||||| ||
 ACAC TATATAGTCT AA
 AT_ A
 GAM1511 HSPC063 3' AAGTCTGATCTGTATACCCA 15437 T TGT
 TG GGTATGCA ATCAGACTT
 || ||||| |||||
 AC CCATATGT TAGTCTGAA
 _ C_
 GAM1511 KIAA1871 3' AAGTCTGATGGAGACCACA 30699 ATGCATG
 TGTGGT TATCAGACTT
 ||||| |||||

		ACACCA	GTAGTCTGAA		
		GAG_____			
GAM1511	Rab11-FIP2	3'	GAAGTCTAATACATGATAC	17098	G C
			GTAT CATGTAT AGACTTC		
			CATA GTACATA TCTGAAG		
			— A		
GAM1512	DYRK1A	5'	AGAGATTTATTTGGGCAAA	28184	GCTCT
			TTTGTCCAAG TCTCT		
			AAACGGGTTT AGAGA		
			ATTT_		
GAM1512	LZTFL1	3'	GATGAGAGAAGGGAGAGAATAA	21600	CCAAGG
	A		TTTGT CTCTTCTCTCATC		
			AAATA GGGAAGAGAGTAG		
			AGAGA_		
GAM1512	SDC4	3'	ATGAGAGAAGAGCCGGA	8889	AA
			TCC GGCTCTTCTCTCAT		
			AGG CCGAGAAGAGAGTA		
			—		
GAM1512	SDPR	3'	ATGAGAGAAACAGGAAACAAA	11024	— AAGGCTC
			TTTG TCC TTCTCTCAT		
			AAAC AGG AAGAGAGTA		
			AA ACA_____		
GAM1512	CAPN6	3'	GATGAGAGAATTCATCCAGACA	15568	CAA CTC_
			TGTC GG TTCTCTCATC		
			ACAG CC AAGAGAGTAG		
			A_ TACTT		
GAM1512	HHLA2	3'	ATGAGAGAAGACTGTGACAA	13935	CAA C
			TTGTC GG TCTTCTCTCAT		
			AACAG TC AGAAGAGAGTA		
			TG_ _		
GAM1512	ITGA10	3'	GATGAGGCTTTACCTCAGACAA	29863	CA CTCTTC
	G		TTTGTC AGG TCTCATC		
			GAACAG TCC GGAGTAG		
			AC ATTC_		
GAM1512	SIMRP7	3'	GAGAAGTAACCCTGGACAGA	44370	A CT_
			TTTGTCCA GG CTTCTC		
			AGACAGGT CC GAAGAG		
			C AAT		
GAM1512	LOC145497	5'	GATGAGAAATTTTTCACCACTG	37873	A_ CTCTTC_
	GACAAA		TTGTCCA GG TCTCATC		

	AACAGGT CC AGAGTAG		
	CA ACTTTTTAA		
GAM1512 LOC153469 3'	GATAGAGCACTGGACAAA 39378	AG	_
	TTTGTCCA GCTCT TC		
	AAACAGGT CGAGA AG		
	CA T		
GAM1512 LOC220766 5'	GATGAAAAAGAGCTTTCAAG 43654	TCC	CTC
	TTTG AAGGCTCTT TCATC		
	GAAC TTTCGAGAA AGTAG		
	AAA		
GAM1512 LOC221431 3'	ATGAGAAAGCTGGGCAAA 44222	AG	CTTC
	TTTGTCCA GCT TCTCAT		
	AAACGGGT CGA AGAGTA		
	A		
GAM1512 LOC222787 5'	AGAAGGTTTTGGATAAA 45304	T	
	TTTGTCCAAGGC CTTCT		
	AAATAGGTTTTG GAAGA		
	-		
GAM1512 LOC257396 5'	AGAAAACTTTGGACAAA 46406	CTC	
	TTTGTCCAAGG TTCT		
	AAACAGGTTTC AAGA		
	AAA		
GAM1513 B3GALT2 5'	AAAAGCAATCGCAGGAGGCA 9868	AA GA	A
	TGT TC TGC ATTGCTTTT		
	ACG AG ACG TAACGAAAA		
	G_ G_ C		
GAM1513 DXS1283E 3'	AAGTATCTTGTATCGACTACA 35059	A	T_
	TGTA TCGATGCAA TGCTT		
	ACAT AGCTATGTT ATGAA		
	C CT		
GAM1513 DKFZp434N074 5'	AAAAGCATCGTTGATTACA 31388	CAAT	
	TGTAATCGATG TGCTTTT		
	ACATTAGTTGC ACGAAAA		
	T__		
GAM1513 FLJ10759 3'	AAAAGCAACTGCAGGACA 20098	AATCGA	A
	TGT TGCA TTGCTTTT		
	ACA ACGT AACGAAAA		
	GG__ C		
GAM1513 LOC153561 3'	AAAAGCAGGCTCATCGAATACA 39400	A	CAA
	TGTA TCGATG TTGCTTTT		

		ACAT AGCTAC GACGAAAA	
		A TCG	
GAM1514 BNC	3'	CCTGGGGGTGGCTTTAAAT 7450	GA__
		GTTTAAAGCCAT AGG	
		TAAATTCGGTG TCC	
		GGGG	
GAM1514 NDN	3'	GCCCTTCATGACCTTGCTGG 8312	TTA C_
		TCAGT AAG CATGAAGGGC	
		GGTCG TTC GTACTTCCCG	
		__ CA	
GAM1514 OLIG2	3'	GCTGTCTGGCTTTAACCTGA 12382	T T AG
		TCAG TTAAAGCCA GA GGC	
		AGTC AATTCGGT CT TCG	
		C _ G_	
GAM1514 RASGRP1	3'	CCTGAGGAACCTTTACACTGA 12302	T __ ATGA
		TCAGT TAAAG CC AGG	
		AGTCA ATTC GG TCC	
		C AA AG__	
GAM1514 SNL	3'	GCCCCCTTGCCTTTCAAAGTGG 9064	_ C TGAA
		TCAGTTT AAAG CA GGGC	
		GGTCAA TTTC GT CCCG	
		C C TCC_	
GAM1514 WNT5A	5'	CATCGGCTCGTAAACTGA 9429	A_ _
		TCAGTTTA AGCC ATG	
		AGTCAAAT TCGG TAC	
		GC C	
GAM1514 BTN2A2	3'	CTTTCAGACTTAAACTGA 13859	A CCA
		TCAGTTTAA G TGAAGG	
		AGTCAAATT C ACTTTC	
		_ AG_	
GAM1514 C17orf1A	5'	GCCCCTGACTCTAAGCTGA 13086	A C TGAA
		TCAGTTTA AG CA GGGC	
		AGTCGAAT TC GT CCCG	
		C A C__	
GAM1514 CABYR	3'	CCCTTTATTGTCTAACTGA 14477	TAAA C
		TCAGTT GC ATGAAGGG	
		AGTCAA TG TATTTCCC	
		TC__ T	
GAM1514 CD36L1	3'	GCCCTTTTCCTCCAGCCTAAAC 12019	AA CAT__
TGA		TCAGTTTA GC GAAGGGC	

AGTCAAAT CG TTTCCCG
 C_ ACCTCCT
 GAM1514 CGI-01 3' GCCCTCCTGCCTAGACTGA 18055 AA CAT A
 TCAGTTTA GC GA GGGC
 ||||| || ||||
 AGTCAGAT CG CT CCCG
 C_ TC_ _
 GAM1514 DKFZp434C0328 5' GCCCTTTGATTTAACCTGA 19014 T GCCAT
 TCAG TTAAA GAAGGGC
 ||| |||| |||||
 AGTC AATTT TTTCCCG
 C AG__
 GAM1514 FLJ11588 5' CCCTTGCCTGAACTGA 23853 AA CATG
 TCAGTTTA GC AAGGG
 ||||| || ||||
 AGTCAAGT CG TTCCC
 C_ ____
 GAM1514 FLJ12838 3' CCTGAAATGGCTTTAAATT 23923 GA_
 AGTTTAAAGCCAT AGG
 ||||| ||||| |||
 TTAAATTTCCGTA TCC
 AAG
 GAM1514 FLJ20400 3' CCTCAAAATTTAAACTGA 33044 GCCA A
 TCAGTTTAAA TGA GG
 ||||| ||||| ||| ||
 AGTCAAATTT ACT CC
 AAA_ _
 GAM1514 KIAA0638 3' GCCCTTCACGCCTTAACACT 35846 _ A CA
 AGT TTAA GC TGAAGGGC
 ||| |||| || |||||
 TCA AATT CG ACTTCCCG
 C C C_
 GAM1514 KIAA0894 3' GCCCCCATGTTCATTTAGACT 17057 GC_ AA
 AGTTTAAA CATG GGGC
 ||||| |||| ||||
 TCAGATTT GTAC CCCG
 ACT C_
 GAM1514 KIAA1204 5' GCCCTCCCTCTTAAGCTGA 34315 _ CCAT A
 TCAGTTTAA AG GA GGGC
 ||||| || |||||
 AGTCGAATT TC CT CCCG
 C C_ _
 GAM1514 LGI4 3' GCCCTTCAGGTCTAAAGC 29288 AAA A
 GTTT GCC TGAAGGGC
 |||| ||| |||||
 CGAA TGG ACTTCCCG
 ATC _
 GAM1514 MGC4172 3' CCCTTCATGGCTTGCCTCCTG 23598 TTTA_
 CAG AAGCCATGAAGGG
 ||| ||||| |||||

		GTC TTCGGTACTTCCC	
		CTCCG	
GAM1514 MIDORI	3'	GCCCTTCATGGCTCTGCAC	36529 T A
		GT TA AGCCATGAAGGGC	
		CA GT TCGGTACTTCCCG	
		C C	
GAM1514 ZF5128	3'	GCCCTTCATGGCAGGGAC	15671 AAA
		GTTT GCCATGAAGGGC	
		CAGG CGGTACTTCCCG	
		GA_	
GAM1514 LOC145989	3'	GCCCCCTTGCCCTTTCAAACCTGG	29952 _ C TGAA
		TCAGTTT AAAG CA GGGC	
		GGTCAAA TTTC GT CCCG	
		C C TCC_	
GAM1514 LOC148195	5'	GCCCTCTCCTCTAACCTATAAA	40877 A CCAT ____
		CTGA TCAGTTTA AG GA AGGGC	
		AGTCAAAT TC CT TCCCG	
		A CAAT CCTC	
GAM1514 LOC158714	5'	GCCCTTCATGGTGGTGAAT	39885 AA
		GTTTA GCCATGAAGGGC	
		TAAGT TGGTACTTCCCG	
		GG	
GAM1514 LOC257407	5'	GCCCAGTGGCTTTAAAC	46336 GAA
		GTTTAAAGCCAT GGGC	
		CAAATTTCGGTG CCCG	
		A_	
GAM1514 LOC91115	3'	GCCAGTGGCTTTAAACTG	32397 GAAG
		CAGTTTAAAGCCAT GGC	
		GTCAAATTTCGGTG CCG	
		A_	
GAM1514 LOC92305	3'	CCTAGCTTTGAACTGA	28759 CATGAA
		TCAGTTTAAAGC GGC	
		AGTCAAGTTTCG TCC	
		A_	
GAM1514 LOC92997	3'	GCCCAGTGGCTTTAAAC	35221 GAA
		GTTTAAAGCCAT GGGC	
		CAAATTTCGGTG CCCG	
		A_	
GAM1515 JAM3	3'	TTTGGCATTGTGTTAACCTCA	26557 TA ATT
		TGAG TTAGG GTGCCAAA	

		ACTC AATTT TACGGTTT		
		C_ GTT		
GAM1515 MATN3	3'	TTGGTGTACTTAATACTCA 8198	AT	TG
		TGAGTATTAGG TG CCAA		
		ACTCATAATTC AT GGTT		
		_ GT		
GAM1515 ZNF278	3'	AGTGACCCCAATCCTATACCCA 15623	A T	TGCCAA
		TG GTAT AGGATTG ACT		
		AC CATA TCCTAAC TGA		
		C _ CCCAG_		
GAM1515 ZNF278	3'	AGTGACCCCAATCCTATACCCA 25772	A T	TGCCAA
		TG GTAT AGGATTG ACT		
		AC CATA TCCTAAC TGA		
		C _ CCCAG_		
GAM1515 ZNF278	3'	AGTGACCCCAATCCTATACCCA 25781	A T	TGCCAA
		TG GTAT AGGATTG ACT		
		AC CATA TCCTAAC TGA		
		C _ CCCAG_		
GAM1515 FLJ20972	3'	AGTTTGCA GTGCCCTAATCTC 24624	T	ATT TG _
A		TGAG ATTAGG G C CAAACT		
		ACTC TAATCC C G GTTTGA		
		_ C_ GT AC		
GAM1515 HSMPP8	3'	GCCTGTAGTCCCAGATACTCA 44902	A_ T_	
		TGAGTATT GGATTG GC		
		ACTCATAG CCTGAT CG		
		AC GTC		
GAM1515 TINF2	3'	AGTTTGACACCTTGATACCCA 14834	A	ATT C
		TG GTATTAGG GTG CAAACT		
		AC CATAGTTC CAC GTTTGA		
		C _ A		
GAM1515 LOC154386	3'	GCCCCTCGATCCTAACCTCA 39473	TA	T_
		TGAG TTAGGATTG GC		
		ACTC AATCCTAGC CG		
		C_ TCCC		
GAM1515 LOC256158	5'	TTTGGCGTGGCCACACTCA 46637	ATTA A TG	
		TGAGT GG T TGCCAAA		
		ACTCA CC G GCGGTTT		
		CA_ _ GT		
GAM1516 TRPC6	5'	TCTGTTGACATAGTAACTC 10979	CATGC	
		GAGTTACTAT GCAGA		

		CTCAATGATA TGTCT	
		CAGT_	
GAM1516 ASB13	3'	GTTTCTGCATGGAATAAC 24014	CTA GC
		GTTA TCATGC AGAAAC	
		CAAT GGTACG TCTTTG	
		AA_ _	
GAM1516 CSMD1	5'	TCCGCGCTCGGAGCAGCTCA 27071	A A AT A
		TGAGTT CT TC GCGC GA	
		ACTCGA GA GG CGCG CT	
		C _ CT C	
GAM1516 CSMD1	5'	TCCGCGCTCGGAGCAGCTCA 36194	A A AT A
		TGAGTT CT TC GCGC GA	
		ACTCGA GA GG CGCG CT	
		C _ CT C	
GAM1516 FLJ10583	3'	TTTCCAGAATAGTAACTCA 19952	CA CGCA
		TGAGTTACTAT TG GAAA	
		ACTCAATGATA AC CTTT	
		AG _	
GAM1516 HEY2	3'	TTCTTGCAATAGTAACT 14566	CA C
		AGTTACTAT TGCG AGAA	
		TCAATGATA ACGT TCTT	
		_ _	
GAM1516 KIAA1944	3'	GTTTCTGCAGCCAGTAAGTCA 37230	G ATCAT _
		TGA TTA CT GC GCAGAAAC	
		ACT AATGA CG CGTCTTTG	
		G C _ A	
GAM1516 KIAA1956	3'	TCTGACAGCAGTAAGTCA 38362	ATCA CG
		TGAGTTACT TG CAGA	
		ACTCAATGA AC GTCT	
		CG _ A _	
GAM1516 PPP4R2	5'	GTTTCTCCATTAATAGTAACTC 21257	C _ CGC
		GAGTTACTAT ATG AGAAAC	
		CTCAATGATA TAC TCTTTG	
		AT C _	
GAM1516 LOC155438	3'	TTGAGACATAATAGTAGCTCA 41769	C CG _
		TGAGTTACTAT ATG CAG	
		ACTCGATGATA TAC GTT	
		A AGA	
GAM1516 LOC200854	5'	GTTTCTCCATTAATAGTAACTC 42253	C _ CGC
		GAGTTACTAT ATG AGAAAC	

CTCAATGATA TAC TCTTTG
 AT C__
 GAM1517 KRT16 5' ACCATTGAGAATGCGCAGC 45627 AT C
 GCT GTGT TTCTCAATGGT
 ||| ||| |||||
 CGA CGCG AAGAGTTACCA
 __ T
 GAM1517 MGC3248 3' ACCACCAAATACATAGCTT 26234 CTTCTCAA
 AAGCTATGTGT TGGT
 ||||| |||
 TTCGATACATA ACCA
 AAACC__
 GAM1517 LOC146515 5' CCACTGAGAAGACCGCT 38192 TAT T A
 AGC G GTCTTCTCA TGG
 ||| | ||||| |||
 TCG C CAGAAGAGT ACC
 __ _ C
 GAM1517 LOC158301 3' ACCATTGAGAAGACATTCCGCT 39809 TAT
 T AAGC GTGTCTTCTCAATGGT
 ||| |||||
 TTCG TACAGAAGAGTTACCA
 CCT
 GAM1518 DNMT3B 3' CAGACAAGCTGCATTTC A 13761 _ CATTATC
 TGAAATGC GC TGTCTG
 ||||| || |||||
 ACTTTACG CG ACAGAC
 T A_____
 GAM1518 SIAT8C 5' CAGACAGATAATAACATT 18025 CGCC
 AATG ATTATCTGTCTG
 ||| |||||
 TTAC TAATAGACAGAC
 AA__
 GAM1518 LOC149301 3' TCAAACAGATGTTGCATTTC A 38691 CCAT C
 TGAAATGCG TATCTGT TGA
 ||||| ||||| |||
 ACTTTACGT GTAGACA ACT
 T__ A
 GAM1519 APPBP2 3' GCAAGATGCTCTGATA 13082 CAAAC A
 TATCAGAGC ATC TTGC
 ||||| || |||
 ATAGTCTCG TAG AACG

 GAM1519 DOCK1 3' AGTGTGTCTGGCTCTGA 7051 A T
 TCAGAGCCA ACA CATT
 ||||| || |||
 AGTCTCGGT TGT GTGA
 C _
 GAM1519 FUT5 3' GGCGTGA CTCTGATA 7788 CCAAACA T
 TATCAGAG TCAT GCC
 ||||| ||| |||

ATAGTCTC AGTG CGG

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GAM1519 PCDHB16 5' GGCTGCTTGGTTCTGA 21947 A TCATT
TCAGAGCCAA CA GCC
||||||| || |||
AGTCTTGGTT GT CGG
C
GAM1519 PPIL1 3' TGCATGTCTGCTCTGATA 18134 CAA _
TATCAGAGC ACAT CA
||||||| ||| ||
ATAGTCTCG TGTA GT
TC_ C
GAM1519 RET 3' TGGTGTTTGGCTCTTATA 21788 C
TAT AGAGCCAAACATCA
||| |||||||||
ATA TCTCGGTTTGTGGT
T
GAM1519 RET 3' TGGTGTTTGGCTCTTATA 21962 C
TAT AGAGCCAAACATCA
||| |||||||||
ATA TCTCGGTTTGTGGT
T
GAM1519 ZNF135 3' GGTCAGTTGACTCTGATA 9489 C AACATC _
TATCAGAG CA ATTG CC
||||||| || ||| ||
ATAGTCTC GT TGAC GG
A T
GAM1519 DKFZp762A227 3' GGCCTGTTTGGCTCCGA 15320 A TCATT
TC GAGCCAAACA GCC
|| |||||||| |||
AG CTCGGTTTGT CGG
C C
GAM1519 DKFZp762A227 3' GGCCTGTTTGGCTCCGA 19108 A TCATT
TC GAGCCAAACA GCC
|| |||||||| |||
AG CTCGGTTTGT CGG
C C
GAM1519 FLJ11608 3' TGGGGACTGTTTTACTCTGATA 23779 CC TCA G
TATCAGAG AAACA TT CCA
||||||| ||| || |||
ATAGTCTC TTTGT AG GGT
AT C_ G
GAM1519 FLJ14146 3' CAAGCCTGTTTGGCCCTGA 24031 A TCA
TCAG GCCAAACA TTG
||| |||||||| |||
AGTC CGGTTTGT AAC
C CCG
GAM1519 FLJ20449 3' TGGCATGGTTTGGCTTCTGATA 19488 _ ATCAT
TATCAGA GCCAAAC TGCCA
||||||| ||||||| |||||
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		ATAGTCT CGGTTTG	ACGGT		
		T GT__			
GAM1519	FLJ23548	3'	GCAAATTTGGCTCGATA	23824	A CATCA
			TATC GAGCCAAA TTGC		
			ATAG CTCGGTTT AACG		
			_ A__		
GAM1519	KIAA0016	3'	GGTGTCACCTTGGCTCTGA	16531	__
			TCAGAGCCAA ACATC		
			AGTCTCGGTT TGTGG		
			CAC		
GAM1519	KIAA1600	3'	GCAATGATATTACCTCTGA	35394	CCA C
			TCAGAG AA ATCATTGC		
			AGTCTC TT TAGTAACG		
			CA_ A		
GAM1519	MGC11287	3'	GGTCCACGTGCCTGGCTCTGA	25501	AA CATT
			TCAGAGCCA CAT GCC		
			AGTCTCGGT GTG TGG		
			CC CACC		
GAM1519	MGC17330	3'	TGGCAATGATGTGCCTTGA	27461	A CAA
			TCAG GC ACATCATTGCCA		
			AGTT CG TGTAGTAACGGT		
			C __		
GAM1519	LOC116068	3'	TGATTATATTTGCCTCTGATA	36502	C C__
			TATCAGAG CAAA ATCA		
			ATAGTCTC GTTT TAGT		
			C ATAT		
GAM1519	LOC202754	3'	TGGCAATGGCAGAAGCCCTGA	40248	A CAAACA
			TCAG GC TCATTGCCA		
			AGTC CG GGTAACGGT		
			C AAGAC_		
GAM1519	LOC90826	5'	TGGAGGATATTTGGCTTTGA	32052	C ATTG
			TCAGAGCCAAA ATC CCA		
			AGTTTCGGTTT TAG GGT		
			A GA__		
GAM1520	HMGB3	3'	AACACGATTCGCAACGTTCTG	11816	CG T
			CAGAATGT GTGA TCGTGTT		
			GTCTTGCA CGCT AGCACAA		
			A_ T		
GAM1520	SMAC	5'	GGCGTGAGCCACCAACACCCTG	29054	AA C AT
			CAG TGT GGTG TCGTGTT		

GTC ACA CCAC AGTGCGG
 CC A CG
 GAM1520 DKFZp547D155 3' AACACGAGACAAAACAATC 34865 A CGG A
 GA TGT TG TTCGTGTT
 || ||| || |||||
 CT ACA AC GAGCACAA
 A AA_ A
 GAM1520 FLJ11126 3' AACACGAAAGTCTGAATCCTG 20333 AATG TGA
 CAG TCGG TTCGTGTT
 ||| |||| |||||
 GTC AGTC AAGCACAA
 CTA_ TGA
 GAM1520 FLJ12704 3' AACATCACCAGTACATTCTG 24560 ATTC
 CAGAATGTCGGTG GTGTT
 ||||| ||||
 GTCTTACAGTCAC TACAA
 CAC_
 GAM1520 FLJ20309 3' ATGAGATCACTGACATTC 19370 _
 GAATGTCGGTGAT TCGT
 ||||| ||||
 CTTACAGTCACTA AGTA
 G
 GAM1520 LOC148696 5' CACGGGTCTGACACGTCTG 40892 A_ GT
 CAGA TGTCG GATTCGTG
 ||| |||| |||||
 GTCT ACAGT CTGGGCAC
 GC _
 GAM1520 LOC149276 5' AACACAAAATGTGGGCATTCTG 40973 G TGATTC
 CAGAATGTC G GTGTT
 ||||| | ||||
 GTCTTACGG T CACAA
 G GTAAAA
 GAM1521 TRIM 3' CAAATGTAAGGCCATGA 18528 AA GAC
 TCAT GCTT TACATTTG
 ||| ||| |||||
 AGTA CGGA ATGTAAAC
 C_ _
 GAM1521 PRO2037 5' CAAATGCTGTTTATGATA 20687 TTGACTA
 TATCATAAGC CATTG
 ||||| ||||
 ATAGTATTTG GTAAAC
 TC____
 GAM1522 KIAA1691 3' CCAATGGTGCTTTTGGCTTTA 44464 TA TTGGAT
 TAA CCA GCACCATTGG
 ||| ||| |||||
 ATT GGT CGTGGTAACC
 TC TTT____
 GAM1522 LOC154813 5' CCAATGGTGCTGCATGG 39492 T GAT
 CCAT G GCACCATTGG
 ||| | |||||

			GGTA C CGTGGTAACC		
			_ GT_		
GAM1523	ABCB10	3'	ATTATAGTCTCAAAATTCCT 14374	CCAAA	_
			AGGAAT GAG CTATAAAT		
			TCCTTA CTC GATATTTA		
			AAA_ T		
GAM1523	ADD1	3'	TGGGTCTCTGGATTCCTG 15470	A	G
			CAGGAATCCA AGA CTA		
			GTCCTTAGGT TCT GGT		
			C G		
GAM1523	ADD1	3'	TGGGTCTCTGGATTCCTG 15474	A	G
			CAGGAATCCA AGA CTA		
			GTCCTTAGGT TCT GGT		
			C G		
GAM1523	CCR9	3'	AGGTCTTATAGATTCCTGA 25249	CA_	G
			TCAGGAATC AAGA CT		
			AGTCCTTAG TTCT GA		
			ATA G		
GAM1523	CCR9	3'	AGGTCTTATAGATTCCTGA 13432	CA_	G
			TCAGGAATC AAGA CT		
			AGTCCTTAG TTCT GA		
			ATA G		
GAM1523	CDC25B	3'	AGCACCTCTGGATTCTGA 22412	G	A A_
			TCAG AATCCA AG GCT		
			AGTC TTAGGT TC CGA		
			_ C CCA		
GAM1523	CDC25B	3'	AGCACCTCTGGATTCTGA 22416	G	A A_
			TCAG AATCCA AG GCT		
			AGTC TTAGGT TC CGA		
			_ C CCA		
GAM1523	CGTHBA	3'	GGCCCCTTGGATTCCTGG 14364	AGA	
			TCAGGAATCCAA GCT		
			GGTCCTTAGGTT CGG		
			CCC		
GAM1523	EIF1A	3'	ATTTATACTCTTTGGACTCC 42721	A	C
			GGA TCCAAAGAG TATAAAT		
			CCT AGGTTTCTC ATATTTA		
			C _		
GAM1523	EXTL3	3'	TGTGGTTTTTGGACCCCT 7171	AA	G
			AGG TCCAAAGA CTATA		

		TCC AGGTTTTT GGTGT	
		CC _	
GAM1523	GHR	3' ATTTATTTTCTTGGATTCCTGA 5671	A CT
		TCAGGAATCCAA GAG ATAAAT	
		AGTCCTTAGGTT CTT TATTTA	
		_ T_	
GAM1523	HS2ST1	3' GGTGCTTCTGAATTCCTGA 14576	C _ A
		TCAGGAAT CA AAG GCT	
		AGTCCTTA GT TTC TGG	
		A C G	
GAM1523	NUCB1	3' AGCCCTCAGGATTCCTGA 12851	AA A
		TCAGGAATCC AG GCT	
		AGTCCTTAGG TC CGA	
		AC C	
GAM1523	CDC42BPB	3' AGTCTTTTCCCTAGTTCCTGA 12658	CCA__ _
		TCAGGAAT AAGAG CT	
		AGTCCTTG TTTTC GA	
		ATCCC T	
GAM1523	DKFZP566B183	3' TTATGTATTTGAATTCCTGA 17769	C GA T
		TCAGGAAT CAAA GC ATAA	
		AGTCCTTA GTTT TG TATT	
		A A_ _	
GAM1523	DKFZP566I1024	3' TAGCCTTGAATTCCTGG 34735	CCA A
		TCAGGAAT AAG GCTA	
		GGTCCTTA TTC CGAT	
		AG_ _	
GAM1523	DKFZp761B0514	3' TGGCCCCCTGGCATTTCCTGA 26053	_ AAGA
		TCAGGAAT CCA GCTA	
		AGTCCTTA GGT CGGT	
		C CCCC	
GAM1523	FLJ13305	5' TGGTCTCGGATTCCTGA 43345	AAA _
		TCAGGAATCC GAG CTA	
		AGTCCTTAGG CTC GGT	
		_ T	
GAM1523	KIAA0265	3' AGCACTCGGAATTCCTGA 34620	_ AA A
		TCAGGAAT CC AG GCT	
		AGTCCTTA GG TC CGA	
		A C_ A	
GAM1523	KIAA1117	3' ATACCTCTGAGTTCCTGA 30632	CCAA C
		TCAGGAAT AGAG TAT	

		AGTCCTTG TCTC ATA	
		AG__ C	
GAM1523 KIAA1319	3'	TTGTGCTCCCTGGATTCCTG 21870	AA T
		CAGGAATCCA GAGC ATAA	
		GTCCTTAGGT CTCG TGTT	
		CC _	
GAM1523 NUDT13	3'	GCTCCTTGGTATTCCTGA 31664	_ A
		TCAGGAAT CCAA GAGC	
		AGTCCTTA GGTT CTCG	
		T C	
GAM1523 SSH2	3'	AGCCCTTTAGAGTTCCTGA 31176	_ C A
		TCAGGAA TC AAAG GCT	
		AGTCCTT AG TTTC CGA	
		G A C	
GAM1523 SSR1	3'	GTGGCTCTTTAATTCCTGA 9113	CC
		TCAGGAAT AAAGAGCTAT	
		AGTCCTTA TTTCTCGGTG	
		A_	
GAM1523 TAF9L	3'	ATTATAGCCAAGGATCCT 18072	A AAAGA
		AGGA TCC GCTATAAAT	
		TCCT AGG CGATATTTA	
		_ AAC__	
GAM1523 LOC115294	3'	TAGTTACCTTGAATTCCTGG 36145	C AG_
		TCAGGAAT CAA AGCTA	
		GGTCCTTA GTT TTGAT	
		A CCA	
GAM1523 LOC150271	5'	AGAATTCTGGATTCCTGA 41166	A AG
		TCAGGAATCCA AG CT	
		AGTCCTTAGGT TT GA	
		C AA	
GAM1523 LOC151877	3'	TGTCTGCCTTGGGTTCC 41398	A A T_
		GGAATCCAA G GC ATA	
		CCTTGGGTT C CG TGT	
		_ _ TC	
GAM1523 LOC152300	5'	AGCTCTTTGGCCCCTGA 39248	AAT
		TCAGG CCAAAGAGCT	
		AGTCC GGTTCCTCGA	
		CC_	
GAM1523 LOC154084	5'	TATTGCGTTTGGATTCTT 41685	GA T
		AGGAATCCAAA GC ATA	

TTCTTAGGTTT CG TAT
 G_ T
 GAM1523 LOC158402 5' TATAGCTCTTAGCCATGA 41976 _ AATCCA
 TCA GG AAGAGCTATA
 ||| || |||||
 AGT CC TTCTCGATAT
 A GA____
 GAM1523 LOC162333 5' ATTTATAGCCATCCGAATCCTG 42124 A CAAAGA
 A TCAGGA TC GCTATAAAT
 ||||| || |||||
 AGTCCT AG CGATATTTA
 A CCTAC_
 GAM1524 TMC1 5' AAAATGAGATGCCAGAAGCCTC 28931 AT ATTTTA
 A TGAG CTTCT TCATTTT
 ||| |||| |||||
 ACTC GAAGA AGTAAAA
 C_ CCGTAG
 GAM1524 KIAA0546 3' GTGAAATAGAAAATGTCA 35332 G C
 TGA AT TTCTATTTTAT
 ||| |||||
 ACT TA AAGATAAAGTG
 G A
 GAM1524 LOC143879 3' AAAATGATAGGTAAAAAGATCT 37656 CTAT
 AGATCTT TTTATCATTTT
 ||||| |||||
 TCTAGAA GGATAGTAAAA
 AAAT
 GAM1524 LOC153222 5' AAAATGATTCTGTAGAAGACCT 39366 A TTT
 AG TCTTCTAT ATCATTTT
 || ||||| |||||
 TC AGAAGATG TAGTAAAA
 C TCT
 GAM1524 LOC219988 5' ATGAACTAGAAGATCCA 44041 A T
 TG GATCTTCTA TTTAT
 || ||||| |||||
 AC CTAGAAGAT AAGTA
 _ C
 GAM1525 LOC170409 3' GCATATGAAATTTTTGAT 40314 C C
 ATCGA AATTCATA GC
 |||| ||||| ||
 TAGTT TTAAAGTAT CG
 T A
 GAM1526 ETV5 3' GGGGAGGCTCAAACCATTA 10749 C C ACTC
 TAAT GTT GA GTCTCCCC
 ||| ||| || |||||
 ATTA CAA CT CGGAGGGG
 C A ____
 GAM1526 WWOX 3' TGGGGAGACAAATCTCAGAAC 18507 _ ACTC_
 GTTC GA GTCTCCCCA
 ||| || |||||

			CAAG CT CAGAGGGGT		
			A CTAAG		
GAM1526	Cab45	3'	GGAAACTGAACGATTA 18620	AACTC C	
			TAATCGTTTCG GT TCC		
			ATTAGCAAGT CA AGG		
			_____ A		
GAM1527	ANK3	3'	AAACCATACACTGGATGACCTA 21980	GA T	
			TAGGTTATT CA TGTATGGTTT		
			ATCCAGTAG GT ACATACCAAA		
			___ C		
GAM1527	FLJ22029	3'	AAACCATACTTATTACTCAATA 24503	CATT___	
			ACC GGTATTGA GTATGGTTT		
			CCAATAACT CATACCAAA		
			CATTATT		
GAM1527	KIAA1579	3'	AAACCAGCCAATCAATAAC 20115	CA TA	
			GTTATTGA TTG TGGTTT		
			CAATAACT AAC ACCAAA		
			___ CG		
GAM1527	LOC149153	3'	AAACCATTTAGAAAATACCAAT 40961	AC GT___	
			AACC GGTATTG ATT ATGGTTT		
			CCAATAAC TAA TACCAAA		
			CA AAGATT		
GAM1528	M11S1	3'	ATTATGTTTAATCGCCA 12516	GC AATG	
			TGGCG TAG GCATAAT		
			ACCGC ATT TGTATTA		
			TA _____		
GAM1528	PLAC1	5'	ATTATCCCCAGCTGCCAGA 22352	AGAAT C	
			TCTGGCGGCT GG ATAAT		
			AGACCGTCGA CC TATTA		
			C___ C		
GAM1528	UBE3A	3'	ATTACTGCTGTTCTAGCCCCCA 28360	C _	
			TGG GGCTAGAATGGCA TAAT		
			ACC CCGATCTTGTCGT ATTA		
			C C		
GAM1528	UBE3A	3'	ATTACTGCTGTTCTAGCCCCCA 28364	C _	
			TGG GGCTAGAATGGCA TAAT		
			ACC CCGATCTTGTCGT ATTA		
			C C		
GAM1528	UBE3A	3'	ATTACTGCTGTTCTAGCCCCCA 6079	C _	
			TGG GGCTAGAATGGCA TAAT		

ACC CCGATCTTGTTCGT ATTA
 C C
 GAM1528 SIAT4B 5' ATTATTTCAAGCCGCCA 13812 A TGGC
 TGGCGGCT GAA ATAAT
 ||||| || ||||
 ACCGCCGA CTT TATTA
 A ____
 GAM1528 LOC91250 5' GATTACAGGCATCAGCCACCA 32548 C A ATG A__
 TGG GGCT GA GC TAATC
 || ||| || || ||||
 ACC CCGA CT CG ATTAG
 A _ A__ GAC
 GAM1529 HGF 3' AATACCACCAATAAATCA 45216 CGA
 TGATTTAT TGGTATT
 ||||| |||||
 ACTAAATA ACCATAA
 ACC
 GAM1529 C20orf43 3' TCTTGCTACCAGCAATAAATCA 30113 CGA T
 TGATTTAT TGGTA TAAGA
 ||||| ||||| |||||
 ACTAAATA ACCAT GTTCT
 ACG C
 GAM1529 KIAA1559 3' ATTCTTGAAATCAATAAATCA 36160 CGA A
 TGATTTAT TGGT TTAAGAAT
 ||||| ||| |||||
 ACTAAATA ACTA AGTTCTTA
 ____ A
 GAM1529 LOC152179 5' ATTCTTAATGAGGTGATATAAT 41431 _ ATGG
 CA TGATT TATCG TATTAAGAAT
 |||| |||| |||||
 ACTAA ATAGT GTAATTCTTA
 T GGA_
 GAM1530 KIAA0429 5' CATTTTGTATCTCCGCACTCA 16467 C A T C
 TGA GT CG AG GTACAAAATG
 || || || || |||||
 ACT CA GC TC TATGTTTTAC
 _ C C _
 GAM1530 PCDH17 3' CATTTTGTCTGCACACACGT 15812 AC A T_
 ACGT GT GCG ACAAATG
 ||| || || |||||
 TGCA CA CGT TGTTTTAC
 CA _ CC
 GAM1530 LOC256806 5' TCACTTTGACCATGCTACGTCA 46143 _ A__ A
 C GT ACGTAGCGT CAAA TGA
 || ||||| ||| |||
 CA TGCATCGTA GTTT ACT
 C CCA C
 GAM1531 UBE2L3 3' GTGCAGTGCATTGAGACA 9361 G TA T
 TG CTGA GTG CACTGCAC
 || ||| || |||||

AC GACT TAC GTGACGTG
 A _ _
 GAM1531 ABCA5 5' CTTGTGCAGCTGCAACCACCA 20745 C ATAG CA
 TGG TG TGT CTGCACAAG
 ||| || ||| |||||
 ACC AC ACG GACGTGTTC
 _ CA_ TC
 GAM1531 DKFZP434B103 5' CTTGTGCAGTAACAGTGCACAC 17895 GC A G C
 A TG TG TA TGT ACTGCACAAG
 || || ||| |||||
 AC AC GT ACA TGACGTGTTC
 AC _ G A
 GAM1531 FLJ13693 3' CTTGTGCAGTGCTGGACTCACC 24188 C TAGT_ T
 CA TGG TGA G CACTGCACAAG
 ||| ||| | |||||
 ACC ACT C GTGACGTGTTC
 C CAGGT_
 GAM1531 FLJ20699 3' TGCAGTGAGCCAGCC 19619 ATA G
 GGCTG GT TCACTGCA
 |||| || |||||
 CCGAC CG AGTGACGT
 _ _
 GAM1531 KCNE4 3' TGCGGGTGGCTCCATCAGCCA 27968 AGT _
 TGGCTGAT GTCACT GCA
 ||||| ||||| |||
 ACCGACTA CGGTGG CGT
 CCT G
 GAM1531 LOC147976 3' TGTACAAGCTCATGATCAGCCA 38431 A TCAC C
 TGGCTGAT GTG TG ACA
 ||||| ||| || |||
 ACCGACTA TAC AC TGT
 G TCGA A
 GAM1531 LOC51236 3' TGTGCAGTGTTGCTACCAGC 18575 A T
 GCTG TAGTG CACTGCACA
 ||| |||| |||||
 CGAC ATCGT GTGACGTGT
 C T
 GAM1532 DUSP10 3' AACTGACAAATTAAGGAGGTTA 14071 C A CTC
 G GC TCTTTAA GTCAGTT
 | || ||||| |||||
 A TG AGGAATT CAGTCAA
 T G AAA
 GAM1532 DUSP10 3' AACTGACAAATTAAGGAGGTTA 29555 C A CTC
 G GC TCTTTAA GTCAGTT
 | || ||||| |||||
 A TG AGGAATT CAGTCAA
 T G AAA
 GAM1532 LOC255533 5' AACTTCTGTTTAAAGATGC 46327 CT TC
 GCATCTTTAA CG AGTT
 ||||| || |||

CGTAGAAATT GT TCAA
T_ CT

GAM1533 CLN2 3' CCTGAAATGCGGTGA 5964 ACGT
TCACC GTGTTTCAGG
||||| |||||
AGTGG CGTAAAGTCC

GAM1533 DDX11 3' ATCCTGAATGAACAGTGG 24983 G GT_
CCAC TGT TTCAGGAT
||||| |||||
GGTG ACA AAGTCCTA
_ AGT

GAM1533 DDX11 3' ATCCTGAATGAACAGTGG 10651 G GT_
CCAC TGT TTCAGGAT
||||| |||||
GGTG ACA AAGTCCTA
_ AGT

GAM1533 DPYSL3 3' GATCCTGGCACATCCATGA 7072 CCAC TT
TCA GTGTGT CAGGATC
||| ||||| |||||
AGT TACACG GTCCTAG
ACC_ _

GAM1533 EPS8 5' GATCCGAGAACACACAAGTGA 10743 CAC CA
TCAC GTGTGTTT GGATC
||||| ||||| |||||
AGTG CACACAAG CCTAG
AA_ AG

GAM1533 F7 3' GATATGCACACACATGGATGA 21237 _ C TT GG
TCA CCA GTGTGT CA ATC
||||| ||||| || |||
AGT GGT CACACA GT TAG
A A C_ A_

GAM1533 F7 3' GATATGCACACACATGGATGA 5608 _ C TT GG
TCA CCA GTGTGT CA ATC
||||| ||||| || |||
AGT GGT CACACA GT TAG
A A C_ A_

GAM1533 FGF23 3' GATCCCAAAAGGATTTTGGTGG 21793 CGT G CA_
TCACCA GT TTT GGATC
||||| || ||| |||||
GGTGGT TA GAA CCTAG
TT_ G AAC

GAM1533 FMR1 3' CCTGAAATGTGTGTGATG 7775 C TG
CA CACG TGTTTCAGG
|| ||| |||||
GT GTGT GTAAAGTCC
A GT

GAM1533 LFG 3' ATCCTGAAACACCAGGAGA 37687 A ACGT
TC CC GTGTTTCAGGAT
|| || |||||

			AG GG CACAAAGTCCTA		
			A AC__		
GAM1533 OTX1	5'	CCTGAAGGACTGCGTGGTGG	15898		_ G
		TCACCACGT GT TTTCAGG			
		GGTGGTGCG CA GAAGTCC			
		T G			
GAM1533 SNAP23	3'	GATCCTGAAAAGTGTTATGA	9919	CC	TGTG
		TCA ACG TTTCAGGATC			
		AGT TGT AAAGTCCTAG			
		AT GA__			
GAM1533 SNAP23	3'	GATCCTGAAAAGTGTTATGA	28284	CC	TGTG
		TCA ACG TTTCAGGATC			
		AGT TGT AAAGTCCTAG			
		AT GA__			
GAM1533 ZNF26	5'	GACTCTATAACACACGTGG	36129	TC	GA
		CCACGTGTGTT AG TC			
		GGTGACACAA TC AG			
		TA TC			
GAM1533 AKAP12	3'	ATCCTGAGGCAAAGTAGTGA	11572	C	GTG
		TCAC AC TGTTTCAGGAT			
		AGTG TG ACGGAGTCCTA			
		A AA_			
GAM1533 AKAP12	3'	ATCCTGAGGCAAAGTAGTGA	29312	C	GTG
		TCAC AC TGTTTCAGGAT			
		AGTG TG ACGGAGTCCTA			
		A AA_			
GAM1533 C1QR1	3'	ATCCTGAAGTGTGGGTGG	14330	G	TG
		CCAC TG TTTCAGGAT			
		GGTG GT GAAGTCCTA			
		G GT			
GAM1533 DDX12	3'	ATCCTGAATGAACAGTGG	30021	G	GT_
		CCAC TGT TTCAGGAT			
		GGTG ACA AAGTCCTA			
		_ AGT			
GAM1533 ERO1L	3'	ATCCTAAAATACATTGGT	15940	C	C
		ACCA GTGTGTTT AGGAT			
		TGGT TACATAAA TCCTA			
		_ A			
GAM1533 FLJ11413	3'	CCCAAACAGGACTGTGGTGA	23772	_ G_	CA
		TCACCAC GT TGTTT GG			

AGTGGTG CA ACAA CC
 T GG AC
 GAM1533 FLJ20040 3' GATCCTGAAGATCGTGTGA 21066 C TGTG
 TCAC ACG TTTCAGGATC
 ||| ||| |||||
 AGTG TGC GAAGTCCTAG
 _ TA_

GAM1533 FLJ20772 3' GATCCTGGGACACATGGG 19665 A TT
 CC CGTGTGT CAGGATC
 || ||||| |||||
 GG GTACACA GTCCTAG
 _ GG

GAM1533 FLJ30574 3' ATCCTGAAGAATGTTGA 29447 CC GTGT
 TCA ACGT TTCAGGAT
 ||| ||| |||||
 AGT TGTA AAGTCCTA
 _ AG_

GAM1533 FLJ31168 3' ATCCTAGCACGTGGGGA 29536 A GTTTC
 TC CCACGTGT AGGAT
 || ||||| |||||
 AG GGTGCACG TCCTA
 G A_

GAM1533 GAGED3 5' CCTTTGCCACGTGGTGA 28268 T TTC
 TCACCACGTG GT AGG
 ||||| || |||
 AGTGGTGCAC CG TCC
 C TT_

GAM1533 IDI2 3' GATCCTGAAAGTCTTGGGGA 27091 A A TGTG
 TC CC CG TTTCAGGATC
 || ||| |||||
 AG GG GT AAAGTCCTAG
 _ _ TCTG

GAM1533 IPLA2(GAMMA) 3' ATCCTGAAAAAGACGGTG 30444 AC GTG
 CACC GT TTTCAGGAT
 ||| || |||||
 GTGG CA AAAGTCCTA
 _ GAA

GAM1533 KIAA0737 3' GATCCTGAAACAGTG 16820 GTG
 CAC TGTTTCAGGATC
 || |||||
 GTG ACAAAGTCCTAG
 _

GAM1533 KIAA0870 3' ATCCGTGTGCACACGTGTGA 39609 C TTCA
 TCAC ACGTGTGT GGAT
 ||| ||||| |||
 AGTG TGCACACG CCTA
 _ TGTG

GAM1533 KIAA1028 3' GATCCTGAAGAAAAAGGTGA 44160 ACGTGTG
 TCACC TTTCAGGATC
 ||| |||||

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AGTGG GAAGTCCTAG
AAAAA__
GAM1533 KIAA1357 3' TGGGACACACGTGTGTGA 35629 _ TT
TCAC CACGTGTGT CA
||||| |||
AGTG GTGCACACA GT
T GG
GAM1533 KIAA1617 3' CCTGAGGGTGCGGTGGTGA 43941 G TG _
TCACCAC TG TT TCAGG
||||| || |||
AGTGGTG GC GG AGTCC
_ GT G
GAM1533 LHFPL2 3' GATCCTGAAAGCAGACTG 34660 C G _
CA GT TGT TT CAGGATC
|| ||| |||
GT CA ACGAA GTCCTAG
_ G A
GAM1533 MAP2K4 3' ATCCTGGAAGGACACAGTGATG 8914 C _ G _
A
TCA CAC GTGT TTTC AGGAT
||| ||| ||| |||
AGT GTG CACA GAAG TCCTA
A A G G
GAM1533 PCQAP 3' CCTTAAACACACATGGGA 18031 A C C_
TC CCA GTGTGTTT AGG
|| ||| ||| |||
AG GGT CACACAAA TCC
_ A AT
GAM1533 PTK6 3' ATCCCAGCTACGTGGGA 12597 A T TCA
TC CCACGTG GTT GGAT
|| ||| ||| |||
AG GGTGCAT CGA CCTA
_ _ C_
GAM1533 RODH-4 3' GATCCCTGTACACGTGGTG 9809 TTT _
CACCACGTGTG CAGG ATC
||||| ||| |||
GTGGTGACAT GTCC TAG
_ C
GAM1533 TSGA14 3' CTGTGGACACACAAGGTGA 20794 AC _
TCACC GTGTGTTT CAG
||||| ||| |||
AGTGG CACACAGG GTC
AA T
GAM1533 WNT16 3' GATCCTGAAACATGCGGG 27674 A
CC CGTGTGTTTCAGGATC
|| ||| ||| |||
GG GCGTACAAAGTCCTAG
_
GAM1533 WNT16 3' GATCCTGAAACATGCGGG 18170 A
CC CGTGTGTTTCAGGATC
|| ||| ||| |||

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GG GCGTACAAAGTCCTAG

GAM1533 LOC143286 5' ATCCTGAAAGAGATGATGG 40353 _ GTG
CCA CGT TTTCAGGAT
||| ||| |||||
GGT GTA AAAGTCCTA
A GAG

GAM1533 LOC144373 3' ATCCTGAATGAACAGTGG 37726 G GT_
CCAC TGT TTCAGGAT
||| ||| |||||
GGTG ACA AAGTCCTA
_ AGT

GAM1533 LOC146728 5' GATCGGCACACATGTGTGA 40723 C T AG
TCAC ACGTGTGT TC GATC
||| ||||| || |||
AGTG TGTACACA GG CTAG
_ C _

GAM1533 LOC149566 3' GATCCTGGGCCCCAGGTGGTGA 41016 G TGT
TCACCAC TG TTCAGGATC
||||| || |||||
AGTGGTG AC GGGTCCTAG
G CCC

GAM1533 LOC150113 5' ATCCTGAAACTATGACGG 42167 A_ T
CC CGTG GTTTCAGGAT
|| ||| |||||
GG GTAT CAAAGTCCTA
CA _

GAM1533 LOC151414 3' ATCCTGAATGGCAGCCAGTGA 39109 CACG GT
TCAC TGT TTCAGGAT
||| ||| |||||
AGTG ACG AAGTCCTA
ACCG GT

GAM1533 LOC158427 3' GATCCCAAGAGACGCACATGAT 29246 C C A_
G CA CA GTGTGTTTC GGATC
|| ||||| |||||
GT GT CACGCAGAG CCTAG
A A AAC

GAM1533 LOC197196 3' ATCCCAGCTACGTGGGA 43199 A T TCA
TC CCACGTG GTT GGAT
|| ||||| ||| |||
AG GGTGCAT CGA CCTA
_ _ C_

GAM1533 LOC199699 3' CCGAGAGACACAGTGTGA 42594 C G A_
TCA CAC TGTGTTTC GG
||| ||| ||||| ||
AGT GTG ACACAGAG CC
A _ AG

GAM1533 LOC219401 3' CCTATGCATGTAGTGA 44591 C TTC
TCAC ACGTGTGT AGG
||| ||||| |||

AGTG TGTACGTA TCC
 A ____
 GAM1533 LOC256112 3' ATCAGAGAACACACGTGGGGA 46103 A CAG
 TC CCACGTGTGTTT GAT
 || ||||| |||
 AG GGTGCACACAAG CTA
 G AGA
 GAM1533 LOC91464 5' GATCCTGGCCTAACCTGGTGA 32876 C GTGTT
 TCACCA GT TCAGGATC
 ||||| || |||||
 AGTGGT CA GGTCTAG
 C ATCC_
 GAM1534 MAP1A 3' CAACATTCCACTATGCCAT 8181 ATC _
 ATGGCATA TGGA TGTG
 ||||| ||| |||||
 TACCGTAT ACCT ACAAC
 C__ T
 GAM1534 MGC20253 3' CAACATCACATCACTCACCATT 29394 CATAATC _
 TTA TAAATGG TG GATGTTG
 ||||| || |||||
 ATTTTACC AC CTACAAC
 ACTCACT A
 GAM1534 LOC120856 3' CAACATCCAGATCTGACA 36635 G TA
 TG CA ATCTGGATGTTG
 || || |||||
 AC GT TAGACCTACAAC
 A C_
 GAM1534 LOC143425 3' AACATCCAGACGATTTC A 42347 C AA
 TGG AT TCTGGATGTT
 || || |||||
 ACT TA AGACCTACAA
 T GC
 GAM1534 LOC201685 3' CAGCTAAGATTATGCCA 43385 GGAT
 TGGCATAATCT GTTG
 ||||| |||
 ACCGTATTAGA CGAC
 AT_
 GAM1535 KCND2 3' AAATAAATAACATAAATCGTTG 14605 CT_
 AA TTCAACGAT TGTTATTTATTT
 ||||| |||||
 AAGTTGCTA ACAATAAATAAA
 AAT
 GAM1535 PMP2 3' AAATAAATAACAAGATAATTGA 8542 CG
 AA TTTCAA ATCTTGTTATTTATTT
 |||| |||||
 AAAGTT TAGAACAATAAATAAA
 AA
 GAM1535 KIAA1229 3' AGATGAAACAAGATCATGAAA 31093 AC AT
 TTTCA GATCTTGTT TTATT
 |||| ||||| |||||

AAAGT CTAGAACAA AGTAGA
A_ _
GAM1536 HGF 3' AATACCACCAATAAATCA 45216 CGA
TGATTTAT TGGTATT
||||| |||||
ACTAAATA ACCATAA
ACC
GAM1536 C20orf43 3' TCTTGCTACCAGCAATAAATCA 30113 CGA T
TGATTTAT TGGTA TAAGA
||||| |||||
ACTAAATA ACCAT GTTCT
ACG C
GAM1536 KIAA1559 3' ATTCTTGAAATCAATAAATCA 36160 CGA A
TGATTTAT TGGT TTAAGAAT
||||| ||| |||||
ACTAAATA ACTA AGTTCTTA
_ A
GAM1536 LOC152179 5' ATTCTTAATGAGGTGATATAAT 41431 _ ATGG
CA TGATT TATCG TATTAAGAAT
||||| ||||| |||||
ACTAA ATAGT GTAATTCTTA
T GGA_
GAM1537 APXL 3' ACTTACTTATTTTATCTA 7352 CT C
TAGATAAA AT AGTAAGT
||||| || |||||
ATCTATTT TA TCATTCA
T_ T
GAM1537 CKN1 3' ACTTCTGTATAGTTTATTTAGT 5529 _ T
CA TGACTAGATAAACTAT CAG AAGT
||||||| ||| |||
ACTGATTTATTTGATA GTC TTCA
T _
GAM1537 HMGA2 3' ACCTACTAATAGTTTGTTGATC 9561 CTA C A
GA GATAAACTAT AGTA GT
|| ||||| ||| ||
CT TTGTTTGATA TCAT CA
AG_ A C
GAM1537 ZNF36 3' ACTTAAGGATCCTTCTAGTCA 45101 TAACT AG
TGACTAGA ATC TAAGT
||||| ||| |||||
ACTGATCT TAG ATTCA
TCC_ GA
GAM1537 FLJ23191 3' GTTGATAGCCCTCTAGTCA 23803 TAAA
TGACTAGA CTATCAGT
||||| |||||
ACTGATCT GATAGTTG
CCC_
GAM1537 KIAA0841 3' ACTTACTGAAATCCCAGTCA 35359 A_ TAAACTA
TGACT GA TCAGTAAGT
|||| || |||||

		ACTGA CT AGTCATTCA		
		CC TAA_____		
GAM1537	RNF20	3' CTGTAGGACAGTTTATCAGTCA 21213	A	A AGTA
		TGACT GATAAACT TC AG		
		ACTGA CTATTTGA AG TC		
		_ C GATG		
GAM1537	LOC118851	3' ACTTTGGGAAATTCATCTGGTC 37199	A	CTA AGT
	A	TGACTAGAT AA TC AAGT		
		ACTGGTCTA TT AG TTCA		
		C AA_ GGT		
GAM1537	LOC150005	3' ACTAGCTGCTTCTAGTCA 41122	TAAACTAT	A
		TGACTAGA CAGT AGT		
		ACTGATCT GTCG TCA		
		TC_____ A		
GAM1538	CLCN4	3' ATAGTGCTGTATCACTTA 7569	AA	
		TAAGTGATACA ACTAT		
		ATTCACTATGT TGATA		
		CG		
GAM1538	HPGD	3' GTCGGTTTGCCAGTATCACTT 6522	AAAAC	TC
	A	TAAGTGATAC TA TCGAC		
		ATTCACTATG GT GGCTG		
		ACCC_ TT		
GAM1538	TIMELESS	3' CGGGAGTTTTGTACCACTT 10006	A	TA
		AAGTG TACAAAAC TCTCG		
		TTCAC ATGTTTTG AGGGC		
		C _		
GAM1538	TLR5	5' TCCTGATGTATTTGTATCACTT 38774	AC	TC
	A	TAAGTGATACAAA TATC GA		
		ATTCACTATGTTT GTAG CT		
		AT TC		
GAM1538	KIAA1557	3' GTCAAAACAGTTTTGTGGAACT 30641	GA	ATCTC
		AGT TACAAAAC GAC		
		TCA GTGTTTTGA CTG		
		AG CAAAA		
GAM1538	PLEKHA3	3' GTCAAGATGACTGCTCTATATC 21167	CAAAAC_____	C
	ACTTG	TAAGTGATA TATCT GAC		
		GTTCACTAT GTAGA CTG		
		ATCTCGTCA A		
GAM1538	LOC133022	3' GTCAAAATAGTTTTGGGGATCA 37375	A_____	CTC
	C	GTGAT CAAAACATAT GAC		

		CACTA GTTTTGATA CTG	
		GGG AAA	
GAM1539	HGF	3' AATACCACCAATAAATCA 45216	CGA
		TGATTTAT TGGTATT	
		ACTAAATA ACCATAA	
		ACC	
GAM1539	C20orf43	3' TCTTGCTACCAGCAATAAATCA 30113	CGA T
		TGATTTAT TGGTA TAAGA	
		ACTAAATA ACCAT GTTCT	
		ACG C	
GAM1539	KIAA1559	3' ATTCTTGAAATCAATAAATCA 36160	CGA A
		TGATTTAT TGGT TTAAGAAT	
		ACTAAATA ACTA AGTTCTTA	
		___ A	
GAM1539	LOC152179	5' ATTCTTAATGAGGTGATATAAT 41431	_ ATGG
	CA	TGATT TATCG TATTAAGAAT	
		ACTAA ATAGT GTAATTCTTA	
		T GGA_	
GAM1540	APXL	3' ACTTACTTATTTTATCTA 7352	CT C
		TAGATAAA AT AGTAAGT	
		ATCTATTT TA TCATTCA	
		T_ T	
GAM1540	CKN1	3' ACTTCTGTATAGTTTATTTAGT 5529	_ T
	CA	TGACTAGATAAACTAT CAG AAGT	
		ACTGATTTATTTGATA GTC TTCA	
		T _	
GAM1540	HMGA2	3' ACCTACTAATAGTTTGTTGATC 9561	CTA C A
		GA GATAAACTAT AGTA GT	
		CT TTGTTTGATA TCAT CA	
		AG_ A C	
GAM1540	ZNF36	3' ACTTAAGGATCCTTCTAGTCA 45101	TAAACT AG
		TGACTAGA ATC TAAGT	
		ACTGATCT TAG ATTCA	
		TCC___ GA	
GAM1540	FLJ23191	3' GTTGATAGCCCTCTAGTCA 23803	TAAA
		TGACTAGA CTATCAGT	
		ACTGATCT GATAGTTG	
		CCC_	
GAM1540	KIAA0841	3' ACTTACTGAAATTCCTCAGTCA 35359	A_ TAAACTA
		TGACT GA TCAGTAAGT	

		ACTGA CT AGTCATTCA		
		CC TAA_____		
GAM1540	RNF20	3' CTGTAGGACAGTTTATCAGTCA 21213	A	A AGTA
		TGACT GATAAACT TC AG		
		ACTGA CTATTTGA AG TC		
		_ C GATG		
GAM1540	LOC118851	3' ACTTTGGGAAATTCATCTGGTC 37199	A	CTA AGT
	A	TGACTAGAT AA TC AAGT		
		ACTGGTCTA TT AG TTCA		
		C AA_ GGT		
GAM1540	LOC150005	3' ACTAGCTGCTTCTAGTCA 41122	TAAACTAT	A
		TGACTAGA CAGT AGT		
		ACTGATCT GTCG TCA		
		TC_____ A		
GAM1541	ABCB10	3' ATTTATAGTCTCAAAATTCCT 14374	CCAAA	_
		AGGAAT GAG CTATAAAT		
		TCCTTA CTC GATATTTA		
		AAA_ T		
GAM1541	ADD1	3' TGGGTCTCTGGATTCCTG 15474	A	G
		CAGGAATCCA AGA CTA		
		GTCCTTAGGT TCT GGT		
		C G		
GAM1541	ADD1	3' TGGGTCTCTGGATTCCTG 15470	A	G
		CAGGAATCCA AGA CTA		
		GTCCTTAGGT TCT GGT		
		C G		
GAM1541	CCR9	3' AGGTCTTATAGATTCCTGA 25249	CA_	G
		TCAGGAATC AAGA CT		
		AGTCCTTAG TTCT GA		
		ATA G		
GAM1541	CCR9	3' AGGTCTTATAGATTCCTGA 13432	CA_	G
		TCAGGAATC AAGA CT		
		AGTCCTTAG TTCT GA		
		ATA G		
GAM1541	CDC25B	3' AGCACCCCTCTGGATTCTGA 22412	G	A A_
		TCAG AATCCA AG GCT		
		AGTC TTAGGT TC CGA		
		_ C CCA		
GAM1541	CDC25B	3' AGCACCCCTCTGGATTCTGA 22416	G	A A_
		TCAG AATCCA AG GCT		

			AGTC TTAGGT TC CGA		
			— C CCA		
GAM1541	CGTHBA	3'	GGCCCCTTGGATTCCTGG 14364	AGA	
			TCAGGAATCCAA GCT		
			GGTCCTTAGGTT CGG		
			CCC		
GAM1541	EIF1A	3'	ATTTATACTCTTTGGACTCC 42721 A C		
			GGA TCCAAAGAG TATAAAT		
			CCT AGGTTTCTC ATATTTA		
			C —		
GAM1541	EXTL3	3'	TGTGGTTTTTTGGACCCCT 7171 AA G		
			AGG TCCAAAGA CTATA		
			TCC AGGTTTTTT GGTGT		
			CC —		
GAM1541	GHR	3'	ATTTATTTTCTTGGATTCCTGA 5671 A CT		
			TCAGGAATCCAA GAG ATAAAT		
			AGTCCTTAGGTT CTT TATTTA		
			— T—		
GAM1541	HS2ST1	3'	GGTGCTTCTGAATTCCTGA 14576 C _ A		
			TCAGGAAT CA AAG GCT		
			AGTCCTTA GT TTC TGG		
			A C G		
GAM1541	NUCB1	3'	AGCCCTCAGGATTCCTGA 12851 AA A		
			TCAGGAATCC AG GCT		
			AGTCCTTAGG TC CGA		
			AC C		
GAM1541	CDC42BPB	3'	AGTCTTTTCCCTAGTTCCTGA 12658 CCA__ _		
			TCAGGAAT AAGAG CT		
			AGTCCTTG TTTTC GA		
			ATCCC T		
GAM1541	DKFZP566B183	3'	TTATGTATTTGAATTCCTGA 17769 C GA T		
			TCAGGAAT CAAA GC ATAA		
			AGTCCTTA GTTT TG TATT		
			A A_ _		
GAM1541	DKFZP566I1024	3'	TAGCCTTGAATTCCTGG 34735 CCA A		
			TCAGGAAT AAG GCTA		
			GGTCCTTA TTC CGAT		
			AG_ _		
GAM1541	DKFZp761B0514	3'	TGGCCCCCTGGCATTTCCTGA 26053 _ AAGA		
			TCAGGAAT CCA GCTA		

		AGTCCTTA GGT CGGT	
		C CCCC	
GAM1541 FLJ13305	5'	TGGTCTCGGATTCCTGA 43345	AAA _
		TCAGGAATCC GAG CTA	
		AGTCCTTAGG CTC GGT	
		_ T	
GAM1541 KIAA0265	3'	AGCACTCGGAATTCCTGA 34620	_ AA A
		TCAGGAAT CC AG GCT	
		AGTCCTTA GG TC CGA	
		A C_ A	
GAM1541 KIAA1117	3'	ATACCTCTGAGTTCCTGA 30632	CCAA C
		TCAGGAAT AGAG TAT	
		AGTCCTTG TCTC ATA	
		AG_ C	
GAM1541 KIAA1319	3'	TTGTGCTCCCTGGATTCCTG 21870	AA T
		CAGGAATCCA GAGC ATAA	
		GTCCTTAGGT CTCG TGTT	
		CC _	
GAM1541 NUDT13	3'	GCTCCTTGGTATTCCTGA 31664	_ A
		TCAGGAAT CCAA GAGC	
		AGTCCTTA GGTT CTCG	
		T C	
GAM1541 SSH2	3'	AGCCCTTTAGAGTTCCTGA 31176	_ C A
		TCAGGAA TC AAAG GCT	
		AGTCCTT AG TTTC CGA	
		G A C	
GAM1541 SSR1	3'	GTGGCTCTTTAATTCCTGA 9113	CC
		TCAGGAAT AAAGAGCTAT	
		AGTCCTTA TTTCTCGGTG	
		A_	
GAM1541 TAF9L	3'	ATTTATAGCCAAGGATCCT 18072	A AAAGA
		AGGA TCC GCTATAAAT	
		TCCT AGG CGATATTTA	
		_ AAC_	
GAM1541 LOC115294	3'	TAGTTACCTTGAATTCCTGG 36145	C AG_
		TCAGGAAT CAA AGCTA	
		GGTCCTTA GTT TTGAT	
		A CCA	
GAM1541 LOC150271	5'	AGAATTCTGGATTCCTGA 41166	A AG
		TCAGGAATCCA AG CT	

	AGTCCTTAGGT TT GA	
	C AA	
GAM1541 LOC151877 3'	TGTCTGCCTTGGGTTCC 41398	A A T_
	GGAATCCAA G GC ATA	
	CCTTGGGTT C CG TGT	
	_ _ TC	
GAM1541 LOC152300 5'	AGCTCTTTGGCCCCTGA 39248	AAT
	TCAGG CCAAAGAGCT	
	AGTCC GGTTCCTCGA	
	CC_	
GAM1541 LOC154084 5'	TATTGCGTTTGGATTCTT 41685	GA T
	AGGAATCCAAA GC ATA	
	TTCTTAGGTTT CG TAT	
	G_ T	
GAM1541 LOC158402 5'	TATAGCTCTTAGCCATGA 41976	_ AATCCA
	TCA GG AAGAGCTATA	
	AGT CC TTCTCGATAT	
	A GA_	
GAM1541 LOC162333 5'	ATTTATAGCCATCCGAATCCTG 42124	A CAAAGA
A	TCAGGA TC GCTATAAAT	
	AGTCCT AG CGATATTTA	
	A CCTAC_	
GAM1542 LOC147057 3'	CAAAGGATTAATAATTAACCTA 40782	TATTT
	TAG TTATTAATCCTTTG	
	ATC AATAATTAGGAAAC	
	CAATT	
GAM1542 LOC154739 5'	CAAAGGATATAAATGACTAA 41716	ATT TA
	TTAGT TTTAT ATCCTTTG	
	AATCA AAATA TAGGAAAC	
	GT_ _	
GAM1542 LOC203276 3'	CAAAGGATATAAATGACTAA 43483	ATT TA
	TTAGT TTTAT ATCCTTTG	
	AATCA AAATA TAGGAAAC	
	GT_ _	
GAM1542 LOC203305 3'	CAAAGGATATAAATGACTAA 43507	ATT TA
	TTAGT TTTAT ATCCTTTG	
	AATCA AAATA TAGGAAAC	
	GT_ _	
GAM1542 LOC254243 3'	CAAAGGATATAAATGACTAA 46509	ATT TA
	TTAGT TTTAT ATCCTTTG	

		AATCA AAATA TAGGAAAC		
		GT_ _		
GAM1542	LOC90038	3' CAAAGGATATAAATGACTAA 30646	ATT	TA
		TTAGT TTTAT ATCCTTTG		
		AATCA AAATA TAGGAAAC		
		GT_ _		
GAM1543	ABCB10	3' ATTTATAGTCTCAAAATTCCT 14374	CCAAA	_
		AGGAAT GAG CTATAAAT		
		TCCTTA CTC GATATTTA		
		AAA_ T		
GAM1543	ADD1	3' TGGGTCTCTGGATTCCTG 15470	A	G
		CAGGAATCCA AGA CTA		
		GTCCTTAGGT TCT GGT		
		C G		
GAM1543	ADD1	3' TGGGTCTCTGGATTCCTG 15474	A	G
		CAGGAATCCA AGA CTA		
		GTCCTTAGGT TCT GGT		
		C G		
GAM1543	CCR9	3' AGGTCTTATAGATTCCTGA 13432	CA_	G
		TCAGGAATC AAGA CT		
		AGTCCTTAG TTCT GA		
		ATA G		
GAM1543	CCR9	3' AGGTCTTATAGATTCCTGA 25249	CA_	G
		TCAGGAATC AAGA CT		
		AGTCCTTAG TTCT GA		
		ATA G		
GAM1543	CDC25B	3' AGCACCCCTCTGGATTCTGA 22412	G	A A_
		TCAG AATCCA AG GCT		
		AGTC TTAGGT TC CGA		
		_ C CCA		
GAM1543	CDC25B	3' AGCACCCCTCTGGATTCTGA 22416	G	A A_
		TCAG AATCCA AG GCT		
		AGTC TTAGGT TC CGA		
		_ C CCA		
GAM1543	CGTHBA	3' GGCCCCTTGGATTCCTGG 14364	AGA	
		TCAGGAATCCAA GCT		
		GGTCCTTAGGTT CGG		
		CCC		
GAM1543	EIF1A	3' ATTTATACTCTTTGGACTCC 42721	A	C
		GGA TCCAAAGAG TATAAAT		

CCT AGGTTTCTC ATATTTA
 C _
 GAM1543 EXTL3 3' TGTGGTTTTTGGACCCCT 7171 AA G
 AGG TCCAAAGA CTATA
 ||| ||||| |||||
 TCC AGGTTTTT GGTGT
 CC _
 GAM1543 GHR 3' ATTTATTTTCTTGGATTCCTGA 5671 A CT
 TCAGGAATCCAA GAG ATAAAT
 ||||| ||| |||||
 AGTCCTTAGGTT CTT TATTTA
 _ T_
 GAM1543 HS2ST1 3' GGTGCTTCTGAATTCCTGA 14576 C _ A
 TCAGGAAT CA AAG GCT
 ||||| || ||| |||
 AGTCCTTA GT TTC TGG
 A C G
 GAM1543 NUCB1 3' AGCCCTCAGGATTCCTGA 12851 AA A
 TCAGGAATCC AG GCT
 ||||| || |||
 AGTCCTTAGG TC CGA
 AC C
 GAM1543 CDC42BPB 3' AGTCTTTTCCCTAGTTCCTGA 12658 CCA__ _
 TCAGGAAT AAGAG CT
 ||||| |||| ||
 AGTCCTTG TTTTC GA
 ATCCC T
 GAM1543 DKFZP566B183 3' TTATGTATTTGAATTCCTGA 17769 C GA T
 TCAGGAAT CAAA GC ATAA
 ||||| |||| || |||||
 AGTCCTTA GTTT TG TATT
 A A_ _
 GAM1543 DKFZP566I1024 3' TAGCCTTGAATTCCTGG 34735 CCA A
 TCAGGAAT AAG GCTA
 ||||| ||| |||||
 GGTCTTA TTC CGAT
 AG_ _
 GAM1543 DKFZp761B0514 3' TGGCCCCCTGGCATTTCCTGA 26053 _ AAGA
 TCAGGAAT CCA GCTA
 ||||| ||| |||||
 AGTCCTTA GGT CGGT
 C CCCC
 GAM1543 FLJ13305 5' TGGTCTCGGATTCCTGA 43345 AAA _
 TCAGGAATCC GAG CTA
 ||||| ||| |||||
 AGTCCTTAGG CTC GGT
 _ T
 GAM1543 KIAA0265 3' AGCACTCGGAATTCCTGA 34620 _ AA A
 TCAGGAAT CC AG GCT
 ||||| || || |||

		AGTCCTTA GG TC CGA	
		A C_ A	
GAM1543 KIAA1117	3'	ATACCTCTGAGTTCCTGA 30632	CCAA C
		TCAGGAAT AGAG TAT	
		AGTCCTTG TCTC ATA	
		AG__ C	
GAM1543 KIAA1319	3'	TTGTGCTCCCTGGATTCCTG 21870	AA T
		CAGGAATCCA GAGC ATAA	
		GTCCTTAGGT CTCG TGTT	
		CC _	
GAM1543 NUDT13	3'	GCTCCTTGGTATTCCTGA 31664	_ A
		TCAGGAAT CCAA GAGC	
		AGTCCTTA GGTT CTCG	
		T C	
GAM1543 SSH2	3'	AGCCCTTTAGAGTTCCTGA 31176	_ C A
		TCAGGAA TC AAAG GCT	
		AGTCCTT AG TTTC CGA	
		G A C	
GAM1543 SSR1	3'	GTGGCTCTTTAATTCCTGA 9113	CC
		TCAGGAAT AAAGAGCTAT	
		AGTCCTTA TTTCTCGGTG	
		A_	
GAM1543 TAF9L	3'	ATTTATAGCCAAGGATCCT 18072	A AAAGA
		AGGA TCC GCTATAAAT	
		TCCT AGG CGATATTTA	
		_ AAC_	
GAM1543 LOC115294	3'	TAGTTACCTTGAATTCCTGG 36145	C AG_
		TCAGGAAT CAA AGCTA	
		GGTCCTTA GTT TTGAT	
		A CCA	
GAM1543 LOC150271	5'	AGAATTCTGGATTCCTGA 41166	A AG
		TCAGGAATCCA AG CT	
		AGTCCTTAGGT TT GA	
		C AA	
GAM1543 LOC151877	3'	TGTCTGCCTTGGGTTCC 41398	A A T_
		GGAATCCAA G GC ATA	
		CCTTGGGTT C CG TGT	
		_ _ TC	
GAM1543 LOC152300	5'	AGCTCTTTGGCCCCTGA 39248	AAT
		TCAGG CCAAAGAGCT	

		AGTCC GGTTCCTCGA		
		CC_		
GAM1543	LOC154084 5'	TATTGCGTTTGGATTCTT	41685	GA T
		AGGAATCCAAA GC ATA		
		TTCTTAGGTTT CG TAT		
		G_ T		
GAM1543	LOC158402 5'	TATAGCTCTTAGCCATGA	41976	_ AATCCA
		TCA GG AAGAGCTATA		
		AGT CC TTCTCGATAT		
		A GA_____		
GAM1543	LOC162333 5'	ATTTATAGCCATCCGAATCCTG	42124	A CAAAGA
	A	TCAGGA TC GCTATAAAT		
		AGTCCT AG CGATATTTA		
		A CCTAC_		
GAM1544	ABCA3 3'	CAGTGACTTGTCCAAGTTTACA	6743	_ AA_
		TGTAAACTTG ACAA ATTG		
		ACATTTGAAC TGTT TGAC		
		C CAG		
GAM1544	CTSB 3'	TCACCCTGTCAAGTTAACA	32328	A AAAATT
		TGT AACTTGACA GTGA		
		ACA TTGAACTGT CACT		
		A CC_____		
GAM1544	OXTR 3'	TCACAATGAGATTCCAGTTTAC	6622	T CAAAA
	A	TGTAAACT GA ATTGTGA		
		ACATTTGA CT TAACACT		
		C TAGAG		
GAM1544	PRKAA2 3'	CACAATTTTCAGGTTT	12928	CAA
		AAACTTGA AAATTGTG		
		TTTGGACT TTTAACAC		

GAM1544	KIAA0970 3'	CACTGTGTCAAGTTACA	17202	A AAAATT
		TGTAA CTTGACA GTG		
		ACATT GAACTGT CAC		
		_ GT_____		
GAM1544	LOC91694 3'	GTCATTTATTGCCCAAGTTTAC	33249	A_ AAATT
	A	TGTAAACTTG CAA GTGAC		
		ACATTTGAAC GTT TACTG		
		CC ATT_		
GAM1545	CLECSF5 3'	CTAGATCAGCTGAAACTCTAA	14918	A _
		TTAGAG TTTCAGCT TCTGG		

			AATCTC AAAGTCGA AGATC		
			— CT		
GAM1545	EGR3	3'	TATTCCTAGCAAAATAAAATCT 29956	CA_____	TCT
			CTAA TAGAGATTT GCT GGAATA		
			ATCTCTAAA CGA CCTTAT		
			ATAAAA T__		
GAM1545	FCMD	3'	TCAGACTGAAATCCTAA 13577	A	CT
			TTAG GATTTTCAG TCTGG		
			AATC CTAAAGTC AGACT		
			— —		
GAM1545	NR3C1	3'	CCAAAACTAAATCTCTAA 5686	C C C	
			TTAGAGATTT AG TT TGG		
			AATCTCTAAA TC AA ACC		
			— A A		
GAM1545	SMARCA3	3'	ATTCCAGAACCAAATCTT 9037	CAGC	
			GAGATTT TTCTGGAAT		
			TTCTAAA AAGACCTTA		
			CC__		
GAM1545	C12orf22	3'	CCCTGAAGTCTCTAA 25125	CTTCT	
			TTAGAGATTTTCAG GG		
			AATCTCTGAAGTC CC		
			————		
GAM1545	FLJ10687	3'	TCTTTCTGGCCAAATCTCTAA 20009	CA TCT_	
			TTAGAGATTT GCT GGA		
			AATCTCTAAA CGG TCT		
			C_ TCTT		
GAM1545	FLJ21140	5'	TTCCTTGCTGAAGTCCCTAA 24143	A	TTCT
			TTAG GATTTTCAGC GGAA		
			AATC CTGAAGTCG CCTT		
			C TT__		
GAM1545	KIAA0872	3'	GGAAGCTGAAACCTCTGA 17247	A	
			TTAGAG TTTCAGCTTCT		
			AGTCTC AAAGTCGAAGG		
			C		
GAM1545	KIAA1211	3'	CATGAAGCAAAATCTCTAA 34161	CA _	
			TTAGAGATTT GCTTC TG		
			AATCTCTAAA CGAAG AC		
			A_ T		
GAM1545	R3HDM	3'	TTCCCCTGAATCTCTAA 17663	T	CTTCT
			TTAGAGATT CAG GGAA		

			AATCTCTAA GTC CCTT	
			— C —	
GAM1545	LOC148946	5'	TATTCCAGAAGCTCTTTTCTGA 40941	TTTC
			TTAGAGA AGCTTCTGGAATA	
			AGTCTTT TCGAAGACCTTAT	
			TC—	
GAM1546	CAV3	3'	ACAGGGAGAGTTGGTT 27190	CTTTT G
			AACCAATTC T CCTGT	
			TTGGTTGAG A GGACA	
			— G	
GAM1546	CD1D	5'	ATATAGAAAAAGGAATT 38789	GC
			AATTCCTTTTT CTGTAT	
			TTAAGGAAAAA GATATA	
			—	
GAM1546	COX10	3'	ATACAAAAAAGGAATT 6979	GCC
			AATTCCTTTTT TGTAT	
			TTAAGGAAAAA ACATA	
			—	
GAM1546	JRKL	3'	ATACATATAAAAAGGGATT 9854	CC
			AATTCCTTTTTG TGTAT	
			TTAGGGAAAAAT ACATA	
			AT	
GAM1546	MAP7	3'	ATAGAAAAAGAATTGGTT 10116	C GC
			AACCAATTC TTTTT CTGT	
			TTGGTTAAG AAAAA GATA	
			— —	
GAM1546	NGFR	3'	ATGCGGCAAGAAGGAATTG 8329	T
			CAATTCCTTTTTGCC GTAT	
			GTTAAGGAAGAACGG CGTA	
			—	
GAM1546	CNIL	3'	ACACACAGAAGAATTGGT 12352	CT CC
			ACCAATTC TTTTG TGT	
			TGGTTAAG AAGAC ACA	
			— AC	
GAM1546	FLJ10154	3'	GATACAGGTAAGGAA 19745	TTT
			TTCCT TGCCTGTATC	
			AAGGA ATGGACATAG	
			—	
GAM1546	FLJ10607	3'	ATACAGGCAACAACCTGGT 37834	ATTCCTT
			ACCA TTTGCCTGTAT	

			TGGT	AAACGGACATA		
			CCAAC__			
GAM1546	FLJ20189	3'	ACAGGGGAAAAGGAATTAGT	19278	C	G
			AC AATTCCTTTTT CTGT			
			TG TTAAGGAAAAG GGACA			
			A G			
GAM1546	KIAA1237	3'	ATACAGAGGTAAAAGAATTG	39217	CT	__
			CAATTC TTTTGCCT GTAT			
			GTTAAG AAAATGGA CATA			
			__ GA			
GAM1546	KIAA1573	3'	GATACAATGTAAAAACAATTG	31413	CC	C_
		GTT	AACCAATT TTTTGC TGTATC			
			TTGGTTAA AAAAATG ACATAG			
			CA TA			
GAM1546	KIAA1579	3'	ATACTCAGAAAAATTGGTT	20118	CC	CCT
			AACCAATT TTTTGT GTAT			
			TTGGTTAA AAAGAC CATA			
			__ T__			
GAM1546	OSBPL8	3'	ACACAAAACTCAGGAATTGGT	21903	__	CC
			ACCAATTCCT TTTTGT TGT			
			TGGTTAAGGA AAAAC ACA			
			CTC __			
GAM1546	PAK2	5'	ACAGCCAAAGAAGGAATTG	33061	GC_	
			CAATTCCTTTTT CTGT			
			GTTAAGGAAGAA GACA			
			ACC			
GAM1546	RAB33B	3'	ACAGGAAAAGTTGGTT	25328	TCCT	G
			AACCAAT TTTT CTGT			
			TTGGTTG AAAA GGACA			
			__ _			
GAM1546	TOB2	3'	ACACTGCAGAAGGAAGTGGTT	45760	A	T C_
			AACCA TTCCTTTT GC TGT			
			TTGGT AAGGAAGA CG ACA			
			C _ TC			
GAM1546	LOC158038	5'	GATACAAATGCAGGAATTG	39699	TTTT	C_
			CAATTCCT GC TGTATC			
			GTTAAGGA CG ACATAG			
			__ TAA			
GAM1546	LOC51141	3'	GATACAGGGTGAAAATGAA	34047	C	TG _
			TTC TTTT CC TGTATC			

AAG AAAA GG ACATAG
 T GT G
 GAM1547 APXL 3' ACTTACTTATTTTATCTA 7352 CT C
 TAGATAAA AT AGTAAGT
 ||||| || |||||
 ATCTATTT TA TCATTCA
 T_ T
 GAM1547 CKN1 3' ACTTCTGTATAGTTTATTTAGT 5529 _ T
 CA TGACTAGATAAACTAT CAG AAGT
 ||||| ||||| |||||
 ACTGATTTATTTGATA GTC TTCA
 T _
 GAM1547 HMGA2 3' ACCTACTAATAGTTTGTTGATC 9561 CTA C A
 GA GATAAACTAT AGTA GT
 || ||||| ||||| |||||
 CT TTGTTTGATA TCAT CA
 AG_ A C
 GAM1547 ZNF36 3' ACTTAAGGATCCTTCTAGTCA 45101 TAACT AG
 TGACTAGA ATC TAAGT
 ||||| ||||| |||||
 ACTGATCT TAG ATTCA
 TCC_ GA
 GAM1547 FLJ23191 3' GTTGATAGCCCTCTAGTCA 23803 TAAA
 TGACTAGA CTATCAGT
 ||||| |||||
 ACTGATCT GATAGTTG
 CCC_
 GAM1547 KIAA0841 3' ACTTACTGAAATTCCCAGTCA 35359 A_ TAACTA
 TGACT GA TCAGTAAGT
 |||| || |||||
 ACTGA CT AGTCATTCA
 CC TAA_
 GAM1547 RNF20 3' CTGTAGGACAGTTTATCAGTCA 21213 A A AGTA
 TGACT GATAAACT TC AG
 |||| ||||| || |||||
 ACTGA CTATTTGA AG TC
 _ C GATG
 GAM1547 LOC118851 3' ACTTTGGGAAATTCATCTGGTC 37199 A CTA AGT
 A TGACTAGAT AA TC AAGT
 ||||| || |||||
 ACTGGTCTA TT AG TTCA
 C AA_ GGT
 GAM1547 LOC150005 3' ACTAGCTGCTTCTAGTCA 41122 TAACTAT A
 TGACTAGA CAGT AGT
 ||||| ||||| |||||
 ACTGATCT GTCG TCA
 TC_ A
 GAM1548 LOC92249 3' ATCACAACGCCCTATCCA 34020 TCC AC
 TGGGT GGGGGCGTT GAT
 |||| ||||| |||||

			ACCTA TCCCCGCAA CTA		
			CA		
GAM1549	MSX2	3'	ACAGCCCATTAAGTTCCTGGT 32660	TACA	
		ATTT	AAATACCAGGGA GGCTGT		
			TTTATGGTCCCT CCGACA		
			TGAATTAC		
GAM1549	FLJ10244	3'	CCTTTCTATCCCTATGTATTTA 19780	C_	C_
		A	TTAAATAC AGGGATA AGG		
			AATTTATG TCCCTAT TCC		
			TA CTT		
GAM1550	VCL	3'	ATGAAACCTTATTTTTTCCA 9401	T	C G
			TGGAAAAA TAAGG TTT CGT		
			ACCTTTTT ATTCC AAA GTA		
			T _ _		
GAM1550	VCL	3'	ATGAAACCTTATTTTTTCCA 15190	T	C G
			TGGAAAAA TAAGG TTT CGT		
			ACCTTTTT ATTCC AAA GTA		
			T _ _		
GAM1550	LOC144473	3'	AGAGCCTTACTCTTTCCA 40411	AAT	
			TGGAAA TAAGGCTTT		
			ACCTTT ATTCCGAGA		
			CTC		
GAM1550	LOC145231	5'	GCCCCACCTTCATTTTTTCCA 40519	T	CTTT
			TGGAAAAT AAGG GC		
			ACCTTTTTA TTCC CG		
			C ACCC		
GAM1550	LOC221398	3'	ATGCAGGCCTTAACCTTCC 43750	AA	T
			GGAAA TTAAGGCTT GCGT		
			CCTTT AATTCCGGA CGTA		
			C_ _		
GAM1550	LOC90594	3'	TAAAGCCTTAATTGTTCCA 31774	A	
			TGGAA AATTAAGGCTTTG		
			ACCTT TTAATTCCGAAAT		
			G		
GAM1551	CACNG3	5'	TGAGGAATGAAAGGAACCCA 13292	C	C CG G
			TGGGT CCTT CA TC CA		
			ACCCA GGAA GT GG GT		
			A A AA A		
GAM1551	GORASP1	3'	CATCTGTACTGGAAGGGACCC 25646	C	C _
			GGGTCCCTTCCA GT GCA ATG		

		CCCAGGGAAGGT CA TGT TAC		
		— — C		
GAM1551	LIFR	3' CATGTTGTGGAAGGACC 8100 CCC_ TC A		
		GGT TTCCACG GCA TG		
		CCG AAGGTGT TGT AC		
		AAAA — —		
GAM1551	PPP2R5D	3' TCACAGACATGGAAGGGACC 12918 C GCAA		
		GGTCCCTTCCA GTC TGA		
		CCAGGGAAGGT CAG ACT		
		A AC_		
GAM1551	C21orf108	3' GTGTCGTGGGAAGGACCCA 42772 C T		
		TGGGTCC TTCCACG CGC		
		ACCCAGG AGGGTGC GTG		
		A T		
GAM1551	KIAA1161	5' CATGTGTTGTGGGAAGGACCCA 39751 C T A		
		TGGGTCC TTCCACG CGCA TG		
		ACCCAGG AGGGTGT GTGT AC		
		A T _		
GAM1551	KIAA1862	3' TGGAGGCAGAAGGGACCCA 34176 CAC G_		
		TGGGTCCCTTC GTC CA		
		ACCCAGGGAAG CGG GT		
		A_ AG		
GAM1551	LOC148936	5' CATGCGTTGTGGGAGGGACCCA 40930 T A		
		TGGGTCCCTTCCACG CGCA TG		
		ACCCAGGGAGGGTGT GCGT AC		
		T _		
GAM1551	LOC148938	5' CATGCGTTGTGGGAGGGACCCA 40923 T A		
		TGGGTCCCTTCCACG CGCA TG		
		ACCCAGGGAGGGTGT GCGT AC		
		T _		
GAM1551	LOC157273	3' CACTGTTGTGGGAGGGACCCA 41782 TC A		
		TGGGTCCCTTCCACG GCA TG		
		ACCCAGGGAGGGTGT TGT AC		
		_ C		
GAM1551	LOC254057	3' TCTCTGCCGTGGAAGGGACTCA 46350 TC AT		
		TGGGTCCCTTCCACG GCA GA		
		ACTCAGGGAAGGTGC CGT CT		
		_ CT		
GAM1551	LOC255465	5' CATGTGTTGTGGGAGGGACCCA 46449 T A		
		TGGGTCCCTTCCACG CGCA TG		

ACCCAGGGAGGGTGT GTGT AC
 T _
 GAM1551 LOC91947 3' TGGACACATGGAAGGGAGCCA 33571 G C_ G
 TGG TCCCTTCCA GTC CA
 ||| ||||| ||| ||
 ACC AGGGAAGGT CAG GT
 G ACA _
 GAM1552 CDH23 5' GGCCGGACGCTGAGGTGGTCG 22671 ACGCGC AA
 CGGCCA CAGCGTCC CC
 ||||| ||||| ||
 GCTGGT GTCGCAGG GG
 GGA_ CC
 GAM1552 CDH23 5' GGCCGGACGCTGAGGTGGTCG 27419 ACGCGC AA
 CGGCCA CAGCGTCC CC
 ||||| ||||| ||
 GCTGGT GTCGCAGG GG
 GGA_ CC
 GAM1552 HS3ST3A1 5' GGCCTCCGTCCAGCGCGCTGGC 12677 A CA_ T_
 C GGCCA CGCGC GCG CC
 ||||| ||||| ||| ||
 CCGGT GCGCG TGC GG
 C ACC CTCC
 GAM1552 INPP4A 5' GGCTCTGGCGCGCCAGCCG 7295 CAA C
 CGGC CGCGCCAG GTC
 ||| ||||| |||
 GCCG GCGCGGTC CGG
 ACC T
 GAM1552 INPP4A 5' GGCTCTGGCGCGCCAGCCG 10247 CAA C
 CGGC CGCGCCAG GTC
 ||| ||||| |||
 GCCG GCGCGGTC CGG
 ACC T
 GAM1552 PIG3 5' GGGCAGCGAGGCGCTGGCCG 11317 AC A_ _
 CGGCCA GCGCC GC GTCC
 ||||| ||||| ||| |||
 GCCGGT CGCGG CG CGGG
 _ AG A
 GAM1552 TOP3B 5' GGCTTGTTTCCTGAACGTTGGC 10038 CGC CGTC _
 CG CGGCCAACG CAG CAA CC
 ||||| ||| ||| ||
 GCCGGTTGC GTC GTT GG
 AA_ CTTT C
 GAM1552 USP1 5' GGTTGGA CTGCGGCGTCACC 9392 CCAAC A _
 G CGG GCGCC GC GTCCAACC
 ||| ||||| ||| |||||
 GCC TCGCG CG CAGGTTGG
 AC_ C TT
 GAM1552 XT3 3' ACCTGGGACGTTGGCCG 21439 CG C
 CGGCCAACG CCAG GT
 ||||| ||| ||

GCCGGTTGC GGTC CA
 AG _
 GAM1552 C20orf39 5' GGCCGCTTGGGCGCACTTGCCG 24369 CAAC _ T
 CGGC GCGCC AGCG CC
 |||| |||| ||||
 GCCG CGCGG TCGC GG
 TTCA GT C
 GAM1552 EHM2 5' GGCCACTCGCAGCGGCGCTGGC 21189 AC A_ TCCAA
 CG CGGCCA GCGCC GCG CC
 ||||| |||| ||| ||
 GCCGGT CGCGG CGC GG
 _ CGA TCACC
 GAM1552 FLJ10116 5' TGGACGCTGGCGCGGTGGCCG 19727 A
 CGGCCA CGCGCCAGCGTCCA
 ||||| |||||
 GCCGGT GCGCGGTGCGAGGT
 G
 GAM1552 KIAA0217 3' GGCGAGGGCGCTGGCCG 33283 AC AG
 CGGCCA GCGCC CGTC
 ||||| |||| ||||
 GCCGGT CGCGG GCGG
 _ GA
 GAM1552 KIAA0427 5' GGCTTGGCGCGGCGGCC 16577 AA C
 GGCC CGCGCCAG GTC
 ||| ||||| |||
 CCGG GCGCGGTT CGG
 CG _
 GAM1552 KIAA0618 5' GTGGACGCTGACCGCCCG 16836 CCAAC C_ A
 CGG GCG CAGCGTCCA C
 ||| ||| ||||| |
 GCC CGC GTCGCAGGT G
 _ CA C
 GAM1552 KIAA0649 5' GGGCGGAGCGCGCTGGCC 16774 A CAG
 GGCCA CGCGC CGTCC
 ||||| |||| ||||
 CCGGT GCGCG GCGGG
 C AG_
 GAM1552 PCQAP 3' GGTTGCTTGGGGGGCGTTGGCC 18033 G AG TC
 G CGGCCAACGC CC CG CAACC
 ||||| || || ||||
 GCCGGTTGCG GG GT GTTGG
 G G_ TC
 GAM1552 SLC16A10 5' GGCCGCCTGCGCGCTGGCCG 20673 A CA T
 CGGCCA CGCGC GCG CC
 ||||| |||| ||| ||
 GCCGGT GCGCG CGC GG
 C TC C
 GAM1552 LOC125704 5' GGGCGGCACGCTGGCCG 36800 A C AGC
 CGGCCA CG GCC GTCC
 ||||| || ||| ||||

GCCGGT GC CGG CGGG
 C A ____
 GAM1552 LOC134121 5' GGCTAGACGCTGGCGCTGAGC 37064 _ AC CAA
 GC CA GCGCCAGCGTC CC
 || || ||||| ||
 CG GT CGCGGTGCGAG GG
 A ____ ATC
 GAM1552 LOC145945 5' GGTCTTGCGCGCTGGCCG 40634 A CGT
 CGGCCA CGCGCCAG CC
 ||||| ||||| ||
 GCCGGT GCGCGGTT GG
 C CT_
 GAM1552 LOC158263 5' GGTTGGAGGGCAGGGGGCGCTG 39799 A G A_ G_
 GCC GGCCA CGC CC GC TCCAACC
 ||||| || || |||||
 CCGGT GCG GG CG AGGTTGG
 C G GA GG
 GAM1552 LOC253502 3' GGCCAAGTGCGTGCTGGCCG 45383 A CA GT_
 CGGCCA CGCGC GC CC
 ||||| ||||| || ||
 GCCGGT GTGCG TG GG
 C ____ AACC
 GAM1553 DKFZP564O0463 3' ATGTTTCCAGCAGTTTA 15442 GAAA CGT
 TAAACTGC GGG ACAT
 ||||| ||| ||||
 ATTTGACG CCC TGTA
 A____ TT_
 GAM1553 KIAA0987 3' ATGCCTTTCATAGTTTA 14675 C G
 TAAACTG GAAAGG CGT
 ||||| ||||| ||||
 ATTTGAT CTTTCC GTA
 A _
 GAM1553 LOC116411 5' GATTGCCCTTTACAGTT 36571 CG TAC
 AACTG AAAGGGCG ATC
 ||||| ||||| ||||
 TTGAC TTTCCCGT TAG
 A_ ____
 GAM1553 LOC90620 5' TGTGTGTCCCGCAGTT 31806 AAA
 AACTGCG GGGCGTACA
 ||||| ||||| ||||
 TTGACGC CCTGTGTGT

 GAM1554 ATP8A2 3' GGCGAGCTCCCCCGCGCCGCA 44923 AT T__ GA
 TGCG CGCGGGG CT CC
 ||||| ||||| || ||
 ACGC GCGCCCC GA GG
 C_ CTC GC
 GAM1554 LPIN1 3' CAGATCTGCCATCGATCGCA 33465 C_ _
 TGCGATCG GG GGTCTG
 ||||| || |||||

ACGCTAGC CC CTAGAC
 TA GT
 GAM1554 CLDN15 3' GGGGGTCCCCCTCAACCGCA 28793 ATCGC TCT A
 TGCG GGGG GACCC CC
 ||| ||| |||| ||
 ACGC CCCC CTGGG GG
 CAACT ____ _
 GAM1554 DKFZp762K222 5' GGTGGGCCAGGCAGCGCACCGC 35235 ATC GG A
 A TGCG GCG GTCTG CCCACC
 ||| || |||| |||||
 ACGC CGC CGGAC GGGTGG
 CA_ GA C
 GAM1554 FLJ10932 3' TCAGACCCTCTAGTTGCA 20265 CGC
 TGCGAT GGGGTCTGA
 |||| |
 ACGTTG TCCCAGACT
 ATC
 GAM1554 FLJ23231 3' GTGGGTCAGAAGCGATC 24680 GGGG
 GATCGC TCTGACCCAC
 |||| |
 CTAGCG AGACTGGGTG
 A____
 GAM1554 PIG7 5' GGCGGGCACCCCGCGAGCGCA 11270 A CT A A
 TGCG TCGCGGGGT G CCC CC
 ||| ||||| | ||| ||
 ACGC AGCGCCCCA C GGG GG
 G ____ C
 GAM1554 LOC152317 3' TGGGTCAGACCCGGGTCACA 41469 C G G
 TG GATC CGGG TCTGACCCA
 || ||| ||| |||||
 AC CTGG GCCC AGACTGGGT
 A _ _
 GAM1554 LOC196761 3' GTGAGCCCAGATCCCGCAACTG 43129 ATC ACC_
 CA TGCG GCGGGGTCTG CAC
 ||| ||||| |||
 ACGT CGCCCTAGAC GTG
 CAA CCGA
 GAM1555 CSF1R 3' GGCGACACGGGGGAGAACATACA 11709 A GATGA C_
 TG TATGTTCT CCG CGCC
 || ||||| ||| |||
 AC ATACAAGA GGC GCGG
 _ GG_ ACA
 GAM1555 NBEA 3' GGCAC TTTGCACCAGAAACATA 45493 _ A ACC_
 TCA TGATATGTT CTG TG GCC
 ||||| ||| |||
 ACTATACAA GAC AC CGG
 A C GTTCA
 GAM1555 EDR3 5' GCAGCGAGAGAACATATC 46068 GATGAC C
 GATATGTTCT CGC GC
 ||||| ||| |||

		CTATACAAGA	GCG CG	
		GA_____A		
GAM1555	FLJ14621	3'	GGCAGCAGTGTTTAGAGCA	26581
			TGTTCTGA AC GC GCC	
			ACGAGATT TG CG CGG	
			TG A A	
GAM1555	KIAA1157	5'	GGCGGCGGCCACCGCGGCA	35753
			TGT TG TG CCGCCGCC	
			ACG GC AC GGCGGCGG	
			GC C C	
GAM1555	OSBPL6	5'	GCAAGGTCAAAGACATATCA	26270
			TGATATGT CT TGACC GC	
			ACTATACA GA ACTGG CG	
			_ A_ AA_	
GAM1555	LOC221583	3'	GGCGTCCACTCCAAAACATATC	44246
		A	TGATATGTT TG TG CGCC	
			ACTATACAA AC AC GCGG	
			A CTC CT	
GAM1555	LOC253943	5'	GCGGCGGCTGGAACAATCA	45984
			TGAT TGTTCTG CCGCCGC	
			ACTA ACAAGGT GGCGGCG	
			_ C_	
GAM1556	ARHGEF6	3'	ACAAACACATCTGCCCAA	33841
			TTGGGCAG GTGT TGT	
			AACCCGTC CACA ACA	
			TA_____A	
GAM1556	MEN1	5'	ACAGACACTGATACCCAG	28295
			TTGGG ATCAGTGTCTGT	
			GACCC TAGTCACAGACA	
			A_____	
GAM1556	MYO10	3'	ACAAACACAGAGTGCCCA	14728
			TTGGGCAGC TC GTGT TGT	
			GACCCGTCG AG CACA ACA	
			___ A A	
GAM1556	BRD4	3'	GACAGACGTCCCGCCACCCA	27777
			TGGG GCG TGTCTGTC	
			ACCC CGC GCAGACAG	
			AC CCT___	
GAM1556	FLJ10415	3'	GCGCCGACTCGCTGCCCA	19852
			TTGGGCAGCGA TC GTGT	

			GACCCGTCGCT AG CGCG		
			C C		
GAM1556	FLJ12768	3'	GACAGAGCACCCACTGCCCAA 24802	CGAATCA _	
			TTGGGCAG GTG TCTGTC		
			AACCCGTC CAC AGACAG		
			ACC___ G		
GAM1556	ISL2	3'	ACAGACACTCAAACCTCCCAA 35079	C CGAATC	
			TTGGG AG AGTGTCTGT		
			AACCC TC TCACAGACA		
			_ AAAC_		
GAM1556	PDEF	5'	ACAGACACAGCCGCCAGCCCAA 14745	A_ AATCA	
			TTGGGC GCG GTGTCTGT		
			AACCCG CGC CACAGACA		
			AC CGA_		
GAM1556	SCYB11	3'	GACAATCAGAATTCCACTGCCC 42258	C_ CAG TC	
	AA		TTGGGCAG GAAT TG TGTC		
			AACCCGTC CTTA AC ACAG		
			AC AG_ TA		
GAM1556	LOC147299	3'	ACAGACACAGCGCTGCCAG 38328	AATCA	
			TTGGGCAGCG GTGTCTGT		
			GACCCGTCGC CACAGACA		
			GA_		
GAM1556	LOC93268	5'	ACAAACACTGATCTCC 35585	C CGA C	
			GG AG ATCAGTGT TGT		
			CC TC TAGTCACA ACA		
			_ _ _ A		
GAM1557	ENAH	3'	ATTCATTTTATAGATTAAACT 20124	GG_ C	
			AG AATCTAAAAA GAAAT		
			TC TTAGATTTT CTTA		
			AAA A		
GAM1557	FLJ12484	3'	TTTGTTCCTAGATTCCTTAA 23024	AA	
			TTAGGGAATCTA AACGAA		
			AATTCCTTAGAT TTGTTT		
			C_		
GAM1557	FLJ12484	3'	TTTGTTCCTAGATTCCTTAA 34522	AA	
			TTAGGGAATCTA AACGAA		
			AATTCCTTAGAT TTGTTT		
			C_		
GAM1557	VPS4B	3'	GATGAACTAGATTCCTTAA 11294	AAAACGAA	
			TTAGGGAATCTA ATC		

		AATCCCTTAGAT TAG	
		CAAG____	
GAM1557	ZNF185	3' GAATTCCATCTTGGCTTCCCTA 14002	T AAAC A
	A	TTAGGGAA CTAA GAA TC	
		AATCCCTT GGTT CTT AG	
		C CTAC A	
GAM1557	LOC145828	5' CGTTTAAATTCCTAA 40612	CTA
		TTAGGGAAT AAAACG	
		AATCCCTTA TTTTGC	
		AAA	
GAM1557	LOC152926	3' ATTTTTCAGACTTCCCTAA 39340	_ AA C
		TTAGGGAA TCT AAA GAAAT	
		AATCCCTT AGA TTT TTTTA	
		C CC _	
GAM1557	LOC220662	3' GGATTCTAAAGATTTC 43824	AAAAAC
		GGGAATCT GAAATCC	
		CCTTTAGA CTTTAGG	
		AAAT__	
GAM1558	CLN6	3' AGCCACGGGGACGCGGGATTCA 19549	C CA AC_
	A	TTGAATCTC TG CC GGCT	
		AACTTAGGG GC GG CCGA	
		C AG GCA	
GAM1558	ENC1	3' AGCTGCTGCTGGAGATTCAA 9696	T CCA
		TTGAATCTCC GCA CGGCT	
		AACTTAGAGG CGT GTCGA	
		T C__	
GAM1558	PLOD	3' AGCCACCAATCAAAGAGATTCA 5843	C_ CACCAC
	A	TTGAATCTC TG GGCT	
		AACTTAGAG AC CCGA	
		AA TAACCA	
GAM1558	PYCS	3' AGCTGCAGCAGGAGATGCAA 8760	A ACCA
		TTG ATCTCCTGC CGGCT	
		AAC TAGAGGACG GTCGA	
		G AC__	
GAM1558	CASPR3	3' AGTCACCAGAGGAGATTCAA 24315	GCACCAC
		TTGAATCTCCT GGCT	
		AACTTAGAGGA CTGA	
		GACCA__	
GAM1558	KIAA1040	3' TCGATGCCAGGAGATTCAA 35745	_ CCA
		TTGAATCTCCTG CA CGG	

		AACTTAGAGGAC GT GCT		
		C A__		
GAM1558 KIAA1764	5'	CCGTGATAGAATGCAGATTCAA 34352	CCT	C_____
		TTGAATCT GCA CACGG		
		AACTTAGA CGT GTGCC		
		__ AAGATA		
GAM1558 KIAA1854	3'	CGGGTTACAGGAGATCCGA 35529	A	C_ A
		TTG ATCTCCTG ACC CG		
		AGC TAGAGGAC TGG GC		
		C AT _		
GAM1558 LOC200197	3'	AGCCACATGCCAGAGATTCA 42729	CT	CCAC
		TGAATCTC GCA GGCT		
		ACTTAGAG CGT CCGA		
		AC ACA_		
GAM1558 LOC203232	5'	AGCCTTTCTGCAGGAGATTCAA 35373		CCAC
		TTGAATCTCCTGCA GGCT		
		AACTTAGAGGACGT CCGA		
		CTTT		
GAM1558 LOC90233	3'	AGTTGTCCACAGGAGATCCA 28742	A	CACC
		TG ATCTCCTG ACGGCT		
		AC TAGAGGAC TGTTGA		
		C ACC_		
GAM1559 GNAI3	3'	CAAACAATCTTAAGTATGCACA 13239	T	C CA
		TGTGCAT GTTGA AT TTTG		
		ACACGTA CAATT TA AAAC		
		T C AC		
GAM1559 CHODL	3'	CAAATGAAATGGACAATGCA 24489		GACA
		TGCATTGTT TCATTTG		
		ACGTAACAG AGTAAAC		
		GTAA		
GAM1559 KIAA0416	3'	CAAATGATAAGGATGCCACA 17832	_	G GAC
		TGTG CATT TT ATCATTTG		
		ACAC GTAG AA TAGTAAAC		
		C G _		
GAM1559 LOC145951	5'	AGTGGTCAACAATGACA 38016	G	AT
		TGT CATTGTTGAC CATT		
		ACA GTAACAAC TG GTGA		
		_ _		
GAM1560 EPB72	3'	ACCCAATTCAAGCTTATTTTA 10303		CCA
		TGAAATAAGCTTGAATT GGT		

		ATTTTATTCGAACTTAA CCA	
		C__	
GAM1560 HMMR	3'	AACCTGTTGAAGATTATTTCA 14861	G G TTC
		TGAAATAA CTT AA CAGGTT	
		ACTTTATT GAA TT GTCCAA	
		A G __	
GAM1560 HMMR	3'	AACCTGTTGAAGATTATTTCA 14863	G G TTC
		TGAAATAA CTT AA CAGGTT	
		ACTTTATT GAA TT GTCCAA	
		A G __	
GAM1560 FLJ12783	3'	ACCAGTCAGGCTTATTTCA 25415	ATTCCA
		TGAAATAAGCTTGA GGT	
		ACTTTATTCGGACT CCA	
		GA__	
GAM1560 KIAA0354	3'	AACCTGGAATCTCTCATCT 16995	CT __
		AG TGA ATTCCAGGTT	
		TC ACT TAAGGTCCAA	
		T_ CTC	
GAM1560 LOC144308	3'	AACCTGGGTGTAGCTCATTT 40403	A TGAAT
		AAAT AGCT TCCAGGTT	
		TTTA TCGA GGGTCCAA	
		C TGT__	
GAM1561 KIAA0872	3'	CCAAAAGAAAAAAATCTCA 17243	GAATTC
		TGAGATTTT TTCTTTTGG	
		ACTCTAAAA AAGAAAACC	
		AAA__	
GAM1561 LOC219445	5'	CCAAAAGAGCCACAGAATCTCA 44011	AATTC
		TGAGATTTTG TTCTTTTGG	
		ACTCTAAGAC GAGAAAACC	
		ACC__	
GAM1561 LOC58525	3'	CCAAAGGAGCAAGCCAAAACCT 38455	A AA C
CA		TGAG TTTTG TT TTCTTTTGG	
		ACTC AAAAC AA GAGGAAACC	
		C CG C	
GAM1562 CCRL1	3'	AACATCTGCATTATTCTGAA 18630	CATT_
		TTCAGAATA GGTGTT	
		AAGTCTTAT CTACAA	
		TACGT	
GAM1562 SLC26A4	3'	GAACCAGGCCAATATATTTTGA 6027	C __
A		TTCAGAATA ATTGGT GTTC	

			AAGTTTTAT TAACCG CAAG	
			A GAC	
GAM1562	ALK7	3'	GAGCATTAATGTTTTCTGAA 37296	T
			TTCAGAA ACATTGGTGTTT	
			AAGTCTT TGTAATTACGAG	
			T	
GAM1562	DKFZp761F2014	3'	ATGGACGCCATAAATTCTGAA 21458	ACAT T
			TTCAGAAT TGGTGT CCAT	
			AAGTCTTA ACCGCA GGTA	
			AAT_ _	
GAM1562	FBXO4	3'	ACACTATTCATATATTCTGAA 27261	CAT__
			TTCAGAATA TGGTGT	
			AAGTCTTAT ATCACA	
			ATACTT	
GAM1562	FLJ10619	3'	AATATCAAATATTCTGAA 19967	CA
			TTCAGAATA TTGGTGTT	
			AAGTCTTAT AACTATAA	
			A_	
GAM1562	FLJ11210	3'	GGGATTTAATATATTTTGAA 29974	C T
			TTCAGAATA ATTGG GTTCC	
			AAGTTTTAT TAATT TAGGG	
			A _	
GAM1562	FLJ12619	3'	GAACACTATGCATTTTGAA 25210	A T
			TTCAGAAT CAT GGTGTTT	
			AAGTTTGA GTA TCACAAG	
			C _	
GAM1562	FLJ20086	3'	AACATCAAATTCTGAA 19187	ACA
			TTCAGAAT TTGGTGTT	
			AAGTCTTA AACTACAA	

GAM1562	FLJ21916	3'	TGGGACTGCATTCTGAA 23385	A TTGGT
			TTCAGAAT CA GTTCCA	
			AAGTCTTA GT CAGGGT	
			C _____	
GAM1562	FLJ23511	3'	AGCACTTATTCTGAA 25962	CATT
			TTCAGAATA GGTGTT	
			AAGTCTTAT TCACGA	

GAM1562	HSAJ1454	3'	ATGGAAAACCATGGATTCTGAA 18866	A T G
			TTCAGAAT CAT GGT TTCCAT	

			AAGTCTTA GTA CCA AAGGTA		
			G _ A		
GAM1562	KIAA0992	3'	ACTACAATGATTCTGAA 18156	A	GT
			TTCAGAAT CATTG GT		
			AAGTCTTA GTAAC CA		
			_ AT		
GAM1562	KIAA1323	3'	GAACACCAACTAAATTTGAA 31562	ATACA	
			TTCAGA TTGGTGTTC		
			AAGTTT AACCACAAG		
			AAATC		
GAM1562	RASGRF2	3'	ATGGTTGTCAGTGCATTCT 30597	A	GT TT
			AGAAT CATTG G CCAT		
			TCTTA GTGAC T GGTA		
			C TG T_		
GAM1562	SAMSN1	5'	GAAAACAATGTATTTGAA 22696	A	GTG
			TTCAGA TACATTG TTC		
			AAGTTT ATGTAAC AAG		
			_ AA_		
GAM1562	STIP-1	3'	AGCTCTATCATATTCTGAA 34526	CAT	T
			TTCAGAATA TGG GTT		
			AAGTCTTAT ATC CGA		
			ACT T		
GAM1562	TA-KRP	3'	GGGAATGTTTTCTGAA 26252	T	TGGTG
			TTCAGAA ACAT TTCC		
			AAGTCTT TGTA AGGG		
			T _ _ _ _		
GAM1562	TIAM2	3'	ATGGAAGATGGTACATTCTGGA 14822	ACATTG	G
			TTCAGAAT GT TTCCAT		
			AGGTCTTA TA AAGGTA		
			CATGG_ G		
GAM1562	LOC150605	5'	AGCTTAATGTATCTGAA 41228	A	T
			TTCAGA TACATTGG GTT		
			AAGTCT ATGTAATT CGA		
			_ _		
GAM1562	LOC152756	3'	GAATAAGATGCAGTTCTGAA 41549	A_	GG
			TTCAGAAT CATT TGTTT		
			AAGTCTTG GTAG ATAAG		
			AC A_		
GAM1563	ADRA1A	5'	TCCAGCCGAGACCTTTTGAT 6334	C AG A A	
			ATCAAAAG GT CG GCT GA		

			TAGTTTTC CA GC CGA CT	
			_ GA _ C	
GAM1563	ADRA1A	5'	TCCAGCCGAGACCTTTTGAT 27135	C AG A A
			ATCAAAAG GT CG GCT GA	
			TAGTTTTC CA GC CGA CT	
			_ GA _ C	
GAM1563	ADRA1A	5'	TCCAGCCGAGACCTTTTGAT 27136	C AG A A
			ATCAAAAG GT CG GCT GA	
			TAGTTTTC CA GC CGA CT	
			_ GA _ C	
GAM1563	ADRA1A	5'	TCCAGCCGAGACCTTTTGAT 27134	C AG A A
			ATCAAAAG GT CG GCT GA	
			TAGTTTTC CA GC CGA CT	
			_ GA _ C	
GAM1563	COX15	3'	CTAGTTCCTCTTTTGAT 27787	CGT C
			ATCAAAAG AG GAGCTAG	
			TAGTTTTC TC CTTGATC	
			— —	
GAM1563	HGF	3'	TCTAGCTCACTGCCTTT 45228	C C
			AAAG GTAG GAGCTAGA	
			TTTC CGTC CTCGATCT	
			_ A	
GAM1563	OCLN	3'	CTAGCACACACTTTTGGT 8380	C AGCGA
			ATCAAAAG GT GCTAG	
			TGGTTTTC CA CGATC	
			A CA__	
GAM1563	SIRT1	3'	TCTGTTACGCTAAACTTTTGAT 14543	CG _ T
			ATCAAAAG TAGCG AGC AGA	
			TAGTTTTC ATCGC TTG TCT	
			AA A _	
GAM1563	CMG2	3'	TCTAGCTTGAAACTTTTG 27723	CGTAG
			CAAAAG CGAGCTAGA	
			GTTTTC GTTCGATCT	
			AAA__	
GAM1563	DKFZp434F142	3'	AGCTCCTGCCTTTTGGT 25993	C C
			ATCAAAAG GTAG GAGCT	
			TGGTTTTC CGTC CTCGA	
			— —	
GAM1563	DKFZp547J036	3'	CTAGCTTGTTCTTGAT 26041	AAGCGT
			ATCAA AGCGAGCTAG	

			TAGTT TTGTTGATC	
			C_____	
GAM1563	GRIN3A	3'	TCTAGGGTTGTAGCTTTTGAT 28539	GTA G_
			ATCAAAAGC GCGA C TAGA	
			TAGTTTTCG TGTT G ATCT	
			A__ G G	
GAM1563	KIAA0367	3'	TCTAGCTCTTGCACTCTGA 33425	AA C C
			TCA AG GTAG GAGCTAGA	
			AGT TC CGTT CTCGATCT	
			C_ A _	
GAM1563	KIAA0537	5'	CTGGTTTGCCACCTCCGAT 16866	AAA C A_
			ATC AG GT GCGAGCTAG	
			TAG TC CA CGTTTGGTC	
			CC_ _ CC	
GAM1563	KIAA1713	3'	TCTGGTTCTAGGCCTTTGA 35811	A G GC
			TCAAA GC TA GAGCTAGA	
			AGTTT CG AT CTTGGTCT	
			C G _	
GAM1563	MGC10818	3'	TTGGCTTCGCTTTTGAT 24944	TAGC
			ATCAAAAGCG GAGCTAG	
			TAGTTTTCGC TTCGTT	

GAM1563	PDP	3'	TCTAAGCATTTACCCTTTTGAT 20515	C CGA _
			ATCAAAAG GTAG GCT AGA	
			TAGTTTTC CATT CGA TCT	
			C TA_ A	
GAM1563	ZNF323	3'	TCTAACTCATGTTTTTGAT 25171	AGC C
			ATCAAAAGCGT GAG TAGA	
			TAGTTTTTGTA CTC ATCT	
			_____ A	
GAM1563	LOC146485	5'	GGCTTTACCTTTTGAT 30070	C GC
			ATCAAAAG GTA GAGCT	
			TAGTTTTC CAT TTCGG	

GAM1563	LOC153785	5'	TCTAGCCCTAGTTTGCTCCTGA 39409	AA T GA_
			TCA AGCG AGC GCTAGA	
			AGT TCGT TTG CGATCT	
			CC _ ATCC	
GAM1563	LOC157663	3'	TCTAAGCATTTACCCTTTTGAT 39639	C CGA _
			ATCAAAAG GTAG GCT AGA	

			TAGTTTTC CATT CGA TCT		
			C TA_ A		
GAM1563	LOC158377	5'	AGCTCCTCCTGCTCGTTGAT 41970	A_ T_ C	
			ATCAA AGCG AG GAGCT		
			TAGTT TCGT TC CTCGA		
			GC CC _		
GAM1563	LOC169611	3'	TCTAGCTTTCTGCTTTT 40288	GT C	
			AAAAGC AG GAGCTAGA		
			TTTTCG TC TTCGATCT		
			_ T		
GAM1563	LOC93624	5'	TCCAGCCCCGCTACGTGACTG 36017	AAA A A	
			CA GCGTAGCG GCT GA		
			GT TGCATCGC CGA CT		
			CAG C C		
GAM1564	BMF	3'	TGCTAGCCTTCTACCCCA 27282	A AAAAA C	
			TG GGTAGAAG CT GCG		
			AC CCATCTTC GA CGT		
			C C_ T		
GAM1564	C4orf6	5'	TGCCAGCCTCCTACCTCA 12312	A AAAAA C	
			TGAGGTAG AG CT GCG		
			ACTCCATC TC GA CGT		
			C C_ C		
GAM1564	DKFZp434F142	3'	TACGCCCATCTCCTACCTCA 25995	A CAAACTC	
			TGAGGTAG AGA GCGTA		
			ACTCCATC TCT CGCAT		
			C ACC_		
GAM1564	GAB3	3'	TGCAAGCTCATTCCTCTACCTC 27930	A CAAA_ C	
	A		TGAGGTAGA GA CT GCG		
			ACTCCATCT CT GA CGT		
			C TACTC A		
GAM1564	KIAA0895	3'	TGAGAGTTTATCTTTACCTCA 44548	A C G	
			TGAGGTAGA GA AAACTC CG		
			ACTCCATTT CT TTTGAG GT		
			_ A A		
GAM1564	KIAA1193	3'	ACGCGATTCTCCTGCCTCA 33578	A CAAAC	
			TGAGGTAG AGA TCGCGT		
			ACTCCGTC TCT AGCGCA		
			C T_		
GAM1564	MGC2560	3'	TGCTTGACTTCTACCTCA 25468	A ACTC	
			TGAGGTAGAAG CAA GCG		

		ACTCCATCTTC GTT CGT	
		A ____	
GAM1564	LOC145497 5'	GTGCCTGTCTCCTACTTCA 37875	A AACT
		TGAGGTAG AGACA CGC	
		ACTTCATC TCTGT GTG	
		C CC__	
GAM1565	ABCF1 3'	GGATCCCACTCTGATTG 6746	AGT C
		CAAT GA GTGGGATCC	
		GTTA CT CACCCTAGG	
		GT_ _	
GAM1565	CARKL 3'	GGATCCCAGAGCGTTGTA 14938	A GACG
		TACAAT GT TGGGATCC	
		ATGTTG CG ACCCTAGG	
		_ AG__	
GAM1565	CRY2 3'	ATCCCAGCTGTCATTGTT 35731	__
		AATAGTGACG TGGGAT	
		TTGTTACTGT ACCCTA	
		CG	
GAM1565	DGAT2 5'	GGACATCTCGTCACTCTGTA 26292	AT T GA
		TACA AGTGACG GG TCC	
		ATGT TCACTGC CT AGG	
		C_ T AC	
GAM1565	DMD 5'	GGA CTGACCACTATTG 10222	AC G A
		CAATAGTG GT GG TCC	
		GTTATCAC CA TC AGG	
		_ G _	
GAM1565	DMD 5'	GGA CTGACCACTATTG 10234	AC G A
		CAATAGTG GT GG TCC	
		GTTATCAC CA TC AGG	
		_ G _	
GAM1565	DMD 5'	GGA CTGACCACTATTG 10195	AC G A
		CAATAGTG GT GG TCC	
		GTTATCAC CA TC AGG	
		_ G _	
GAM1565	DPYD 5'	GGACCCCAAATGTCACTG 30317	_ A
		TAGTGACG TGGG TCC	
		GTCAC TGT ACCC AGG	
		AA C	
GAM1565	GALNT3 3'	ATCCTCAACACTATTGTA 10802	ACGT
		TACAATAGTG GGGAT	

		ATGTTATCAC TCCTA		
		AAC_		
GAM1565	HCFC1	3' GAGTACACCGTTCAC TATTGTA	35158	_ _ GGA
		TACAATAGTGA CG TG TC		
		ATGTTATCACT GC AC AG		
		T C ATG		
GAM1565	HOXA7	3' GAATCCACCTTCCACTATTGT	13769	AC_ A
		ACAATAGTG GTGGG TC		
		TGTTATCAC CACCT AG		
		CTTC A		
GAM1565	KCNAB1	3' ATGCTATGTCAC TATTCA	30546	C G
		A AATAGTGACGTGG AT		
		A TTATCACTGTATC TA		
		C G		
GAM1565	LBR	3' GAATTCATTCAC TATTGTA	29852	C A
		TACAATAGTGA GTGGG TC		
		ATGTTATCACT TACTT AG		
		_ A		
GAM1565	LMO7	5' GATTCTACCACTTTTG	17970	T AC
		CAA AGTG GTGGGATC		
		GTT TCAC CATCTTAG		
		T _		
GAM1565	LMO7	5' GATTCTACCACTTTTG	11827	T AC
		CAA AGTG GTGGGATC		
		GTT TCAC CATCTTAG		
		T _		
GAM1565	MAB21L1	5' GGATCCACAGCTTACTG	12113	C_
		TAGTGA GTGGGATCC		
		GTCATT CACCCTAGG		
		CGA		
GAM1565	RNASE1	5' GGATTTTAGGTCACTTTGTA	31945	T G
		TACAA AGTGAC TGGGATCC		
		ATGTT TCACTG ATTTTAGG		
		_ G		
GAM1565	RNMT	3' GGATCCAGGGCACTGTCA	9889	A ACG
		C ATAGTG TGGGATCC		
		A TGTCAC ACCCTAGG		
		C GGG		
GAM1565	RUNX1	3' GATTCATGTCACTACTGT	7500	A G
		ACA TAGTGACGTGG ATC		

		TGT ATCACTGTACT TAG		
		C _		
GAM1565	SNCA	3' GACCCCAACTACTATTGTA 5896	ACG	A
		TACAATAGTG TGGG TC		
		ATGTTATCAT ACCC AG		
		CA_ C		
GAM1565	USP6	3' GATCCCACCATTAGCCTGTA 43810	A__	AC
		TACA TAGTG GTGGGATC		
		ATGT ATTAC CACCCTAG		
		CCG _		
GAM1565	ALS2CR3	3' GATCCCAAATCTTATGTA 17412	A T	CG
		TACA TAG GA TGGGATC		
		ATGT ATT CT ACCCTAG		
		_ _ AA		
GAM1565	CD36L2	3' ATTTTGTGACCACTATTGTG 12020	A_	TG
		TACAATAGTG CG GGAT		
		GTGTTATCAC GT TTTA		
		CA GT		
GAM1565	DCAMKL1	3' GGATCCCAGCACATCACTGT 11117	C _	
		ATAGTGA GT GGGATCC		
		TGTCACT CA CCCTAGG		
		A CGA		
GAM1565	FKSG28	3' GATCTTATACCACTCTGTA 25202	AT	AC
		TACA AGTG GTGGGATC		
		ATGT TCAC TATTCTAG		
		C_ CA		
GAM1565	KIAA0173	3' GGAGCAGTCACTATTGTA 16041		GTGGGA
		TACAATAGTGAC TCC		
		ATGTTATCACTG AGG		
		ACG__		
GAM1565	KIAA0317	3' CCCTTTGGCACTATTGTG 16793	A T_	
		TACAATAGTG CG GGG		
		GTGTTATCAC GT CCC		
		G TT		
GAM1565	KIAA0663	3' GGACTTAGTTTCATCTATTGTA 16813	_ CG_	A
		TACAATAG TGA TGGG TCC		
		ATGTTATC ACT ATTC AGG		
		T TTG _		
GAM1565	KIAA1001	3' GGACTGCTCAATCACTATT 17328	CG	A__
		AATAGTGA TGGG TCC		

		TTATCACT ACTC AGG		
		A_ GTC		
GAM1565 KIAA1128	3'	GGATCCCACGGA	33971	GA
		AATAGT CGTGGGATCC		
		TTGTCA GCACCCTAGG		
		G_		
GAM1565 KPNA6	3'	ATCCCACCCATGTTGTA	14685	G AC
		TACAATA TG GTGGGAT		
		ATGTTGT AC CACCCTA		
		_ C_		
GAM1565 NUP54	3'	ATTGTATGTACTATTGTA	30179	A G
		TACAATAGTG CGTG GAT		
		ATGTTATCAT GTAT TTA		
		_ G		
GAM1565 TNFRSF21	3'	GACCCCATTGAGTTACTGT	15803	___ A
		ATAGTGAC GTGGG TC		
		TGTCATTG TACCC AG		
		AGT C		
GAM1565 LOC158527	5'	GATCTCACTCACTATCATG	39861	___ C
		CA ATAGTGA GTGGGATC		
		GT TATCACT CACTCTAG		
		AC _		
GAM1565 LOC162239	3'	GGATCCCATGAGAACATTAT	40052	A___
		ATAGTG CGTGGGATCC		
		TATTAC GTACCCTAGG		
		AAGA		
GAM1565 LOC220477	5'	GGAGTACAACACTACTATTGTA	37409	ACG GGA
		TACAATAGTG TG TCC		
		ATGTTATCAT AC AGG		
		CA_ ATG		
GAM1565 LOC220573	3'	GATCCCACCATTAGCCTGTA	34484	A___ AC
		TACA TAGTG GTGGGATC		
		ATGT ATTAC CACCCTAG		
		CCG _		
GAM1565 LOC221337	3'	GGATCCCAGGCTACTAGTG	44236	A ACG
		CA TAGTG TGGGATCC		
		GT ATCAT ACCCTAGG		
		G CGG		
GAM1565 LOC253019	3'	GGACTTAGTTTCATCTATTGTA	45668	_ CG_ A
		TACAATAG TGA TGGG TCC		

ATGTTATC ACT ATTC AGG
 T TTG _
 GAM1565 LOC253975 3' GGA CT TAG TTTCATCTATTGTA 45935 _ CG_ A
 TACAATAG TGA TGGG TCC
 ||||| ||| ||| |||
 ATGTTATC ACT ATTC AGG
 T TTG _
 GAM1565 LOC51279 3' ATCCTATTACATCACTGTTG 18615 C ____
 CAATAGTGA GTG GGAT
 ||||| ||| |||
 GTTGTCAC T CAC CCTA
 A TTAT
 GAM1565 LOC93190 3' GATCTTTGACACTATTG 35489 A T
 CAATAGTG CG GGGATC
 ||||| || |||||
 GTTATCAC GT TTCTAG
 A _
 GAM1566 ANKH 3' CTACTCCACACATGCAGGAGGC 27636 G ____ ACGA
 GGGTG CACCCGTCTC TG GT AGTAG
 ||||| || || |||||
 GTGGGCGGAG AC CA TCATC
 G GTA CACC
 GAM1566 SIGLEC6 3' GCAATGTACCACAAACCGAGTG 30109 C TCTC AA
 CAC CG GTGGTACG GT
 ||| || ||||| ||
 GTG GC CACCATGT CG
 A CAAA AA
 GAM1566 FLJ14596 3' ACCTCTGTCACCACCAAAGACG 26569 C__ _ _ A
 GG CCCGTCT GTGGT AC GA GT
 ||||| |||| ||||| ||
 GGGCAGA CACCA TG CT CA
 AAC C T C
 GAM1566 LOC147276 5' CTACTTCGGTGATGGAGATGGG 38327 GTGGTA
 CCCGTCTC CGAAGTAG
 ||||| |||||
 GGGTAGAG GCTTCATC
 GTAGTG
 GAM1567 FAP 5' AACGCCCCCAAATCTGTTTC 10765 TG CCC A
 GAGAT AGAT GGG GCGTT
 |||| ||| ||| |||||
 CTTTG TCTA CCC CGCAA
 _ AAA C
 GAM1567 LOC145739 3' TTCCCAAATCTCAATTTCA 37965 CCC
 TGAGATTGAGAT GGGAG
 ||||| |||||
 ACTTTAACTCTA CCCTT
 AAA
 GAM1568 PACSIN1 3' GACTCCATTAGTTCCGA 44317 CGAAA C
 TCGGAACTGA GAG TC
 ||||| ||| ||

AGCCTTGATT CTC AG
 AC____ _
 GAM1568 FLJ22060 3' AGCTCATCAGTTCCCATATA 23864 C CGAAA
 TAT GGAAGCTGA GAGCT
 ||| ||||| ||||
 ATA CCTTGACT CTCGA
 C A____
 GAM1568 GLP 3' TGAGCTCTTCATTAGCTC 20724 A C A
 GA CTGA GAA GAGCTCA
 || |||| ||| |||||
 CT GATT CTT CTCGAGT
 C A _
 GAM1568 GOLGIN-67 3' TGAGCTCTTCTATAGCTC 45537 A AC A
 GA CTG GAA GAGCTCA
 || ||| ||| |||||
 CT GAT CTT CTCGAGT
 C AT _
 GAM1568 KIAA0855 3' TGAGCTCTTCTATAGCTC 17377 A AC A
 GA CTG GAA GAGCTCA
 || ||| ||| |||||
 CT GAT CTT CTCGAGT
 C AT _
 GAM1568 ZNF238 3' TGAGCTCTTTTTTCCCCCCC 13046 AACT C
 GG GA GAAAGAGCTCA
 || || |||||
 CC CT TTTTCTCGAGT
 CCCC T
 GAM1568 LOC204301 3' TGAGCTCTTCCTTAGCTC 43095 A C A
 GA CTGA GAA GAGCTCA
 || |||| ||| |||||
 CT GATT CTT CTCGAGT
 C C _
 GAM1568 LOC220534 3' TGAGCTCTTCATTAGCTC 43618 A C A
 GA CTGA GAA GAGCTCA
 || |||| ||| |||||
 CT GATT CTT CTCGAGT
 C A _
 GAM1568 LOC220538 3' TGAGCTCTTCATTAGCTC 43628 A C A
 GA CTGA GAA GAGCTCA
 || |||| ||| |||||
 CT GATT CTT CTCGAGT
 C A _
 GAM1568 LOC220963 3' TGAGCTCTTCAAGTGATTCTGA 43959 CTG GA_
 TA TATCGGAA AC AAGAGCTCA
 ||||| || |||||
 ATAGTCTT TG TTCTCGAGT
 AG_ AAC
 GAM1568 LOC254358 3' TGAGCTCTTCCTTAGCTC 45533 A C A
 GA CTGA GAA GAGCTCA
 || |||| ||| |||||

			CT GATT CTT CTCGAGT		
			C C _		
GAM1568	LOC257286	3'	TGAGCTCTTCATTAGCTC	45375	A C A
			GA CTGA GAA GAGCTCA		
			CT GATT CTT CTCGAGT		
			C A _		
GAM1569	MARK3	5'	CCTCACTAAACCATCCAA	8189	TCCAA C
			TTGG GTGGTTTAG GAGG		
			AACC TACCAAATC CTCC		
			_____ A		
GAM1569	TEX15	3'	GCCTCTTTATACTCACTTAAAC	25295	CC _ T C
	CAA		TTGGT AAGTG GT TAG GAGGC		
			AACCA TTCAC CA ATT CTCCG		
			AA T T T		
GAM1569	TP63	3'	GCTTAAACCACTTAAACGAA	9817	G CC _
			TT GT AAGTGGTTTA GC		
			AA CA TTCACCAAAT CG		
			G AA T		
GAM1569	GPR88	3'	CCCAGCGGGCTACCTGAACCAA	22572	C A A GA
			TTGGT CA GTGGTTT GC GG		
			AACCA GT CATCGGG CG CC		
			A C _ AC		
GAM1569	LOC223009	5'	GCCTCACTGTGGACCACCCAAG	45314	CCAA _ C
	CCAA		TTGGT GTGGTT TAG GAGGC		
			AACCG CACCAG GTC CTCCG		
			AACC GT A		
GAM1569	LOC254173	3'	CCTCGGCGGCCACTTGACCAA	46288	C TAG
			TTGGTC AAGTGGTT CGAGG		
			AACCAG TTCACCGG GCTCC		
			_ CG_		
GAM1570	B3GAT1	3'	AAGCGCCTTTTCCTGCAGCT	20714	CCGCCTA
			AGCTGCAGG GCGCTT		
			TCGACGTCC CGCGAA		
			TTTTC_		
GAM1570	B3GAT1	3'	AAGCGCCTTTTCCTGCAGCT	27626	CCGCCTA
			AGCTGCAGG GCGCTT		
			TCGACGTCC CGCGAA		
			TTTTC_		
GAM1570	FLJ10241	3'	GAAGCACCAGGCGGTCAGCAGC	19775	A AGC
	TG		TAGCTGC GGCCGCCT GCTTC		

GTCGACG CTGGCGGA CGAAG
 A CCA
 GAM1570 LOC144667 5' AAGCACCAGACACCATGCAGCT 40449 _ CCGC AGC
 G TAGCTGCA GG CT GCTT
 ||||| || || ||||
 GTCGACGT CC GA CGAA
 A ACA_ CCA
 GAM1571 CALM1 3' TGCTGTTCAAAGAAATTACAGT 13756 C C AA
 T AGC GTAATT CT TGAGCAGCA
 || ||||| || |||||
 TTG CATTAA GA ACTTGTCGT
 A A A_
 GAM1571 FLRT3 5' CTGTCAATGGAATTACAGCT 14948 C TAA G
 AGC GTAATTCC TGA CAG
 || ||||| || ||||
 TCG CATTAAAGG ACT GTC
 A TA_ _
 GAM1571 PIK3R2 3' TGCTGCTTCCGAGAACCTCGGC 11468 TAA CTAAT
 GCCG TTC GAGCAGCA
 ||| || |||||
 CGGC AAG TTCGTCGT
 TCC AGCC_
 GAM1571 PRKG1 3' TGCTGCTCCAGTAACTAC 12938 A C AAT
 GTA TT CT GAGCAGCA
 ||| || |||||
 CAT AA GA CTCGTCGT
 C T C_
 GAM1571 RAB23 3' TGCTGCTCACTGAGAACCCAGC 18402 CGTAA C A
 T AGC TTC TA TGAGCAGCA
 || ||| || |||||
 TCG AAG GT ACTCGTCGT
 ACCC_ A C
 GAM1571 C20orf121 3' TGCTGCTCATCAGGAACTTAC 23636 _ A
 GTAA TTCCT ATGAGCAGCA
 ||| |||| |||||
 CATT AAGGA TACTCGTCGT
 CA C
 GAM1571 FLJ22021 3' TGCTGCTCATCAGCTGCCCGCT 23746 C_ ATT C A
 AGC GTA CT ATGAGCAGCA
 ||| || || |||||
 TCG CGT GA TACTCGTCGT
 CC C_ C
 GAM1571 KIAA0265 3' TGCTGAAATTAGGAACACAGG 34630 _ AA GAG
 T GCC GT TTCCTAAT CAGCA
 ||| || ||||| ||||
 TGG CA AAGGATTA GTCGT
 A CC AA_
 GAM1571 KIAA1483 3' GCTGCTTAGAAATACGGCT 34616 A CTAA
 AGCCGTA TTC TGAGCAGC
 ||||| || |||||

TCGGCAT AAG ATTCGTCG
A ____

GAM1571 KIAA1795 3' CTGCTCATTCTTGACATAGCT 35700 CG AAT CT_
AGC T TC AATGAGCAG
||| | || |||||
TCG A AG TTA CTGTC
AT C__ TTC

GAM1571 MGC13061 3' TGGACACTAGGAATTGCAGC 26131 C A AG
GC GTAATTCCTA TG CA
|| ||||| || ||
CG CGTTAAGGAT AC GT
A C AG

GAM1571 SMARCF1 3' TGCTGCTCATCCTGGGCAAGCT 20524 CGTAATT ____
AGC CCTA ATGAGCAGCA
||| ||| |||||
TCG GGGT TACTCGTCGT
AAC____ CC

GAM1571 TIMM9 5' TGCTTAAGTAAGAATCAGGC 14833 GTA C A_
GCC ATTC TA TGAGCA
||| ||| || |||||
CGG TAAG AT ATTCGT
AC_ A GA

GAM1571 LOC143308 5' TGCCACTCATTGGGCCACACGC 40348 C AATT CA
T AGC GT CCTAATGAG GCA
||| || ||||| |||
TCG CA GGGTTACTC CGT
_ CACC AC

GAM1571 LOC51619 3' TGCCATTTTCAGCAATTACGGC 18078 C ____ A
T AGCCGTAATT CT AATG GCA
||||||| || ||| |||
TCGGCATTAA GA TTAC CGT
C CTT _

GAM1572 FLJ13052 3' GCCTTATTACGCTTTTCA 23285 T C T
TG AAAGCGTAA AA GGC
|| ||||| || |||
AC TTTCGCATT TT CCG
T A _

GAM1572 KIAA0976 3' AAAATGCCCAGTAAC TTTACA 17161 CGTA AAT
TGTAAG AC GGCATTTT
||||| || |||||
ACATTTT TG CCGTAAAA
AA__ AC__

GAM1572 KIAA1387 3' AAAATACCACTGTACTTGT TTT 35104 TA_ A C
ACA TGTAAGCG ACA TGG ATTTT
||||| ||| ||| |||||
ACATTTTGT TGT ACC TAAAA
TCA C A

GAM1573 CDC25A 5' GTGTTTGTGTTTGACCCGC 7540 AGCA
GCG CAAACACAAACAC
||| |||||

			CGC GTTTGTGTTTGTG		
			CCA_		
GAM1573	GRAF	3'	CCGTGTGTCTGTGCAGTGC 17442	AAA	A
			GCAC CACA ACACACGG		
			CGTG GTGT TGTGTGCC		
			AC_ C		
GAM1573	KCNH2	5'	CCAGTCTGTGCGCGCCCGTGCT 5755	AAACACAA	C _
	CGC		GCGAGCAC ACA AC GG		
			CGCTCGTG TGT TG CC		
			CCCGCGCG C A		
GAM1573	DGKD	3'	CCGTGTGTCCTTCTGTGGCCGC 29881	A A	AACACAA
			GCG GC CA ACACACGG		
			CGC CG GT TGTGTGCC		
			_ _ GTCTTCC		
GAM1573	FLJ12484	3'	CCGTGTGTCTTGTCTGTG 34516	A	CAA
			CACA ACA ACACACGG		
			GTGT TGT TGTGTGCC		
			C TC_		
GAM1573	FLJ12484	3'	CCGTGTGTCTTGTCTGTG 23018	A	CAA
			CACA ACA ACACACGG		
			GTGT TGT TGTGTGCC		
			C TC_		
GAM1573	FLJ22965	3'	CCATGTGTTTGTATCCATGTTT 22643	CAAAC	C
			GAGCA ACAACACA GG		
			TTTGT TGTGTGTGT CC		
			ACCTA A		
GAM1573	MGC1842	3'	CCGTGTGTTGTGCATGTCACTC 32687	C_ AAC	A
			GAG ACA ACAA CACACGG		
			CTC TGT TGTT GTGTGCC		
			AC AC_ _		
GAM1574	DPEP1	5'	CTCACAGCCTGAAGCTCATCCT 10674	A A	A GC
			AG AT AGCTTCAG CTG GAG		
			TC TA TCGAAGTC GAC CTC		
			C C C A_		
GAM1574	FGF2	3'	CCAGTGAAGCTTACCTA 7733	AA	AG
			TAG TAAGCTTC ACTGG		
			ATC ATTCGAAG TGACC		
			C_ _		
GAM1574	KIAA0172	5'	CTCGCCGGTGAAAGCTCAGCCT 32411	AATA	CAG
	A		TAG AGCTT ACTGGCGAG		

		ATC TCGAA TGGCCGCTC		
		CGAC AG_		
GAM1574	KIAA0316	3' CTCAACATCCTGAAGCTGATC 34530	ATA	AC GC
		GA AGCTTCAG TG GAG		
		CT TCGAAGTC AC CTC		
		AG_ CT AA		
GAM1574	KIAA0483	3' CTCACCAAATGAAGCTTTTCT 17528	T	GAC C
	A	TAGAA AAGCTTCA TGG GAG		
		ATCTT TTCGAAGT ACC CTC		
		T AA_ A		
GAM1574	KIAA1538	3' CGCCTTGTTCTGAAGCTTTCTC 35425	AT	_ T_
	TA	TAGA AAGCTTCAGA C GGCG		
		ATCT TTCGAAGTCT G CCGC		
		CT T TT		
GAM1574	LOC133088	5' TCAGTGTGAAGCTTATTC 37033		G
		GAATAAGCTTCA ACTGG		
		CTTATTCGAAGT TGA CT		
		G		
GAM1575	FAT2	3' CCCAGGCTGTTGTCCCTTGAA 7173	A T	TC
		TTCAA GG ACAATAGT GGG		
		AAGTT CC TGTTGTCG CCC		
		C _ GA		
GAM1575	GPLD1	3' CCTGCGCATGTACCCCTGAA 44180	AA	ATA T
		TTCA GGTACA GT CGGG		
		AAGT CCATGT CG GTCC		
		CC A_ C		
GAM1575	PDE4B	3' CCCGAAGTACTGACTTTTGAA 8466	GTA	A
		TTCAAAG CA TAGTTCGGG		
		AAGTTTC GT ATCAAGCCC		
		A_ C		
GAM1575	C20orf44	3' CTGAACTGACCTCTGAA 20207	A	ACAA
		TTCA AGGT TAGTTCGG		
		AAGT TCCA GTCAAGTC		
		C _		
GAM1575	FLJ20445	3' CCCGAATTGAACACTTTT 19479	ACAA	
		AAAGGT TAGTTCGGG		
		TTTTCA GTTAAGCCC		
		CAA_		
GAM1575	FLJ21034	3' CCCATATTGCATCTTTGAA 24483	A	GTTC
		TTCAAAGGT CAATA GGG		

AAGTTTCTA GTTAT CCC
 C A____
 GAM1575 KIAA1272 3' CCCGAATGGCCTTGTGCCT 34760 TA____
 AGGTACAA GTTCGGG
 ||||| |||||
 TCCGTGTT TAAGCCC
 CCGG
 GAM1575 KIAA1911 3' CTGAACTATACTTTGAA 36393 GTACA
 TTCAAAG ATAGTTCGG
 ||||| |||||
 AAGTTTC TATCAAGTC
 A____
 GAM1575 NCUBE1 3' CCTATATTGCCCTTTGAA 18093 TA GTTC
 TTCAAAGG CAATA GG
 ||||| |||||
 AAGTTTCC GTTAT CC
 C_ AT____
 GAM1575 SH3BGL2 3' CCTGGATTGCACCTTTGAA 25529 ACAA
 TTCAAAGGT TAGTTCGGG
 ||||| |||||
 AAGTTTCCA GTTAGGTCC
 C____
 GAM1575 ZIC4 5' CCAGCCGTCCTTTGAA 25853 T AATA C
 TTCAAAGG AC GTT GG
 ||||| || |||||
 AAGTTTCC TG CGA CC
 _ C____ _
 GAM1575 LOC144017 3' CCCAAACTTAACCTTTGA 40387 ACAAT C
 TCAAAGGT AGTT GGG
 ||||| |||||
 AGTTTCCA TCAA CCC
 AT____ A
 GAM1575 LOC201689 5' CCTGAATCATACCCTTGGA 33334 A CAATA
 TTCAA GGTA GTTCGGG
 ||||| |||||
 AGGTT CCAT TAAGTCC
 C AC____
 GAM1575 LOC84549 3' CTGAACTGTACACTTT 26260 _ ATA
 AAAG GTACA GTTCGG
 ||||| |||||
 TTTC CATGT CAAGTC
 A ____
 GAM1576 KIAA1350 3' GCCTGGTACTTTTTTGT 36001 C ATT
 ACGAAAAAG ACCA GC
 ||||| |||||
 TGTTTTTTC TGGT CG
 A C____
 GAM1576 PCDH10 5' GCCGTTCTGTGCTTTTCCG 21884 A C_ T
 CG AAAAGCAC AAT GC
 || ||||| |||||

GC TTTTCGTG TTG CG
 C TC C
 GAM1576 PCDH10 5' GCCGTTCTGTGCTTTTCCG 26770 A C_ T
 CG AAAAGCAC AAT GC
 || ||||| ||| ||
 GC TTTTCGTG TTG CG
 C TC C
 GAM1576 SMOC2 3' GCTGCAATCGTATGGCTTTCTC 35834 A ACCA__
 GA AAAGC ATTGCAGC
 || |||| |||||
 CT TTTTCG TAACGTCG
 C GTATGC
 GAM1576 TAF9L 3' CTGCAGTATTTTTCGT 18073 GC CAAT
 ACGAAAAA AC TGCAG
 ||||| || |||||
 TGCTTTTT TG ACGTC
 A_ ____
 GAM1576 TGOLN2 3' CTGCAGGTGGAAGTGCTTTTC 32024 A ____ A
 GAAAA GCA CCA TTGCAG
 ||||| ||| |||||
 CTTTT CGT GGT GACGTC
 _ GAA G
 GAM1576 LOC153364 5' GCTGCAGTGGCCCCTGCGTTA 39370 AAAAAGCA A
 TAACG CCA TTGCAGC
 |||| ||| |||||
 ATTGC GGT GACGTCG
 GTCCCC__ _
 GAM1576 LOC155072 5' CTGCATGGTGCTTCGTC 41761 AA AT
 GA AAGCACCA TGCAG
 || ||||| |||||
 CT TTCGTGGT ACGTC
 GC ____
 GAM1576 LOC202868 5' CTGCATGGTGCTTTGTC 43448 A AT
 GA AAAGCACCA TGCAG
 || ||||| |||||
 CT TTTTCGTGGT ACGTC
 G ____
 GAM1577 EGFR 3' GACTGGTTTTGCAACGTTTACA 11724 TTAGA
 TGTAACGTTGTAAA AGTC
 ||||| |||||
 ACATTTGCAACGTTT TCAG
 TGG__
 GAM1577 GLUL 3' ACTTCTAATTGCCATGTACA 7833 AA T A
 TGT ACGT GTAA TTAGAAGT
 ||| |||| |||||
 ACA TGTA CGTT AATCTTCA
 _ C _
 GAM1577 SMUG1 3' ACTTCTAAGGTCACGTTTAC 15608 T TAAA
 GTAAACGT G TTAGAAGT
 ||||| | |||||

			CATTTGCA C AATCTTCA		
			_ TGG _		
GAM1578	CCNF	3'	GGCAATGATACCTACCTCA 7527	ATT	ATA
			TGAG GGTATCGT GCC		
			ACTC CCATAGTA CGG		
			CAT A _		
GAM1578	CKN1	3'	CTATAAGATGCAGTCTCA 5531	G	G
			TGAGATTG TATC TATAG		
			ACTCTGAC GTAG ATATC		
			_ A		
GAM1578	COL4A3	3'	GGCTACTGCTTCAATCTCA 5549	TATC	_
			TGAGATTGG GTA TAGCC		
			ACTCTAACT CGT ATCGG		
			T _ C		
GAM1578	COL4A3	3'	GGCTACTGCTTCAATCTCA 25356	TATC	_
			TGAGATTGG GTA TAGCC		
			ACTCTAACT CGT ATCGG		
			T _ C		
GAM1578	COL4A3	3'	GGCTACTGCTTCAATCTCA 25362	TATC	_
			TGAGATTGG GTA TAGCC		
			ACTCTAACT CGT ATCGG		
			T _ C		
GAM1578	FGF2	3'	GCCACATCTAATCTCA 7739	T C	ATA
			TGAGATTGG AT GT GC		
			ACTCTAATC TA CA CG		
			_ _ C _		
GAM1578	PCDHB16	3'	GGCTAACAACCTCAATCTCA 21946	_	ATC A
			TGAGATTG GT GT TAGCC		
			ACTCTAAC CA CA ATCGG		
			T A _ _		
GAM1578	TGFBR2	3'	GGCATGCTGATACCATCCCA 9243	A T	_ A
			TG GAT GGTATC GTAT GCC		
			AC CTA CCATAG CGTA CGG		
			C _ T _		
GAM1578	ZNF146	5'	GCTAGATGACAATCTCA 13995	GTA	A
			TGAGATTG TCGT TAGC		
			ACTCTAAC AGTA ATCG		
			_ G		
GAM1578	AMOT	3'	GGCTAATTGCCACCAATTTCA 28415	AT	TA
			TGAGATTGGT CG TAGCC		

ACTTTAACCA GT ATCGG
 CC TA
 GAM1578 C20orf20 3' GGCCACAGTGATACCATCCCA 20246 A T TATA_
 TG GAT GGTATCG GCC
 || ||| ||||| |||
 AC CTA CCATAGT CGG
 C _ GACAC
 GAM1578 DIO2 3' GGCTTAAGTACCAATCTC 15171 CGTAT
 GAGATTGGTAT AGCC
 ||||| |||
 CTCTAACCATG TCGG
 AAT_
 GAM1578 DIO2 3' GGCTTAAGTACCAATCTC 6460 CGTAT
 GAGATTGGTAT AGCC
 ||||| |||
 CTCTAACCATG TCGG
 AAT_
 GAM1578 DKFZP434L187 3' GGCTCACTGATACCAGATCCCA 34122 A _ TATA
 TG GAT TGGTATCG GCC
 || ||| ||||| |||
 AC CTA ACCATAGT TGG
 C G CAC_
 GAM1578 FLJ10120 3' GGCTATACTGACAACTCA 19730 A GTATC
 TGAG TTG GTATAGCC
 ||| ||| |||||
 ACTC AAC CATATCGG
 A AGT_
 GAM1578 FLJ11722 3' GGCTCACGCCTACAATCTCA 24522 GTAT AT
 TGAGATTG CGT AGCC
 ||||| ||| |||
 ACTCTAAC GCA TCGG
 ATCC C_
 GAM1578 ILF3 3' GGCTCGGGCTACCAAGTCCCA 10846 A TC AT_
 TG GATTGGTA GT AGCC
 || ||||| || |||
 AC CTGACCAT CG TCGG
 C _ GGC
 GAM1578 KIAA1005 3' GCTTTTACCCAATCTCA 35777 TATC T_
 TGAGATTGG GTA AGC
 ||||| ||| |||
 ACTCTAACC CAT TCG
 _ TT
 GAM1578 KIAA1924 3' GCTATACGACTTCACATC 36480 _ TA
 GAT TGG TCGTATAGC
 ||| ||| |||||
 CTA ACT AGCATATCG
 C TC
 GAM1578 LOC150005 3' GGCTCCATACCAATCCCA 41123 A CGTAT
 TG GATTGGTAT AGCC
 || ||||| |||

			AC CTAACCATA	TCGG		
			C	CC__		
GAM1578	LOC255231	3'	GGTTGCAATACCAATCT	45674	C	TA
			AGATTGGTAT GTA	GCC		
			TCTAACCATA CGT	TGG		
			A	__		
GAM1579	MFN1	3'	CGCCTTAGTGCTTCAGACCC	19601	AT_	AA
			GGGTT GGC	ACTAA CG		
			CCCAG TCGTGATT	GC		
			ACT	CC		
GAM1579	LOC148764	5'	AAGCGTTTTCCCTTCTCATAAC	38588	CACT__	
			CCC	GGGGTTATGG	AAAACGCTT	
			CCCCAATACT	TTTTGCGAA		
			CTTCCC			
GAM1580	PER2	3'	ATTCCAAAGATGGTTCAGA	23088	C	__
			TC GAACCATCT	GAAT		
			AG CTTGGTAGA	CTTA		
			A	AAC		
GAM1580	AKL3L	3'	TGTGCCAAATGATTCCGGATA	18410	C	C AATTA
			TATCCGAA CAT TG	CACA		
			ATAGGCTT GTA AC	GTGT		
			A	A C__		
GAM1580	FLJ20793	3'	TGTAATTCATGGTCTGGA	44110	A	TC
			TCCG ACCA TGAATTACA			
			AGGT TGGT ACTTAATGT			
			C	__		
GAM1580	KIAA1715	3'	TGTAATTCAGCTTCTCAGAT	33794	C	ACCAT
			ATC GA	CTGAATTACA		
			TAG CT	GACTTAATGT		
			A	CTTC_		
GAM1580	PTPRN2	3'	GTAGAGATGATTCGGAT	28370	C	GAA
			ATCCGAA CATCT	TTAC		
			TAGGCTT GTAGA	GATG		
			A	__		
GAM1580	PTPRN2	3'	GTAGAGATGATTCGGAT	28375	C	GAA
			ATCCGAA CATCT	TTAC		
			TAGGCTT GTAGA	GATG		
			A	__		
GAM1580	STK38L	3'	TGTATAATTCAGATTTATC	34295	ACC	C
			GA	ATCTGAATTA ACA		

CT TAGACTTAAT TGT
 ATT A
 GAM1580 LOC203286 5' TGTAATAGATGGTCCCG 43498 A_ AA
 CG ACCATCTG TTACA
 || ||||| ||||
 GC TGGTAGAT AATGT
 CC A_
 GAM1581 ARHGEF6 3' CAAACACATCTGCCAA 33845 AAT
 TTG CAGATGTGTTTG
 ||| |||||
 AAC GTCTACACAAAC
 CC_
 GAM1581 D4ST-1 3' GCAACACATCTGATCTAA 28228 A T
 TTG ATCAGATGTGTT GC
 ||| ||||| ||
 AAT TAGTCTACACAA CG
 C _
 GAM1581 KIAA0700 3' ATCCTGCAACAGCTGGACTCAA 35658 A_ A GTT
 TTGA TCAG TGT TGCAGGAT
 ||| ||| ||| |||||
 AACT GGTC ACA ACGTCCTA
 CA G _
 GAM1581 RODH-4 5' ATCCTGCAATCCTTCTGCCCA 9808 AAT TGTGT
 A TTG CAGA TTGCAGGAT
 ||| ||| |||||
 AAC GTCT AACGTCCTA
 CCC TCCT_
 GAM1581 SPTLC2 3' GTTTAACACAGCCTGATTCAA 11283 A_ T_
 TTGAATCAG TGTGTT GC
 ||||| ||||| ||
 AACTTAGTC ACACAA TG
 CG TT
 GAM1581 LOC147669 5' TCCCATACATCTGTCCAA 40856 AAT TTGCA
 TTG CAGATGTGT GGA
 ||| ||||| |||
 AAC GTCTACATA CCT
 CT_ C_
 GAM1581 LOC151438 3' CCTGCAGGCCAATTCAA 41347 CAGA T
 TTGAAT TG GTTTGCAGG
 ||||| || |||||
 AACTTA AC CGGACGTCC
 _ _
 GAM1582 CDKN2A 3' TGAAAGAACCAGAGAGGCTCTG 27759 T GGAGTT
 A TCAG GCCT GTTCTTTCA
 ||| ||| |||||
 AGTC CGGA CAAGAAAGT
 T GAGAC_
 GAM1582 SFRP1 3' AAAGAACAATGACAAACAC 8924 CC GA
 GTG TG GTTGTCTTT
 ||| || |||||

CAC AC TAACAAGAAA
AA AG
GAM1582 APACD 3' GAAAACTATTCCAGGACT 12362 G T CT
AGT CCTGGAGT GTT TTC
||| ||||| ||| |||
TCA GGACCTTA CAA AAG
_ T _
GAM1582 ARNTL2 3' AAAAAATTACCCAGGCACT 21409 A T C
AGTGCCTGG GT GTT TTT
||||||| || ||| |||
TCACGGACC CA TAA AAA
_ T A
GAM1582 DIS3 3' TGAAAGAACACTTCTAAGCCT 17304 T C T
AG GC TGGAG TGTTCTTTCA
|| || |||| |||||
TC CG ATCTT ACAAGAAAGT
_ A C
GAM1582 DKFZP564B1162 5' TGAAAGAAATCTATCATGCACT 25339 C _ TTG
GA TCAGTGC TGG AG TTCTTTCA
||||||| ||| || |||||
AGTCACG ACT TC AAGAAAGT
T A TA_
GAM1582 GT650 3' TGAATTCAACTCCAGACAC 27433 C TTCT
GTG CTGGAGTTG TTCA
||| ||||| ||| |||
CAC GACCTCAAC AAGT
A TT_
GAM1582 HTEX4 5' TGAAAGAAGAGACAGGCAATGA 44218 G GAGT G
TCA TGCCTG T TTCTTTCA
||| ||||| | |||||
AGT ACGGAC A AAGAAAGT
A AG_ G
GAM1582 HTEX4 5' TGAAAGAAGAGACAGGCAATGA 46654 G GAGT G
TCA TGCCTG T TTCTTTCA
||| ||||| | |||||
AGT ACGGAC A AAGAAAGT
A AG_ G
GAM1582 HTEX4 5' TGAAAGAAGAGACAGGCAATGA 46723 G GAGT G
TCA TGCCTG T TTCTTTCA
||| ||||| | |||||
AGT ACGGAC A AAGAAAGT
A AG_ G
GAM1582 KIAA0789 3' AAGGAACCTCAGGCAC 31842 G TT
GTGCCTG AG GTTCTTT
||||||| || |||||
CACGGAC TC CAAGGAA
_ _
GAM1582 KIAA0830 3' AACAGACTCCAGGCCCTGA 34544 T _
TCAG GCCTGGAGT TGTT
||||| ||||| |||

			AGTC CGGACCTCA ACAA		
			C G		
GAM1582	KIAA1254	3'	GAAAACTCCAGGCATCGA 34697	A	G
			TC GTGCCTGGAGTT TTC		
			AG TACGGACCTCAA AAG		
			C _		
GAM1582	MGC2827	3'	TGAAAGAACAGATTAAGCATTG 23427		CTG G
	A		TCAGTGC GA TTGTTCTTTCA		
			AGTTACG TT GACAAGAAAGT		
			AA_ A		
GAM1582	LOC158798	5'	AATGACTTCAGACACTGA 39891	C	TG
			TCAGTG CTGGAGT TT		
			AGTCAC GACTTCA AA		
			A GT		
GAM1582	LOC161357	3'	AAAGATTCAACAGGCACTGG 40017		AGTTGT
			TCAGTGCCTGG TCTTT		
			GGTCACGGACC AGAAA		
			ACTT__		
GAM1582	LOC199863	5'	AGCAACCCAGACACTGA 43253	C	A
			TCAGTG CTGG GTTGT		
			AGTCAC GACC CAACGA		
			A _		
GAM1582	LOC221895	3'	AAAGGGTGATCCAGACAT 44440	C	G TG
			GTG CTGGA T TTCTTT		
			TAC GACCT A GGGAAA		
			A _GT		
GAM1583	FLRT2	5'	AAGACATTTAGAAATATGT 14874		GATAT
			ACATATTT GATGTCTT		
			TGTATAAA TTACAGAA		
			GAT__		
GAM1583	PDE4D	3'	AGCAACAAATATGTCA 36427		ATATGA T
			TGACATATTTG TG CT		
			ACTGTATAAAC AC GA		
			A_____ _		
GAM1583	TLL1	3'	AAGACTTGTCAAATATATCA 14836	C	TGAT
			TGA ATATTTGATA GTCTT		
			ACT TATAAACTGT CAGAA		
			A T__		
GAM1583	AKR1D1	3'	AAGACATCAAAGGCAACATATG 12609	_	ATA_
			CATAT TTG TGATGTCTT		

			GTATA AAC ACTACAGAA			
			C GGAA			
GAM1583	FLJ14803	3'	GAAAATATCAAACATGTTA	26625	A	GATG
			TGACAT TTTGATAT TC			
			ATTGTA AAACATA AG			
			C AA__			
GAM1583	FLJ22795	3'	AAGACACCTGTCAAATGTCA	24686	AT	TGA
			TGACAT TTGATA TGTCTT			
			ACTGTA AACTGT ACAGAA			
			__ CC_			
GAM1583	H2AFJ	3'	AAGATAGGACCAAATATGT	20235	ATATGA	
			ACATATTTG TGTCTT			
			TGTATAAAC ATAGAA			
			CAGG__			
GAM1583	KIAA0737	3'	ATCATATCAAATATGCCA	16818	A	
			TG CATATTTGATATGAT			
			AC GTATAAACTATACTA			
			C			
GAM1583	KIAA1582	3'	AAGACATATCAAACATGCA	32577	A A	TGA
			TG CAT TTTGATA TGTCTT			
			AC GTA AAACAT ACAGAA			
			_ C _			
GAM1583	PRPF8	5'	GAAGACATGCCCCCAGAACATG	30683	A_	ATATG
	TCA		TGACAT TTTG ATGTCTTC			
			ACTGTA AGAC TACAGAAG			
			CA CCCCCG			
GAM1583	SNTG1	3'	GTCAATCAAATATGCCA	21040	A	A
			TG CATATTTGAT TGAT			
			AC GTATAAACTA ACTG			
			C _			
GAM1583	LOC143465	5'	GCTTCATGTCAAACATGTCA	40363	A	T
			TGACAT TTTGATATGA GT			
			ACTGTA AAACGTACT CG			
			C T			
GAM1583	LOC145717	3'	AAGACACCTGTCAAATGTCA	33186	AT	TGA
			TGACAT TTGATA TGTCTT			
			ACTGTA AACTGT ACAGAA			
			__ CC_			
GAM1583	LOC145725	3'	AAGACACCTGTCAAATGTCA	37943	AT	TGA
			TGACAT TTGATA TGTCTT			

		ACTGTA AACTGT ACAGAA		
		— CC_		
GAM1583	LOC145732 3'	AAGACACCTGTCAAATGTCA 37952	AT	TGA
		TGACAT TTGATA TGTCTT		
		ACTGTA AACTGT ACAGAA		
		— CC_		
GAM1583	LOC196957 3'	AAGACACCTGTCAAATGTCA 42424	AT	TGA
		TGACAT TTGATA TGTCTT		
		ACTGTA AACTGT ACAGAA		
		— CC_		
GAM1583	LOC196961 3'	AAGACACCTGTCAAATGTCA 42433	AT	TGA
		TGACAT TTGATA TGTCTT		
		ACTGTA AACTGT ACAGAA		
		— CC_		
GAM1583	LOC197138 3'	AAGACACCTGTCAAATGTCA 42451	AT	TGA
		TGACAT TTGATA TGTCTT		
		ACTGTA AACTGT ACAGAA		
		— CC_		
GAM1583	LOC201475 5'	GAAAACATCATATATTTTGATG 42577	ATTG_	C
	TTA	TGACAT ATATGATGT TTC		
		ATTGTA TATACTACA AAG		
		GTTTTA A		
GAM1583	LOC220537 3'	AAGACACCTGTCAAATGTCA 43619	AT	TGA
		TGACAT TTGATA TGTCTT		
		ACTGTA AACTGT ACAGAA		
		— CC_		
GAM1583	LOC221806 5'	AAGACCTCAATCATGTCA 44452	TATT	A T
		TGACA TGAT TGA GTCTT		
		ACTGT ACTA ACT CAGAA		
		— C		
GAM1583	LOC245727 3'	AAGACACCTGTCAAATGTCA 43793	AT	TGA
		TGACAT TTGATA TGTCTT		
		ACTGTA AACTGT ACAGAA		
		— CC_		
GAM1583	LOC254065 5'	GTCATATCAAAAATATCA 46524	C A	
		TGA AT TTTGATATGAT		
		ACT TA AA ACTATACTG		
		A A		
GAM1584	FLJ20456 3'	AACAAAGTGCAGACATTCA 19493	T	TTT TC
		TGA ATGTCTGT A TTGTT		

ACT TACAGACG T AACAA
 _ _ GA
 GAM1584 KIAA1582 3' AAGTAAAAAAGACATATCA 32578 G_ T
 TGATATGTCT TTTTA CTT
 ||||| |||||
 ACTATACAGA AAAAT GAA
 AA T
 GAM1584 TRIM38 3' AAACAAAACAAAACAGAAAAAT 13049 ATG ATC
 CA TGAT TCTGTTTT TTGTTT
 ||| ||||| |||||
 ACTA AGACAAAA AACAAA
 AAA CAA
 GAM1584 LOC219673 5' AACAAAGATAAAAAATACA 44691 CTG
 TGT TTTTATCTTGTT
 ||| |||||
 ACA AAAATAGAACAA
 TAA
 GAM1585 CLCA3 3' ATATAGAAAATGAAGAGGGACA 11353 A TT A _ |||
 TCAAGT ATGT C CTT TCTATA T
 ||| ||| ||||| |
 TACA G GAA AGATAT A
 C GG A GTAAA |||
 GAM1585 EGFR 3' AAAGTGTCTCTGCCTTGAGTCA 11719 T TT_
 TGA CTCAA GT CACTTT
 ||||| || |||||
 ACTGAGTT CG GTGAAA
 C TCTCT
 GAM1585 GPR48 3' TATAGAAAGTAAACTGTGGTCA 20552 T AT C
 TGAC CA GTTT ACTTTCTATA
 ||| || ||| |||||
 ACTG GT CAAA TGAAAGATAT
 _ GT _
 GAM1585 PLAG1 3' TATACTGACTGAAACATGAGCC 8525 A A C TC
 A TG CTCA TGTTTCA TT TATA
 || ||| ||||| || |||
 AC GAGT ACAAAGT AG ATAT
 C _ C TC
 GAM1585 DIO2 3' GAGCAAAACATTGGGCCA 6459 A CA
 TG CTCAATGTTT CTT
 || ||||| |||
 AC GGGTTACAAA GAG
 C AC
 GAM1585 DIO2 3' GAGCAAAACATTGGGCCA 15170 A CA
 TG CTCAATGTTT CTT
 || ||||| |||
 AC GGGTTACAAA GAG
 C AC
 GAM1585 KIAA0210 5' AGAAAAATGAAGCATTGGTCA 16419 T C
 TGAC CAATGTTTCA TTTCT
 ||| ||||| |||||

ACTG GTTACGAAGT AAAGA
 _ A
 GAM1585 SLC7A11 3' TATAGAAAGTGAATATGCAGTT 15646 _ ATGT
 A TGA CT CA TTC ACT TTT CTATA
 ||||| || |||||
 ATTGA GT AAGTGAAAGATAT
 C AT__
 GAM1585 SOX7 3' AGAAAATGGGATTGAGTTA 25450 AT TT C
 TGA CT CA GT CA TTT CT
 ||||| || || |||||
 ATTGAGT TA GT AAAGA
 __ GG A
 GAM1585 LOC158629 5' AGAAAGTGACCCTGATCA 42017 C ATGTT
 TGA TCA TCA CT TTT CT
 ||| ||| |||||
 ACT AGT AGTGAAAGA
 _ CCC__
 GAM1585 LOC168512 5' TATACGAGGTGAAACATT 40252 C
 AATGTTTCACTTT TATA
 ||||| ||||| |||||
 TTACAAAGTGGAG ATAT
 C
 GAM1585 LOC51205 5' TATAGAAAAGTGGAATCGAGT 18501 AAT _
 ACTC GTTTC ACTTT CTATA
 ||| ||||| |||||
 TGAG TAAGGTGAAA GATAT
 C__ A
 GAM1586 GNGT2 5' AACTAGGAGGCTCAAA 25578 GA T
 TTTGAGCT C CTAGTT
 ||||| | |||||
 AAAC TCGG G GATCAA
 A__
 GAM1586 GOCAP1 3' AACTAGAATGTTCAAAA 22937 TGAC
 TTTTGAGC TCTAGTT
 ||||| |||||
 AAAACTTG AGATCAA
 TA__
 GAM1586 LIMD1 3' AACCAGAGTCAAGATTTGAAAT 15498 TG _ _ A
 A TATTT AG CT GACTCT GTT
 ||||| || || ||||| |||
 ATAAA TT GA CTGAGA CAA
 GT A A C
 GAM1586 NRG1 5' AACTAGAAAAGTGGCCCAGAA 15139 A AC__
 TTTTG GCTG TCTAGTT
 ||||| ||||| |||||
 AAGAC CGGT AGATCAA
 C GAAA
 GAM1586 ADMP 3' AACTAAAGTATAATCAAAGTA 29653 GCTG C
 TATTTTGA ACT TAGTT
 ||||| || |||||

		ATGAAACT TGA ATCAA		
		AATA A		
GAM1586	BM045	5' AACTAGAATCAGCAACGAGA 38214	A_	C
		TTTTG GCTGA TCTAGTT		
		AGAGC CGACT AGATCAA		
		AA A		
GAM1586	C1orf24	3' AACTAGAGTGCATTTAAAATA 27526	C	_
		TATTTTGAG TG ACTCTAGTT		
		ATAAAATTT AC TGAGATCAA		
		_ G		
GAM1586	FLJ20093	3' AACTGTCAGGTCAAAATA 19204	G	TCT
		TATTTTGA CTGAC AGTT		
		ATAAAACT GACTG TCAA		
		G _		
GAM1586	FLJ22037	5' AACTCTGTCAACTCGAAATA 45074	C	TCT
		TATTTTGAG TGAC AGTT		
		ATAAAGCTC ACTG TCAA		
		A TC_		
GAM1586	KIAA0564	3' AACTGTAATGCTCAAAATA 32899	TGACTC	
		TATTTTGAGC TAGTT		
		ATAAAACTCG GTCAA		
		TAAT_		
GAM1586	KIAA0694	3' GACAGAGCTGAGCTCAAAATA 35929	GA_	A
		TATTTTGAGCT CTCT GTT		
		ATAAAACTCGA GAGA CAG		
		GTC _		
GAM1586	P15-2	3' AACTAGAGAGGTGCAAAA 20781	A	GA
		TTTTG GCT CTCTAGTT		
		AAAAC TGG GAGATCAA		
		G A_		
GAM1586	PHCA	3' AACTAGAGTGTACAAAA 20375	A	TG
		TTTTG GC ACTCTAGTT		
		AAAAC TG TGAGATCAA		
		A _		
GAM1586	LOC196549	5' AACTAAATTCATCTCAAAATG 29807	C	CTC
		TATTTTGAG TGA TAGTT		
		GTAAAACTC ACT ATCAA		
		T TAA		
GAM1586	LOC221477	5' AACTGCCAGCTCAGAATA 44248	ACTC	
		TATTTTGAGCTG TAGTT		

		ATAAGACTCGAC	GTCAA		
		C__			
GAM1586	LOC257017	5'	AACTGCCAGACTCAAAATA	46490	_ ACTC
			TATTTTGAG CTG TAGTT		
			ATAAACTC GAC GTCAA		
			A C__		
GAM1586	LOC257117	5'	AACTAGAGTCAGAACGAA	46024	AG
			TTTG CTGACTCTAGTT		
			AAGC GACTGAGATCAA		
			AA		
GAM1586	LOC92973	5'	AACTAGAACCAGCACACGAAA	35181	A__ AC
			TTTTG GCTG TCTAGTT		
			AAAGC CGAC AGATCAA		
			ACA CA		
GAM1586	LOC93550	5'	AACTAGAAAAGTCAAAGTA	35931	G GAC
			TATTTTGA CT TCTAGTT		
			ATGAAACT GA AGATCAA		
			_ AA_		
GAM1587	CLN2	3'	ATCTTCCAGAGTAAAATGC	5962	TAAAA A
			GCATTTTG CTG AAGAT		
			CGTAAAAT GAC TTCTA		
			GA__ C		
GAM1587	MASP1	3'	ATCTTTCAGCCTTGAAATGT	29158	TAAAA
			GCATTTTG CTGAAAGAT		
			TGTAAAGT GACTTTCTA		
			TCC__		
GAM1587	RASA1	3'	CTTTCACAAAACGAAATGCTA	22905	AAAAC
			TAGCATTTTGT TGAAAG		
			ATCGTAAAGCA ACTTTC		
			AAAC_		
GAM1587	FXYD3	5'	ATCTCTCAGCCCAGCGAGATGC	22434	AAAA A
			GCATTTTGT CTGA AGAT		
			CGTAGAGCG GACT TCTA		
			ACCC C		
GAM1587	KIAA0555	3'	ATCCTTCAGTTTTAGCACTGGC	16680	ATTT _ A
			GC TGT AAAACTGAA GAT		
			CG ACG TTTTGACTT CTA		
			GTC_ A C		
GAM1587	KIAA0738	3'	CTTTCAGATAAAATGT	16278	AAAA
			GCATTTTGT CTGAAAG		

TGTAAAATA GACTTTC

GAM1587 PRO2086 5' ATCTAGAGTGTTTTACAAAAT 15345 TGAA_
ATTTTGTA AAC AGAT
||||| |||
TAAACATTTTG TCTA
TGAGA

GAM1587 LOC253955 5' CTTTCAGTTTTCCATAGC 45326 ATTT T
GC TG AAAACTGAAAG
|| || |||||
CG AC TTTTGACTTTC
AT__ C

GAM1587 LOC51696 3' ATCTTTCAGCCACAGAATCTA 18307 C AAAA
TAG ATTTTGT CTGAAAGAT
||| ||||| |||||
ATC TAAGACA GACTTTCTA
_ CC__

GAM1588 BRCA1 3' CCTGTTGCTGAAACCATACA 14169 A TC
TGTGT GTTTCAGTA TAGG
|||| ||||| |||
ACATA CAAAGTCGT GTCC
C T_

GAM1588 BRCA1 3' CCTGTTGCTGAAACCATACA 14175 A TC
TGTGT GTTTCAGTA TAGG
|||| ||||| |||
ACATA CAAAGTCGT GTCC
C T_

GAM1588 BRCA1 3' CCTGTTGCTGAAACCATACA 14181 A TC
TGTGT GTTTCAGTA TAGG
|||| ||||| |||
ACATA CAAAGTCGT GTCC
C T_

GAM1588 BRCA1 3' CCTGTTGCTGAAACCATACA 14188 A TC
TGTGT GTTTCAGTA TAGG
|||| ||||| |||
ACATA CAAAGTCGT GTCC
C T_

GAM1588 BRCA1 3' CCTGTTGCTGAAACCATACA 14194 A TC
TGTGT GTTTCAGTA TAGG
|||| ||||| |||
ACATA CAAAGTCGT GTCC
C T_

GAM1588 BRCA1 3' CCTGTTGCTGAAACCATACA 14200 A TC
TGTGT GTTTCAGTA TAGG
|||| ||||| |||
ACATA CAAAGTCGT GTCC
C T_

GAM1588 BRCA1 3' CCTGTTGCTGAAACCATACA 14208 A TC
TGTGT GTTTCAGTA TAGG
|||| ||||| |||

			ACATA CAAAGTCGT GTCC		
			C T_		
GAM1588	BRCA1	3'	CCTGTTGCTGAAACCATACA 14214	A	TC
			TGTGT GTTTCAGTA TAGG		
			ACATA CAAAGTCGT GTCC		
			C T_		
GAM1588	BRCA1	3'	CCTGTTGCTGAAACCATACA 14220	A	TC
			TGTGT GTTTCAGTA TAGG		
			ACATA CAAAGTCGT GTCC		
			C T_		
GAM1588	BRCA1	3'	CCTGTTGCTGAAACCATACA 14163	A	TC
			TGTGT GTTTCAGTA TAGG		
			ACATA CAAAGTCGT GTCC		
			C T_		
GAM1588	CALM1	3'	CCTAAAGATCAAGCTACACA 13755		CAGT _
			TGTGTAGTTT ATCT AGG		
			ACACATCGAA TAGA TCC		
			C_ AA		
GAM1588	ICMT	3'	CCTAGATAACTCTACACG 14779		TTTCAG
			TGTGTAG TATCTAGG		
			GCACATC ATAGATCC		
			TCA_		
GAM1588	IL13RA1	3'	CCTCTCTACTAAAACTACA 7283	C	TCT
			TGTAGTTT AGTA AGG		
			ACATCAAA TCAT TCC		
			A CTC		
GAM1588	IRTA2	3'	CCCAGAATGATAACTGCACA 25296	_	GTA A
			TGTGTAGTT TCA TCT GG		
			ACACGTCAA AGT AGA CC		
			T A_ C		
GAM1588	MYLK2	3'	CCGGGGCTGAAGCCACACA 26964	A	ATCTA
			TGTGT GTTTCAGT GG		
			ACACA CGAAGTCG CC		
			C GGG_		
GAM1588	NPY1R	3'	CCTAGCAGGGAAAAATACACA 6607	G_	AGTAT
			TGTGTA TTTC CTAGG		
			ACACAT AAAG GATCC		
			AA GGAC_		
GAM1588	RAB27A	3'	CCCAGACTTTACGACTACACA 10928		TC TA A
			TGTGTAGTT AG TCT GG		

			ACACATCAG TT AGA CC		
			CA TC C		
GAM1588	SALL1	3'	CCCAGATCTATGAACTACA 8877	C_ T A	
			TGTAGTTT AG ATCT GG		
			ACATCAAG TC TAGA CC		
			TA _ C		
GAM1588	SLC1A3	5'	CCCAGACACTGAAGTGCA 10382	G A A	
			TGTA TTTCAGT TCT GG		
			ACGT GAAGTCA AGA CC		
			_ C C		
GAM1588	ZNF134	5'	CCATGGACTGAAACTTCACA 9487	T TA _	
			TGTG AGTTTCAG TCTA GG		
			ACAC TCAAAGTC AGGT CC		
			T _ A		
GAM1588	DKFZP434D193	3'	CCTGGTATAAACTACA 42850	CA T	
			TGTAGTTT GTA CTAGG		
			ACATCAA TAT GGTCC		
			A_ _		
GAM1588	DKFZp547I224	5'	CCTAATATTTGTAACACACA 21474	T _ C	
			TGTGTAGTT CAG TAT TAGG		
			ACACATCAA GTT ATA ATCC		
			T T _		
GAM1588	FLJ20514	3'	CTGTCTGAACTACACA 19534	T TATC	
			TGTGTAGTT CAG TAG		
			ACACATCAA GTC GTC		
			_ T _		
GAM1588	FLJ32332	3'	CCCAGATGCTGATACACA 29468	GTT A	
			TGTGTA TCAGTATCT GG		
			ACACAT AGTCGTAGA CC		
			_ C		
GAM1588	KIAA1349	3'	CCTAGATGTCAACTCCACA 35013	T TCAG	
			TGTG AGTT TATCTAGG		
			ACAC TCAA GTAGATCC		
			C CT_		
GAM1588	KIAA1918	3'	CCTAACACAGGCTGAACTAAA 36214	G ATC_	
	CA		TGT TAGTTTCAGT TAGG		
			ACA ATCAAAGTCG ATCC		
			A GACACA		
GAM1588	SYTL2	3'	CCTAAGGAATACTACACA 26758	_ AGTATC	
			TGTGTAGT TTC TAGG		

		ACACATCA AAG	ATCC	
		T GA_____		
GAM1588	SYTL2	3' CCTAAGGAATACTACACA	26174	_ AGTATC
		TGTGTAGT TTC	TAGG	
		ACACATCA AAG	ATCC	
		T GA_____		
GAM1588	VPS39	3' CCTAGATACATGTTCCCACA	31469	TAGTTT _
		TGTG CA GTATCTAGG		
		ACAC GT CATAGATCC		
		CCTT__ A		
GAM1588	LOC125704	3' CCTTGAGCAAAACTGCACA	36798	CA A T
		TGTGTAGTTT GT TC AGG		
		ACACGTCAAA CG AG TCC		
		A_ _ T		
GAM1588	LOC221738	5' CTGGTAATAAAACTACACA	45028	CAG T
		TGTGTAGTTT TA CTAG		
		ACACATCAAA AT GGTC		
		ATA _		
GAM1589	EIF1A	3' AAAGCCTTTTTCAACATATC	42715	ATCTAGC
		GATATGTT AAGGCTTT		
		CTATACAA TTCCGAAA		
		CTTT_____		
GAM1589	LDHB	5' AAAGCCTTGCCAGATTCAGACA	8084	___ A
		TGTT ATCT GCAAGGCTTT		
		ACAG TAGA CGTTCCGAAA		
		ACT C		
GAM1589	NBEA	3' CTTTGCACCAGAAACATATCA	45492	A A__
		TGATATGTT TCT GCAAGG		
		ACTATACAA AGA CGTTTC		
		_ CCA		
GAM1589	REGL	3' AAGGTATACTAAATAATATATC	13255	C CAAG
	A	TGATATGTTAT TAG GCTTT		
		ACTATATAATA ATC TGGAA		
		A ATA_		
GAM1589	FLJ21934	3' CCTTGCTATTTTCATATTA	24079	TTATC
		TGATATG TAGCAAGG		
		ATTATAC ATCGTTCC		
		TTTT_		
GAM1589	TRIM2	3' AAGTATAGATAACATTTCA	17594	T GCAAG
		TGA ATGTTATCTA GCTT		

		ACT TACAATAGAT	TGAA		
		T	A		
GAM1590	EGFL5	5' CAGTGCCCACCCCTGTTATA	41881	T	TTT_
		TATAACAG GGTG	CTG		
		ATATTGTC CCAC	GAC		
		C	CCGT		
GAM1590	LMAN1	3' ATTACAGAAACAGTCTGT	12098	TGG	C
		ACAG	TGTTTCTG AAT		
		TGTC	ACAAAGAC TTA		
		TG_	A		
GAM1590	PTHLH	3' TGCAGAACAGCATCATGTCATA	8686	A	G _
		TAT ACA TGGTGT	TTCTGCA		
		ATA TGT ACTACG	AAGACGT		
		C _	AC		
GAM1590	RRM2B	3' TGCTAACATCACTGTCATA	33690	A	TCT
		TAT ACAGTGGTGTT	GCA		
		ATA TGTCACTACAA	CGT		
		C	T_		
GAM1590	FLJ14641	3' TGCAGAAATGAGGACGTTAT	26591	A	GG_
		ATAAC GT	TGTTTCTGCA		
		TATTG CA	GTAAAGACGT		
		_	GGA		
GAM1590	FLJ20373	3' TATTGCAATGACACCATT	19427	TC	
		AGTGGTGTT	TGCAATA		
		TTACCACAG	ACGTTAT		
		TA			
GAM1590	NP220	5' GTTCAACACCACCTTATA	15836	CA	TCT
		TATAA GTGGTGTT	GC		
		ATATT	CACCACAA TG		
		C_	CT_		
GAM1590	LOC148894	3' ATTGCAGAAAATAACATTGT	40916	GTG_	
		ACAGTG	TTTCTGCAAT		
		TGTTAC	AAAGACGTTA		
		AATA			
GAM1591	BAPX1	3' CCAAGGGGTGCGAAACCCTG	6861	_G	TT C
		CAGGGTTT G G	CC TGG		
		GTCCCAAA C T	GG ACC		
		G G	GG A		
GAM1591	CCND2	3' GCCAACAAACCCTCTGTA	7517	C	_
		TACA	AGGGTTTG GGT		

ATGT TCCCAAAC CCG
 C AA
 GAM1591 DDX6 5' GCCAGAACAGAGAACCCTGTTA 10646 C GG_ CC
 A ACAGGGTTT GTTC TGGC
 | ||||| ||| |||
 A TGTCCCAAG CAAG ACCG
 T AGA _
 GAM1591 DNASE1L1 3' CCAGGAAACCATTAAGCCC 13565 _ C
 GGGTTTG GGTTCCTGG
 ||||| ||| |||||
 CCCGAAT CCAA GGACC
 TA A
 GAM1591 HNRPD 3' CCAGAAAACGCTGTCCTGTG 11950 TT _ CC
 CACAGGG TGG GTT CTGG
 ||||| ||| ||| |||
 GTGTCCT GTC CAA GACC
 _ G AA
 GAM1591 HSPA8 5' GCCAGGGAAGCCAACCCC 13370 T G
 GGG TTGG TTCCCTGGC
 ||| ||| |||||
 CCC AACC AAGGGACCG
 C G
 GAM1591 THBD 5' GCCAGAGAACCCAGCAATCCGA 5920 ACA _ C
 GTA TAC GGGTT TGGGTTCTGGC
 ||| ||||| ||||| |||||
 ATG CCTAA ACCCAAG GACCG
 AG_ CG A
 GAM1591 C4orf6 5' CCAGAAAACAAGCCCTG 12310 GG CC
 CAGGGTTTG TTC TGG
 ||||| ||| |||
 GTCCCGAAC AAG ACC
 AA _
 GAM1591 HT002 3' GCCAAGGAACCCAAGGACTG 15283 GG C
 CAG TTTGGGTTCC TGGC
 ||| ||||| ||||| |||||
 GTC GAACCCAAGG ACCG
 AG A
 GAM1591 KIAA0775 5' CCAGGGACAAACCCT 16319 GGT
 AGGGTTTG TCCCTGG
 ||||| |||||
 TCCCAAAC AGGGACC
 _
 GAM1591 KIAA0821 3' GCCAGGGAGGGGAACCCTG 17199 GGG
 CAGGGTTT TTCCCTGGC
 ||||| |||||
 GTCCCAAG GAGGGACCG
 G_
 GAM1591 KIAA1297 5' GCCAGGAAACCCACCGTGTGTG 35713 G TT C
 TACACA GGT GGGTTCTGGC
 ||||| ||| ||||| |||||

		GTGTGT CCA CCCAA GGACCG		
		G _ A		
GAM1591	MGC14161	3' CCAAGGAACCCGGCTACCC	26720	_ C
		GGGT TTGGGTTCC TGG		
		CCCA GGCCCAAGG ACC		
		TC A		
GAM1591	MGC4161	5' CCAGAGGAAGCCTGTGTA	23595	G TTGGGT _
		TACACAGG T TCC CTGG		
		ATGTGTCC A AGG GACC		
		G _ _ _ A		
GAM1591	PCSK7	5' CCAGGAGCTCAACCTCATGTA	11075	CA T C
		TACA GGGTT GGGTTCC TGG		
		ATGT TCCAA CTCGAGG ACC		
		AC _ _		
GAM1591	PRIC285	3' CCAGGAAGGAAACCCTGTG	30803	GGG C
		CACAGGGTTT TTCC TGG		
		GTGTCCCAAA AAGG ACC		
		GG _ _		
GAM1591	LOC135763	3' GCCAGCTCCAACCCAAAGCCCT	28882	_ CC _
	G	CAGGGTTT GGGTT CTGGC		
		GTCCCGAA CCCAA GACCG		
		A CCTC		
GAM1591	LOC149464	5' GCCAGGGAAGCTGTGACCCAG	40992	ACA _ G
	TA	TAC GGGTT TGG TTCCCTGGC		
		ATG CCCAG GTC AAGGGACCG		
		AC _ T G		
GAM1591	LOC200531	5' GCCAGGAAAATGCCCTGTGTG	42818	TTGGG C
		TACACAGGGT TTCC TGGC		
		GTGTGTCCCG AAGG ACCG		
		TAA _ _		
GAM1591	LOC201689	3' CCAGGGAAGCCCCCTG	33333	TTT G
		CAGGG GG TTCCCTGG		
		GTCCC CC AAGGGACC		
		_ G		
GAM1592	KIAA1560	3' CATAGTGGTAAATAATTATGAA	32102	CT _
		TTCATAATTAT TTATTATG		
		AAGTATTAATA GGTGATAC		
		AAT		
GAM1592	LANO	3' CATGATAATAATTATGAAGA	24805	A CTT
		TC TTCATAATTAT TATTATG		

AG AAGTATTAATA ATAGTAC

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      ———
GAM1592 ROBO4  3' CATGGAAGAAAATAATTATGA 21133  ____  A
      ATG      CATTCATAATTA TCTTTT TTATG
              ||||| |||| ||||
              GTAAGTATTAAT AGAAA GGTAC
              AAA _
GAM1592 ULK2   3' TAAAGATAATTAATAAATGA 16183  CA
              TCATT TAATTATCTTTA
              |||| ||||| |||||
              AGTAA ATTAATAGAAAT
              AA
GAM1593 ATP7A  3' GTAGCTCAAAAGACCTTA 5493  A  T G
              TAAG TCTTTTG AG TAT
              ||| ||||| || |||
              ATTC AGAAAAC TC ATG
              C _ G
GAM1593 FGD1   3' TCAATACCCTACCACAGATC 10768  TTT _
              GATCT GTAGG TATTGA
              |||| |||| |||||
              CTAGA CATCC ATAACT
              CAC C
GAM1593 PAG    3' TCACCACCCACAAAAGATC 20510  A AT
              GATCTTTTGT GGT TGA
              ||||| ||| |||
              CTAGAAAACA CCA ACT
              C CC
GAM1593 SIAT1  3' TTTCAATACCTACCCCCAAATC 8976  CTTTT_
      TT      AAGAT GTAGGTATTGAAA
              |||| ||||| |||||
              TTCTA CATCCATAACTTT
              AACCCC
GAM1593 ZNF10  3' TTAATAACCCACAAAAGATTCA 17696  A  A _
              A GATCTTTTGT GGT ATTGA
              | ||||| ||| |||||
              A TTAGAAAACA CCA TAATT
              C C A
GAM1593 CALN1  3' TCAATACCTGCCCTGTCT 25518  CTTT
              AGAT GTAGGTATTGA
              ||| ||||| |||||
              TCTG CGTCCATAACT
              TCC__
GAM1593 CTSO   3' TACCTACAAAAGATTCTA 7017  AG
              TA ATCTTTTGTAGGTA
              || ||||| |||||
              AT TAGAAAACATCCAT
              CT
GAM1593 FLJ21106 3' TTCAACAAATGTAAAAGATC 24737  GGTA
              GATCTTTTGTGTA TTGAA
              ||||| ||||
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		CTAGAAAATGT AACTT	
		AAAC	
GAM1593 M96	3'	TTTCAATACCTTTTAGATT 14289	TTTGT
		AGATCT AGGTATTGAAA	
		TTTAGA TCCATAACTTT	
		TTT__	
GAM1593 PRO1843	5'	TTCAATACTCTTTAAAAG 20575	T _
		CTTTTG AG GTATTGAA	
		GAAAAT TC CATAACTT	
		T T	
GAM1593 PRO2958	3'	TTTCAATACCTTTCAGATC 20628	TTTGT
		GATCT AGGTATTGAAA	
		CTAGA TCCATAACTTT	
		CTT__	
GAM1593 LOC129676	5'	TTTCGGGGCTACAAAGGATCT 37290	GTA
		AGATCTTTTGTAG TTGAAA	
		TCTAGGAAACATC GGCTTT	
		GG_	
GAM1593 LOC131583	3'	TCTTGCTCAAAAGATCT 37357	TA TT
		AGATCTTTTG GGTA GA	
		TCTAGAAAAC TCGT CT	
		_ T_	
GAM1593 LOC91291	5'	TTCAATACCTTGAAGAAAGATT 32632	A GT__
CA		A GATCTTTT AGGTATTGAA	
		A TTAGAAAG TCCATAACTT	
		C AAGT	
GAM1594 PTPRO	3'	ACAACAGAAAACACTTTG 25001	ATAAGGTG
		CAAAGTGTTT GTTGT	
		GTTTCACAAA CAACA	
		AGA_____	
GAM1594 PTPRO	3'	ACAACAGAAAACACTTTG 25025	ATAAGGTG
		CAAAGTGTTT GTTGT	
		GTTTCACAAA CAACA	
		AGA_____	
GAM1594 PTPRO	3'	ACAACAGAAAACACTTTG 25016	ATAAGGTG
		CAAAGTGTTT GTTGT	
		GTTTCACAAA CAACA	
		AGA_____	
GAM1594 PTPRO	3'	ACAACAGAAAACACTTTG 8736	ATAAGGTG
		CAAAGTGTTT GTTGT	

			GTTTCACAAA	CAACA	
			AGA_____		
GAM1594	PTPRO	3'	ACAACAGAAAACACTTTG	25007	ATAAGGTG
			CAAAGTGTTT	GTTGT	
			GTTTCACAAA	CAACA	
			AGA_____		
GAM1594	FLJ21126	3'	ACAACCACCTGCTCCAACAC	43416	TATA_
			GTGTT	AGGTGGTTGT	
			CACAA	TCCACCAACA	
			CCTCG		
GAM1594	PGLYRP	3'	ACAACCACCCCCAAGCCTCA	27480	A T ATAA
			A AG GTTT	GGTGGTTGT	
			A TC CGAA	CCACCAACA	
			C _ CCC_		
GAM1594	PTPNS1	3'	CACCTCTCATAAGCACTTT	28051	A__
			AAAGTGTTTAT	AGGTG	
			TTTCACGAATA	TCCAC	
			CTC		
GAM1594	LOC146540	3'	TACATTTCACTTCTAAACACTT	38200	A TA T_
			CA	C AAGTGTTTA	AGGTGG TGTA
			A TTCACAAAT	TTCAC	ACAT
			C	C_ TT	
GAM1594	LOC162333	5'	TACAACACTTTTACAACACTC	42134	A TAT
			TG	CA AGTGTT	AAGGTGGTTGTA
			GT TCACAA	TTTCATCAACAT	
			C	CAT	
GAM1594	LOC92597	3'	ACCAATTCTTAGAAACACTTT	34672	A _
			AAAGTGTTT	TAAGG TGGT	
			TTTCACAAA	ATTCT	ACCA
			G	TA	
GAM1595	FHOD2	3'	CAAACAGGATGCAACTGCAGTG	36552	ACTGG _
			TACTGCA	TGCG CCTGTTTG	
			GTGACGT	ACGT GGACAAAC	
			CA__	A	
GAM1595	PCDH19	3'	CAAACCAGCTAACACCATTACA	31861	C C C__ CT
			G	CTG AA TGGTG	GC GTTTG
			GAC TT ACCAC	CG CAAAC	
			A _	AAT AC	
GAM1595	LOC124222	3'	CAAACAGGCAGGGAGCCACAGT	36740	CAAC GC__
			ACTG	TGGT GCCTGTTTG	

		TGAC ACCG CGGACAAAC		
		AGGGA		
GAM1595	LOC195977 3'	AAACAGGCTCGCTGCAG 42298	ACTG	C
		CTGCA GTG GCCTGTTT		
		GACGT CGC CGGACAAA		
		T		
GAM1595	LOC202134 3'	CAAACAGGCATTTTTGCA 43413	CT	GC
		TGCAA GGT GCCTGTTT		
		ACGTT TTA CGGACAAAC		
		T_ _		
GAM1596	DLG5 5'	TCAAGGAACAGATGGAATCCCA 40340	CCG	AAG
		TGGGAT CATCTGTT TTGA		
		ACCCTA GTAGACAA AACT		
		AG_ GG_		
GAM1596	EZH1 3'	CAACTTAGGCAGTTCCCA 7716	TCC	ATCTG
		TGGGA GC TTAAGTTG		
		ACCCT CG GATTCAAC		
		TGA _		
GAM1596	ALDH5A1 3'	CTTAAACAGATGCAAATCCTA 6741	CC	_
		TGGGAT GCATCTGTT AAG		
		ATCCTA CGTAGACAA TTC		
		AA A		
GAM1596	C20orf121 3'	TCAACCTAAAATGCTGGATCCC 23635	_	CTG A
	A	TGGGATCC GCAT TTA GTTGA		
		ACCCTAGG CGTA AAT CAACT		
		T A_ C		
GAM1596	SLC26A7 5'	CAACTTAACACTGAACCCA 27412	A	CGCATC
		TGGG TC TGTTAAGTTG		
		ACCC AG ACAATTCAAC		
		A TC_		
GAM1596	SLC26A7 5'	CAACTTAACACTGAACCCA 28624	A	CGCATC
		TGGG TC TGTTAAGTTG		
		ACCC AG ACAATTCAAC		
		A TC_		
GAM1596	LOC92340 3'	CAACTCCATCCACGGATCCC 34196	CATC	TTA
		GGGATCCG TG AGTTG		
		CCCTAGGC AC TCAAC		
		ACCT C_		
GAM1597	CSNK2A1 3'	CCTGTTTCATCTCCCAACATGCT 7621	A	AAA
		AGCGT GTT AGATGAACAGG		

TCGTA CAA TCTACTTGTCC
 _ CCC
 GAM1597 SORCS1 3' CCTGTTACCTCTTTCCAC 27484 TA _
 GT AAAGA TGAACAGG
 || |||| |||||
 CA TTTCT ACTTGTCC
 CC CC
 GAM1597 DKFZP564O0423 3' CCTGTTTCATCTCCTCCTTTCTC 44065 CGT TTAAA
 GAG AG AGATGAACAGG
 ||| || |||||
 CTC TC TCTACTTGTCC
 TT_ CTCC_
 GAM1597 DKFZP586J0619 3' CCTGTTACCCCTCTGACCGC 39581 TA AAAGA_
 GCG GTTA TGAACAGG
 ||| ||| |||||
 CGC CAGT ACTTGTCC
 _ CTCCCC
 GAM1597 GFR 3' CCTGTTTCATCTCTTTCATGCC 14637 A AGTT A
 G GCGT AA AGATGAACAGG
 | ||| || |||||
 C CGTA TT TCTACTTGTCC
 C CT_ C
 GAM1597 KIAA0429 5' CACCTTCCAGACTACGCTC 16466 AA_ A
 GAGCGTAGTT AAG TG
 ||||| ||| ||
 CTCGCATCAG TTC AC
 ACC C
 GAM1597 MGC11115 3' CGTTGACTAACTATGCTC 26093 AAA
 GAGCGTAGTTA GATG
 ||||| |||
 CTCGTATCAAT TTGC
 CAG
 GAM1597 LOC151391 3' CCTGTTTCATCTTTCAGGGCTT 41336 GTAGTTA
 GAGC AAAGATGAACAGG
 ||| |||||
 TTCG TTTCTACTTGTCC
 GGAC_
 GAM1597 LOC163882 3' CCTGTTACCTCTTGGGTCTC 39972 _G TTAAA A
 GAG C TAG AG TGAACAGG
 ||| ||| || |||||
 CTC G GTT TC ACTTGTCC
 T G C_ C
 GAM1598 SPAG8 3' CTGACAGCCCAAACCTGTCAGA 14816 TGA GA
 TTTGACAGTTTGG TG TCAG
 ||||| || |||
 AGACTGTCAAACC AC AGTC
 CG_ _
 GAM1598 KIAA0471 3' CTGATCCTTTCAAACCAACCA 16912 ACA_ TGAT
 A TTTG GTTTGG GGATCAG
 ||| |||| |||||

AAAC CAAACT CCTAGTC
 CAAC TT__
 GAM1598 RAB35 3' CCACTTGCCCCAACTGCCAAA 13731 A _TG_
 TTTG CAGTTTG G A TGG
 ||| ||||| | |||
 AAAC GTCAAAC C T ACC
 C C GT C
 GAM1598 LOC129138 3' ATCCCAGGAACCTGTCAAA 29018 ____ T
 TTTGACAG TTTGG GAT
 ||||| |||||
 AAACTGTC GGACC CTA
 CAA _
 GAM1598 LOC164955 3' CTAAATCCAAACTGTCAAA 40112 TGA
 TTTGACAGTTTG TGG
 ||||| |||
 AAACTGTCAAACC ATC
 TAA
 GAM1599 ANK2 3' CAGAAGAACTTCACCTGCAGA 6822 CA ACCCTT
 TC CAG GAGTTCTTCTG
 || ||| |||||
 AG GTC TTCAAGAAGAC
 AC CAC__
 GAM1599 ANK2 3' CAGAAGAACTTCACCTGCAGA 21966 CA ACCCTT
 TC CAG GAGTTCTTCTG
 || ||| |||||
 AG GTC TTCAAGAAGAC
 AC CAC__
 GAM1599 GFRA1 5' CAGAAGAAATCTGGCCTCGGA 11772 AC A CTT G
 TCC AG CC GA TTCTTCTG
 ||| ||| || |||||
 AGG TC GG CT AAGAAGAC
 C_ C T__ A
 GAM1599 ITGA5 3' CAGAAGGAGGAGGACCTGGGA 30721 A AC GAG
 TCC CAG CCTT TTCTTCTG
 ||| ||| |||||
 AGG GTC GGAG AGGAAGAC
 _ CA G_
 GAM1599 KCNJ5 3' CAGAAGAATGGCATGAACCTGG 6586 A ACCCT A_
 GA TCC CAG TG GTTCTTCTG
 ||| ||| || |||||
 AGG GTC AC TAAGAAGAC
 _ CAAGT GG
 GAM1599 LEP 3' CAGAAGGGAGAAGGATCT 5735 C GAG
 AGA CCTT TTCTTCTG
 ||| ||| |||||
 TCT GGAA GGGAAGAC
 A GA_
 GAM1599 MSH3 3' CAGAAGGAATAAGGTCATG 8282 _ C AG
 CA GACC TTG TTCTTCTG
 || ||| ||| |||||

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GT CTGG AAT AGGAAGAC
A _ A_
GAM1599 MTCP1 5' CAGAAGTTTAGCAAGGGTCATG 15485 _ AGTT_
CA GACCCTTG CTTCTG
|| ||||| |||||
GT CTGGGAAC GAAGAC
A GATTT
GAM1599 RNMT 3' CAGAGGGTCTCTAGGGTCTG 9881 T TT
CAGACCCT GAG CTTCTG
||||| ||| |||||
GTCTGGGA CTC GGAGAC
T TG
GAM1599 TNFSF4 3' AGAAGAATCAGCTTGTG 9328 ACCC G
CACAG TTGA TTCTTCT
|||| ||| |||||
GTGTT GACT AAGAAGA
C__ _
GAM1599 APOL4 3' CAGAAGAACGTGGATTGTG 24975 A CTTGA
CACAG CC GTTCTTCTG
|||| || |||||
GTGTT GG CAAGAAGAC
A TG__
GAM1599 C21orf42 3' CAGAAGAACTCCATTCTTGT 27749 ACCCTT
ACAG GAGTTCTTCTG
||| |||||
TGTT CTCAAGAAGAC
CTTAC_
GAM1599 CDC14B 3' CAGAAGAATTGAGGATCTGATG 27163 _ C G
GA TCCA CAGA CCTT AGTTCTTCTG
||| ||| ||| |||||
AGGT GTCT GGAG TTAAGAAGAC
A A _
GAM1599 CDC14B 3' CAGAAGAATTGAGGATCTGATG 9759 _ C G
GA TCCA CAGA CCTT AGTTCTTCTG
||| ||| ||| |||||
AGGT GTCT GGAG TTAAGAAGAC
A A _
GAM1599 DKFZP564A022 3' CAGAAGAATGGCGTAAACCCAG 25228 ACAG__ _ TTGA
GA CC AC CC GTTCTTCTG
|| ||| |||||
GG TG GG TAAGAAGAC
ACCCAAA C ____
GAM1599 DOCK3 3' GAATTCAAGAGCCTGTGGA 33034 ACC
TCCACAG CTTGAGTTC
||||| |||||
AGGTGTC GAACTTAAG
CGA
GAM1599 FLJ11850 3' CAGAAGGGTGAAGGCTGTAGA 22949 C AC GA TT
TC ACAG CCTT G CTTCTG
|| ||| ||| | |||||

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AG TGTC GGAA T GAAGAC
A _ G_ GG
GAM1599 FLJ33069 3' GACTCAAGGGCTGTAGA 29474 C A
TC ACAG CCCTTGAGTT
|| ||| |||||
AG TGTC GGGA ACTCAG
A _
GAM1599 GMPPB 5' CAGAAGAGGGTGAGTCCTGGA 45810 CA CC AG
TCCA GAC TTG TTCTTCTG
||| ||| ||| |||||
AGGT CTG AGT GAGAAGAC
C_ _ GG
GAM1599 HCA4 3' CAGAGGTAACAAAAGTCTGTGG 38021 CC AGTT
CCACAGAC TTG CTTCTG
||||| ||| |||||
GGTGTCTG AAC GGAGAC
AA AAT_
GAM1599 HNK-1ST 5' AGAAGGAAGAGTCAGTG 11265 A C TGAG
CAC GAC CT TTCTTCT
||| ||| ||| |||||
GTG CTG GA AGGAAGA
A A _
GAM1599 KIAA0618 3' CAGAAGGAAGAGGATCT 16833 C GAG
AGA CCTT TTCTTCTG
||| ||| |||||
TCT GGAG AGGAAGAC
A A_
GAM1599 KIAA0763 3' AAGCTTATCAAAAAGTTTGTGGA 16965 CC GTT_
TCCACAGAC TTGA CTT
||||| ||| |||
AGGTGTTTG AACT GAA
AA ATT C
GAM1599 KIAA1884 3' CAGAAAAGGAAGAGGGGCTGCA 36292 CA A GAGTTC
GA TC CAG CCCTT TTCTG
|| ||| ||||| |||||
AG GTC GGGAG AAGAC
AC G AAGGAA
GAM1599 MGC13017 3' CAGAAGAACTGCTTGAACCTGG 27944 A ACCCTTG_
GA TCC CAG AGTTCTTCTG
||| ||| |||||
AGG GTC TCAAGAAGAC
_ CAAGTT CG
GAM1599 MGC22805 5' CAGAAGATTCAAGGAGCTGTAG 29409 C AC T
A TC ACAG CCTTGAGT CTTCTG
|| ||| ||||| |||||
AG TGTC GGA ACTTA GAAGAC
A GA _
GAM1599 PSR 3' AACTAAGGATCTGTGGG 32494 C G
TCCACAGA CCTT AGTT
||||| ||| |||

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GGGTGTCT GGAA TCAA
A _
GAM1599 TGIF2 3' AGAGGAACCCAGTGG 22363 AGACCCT A
TCCAC TG GTTCTTCT
|||| | |||||
AGGTG AC CAAGGAGA
_____ C
GAM1599 VAV3 3' AGAAAGAGGGTCAGTGG 12757 A GAG
TCCAC GACCCTT TTCT
|||| ||||| |||
AGGTG CTGGGAG AAGA
A A_
GAM1599 LOC139770 3' CAGAAGAATAGCTTGAGCCAG 37144 ACAGACC TG _
GA TCC CT AGT TCTTCTG
|| | || |||||
AGG GA TCG AGAAGAC
ACCC_ GT ATA
GAM1599 LOC148413 3' CAGAAGGAATGAAGGCCTG 38532 AC GAG
CAG CCTT TTCTTCTG
|| || |||||
GTC GGAA AGGAAGAC
C_ GTA
GAM1599 LOC154881 3' CAGAAGAAGGGTTGGGTCTG 39495 TTGAG
CAGACCC TTCTTCTG
|||| |||||
GTCTGGG AAGAAGAC
TTGGG
GAM1599 LOC158376 5' CAGCTGTGACTCAAGGGCCAG 41971 ACAGA CTT_
GA TCC CCCTTGAGTT CTG
|| ||||| |||
AGG GGGAAGTCAG GAC
ACCC_ TGTC
GAM1599 LOC168448 3' CAGAAGAATTGAGGATCTGATG 40247 _ C G
GA TCCA CAGA CCTT AGTTCTTCTG
|||| ||| |||||
AGGT GTCT GGAG TTAAGAAGAC
A A _
GAM1599 LOC200772 3' AGAAGAACAAAGCTGCAGA 43346 CA ACC GA
TC CAG CTT GTTCTTCT
|| || || |||||
AG GTC GAA CAAGAAGA
AC _ A_
GAM1599 LOC220074 3' CAGAGTACCAGGGTCTGTAGA 29823 C T A TC
TC ACAGACCCT G GT TTCTG
|| ||||| || |||||
AG TGTCTGGGA C CA GAGAC
A _ T_
GAM1599 LOC222962 3' GACCCAAGGGTCCCTGGA 44630 CA A
TCCA GACCCTTG GTT
|||| ||||| |||

AGGT CTGGGAAC CAG
 CC C
 GAM1599 LOC256401 3' CAGAAGAATTGAGGATCTGATG 45945 _ C G
 GA TCCA CAGA CCTT AGTTCTTCTG
 |||| |||| |||| ||||
 AGGT GTCT GGAG TTAAGAAGAC
 A A _
 GAM1599 LOC90408 3' CAGAAGAACATAAATTGTG 31395 ACCC A
 CACAG TTG GTTCTTCTG
 |||| || ||||
 GTGTT AAT CAAGAAGAC
 A _ A
 GAM1599 LOC91516 5' CAGAAGAGCCAGGATCTGCTGG 32954 _ C T A
 A TCCA CAGA CCT G GTTCTTCTG
 |||| |||| |||| ||||
 AGGT GTCT GGA C CGAGAAGAC
 C A _ _
 GAM1600 AQP6 5' GCCACCTTGAGGCAGCCTATCC 27613 C_ C G G
 CA TGGGA GGC GC TCG AGGTGGC
 |||| || || ||||
 ACCCT CCG CG AGT TCCACCG
 AT A G _
 GAM1600 CDH5 3' GCCACCTCCACACCCACCCC 7547 AC CCGC C
 GGG GG GT GGAGGTGGC
 || || || ||||
 CCC CC CA CCTCCACCG
 CA CA _ _
 GAM1600 HUNK 3' CCACCTCTGTGGCCACCTCA 15946 AC GTC
 TGGG GGCCGC GGAGGTGG
 |||| |||| ||||
 ACTC CCGGTG TCTCCACC
 CA _ _
 GAM1600 LTA 3' CCACCTCTCCTTTGGCCATTCC 6195 C CGTC
 A TGGGA GGCCG GGAGGTGG
 |||| |||| ||||
 ACCTT CCGGT TCTCCACC
 A TTCC
 GAM1600 SNL 3' GCCACCTCCTCCAGCCCCCA 9063 AC CGCGTC
 TGGG GGC GGAGGTGGC
 |||| || ||||
 ACCC CCG CCTCCACCG
 C_ ACCCT_
 GAM1600 SORCS3 5' GCCACCTCCTTCCCGGCCGCC 17364 A CGTC
 GGG CGGCCG GGAGGTGGC
 || |||| ||||
 CCC GCCGGC CCTCCACCG
 _ CCTT
 GAM1600 VIPR2 3' CCACCGGGTGACATCCGTCCCA 9412 CCGC GA_
 TGGGACGG GTCG GGTGG
 |||| || ||||

ACCCTGCC CAGT CCACC
 TA__ GGG
 GAM1600 WNT1 3' CCACCTCCAACCCAACCCA 11895 AC CCGC C
 TGGG GG GT GGAGGTGG
 |||| || || |||||
 ACCC CC CA CCTCCACC
 AA ____ A
 GAM1600 DKFZP434P0111 3' CCACTTCCCAGCCGCCCA 33454 A CGCGTC
 TGGG CGGC GGAGGTGG
 |||| ||| |||||
 ACCC GCCG CCTTCACC
 C AC____
 GAM1600 DKFZp586I021 3' GCCACCTCCGCCAGCCGCCTCC 26028 C C GT_
 GGA GGC GC CGGAGGTGGC
 ||| ||| || |||||
 CCT CCG CG GCCTCCACCG
 _ C ACC
 GAM1600 PDK2 3' GCCACCTCCTGAGCCCTCCCA 8475 C CGCG _
 TGGGA GGC TC GGAGGTGGC
 |||| ||| || |||||
 ACCCT CCG AG CCTCCACCG
 C ____ T
 GAM1600 REC8 5' CCACACCGCGGCCGCCCA 11608 A TCGGAG
 TGGG CGGCCGCG GTGG
 |||| ||||| |||
 ACCC GCCGGCGC CACC
 _ CA____
 GAM1600 SIMRP7 3' GCCACCCTGCGCAACCAGCCC 44371 AC CC T A
 GGG GG GCG CGG GGTGGC
 ||| || ||| ||| |||||
 CCC CC CGC GTC CCACCG
 GA AA _ _
 GAM1600 TNFSF13 5' CCACCTCCTTGCTACCCCA 9898 AC CGCGTC
 TGGG GGC GGAGGTGG
 |||| ||| |||||
 ACCC TCG CCTCCACC
 CA TT____
 GAM1600 LOC145989 3' GCCACCTCCTCCCAGCCCCCA 29951 AC CGCGTC
 TGGG GGC GGAGGTGG
 |||| ||| |||||
 ACCC CCG CCTCCACCG
 C_ ACCCT_
 GAM1601 CHS1 3' GAATTATAAAAGCTTACTTTA 5527 _ T
 TAAGGTAAGCTTT ATG TTC
 ||||| ||||| ||| |||
 ATTTCATTGAAA TAT AAG
 A T
 GAM1601 DSC3 3' AAACATTTTAAACTTACCTT 7650 C ____
 AAGGTAAG TTTA TGTTT
 ||||| |||| |||||

			TTCCATTTC AAAT ACAAA		
			A TTT		
GAM1601	DSC3	3'	AAACATTTTAAAACTTACCTT 23661	C	___
			AAGGTAAG TTTA TGTTT		
			TTCCATTTC AAAT ACAAA		
			A TTT		
GAM1601	GRLF1	3'	GATAGAAACATAGGCACC 38414	AA	T C
			GGT GCTT ATGTTTC ATC		
			CCA CGGA TACAAAG TAG		
			___ _ A		
GAM1601	MAP3K9	3'	GATGGAAACAGGGCCACTT 30459	AA	TA
			AGGT GCTT TGTTTCCATC		
			TTCA CGGG ACAAAGGTAG		
			C_ _		
GAM1601	NEU3	3'	ATGGAAACCAGGGGACTTACCT 13453	_	AT
	T		AAGGTAAG CTTT GTTTCCAT		
			TTCCATTTC GGGG CAAAGGTA		
			A AC		
GAM1601	NR3C2	3'	GAACGTTTTTAAAGCTTACC 6597		___
			GGTAAGCTTT ATGTTT		
			CCATTGCGAAA TGCAAG		
			TTT		
GAM1601	PCDHA1	3'	ATGGAAACAAGCCACTTA 25380	GTAA	TTA
			TAAG GCT TGTTTCCAT		
			ATTC CGA ACAAAGGTA		
			AC_ _		
GAM1601	PCDHA1	3'	ATGGAAACAAGCCACTTA 20861	GTAA	TTA
			TAAG GCT TGTTTCCAT		
			ATTC CGA ACAAAGGTA		
			AC_ _		
GAM1601	PCDHA10	3'	ATGGAAACAAGCCACTTA 20871	GTAA	TTA
			TAAG GCT TGTTTCCAT		
			ATTC CGA ACAAAGGTA		
			AC_ _		
GAM1601	PCDHA10	3'	ATGGAAACAAGCCACTTA 25612	GTAA	TTA
			TAAG GCT TGTTTCCAT		
			ATTC CGA ACAAAGGTA		
			AC_ _		
GAM1601	PCDHA11	3'	ATGGAAACAAGCCACTTA 20881	GTAA	TTA
			TAAG GCT TGTTTCCAT		

		ATTC CGA ACAAAGGTA		
		AC__ __		
GAM1601	PCDHA12	3' ATGGAAACAAGCCACTTA	20892	GTAA TTA
		TAAG GCT TGTTTCCAT		
		ATTC CGA ACAAAGGTA		
		AC__ __		
GAM1601	PCDHA13	3' ATGGAAACAAGCCACTTA	20902	GTAA TTA
		TAAG GCT TGTTTCCAT		
		ATTC CGA ACAAAGGTA		
		AC__ __		
GAM1601	PCDHA2	3' ATGGAAACAAGCCACTTA	20912	GTAA TTA
		TAAG GCT TGTTTCCAT		
		ATTC CGA ACAAAGGTA		
		AC__ __		
GAM1601	PCDHA3	3' ATGGAAACAAGCCACTTA	20922	GTAA TTA
		TAAG GCT TGTTTCCAT		
		ATTC CGA ACAAAGGTA		
		AC__ __		
GAM1601	PCDHA4	3' ATGGAAACAAGCCACTTA	20932	GTAA TTA
		TAAG GCT TGTTTCCAT		
		ATTC CGA ACAAAGGTA		
		AC__ __		
GAM1601	PCDHA5	3' ATGGAAACAAGCCACTTA	20942	GTAA TTA
		TAAG GCT TGTTTCCAT		
		ATTC CGA ACAAAGGTA		
		AC__ __		
GAM1601	PCDHA6	3' ATGGAAACAAGCCACTTA	20952	GTAA TTA
		TAAG GCT TGTTTCCAT		
		ATTC CGA ACAAAGGTA		
		AC__ __		
GAM1601	PCDHA6	3' ATGGAAACAAGCCACTTA	25584	GTAA TTA
		TAAG GCT TGTTTCCAT		
		ATTC CGA ACAAAGGTA		
		AC__ __		
GAM1601	PCDHA7	3' ATGGAAACAAGCCACTTA	20962	GTAA TTA
		TAAG GCT TGTTTCCAT		
		ATTC CGA ACAAAGGTA		
		AC__ __		
GAM1601	PCDHA8	3' ATGGAAACAAGCCACTTA	20972	GTAA TTA
		TAAG GCT TGTTTCCAT		

			ATTC CGA ACAAAGGTA		
			AC__ __		
GAM1601	PCDHA9	3'	ATGGAAACAAGCCACTTA	25597	GTAA TTA
			TAAG GCT TGTTTCCAT		
			ATTC CGA ACAAAGGTA		
			AC__ __		
GAM1601	PCDHAC1	3'	ATGGAAACAAGCCACTTA	20841	GTAA TTA
			TAAG GCT TGTTTCCAT		
			ATTC CGA ACAAAGGTA		
			AC__ __		
GAM1601	PCDHAC2	3'	ATGGAAACAAGCCACTTA	20851	GTAA TTA
			TAAG GCT TGTTTCCAT		
			ATTC CGA ACAAAGGTA		
			AC__ __		
GAM1601	HIC	3'	GATGAAAACATAATGCCTTA	33492	AGCT C
			TAAGGTA TTATGTTT CATC		
			ATTCCGT AATACAAA GTAG		
			____ A		
GAM1601	KIAA0648	3'	GAAAATGAAGCTCACTT	40219	A G
			AGGT AGCTTTAT TTTC		
			TTCA TCGAAGTA AAAG		
			C _		
GAM1601	SH3BGRL2	3'	ATGGAAACTCTTACCT	25525	CTTTAT
			AGGTAAG GTTTCCAT		
			TCCATTC CAAAGGTA		
			T_____		
GAM1601	LOC51133	5'	GATGGAAACTTTTCTTACC	18204	CTTTAT
			GGTAAG GTTTCCATC		
			CCATTC CAAAGGTAG		
			TTTT__		
GAM1601	LOC91286	5'	GAAATATTATTACCTTA	32622	CTTT
			TAAGGTAAG ATGTTTC		
			ATTCCATTT TATAAAG		
			AT__		
GAM1602	DGUOK	3'	GTAACCAAACAAGAAGACCTCA	28137	A GG C
			TGAGGT CTTCTTGT GG TTAC		
			ACTCCA GAAGAACA CC AATG		
			_ AA _		
GAM1602	DGUOK	3'	GTAACCAAACAAGAAGACCTCA	28140	A GG C
			TGAGGT CTTCTTGT GG TTAC		

			ACTCCA GAAGAACA CC AATG		
			— AA —		
GAM1602	CL683	3'	AATCCAAACAATACCTCA 17924	CTTC	GG C
			TGAGGTA TTGT GG TT		
			ACTCCAT AACA CC AA		
			— AA T		
GAM1602	FLJ12505	5'	AAGCCCCAGCAGCCCCA 24091	A	ACTTCT _
			TG GGT TG TGGGGCTT		
			AC CCG AC ACCCCGAA		
			C — G		
GAM1602	LOC147639	5'	AAGCTACAAGAAGTCCCCA 38343	A T	GG
			TG GG ACTTCTTGT GGCTT		
			AC CC TGAAGAACA TCGAA		
			_ C _		
GAM1602	LOC203286	5'	CCCCACAAGAAGCACCTC 43495	A	
			GAGGT CTTCTTGTGGGG		
			CTCCA GAAGAACACCCC		
			C		
GAM1602	LOC221773	3'	TAAACTTAAAAAGAAACCTCA 43766	AC	GTG C
			TGAGGT TTCTT GGG TTA		
			ACTCCA AAGAA TTC AAT		
			A_ AAA A		
GAM1603	MAP1B	3'	TGCGTGTTGAATCCCA 12536	T A	
			TGGGATTCAAC AC GCA		
			ACCCTAAGTTG TG CGT		
			— —		
GAM1603	MAP1B	3'	TGCGTGTTGAATCCCA 25713	T A	
			TGGGATTCAAC AC GCA		
			ACCCTAAGTTG TG CGT		
			— —		
GAM1603	MFAP3	3'	AAAGCACTGAAC TAAGAGTCCC 12553	AACTA_	CA
	A		TGGGATTC CAG CTTT		
			ACCCTGAG GTC GAAA		
			AATCAA AC		
GAM1603	C22orf5	3'	AAAGTGCTGCTGATTCCCA 14582	T	ACTA
			TGGGA TCA CAGCACTTT		
			ACCCT AGT GTCGTGAAA		
			T C_		
GAM1603	CHL1	3'	AAAGTGCTAATAATAATCTCA 13389	CAACTAC	
			TGGGATT AGCACTTT		

		ACTCTAA	TCGTGAAA		
		TAATAA_			
GAM1603	KIAA1910	3'	AAAGTGCTGCATGGCTCGCA	36283	G TT ACTA
			TG GA CA CAGCACTTT		
			AC CT GT GTCGTGAAA		
			G CG AC_		
GAM1603	PCANAP7	5'	AAAGTGCTGTACAAATTCCA	44836	CAAC
			TGGGATT TACAGCACTTT		
			ACCTTAA ATGTCGTGAAA		
			AC_		
GAM1603	PFDN1	3'	TGTTACAGCTGAATCTCA	8485	A AC_
			TGGGATTCA CT AGCA		
			ACTCTAAGT GA TTGT		
			C CAC		
GAM1603	LOC148709	3'	AAAGTGCTGCAGTAAACCA	38577	GATTCA A
			TGG ACT CAGCACTTT		
			ACC TGA GTCGTGAAA		
			AAA_ C		
GAM1603	LOC257319	3'	AAAGTGCAACAGGCAATTGAAT	45827	____ ACA
	CC		GGATTCAA CT GCACTTT		
			CCTAAGTT GA CGTGAAA		
			AACG CAA		
GAM1604	HMGA2	5'	TTCAAGGGACACAATTCA	9573	C GCC
			TGAATTG GT TCCTTGAG		
			ACTTAAC CA GGGAAGTT		
			A _		
GAM1604	C20orf110	3'	GACTCAAGGAGACAACCACCTC	38838	AT CG C
	A		TGA TG TG CTCCTTGAGTC		
			ACT AC AC GAGGAACTCAG		
			CC CA A		
GAM1604	FLJ14621	3'	AAGAAGGCAGCAATTCA	26577	G C
			TGAATTGC TGCCT CTT		
			ACTTAACG ACGGA GAA		
			_ A		
GAM1604	MRPS27	3'	ACTCAAGGCCATGAACTCA	17472	A G CCT
			TGA TT CGTG CCTTGAGT		
			ACT AA GTAC GGAACTCA		
			C _ C_		
GAM1604	LOC152766	5'	GACTCAAGGAAACGGAATT	41553	G GCC
			AATT CGT TCCTTGAGTC		

TTAA GCA AGGAACTCAG
 G A__
 GAM1604 LOC257206 3' ACTCAAGGAGGCTGGGTTTC 46385 TTG T
 GAA CG GCCTCCTTGAGT
 ||| || |||||
 CTT GT CGGAGGAACTCA
 TGG _
 GAM1605 SCG3 3' TCATTTCCACCAGCAGTTCCCT 14903 T AGAAC
 TA TAAG GGATTG GGAAATGA
 |||| ||||| |||||
 ATTG CTTGAC CCTTTACT
 C GACCA
 GAM1605 SLC21A2 3' TCATTTCCAAACATCTCACTC 12159 T AC__
 GA TGAGA GGAAATGA
 || ||||| |||||
 CT ACTCT CCTTTACT
 C ACAA
 GAM1605 CYLD 3' TCTACTCTCAATCCAGTTA 17577 G AC
 TAA TGGATTGAGA GGA
 ||| ||||| |||
 ATT ACCTAACTCT TCT
 G CA
 GAM1605 DKFZp434G179 3' TCATTTCCATTCCCATAAACT 39042 GGAT A C
 T AAGT TG GAA GGAAATGA
 |||| || ||| |||||
 TTCA AC CTT CCTTTACT
 AAAT C A
 GAM1605 FLJ21168 3' TCATTCCCGTCCCAGTTTACT 24673 A A A
 AGTGGATTG GA CGG AATGA
 ||||| || ||| |||||
 TCATTGAC CT GCC TTACT
 C _ C
 GAM1605 MGC9753 5' TCACTTCCGCTCCCGC 27244 ATT AA A
 GTGG GAG CGGAA TGA
 |||| ||| ||||| |||
 CGCC CTC GCCTT ACT
 _ _ C
 GAM1605 PDZD2 3' TCATTTCCATCTTCCAC 39395 ATT AC
 GTGG GAGA GGAAATGA
 |||| ||||| |||||
 CACC TTCT CCTTTACT
 C__ A_
 GAM1605 SLC17A6 3' TCATTTCCATTCAAGTCATCCA 21597 T __ C
 TGGAT GA GAA GGAAATGA
 ||||| || ||| |||||
 ACCTA CT CTT CCTTTACT
 _ GAA A
 GAM1605 ZNF262 3' TCATCTCCATTCTCAGTTTCTT 11557 T C A
 AAG GGATTGAGAA GGA ATGA
 ||| ||||| ||| |||||

		TTC TTTGACTCTT CCT TACT		
		— A C		
GAM1605	LOC115129 3'	TCACCTCCGTTTGGACCA 36253	A G	AA
		TGG TT AGAACGGA TGA		
		ACC AG TTTTGCCT ACT		
		— — CC		
GAM1605	LOC149478 3'	TCATTTCCGTGGACACCCAC 38756	AT AGA	
		GTGG TG ACGGAAATGA		
		CACC AC TGCCTTTACT		
		C_ AGG		
GAM1605	LOC158318 5'	TCATTCTAGGCAATCCAC 41958	AGAAC	A
		GTGGATTG GGAA TGA		
		CACCTAAC TCTT ACT		
		GGA_ _		
GAM1605	LOC90784 5'	CACTTCCGTCCAAAGTCCACTT 32003	GAGA	A
	A	TAAGTGGATT ACGGAA TG		
		ATTCACCTGA TGCCTT AC		
		AACC C		
GAM1605	LOC92492 5'	TCACTTCCACTCATAATCCAC 34455	A AC	A
		GTGGATTG GA GGAA TGA		
		CACCTAAT CT CCTT ACT		
		A CA C		
GAM1606	ATP11B 3'	TGTCAGTAAATGTAGTA 39149	CACC	
		TACTACATTTGC GCA		
		ATGATGTAAATG TGT		
		AC_		
GAM1606	PTP4A2 5'	GTGCCTAAATGTAGTA 27831	CCACC	
		TACTACATTTG GCAC		
		ATGATGTAAAT CGTG		
		C_		
GAM1606	PTP4A2 5'	GTGCCTAAATGTAGTA 9554	CCACC	
		TACTACATTTG GCAC		
		ATGATGTAAAT CGTG		
		C_		
GAM1606	SRGAP1 5'	GCCAAATGGCAAATGTGTA 35757	T	CC_
		TAC ACATTTGCCA GC		
		ATG TGTAACGGT CG		
		— AAAC		
GAM1606	DNAM-1 3'	GCCTTAGGAGCAAATGTAGTA 13340	CA	_____
		TACTACATTTGC CC GC		

		ATGATGTAAACG GG CG		
		A_ ATTC		
GAM1606	KIAA0426	3' TGCAGTAAGTGTAGTA 16313		CACC
		TACTACATTTGC GCA		
		ATGATGTGAATG CGT		
		A__		
GAM1606	KIAA1025	3' GTGCGGTGGTGTGTGTAG 31996	T	
		CTACAT TGCCACCGCAC		
		GATGTG GTGGTGGCGTG		
		T		
GAM1606	KIAA1078	3' GTTGTGACAAATGTGTA 32471	T	C C
		TAC ACATTTG CAC GC		
		ATG TGTAAAC GTG TG		
		_ A T		
GAM1606	LOC147353	3' GCTATGTGCAAATGTAGTA 40836		_ CC
		TACTACATTTGC CA GC		
		ATGATGTAAACG GT CG		
		T AT		
GAM1606	LOC91179	5' GGTGCGAGACCAAGTGTAG 32493		CCAC
		CTACATTTG CGCACC		
		GATGTGAAC GCGTGG		
		CAGA		
GAM1607	DKFZp761G0313	3' GCCCAAACCCACATTCCA 32740		TGA TA
		TGGAATGTG TTTG GC		
		ACCTTACAC AAAC CG		
		CC_ C_		
GAM1607	HML2	5' ACGTGGAATCACACCCTCCA 13040	AT	GTA
		TGGA GTGTGATTT GCGT		
		ACCT CACACTAAG TGCA		
		CC GG_		
GAM1607	LOC139248	5' GACGGTACCACCATCCCA 37336	A T	ATTT G
		TGG ATG GTG GTA CGTC		
		ACC TAC CAC CAT GCAG		
		C _ _ _ G		
GAM1607	LOC196746	3' TGCAAATCAACATTCCA 42290		G
		TGGAATGT TGATTTGTA		
		ACCTTACA ACTAAACGT		
		-		
GAM1608	LFG	3' CACGCATCACAGCCATTTGA 37689		CCA AC
		TTAGAT GCT GATGCGTG		

		AGTTTA CGA CTACGCAC	
		C__ CA	
GAM1608	MLLT4	5' GCGCGCTGCTGGATCTAA 35888	TACGAT
		TTAGATCCAGC GCGTGC	
		AATCTAGGTCG CGCGCG	
		T_____	
GAM1608	VANGL2	3' TACAGTTTGCAGTGGATCTA 35484	G A TGC
		TAGATCCA CT CGA GTG	
		ATCTAGGT GA GTT CAT	
		_ C TGA	
GAM1608	NY-REN-25	3' TGCACGCATCGAAGGATCTGA 30420	AGCTA
		TTAGATCC CGATGCGTGCA	
		AGTCTAGG GCTACGCACGT	
		AA_____	
GAM1608	LOC219333	3' ATGCAGCTGGATCTAA 44933	ACGAT
		TTAGATCCAGCT GCGT	
		AATCTAGGTCGA CGTA	

GAM1609	MYCBP	3' ACAGCCATCTAACTCATT 14722	CT TAA
		TAATGGGT GGTGG CTGT	
		ATTACTCA CTACC GACA	
		AT _____	
GAM1609	PPT2	3' ATACAGAAACCGGACCCA 29060	GGTAA
		TGGGTCTGGT CTGTAT	
		ACCCAGGCCA GACATA	
		AA_____	
GAM1609	PTPRA	5' ACAGTTACCACCCTCATT 8713	TCT
		AATGGG GGTGGTAACTGT	
		TTACTC CCACCATTGACA	

GAM1609	FLJ12681	3' ACAGCGCACACCCAGACCC 23034	_ _ AA
		GGGTCTGG TG GT CTGT	
		CCCAGACC AC CG GACA	
		C A C_	
GAM1609	KIAA0284	3' ACAGTTGCCAAACCCATTG 31615	CTGG
		TAATGGGT TGGTAACTGT	
		GTTACCCA ACCGTTGACA	
		A_____	
GAM1609	LOC222161	5' TACAGTTAGCAGACCC 44581	GTGG
		GGGTCTG TAACTGTA	

		CCCAGAC ATTGACAT	
		G__	
GAM1610 CYP1A2	3'	ACCCAGAGCTGTGGGAGGACCC 34254	A AT TG
C		GGG TCCTC G GCTCTGGGT	
		CCC AGGAG T CGAGACCCA	
		C GG GT	
GAM1610 PVR	3'	ACCCAGAGTGGCCCAAGACTCC 13252	TC CAT G
C		GGGA CT GT GCTCTGGGT	
		CCCT GA CG TGAGACCCA	
		CA ACC G	
GAM1610 TNFRSF8	3'	ACCCAGAGCCTAGGGGATCC 6909	ATGT
		GGATCCTC GGCTCTGGGT	
		CCTAGGGG CCGAGACCCA	
		AT__	
GAM1610 HABP4	3'	ACCCAGAGCCACACACGCCCG 34924	ATCCTCA
		CGGG TGTGGCTCTGGGT	
		GCCC ACACCGAGACCCA	
		GCAC__	
GAM1610 KIAA1280	5'	CCCAGATTGAGGATCC 34549	TGTGGC
		GGATCCTCA TCTGGG	
		CCTAGGAGT AGACCC	
		T__	
GAM1610 KLHL6	3'	ACCCAGAGACAAAGAACCC 28208	A CTCATG G
		GGG TC TG CTCTGGGT	
		CCC AG AC GAGACCCA	
		A AA__ A	
GAM1610 OS4	5'	CCCAAAGTGGAGAGCCCG 12286	A T GGCTC
		CGGG TCCTCA GT TGGG	
		GCCC AGGAGT CA ACCC	
		G _ A__	
GAM1610 PME-1	3'	ACCCAGAGAGGCCAAGATCCC 18230	CTCAT GG
		GGGATC GT CTCTGGGT	
		CCCTAG CG GAGACCCA	
		AAC__ GA	
GAM1610 SARM	3'	ACCCAGAGGGTAAGGATTCC 17451	C GTGG
		GGGATCCT AT CTCTGGGT	
		CCTTAGGA TG GAGACCCA	
		A G__	
GAM1610 LOC124930	3'	ACCCAGAGAAGCACAGACCCCG 36765	A CTCA GG
		CGGG TC TGT CTCTGGGT	

GCCC AG ACG GAGACCCA
 C AC__ AA
 GAM1610 LOC149276 3' ACCCAGGATGAGCAAAAGGATC 40974 CA GGC_
 CC GGGATCCT TGT TCTGGGT
 ||||| || |||||
 CCCTAGGA ACG GGACCCA
 AA AGTA
 GAM1610 LOC157848 3' ACCCAGAGAGAAAAAGCATCCC 39671 C CATGTGG
 GGGAT CT CTCTGGGT
 |||| || |||||
 CCCTA GA GAGACCCA
 C AAAAGA_
 GAM1610 LOC158292 5' ACCCAGAGGAGGAGAGAACCCG 41930 A _ ATGTGG
 CGGG TC CTC CTCTGGGT
 ||| || || |||||
 GCCC AG GAG GAGACCCA
 A A GAG__
 GAM1610 LOC253893 3' ACCCAGAGAGAAAAAGCATCCC 45970 C CATGTGG
 GGGAT CT CTCTGGGT
 |||| || |||||
 CCCTA GA GAGACCCA
 C AAAAGA_
 GAM1611 LIFR 3' CTAGCAGCGTTAGTTC 8102 C GC
 GA ACTGACGC GCTAG
 || ||||| ||||
 CT TGATTGCG CGATC
 _ A_
 GAM1611 BTBD3 3' CTAACGCTCACTGTGCTGCCCC 17338 AGA C__ C
 ATGT ACAT CACTGACG GCG TAG
 ||| ||||| ||| |||
 TGTA GTGACTGT CGC ATC
 CCC CACT A
 GAM1611 LOC149351 3' AGGCCATGTCTATGTA 38716 C ACGC G
 TACATAGACA TG GC CT
 ||||| || |||
 ATGTATCTGT AC CG GA
 _ _ _
 GAM1612 KIAA1679 3' CAGTTGTAATTCAGTTTAATGA 34750 A C
 TCATTGAACTGAAT ATA CTG
 ||||| ||| |||
 AGTAATTTGACTTA TGT GAC
 A T
 GAM1613 CRLF1 5' CACCGCCGCCGAGCCGC 11139 AACC _
 GCG GC CGGCGGCGGTG
 || || |||||
 CGC CG GCCGCCGCCAC
 _ A
 GAM1613 ENO2 5' CCACCGCCACCGCCACCGCCA 7705 A AACC C C
 TG GCG GC GG GGCGGTGG
 || || || |||||

AC CGC CG CC CCGCCACC
 _ CAC_ _ A
 GAM1613 KCNS2 5' CCACCGCCGCGATGCTCGCCCG 33900 A ACC CG_
 TG GCGA GC GCGGCGGTGG
 || ||| || |||||
 GC CGCT CG CGCCGCCACC
 C _ TAG
 GAM1613 MMP14 3' CCACCGCCGCGCCGCCCA 11435 A AACC C
 TG GCG GCCGGCGG GG
 || ||| ||||| ||
 AC CGC CGGCCGCC CC
 C C_ A
 GAM1613 FLJ14753 3' CCACCGCCATCATTCTGCTCA 26285 _ CCGCC GC
 TGAGC GAA G GCGGTGG
 ||||| ||| | |||||
 ACTCG CTT C CCGCCACC
 T A_ TA
 GAM1613 KIAA0229 3' CACCACCGCCATCGCCTCA 44397 _ ACCGCC C
 TGAG CGA GGCGG GGTG
 ||||| ||| ||||| |||||
 ACTC GCT CCGCC CCAC
 C A_ A
 GAM1613 KIAA0537 5' CCACCGCCGCCACCTCGCCCG 16865 A ACCGCC
 TG GCGA GGCGGCGGTGG
 || ||| |||||
 GC CGCT CCGCCGCCACC
 C CCA_
 GAM1613 MGC20235 5' CCACACCGCCCGAGCTCAGCTC 29664 GAACC C_ C
 A TGAG GC GGCGG GGTGG
 ||||| || ||||| |||||
 ACTCG CG CCGCC CCACC
 ACT_ AC A
 GAM1613 SEMA4G 5' CCACCGCCACCGGCTGAGCT 45410 GAACC C
 AGC GCCGG GCGGTGG
 ||| ||||| |||||
 TCG CGGCC CCGCCACC
 AGT_ A
 GAM1613 VIAAT 5' CCACCGCCGCCGCCGCCGCTC 27884 AAC C
 GAGCG CG CGGCGGCGGTGG
 ||||| || |||||
 CTCGC GC GCCGCCGCCACC
 C_ C
 GAM1613 LOC145989 5' CCACCGCCACCATGACCGCCA 29948 A AAC CC C
 TG GCG CG GG GCGGTGG
 || ||| || || |||||
 AC CGC GT CC CCGCCACC
 _ CA_ A_ A
 GAM1613 LOC148946 5' CCACACCGCCTCCGCTC 40938 AACCGCC C
 GAGCG GGCGG GGTGG
 ||||| ||||| |||||

CTCGC CCGCC CCACC
 CT_____ A
 GAM1613 LOC151127 5' CCACCGCCGCGCTGCTACCGC 39060 A AACC ____
 CA TG GCG GC CGGCGGCGGTGG
 || ||| || |||||
 AC CGC CG GCCGCCGCCACC
 _ CAT_ TC
 GAM1613 LOC201175 5' CCACCGCCGCTCCGCCCA 42533 A AACC C
 TG GCG GCCGGCGG GG
 || ||| ||||| ||
 AC CGC CGGCCGCC CC
 C CT_ A
 GAM1613 LOC220558 5' CCACCGCCGCCGACAGCG 43804 ____
 CGC CGGCGGCGGTGG
 ||| |||||
 GCG GCCGCCGCCACC
 ACA
 GAM1613 LOC221250 5' CCACCGCCGCCGCCGCCCA 44118 A AAC C
 TG GCG CG CGGCGGCGGTGG
 || ||| |||||
 AC CGC GC GCCGCCGCCACC
 _ C_ C
 GAM1613 LOC221250 5' CCACCGCCGGCGGCGGCAGC 44119 GAA G
 GC CCGCCG CGGCGGTGG
 || ||||| |||||
 CG GGCGGC GCCGCCACC
 AC_ G
 GAM1613 LOC91272 5' CCACCGCCCTGCCGCCA 32611 A AACC C C
 TG GCG GC GG GGCGGTGG
 || ||| || |||||
 AC CGC CG CC CCGCCACC
 _ ____ T _
 GAM1614 ATP8B2 5' CTCAAACCGGGATCATGACG 32514 ____ TCAA
 CGTCATGA CCG TGAG
 ||||| ||| |||
 GCAGTACT GGC ACTC
 AG CAA_
 GAM1614 PRV1 3' CTCATTGTTATGATG 36398 CGTC
 CGTCATGAC AATGAG
 ||||| |||||
 GTAGTATTG TTA CTC

 GAM1614 C1QTNF6 3' CGCCCATGGTGCTCATGC 25657 T C GT A
 G CATGA C CAATG GCG
 | |||| | ||||| |||
 C GTACT G GTTAC CGC
 _ C TG C
 GAM1614 FLJ10726 3' CTCATTGGTTATGAGG 20057 G TCA
 C TCATGACCG ATGAG
 | ||||| |||||

G AGTATTGGT TACTC
 G ____
 GAM1614 LOC145854 3' CTCTTTGATCATGGCG 38007 CCG T
 CGTCATGA TCAA GAG
 ||||| ||| |||
 GCGGTACT AGTT CTC
 ____ T
 GAM1614 LOC157273 3' CTCATTGAGTCATCCAAC 41783 C__ CG
 GT ATGAC TCAATGAG
 || |||| |||||
 CA TACTG AGTTACTC
 ACC ____
 GAM1615 BMP6 5' CGCCCCGACGACCATGAGA 7453 _ G_ TA
 TCTCATGG CG TG GCG
 ||||| || || |||
 AGAGTACC GC GC CGC
 A AG CC
 GAM1615 CSDA 5' CGCCGCCTGCGCCGCGAGA 9727 ATG _
 TCTC GCGGTGTAG CGGCG
 ||| ||||| |||||
 AGAG CGCCGCGTC GCCGC
 ____ C
 GAM1615 EN1 3' CGCCGCTACAAGCCAAAGA 7141 CA GG
 TCT TGGC TGTAGCGGCG
 ||| |||| |||||
 AGA ACCG ACATCGCCGC
 A_ A_
 GAM1615 FOXE1 5' CGCCGCTGCCCGCCTCGAGA 10781 AT T
 TCTC GGCGG GTAGCGGCG
 ||| |||| |||||
 AGAG CCGCC CGTCGCCGC
 CT _
 GAM1615 RFX2 5' CGCCGCCGCCATAGA 6271 C TA
 TCT ATGGCGGTG GCG
 ||| ||||| |||
 AGA TACCGCCGC CGC
 _ _
 GAM1615 RORB 3' CCGCTACAGTTTGAAGA 13786 _ T GG
 TCT CA GGC TGTAGCGG
 ||| || |||||
 AGA GT TTG ACATCGCC
 A _ _
 GAM1615 SCN1A 3' CCCTCCACCGCCAGAAGA 42833 CA T C
 TCT TGGCGGTG AG GG
 ||| ||||| || |||
 AGA ACCGCCAC TC CC
 AG C _
 GAM1615 CCNI 5' CCGCCTCCGCGCGCCTATGAGA 13713 _ _ TA_
 TCTCAT GGCG GTG GCGG
 ||||| |||| ||| ||||

	AGAGTA CCGC CGC CGCC		
	T G CTC		
GAM1615 FLJ10099 5'	CGCCACGCGCCGCCACGAG 19725	A	AGC
	CTC TGGCGGTGT GGCG		
	GAG ACCGCCGCG CCGC		
	C CA_		
GAM1615 FLJ10350 5'	CGCCGCTGAGACCCCGAGA 45730	AT C G_	
	TCTC GG GGT TAGCGGCG		
	AGAG CC CCA GTCGCCGC		
	__ _ GA		
GAM1615 FLJ10846 5'	CGCCAATAGCACCTGAGA 20198	TG C AGC_	
	TCTCA G GGTGT GGCG		
	AGAGT C CCACG CCGC		
	__ _ ATAA		
GAM1615 KIAA1655 5'	CCAGTTGCTCACCATGAGA 33086	C T _	
	TCTCATGG GG GTAGC GG		
	AGAGTACC CT CGTTG CC		
	A _ A		
GAM1615 MAGE-E1 3'	CGAGCCCGCCATGAGA 25105	T AG	
	TCTCATGGCGG GT CG		
	AGAGTACCGCC CG GC		
	_ A_		
GAM1615 MGC15631 3'	CCGTGTGCTCGCCATGTGA 26492	T T _	
	TC CATGGCGG GTA GCGG		
	AG GTACCGCT CGT TGCC		
	T _ G		
GAM1615 LOC143920 3'	CTGGGTACCGCCAGAAGA 37640	CA AG	
	TCT TGGCGGTGT CGG		
	AGA ACCGCCATG GTC		
	AG G_		
GAM1615 LOC164397 5'	CGCCTGGTCCCTCCATGAGA 40151	C TG AGC	
	TCTCATGG GG T GGCG		
	AGAGTACC CC G CCGC		
	T CT GT_		
GAM1615 LOC220549 5'	CGCCGCTATCGCACGGGA 44650	ATG GT	
	TCTC GCG GTAGCGGCG		
	AGGG CGC TATCGCCGC		
	CA_ _		
GAM1615 LOC220558 5'	CGCCGCCTGCGCCGCGAGA 43805	ATG _	
	TCTC GCGGTGTAG CGGCG		

			AGAG CGCCGCGTC GCCGC		
			_____ C		
GAM1616 AKAP2	3'	ACATATATATACACACAC	14057	A	_____
		GT TGTGTATATATG GT			
		CA ACACATATATAT CA			
		C A			
GAM1616 GHR	3'	CTATAACCAGACACATACT	5672	ATATA	
		AGTATGTGT TGGTTATAG			
		TCATACACA ACCAATATC			
		G_____			
GAM1616 ICOS	3'	CTATGCATACATATATACACAC	14387	A	GT_____
AT		GT TGTGTATATATG TATAG			
		TA ACACATATATAC GTATC			
		C ATAC			
GAM1616 TJP1	3'	CCATATTACCACAGACATACTA	9263	_____ T	
		TAGTATGT GTA ATATGG			
		ATCATACA CAT TATACC			
		GACAC _			
GAM1616 ARHGAP5	3'	CTATTTCTTTTACACACATAC	37818	A TAT TT	
		GTATGTGT TA GG ATAG			
		CATACACA AT TC TATC			
		C TT_ TT			
GAM1616 FLJ12960	3'	CTATAAGGAATACACATAC	23915	A_____	
		GTATGTGTAT TATGG			
		CATACACATA ATATC			
		AGGA			
GAM1616 KIAA1762	3'	CCATAAATGCATACACATAC	31909	A_____	
		GTATGTGTAT TATGG			
		CATACACATA ATACC			
		CGTAA			
GAM1616 MGC15482	3'	ACACATACATACACATAC	26695	A _	
		GTATGTGTAT TATG GT			
		CATACACATA ATAC CA			
		C A			
GAM1616 LOC124045	3'	CTATGTAGTATATACACACAT	37440	A	GGT
		GT TGTGTATATAT TATAG			
		TA ACACATATATG GTATC			
		C AT_			
GAM1616 LOC143465	5'	CTATGTATGTATATACACACAT	40362	A	GT
		GT TGTGTATATATG TATAG			

TA ACACATATATGT GTATC
 C AT
 GAM1616 LOC203378 5' CCATAATATACACACTCTA 43550 TA _
 TAG TGTGTATAT ATGG
 ||| ||||| |||
 ATC ACACATATA TACC
 TC A
 GAM1617 LOC257463 5' CATCGAGACATTAAATCTCAGA 35208 GA CGG TAC
 TC AGA TA GTCTCGATG
 || ||| || |||||
 AG TCT AT CAGAGCTAC
 AC AA_ TA_
 GAM1618 C1orf16 3' CGCTCATTGCTCTTCAGA 16855 G A CGTTC
 TC GAA AGC GATGAGCG
 || ||| || |||||
 AG CTT TCG TTA CTGCG
 A C _
 GAM1618 C5orf4 3' GCGCTCATCACCTCTTCC 26182 A CC TC
 GGAA AG GT GATGAGCGC
 ||| || || |||||
 CCTT TC CA CTACTCGCG
 C _ _
 GAM1618 DKFZP586J0619 3' CATGAAACGGCTTTCCCGG 39580 A CG
 TCGG AAAGCCGTT ATG
 ||| ||||| |||
 GGCC TTTCGGCAA TAC
 C AG
 GAM1618 LOC161244 5' GCGCTCACTGGACACCCTCC 42107 AAAGCC A
 GGA GTTCG TGAGCGC
 || |||| |||||
 CCT CAGGT ACTCGCG
 CCCA_ C
 GAM1618 LOC255718 5' CGCCCAACGGCTTTTC 46580 TCGA A
 GAAAAGCCGT TG GCG
 ||||| |||
 CTTTTCGGCA AC CGC
 _ C
 GAM1619 SNAI1 3' CCCACAAGGAACCCTCAGGCC 12607 A C_ C A
 GG CT GGGTTCCT GT GG
 || || ||||| || ||
 CC GA CCCAAGGA CA CC
 G CT A C
 GAM1619 PIPPIN 3' CACGAGGAGGGCCCCCA 38909 A A GGGT A
 TG GGG CTC TCCTCGT G
 || ||| || ||||| |
 AC CCC GGG AGGAGCA C
 C _ _ C
 GAM1619 VDAC3 3' CCCACGACCTTGCCCCGAGCCC 12203 A CC_ A
 CTC GAGGG CTCGGGT TCGT GG
 |||| ||||| ||| ||

CTCCC GAGCCCGG AGCA CC
C TTCC C
GAM1619 LOC255452 3' CCCACGAGCCCCAAGCCCCT 46572 A C TTC A
AGGG CT GGG CTCGT GG
|||| ||| ||||| ||
TCCC GA CCC GAGCA CC
C A C__ C
GAM1620 IARS 5' TCAAAGACGAGGGTCACGCACG 15080 A _ GAG
CGTGC TG CC TTCGTCTTTGA
|||| ||| ||||| |||||
GCACG AC GG GAGCAGAAACT
C T ____
GAM1620 KIAA0795 5' CAAAGACGCCTGCTGCAC 24583 T CG TT
GTGCA GC AG CGTCTTTG
|||| ||| ||||| |||||
CACGT CG TC GCAGAAAC
_ _ C_
GAM1620 LOC145693 5' CAAAGCTGCAGCATGCAC 37922 CGA TC T
GTGCATGC GT G CTTTG
||||| || |||||
CACGTACG CG C GAAAC
A__ T__
GAM1620 LOC254431 3' TCAAAAACGCTGACATGCA 46293 C G TT C
TGCATG C AG CGT TTTGA
||||| || |||||
ACGTAC G TC GCA AACT
A _ _ A
GAM1620 LOC90591 3' TCAAAGACATAAAAGGATGCAC 31760 G GAGTTC
GTGCAT CC GTCTTTGA
||||| || |||||
CACGTA GG CAGAAACT
_ AAAATA
GAM1621 CIT 3' CCCACCCCCCAGCGTCATCTC 34563 CA AAGCA
GAGATGGC TTGGG GG
||||| ||||| ||
CTCTACTG GACCC CC
C_ CCCAC
GAM1621 CRAT 3' CCTGCTTCCCAAACCTCCCA 10152 CCA_
TGG TTGGGAAGCAGG
||| ||||| |||||
ACC AACCCCTTCGTCC
CTCA
GAM1621 CRAT 3' CCTGCTTCCCAAACCTCCCA 6407 CCA_
TGG TTGGGAAGCAGG
||| ||||| |||||
ACC AACCCCTTCGTCC
CTCA
GAM1621 DDX3 5' TCCTGCTTCACAAAATGGCCAC 7038 AGA GG_
CGCA TG TGGCCATT GAAGCAGGA
|| ||||| |||||

		AC ACCGGTAA CTTCGTCCT	
		GCC AACA	
GAM1621 DDX3	5'	TCCTGCTTCACAAAATGGCCAC 23434	AGA GG__
		CGCA TG TGGCCATT GAAGCAGGA	
		AC ACCGGTAA CTTCGTCCT	
		GCC AACA	
GAM1621 DRPLA	5'	CCTGCTTCCCAGACCA 7649	CCA
		TGG TTGGGAAGCAGG	
		ACC GACCCTTCGTCC	
		A__	
GAM1621 DVL3	3'	CCTGCTTCAGCAGCCCCTCA 10697	AT CAT G_
		TGAG GGC TG GAAGCAGG	
		ACTC CCG AC CTTCGTCC	
		C_ __ GA	
GAM1621 EIF4G1	5'	TCCTGCTTCCCACTCATCTTA 11397	CCAT
		TGAGATGG TGGGAAGCAGGA	
		ATTCTACT ACCCTTCGTCCT	
		C__	
GAM1621 EPHA2	3'	TCCCACATGAGGCCATCTCA 10716	AT__
		TGAGATGGCC TGGGA	
		ACTCTACCGG ACCCT	
		AGTAC	
GAM1621 IGFBP5	5'	TCCCACCCCCAACGCCATCTC 6202	CA AAGCA
		GAGATGGC TTGGG GGA	
		CTCTACCG AACCC CCT	
		C_ CCAC_	
GAM1621 NGFR	3'	CCTGCCCGTCACCATCTCA 8332	CCAT AA
		TGAGATGG TGGG GCAGG	
		ACTCTACC GCCC CGTCC	
		ACT_ __	
GAM1621 PAK1	5'	TCCTGCCTCAGAGGCCATCT 8435	A AA
		AGATGGCC TTGGG GCAGGA	
		TCTACCGG GACTC CGTCCT	
		A __	
GAM1621 PTPRO	5'	CCTACGTTCATAGCCGTCTCA 25010	CAT AAGC
		TGAGATGGC TGGG AGG	
		ACTCTGCCG ACTT TCC	
		AT_ GCA_	
GAM1621 PTPRO	5'	CCTACGTTCATAGCCGTCTCA 25019	CAT AAGC
		TGAGATGGC TGGG AGG	

		ACTCTGCCG ACTT TCC	
		AT_ GCA_	
GAM1621	PTPRO	5' CCTACGTTTCATAGCCGTCTCA 25029	CAT AAGC
		TGAGATGGC TGGG AGG	
		ACTCTGCCG ACTT TCC	
		AT_ GCA_	
GAM1621	RAB1A	5' TCCCGGAACAGCCTATCTCA 34790	_ CA__
		TGAGAT GGC TTGGGA	
		ACTCTA CCG GGCCCT	
		T ACAA	
GAM1621	SMARCD1	3' CCTGCTTCCCCACCCCCTCCTC 29144	AT CCATT
	A	TGAG GG GGGAAAGCAGG	
		ACTC CC CCCTTCGTCC	
		CT CCCAC	
GAM1621	SMARCD1	3' CCTGCTTCCCCACCCCCTCCTC 9046	AT CCATT
	A	TGAG GG GGGAAAGCAGG	
		ACTC CC CCCTTCGTCC	
		CT CCCAC	
GAM1621	SYNGR3	3' CCTGCTTCCTGGCCCAGTCCCA 10407	A _ TTG
		TG GAT GGCCA GGAAGCAGG	
		AC CTG CCGGT CCTTCGTCC	
		C AC _	
GAM1621	C11orf9	3' CCTACTTCCCAGTTAACTC 14944	A CAT C
		GAG TGGC TGGGAAG AGG	
		CTC ATTG ACCCTTC TCC	
		A _ A	
GAM1621	CENTG1	3' CCTACCCCTTCCATGCTCATCT 16566	GC TG C__
	CA	TGAGATG CAT GGAAG AGG	
		ACTCTAC GTA CCTTC TCC	
		TC _ CCCA	
GAM1621	CLDN6	3' CCTGCCCCCTCGTCTCA 22170	CCATT AA
		TGAGATGG GGG GCAGG	
		ACTCTGCT CCC CGTCC	
		_ CC	
GAM1621	DGKZ	3' CCCGCTCCCCTGTCAATTCA 9719	CATT A A
		TGAGATGGC GGG AGC GG	
		ACTTTACTG CCC TCG CC	
		T_ C C	
GAM1621	DKFZP586P0123	5' CCTCAGACTCAAACGGCCATCT 45464	A_ AAGC
	CA	TGAGATGGCC TTGGG AGG	

ACTCTACCGG AACTC TCC
 CA AGAC
 GAM1621 EPB41L1 3' TCCCGCCTCCCCTCACCTCA 34944 AT CCATT A A
 TGAG GG GGA GC GGA
 ||| || ||| |||
 ACTC CC CCCT CG CCT
 _ ACTC_ C C
 GAM1621 FLJ13102 3' CCTGCCCTCACCATCTCA 24343 CCAT AA
 TGAGATGG TGGG GCAGG
 ||||| ||| |||||
 ACTCTACC ACTC CGTCC
 _ C_
 GAM1621 FLJ13840 5' TCCTGAGGAACGACTATCTCA 24081 CCA GGAAG
 TGAGATGG TTG CAGGA
 ||||| || |||||
 ACTCTATC AGC GTCCT
 _ AAGGA
 GAM1621 FLJ23040 3' CCTGCCTTGGGCCTCCCA 24808 A T ATT GAA
 TG GA GGCC GG GCAGG
 || |||| || |||||
 AC CT CCGG TC CGTCC
 C _ GT_ _
 GAM1621 GMPPB 5' CCTGCTTCCCAAACCCCA 45813 CCA
 TGG TTGGGAAGCAGG
 || |||||
 ACC AACCTTCGTCC
 CCA
 GAM1621 GPA33 3' TCCCACTCCCTTTCCAACCTCA 12406 A_ CCATT A CA
 TGAG TGG GGA G GGA
 ||| || |||| | |||
 ACTC ACC CCCT C CCT
 CA TTT_ _ AC
 GAM1621 KIAA0720 3' CCTGCCCCCACCCTTCCCA 31233 A T CCAT AA
 TG GA GG TGGG GCAGG
 || ||| |||| |||||
 AC CT CC ACCC CGTCC
 C T _ C_
 GAM1621 KIAA1257 3' CCTGCTGCGTGCCACCTCA 31432 A C TGGGA
 TGAG TGGC AT AGCAGG
 ||| |||| || |||||
 ACTC ACCG TG TCGTCC
 C _ CG_
 GAM1621 KIAA1257 3' CTGCTTCAGCCTCTCA 31434 T CATTGG
 TGAGA GGC GAAGCAG
 |||| || |||||
 ACTCT CCG CTTCGTC
 _ A_
 GAM1621 KIAA1503 5' CCCGCTTCCTGCCATC 33916 CATT A
 GATGGC GGAAGC GG
 |||| ||||| ||

CTACCG TCCTTCG CC
 _____ C
 GAM1621 KIAA1649 3' CTGCTTCAGCCTCTCA 26106 T CATTGG
 TGAGA GGC GAAGCAG
 ||||| ||| |||||
 ACTCT CCG CTTCGTC
 _ A _____
 GAM1621 KIAA1822 3' TCCCGCTTCCCACCTGCATC 33556 G CAT A
 GATG C TGGGAAGC GGA
 ||||| | ||||| |||
 CTAC G ACCCTTCG CCT
 _ TCC C
 GAM1621 KIAA1853 3' CCCACTTCCCAAATATGCCTC 34385 T CA__ CA
 GA GGC TTGGGAAG GG
 || ||| ||||| ||
 CT CCG AACCCTTC CC
 _ TATA AC
 GAM1621 KIAA1944 3' CCTGCTTCTCTCCATCTCA 37228 CCATT
 TGAGATGG GGGAAGCAGG
 ||||| |||||
 ACTCTACC TCCTTCGTCC
 TC____
 GAM1621 MGC2477 5' TCCTACCCTTGTTGCCATCCCA 23545 A C T_ AAGC
 TG GATGGC AT GGG AGGA
 || ||||| || ||| ||||
 AC CTACCG TG CCC TCCT
 C T TT A____
 GAM1621 OSBPL3 3' TCCTGCTTCCCACCCCA 17816 CCAT
 TGG TGGGAAGCAGGA
 ||| |||||
 ACC ACCCTTCGTCCT
 CC____
 GAM1621 TSPAN-5 5' CCTGCTTTCTCGCGCCA 12275 ATT
 TGGCC GGGAAGCAGG
 ||||| |||||
 ACCGG TCTTTCGTCC
 CGC
 GAM1621 VILL 3' CCTGCTTCCACTCCCCTCA 33946 AT CCATTG
 TGAG GG GGAAGCAGG
 |||| || |||||
 ACTC CC CCTTCGTCC
 C_ TCA____
 GAM1621 LOC112616 3' TCCTGCTTCTAGAACCACCTCA 28773 A CCATTG
 TGAG TGG GGAAGCAGGA
 |||| ||| |||||
 ACTC ACC TCTTCGTCCT
 C AAGA____
 GAM1621 LOC126528 5' CCCGCTTTCTGAACCTCTCA 36843 T CCA TG A
 TGAGA GG T GGAAGC GG
 ||||| || | ||||| ||

ACTCT CC A CTTTCG CC
 _ A_ GT C
 GAM1621 LOC146268 3' CCTGCTTCCCACCACTTC 38122 A CCAT
 GAG TGG TGGGAAGCAGG
 ||| ||| |||||
 CTT ACC ACCCTTCGTCC
 C ____
 GAM1621 LOC147165 5' CCCACTTTCCAGACCATTCCA 40813 AG CCA CA
 TG ATGG TTGGGAAG GG
 || ||| ||||| ||
 AC TACC GACCTTTC CC
 CT A_ AC
 GAM1621 LOC153020 3' CTTCCCAATGGCCATGTCA 39355 G
 TGA ATGGCCATTGGGAAG
 ||| |||||
 ACT TACCGGTAACCCTTC
 G
 GAM1621 LOC222237 3' CCTGCCTCCTATGGCCTCTCA 45268 T T A
 TGAGA GGCCAT GGGA GCAGG
 |||| |||| ||| ||||
 ACTCT CCGGTA TCCT CGTCC
 _ _ C
 GAM1621 LOC253868 5' CCTGCCCCCACCAGCACCTCA 45748 ATG CAT AA
 TGAG GC TGGG GCAGG
 |||| || ||| ||||
 ACTC CG ACCC CGTCC
 CA_ ACC CC
 GAM1621 LOC51246 3' CCTGCTTCCCGACACCAGCCTC 18578 A_ CCA
 A TGAG TGG TTGGGAAGCAGG
 |||| ||| |||||
 ACTC ACC AGCCCTTCGTCC
 CG AC_
 GAM1621 LOC51667 3' TCCTGCTTCCCACGCTGCCATC 18197 CAT_
 TC GAGATGGC TGGGAAGCAGGA
 ||||| |||||
 CTCTACCG ACCCTTCGTCCT
 TCGC
 GAM1621 LOC92223 5' CCTGCTTCCCTTCCACCACCTC 33993 A CCATT
 A TGAG TGG GGGAAGCAGG
 |||| ||| |||||
 ACTC ACC CCCTTCGTCC
 C ACCTT
 GAM1621 LOC93259 5' TCCTGCTTCCCCGGCACCCT 35562 ATG ATT
 AG GCC GGGAAGCAGGA
 || ||| |||||
 TC CGG CCCTTCGTCCT
 CCA C_
 GAM1621 LOC93512 5' CCCACTTTCCAGACCATTCCA 35877 AG CCA CA
 TG ATGG TTGGGAAG GG
 || ||| ||||| ||

		AC TACC GACCTTTC CC	
		CT A__ AC	
GAM1622	CAMK4	3' TGAAAATCTAGCCATCCTA 7483	A CTTTA
		TAGGATG GTT ATTTTCA	
		ATCCTAC CGA TAAAAGT	
		_ TC__	
GAM1622	DEDD	3' TTGAAAATTAATCGCCACCCT 26882	A A TCT
		AGG TG GT TTAATTTTCAA	
		TCC AC CG AATTAAAAGTT	
		C _ CT_	
GAM1622	MAP3K5	3' AAAATTAAAGAGACTCTC 12545	T _
		GA GAGT TCTTTAATTTT	
		CT CTCA AGAAATTAAAA	
		_ G	
GAM1622	PRLR	5' TGACAAAACCTAAAGAACTCTCC 6650	T A _
	TA	TAGGA GAGTTCTTTA TTT TCA	
		ATCCT CTCAAGAAAT AAA AGT	
		_ C AC	
GAM1622	KIAA0310	3' TTGAAAATTAATTCCACCATCC 39711	A TCT_
	T	AGGATG GT TTAATTTTCAA	
		TCCTAC CA AATTAAAAGTT	
		_ CCTT	
GAM1623	FLJ23323	3' AGATGAACTTTTGTATCATT 23954	T C TT
		TAATG AT TA AGTTCATCT	
		ATTAC TA GT TCAAGTAGA	
		_ T TT	
GAM1623	HSC3	3' ATAGATGGGTTACAAATACAT 29733	CTAT TT
		ATGTAT TAG CATCTAT	
		TACATA ATT GTAGATA	
		AAC_ GG	
GAM1623	LOC145623	5' TAGATAGATAGATACAT 40546	AGTTC
		ATGTATCTATT ATCTA	
		TACATAGATAG TAGAT	
		A__	
GAM1624	BCL2	3' TCACAGAATCAAGGAAGCACCT 6261	CATT A
	CA	TGAGGTGCTTCT TTCT TGA	
		ACTCCACGAAGG AAGA ACT	
		AACT C	
GAM1624	CNGA3	3' CACAGAAAAAAGCATCTCA 6977	CTCA A
		TGAGGTGCTT TTTTCT TG	

			ACTCTACGAA	AAAAGA AC		
			_____ C			
GAM1624	KCNAB2	3'	TGTAGGAAAAGACCTCA	9710	G	CTCAT
			TGAGGT CTT	TTTCTATG		
			ACTCCA GAA	AAGGATGT		
			— ———			
GAM1624	STAR	3'	CACAGAACAAGCAGCACCCCA	5903	A	T CATT A
			TG GGTGCT CT	TTCT TG		
			AC CCACGA GA	AAGA AC		
			C C AC_ C			
GAM1624	DNAJB5	3'	CATGCACAAGAAGCACTCA	14586	G	CATTTTC
			TGAG TGCTTCT	TATG		
			ACTC ACGAAGA	GTAC		
			— ACAC_			
GAM1624	MAP3K2	3'	TCACAGAATACTAAAGCACCTC	13386		CTCATT A
	A		TGAGGTGCTT	TTCT TGA		
			ACTCCACGAA	AAGA ACT		
			ATCAT_ C			
GAM1624	LOC148809	3'	TCACAGCACAGAGAAGCAACCC	38596	A	_ ATTTT A
	A		TG GGT GCTTCTC	CT TGA		
			AC CCA CGAAGAG	GA ACT		
			_ A ACAC_ C			
GAM1624	LOC149372	3'	CATAGAAAGTAACACCCCA	38726	A	C CTC
			TG GGTG TT	ATTTTCTATG		
			AC CCAC AA	TGAAAGATAC		
			C _ —			
GAM1624	LOC158428	5'	CATAGAAAATGTACACTTCA	34920		CTTCT
			TGAGGTG	CATTTTCTATG		
			ACTTCAC	GTAAAAGATAC		
			AT_			
GAM1624	LOC169026	3'	TCATAGAAAATAAGGAACC	40267	GC	C
			GGT TTCT	ATTTTCTATGA		
			CCA AGGA	TAAAAGATACT		
			_ A			
GAM1625	SYT13	3'	ATATCGAATCCCTCTTTCATGA	44885	GTTTT_	A
	GA		TCTCA	AGGGATTC ATAT		
			AGAGT	TCCCTAAG TATA		
			ACTTTC	C		
GAM1625	LOC148545	3'	ATTGAACAGGACAACCTGAGGA	38552		TTAGGGA
			TTCTCAGTT	TTCAAT		

AGGAGTCAA AAGTTA
 CAGGAC_
 GAM1626 CDK10 3' CCTTCCCCACCGCAA 27554 _ TATGCC
 TTG GGTGGTGG AAGG
 ||| ||||| |||
 AAC CCACCACC TTCC
 G CCT_
 GAM1626 ENG 3' CCCTGTGTATTCACCACC 5594 T _ A
 GGTGGTGG ATGC CA GG
 ||||| ||| ||
 CCACCACT TATG GT CC
 _ T C
 GAM1626 FLJ21438 3' CCCAGGTGGACCCACCCAACGA 30845 A TG A AA
 TC TTGGGTGG GT TGCC GG
 || ||||| || ||| ||
 AG AACCCACC CA GTGG CC
 C _ G AC
 GAM1626 KIAA1610 3' CCTCATTCCACCCCAA 33339 T T_ CCA
 TTGGG GGTGG ATG AGG
 |||| |||| ||| |||
 AACCC CCACC TAC TCC
 _ CT _
 GAM1626 LOC221477 3' CCTCCACCACCACAAT 44253 _ TATGCCA
 ATTG GGTGGTGG AGG
 ||| ||||| |||
 TAAC CCACCACC TCC
 A _
 GAM1627 LNK 3' ACTGTTTCAACTAACACCCATG 11970 CATATC_
 CTA TAGCATGGGTGT AGCAGT
 ||||| |||||
 ATCGTACCCACA TTGTCA
 ATCAACT
 GAM1627 MYO3B 3' TTGCCAAGACACCCACACTA 29094 CA ATATCA
 TAG TGGGTGTC GCAG
 || ||||| |||
 ATC ACCACAG CGTT
 AC AAC_
 GAM1627 LOC219920 5' ACTGCCTGTGGCACCCAT 44802 TCA
 ATGGGTGTCATA GCAGT
 ||||| |||||
 TACCCACGGTGT CGTCA
 C_
 GAM1627 LOC220279 5' ACTGCTGATATTTCCACC 45288 TC_
 GGTG ATATCAGCAGT
 ||| |||||
 CCAC TATAGTCGTCA
 CTT
 GAM1627 LOC255826 5' ACCGCCCCGACGCCCATGC 46569 ATATCA A
 GCATGGGTGTC GC GT
 ||||| |||

		CGTACCCGCAG	CG CA	
		CCCC__ C		
GAM1628 DR1	5'	TCCATATTAGTTCCCA	29858	T A
		TGGGAACTA ATAT GGA		
		ACCCTTGAT TATA CCT		
		— —		
GAM1628 FABP2	3'	TACATTCCACAGTGCCCA	5625	A ATATATA
		TGGG ACT GGAATGTA		
		ACCC TGA CCTTACAT		
		G CA_____		
GAM1628 LDHB	5'	TACATCTCAATATGGTTCCCA	8088	ATA GA
		TGGGAACTATAT G ATGTA		
		ACCCTTGGTATA C TACAT		
		A__TC		
GAM1628 AUTL1	5'	ACATTTTACAGTTCTCCA	26647	_ ATATA
		TGG GAACT TAGGAATGT		
		ACC CTTGA ATTTTACA		
		T C_____		
GAM1628 B3GALT1	3'	ATATTTTACATATATTCCCA	21971	C A
		TGGGAA TATAT TAGGAATGT		
		ACCCTT ATATA ATTTTATA		
		— C		
GAM1628 GNB4	3'	ACATTCCTGTAATCCCA	22267	ACTATA
		TGGGA TATAGGAATGT		
		ACCCT ATGTCCTTACA		
		A_____		
GAM1628 OBTP	3'	TTCTGTACATAGTTCCCA	19081	A
		TGGGAACTAT TATAGGA		
		ACCCTTGATA ATGTCTT		
		C		
GAM1628 LOC157663	3'	ACATCACTCTTATGTAATCCC	39637	ACTA ____
		GGA TATATAGGA ATGT		
		CCCT ATGTATTCT TACA		
		A__ CAC		
GAM1628 LOC199926	3'	TACATTCCTACGTTCTC	43262	TATATA
		GGAAC TAGGAATGTA		
		CTCTTG ATCCTTACAT		
		C_____		
GAM1628 LOC202316	3'	TACATTCCTACGTTCTC	43427	TATATA
		GGAAC TAGGAATGTA		

			CTCTTG	ATCCTTACAT		
			C_____			
GAM1629	DNAJB5	3'	CCCACCCCCATAGTTGT	14587	A T TGTT	
			ACAACTAT GG GT	GGG		
			TGTTGATA CC CA	CCC		
			C C _____			
GAM1629	KIAA1001	5'	CCCCAACATTCCTATAG	17326	TGT	
			CTATAGG TGTTGGGG			
			GATATCC ACAACCCC			
			TT_			
GAM1629	KSR	5'	CCCACCACACCCAGCTGCGA	32020	A A ATA T T	
			TC CA CT GGTGT GT GGG			
			AG GT GA CCACA CA CCC			
			C C CC_ C _			
GAM1629	PRPF8	3'	CCCCACTCTCCTATAAGCATGA	30679	CAAC TGTT T	
			TCA TATAGG GT GGGG			
			AGT ATATCC CA CCCC			
			ACGA TCT_ _			
GAM1629	SR-BP1	3'	CCCCTTCACCTGCAGCTATGA	12484	CAA A TTGTT	
			TCA CT TAGGTG GGGG			
			AGT GA GTCCAC CCCC			
			ATC C TT_____			
GAM1630	FABP2	3'	TATGCAATATATCAATGTAA	5626	G C	
			TTACATTGA ATATT CATG			
			AATGTA ACT TATAA GTAT			
			A C			
GAM1630	PRKAA2	3'	TGGCGAACCATCTCAATGTAA	12929	ATT_____	
			TTACATTGAGAT CCA			
			AATGTA ACTCTA GGT			
			CCAAGC			
GAM1630	GPR88	3'	CATTTAAAATATCTCAATG	22571	CCA	
			CATTGAGATATT TGAATG			
			GTA ACTCTATAA ATTTAC			
			A_____			
GAM1630	LOC148946	3'	CATTCATGGA ACTTATTAGTG	40937	GATA	
			CATTGA TTCCATGAATG			
			GTGATT AAGGTA CTTAC			
			ATTC			
GAM1630	LOC90750	3'	CATCCATGGAATTTTGGAATG	31966	GA T A	
			CATT GA ATTCCATG ATG			

			GTAA TT TAAGGTAC TAC		
			GG T C		
GAM1631	HGF	3'	CCTTAAATCAATTTATTGA 45221	GTAA	
			TCAATAAAT TTAAGG		
			AGTTATTTA AATTCC		
			ACTA		
GAM1631	MBNL	3'	CTTTGTACATTTTAATTGATA 22028	_	ATT
			TATCAAT AAATGTA AAG		
			ATAGTTA TTTACAT TTC		
			A GT_		
GAM1631	PPP3R1	3'	CCTTAATTACATTTTTTG 37530	T	
			CAA AAATGTAATTAAGG		
			GTT TTTACATTAATTCC		
			-		
GAM1631	LOC116068	3'	CCTTAATTACATTTAATG 36500	A	
			CA TAAATGTAATTAAGG		
			GT ATTTACATTAATTCC		
			A		
GAM1632	ARHGAP6	3'	AAAACAAACAGAACCCTAA 6838	CA	A
			TTGGG TCT TTTGTTTT		
			AACCC AGA AAACAAAA		
			A_ C		
GAM1632	ARHGAP6	3'	AAAACAAACAGAACCCTAA 15082	CA	A
			TTGGG TCT TTTGTTTT		
			AACCC AGA AAACAAAA		
			A_ C		
GAM1632	VHL	3'	CCATGAAAACAGAACCCTAA 6160	CATCTA	_
			TTGGG TTTGTTTT TGG		
			AACCC AGACAAAAG ACC		
			A_____ T		
GAM1632	FLJ10743	3'	CCAGATTCTCAAGCAGATGCCC 20075	A	TTT_
	AA		TTGGGCATCT TTTG TTTGG		
			AACCCGTAGA GAAC AGACC		
			C TCTT		
GAM1632	HERPUD1	3'	GAACAAAAAATGCCCAA 16186	CTA	
			TTGGGCAT TTTGTTT		
			AACCCGTA AAACAAG		
			AA_		
GAM1632	ZFP95	3'	CTGGCTTACAATAAATGCCCAA 15920	C	T TTT TG
			TTGGGCAT TATT GT T G		

AACCCGTA ATAA CA G C
 A _ TTC GT
 GAM1632 ZFP95 3' CTGGCTTACAATAAATGCCCAA 29710 C T TTT TG
 TTGGGCAT TATT GT T G
 ||||| ||| || ||
 AACCCGTA ATAA CA G C
 A _ TTC GT
 GAM1632 LOC153778 5' CCAGAAACAAATACCCAA 39407 CATC T
 TTGGG TATTTGTTTTT GG
 |||| ||||| ||
 AACCC ATAAACAAAGA CC

 GAM1632 LOC255030 5' CCAAAAAACAAAAAACC 46439 CATCTA
 GGG TTTGTTTTTTGG
 || |||||
 CCC AAACAAAAAACC
 AAA____
 GAM1633 RABIF 3' AAAATCTCATCTCTTCCCT 8779 TCT _
 AGG AG GATGAGATTTT
 || || |||||
 TCC TC CTA CTCTAAAA
 CT_ T
 GAM1633 KIAA0596 3' CTGTCCTCCACCCTGGACCCCA 31461 A A A TTTT
 TG GGTCTAGG TG GA CAG
 || ||||| || ||
 AC CCAGGTCC AC CT GTC
 C C _ CCT_
 GAM1633 LOC144501 3' CTGGGCCCATCCCAGGCCTCA 40425 A AGATT
 TGAGGTCT GGATG TTCAG
 ||||| |||| ||||
 ACTCCGGA CCTAC GGGTC
 C CC____
 GAM1633 LOC163412 5' GGAATCTTCCCAGACCCCA 39955 A A TG
 TG GGTCT GGA AGATTTT
 || |||| || |||||
 AC CCAGA CCT TCTAAGG
 C C _
 GAM1633 LOC222182 3' CTGAAAAGTCTCCAACCCCA 45197 A CTA AT _
 TG GGT GG GAGATTTT CAG
 || || || ||||| ||
 AC CCA CC CTCTGAAA GTC
 C A_ _ A
 GAM1634 NR5A2 3' CAGCCCCAGAGGATTCCATA 9915 T A
 TATGG ATCCTCTGG GTTG
 |||| ||||| ||||
 ATACC TAGGAGACC CGAC
 T C
 GAM1634 WNT3A 3' CCCCAACCCCAAGACCA 26973 ATC C A
 TGGT CT TGG GTTGGGG
 |||| || || |||||

ACCA GA ACC CAACCCC
 ____ C
 GAM1634 CDC14B 3' CCCCCAACCCCAAACCTTTCACC 27166 ATCCTC_ A
 A TGGT TGG GTTGGGGG
 |||| ||| |||||
 ACCA ACC CAACCCCC
 CTTTCAA C
 GAM1634 KIAA1656 5' CCCCCAACCTGCAGGGAAGATG 32727 _ _ G _
 ACCATA ATGGT ATC CTCTG AG TTGGGGG
 ||||| ||| ||||| ||| |||||
 TACCA TAG GGGAC TC AACCCCC
 G AA G C
 GAM1634 PRO1914 5' CCCCCAACCCACAGATACCA 15329 CTC A
 TGGTATC TGG GTTGGGGG
 ||||| ||| |||||
 ACCATAG ACC CAACCCCC
 AC_ _
 GAM1634 PRO2859 5' CCCCCAACCCAGCAGACAC 20616 A CT A
 GT TC CTGG GTTGGGGG
 || || ||| |||||
 CA AG GACC CAACCCCC
 C AC C
 GAM1634 RDH-E2 3' CCCTCTCTCCAGAGGACAC 29079 A TT
 GT TCCTCTGGAG GGGG
 || ||||| |||
 CA AGGAGACCTC TCCC
 C TC
 GAM1634 LOC131583 5' CCCCCAACTCCCTACCA 37356 TCCTCT
 TGGTA GGAGTTGGGG
 |||| |||||
 ACCAT CCTCAACCCC
 C____
 GAM1634 LOC204593 5' CCCCAGCCAGAAAATCCA 43583 T CC AG
 TGG AT TCTGG TTGGGG
 ||| || |||| |||||
 ACC TA AGACC GACCCC
 _ AA _
 GAM1634 LOC254042 3' CCCCCAACCCCAAGCCCTTCCGT 45791 TATCCT A
 A TATGG CTGG GTTGGGGG
 |||| ||| |||||
 ATGCC GACC CAACCCCC
 TTCCC_ C
 GAM1635 CRNKL1 3' AACTGCATTAACCGATCTGA 18771 ACCCG CTA
 TCAGATCG GA CAGTT
 ||||| || |||||
 AGTCTAGC TT GTCAA
 CAA_ AC_
 GAM1635 KIAA1190 3' GGTGCCCCGAGTGATCTGA 35223 G C _
 TCAGATC AC CGG ACT
 ||||| || ||| |||

		AGTCTAG TG GCC TGG	
		_ A CG	
GAM1636 CBFA2T2	3'	AAACCCCGGACCTCAGGTG 11545	TA CCATT
		CACCTGAG CC GGTTC	
		GTGGACTC GG CCAAA	
		CA CC__	
GAM1636 DFFB	3'	AAACTCCTGACCTCAGGTG 42236	TACCC TT
		CACCTGAG CA GGTTC	
		GTGGACTC GT TCAAA	
		CA__ CC	
GAM1636 DLEC1	3'	AACCAGACCACTCAGGTGG 14261	ACCCCA
		CCACCTGAGT TTGGTT	
		GGTGGACTCA GACCAA	
		CCA__	
GAM1636 DLEC1	3'	AACCAGACCACTCAGGTGG 14267	ACCCCA
		CCACCTGAGT TTGGTT	
		GGTGGACTCA GACCAA	
		CCA__	
GAM1636 MAK	3'	AAACTCCTGACCTCAGGTG 12526	TACCC TT
		CACCTGAG CA GGTTC	
		GTGGACTC GT TCAAA	
		CA__ CC	
GAM1636 MEFV	3'	AAACTCCTGACCTCAGGTG 5766	TACCC TT
		CACCTGAG CA GGTTC	
		GTGGACTC GT TCAAA	
		CA__ CC	
GAM1636 MICB	3'	AAACTCCTGACCTCAGGTG 12563	TACCC TT
		CACCTGAG CA GGTTC	
		GTGGACTC GT TCAAA	
		CA__ CC	
GAM1636 MLANA	3'	AAACTCCTGACCTCAGGTG 12026	TACCC TT
		CACCTGAG CA GGTTC	
		GTGGACTC GT TCAAA	
		CA__ CC	
GAM1636 NDRG3	3'	AAACTCCTGACCTCAGGTG 25719	TACCC TT
		CACCTGAG CA GGTTC	
		GTGGACTC GT TCAAA	
		CA__ CC	
GAM1636 NQO1	3'	AAACTCCTGACCTCAGGTG 6604	TACCC TT
		CACCTGAG CA GGTTC	

			GTGGACTC GT TCAAA		
			CA__ CC		
GAM1636 PBX2	3'	TAAACCAATAGAATCGCTCGGT 8449		T	ACCCC_
GG		CCACC GAGT ATTGGTTTA			
		GGTGG CTCG TAACCAAAT			
		_ CTAAGA			
GAM1636 PER2	3'	CAGCGAGGTACACCAGGTGG 23089		A_	CCA
		CCACCTG GTACC TTG			
		GGTGGAC CATGG GAC			
		CA AGC			
GAM1636 PPT1	3'	AGGCCTGAGGTACTCA 30954		C	TT
		TGAGTACC CA GGTTT			
		ACTCATGG GT CCGGA			
		A _			
GAM1636 PSMD9	3'	AAACCAAAGCTCAGATGG 8677		C	ACCCCA
		CCA CTGAGT TTGGTTT			
		GGT GACTCG AACCAAA			
		A A_			
GAM1636 SCML2	3'	AAACTCCTGACCTCAGGTG 12733			TACCC TT
		CACCTGAG CA GGTTT			
		GTGGACTC GT TCAAA			
		CA__ CC			
GAM1636 SEPX1	3'	ACTTTCTGGAGTAATCAGGTGG 18456		G C	TT_
		CCACCTGA TAC CCA GGT			
		GGTGGACT ATG GGT TCA			
		A A CTT			
GAM1636 SULT2B1	5'	AAACTCCTGACCTCAGGTG 10948			TACCC TT
		CACCTGAG CA GGTTT			
		GTGGACTC GT TCAAA			
		CA__ CC			
GAM1636 VHL	3'	AAACTCCTGACCTCAGGTG 6154			TACCC TT
		CACCTGAG CA GGTTT			
		GTGGACTC GT TCAAA			
		CA__ CC			
GAM1636 ATF3	3'	TCAAGATATTCAGGTGG 10246			CCCCA
		CCACCTGAGTA TTGG			
		GGTGGACTTAT AACT			
		AG_			
GAM1636 BOP	5'	GCCTGGAGTCTCAGGTGG 41209		T C	TT
		CCACCTGAG AC CCA GGT			

			GGTGGACTC TG GGT CCG	
			— A —	
GAM1636	CED-6	3'	AACACAATGGAGTACTAAGATG 18429	C G C —
	G		CCA CT AGTAC CCATTG GTT	
			GGT GA TCATG GGTAAC CAA	
			A A A A	
GAM1636	CXYorf1	3'	TAAACCAATGGAAAGAAGGGG 39912	A GAGTACC
			CC CCT CCATTGGTTTA	
			GG GGA GGTAACCAAAT	
			— AGAAA—	
GAM1636	DDX34	3'	TGATGAGGTATCAGGTGG 16168	G C
			CCACCTGA TACC CATTG	
			GGTGGACT ATGG GTAGT	
			— A	
GAM1636	EVI5	3'	AAACTTCTGACCTCAGGTG 12205	TACCC TT
			CACCTGAG CA GGTTT	
			GTGGACTC GT TCAAA	
			CA__ CT	
GAM1636	FBP17	3'	AAACTCCTGACCTCAGGTG 36045	TACCC TT
			CACCTGAG CA GGTTT	
			GTGGACTC GT TCAAA	
			CA__ CC	
GAM1636	FLJ10159	3'	AAACCAATGAAAACAAGAGGG 19747	AC GA ACCC
			CC CT GT CATTGGTTT	
			GG GA CA GTAACCAAA	
			GA A_ AAA_	
GAM1636	FLJ12363	3'	AAACTCCTGACCTCAGGTG 25864	TACCC TT
			CACCTGAG CA GGTTT	
			GTGGACTC GT TCAAA	
			CA__ CC	
GAM1636	FLJ12816	3'	TAAGCTAGGGACACTCAAGTG 22605	C AC AT
			CAC TGAGT CCC TGGTTTA	
			GTG ACTCA GGG ATCGAAT	
			A CA _	
GAM1636	FLJ12891	3'	AAACCAATGTATTCTCAAATG 24508	CC TACCC
			CA TGAG CATTGGTTT	
			GT ACTC GTAACCAAA	
			AA TTTAT	
GAM1636	FLJ20241	5'	AAACCAATTCACCCAGCTGG 19311	C A ACCCC
			CCA CTG GT ATTGGTTT	

	GGT GAC CA TAACCAA C C CT__	
GAM1636 FLJ21168	3' AATTAAAGGTATCAGGTGG 24670 CCACCTGA TACC TTGGTT GGTGGACT ATGG AATTAA _ A_	G CCA
GAM1636 FLJ22684	3' AAACCTCCTGACCTCAGGTG 24642 CACCTGAG CA GGTTT GTGGACTC GT TCAAA CA__ CC	TACCC TT
GAM1636 KIAA0161	3' AAACCTCCTGACCTCAGGTG 16427 CACCTGAG CA GGTTT GTGGACTC GT TCAAA CA__ CC	TACCC TT
GAM1636 KIAA0391	3' AAACCTCCTGACCTCAGGTG 16133 CACCTGAG CA GGTTT GTGGACTC GT TCAAA CA__ CC	TACCC TT
GAM1636 KIAA0472	3' TAATCCAAGATACTCAGGAGG 35581 CC CCTGAGTA TTGG TTA GG GGACTCAT AACC AAT A AG__ T	A CCCCC T
GAM1636 KIAA1170	3' AAACCTCCTGACCTCAGGTG 34609 CACCTGAG CA GGTTT GTGGACTC GT TCAAA CA__ CC	TACCC TT
GAM1636 KIAA1198	3' AAACCTCCTGACCTCAGGTG 31699 CACCTGAG CA GGTTT GTGGACTC GT TCAAA CA__ CC	TACCC TT
GAM1636 KIAA1493	3' AAACCTCCTGACCTCAGGTG 32085 CACCTGAG CA GGTTT GTGGACTC GT TCAAA CA__ CC	TACCC TT
GAM1636 KIAA1712	3' AAACCTCCTGACCTCAGGTG 33535 CACCTGAG CA GGTTT GTGGACTC GT TCAAA CA__ CC	TACCC TT
GAM1636 MGC35558	3' GGACGAGGCATCTCAGGTGG 29615 CCACCTGAG CC T GTTT 	TAC CAT G

	GGTGGACTC GG A CAGG	
	TAC ____ G	
GAM1636 MGC4730	3' TAAACCAACGGGAAAATTAG 32134	GTAC A
	CTGA CCC TTGGTTTA	
	GATT GGG AACCAAAT	
	AAAA C	
GAM1636 PIP3-E	3' AAACCTCCTGACCTCAGGTG 33173	TACCC TT
	CACCTGAG CA GGTTT	
	GTGGACTC GT TCAAA	
	CA____ CC	
GAM1636 PRO2955	3' AAACCTCCTGACCTCAGGTG 20619	TACCC TT
	CACCTGAG CA GGTTT	
	GTGGACTC GT TCAAA	
	CA____ CC	
GAM1636 PSTPIP2	3' AAACCTCCTGACCTCAGGTG 23678	TACCC TT
	CACCTGAG CA GGTTT	
	GTGGACTC GT TCAAA	
	CA____ CC	
GAM1636 UBE2V2	3' TAAACCTGGAGTACTCG 9376	C TT
	TGAGTAC CCA GGTTTA	
	GCTCATG GGT CCAAAT	
	A ____	
GAM1636 VDU1	3' AAACCTCCTGACCTCAGGTG 17380	TACCC TT
	CACCTGAG CA GGTTT	
	GTGGACTC GT TCAAA	
	CA____ CC	
GAM1636 VPS33A	3' AAACCTCCTGACCTCAGGTG 23229	TACCC TT
	CACCTGAG CA GGTTT	
	GTGGACTC GT TCAAA	
	CA____ CC	
GAM1636 WBSCR23	3' AAACCTCCTGACCTCAGGTG 24636	TACCC TT
	CACCTGAG CA GGTTT	
	GTGGACTC GT TCAAA	
	CA____ CC	
GAM1636 LOC133362	5' TGGGAGTACCTCAGGCGG 37380	A _ _
	CC CCTGAG TAC CCCA	
	GG GGA CTC ATG GGGT	
	C C A	
GAM1636 LOC143916	3' AAACCTCCTGACCTCAGGTG 37649	TACCC TT
	CACCTGAG CA GGTTT	

	GTGGACTC GT TCAAA	
	CA__ CT	
GAM1636 LOC144524 5'	AAACTCCTGAAGTCAGGTG 40432	ACCC TT
	CACCTGAGT CA GGTTT	
	GTGGACTCA GT TCAAA	
	A__ CC	
GAM1636 LOC146229 3'	AAACTCCTGACCTCAGGTG 38103	TACCC TT
	CACCTGAG CA GGTTT	
	GTGGACTC GT TCAAA	
	CA__ CC	
GAM1636 LOC149711 3'	AAACTCCTGACCTCAGGTG 41066	TACCC TT
	CACCTGAG CA GGTTT	
	GTGGACTC GT TCAAA	
	CA__ CC	
GAM1636 LOC169611 3'	AAACTCCTGACCTCAGGTG 40284	TACCC TT
	CACCTGAG CA GGTTT	
	GTGGACTC GT TCAAA	
	CA__ CC	
GAM1636 LOC196047 5'	AAACTCCTGACCTCAGGTG 43142	TACCC TT
	CACCTGAG CA GGTTT	
	GTGGACTC GT TCAAA	
	CA__ CC	
GAM1636 LOC196510 3'	AAACCAATGGAGGACTCAGG 42392	A _
	CCTGAGT CC CCATTGGTTT	
	GGAAGTCA GG GGTAACCAAA	
	_ A	
GAM1636 LOC199699 3'	AAACTCCTGGCCTCAGGTG 42593	TACC TT
	CACCTGAG CCA GGTTT	
	GTGGACTC GGT TCAAA	
	C__ CC	
GAM1636 LOC199958 3'	AAACCAGGGTGAACCCTCAGGT 43263	_____ CAT
G	CACCTGAG TACCC TGGTTT	
	GTGGACTC GTGGG ACCAAA	
	CCAA _____	
GAM1636 LOC200093 3'	TAAACCAATGGAAAGAAGGGG 31604	A GAGTACC
	CC CCT CCATTGGTTTA	
	GG GGA GGTAACCAAAT	
	_ AGAAA__	
GAM1636 LOC200220 3'	AAACCAATGGAGGACTCAGG 42741	A _
	CCTGAGT CC CCATTGGTTT	

GGACTCA GG GGTAACCAAA
_ A
GAM1636 LOC220074 3' AAACCTCCTGACCTCAGGTG 29821 TACCC TT
CACCTGAG CA GGTTT
||||||| || |||||
GTGGACTC GT TCAAA
CA__ CC
GAM1636 LOC222160 5' AACTAGTGAGGTCTCAAGCGG 45163 ACC T C
CC TGAG ACC CATTGGTT
|| |||| ||| |||||||
GG ACTC TGG GTGATCAA
CGA _ A
GAM1636 LOC256364 5' AAACCTCCTGGCCTCAGGTG 45444 TACC TT
CACCTGAG CCA GGTTT
||||||| ||| |||||
GTGGACTC GGT TCAAA
C__ CC
GAM1636 LOC91040 3' TAAACCAATGGAAAGAAGGGG 32321 A GAGTACC
CC CCT CCATTGGTTTA
|| ||| |||||||||
GG GGA GGTAACCAAAT
_ AGAAA_
GAM1637 GORASP1 3' AATGTCTGCTCTGGGGGGCA 25643 GA G C AA
TGC CCT CA GA CAGACATT
||| ||| || ||| |||||||
ACG GGG GT CT GTCTGTAA
_ G _ C_
GAM1637 KIAA0884 5' AATGTCTGATTTTGAAGTCACA 34771 C CTGCA _
TG GAC CGAAA CAGACATT
|| ||| ||||| |||||||
AC CTG GTTTT GTCTGTAA
A AA__ A
GAM1638 MSF 3' AGCCCACCAGGAGCAC 42519 TATTAT
GTG CTCCTGGTGGGCT
||| |||||||||
CAC GAGGACCACCCGA

GAM1638 PYGB 3' AGCCCACCAGAGCACTACA 8763 TTAT C
TGTA CTC TGGTGGGCT
||| ||| |||||||
ACAT GAG ACCACCCGA
CAC_ _
GAM1638 C20orf108 3' GCAACCATGAGATAATACA 28086 C GG
TGTATTATCTC TGGT GC
||||||||| ||| ||
ACATAATAGAG ACCA CG
T A_
GAM1638 FLJ10378 5' CAATAGGAGAAATGATACAC 19839 _ G
GTGTATTA TCTCCTG TG
||||||| ||||||| ||

		CACATAGT AGAGGAT AC		
		AA A		
GAM1638	HDCMA18P 5'	CCCACCAGAAGAAGCAC	18766	ATTA C
		GTGT TCT CTGGTGGG		
		CACG AGA GACCACCC		
		A__ A		
GAM1638	KIAA0164 3'	AGTGCTAGGAAATAACTCAC	16403	TA C GG
		GTG TTAT TCCTGGT GCT		
		CAC AATA AGGATCG TGA		
		TC A _		
GAM1638	SLK 3'	TAGCTCATGAAGACAATCAC	16282	T A CCTG
		GTG ATT TCT GTGGGCTA		
		CAC TAA AGA TACTCGAT		
		_ C AG__		
GAM1638	LOC144811 3'	AGTGAAGGAGATAAACAC	40454	A GGTGG
		GTGT TTATCTCCT GCT		
		CACA AATAGAGGA TGA		
		_ AG__		
GAM1638	LOC145786 5'	GTAGCCTACCAAATTATACAC	40592	TATCTCC
		GTGTAT TGGTGGGCTAC		
		CACATA ACCATCCGATG		
		TTAAA__		
GAM1638	LOC158696 3'	TACCAGAAAATAATACAT	39880	CTC
		GTGTATTAT CTGGTG		
		TACATAATA GACCAT		
		AAA		
GAM1638	LOC254556 3'	AGCCCACCAGATGTAGCAC	45391	AT CCT
		GTGT TATCT GGTGGGCT		
		CACG GTAGA CCACCCGA		
		AT _		
GAM1638	LOC257415 3'	CTCTGGGAGATAATACAC	45958	TG T
		GTGTATTATCTCC G GG		
		CACATAATAGAGG C TC		
		GT _		
GAM1638	LOC90342 5'	GCTCCAAGAGATAACACAT	31254	A C TG
		GTGT TTATCTC TGG GGC		
		TACA AATAGAG ACC TCG		
		C A _		
GAM1639	LOC114971 3'	AACCAGCTGAGCAGCAGTC	36206	GTA G A
	TA	TAGA CTGC GTTTAGCT GTT		

		ATCT GACG CGAGTCGA CAA	
		GAC A C	
GAM1639	LOC221773 3'	ACTAGCTATGAAATACTC 43759	CTG GTT
		GAGTA CG TAGCTAGT	
		CTCAT GT ATCGATCA	
		AAA ____	
GAM1639	LOC255533 5'	AACTAGCTAACTTTGTACTT 46326	TGC T
		GAGTAC GGTT AGCTAGTT	
		TTCATG TCAA TCGATCAA	
		TT_ _	
GAM1640	RTN3 3'	TAATGAAACTGTGTGTAC 36586	_ A
		GTGC CACA TTTCATTA	
		CATG GTGT AAAGTAAT	
		T C	
GAM1640	TUFT1 3'	TTGTTAATGTCAGAGTGACACT 21320	C AATTT
		AGTG CAC CATTAACAA	
		TCAC GTG GTAATTGTT	
		A AGACT	
GAM1640	C6orf33 3'	TTGTTAATGGCCTGTGACAT 28494	C ATT
		GTG CACA TCATTAACAA	
		TAC GTGT GGTAATTGTT	
		A CC_	
GAM1640	FLJ23191 5'	TTAATGAGGAAGGCACTGA 23805	ACAA
		TCAGTGCC TTTCATTAA	
		AGTCACGG GGAGTAATT	
		AA_	
GAM1640	FLJ30213 3'	TTGTTAGTTTATCTTG GCACTG 29610	CA TTC
	A	TCAGTGCCA AT ATTAACAA	
		AGTCACGGT TA TGATTGTT	
		TC TT_	
GAM1640	KIAA1184 3'	TTGTCAATGCTTCTCTGTGGC 22898	TTT__ A
	ACT	AGTGCCACAA CATT ACAA	
		TCACGGTGTT GTAA TGTT	
		CTCTTC C	
GAM1640	NDP52 3'	AGTGGAGTTATGTCACTGA 12442	C C
		TCAGTG CA AATTCATT	
		AGTCAC GT TTGAGGTGA	
		T A	
GAM1640	TNRC6 3'	TTAATGAAAGTGTTCAC 34901	C A
		GTGC ACA TTTCATTAA	

CACG TGT AAAGTAATT
T G
GAM1640 LOC129676 5' GTGCAAATTGCAGGCACTGA 37287 A_ _
TCAGTGCC CAATTT CAT
||||| ||||| ||
AGTCACGG GTTAAA GTG
AC C
GAM1640 LOC152905 3' TAATGAAACTGTGTGTAC 30331 _ A
GTGC CACA TTTCATTA
||| ||| |||||
CATG GTGT AAAGTAAT
T C
GAM1640 LOC254402 5' AGTGGCTGTGGCACTGA 46583 ATT
TCAGTGCCACA TCATT
||||||| ||||
AGTCACGGTGT GGTGA
C_
GAM1640 LOC56267 3' TTGTTGTAATTATGGCACTG 21230 C TCAT
CAGTGCCA AATT TAACAA
||||| ||| |||||
GTCACGGT TTAA GTTGTT
A T____
GAM1641 HGF 3' CACGAACACACTTTTTAC 45219 TTTT
GTA GAGTGTGTTCGTG
||| |||||
CAT TTCACACAAGCAC
TT_
GAM1642 LOC254122 3' GGCCTGGCAGACGATTATA 45437 C ACCC
TGTAATCGTC TGTTG GCC
||||||| |||| ||
ATATTAGCAG ACGGT CGG
_ C_
GAM1642 LOC254830 5' GCGAGCAGAACTGATTACA 46612 _ C GACC
TGTAATC GT CTGTT CGC
||||| || |||| ||
ACATTAG CA GACGA GCG
T A ____
GAM1643 GNAS 3' ACAGATGGCTGCGCACC 18676 AT T CAA
GGT G CGC CCATCTGT
||| ||| |||||
CCA C GCG GGTAGACA
__ TC_
GAM1643 ZNF43 5' ACAGATGGGATTGTGACATATC 9470 CAA_
GCT AGCGGTATGTCGC CCATCTGT
||||||| |||||
TCGCTATACAGTG GGTAGACA
TTAG
GAM1643 LEPROTL1 3' CAGACGGTTGGCATAC 17650 GTC A
GTAT GCCAACC TCTG
||| ||||| |||

CATA CGGTTGG AGAC
 _____ C
 GAM1644 ADAMTS5 3' CTGTCTTTACCTTTCCA 13918 TGATGC G
 TGGAA TGAG AGACAG
 ||||| ||| |||||
 ACCTT ACTT TCTGTC
 TCC____ _
 GAM1644 ALPI 3' TGCTGTCTCCCCACTAGGATCA 7345 G A____
 TTCCA TGGAAATGAT CTG GGAGACAGCA
 ||||| ||| |||||
 ACCTTACTA GAT CCTCTGTCGT
 G CACC
 GAM1644 DUSP2 3' TGCTACCTCCTCAGAGTTTCA 10682 GATG AC
 TGGAAAT CTGAGGAG AGCA
 ||||| ||||| |||
 ACTTTG GACTCCTC TCGT
 A____ CA
 GAM1644 FKBP1B 3' CTGCCTCATGGCATCATCCA 27643 A GAG A
 TGGATGATGCT GAG CAG
 ||| ||||| ||| |||
 ACCT ACTACGG CTC GTC
 _ TA_ C
 GAM1644 HOXB6 3' GCTGTCCCCTCAGCGGGGGCC 30088 AATGA A
 GG TGCTGAGG GACAGC
 || ||||| |||||
 CC GCGACTCC CTGTCTG
 GGGG_ C
 GAM1644 KIF5C 3' TGCTGAAGAAATCCAACATCAT 10858 CTGA GA____
 TCCA GGAATGATG GGA CAGCA
 ||||| ||| |||||
 CCTTACTAC CCT GTCGT
 AA__ AAAGAA
 GAM1644 LZTFL1 3' CTGTCTACTAAGAGACATCATT 21599 _ GA_ _
 CCA TGGAAATGATG CT GG AGACAG
 ||||| || |||||
 ACCTTACTAC GA TC TCTGTC
 A GAA A
 GAM1644 PIGA 3' TGCTACCTCTATATCATTC 21713 CT AGAC
 GAATGATG GAGG AGCA
 ||||| ||| |||
 CTTACTAT CTCC TCGT
 AT A____
 GAM1644 PIGA 3' TGCTACCTCTATATCATTC 21720 CT AGAC
 GAATGATG GAGG AGCA
 ||||| ||| |||
 CTTACTAT CTCC TCGT
 AT A____
 GAM1644 PIGA 3' TGCTACCTCTATATCATTC 8500 CT AGAC
 GAATGATG GAGG AGCA
 ||||| ||| |||

CTTACTAT CTCC TCGT
 AT A__
 GAM1644 SHMT2 3' CTGCCTCCTCATTTTTCA 11880 TGATGC A
 TGGAA TGAGGAG CAG
 |||| ||||| ||
 ACTTT ACTCCTC GTC
 TT__ C
 GAM1644 STXBP1 3' TGTCCCCAGGCATCATCCCA 9143 A GA A
 TGG ATGATGCT GG GACA
 || ||||| || ||||
 ACC TACTACGG CC CTGT
 C AC _
 GAM1644 TFE3 3' TGTCCCTCAGCAACATCCCA 13277 A A A
 TGG ATG TGCTGAGG GACA
 || || ||||| ||||
 ACC TAC ACGACTCC CTGT
 C A _
 GAM1644 XK 3' CCATCAGCAACATCATTCC 22058 _ _
 GGAATGA TGCTGA GG
 ||||| ||||| ||
 CCTTACT ACGACT CC
 ACA A
 GAM1644 APOA5 3' GCTGTCTCCTGCATATCCA 27539 ATG TG
 TGGA ATGC AGGAGACAGC
 ||| ||| ||||| ||||
 ACCT TACG TCCTCTGTCTG
 A__ _
 GAM1644 BANP 5' CTGCCCTGGCATCACCCA 32913 AA G AGA
 TGG TGATGCT AGG CAG
 || ||||| || ||
 ACC ACTACGG TCC GTC
 C_ _ C_
 GAM1644 CD109 3' TGCTGTCTCCTTCCCACATCC 28573 A A CT
 GGA TG TG GAGGAGACAGCA
 || || || ||||| ||||
 CCT AC AC TTCCTCTGTCTG
 _ _ CC
 GAM1644 CPSF2 3' TGCTGTCTCCTAAGGTCACCCA 30866 AA G G
 TGG TGAT CT AGGAGACAGCA
 || |||| || ||||| ||||
 ACC ACTG GA TCCTCTGTCTG
 C_ _ A
 GAM1644 FLJ12057 3' CTGTCTCCTTCCTCCCA 24126 AAT TGCT
 TGG GA GAGGAGACAG
 || || ||||| ||||
 ACC CT TTCCTCTGTCTG
 _ _ CC_
 GAM1644 FLJ20203 3' TGCCATCCTAGGCATCATTC 19291 G GACA
 GAATGATGCT AGGA GCA
 ||||| |||| |||

CTTACTACGG TCCT CGT
 A AC__
 GAM1644 FLJ20508 3' CTGCCCTTGGCATCATCCA 19518 A TG AGA
 TGGA TGATGC AGG CAG
 ||| ||||| ||| |||
 ACCT ACTACG TCC GTC
 _ GT C__
 GAM1644 FLJ21140 3' TGCCATCCTTAGCATCAGCCCA 24142 AA GACA
 TGG TGATGCTGAGGA GCA
 ||| ||||| ||||| |||
 ACC ACTACGATTCCT CGT
 CG AC__
 GAM1644 FLJ21459 3' CTGTCTCCCGTCACCCC 23719 AA CTGA
 GG TGATG GGAGACAG
 || ||||| ||||| |||||
 CC ACTGC CCTCTGTC
 CC ____
 GAM1644 GABBR1 3' GCTGCCTCCTCAGCAGCCTC 7206 ATGA A
 GA TGCTGAGGAG CAGC
 || ||||| ||||| |||||
 CT ACGACTCCTC GTCG
 CCG_ C
 GAM1644 GABBR1 3' GCTGCCTCCTCAGCAGCCTC 22423 ATGA A
 GA TGCTGAGGAG CAGC
 || ||||| ||||| |||||
 CT ACGACTCCTC GTCG
 CCG_ C
 GAM1644 KIAA0182 3' CTGTCTCCCCATCCTTCCA 35645 T CTGA
 TGGAA GATG GGAGACAG
 ||||| ||||| ||||| |||||
 ACCTT CTAC CCTCTGTC
 C C__
 GAM1644 KIAA1023 3' GCTGTCTCCCCAGCGTGTCC 19093 ATG A
 GGA ATGCTG GGAGACAGC
 ||| ||||| ||||| |||||
 CCT TGCGAC CCTCTGTCG
 G_ C
 GAM1644 KIAA1317 5' TTTTTCAGCATCACTTCA 41632 A
 TGGA TGATGCTGAGGAG
 ||||| ||||| ||||| |||||
 ACTT ACTACGACTTTTT
 C
 GAM1644 KIAA1617 3' CTGTCTCCTGCTGGCATTG 43942 AT_ TG
 GAATG GC AGGAGACAG
 ||||| || ||||| |||||
 CTTAC CG TCCTCTGTC
 GGT ____
 GAM1644 MGC10966 5' TGCCGCCTCCTCAGCATC 25538 ACA
 GATGCTGAGGAG GCA
 ||||| ||||| ||||| |||

CTACGACTCCTC CGT
 CGC
 GAM1644 NR6A1 3' TGCTGTCTCCTCAACTCAACC 27189 AA TGC
 GG TGA TGAGGAGACAGCA
 || ||| |||||
 CC ACT ACTCCTCTGTCGT
 A_ CA_
 GAM1644 NR6A1 3' TGCTGTCTCCTCAACTCAACC 27183 AA TGC
 GG TGA TGAGGAGACAGCA
 || ||| |||||
 CC ACT ACTCCTCTGTCGT
 A_ CA_
 GAM1644 NR6A1 3' TGCTGTCTCCTCAACTCAACC 7235 AA TGC
 GG TGA TGAGGAGACAGCA
 || ||| |||||
 CC ACT ACTCCTCTGTCGT
 A_ CA_
 GAM1644 PDK2 3' GTCCCCCTCAGCACCTCCA 8476 ATGA A_
 TGGG TGCTGAGG GAC
 ||| ||||| |||
 ACCT ACGACTCC CTG
 CCC_ CC
 GAM1644 PME-1 3' CTGTCTCCTCTCCATCCC 18231 AAT CT
 GG GATG GAGGAGACAG
 || ||| |||||
 CC CTAC CTCCTCTGTC
 _ CT
 GAM1644 SLC38A4 3' TGCCGTCTCCTCATCCTGCA 19759 _ A
 TGC TGAGGAGAC GCA
 ||| ||||| |||
 ACG ACTCCTCTG CGT
 TCCT C
 GAM1644 LOC145739 3' CTGTCTCCTGTTTCATCATCCCA 37961 A CTG
 TGG ATGATG AGGAGACAG
 ||| ||||| |||||
 ACC TACTAC TCCTCTGTC
 C TTG
 GAM1644 LOC147180 5' TGCTGTCTACAGGAGCTCATCC 40818 A T GAGG_
 CA TGG ATGA GCT AGACAGCA
 ||| ||| ||| |||||
 ACC TACT CGA TCTGTCGT
 C _ GGACA
 GAM1644 LOC148293 5' TGCTGTGAAAAGCTTCATTCCA 38519 T GAGGAG
 TGG AATGA GCT ACAGCA
 ||||| ||| |||||
 ACCTTACT CGA TGTCGT
 T AAAG_
 GAM1644 LOC149535 3' TGTTCCCTCAGCATCCCCCA 38772 AAT A
 TGG GATGCTGAGGAG CA
 ||| ||||| ||| ||

ACC CTACGACTCCTT GT
 CC_ _
 GAM1644 LOC150343 5' CTGTCTCCCCAGCAGTGACA 38903 GA GA A
 TG AT TGCTG GGAGACAG
 || || |||| |||||
 AC TG ACGAC CCTCTGTC
 AG _ C
 GAM1644 LOC152048 3' CTGTCTCCCATCACCCC 41426 AA CTGA
 GG TGATG GGAGACAG
 || |||| |||||
 CC ACTAC CCTCTGTC
 CC _
 GAM1644 LOC155179 3' GCTGTCTCCCCAGCGTGTCC 39559 ATG A
 GGA ATGCTG GGAGACAGC
 || |||| |||||
 CCT TGCGAC CCTCTGTCTG
 G_ C
 GAM1644 LOC221466 3' GCTGTCTGTCTCCACCCCA 44994 AA ATGCT _
 TGG TG GAGG AGACAGC
 || || |||| |||||
 ACC AC CTCT TCTGTCTG
 CC _ G
 GAM1644 LOC255779 3' TGCTGTGCATATAATCATTCCA 45943 GCTGAGGA
 TGGAATGAT GACAGCA
 ||||| |||||
 ACCTTACTA CTGTCGT
 ATATA_
 GAM1644 LOC90049 3' TGCTGTGAAAAGCTTCATTCCA 30698 T GAGGAG
 TGGAATGA GCT ACAGCA
 ||||| || |||||
 ACCTTACT CGA TGTCGT
 T AAAG_
 GAM1644 LOC91252 3' CTGCCCCCTCAGCACACACA 32553 GAA A AGA
 TG TG TGCTGAGG CAG
 || ||||| |||||
 AC AC ACGACTCC GTC
 AC_ _ CCC
 GAM1645 COL4A1 3' GAGAACTCCATCAGAAAACCAA 7578 A_ TAT A C
 A TTTGGT TCT TGGA GT CTC
 ||||| || ||||| |||||
 AAACCA AGA ACCT CA GAG
 AA CT_ _ A
 GAM1645 FSTL1 3' ACTTTCAAGATCCAAA 13947 T TAT
 TTTGG ATCT TGGAAGT
 ||||| ||||| |||||
 AAACC TAGA ACTTTCA
 _ _
 GAM1645 M11S1 3' GGAAGTCCTCAAGGAAAAGATA 12518 ATT_ AAGT
 CCAAA GGTATCTT GG CC
 ||||| || ||

			CCATAGAA	CC	GG		
			AAGGAAIIICT	TGAA			
GAM1645	ZNF124	5'	ACCTCCAGATGCCAAA	9481		TATT	A
			TTTGGTATCT	GGA GT			
			AAACCGTAGA	CCT CA			
			_____	C			
GAM1645	DKFZP434O047	5'	GACCCAATAAGCTACCAA	17865		T	AA
			TTTGGTA	CTTATTGG GTC			
			AAACCAT	GAATAACC CAG			
			C	_____			
GAM1645	FXD3	3'	GAGAACTTCCAACAAGCCTCAA	22435		TAT	A C
	A		TTTGG	CTT TTGGAAGT CTC			
			AAACT	GAA AACCTTCA GAG			
			CC_	C A			
GAM1645	FXD3	3'	GAGAACTTCCAACAAGCCTCAA	12592		TAT	A C
	A		TTTGG	CTT TTGGAAGT CTC			
			AAACT	GAA AACCTTCA GAG			
			CC_	C A			
GAM1645	MGC15606	3'	GAAATTAATAAGATACTAAA	29661			AAG
			TTTGGTATCTTATTGG	TC			
			AAATCATAGAATAATT	AG			
			AA_				
GAM1645	RBM11	3'	GAGGACATATGATAATGATACC	29560		_	GAA
	AAA		TTTGGTATC	TTATTG GTCCTC			
			AAACCATAG	AATAGT CAGGAG			
			T	ATA			
GAM1645	LOC203292	5'	AGGACCTAGGAAAATACCAGA	43500		C A	AA
			TTTGGTAT	TT TTGG GTCCT			
			AGACCATA	AA GATC CAGGA			
			A G	_____			
GAM1646	WW45	3'	ACTGAAGAAATGTTGACA	22396		G	C
			TGTCAACAT	TCTTC GT			
			ACAGTTGTA	AGAAG CA			
			A	T			
GAM1646	KIAA1034	3'	GGGAGAAGACATGTTGCA	31310		T	CG
			TG CAACATGTCTTC	TC			
			AC GTTGTACAGAAG	GG			
			_	AG			
GAM1646	SV2B	3'	GAGAGAAGACATATTGAC	16882		C	CG
			GTCAA	ATGTCTTC TC			

		CAGTT TACAGAAG AG		
		A AG		
GAM1646	LOC219738 3'	TGTGGAAGACATGCCGAC 29818	AA	T
		GTC CATGTCTTCCG CG		
		CAG GTACAGAAGGT GT		
		CC _		
GAM1646	LOC220573 3'	ATGACTGTATAAACTTGTGA 34482	T	CTTCCGTC
	CA	TGTCAACA GT GTCAT		
		ACAGTTGT CA CAGTA		
		T AAATATGT		
GAM1646	LOC91960 3'	GACGACAGGAAATGGTGACA 33611	A	GTC _
		TGTCA CAT TTCC GTCGTC		
		ACAGT GTA AAGG CAGCAG		
		G _ A		
GAM1647	CAPN1 3'	ACCACACCAGGCCACCCC 11686	TA	CGA A
		GG GTGGTTTG TGT GT		
		CC CACCGGAC ACA CA		
		C_ C_ C		
GAM1647	KIAA0329 3'	ACCACACCACACCACACCACA 16873	C A	T CGA A
		TG GGT GTGGT TG TGT GT		
		AC CCA CACCA AC ACA CA		
		A _ C C_ C		
GAM1647	KIAA0329 3'	ACCACACCACACCACACCTCA 16874	C A	T CGA A
		TG GGT GTGGT TG TGT GT		
		AC CCA CACCA AC ACA CA		
		T _ C C_ C		
GAM1647	LOC200325 5'	CTACAACACCACCACCCA 43290	C A	TTGCGA
		TG GGT GTGGT TGTAG		
		AC CCA CACCA ACATC		
		_ C CA_		
GAM1648	LDHB 5'	AGACCGGCGCCGGAGGAGACGC 8085	G	GGGAG C
	A	TGCGT TC GGCGCCGG CT		
		ACGCA AG CCGCGGCC GA		
		G GAGG_ A		
GAM1648	PAX6 5'	AGGCCGGCGCCGCACACACAC 5826	CGGGAG	
		GTGT GGCGCCGGCCT		
		CACA CCGCGGCCGGA		
		CACACG		
GAM1648	PAX6 5'	AGGCCGGCGCCGCACACACAC 7310	CGGGAG	
		GTGT GGCGCCGGCCT		

CACA CCGCGGCCGGA
 CACACG
 GAM1648 A2BP1 5' CCAGCACCCCCTTCCGCCGC 20805 T T C__ C
 GCG G CGGGAGGG GC GG
 ||| ||||| ||
 CGC C GCCTTCCC CG CC
 __ CCA A
 GAM1648 FLJ14594 3' GCCGACGAACCGACACGC 26567 GAGGG C
 GCGTGTCCG CG CGGC
 ||||| || ||
 CGCACAGCC GC GCCG
 AA__ A
 GAM1648 KIAA1908 3' CCAGCACCCCCTGCACCCA 36331 C T A GC C
 TG GTG CGGG GG GC GG
 || ||| ||| || ||
 AC CAC GTCC CC CG CC
 C _ _ A_ A
 GAM1648 MGC15875 5' AGACCAGCGCCCGAAGGCCGAC 26747 GA__ C C
 ACGC GCGTGTCCG GGGCGC GG CT
 ||||| ||||| ||
 CGCACAGCC CCCGCG CC GA
 GGAAG A A
 GAM1648 RIN3 3' CCGGCGCCCTCTTCACACGTA 24232 CG
 TCGTGT GGAGGGCGCCGG
 ||||| |||||
 ATGCACA TCTCCGCGGCC
 CT
 GAM1648 UREB1 5' GCCTGCCCCCTGACACACA 25365 C A CC
 TG GTGTCGGG GGGCG GGC
 || ||||| |||| ||
 AC CACAGTCC CCCGT CCG
 A _ _
 GAM1649 CHRNA4 3' GCGGCGGACAGGAACACCA 6397 CATA ATC
 TGG CCTGTCCGC CGT
 || ||||| ||
 ACC GGACAGGCG GCG
 ACAA _
 GAM1649 F7 3' CACGGATGCACAGAGATATGC 5605 C__ CC
 GCATA CTGT GCATCCGTG
 |||| ||| |||||
 CGTAT GACA CGTAGGCAC
 AGA _
 GAM1649 F7 3' CACGGATGCACAGAGATATGC 21234 C__ CC
 GCATA CTGT GCATCCGTG
 |||| ||| |||||
 CGTAT GACA CGTAGGCAC
 AGA _
 GAM1649 FBXO2 5' CACAGACGCGGACAGCGCC 14462 ATAC A C
 GGC CTGTCCGC TC GTG
 || ||||| || ||

		CCG GACAGGCG AG CAC		
		C___ C A		
GAM1649 KIAA0435	3'	GCACGGATGGGGGTGATGCCA 16722	ACC GT G	
		TGGCAT T CC CATCCGTGC		
		ACCGTA G GG GTAGGCACG		
		___ TG G		
GAM1649 LOC154214	3'	ACGATCACGGACAGGTATGC 39466	CATC	
		GCATACCTGTCCG CGT		
		CGTATGGACAGGC GCA		
		ACTA		
GAM1650 SNL	3'	ACAGGGTCTGCCCCGCTGCAC 9058	TC	C
		GTGT CGGGCAGACCC GT		
		CACG GCCCGTCTGGG CA		
		TC A		
GAM1650 DKFZp761A132	3'	ACGGAACCCACCATGCACTGCA 26076	TCC__	CAGACC
		TGCGGTGT GGG CCGT		
		ACGTCACG CCC GGCA		
		TACCA AA___		
GAM1650 GMPPB	5'	CGGGCTGGAACACAGCA 45814	G	GCAGA C
		TGC GTGTTCCGG CCC G		
		ACG CACAAGGTC GGG C		
		A ___ A		
GAM1650 KIAA0125	5'	ACGGAGTCTGCCCAAGACTGCA 30343	G CC	C
		TGCGGT TT GGGCAGAC CCGT		
		ACGTCA AA CCCGTCTG GGCA		
		G _ A		
GAM1650 KIAA0125	5'	ACGGAGTCTGCCCAGGACTGCA 16689	TGT _	C
		TGCGG TCC GGGCAGAC CCGT		
		ACGTC AGG CCCGTCTG GGCA		
		___ A A		
GAM1650 KIAA1229	3'	CGGGCAGGGAACATCACA 31097	C	GG AGAC C
		TG GGTGTTCC GC CC G		
		AC CTACAAGG CG GG C		
		A GA ___ A		
GAM1650 LOC143437	5'	ACGGAGTCTGCCCAGGCCACAC 40358	T_ _	C
C		GGTGT CC GGGCAGAC CCGT		
		CCACA GG CCCGTCTG GGCA		
		CC A A		
GAM1650 LOC145989	3'	CGGGTCTGCCCCGCTGCA 29949	TGTTC	C
		TGCGG CGGGCAGACCC G		

ACGTC GCCCGTCTGGG C
 _____ A
 GAM1650 LOC253531 5' ACGGAGTCTGCCAGGCCACAC 46145 T_ _ C
 C GGTGT CC GGGCAGAC CCGT
 |||| | ||||| ||||
 CCACA GG CCCGTCTG GGCA
 CC A A
 GAM1651 ABL1 5' GGAGGGGGTTAAGGCGCAGGCG 11639 A C AGGG
 G TC CCTGCGCCT AACC TC
 || ||||| ||| ||
 GG GGACGCGGA TTGG GG
 C A GGG A
 GAM1651 C1orf17 5' GCCCGAGGCGCAGGGGA 33854 A AACCA
 TC CCTGCGCCTC GGGT
 || ||||| |||
 AG GGACGCGGAG CCCG
 G _____
 GAM1651 C1orf34 3' ACCCTGGTGGTGCAGTGA 30432 C TCA
 TCAC TGC GCC ACCAGGGT
 ||| ||||| |||||
 AGTG ACGTGG TGGTCCCA

 GAM1651 CHODL 3' TGGTTGAGACCAGGTGA 24493 CGC
 TCACCTG CTCAACCA
 ||||| |||||
 AGTGGAC GAGTTGGT
 CA_
 GAM1651 DJ465N24.2.1 5' GGCTAAAGCCGCAGGTGA 21580 C CAACCAG
 TCACCTGCG CT GGTC
 ||||| || |||
 AGTGGACGC GA TCGG
 C AA_____
 GAM1651 DKFZp547I014 5' TGACCCTGGCTTGTGCTAGT 21469 CT CTCAA
 AC GCGC CCAGGGTCA
 || ||| |||||
 TG CGTG GGTCCCAGT
 AT TTC____
 GAM1651 FLJ13052 3' GACCCTGGGCACAGGGGA 23284 A C TCAAC
 TC CCTG GCC CAGGGTC
 || ||| ||| |||||
 AG GGAC CGG GTCCCAG
 G A _____
 GAM1651 KIAA0350 3' ACCTAAGGGGCAGGTGA 30659 G CAACCA
 TCACCTGC CCT GGGT
 ||||| ||| |||
 AGTGGACG GGA TCCA
 G A_____
 GAM1651 KIAA0980 3' GACCCTGGCTGTCTCAGAGTGA 24810 _ CGCCT A
 TCAC CTG CA CCAGGGTC
 ||| ||| || |||||

AGTG GAC GT GGTCCCAG
 A T___ C
 GAM1651 KIAA1529 5' TGACCCCAGTCATCCTGCAGGT 34949 CCTCA CA
 GA TCACCTGCG AC GGGTCA
 ||||| || |||||
 AGTGGACGT TG CCCAGT
 CCTAC AC
 GAM1651 KIAA1617 3' GACCCTGGTTGAGTGGCA 43943 GC
 TGC CTCAACCAGGGTC
 || |||||
 ACG GAGTTGGTCCCAG
 GT
 GAM1651 KIAA1729 5' TGACCCTGTCTGAGCCAAATGA 42952 CC C C AC
 TCA TG GC TCA CAGGGTCA
 || || || || |||||
 AGT AC CG AGT GTCCCAGT
 AA _ _ CT
 GAM1651 MAFB 3' TGACCCTGGCAGTGCAGTGGT 11944 _ CTCAA
 ACC TGCGC CCAGGGTCA
 || |||| |||||
 TGG ACGTG GGTCCCAGT
 TC AC___
 GAM1651 MGC13040 5' GAACCGAGGCGCAGGGA 26754 A AACCA G
 TC CCTGCGCCTC GG TC
 || ||||| || ||
 AG GGACGCGGAG CC AG
 _ _ _ A
 GAM1651 MIC2L1 3' ACCAGGGTCATAGTGAAACGCA 25487 CC A_____ CAGG
 GGTGA CCTGCG TC AC GT
 |||| || || ||
 GGACGC AG TG CA
 AA TGATIIIIAC GGAC
 GAM1651 RAI 5' TGACCCTGAGGTCAACACAG 13473 C_____ ACCA
 CTG GCCTCA GGGTCA
 || |||| |||||
 GAC TGGAGT CCCAGT
 ACAAC _____
 GAM1651 LOC152059 5' CCCCAGTTGAGGCTCAGATGA 39206 C C CA
 TCA CTG GCCTCAAC GGG
 || || ||||| ||
 AGT GAC CGGAGTTG CCC
 A T AC
 GAM1651 LOC152404 5' TGACCCTGCAGTGTGCAGGCGA 39272 A _ CAAC
 TC CCTGCGC CT CAGGGTCA
 || ||||| || |||||
 AG GGACGTG GA GTCCCAGT
 C T C___
 GAM1651 LOC197414 3' TGA CTGTGTGGAACGCAGGTGA 42516 CC AAC G
 TCACCTGCG TC CA GGTCA
 ||||| || || |||||

AGTGGACGC AG GT TCAGT
 A_ GT_ G
 GAM1651 LOC221463 3' ACCCTGATCAAAGGAGGGTGA 44197 GCG CAAC_
 TCACCT CCT CAGGGT
 ||||| ||| |||||
 AGTGGG GGA GTCCCA
 A__ AACTA
 GAM1651 LOC256222 5' GACCCTGGCTGACTGCA 46426 CC A
 TGCG TCA CCAGGGTC
 ||| ||| |||||
 ACGT AGT GGTCCCAG
 C_ C
 GAM1651 LOC57109 3' GACCCCTGGGCCAGGTGA 21654 C T ACCA
 TCACCTG GCC CA GGGTC
 ||||| ||| || |||||
 AGTGGAC CGG GT CCCAG
 _ _ CC_
 GAM1652 ARNT2 3' TCCCCACTGAAGAGGTCTGT 16937 _____ A
 ACAGACCTCT GG GGA
 ||||| || |||
 TGTCTGGAGA CC CCT
 AGTCA _
 GAM1652 CHRNA4 3' GCTTTTCCCCTGCCTGTGAG 6398 ACCTCT A
 CTCACAG GG GGAAAAGC
 ||||| || |||||
 GAGTGTC CC CCTTTTCG
 CGT__ _
 GAM1652 DGCR2 3' CTTTCTTAAGATGCTGTGAG 11612 ACC GG
 CTCACAG TCT AGGAAAAG
 ||||| ||| |||||
 GAGTGTC AGA TTCTTTTC
 GT_ A_
 GAM1652 ED1 3' TCCTCTAGGCCCTGTGAG 7100 AC T
 CTCACAG C CTGGAGGA
 ||||| | |||||
 GAGTGTC G GATCTCCT
 CC_
 GAM1652 EFNB1 3' CCTCCCCAGGCTTTGTGAG 10709 _ CT
 CTCACAGA CCT GGAGG
 ||||| ||| |||||
 GAGTGTTT GGA CCTCC
 C CC
 GAM1652 GLP1R 3' GCTTCTCCTCCAGGTATTTG 7825 CC A
 CAGA TCTGGAGGA AAGC
 ||| ||||| |||||
 GTTT GGACCTCCT TTCG
 AT C
 GAM1652 IHPK1 3' CCTCTCTGGGCCTGTGCAG 45822 _ A CT
 CT CACAG CCT GGAGG
 || ||||| ||| |||||

			GA GTGTC GGG TCTCC		
			C C TC		
GAM1652	IL1F5	3'	CCTAGAAGCAGAGACTCTGTGA 14597	C_	G____
	G		CTCACAGA CTCTG AGG		
			GAGTGTCT GAGAC TCC		
			CA GAAGA		
GAM1652	JTB	5'	GCCCTTCCTCCAGCGCCCTGCG 13514	A	ACCT AA
	G		TC CAG CTGGAGGAA GC		
			GG GTC GACCTCCTT CG		
			C CCGC CC		
GAM1652	LIF	3'	GCTCTTCCTCTGGGTAAAGGTC 8096	____	TG A
	TGT		ACAGACCT C GAGGAA AGC		
			TGTCTGGA G CTCCTT TCG		
			AATG GT C		
GAM1652	MEN1	5'	CCTCCCCAAGCCTGTGTCTGTG 44841	____	CT_
	A		TCACAGAC CT GGAGG		
			AGTGTCTG GA CCTCC		
			TGTCC ACC		
GAM1652	MSL3L1	5'	GCTTTCTTTAAAAAAGGGTCTG 13670	CTG____	A
	TGA		TCACAGACCT GAGGAAA GC		
			AGTGTCTGGG TTTCTTT CG		
			AAAAAA _		
GAM1652	PIK3C2B	3'	CTTTTCCTCATTCTGTGGG 8506		CCTCTG
			CTCACAGA GAGGAAAAG		
			GGGTGTCT CTCCTTTTC		
			TA____		
GAM1652	PMM2	3'	CCTCCCTCTTGGGTGGGTCTGTG 35678	_	_____
	G		TCACAGACCT CT GGAGG		
			GGTGTCTGGG GG CCTCC		
			T TTCTC		
GAM1652	PROK1	3'	CCTTCACGTGAGGTCTGTGAG 26198	_____	
			CTCACAGACCTC TGGAGG		
			GAGTGTCTGGAG ACTTCC		
			TGC		
GAM1652	SH3BP2	3'	CCTCTGGGTCTGTGAG 8945	CT	
			CTCACAGACCT GGAGG		
			GAGTGTCTGGG TCTCC		

GAM1652	SLC22A12	5'	GCTTTCCCGGGAGGTCTGGAG 29404	A	GGA A
			CTC CAGACCTCT GGAAA GC		

GAG GTCTGGAGG CCTTT CG
 _ GC_ _
 GAM1652 SPARC 3' TTCCCCAGGTGGCCTGGAG 9089 A A _ A
 CTC CAG CC TCTGG GGAA
 ||| ||| || ||||| ||||
 GAG GTC GG GGACC CCTT
 _ C T _
 GAM1652 TH1L 3' CTTTTCCTCCCCATCCTGGAG 18537 A ACCTCT
 CTC CAG GGAGGAAAAG
 ||| ||| ||||| |||||
 GAG GTC CCTCCTTTTC
 _ CTACC_
 GAM1652 TRPC1 3' CTTTTCCTCCACAGCTGTG 9307 AC C
 CACAG CT TGGAGGAAAAG
 ||||| || ||||| |||||
 GTGTC GA ACCTCCTTTTC
 _ C
 GAM1652 AF9Q34 5' GCTTTTCCTGCCGGTCTG 26275 TCT _
 CAGACC GG AGGAAAAGC
 ||||| || ||||| |||||
 GTCTGG CC TCCTTTTCG
 _ G
 GAM1652 AMOTL1 3' CCTCCAGGAAATCTTGAG 36464 C CC_
 CTCA AGA TCTGGAGG
 ||||| ||| ||||| |||||
 GAGT TCT GGACCTCC
 _ AAA
 GAM1652 AQP9 5' TCTCCAGGAATCTGTGAG 21970 CC
 CTCACAGA TCTGGAGG
 ||||| ||||| ||||| |||||
 GAGTGTCT GGACCTCT
 AA
 GAM1652 ARNTL2 3' GCTTTCCAAGGGAGGTCTAGGA 21416 AC GGA A
 TC AGACCTCT GGAAA GC
 || ||||| ||||| ||||| |||||
 AG TCTGGAGG CCTTT CG
 GA GAA _
 GAM1652 BLZF1 5' CTTCCGAATGGAAGAGGTCTGT 9750 _____
 GAG CTCACAGACCTCT GGAGG
 ||||| ||||| ||||| |||||
 GAGTGTCTGGAGA CCTTC
 AGGTAAG
 GAM1652 C20orf160 3' GCTTTGTCCCAGAAGTCCAGAG 27933 ACA C A GA
 CTC GAC TCTGG G AAAGC
 ||| ||| ||||| ||||| |||||
 GAG CTG AGACC C TTTCG
 AC_ A _TG
 GAM1652 DKFZP547E2110 3' GCTTTTCCAACAAATCTTTGA 43730 C CCTC GA
 TCA AGA TG GGAAAAGC
 ||| ||| || ||||| |||||

AGT TCT AC CCTTTTCG
 T AA__ AA
 GAM1652 DKFZP586F1524 3' TTTTCTTCAGAAGACCCATGTG 17855 GACC____
 CACA TCTGGAGGAAA
 |||| |||||
 GTGT AGACTTCTTTT
 ACCCAGA
 GAM1652 FADS2 3' GCTTTTCCTCAGGGTGTCTGA 10467 CA _ G
 G CTCA GAC CTCTG AGGAAAAGC
 |||| ||||| |||||
 GAGT CTG GGGAC TCCTTTTCG
 C_ T _
 GAM1652 FLJ00024 3' GCCCTTCCTCCAGGTGTGTG 31895 G CT AA
 CACA ACCT GGAGGAA GC
 |||| ||||| |||||
 GTGT TGA CCTCCTT CG
 G _ CC
 GAM1652 FLJ10201 3' GCTTTTCTGCAAAGTCTGTGG 19762 CTC GA
 TCACAGAC TG GGAAAAGC
 ||||| || |||||
 GGTGTCTG AC TCTTTTCG
 AA_ G_
 GAM1652 FLJ10330 3' GCTTTTCCCCCATTTGT 19831 CCTC A
 ACAGA TGG GGAAAAGC
 |||| |||||
 TGTTT ACC CCTTTTCG
 _ C
 GAM1652 FLJ10604 3' GCTTTTCCTCTACAGGCCT 19963 A C
 AG CCT TGGAGGAAAAGC
 || |||||
 TC GGA ATCTCCTTTTCG
 C C
 GAM1652 FLJ13181 5' CCTCCTGAGTAGATCTGTGGG 24827 C__ T
 CTCACAGA CTC GGAGG
 ||||| |||||
 GGGTGTCT GAG CCTCC
 AGAT T
 GAM1652 FLJ14050 5' CCTCCCATGCAGAGGTCAGTGA 30255 A ____
 G CTCAC GACCTCT GGAGG
 |||| ||||| |||||
 GAGTG CTGGAGA CCTCC
 A CGTAC
 GAM1652 FLJ14084 3' CCTGTTAGAAGTCTGTGAG 22283 C _
 CTCACAGAC TCTGG AGG
 ||||| |||||
 GAGTGTCTG AGATT TCC
 A G
 GAM1652 FLJ14346 5' CTCCAGGGTGCAGAGGCCTGC 24621 A A ____
 GGG CTC CAG CCTCT GGAG
 ||||| |||||

		GGG GTC GGAGA	CCTC		
		C C CGTGGGAC			
GAM1652	FLJ14816	3'	GCCCTTCCTTCGGACCGTGAG	26640	AGACC AA
			CTCAC TCTGGAGGAA GC		
			GAGTG AGGCTTCCTT CG		
			CC__ CC		
GAM1652	FLJ20297	5'	CCTCCCACGAGATCTGGAG	19650	A C T__
			CTC CAGA CTC GGAGG		
			GAG GTCT GAG CCTCC		
			_ A CAC		
GAM1652	FLJ21313	3'	CCTGGTCAAGAATCTGTGAG	23409	CC _ _
			CTCACAGA TCT GG AGG		
			GAGTGTCT AGA CT TCC		
			A_ A GG		
GAM1652	GOLGIN-67	3'	GCCTTTCCTCCATTTTCTGTG	45535	CCTC A
			CACAGA TGGAGGAAA GC		
			GTGTCT ACCTCCTTT CG		
			TTT_ C		
GAM1652	KIAA0229	3'	CTTTCAGGGCCTGTGAG	44400	A T
			CTCACAG CC CTGGAGG		
			GAGTGTC GG GACTTTC		
			C _		
GAM1652	KIAA0247	3'	CTTTCCTCTCTGCGAG	16376	A CCTCTG A
			CTC CAGA GAGGAAA G		
			GAG GTCT CTCCTTT C		
			C _ C		
GAM1652	KIAA0275	3'	CCTCCCAGCATCTGTGAG	16550	CCT _
			CTCACAGA CTGG AGG		
			GAGTGTCT GACC TCC		
			AC_ C		
GAM1652	KIAA0596	3'	TTCGCCAGAAGTTTGTGAG	31467	C A
			CTCACAGAC TCTGG GGA		
			GAGTGTTTG AGACC CTT		
			A G		
GAM1652	KIAA0682	3'	GCTCTCCCTCCAGGGCTGCTGA	18290	_ A T AAA
	G		CTCA CAG CC CTGGAGG AGC		
			GAGT GTC GG GACCTCC TCG		
			C _ _ CTC		
GAM1652	KIAA0855	3'	GCCTTTCCTCCATTTTCTGTG	17374	CCTC A
			CACAGA TGGAGGAAA GC		

GTGTCT ACCTCCTTT CG
 TTT_ C
 GAM1652 KIAA0977 3' TCTTCCGGAGTCTAGAG 17082 AC C
 CTC AGAC TCTGGAGGA
 ||| ||| |||||
 GAG TCTG AGGCCTTCT
 A_ _
 GAM1652 KIAA1014 3' CTTCTCCTCCAGAACAAGTG 32570 AGACC A
 CAC TCTGGAGGA AAG
 ||| ||||| |||
 GTG AGACCTCCT TTC
 AACA_ C
 GAM1652 KIAA1322 3' GCTGCTCCTCCAGAGGTCTG 36030 AA
 CAGACCTCTGGAGGA AGC
 ||||| |||
 GTCTGGAGACCTCCT TCG
 CG
 GAM1652 KIAA1462 3' TTTCCCAGAGGTCTTGA 43924 C A
 TCA AGACCTCTGG GGAA
 ||| ||||| |||
 AGT TCTGGAGACC CTTT
 _ _
 GAM1652 KIAA1497 5' CTTTTCCTTCTTACTGTGA 33529 ACCTCT
 TCACAG GGAGGAAAAG
 ||||| |||||
 AGTGTC CTTCTTTTC
 ATT____
 GAM1652 KIAA1553 3' CTCCCGAGTGGAGGTCGTGAG 44143 A _____
 CTCAC GACCTCT GGAG
 ||||| ||||| |||
 GAGTG CTGGAGG CCTC
 _ TGAGC
 GAM1652 KIAA1940 3' TCCTCCAGAGGCCTGGAAG 39010 CA A
 CT CAG CCTCTGGAGGA
 || ||| |||||
 GA GTC GGAGACCTCCT
 AG C
 GAM1652 KIF13B 3' CTTTCCTCCCCACTGGAG 17582 A ACCTCT A
 CTC CAG GGAGGAAA G
 ||| ||| ||||| |
 GAG GTC CCTCCTTT C
 _ ACC_ C
 GAM1652 MGC13061 3' CTTTCCTGCAGCCTGGAG 26127 A ACCT G A
 CTC CAG CTG AGGAAA G
 ||| ||| ||| ||||| |
 GAG GTC GAC TCCTTT C
 _ C_ G C
 GAM1652 NEUROD6 5' TTTTATAGAGATCAATGAG 22929 CA C
 CTCA GA CTCTGGAGG
 |||| || |||||

GAGT CT GAGATTTTT
 AA A
 GAM1652 NYD-SP29 5' GCTTTTCCTGAGGGCACTG 36862 A__ TGG
 CAG CCTC AGGAAAAGC
 ||| ||| |||||
 GTC GGAG TCCTTTTCG
 ACG ____
 GAM1652 p25 3' TTTTCCAGAGCCTGTTAG 13895 C AC
 CTACAG CTCTGGAGGA
 || ||| |||||
 GA TGTC GAGACCTTTT
 T C_
 GAM1652 PARVA 3' TCCTCCAGAAGTCTGTGA 20146 C
 TCACAGAC TCTGGAGGA
 ||||| |||||
 AGTGTCTG AGACCTCCT
 A
 GAM1652 RASAL2 3' GCTTTTCCCCCACATCTCTATG 11249 C CCTC A
 CA AGA TGG GGAAAAGC
 || ||| ||| |||||
 GT TCT ACC CCTTTTCG
 A CTAC C
 GAM1652 RNF38 3' CCTTCAGAAACTGTGAG 23060 ACC
 CTCACAG TCTGGAGG
 ||||| |||||
 GAGTGTC AGACTTCC
 AA_
 GAM1652 RNF8 3' TTTCCTTCAGGCTCTGTGA 10101 C T
 TCACAGA C CTGGAGGAAA
 ||||| | |||||
 AGTGTCT G GACTTCCTTT
 C_
 GAM1652 RNPC2 3' TCTTTTAAAGCTCTGTGAG 11336 C CT
 CTCACAGA CT GGAGGA
 ||||| || |||||
 GAGTGTCT GA TTTTCT
 C AT
 GAM1652 SARM 3' GCCTTTCCTCCAAAGCCTG 17460 AC C A
 CAG CT TGGAGGAAA GC
 ||| || ||||| ||
 GTC GA ACCTCCTTT CG
 C_ A C
 GAM1652 SEC10L1 5' CCTCCTGGGATCTGTGGG 13298 C T
 CTCACAGA CTC GGAGG
 ||||| ||| |||||
 GGGTGTCT GGG CCTCC
 A T
 GAM1652 SMARCF1 3' GCTTTTCCCCCAAAGTATCATG 12626 _ C_ C A
 TG CACA GA CT TGG GGAAAAGC
 |||| || ||| |||||

			GTGT CT GA ACC CCTTTTCG		
			A AT A C		
GAM1652	SMARCF1	3'	GCTTTTCCCCCAAAGTATCATG 20521	_ C_ C A	
	TG		CACA GA CT TGG GGAAAAGC		
			GTGT CT GA ACC CCTTTTCG		
			A AT A C		
GAM1652	SMARCF1	3'	GCTTTTCCCCCAAAGTATCATG 29164	_ C_ C A	
	TG		CACA GA CT TGG GGAAAAGC		
			GTGT CT GA ACC CCTTTTCG		
			A AT A C		
GAM1652	SS18L1	3'	CCCTATGAGGAAATCTGGAG 32559	A _ _ A	
			CTC CAGA CCTC TGG GG		
			GAG GTCT GGAG ATC CC		
			_ AAA T _		
GAM1652	TBX4	3'	CTTCTGGAGAGTCTGTGAG 20545	_ TG	
			CTCACAGAC CTC GAGG		
			GAGTGTCTG GAG CTTC		
			A GT		
GAM1652	ZFP106	3'	CTTCAAGAGGGTCTGTGAG 22831	_ G	
			CTCACAGACC TCT GAGG		
			GAGTGTCTGG AGA CTTC		
			G A		
GAM1652	LOC112868	3'	GCCCTTCCTCCATGTGTTTGT 36082	CTC AA	
			ACAGAC TGGAGGAA GC		
			TGTTTG ACCTCCTT CG		
			TGT CC		
GAM1652	LOC124842	3'	GCTCTTCCTCCAGTGGCTCGT 37263	_ A T A	
			AC AG CC CTGGAGGAA AGC		
			TG TC GG GACCTCCTT TCG		
			C _ T C		
GAM1652	LOC126302	3'	GCTCTCCCTCCAGAGCCTGT 36823	AC AAA	
			ACAG CTCTGGAGG AGC		
			TGTC GAGACCTCC TCG		
			C_ CTC		
GAM1652	LOC126661	5'	GCTTTTCCCCCAGTTCCCCAAG 36854	ACAGACCT A	
	AG		CTC CTGG GGAAAAGC		
			GAG GACC CCTTTTCG		
			AACCCCTT C		
GAM1652	LOC130355	5'	TCCTCCCTTGGGGTCTAGAG 36989	AC T_	
			CTC AGACCTC GGAGGA		

	GAG TCTGGGG CCTCCT		
	A_ TTC		
GAM1652 LOC130752 3'	GCTTTGTATAAAGGTCTGT 37006	C GAGGA	
	ACAGACCT TG AAAGC		
	TGTCTGGA AT TTTCG		
	A ATG__		
GAM1652 LOC144501 3'	CCTCCAGGCCTGTGGG 40423	ACC	
	CTCACAG TCTGGAGG		
	GGGTGTC GGACCTCC		
	C__		
GAM1652 LOC145988 3'	GCCTTTCCTCCATTTTCTGTG 38039	CCTC	A
	CACAGA TGGAGGAAA GC		
	GTGTCT ACCTCCTTT CG		
	TTT_ C		
GAM1652 LOC149603 3'	CCTTGGTGCGATGTCTGTGAG 34970	C TG__	
	CTCACAGAC TC GAGG		
	GAGTGTCTG AG TTCC		
	T CGTGG		
GAM1652 LOC149619 5'	TCTCTACATGAAGTCTGTGG 41028	C ____	
	TCACAGAC TC TGGAGG		
	GGTGTCTG AG ATCTCT		
	A TAC		
GAM1652 LOC150819 3'	TCCCTATGTGAGGTTTGT 41247	__ A	
	ACAGACCTC TGG GGA		
	TGTTTGGAG ATC CCT		
	TGT _		
GAM1652 LOC151521 3'	CTTTTCCTAGTATTGTGAG 41369	AC CTGG	
	CTCACAG CT AGGAAAAG		
	GAGTGTT GA TCCTTTTC		
	AT ____		
GAM1652 LOC152765 5'	CTGCCAGAGGTCTAAGAG 39316	AC	A_
	CTC AGACCTCTGG GG		
	GAG TCTGGAGACC TC		
	AA CG		
GAM1652 LOC152925 3'	CTCTTCCTTTTCAGGACCTTGA 39332	C A_ CT	A
	TCA AG CCT GGAGGAA AG		
	AGT TC GGA TTTCCTT TC		
	_ CA CT C		
GAM1652 LOC204301 3'	GCCTTTCCTCCATTTTCTGTG 43093	CCTC	A
	CACAGA TGGAGGAAA GC		

GTGTCT ACCTCCTTT CG
 TTT_ C
 GAM1652 LOC205313 5' GCCCTTCCTCCAGGCTTCT 43594 CC AA
 AGA TCTGGAGGAA GC
 ||| ||||| ||
 TCT GGACCTCCTT CG
 TC CC
 GAM1652 LOC221751 5' TTTCTTTAGATCTGTGCAG 44192 _ CC
 CT CACAGA TCTGGAGGAA
 || |||| |||||
 GA GTGTCT AGATTCTTT
 C _
 GAM1652 LOC253350 5' GCCCTTCCTCGGCATCTGGAG 46587 A CCT G AA
 CTC CAGA CTG AGGAA GC
 ||| ||| ||| ||| ||
 GAG GTCT GGC TCCTT CG
 _ AC_ _ CC
 GAM1652 LOC253981 3' CTTTTCCTTTAGGCCTG 45863 A CT A
 CAG CCT GG GGAAAAG
 ||| ||| || |||||
 GTC GGA TC CCTTTTC
 C TT _
 GAM1652 LOC254358 3' GCCTTTCCTCCATTTTCTGTG 45531 CCTC A
 CACAGA TGGAGGAAA GC
 ||||| ||||| ||
 GTGTCT ACCTCCTTT CG
 TTT_ C
 GAM1652 LOC257476 3' CCTCTCTGGGCCTGTGCAG 30714 _ A CT
 CT CACAG CCT GGAGG
 || |||| ||| ||||
 GA GTGTC GGG TCTCC
 C C TC
 GAM1652 LOC64102 5' GCTTCTCCTCTGGCATCTGTGA 22708 C CCT TG A
 G CT ACAGA C GAGGA AAGC
 || |||| | |||| ||||
 GA TGTCT G CTCCT TTCG
 T AC_ GT C
 GAM1653 IHPK3 3' ACCTTCTGGAGTACACTG 27653 C _ A
 TAG TGT CTCCA AAGGT
 ||| ||| ||||| ||||
 GTC ACA GAGGT TTCCA
 _ T C
 GAM1653 RDS 3' CACCCTTTGGAGACCAGGCCTC 5862 TA _ A
 A TG GCT GTCTCCAAA GGTG
 || ||| ||||| ||||
 AC CGG CAGAGGTTT CCAC
 TC AC C
 GAM1653 UBE2V1 3' CACCTTTTGAAGCAGCAAC 9369 A T C
 GT GCTG CT CAAAAGGTG
 || |||| || |||||

CA CGAC GA GTTTTCCAC
 A _ A
 GAM1653 UBE2V1 3' CACCTTTTGAAGCAGCAAC 22521 A T C
 GT GCTG CT CAAAAGGTG
 || ||| || |||||
 CA CGAC GA GTTTTCCAC
 A _ A
 GAM1653 UBE2V1 3' CACCTTTTGAAGCAGCAAC 22768 A T C
 GT GCTG CT CAAAAGGTG
 || ||| || |||||
 CA CGAC GA GTTTTCCAC
 A _ A
 GAM1653 BS69 5' TGTGAAACAAC TACATTA 13407 C C _
 TAATGTAG TGT TC CA
 ||||| ||| ||
 ATTACATC ACA AG GT
 A A T
 GAM1653 FLJ12903 3' CACCTTTTGGAAATGCCCATTTG 22977 TA T C
 TAATG GC GT TCCAAAAGGTG
 |||| ||| |||||
 GTTAC CG TA AGGTTTCCAC
 C _ _ A
 GAM1653 KIAA0285 5' CACCCCTGGGCAGCTTCA 16750 T CT AAA
 TG AGCTGT CCA GGTG
 || ||||| ||| |||
 AC TCGACG GGT CCAC
 T _ _ CC_
 GAM1653 KIAA0446 5' CCTTTTGAAGAGCTCA 34149 T TG C
 TG AGC TCT CAAAAGG
 || ||| ||| |||||
 AC TCG AGA GTTTTCC
 _ _ A
 GAM1653 KIAA0630 5' CACCTTTTGGATTTTCCACAT 43061 AGCTGTC
 ATGT TCCAAAAGGTG
 ||| |||||
 TACA AGGTTTCCAC
 CCTTTT_
 GAM1653 KIAA0945 3' CACCTCCCAGAGACGGCCAC 17291 A CAAA
 GT GCTGTCTC AGGTG
 || ||||| |||
 CA CGGCAGAG TCCAC
 C ACCC
 GAM1653 SUN1 3' CACTGTGAGGAGACAGCCAC 24793 A AAAA
 GT GCTGTCTCC GGTG
 || ||||| |||
 CA CGACAGAGG TCAC
 C AGTG
 GAM1653 LOC154881 3' CACCTTTTGGAGATTTAACCAT 39494 TAGCT
 ATG GTCTCCAAAAGGTG
 ||| |||||

			TAC TAGAGGTTTTCCAC			
			CAATT			
GAM1653	LOC254122	3'	CACCATCAGAGACAGCCACA	45435	A	CAAAA
			TGT GCTGTCTC GGTG			
			ACA CGACAGAG CCAC			
			C ACTA_			
GAM1654	DSC2	3'	GGGTATAATGACAACAGCCA	11393	A A	__
			TG CT TTGTCAT TGCCT			
			AC GA AACAGTA ATGGG			
			C C AT			
GAM1654	RNF14	3'	TGCCCCAAGCTCTGAATAGTTA	10505		TG TT CTCA
			TGACTAT TCA GC GGCA			
			ATTGATA AGT CG CCGT			
			__ CT AAAC			
GAM1654	CECR1	3'	TGCCTGAGCTATGACAACAG	18886	A	T C
			CT TTGTCAT GC TCAGGCA			
			GA AACAGTA CG AGTCCGT			
			C T _			
GAM1654	KIAA1877	3'	TGTTGCAATGACAATAGCA	32887	A	CT
			TG CTATTGTCATTGC CA			
			AC GATAACAGTAACG GT			
			_ TT			
GAM1654	LOC254848	5'	GCCCCGAGGCAATGAACAGTA	46380	_	A
			TATTGT CATTGCCTC GGC			
			ATGACA GTAACGGAG CCG			
			A C			
GAM1654	LOC255308	3'	GCCTGAAATCCAATAGTC	45356		TC GCC
			GACTATTG ATT TCAGGC			
			CTGATAAC TAA AGTCCG			
			C_ __			
GAM1655	FLJ12443	3'	CTTTGGTAGCTAACAGTCACTG	24224	C	GTAAC
	A		TCAG GAT GTTACCAAAG			
			AGTC CTG CGATGGTTTC			
			A ACAAT_			
GAM1655	KIAA0478	3'	CTTTGGGGACTACATTGCTGA	16980		ACT TA
			TCAGCGATGTA GT CCAAAG			
			AGTCGTTACAT CA GGTTTC			
			_ GG			
GAM1656	DGKI	3'	CTACCTGAGACCATGCC	11079	C C	
			GGCATGGTCTC AGG TGG			

CCGTACCAGAG TCC ATC

GAM1656 HCN2 3' CCAGACCAAAGCCATGCC 6863 T CCA _
GGCATGG CT GG CTGG
||||| || || ||||
CCGTACC GA CC GACC
_ AA_ A

GAM1656 LIFR 3' CTGACCAGCCCAAATCAT 8103 CTCCA
ATGGT GGCTGGTCAG
|||| |||||||
TACTA CCGACCAGTC
AAC_

GAM1656 SLC9A1 5' CTTTTCCTAGAGACTACGCC 34858 A C CT_
GGC TGGTCTC AGG GG
|| ||||| || ||
CCG ATCAGAG TCC TC
C A TTT

GAM1656 SMAC 5' CTGACCAGCCCTCGTCAGCC 29050 A TCTCCA
GGC TGG GGCTGGTCAG
||| || |||||||
CCG ACT CCGACCAGTC
_ GCTC_

GAM1656 TSSC4 5' TGAACAGAGGCCATGCCG 12259 CAGGC G
CGGCATGGTCTC TG TCA
||||||| || |||
GCCGTACCGGAG AC AGT
_____ A

GAM1656 WISP1 3' CCAGCTGCAGACCATGCC 9962 CCA
GGCATGGTCT GGCTGG
||||||| |||||
CCGTACCAGA TCGACC
CG_

GAM1656 C22orf2 3' CCAGTCTGAAAACCAGACCG 45334 CA CTC
CGG TGGT CAGGCTGG
||| ||| |||||||
GCC ACCA GTCTGACC
AG AAA

GAM1656 FLJ00001 3' CCCCTGGAGGCCACGCC 39775 A CT
GGC TGGTCTCCAGG GG
||| ||||||| ||
CCG ACCGGAGGTCC CC
C _

GAM1656 FLJ22037 5' GGCCTGGAAACCACGCTG 45075 A C
CGGC TGGT TCCAGGCT
|||| ||| |||||||
GTCG ACCA AGGTCCGG
C A

GAM1656 KCNT1 3' GGCCTGGACACCACGCCG 30977 A C
CGGC TGGT TCCAGGCT
|||| ||| |||||||

GCCG ACCA AGGTCCGG
 C C
 GAM1656 MDS018 3' CTGAGGTTTCCTGCAGACCATG 22401 C CTGG_
 CC GGCATGGTCT CAGG TCAG
 ||||| ||| |||
 CCGTACCAGA GTCC AGTC
 C TTTGG
 GAM1656 SDC3 3' CTGACCAGCCCAAATCTGCC 16083 T CTCCA
 GGCA GGT GGCTGGTCAG
 ||| ||| |||||
 CCGT CTA CCGACCAGTC
 _ AAC_
 GAM1656 LOC126353 3' CCAACCCTGGGAAACCATCC 36829 C C_ C_
 GG ATGGT TCCAGG TGG
 || ||| ||||| |||
 CC TACCA GGGTCC ACC
 _ AA CA
 GAM1656 LOC128989 3' CCAGCTGGAGACCATGCC 36940 G
 GGCATGGTCTCCAG CTGG
 ||||| |||
 CCGTACCAGAGGTC GACC
 _
 GAM1656 LOC134265 3' CTGAGGTAGCTGGAGACCACAG 37074 A_ G G_
 C GC TGGTCTCCAG CTG TCAG
 || ||||| ||| |||
 CG ACCAGAGGTC GAT AGTC
 AC _ GG
 GAM1656 LOC157349 3' TGACCAGCCCTCCTGCC 39599 T TCTCCA
 GGCA GG GGCTGGTCA
 ||| || |||||
 CCGT CC CCGACCAGT
 _ TC_
 GAM1656 LOC219700 5' CTGACCAGGCTAGACCACACG 44701 GCA CC G
 CG TGGTCT AG CTGGTCAG
 || ||||| || |||||
 GC ACCAGA TC GACCAGTC
 AC_ _ G
 GAM1656 LOC221399 5' CTGACTTCTTTGGAGACACACC 45051 CATG CT
 G CGG GTCTCCAGG GGTCAG
 || ||||| |||||
 GCC CAGAGGTTT TCAGTC
 ACA_ CT
 GAM1656 LOC256158 5' CTGGAGTGCCAGAGCCACGCC 46625 A T CA TGG
 GGC TGG CTC GGC TCAG
 ||| ||| ||| |||
 CCG ACC GAG CCG GGTC
 C _ A_ TGA
 GAM1656 LOC51337 3' TGACCAGCCTGGCCCACC 18765 CA TCT
 GG TGG CCAGGCTGGTCA
 || ||| |||||

CC ACC GGTCCGACCAGT
 _ C_
 GAM1656 LOC54103 5' CTGACCAGCCCAGGAGGAACCA 45208 _ A_
 TGGT CTCC GGCTGGTCAG
 |||| ||| |||||
 ACCA GAGG CCGACCAGTC
 AG AC
 GAM1657 MARK3 5' GCGCGTGCAGCCCCGGACA 8191 C TA ACACA
 TG CCG GCT TACGCGC
 || ||| || |||||
 AC GGC CGA GTGCGCG
 A CC C____
 GAM1657 FLJ21276 3' CGCGTATGTGAGCATAGCA 23901 CC A A
 TGC GT GCT CACATACGCG
 ||| || ||| |||||
 ACG TA CGA GTGTATGCGC
 A _ _ _
 GAM1657 LOC92299 5' CGCGTACGAGTGTCTACGGGC 34130 CT A_
 GCCCGTAG ACAC TACGCG
 ||||| ||| |||||
 CGGGCATC TGTG ATGCGC
 _ AGC
 GAM1658 ARHC 5' GAGCTCCCTTTTCCGTGGA 11663 CA A
 TCCACGAAA AG GAGTTC
 ||||| || |||||
 AGGTGCCTTT TC CTCGAG
 _ C
 GAM1658 HDAC4 5' GAGCTATCGTTTCCGTGGA 12665 AA G
 TCCACGAAAC GA AGTTC
 ||||| || |||||
 AGGTGCCTTTG CT TCGAG
 _ A
 GAM1658 ICOS 3' GATTCTCTTATTTCCGGGA 14391 A C
 TCC CGGAAA AAGAGAGTT
 || ||||| |||||
 AGG GCCTTT TTCTCTTAG
 _ A
 GAM1658 LIMD1 3' TCGCCTTGTTTCCATGGG 15501 C A_
 TCCA GGAAACAAG GA
 ||| ||||| ||
 GGGT CCTTTGTTC CT
 A CG
 GAM1658 ASAH 3' GTGAACTCCACCTCCGTGGA 10518 AACAAGA
 TCCACGGA GAGTTCAC
 ||||| |||||
 AGGTGCCT CTCAAGTG
 CCAC____
 GAM1658 KIAA0934 3' TCTCTTGGCTTCCATGGA 32121 C A_
 TCCA GGAA CAAGAGA
 ||| ||| |||||

		AGGT CCTT GTTCTCT		
		A CG		
GAM1658	KIAA1904	3' GGGCTCTTGTCCCGGTGGA	36383	_ AAACAA
		TCCAC GG GAGAGTTC		
		AGGTG CC TTCTCGGG		
		G CTG__		
GAM1658	LIP8	5' GTGAACTTTTCCTCCTGGA	42547	C AACAA
		TCCA GGA GAGAGTTCAC		
		AGGT CCT TTTTCAAGTG		
		_ CC__		
GAM1658	LOC149478	3' CGTGTTTCTCATTTCCGTGGA	38751	CAA TT
		TCCACGGAAA GAGAG CACG		
		AGGTGCCTTT CTCTT GTGC		
		A__ T__		
GAM1658	LOC196477	3' TGAAGTTGCTTCTGTGGA	42376	AACA AG G
		TCCACGGA AG A TTCA		
		AGGTGTCT TC T AAGT		
		__ GT G		
GAM1658	LOC199990	3' GAGTTCTGTTTCCGTGGA	42682	AGA GT
		TCCACGGAAACA GA TC		
		AGGTGCCTTTGT CT AG		
		__ TG		
GAM1658	LOC245806	3' TGTGCCTCTCACTCCGTGGA	44132	AACAA TT
		TCCACGGA GAGAG CACG		
		AGGTGCCT CTCTC GTGT		
		CA__ C__		
GAM1658	LOC91663	5' GATCTTTCTCCGTGGA	28753	AACAA T
		TCCACGGA GAGAG TC		
		AGGTGCCT CTTTC AG		
		__ T		
GAM1659	EGLN2	5' CCGTCATCCGCCACTGCG	28021	C
		CGCAGTG CGGATGGCGG		
		GCGTCAC GCCTACTGCC		
		C		
GAM1659	EGR4	5' TCCCCGCCACCCGCGCGC	7693	_ A
		GTGC CGG TGGCGGGGA		
		CGCG GCC ACCGCCCT		
		C C		
GAM1659	MX1	5' CCGCACTCCAGCACTGCG	8292	C TG
		CGCAGTGC GGA GCGG		

GCGTCACG CCT CGCC
 A CA
 GAM1659 TBL1X 3' CCCC GCCACCTGTACTCA 12180 C C A
 G AGTGC GG TGGCGGGG
 I ||||| II |||||
 A TCATG CC ACCGCCCC
 C T _
 GAM1659 ATPW 5' CTCGACCCGGCACTGGGTA 17908 G ATGG
 TAC CAGTGCCGG CGGG
 III ||||| III
 ATG GTCACGGCC GCTC
 G CA__
 GAM1659 CCR1 3' CCCC GCCACCCTCCCACTGC 6974 CC_ A
 GCAGTG GG TGGCGGGG
 ||||| II |||||
 CGTCAC CC ACCGCCCC
 CCT C
 GAM1659 FLJ12552 3' TCCTGTATCCGGCACTGC 23115 G
 GCAGTGCCGGATG CGGGG
 ||||| |||||
 CGTCACGGCCTAT GTCCT
 _
 GAM1659 FLJ20306 5' CCCC GCCGCTCACCGGCGC 19368 A__
 GTGCCGG TGGCGGGG
 ||||| |||||
 CGCGGCC GCCGCCCC
 ACTC
 GAM1659 FLJ32865 3' CCCC ACCACCCGGTGCTGC 29424 TG A C
 GCAG CCGG TGG GGGG
 |||| |||| ||||
 CGTC GGCC ACC CCCC
 GT C A
 GAM1659 KIAA1910 3' TCCCC GCCCCAGCAACTGC 36288 _ C AT
 GCAGT GC GG GGC GGGA
 |||| II || |||||
 CGTCA CG CC CCGCCCT
 A A _
 GAM1659 LOC143888 3' CCCC GCCCCCCGTC ACTGC 37668 C AT
 GCAGTG CGG GGC GGGA
 ||||| || |||||
 CGTCAC GCC CCGCCCC
 T CC
 GAM1659 LOC157737 5' CCGCACCTGCACTGCGTA 41842 C ATG
 TACGCAGTGC GG GCGG
 ||||| || ||||
 ATGCGTCACG CC CGCC
 T CA_
 GAM1659 LOC158310 5' TCCCC GCCACCCACGCACTCA 41948 C C__ A
 G AGTGC GG TGGCGGGGA
 I ||||| II |||||

A TCACG CC ACCGCCCCT
 C CAC C
 GAM1659 LOC163033 5' TCCCCGCCACCACCGTCCGCGT 40073 AGTGC A__
 ACGC CGG TGGCGGGGA
 |||| ||| |||||
 TGCG GCC ACCGCCCCT
 CCT__ ACC
 GAM1660 BTG2 3' AGAAAAGACAAAGGTTA 13621 CGAGG
 TAACTTTTGTC TTCT
 ||||| |||
 ATTGGAAACAG AAGA
 AA__
 GAM1660 CSNK1G1 3' AGATTCTTCTGGACAAAAGT 22568 _ T_
 ACTTTTGTCC GAGG TCT
 ||||| ||| |||
 TGAAAACAGG CTTC AGA
 T TT
 GAM1660 KIAA0528 5' CGGAAGAACCCATCAAAG 35840 TCCGA
 TTTTG GGTCTTCCG
 |||| |||||
 GAAAC CCAAGAAGGC
 TAC__
 GAM1660 KIAA0987 3' AGAAACTTTGGAACAAAA 14674 _ _
 TTTTGT CCGAGGTT CT
 |||| ||||| ||
 AAAACA GGTTC AA GA
 A A
 GAM1660 KIAA1117 3' GAGGGCCGGACAAAAG 30634 GA
 CTTTGTCC GGTCTT
 ||||| |||||
 GAAAACAGG CCGGGAG
 _
 GAM1660 LOC149146 5' GAAGAACGACAAAAG 38656 CGAG
 CTTTGTCC GTTCTTC
 ||||| |||||
 GAAAACAG CAAGAAG
 _
 GAM1661 EFNA5 3' CAGCGGGCTATGGACAAGGAAG 7683 GCCG ____
 AA TTCTTC TTGTTTA CCCGCTG
 |||| ||||| |||||
 AAGAAG AACAGGT GGGCGAC
 G__ ATC
 GAM1661 LOC151445 3' CAGCGAGTATATGAACAACAAA 34418 GCC ____ C
 GA TC GTTGTTT AC CGCTG
 || ||||| || |||||
 AG CAACAAG TG GCGAC
 AAA TATA A
 GAM1661 LOC161635 5' CAGCATCACCAACGGTGAAGAA 46183 TTTACCC
 TTCTTCGCCGTTG GCTG
 ||||| |||||

		AAGAAGTGGCAAC	CGAC	
		CACTA__		
GAM1662	DAG1	3' GCCTTTAACTAACTGTA	10635	ATA T
		TACAGTTA TTGA GGC		
		ATGTCAAT AATT CCG		
		CAC T		
GAM1662	HNRPD	3' CCATTGTGTCCAAGTGTAT	11951	A_ T
		ATACAGTT ATAT GATGG		
		TATGTCAA TGTG TTACC		
		CC _		
GAM1662	PDE7A	3' CACCAATGTCCTAGCTGTATTA	32641	_ A
		TAATACAGTTA ATATTG TG		
		ATTATGTCGAT TGTAAC AC		
		CC C		
GAM1662	RFP	3' GTGCCATAGTTTTATTAAGTCC	13262	AC TTG__
	ATTA	TAAT AGTTAATA ATGGCAC		
		ATTA TCAATTAT TACCGTG		
		CC TTTGA		
GAM1662	DKFZp434G179	3' TGCCTTGATTAAATGTATTA	39044	G ATTGAT
		TAATACA TTAAT GGCA		
		ATTATGT AATTA CCGT		
		A GTT__		
GAM1662	FAM8A1	3' TGCCACCAATTTGTATTA	18382	TTAAT A
		TAATACAG ATTG TGGCA		
		ATTATGTT TAAC ACCGT		
		_____ C		
GAM1662	FLJ13456	3' GCAGTTGAAAATTAAGTGCATT	32799	A A_ TG G
	A	TAAT CAGTTAAT T AT GC		
		ATTA GTCAATTA A TG CG		
		C AA GT A		
GAM1662	KIAA1189	3' TGCTAGTCATAACTGTA	35653	ATAT _
		TACAGTTA TGA TGGCA		
		ATGTCAAT ACT ATCGT		
		_____ G		
GAM1662	PLAA	3' GTACATCAAAGTGTATTA	10441	AATAT _
		TAATACAGTT TGATG GC		
		ATTATGTCAA ACTAC TG		
		_____ A		
GAM1662	SLC2A13	3' GTGCCAGATCTTTAACTGTAT	27466	TATTGA
		ATACAGTTAA TGGCAC		

		TATGTCAATT	ACCGTG		
		TCTAG_			
GAM1662	XLKD1	3'	GTGCCATTAACAAATGTAT	13507	GTTAATA
			ATACA TTGATGGCAC		
			TATGT AATTACCGTG		
			AAAC__		
GAM1662	LOC144997	3'	TGCCATCAATATTTTAGACTG	40483	__
			CAGTT AATATTGATGGCA		
			GTCAG TTATAACTACCGT		
			ATT		
GAM1662	LOC149076	3'	GTTTTGAATATTAAGTGTGTTA	38638	GAT
			TAATACAGTTAATATT GGC		
			ATTGTGTCAATTATAA TTG		
			GTT		
GAM1662	LOC152674	3'	CCTTCTATTAAGTGTAT	41538	TT T
			ATACAGTTAATA GA GG		
			TATGTCAATTAT CT CC		
			__ T		
GAM1662	LOC158038	5'	GTGCCATCAGAAAGCTGTAT	39700	AATA
			ATACAGTT TTGATGGCAC		
			TATGTCTGA GACTACCGTG		
			AA__		
GAM1663	EPHA3	5'	CGCACGCTGAAGACGGCA	11741	ATGTA
			TGTCGTCT AGCGTGCG		
			ACGGCAGA TCGCACGC		
			AG__		
GAM1663	NPR1	5'	CGCACGCTACAAACACACA	42234	C CTA A
			TGT GT TGTA GCGTGCG		
			ACA CA ACAT CGCACGC		
			_ CAA _		
GAM1663	SH3BP2	3'	CAGGCCACACAGACGGACA	8943	_ A AA G
			TGTC GTCT TGT GC TG		
			ACAG CAGA ACA CG AC		
			G C C_ G		
GAM1663	CDC14A	3'	CATGTGCCTACATAGACACA	9763	C A__
			TGT GTCTATGTA GCGTG		
			ACA CAGATACAT TGTAC		
			_ CCG		
GAM1663	LOC219376	3'	CACACATACATAGACACA	45068	C AGC
			TGT GTCTATGTA GTG		

ACA CAGATACAT CAC
 _ ACA
 GAM1664 BLAME 3' CCTGGACTATCAGTAA 21307 C CGT
 TTGC GATAGTCC GGG
 ||| ||||| |||
 AATG CTATCAGG TCC
 A _

GAM1664 DXYS155E 3' TCCCCACGGCCTGTCCGGGAA 11543 G _ TC
 TT CCG ATAG CCGTGGGGA
 || ||| ||| |||||
 AA GGC TGTC GGCACCCCT
 G C C_

GAM1664 EN1 5' CCCCACGGGCGCTGGCAA 7140 ATA T
 TTGCCG G CCCGTGGGG
 ||||| | |||||
 AACGGT C GGGCACCCC
 CGC _

GAM1664 SIAT8E 5' CCCCCGTCCCTATCGGCAG 30090 TCC T
 TTGCCGATAG CG GGGG
 ||||| || |||
 GACGGCTATC GC CCCC
 CCT _

GAM1664 TNFRSF6B 5' TCCCCACGGGCTGCAGCA 26762 CGA T
 TGC TAG CCCGTGGGGA
 ||| ||| |||||
 ACG GTC GGGCACCCCT
 AC_ C

GAM1664 FLJ22246 5' TCCAGCGCGGGACCAGCAGCAA 24910 CGATA G_
 TTGC GTCCCGTG GGA
 ||| ||||| |||
 AACG CAGGGCGC CCT
 ACGAC GA

GAM1664 KIAA1091 3' TCCCCGGAACATCGGCAA 34542 AG CGT
 TTGCCGAT TCC GGGGA
 ||||| ||| |||||
 AACGGCTA AGG CCCCT
 CA _

GAM1664 KIAA1691 3' CCCCACATGTCATGGCAA 44466 _ GTCCC
 TTGCC GATA GTGGGG
 |||| ||| |||||
 AACGG CTGT CACCCC
 TA A_

GAM1664 RAB39 3' CCTGGACTATCAGCAG 37644 C CGT
 TTGC GATAGTCC GGG
 ||| ||||| |||
 GACG CTATCAGG TCC
 A _

GAM1664 LOC150407 3' TCCTGCAGGACTGTCAGCAA 38953 C C TG
 TTGC GATAGTCC G GGG
 ||| ||||| | |||

AACG CTGTCAGG C CCT
A A GT
GAM1664 LOC169026 3' CCGTGGGGATGTAACCTATCGGC 40264 T_____ GTG
AA TTGCCGATAG CCC GG
||||||| ||| ||
AACGGCTATC GGG CC
AATGTIIIA GTG
GAM1664 LOC203392 5' CCCCACGGAGACGCGCCAA 43041 C ATA _
TTG CG GTC CCGTGGGG
||| || ||| |||||
AAC GC CAG GGCACCCC
C G_ A
GAM1664 LOC222166 5' CCCCACGGCGGCCCGCAA 45152 CGATA _
TTGC GTC CCGTGGGG
|||| ||| |||||
AACG CGG GGCACCCC
CC_ C
GAM1664 LOC93082 3' CCATGGGACCTCAGCAA 28766 C TA
TTGC GA GTCCCGTGG
|||| ||| |||||
AACG CT CAGGGTACC
A C_
GAM1665 TRPS1 3' CCAGCCCTGCCTGTAC 15348 C C AC
GTACAGGC GG GC TGG
|||||| ||| |||
CATGTCCG CC CG ACC
T _ _
GAM1665 E2IG4 3' TGGGCCGGCCTGACCCGCA 43702 AA A G
TGC GT CAGGCCGGC CA
||| ||| ||||| ||
ACG CA GTCCGGCCG GT
CC _ G
GAM1665 FLJ13710 3' CCAGCATGGGGCCTGTACTT 24204 GG CA
AAGTACAGGCC CG CTGG
||||||| || |||
TTCATGTCCGG GT GACC
G_ AC
GAM1665 KIAA1582 5' CCAGCTGCCTGGCCTGTACTTG 32586 C _
CAAGTACAGGCCGG GCA CTGG
||||||| ||| |||
GTTTCATGTCCGGTC CGT GACC
_ C
GAM1665 KIAA1706 3' CCAACGCGCAGTGTGTATTTGC 44576 G CG AC
A TGCAAGTACA GC GCGC TGG
||||||| || ||| |||
ACGTTTATGT TG CGCG ACC
G A_ CA
GAM1665 P2RXL1 3' CCAGCAGGCACCTGTATTGCA 11928 G CCG GCA
TGCAA TACAGG GC CTGG
|||| ||||| || |||

ACGTT ATGTCC CG GACC
 _ A_ GAC
 GAM1666 F8 3' CCTGACCCCTTCACTATG 5615 C CCTGC
 CA AGTGA GGGTCAGG
 || |||| |||||
 GT TCACT CCCAGTCC
 A TC__
 GAM1666 GRLF1 3' CCCCCGCAGGCCACCAGGCA 38411 ACA A TCA
 TGC GTG CCTGCGGG GG
 ||| ||| ||||| ||
 ACG CAC GGACGCCC CC
 GAC C ____
 GAM1666 IRTA1 3' CTGCACAGGCACTGTGCA 25302 A ____
 TGCACAGTG CCT GCGG
 ||||| ||| |||
 ACGTGTAC GGA CGTC
 _ CA
 GAM1666 PRDM2 3' CCTGGCAAGTCACCTGCA 14533 CA C GGGT
 TGCA GTGAC TGC CAGG
 ||| |||| ||| |||
 ACGT CACTG ACG GTCC
 C_ A ____
 GAM1666 TEM6 3' GCCATGTAAAGTCACTGTGC 22963 CT__ _
 A TGCACAGTGAC GCG GGT
 ||||| ||| |||
 ACGTGTCACTG TGT CCG
 AAAAT A
 GAM1666 TRIM34 3' CCTAACTATTAAGATCACTGTG 28174 C GCG_ C
 TA TGCACAGTGA CT GGT AGG
 ||||| || ||| |||
 ATGTGTCACT GA TCA TCC
 A ATTA A
 GAM1666 TRIM34 3' CCTAACTATTAAGATCACTGTG 22250 C GCG_ C
 TA TGCACAGTGA CT GGT AGG
 ||||| || ||| |||
 ATGTGTCACT GA TCA TCC
 A ATTA A
 GAM1666 DKFZP434A043 3' GCCTGATTAACAGGCACT 17701 A CG
 AGTG CCTG GGTCAAGC
 ||| ||| |||||
 TCAC GGAC TTAGTCCG
 _ AA
 GAM1666 E2IG4 3' GCCTGACCCGCAATGGGCA 43701 A ____
 TG CC TGCGGGTCAGGC
 || || |||||
 AC GG ACGCCAGTCCG
 G TA
 GAM1666 FLJ00001 3' GCCGGTCACCAGGCCACTGTGC 39782 A CG GT A
 A TGCACAGTG CCTG G C GGC
 ||||| ||| | |||

ACGTGTAC GGAC C G CCG
 C CA TG _
 GAM1666 KIAA0513 3' CCTGACCCCAACACCTGCA 16353 CA ACC C
 TGCA GTG TG GGGTCAGG
 ||| ||| || |||||
 ACGT CAC AC CCCAGTCC
 C_ A_ _
 GAM1666 KIAA1061 3' GCCTGACTGCCAAGCCACCTGC 35269 CA ACCT_ G
 A TGCA GTG GCGG TCAGGC
 ||| ||| ||| |||||
 ACGT CAC CGTC AGTCCG
 C_ CGAAC _
 GAM1666 KIAA1297 3' GCCTACCAAGGTGACTGTGCA 35715 G GCG C
 TGCACAGT ACCT GGT AGGC
 ||||| ||| ||| |||
 ACGTGTCA TGGG CCA TCCG
 G A_ _
 GAM1666 KIAA1970 3' GCCTGACTTGTGTAACCACT 36753 ACCT_
 AGTG GCGGGTCAGGC
 ||| |||||
 TCAC TGTTCACTCCG
 CAATG
 GAM1666 LGALS8 5' GCCTAAAATCTTAGGTCAT 13245 C C_
 GTGACCTG GGGT AGGC
 ||||| ||| |||
 TACTGGAT TCTA TCCG
 _ AAA
 GAM1666 MAC30 3' CCTGACCCACAGCATATATGC 31403 CA_ AC C
 GCA GTG CTG GGGTCAGG
 ||| ||| ||| |||||
 CGT TAC GAC CCCAGTCC
 ATA _ A
 GAM1666 MGC1136 3' GCCCCAGGCCACTGTCA 23454 C A C
 TG ACAGTG CCTG GGGT
 || ||||| ||| |||
 AC TGTCAC GGAC CCGG
 _ C _
 GAM1666 MGC12945 5' GCCTGACCCGCAGGCCGCCGC 26118 ACA A
 GC GTG CCTGCGGGTCAGGC
 || ||| |||||
 CG CGC GGACGCCAGTCCG
 C_ C
 GAM1666 SIAT8C 5' ACTCACAGGTCACCTCGCA 18024 ACA C
 TGC GTGACCTG GGGT
 ||| ||||| |||
 ACG CACTGGAC CTCA
 CTC A
 GAM1666 TCL6 5' ACCAGGCAGCCACTGTGCA 21765 AC G_
 TGCACAGTG CTGC GGT
 ||||| ||| |||

		ACGTGTCAC GACG CCA		
		C_ GA		
GAM1666	TCL6	5' ACCAGGCAGCCACTGTGCA	21757	AC G_
		TGCACAGTG CTGC GGT		
		ACGTGTCAC GACG CCA		
		C_ GA		
GAM1666	TCL6	5' ACCAGGCAGCCACTGTGCA	15763	AC G_
		TGCACAGTG CTGC GGT		
		ACGTGTCAC GACG CCA		
		C_ GA		
GAM1666	TCL6	5' ACCAGGCAGCCACTGTGCA	14840	AC G_
		TGCACAGTG CTGC GGT		
		ACGTGTCAC GACG CCA		
		C_ GA		
GAM1666	LOC152002	3' CCGGGCAGGTCACACTGTGC	39194	GGGTCA
		GCACAGTGACCTGC GG		
		CGTGTCACACTGGACG CC		
		GG____		
GAM1666	LOC199990	3' GCCCACGCAGGCCCACTGTGCA	42684	A_ GGTCA
		TGCACAGTG CCTGCG GGC		
		ACGTGTCAC GGACGC CCG		
		CC AC____		
GAM1666	LOC201229	3' GCCTGTCCAAGCCTCTGTGCA	42544	TGAC GC T
		TGCACAG CT GGG CAGGC		
		ACGTGTC GA CCT GTCCG		
		TCC_ A_ _		
GAM1666	LOC86651	5' ACACCAGATCACTGTGCA	34095	C CGG
		TGCACAGTGA CTG GT		
		ACGTGTCAC T GAC CA		
		A CA_		
GAM1666	LOC90378	5' GCCTAACCCGCGGCCGCGTGCA	31335	A A T C
		TGCAC GTG CC GCGGGT AGGC		
		ACGTG CGC GG CGCCCA TCCG		
		_ C _ A		
GAM1666	LOC91694	3' CCTGACATGGTACTGTGCA	33248	A TGCGG
		TGCACAGTG CC GTCAGG		
		ACGTGTCAT GG CAGTCC		
		_ TA____		
GAM1667	DYRK1A	3' CCACAGTCACCACTCCATGACA	28162	CCATC AC
		TGTCATGGA GTGGCT GG		

ACAGTACCT CACTGA CC
 CAC__ CA
 GAM1667 CECR7 5' CCACAGTTTCTGTCCCATGACA 38877 _ C__ C
 TGT CATGG AC AT GTGG
 ||||| || ||||
 ACAGTACC TG TG CACC
 C TCTT A
 GAM1667 FLJ30058 3' CTAGCCGTGTCCACGCA 29582 CA CATCG C
 TGT TGGAC TGGCTA G
 || |||| |||||
 ACG ACCTG GCCGAT C
 C_ T__ A
 GAM1667 LOC146138 3' CCATAGCTGGACCAATCATGAC 40654 ACCA G C
 A TGT CATGG TC TGGCTA GG
 ||||| || ||||| ||
 ACAGTACT AG GTCGAT CC
 AACC _ A
 GAM1667 LOC146443 5' CCGCTCTGTGACAGTCCATGAC 38148 CA TG CTA
 GTCATGGAC TCG G CGG
 ||||| || | |||
 CAGTACCTG AGT C GCC
 AC GT TC_
 GAM1667 LOC221922 5' CCATGAATGGCACCATGACA 44531 A_ _
 TGT CATGG CCAT CGTGG
 ||||| |||||
 ACAGTACC GGTA GTACC
 AC A
 GAM1668 AXL 5' CTCCCCTGCCGCTGTGCCA 7422 AG C CGAA
 TG ACAGCGGT GGG GAG
 || ||||| || |||
 AC TGTCGCCG CCC CTC
 CG T ____
 GAM1668 AXL 5' CTCCCCTGCCGCTGTGCCA 22443 AG C CGAA
 TG ACAGCGGT GGG GAG
 || ||||| || |||
 AC TGTCGCCG CCC CTC
 CG T ____
 GAM1668 DNMT3L 5' CCTCTGGCCACCCGCTGTCCCA 15019 A TCG GA
 TG GACAGCGG GGC AGAGG
 || ||||| || ||||
 AC CTGTGCGC CCG TCTCC
 C CA_ G_
 GAM1668 FZD4 3' CCTCTCCAGGTCACTGTCTCA 14483 C GT_ CGA
 TGAGACAG G C GGG AGAGG
 ||||| | ||| ||||
 ACTCTGTC C G CCC TCTCC
 A TG A ____
 GAM1668 G6PT1 5' CCTCTTCGCCGCCCGCCGCTC 7199 ACA T ____
 GAG GCGG CGGGC GAAGAGG
 || |||| ||||| |||||

CTC CGCC GCCCG CTTCTCC
 — — CCG
 GAM1668 KCNN4 5' CCTCCCCGCCCTGCCTGGCCGT 8037 A — C AA
 C GAC GC GGT GGGCG GAGG
 ||| || ||| ||||| ||||
 CTG CG CCG CCCGC CTCC
 C GT T CC
 GAM1668 MAT1A 3' CTCCCCCACC GTTGTCTCA 43668 C CGAA
 TGAGACAGCGGT GGG GAG
 ||||| ||||| ||| |||
 ACTCTGTTGCCA CCC CTC
 C —
 GAM1668 NRAS 3' CCTCCTCACTTGGCTGTCTG 8360 — C A
 CAG CGGTCGGG GA GAGG
 ||| ||||| ||| ||||
 GTC GTCGGTTC CT CTCC
 T A C
 GAM1668 SFRP1 5' CCTCCCCGCCCGCGCCGCCTC 8929 ACA — AA
 GAG GCGGT CGGGCG GAGG
 ||| ||||| ||||| ||||
 CTC CGCCG GCCCGC CTCC
 — C CC
 GAM1668 FLJ10101 3' CCTCCTCGCCCTGGGCTGC 24045 — A
 GCGGTC GGGCGA GAGG
 ||||| ||||| ||||
 CGTCGG CCCGCT CTCC
 GT C
 GAM1668 FLJ10101 3' CCTCCTCGCCCTGGGCTGC 24046 — A
 GCGGTC GGGCGA GAGG
 ||||| ||||| ||||
 CGTCGG CCCGCT CTCC
 GT C
 GAM1668 KIAA0053 5' CCTCTCCGCCCACTCTTTGCTC 17030 A C _ C A
 A TGAG CAG G GT GGGCG AGAGG
 |||| ||| | ||| ||||| ||||
 ACTC GTT C CA CCCGC TCTCC
 _ TT _ C
 GAM1668 KIAA0285 5' CCCTCCAGACCACTGTCTC 16752 C G CGA A
 GAGACAG GGTC GG AG GG
 ||||| ||||| || |||
 CTCTGTC CCAG CC TC CC
 A A — —
 GAM1668 KIAA0350 3' CTCCTCTGCCGCTGTCCCA 30665 A C CGAA
 TG GACAGCGGT GGG GAG
 || ||||| ||| |||
 AC CTGTCGCCG CTC CTC
 C T —
 GAM1668 KIAA0669 5' CCTCTTCGCCCTCCCACT 16626 C TC
 AG GG GGGCGAAGAGG
 || || ||||| |||||

	TC CC CCCGCTTCTCC	
	A CT	
GAM1668 KIAA0731 3'	CCCCATTGCCAGCACTGTCTC 33239	CG C AGA
A	TGAGACAG GT GGGCGA GG	
	ACTCTGTC CG CCCGTT CC	
	A_ A ACC	
GAM1668 KIAA0872 3'	CCTCTCCCTTCCCTCTGTCTCA 17245	C TC C A
	TGAGACAG GG GGG GA GAGG	
	ACTCTGTC CC TCC CT CTCC	
	T CT _ _	
GAM1668 KIAA1172 5'	CTCTCCGCCTCTGCCTC 35078	ACA TC A
	GAG GCGG GGGCG AGAG	
	CTC CGTC TCCGC TCTC	
	_ _ C	
GAM1668 LOC116411 5'	CCTCCGCCCGGCAGCCGC 36566	_ AA
	GCGGT CGGGCG GAGG	
	CGCCG GCCCGC CTCC	
	ACG _	
GAM1668 LOC116411 5'	CCTCTCCGCCAGCAGCCACCT 36567	ACA G C A
C	GAG GC GT GGGCG AGAGG	
	CTC CG CG CCCGC TCTCC	
	CAC A A C	
GAM1668 LOC116411 5'	TGCCCGGCCGCCATCCCA 36572	A CA
	TG GA GCGGTCGGGCG	
	AC CT CGCCGGCCCGT	
	C AC	
GAM1668 LOC147093 5'	CCTCTTCACCTCATGCTGTCT 40801	GTC C
	AGACAGCG GGG GAAGAGG	
	TCTGTGCT TCC CTTCTCC	
	AC_ A	
GAM1668 LOC152762 3'	CCTCCGCCCAAGTTGAAGTCT 39305	AG TC_ AA
	AGAC CGG GGGCG GAGG	
	TCTG GTT CCCGC CTCC	
	AA GAA _	
GAM1668 LOC200093 3'	CCTCAAACAGCCGCTGTCTCA 31598	CGGGCGAA
	TGAGACAGCGGT GAGG	
	ACTCTGTCGCCG CTCC	
	ACAAA_	
GAM1668 LOC221468 3'	CCTCTCCCTCACCACCATCATC 29826	_ CAGC C C A
A	TGA GA GGT GGG GA GAGG	

ACT CT CCA TCC CT CTCC
 A ACCA C _ _
 GAM1668 LOC92697 5' TGCCCGGCCGCCATCCCA 34806 A CA
 TG GA GCGGTCGGGCG
 || || |||||
 AC CT CGCCGGCCCGT
 C AC
 GAM1669 CROT 3' GCAGCAATGCAAATTATGACA 22123 CTTTAG
 TGT CATAAT GTTGCTGC
 ||||| |||||
 ACAGTATTA TAACGACG
 AACG_
 GAM1669 EIF4EBP2 3' CAGCAACTTTTAAATTAAACA 10300 CA CTTT
 TGT TAAT AGGTTGCTG
 ||| ||| |||||
 ACA ATTA TTCAACGAC
 A_ ATTT
 GAM1669 GPR44 3' AGCAACTCTAAGACTACAGCA 11173 CA A TA
 TGT TA TCTT GGTTGCT
 ||| ||| |||||
 ACG AT AGAA TCAACGA
 AC C TC
 GAM1669 DKFZP434O047 5' GGCAGCAAACAAAATCATGCAC 17868 _ A C AGG
 A
 TGT CAT AT TTT TTGCTGCC
 ||| ||| ||| |||||
 ACA GTA TA AAA AACGACGG
 C C _ CA_
 GAM1669 FLJ20716 3' CAGCATTCAAGATTATGA 19631 TA GT
 TCATAATCTT G TGCTG
 ||||| |||
 AGTATTAGAA C ACGAC
 _ TT
 GAM1669 HNRPA3 3' CAGCAATCAAATTATGGACA 12322 _ CTTTA
 TGTC ATAAT GGTTGCTG
 ||| ||| |||||
 ACAG TATTA CTAACGAC
 G AA_
 GAM1669 MAGE-E1 3' CAGCAACCCACCTGAGTATGA 25103 A TTTA_
 TCATA TC GGTTGCTG
 |||| || |||||
 AGTAT AG CCAACGAC
 G TCCAC
 GAM1669 MAL2 3' GCAGTTGAACAAAATTATGGC 27469 C AGGT
 A
 TGT CATAAT TTT GCTGC
 ||||| ||| |||||
 ACGGTATTA AAA TGACG
 A CAAGT
 GAM1669 MGC15563 3' GACCCAAAGATCATGATA 26699 A A
 TGT CAT ATCTTT GGTT
 ||||| ||||| |||||

		ATAGTA TAGAAA CCAG	
		C C	
GAM1669	LOC204823 5'	CAGCAACCCAAAGAGAAGGGA 43102	ATAA_ A
		TC TCTTT GGTTGCTG	
		AG AGAAA CCAACGAC	
		GGAAG C	
GAM1669	LOC255654 5'	GGCAGCAAACAAAATCATGCAC 46302	_ A C AGG
A		TGT CAT AT TTT TTGCTGCC	
		ACA GTA TA AAA AACGACGG	
		C C _ CA_	
GAM1670	ADAM19 3'	CCTCAGGGTGGCTGTGATA 27095	A GGATTAA
		TATCACAGC CAC AGG	
		ATAGTGTCTG GTG TCC	
		_ GGAC__	
GAM1670	AP2B1 3'	CCTTCAACCATGCTGTGAT 6953	CAC A A
		ATCACAGCA GG TT AAGG	
		TAGTGTCTG CC AA TTCC	
		A__ _ C	
GAM1670	BMPR2 5'	TCCTTTCAAACGTATTGTGAT 6869	CAC A _
A		TATCACAG ACGG TT AAAGGA	
		ATAGTGTT TGTC AA TTTCCT	
		A__ A C	
GAM1670	CYP4F3 3'	TCCTTATGGGTATGCTGTGG 6592	C GG TA
		TCACAGCA AC AT AAGGA	
		GGTGTCTG TG TA TTCCT	
		A GG _	
GAM1670	EXTL1 5'	CCTGGCCTCTGCACTGTGATA 10752	CACA TTAA
		TATCACAG CGGA AGG	
		ATAGTGTC GTCT TCC	
		AC__ CCGG	
GAM1670	IL1F5 3'	CCTTTAATCCTGCCACTGTCAT 14598	C CA_ C
A		TAT ACAG CA GGATTAAAGG	
		ATA TGTC GT CCTAATTTC	
		C ACC _	
GAM1670	OPHN1 3'	CCTTTGCCCACTGTGGTA 8402	CACAC AT
		TATCACAG GG TAAAGG	
		ATGGTGTC CC GTTTC	
		ACA__ _	
GAM1670	PRX 3'	CCTCGCTGTTGTGTGTGTGATA 21934	G ATTAA
		TATCACA CACACGG AGG	

		ATAGTGT GTGTGTT TCC	
		— GTCGC	
GAM1670 ZNF192	3'	TCCCCACTGTACACTGTGGTA 12990	CAC ATTAAA
		TATCACAG ACGG GGA	
		ATGGTGTC TGTC CCT	
		ACA ACC__	
GAM1670 H-L(3)MBT	3'	CCTTTAATCCAATATAGTTGAT 17755	CAGCACAC
A		TATCA GGATTAAAGG	
		ATAGT CCTAATTTCC	
		TGATATAA	
GAM1670 KIAA1456	3'	TCCTTTAATGATTGTGCT 33264	CGG
		AGCACA ATTAAAGGA	
		TCGTGT TAATTCCT	
		TAG	
GAM1670 SZF1	5'	TCCTTGGGAGTCGCTGTGATA 18175	AC GGATTA
		TATCACAGC AC AAGGA	
		ATAGTGTCG TG TTCCT	
		C_ AGGG__	
GAM1670 LOC146243	3'	TCCTTTAATCTGTACTGT 40679	CAC
		ACAG ACGGATTAAAGGA	
		TGTC TGTCTAATTCCT	
		A__	
GAM1670 LOC257117	5'	CCTATCTGTTTGCTGTGATA 46025	C TAA
		TATCACAGCA ACGGAT AGG	
		ATAGTGTCGT TGTCTA TCC	
		T _	
GAM1671 CRACC	3'	TGACTAGAAACATCAAGG 22157	GTG T C
		CCT GGTGTTT CTAG CA	
		GGA CTACAAA GATC GT	
		A_ _ A	
GAM1671 DDX11	3'	GGCCAGGCACCCCCAGGG 24987	T TTT A
		CCCTG GGGTGT CT GCC	
		GGGAC CCCACG GA CGG	
		C _ C	
GAM1671 DHCR24	3'	GCCAGACGAGGTCCTCACAGG 16524	_ _ G T A
		CCTGTG GG T TT TCT GC	
		GGACAC CC G AG AGA CG	
		T T G C C	
GAM1671 DMPK	5'	TGGCCAGAGAGGCCAGGGG 10668	GT G A
		CCCCT GGGT TTTTCT GCCA	

			GGGGA CCCG GAGAGA CGGT		
			— — C		
GAM1671	DUSP4	5'	GCTAGAACACAGCAGGG 27668	GG	TT
			CCCTGT GTGT TCTAGC		
			GGGACG CACA AGATCG		
			A_ _		
GAM1671	GASC1	3'	TAGTGAATCACCCACAAGG 32125	C	_ T
			CC TGTGGGTG TTT CTA		
			GG ACACCCAC AAG GAT		
			A T T		
GAM1671	LMO2	5'	GGCCAGCCCCGCGCCACAAAGG 12100	CC	_ TTTT A
	G		CCC TGTGG GTG CT GCC		
			GGG ACACC CGC GA CGG		
			AA G CCC_ C		
GAM1671	LZTR1	3'	TGGCTCCTGCCACACCCACAGG 13641		TTTCT_
	G		CCCTGTGGGTGT AGCCA		
			GGGACACCCACA TCGGT		
			CCGTCC		
GAM1671	MUC4	3'	AGACACACCCACAGAAGG 28709	CC	TT
			CC CTGTGGGTGT TCT		
			GG GACACCCACA AGA		
			AA C_		
GAM1671	PAK1	5'	GGCTAGGCGCACCCACGGGG 8434		TT
			CCCTGTGGGTGT TCTAGCC		
			GGGGCACCCACG GGATCGG		
			C_		
GAM1671	RALBP1	3'	TGGCCTGGTGCATCCACAGAGG 13666	C	TT TA
			CC CTGTGGGTGT TC GCCA		
			GG GACACCTACG GG CGGT		
			A T_ TC		
GAM1671	SCML2	3'	GCTAAATCCCAAAGGGG 12736	G	T TTC
			CCCCT TGGG GTT TAGC		
			GGGGA ACCC TAA ATCG		
			A _ _		
GAM1671	SPAP1	3'	GCCAGAACGTGCCTCAGGAGG 25049	_ T	TG T A
			CC CCTG GGG T TTCT GC		
			GG GGAC TCC G AAGA CG		
			A _ GT C C		
GAM1671	C11orf15	3'	TGACTAGAAAGAAACAGG 21807	GGGTG	C
			CCTGT TTTTCTAG CA		

GGACA GAAAGATC GT
AA___ A
GAM1671 C21orf42 3' AGAAAACACCCTCAAAGG 27748 CC T
CC TG GGGTGT TTTTCT
|| || |||||
GG AC CCCACAAAAGA
AA T
GAM1671 CGGBP1 5' TGA CTTCCTGGCACCACAGGG 9742 G TTCT C
CCCTGTGG TGTT AG CA
||||| ||| ||
GGGACACC ACGG TC GT
_ TCCT A
GAM1671 DDX12 3' GGCCAGGCACCCCCAGGG 30025 T TTT A
CCCTG GGGTGT CT GCC
|||| |||| ||||
GGGAC CCCACG GA CGG
C _ C
GAM1671 DIO2 3' GAAAGAAACCCACAGAAGG 6457 CC G_
CC CTGTGGGT TTTTC
|| ||||| ||||
GG GACACCCA GAAAG
AA AA
GAM1671 DIO2 3' GAAAGAAACCCACAGAAGG 15168 CC G_
CC CTGTGGGT TTTTC
|| ||||| ||||
GG GACACCCA GAAAG
AA AA
GAM1671 DKFZp434N0650 5' GCCACCGAGGCACCGACAGG 26005 G CTA_
CCTGT GGTGTTTT GC
|||| ||||| ||
GGACA CCACGGAG CG
G CCAC
GAM1671 FLJ10761 3' TGA CTAGAGGGAGCCAAGAGG 20106 GTG G C
CCT GGT TTTTCTAG CA
||| ||| ||||| ||
GGA CCG GGGAGATC GT
GAA A A
GAM1671 FLJ20509 3' TGA CTTGAGACACCCAAGAGG 19525 G_ CT C
CCT TGGGTGTTTT AG CA
||| ||||| ||| ||
GGA ACCCACAGAG TC GT
GA T_ A
GAM1671 FYCO1 3' GCTGTTGT CACACCCAAAGGG 23710 G TTTC_
CCCT TGGGTGT TAGC
|||| ||||| ||||
GGGA ACCCACA GTCG
A CTGTT
GAM1671 GPA33 3' AGTGAACACACACAAGGG 12402 C G T
CCC TGTG GTGTTT CT
||| ||| ||||| ||

GGG ACAC CACAAG GA
A A T
GAM1671 KIAA0258 3' GGCCAGAAGCTCCAGG 16649 T GTT A
CCTG GGGT TTCT GCC
||||| |||||
GGAC CTCG AAGA CGG
_ _ _ C
GAM1671 KIAA0326 3' GCCAGAAACCTTCAGAAGG 32159 CC T GTT A
CC CTG GGGT TTCT GC
|| ||||| |||||
GG GAC TCCA AAGA CG
AA T _ _ C
GAM1671 KIAA0939 3' TGGCTCCTCAGCCCACAGAGGG 31068 _ GTTTTCT
CCC CTGTGGGT AGCCA
||| ||||| |||||
GGG GACACCCG TCGGT
A ACTCC_
GAM1671 KIAA1853 3' GCTGCTTCATCCACAGAAGG 34389 CC TTTC
CC CTGTGGGTG TAGC
|| ||||| |||||
GG GACACCTAC GTCG
AA TTC_
GAM1671 MDS028 3' TGGCCCCAACACCCATAAGG 20536 C TTCTA
CC TGTGGGTGTT GCCA
|| ||||| |||||
GG ATACCCACAA CGGT
A CCC_
GAM1671 MESDC2 3' TGGCTAGAAAGTGGCAGAGGG 35894 G GGTGT
CCCT TG TTTCTAGCCA
||||| |||||
GGGA AC GAAGATCGGT
G GGT_
GAM1671 NDRG4 3' TGGACAACAGCCACAAGGGG 23216 C G T
CCCC TGTGG TGTT TCTA
||||| ||||| |||||
GGGG ACACC ACAA AGGT
A G C
GAM1671 NDRG4 3' TGGACAACAGCCACAAGGGG 21701 C G T
CCCC TGTGG TGTT TCTA
||||| ||||| |||||
GGGG ACACC ACAA AGGT
A G C
GAM1671 ORCTL3 3' GGCCAGGACCCACAGGG 10445 GTTT A
CCCTGTGGGT TCT GCC
||||||| |||||
GGGACACCCA GGA CGG
_ _ _ C
GAM1671 RHOBTB2 3' AGGAAACACCCCCAGGAGG 30558 _ T
CC CCTG GGGTGTTTCT
|| ||||| |||||

		GG GGAC CCCACAAAGGA			
		A C			
GAM1671	SYTL4	5' TGGCCAGTCAGCCACAGGG	28024	G TTTT	A
		CCCTGTGG TG CT GCCA			
		GGGACACC AC GA CGGT			
		G T__ C			
GAM1671	TRIM38	3' CTAAAAATACCACAGATGG	13050	CC G C	
		CC CTGTGG TGTTTT TAG			
		GG GACACC ATAAAA ATC			
		TA _ _			
GAM1671	LOC122970	3' TGGCCAGAAACATACAGAGGGG	36715	G GG T A	
		CCCCT TG TGTTT CT GCCA			
		GGGGA AC ACAA GA CGGT			
		G AT _ C			
GAM1671	LOC126755	3' TGACTAAAAGCCTCCCCCAGG	36857	T T_ C C	
		CCTG GGG GTTTT TAG CA			
		GGAC CCC CGAAA ATC GT			
		C TC _ A			
GAM1671	LOC126782	5' GGCCAGAACCCGTCTACAGAGG	36860	C GT TT A	
		CC CTGTGG G TTCT GCC			
		GG GACATC C AAGA CGG			
		A TG CC C			
GAM1671	LOC144742	5' TAGCCAAAGGCCCAAGGG	37779	G G T_	
		CCCT TGGGT TTT CTA			
		GGGA ACCCG AAA GAT			
		_ G CC			
GAM1671	LOC145468	3' GGCCAGACAACCTCAGGG	36548	T GTTT A	
		CCCTG GGGT TCT GCC			
		GGGAC TCCA AGA CGG			
		_ AC_ C			
GAM1671	LOC150155	3' GGCCAGACAACCTCAGGG	35089	T GTTT A	
		CCCTG GGGT TCT GCC			
		GGGAC TCCA AGA CGG			
		_ AC_ C			
GAM1671	LOC152503	5' CTAGGATCACAGCCACAGG	41518	G T_	
		CCTGTGG TGT TTCTAG			
		GGACACC ACA AGGATC			
		G CT			
GAM1671	LOC153577	3' TGGCCACCGTCACCCACAGGGG	41647	TTTTCTA	
		CCCCTGTGGGTG GCCA			

		GGGGACACCCAC	CGGT		
		TGCCAC_			
GAM1671	LOC154428 5'	GCCAGCTCTGCCCCACAGGG	41702	T TTT_ A	
		CCCTGTGGG GT CT GC			
		GGGACACCC CG GA CG			
		_ TCTC C			
GAM1671	LOC163081 5'	AGAGAACACACACAGGGG	40086	G	
		CCCCTGTG GTGTTTCT			
		GGGGACAC CACAAGAGA			
		A			
GAM1671	LOC196872 3'	TGGCTGCCCTCCCCACAGGGGG	42418	TGTTTTC	
		CCCCCTGTGGG TAGCCA			
		GGGGGACACCC GTCGGT			
		CTCCC_			
GAM1671	LOC199232 5'	TGACTAGACGGTCCGCAGGGG	42881	TG TT C	
		CCCCTGTGGG T TCTAG CA			
		GGGGACGCCT G AGATC GT			
		_ GC A			
GAM1671	LOC219401 3'	AGAGAACACACACAAGGG	44586	C G	
		CCC TGTG GTGTTTCT			
		GGG ACAC CACAAGAGA			
		A A			
GAM1671	LOC221495 3'	GCTAGAACCCAGAGAGG	45058	C G GTTT	
		CC CT TGGGT TCTAGC			
		GG GA ACCCA AGATCG			
		A G _			
GAM1671	LOC255565 3'	AGACATCACCCACAAGGGG	45588	C TTT	
		CCCC TGTGGGTG TCT			
		GGGG ACACCCAC AGA			
		A TAC			
GAM1671	LOC51580 3'	AGAAAATCCACTGGGG	18011	T GT	
		CCCC GTGGGT TTTCT			
		GGGG CACCTA AAAGA			
		T _			
GAM1671	LOC90010 3'	AGACATCACCCACAAGGGG	30621	C TTT	
		CCCC TGTGGGTG TCT			
		GGGG ACACCCAC AGA			
		A TAC			
GAM1671	LOC90249 3'	GCTTTGGCACCCACCAAGG	31013	_ TTCT	
		CCT GTGGGTGTT AGC			

GGA CACCCACGG TCG
 AC TT__
 GAM1672 KIAA0089 3' GTTTTAGCGCCACCATTAACCC 34668 A CAA_ CC
 A TG GTTAATGG GC GAGC
 || ||||| || ||||
 AC CAATTACC CG TTTG
 C ACCG AT
 GAM1672 KIAA0227 3' GGGCCTGCCATTACTCA 30455 T A
 TGAGT AATGGCA GCCC
 |||| ||||| ||||
 ACTCA TTACCGT CGGG
 _ C
 GAM1672 KIAA1708 3' ACGATGCAGCCCACCATTA ACT 33272 CAA CCGAG
 CA TGAGTTAATGG GC CGT
 ||||| || ||||
 ACTCAATTACC CG GCA
 ACC ACGTA
 GAM1673 ADH4 5' AGAAAGAACTTCCAACA 6321 C G_
 TGT GGAAGT CTTTCT
 || ||||| |||||
 ACA CCTTCA GAAAGA
 A AA
 GAM1673 ANK3 3' AGAAAAGAAAACCAACCACACA 21981 C AA C_
 TGT GG GTG TTTCTTTTCT
 ||| || ||| |||||
 ACA CC CAC AAAGAAAAGA
 _ _ CA
 GAM1673 CPNE3 3' AGAAAAAAGAAGACTTTTCCAA 9991 C TGC C
 C GT GGAAG TTTCTTTT TCT
 || |||| ||||| ||||
 CA CCTTT GAAGAAAA AGA
 A TCA A
 GAM1673 JUN 3' AGAAAAAAGAAGTGTCCGA 8009 AG T C
 TCGGA TGCTT CTTTT TCT
 |||| |||| ||||| ||||
 AGCCT GTGAA GAAAA AGA
 _ _ A
 GAM1673 PPP2R2B 3' AAAGAGAGCACTTTTCGACA 10921
 TGT CGGAAGTGCTTTCTTT
 ||||| |||||
 ACAGCTTTCACGAGAGAAA
 GAM1673 C6orf37 3' AGAGAAAAGAACAGCTCCCGAC 33508 A GCT
 GTCGG AGT TTCTTTTCTCT
 |||| ||| |||||
 CAGCC TCG AAGAAAAGAGA
 C AC_
 GAM1673 CNNM1 3' AGAAAAGAAAAGCAACCACA 21603 C AAG _
 TGT GG TGCTTT CTTTTCT
 ||| || ||||| |||||

ACA CC ACGAAA GAAAAGA
 _ A_ A
 GAM1673 EPB41L1 3' AGAAAAAGAAAGCAAGAACAGA 34935 GGAAG_
 TC TGCTTTCTTTTCT
 || |||||
 AG ACGAAAGAAAAGA
 ACAAGA
 GAM1673 FLJ10350 3' GGGAAAAGCACTTCCAGCA 45731 C CTTT
 TGT GGAAGTGCTTT TCTC
 ||| ||||| ||||
 ACG CCTTCACGAAA AGGG
 A _
 GAM1673 FLJ10420 3' AGAAATCTGAAAGCACCTCTGA 19854 A T_
 CA TGTCGGA GTGCTTTC TTTCT
 ||||| ||||| ||||
 ACAGTCT CACGAAAG AAAGA
 C TCT
 GAM1673 FLJ13213 5' AAAAGAAAGCAAGGATA 24098 GGAAG
 TGTC TGCTTTCTTTT
 ||| |||||
 ATAG ACGAAAGAAAA
 GA_
 GAM1673 FLJ13964 3' AGAAGAAGCACCTCCACA 25900 C A T
 TGT GGA GTGCTT CTTTT
 ||| ||| ||||| ||||
 ACA CCT CACGAA GAAGA
 _ C _
 GAM1673 NT5C1B 5' AGAAAAAAGAAAGGAATCTGAC 35283 AGTG C
 A TGTCGGA CTTTCTTT TCT
 ||||| ||||| |||
 ACAGTCT GAAAGAAAA AGA
 AAG_ A
 GAM1673 PRO2133 3' AGAGAAAAAAAAGATCC 20689 AGTG C
 GGA CTTT TTTTCTCT
 ||| ||| |||||
 CCT GAAA AAAAGAGA
 A_ A
 GAM1673 LOC132332 3' AGAAGAAACACTTCCCACA 37485 C C
 TGT GGAAGTG TTTCTTTT
 ||| ||||| |||||
 ACA CCTTCAC AAAGAAGA
 C _
 GAM1673 LOC146713 3' AAAAAAAGCACTTAATGC 40713 CGG C
 GT AAGTGCTTT TTTT
 || ||||| |||
 CG TTCACGAAA AAAA
 TAA A
 GAM1673 LOC146952 5' AGAAAAGAAAGCAAACG 40766 GAAG
 CG TGCTTTCTTTTCT
 || |||||

GC ACGAAAGAAAAGA
 AA__
 GAM1673 LOC148166 5' AGAAAAAAGAAAGAGAGATTCC 38479 GTG__ C
 GGAA CTTTCTTT TCT
 ||| ||||| |||
 CCTT GAAAGAAAA AGA
 AGAGA A
 GAM1673 LOC150174 3' AGAAGAAGTCATTCCCAACA 38868 C A C
 TGT GG AGTG TTTCTTTT
 ||| || ||| |||||
 ACA CC TTAC GAAGAAGA
 A C T
 GAM1673 LOC152620 3' AGAAAAAAGAAAGCAGAAGAGC 30172 AAG__ C
 C GG TGCTTTCTTT TCT
 || ||||| |||
 CC ACGAAAGAAAA AGA
 GAGAAG A
 GAM1673 LOC166042 5' GAAGGAAAACATTCCAACA 40201 C G C
 TGT GGAA TG TTTCTTTT
 ||| ||| || |||||
 ACA CCTT AC AAAGGAAG
 A _ A
 GAM1673 LOC206836 5' AGAGAAAAGTTTGCGACTCCCA 43124 C AG TTT
 CA TGT GGA TGC CTTTCTCT
 ||| ||| || |||||
 ACA CCT GCG GAAAAGAGA
 C CA TTT
 GAM1673 LOC90520 3' AGAGAAGGTTTCAGCACTTCAG 31630 G TTC_
 ACA TGTC GAAGTGCT TTTTCTCT
 ||| ||||| |||||
 ACAG CTTACGA GGAAGAGA
 A CTTT
 GAM1674 EFNB1 3' ACAGGTGGGTAACCCCCAC 10705 AAA GC
 GTG GTTACCCATC GT
 ||| ||||| ||
 CAC CAATGGGTGG CA
 CCC A_
 GAM1674 PPIF 3' TGGGAACAAACCTCACTTGA 12284 AA__ A
 TCAAGTGA GTT CCA
 ||||| ||| |||
 AGTTCACT CAA GGGT
 CCAA _
 GAM1675 RB1CC1 3' CTCCAAAACAGCAGGCCA 16630 A C
 TG CCTGTTGT TTTGGGG
 || ||||| |||||
 AC GGACGACA AAACCTC
 C A
 GAM1675 BCE-1 5' AACAAATTAGAACACAACAGGCC 13867 A C GG GC
 A TG CCTGTTGT TTT GG GTT
 || ||||| ||| || |||

			AC GGACAACA AAG TT CAA	
			C C A_ AA	
GAM1676	GPLD1	3'	GAAAGAACAAGATCATGCCCTT 44181	A _ CCACC
			TGCA TG AAGGGGTAT TC CTTTC	
			AC TTTCCCGTA AG GAAAG	
			G CT AACAA	
GAM1676	POLQ	3'	GAAAGAACAGAGATTACCCTT 13365	GT CCCACC
			CA TGAAAGGG ATT CTTTC	
			ACTTTCCC TAG GAAAG	
			AT AGACAA	
GAM1676	SET	3'	AAAGAGTCTCTACCCCTTTC 8920	TTCCC C
			GAAAGGGGTA AC CTTT	
			CTTTCCCAT TG GAAA	
			CTC_ A	
GAM1676	TGFB3	3'	GAAAGGGTGGAATCAACCCTC 9234	A GT_ C
			TC GA AGGG ATT CCACCCTTTC	
			CT TCCC TAA GGTGGGAAAG	
			C AAC A	
GAM1676	caspr5	5'	GAAAGAGCGAGTGCCTCT 29095	CCACC
			AGGGGTATTC CTTTC	
			TCTCCGTGAG GAAAG	
			CGA_	
GAM1676	caspr5	5'	GAAAGAGCGAGTGCCTCT 28266	CCACC
			AGGGGTATTC CTTTC	
			TCTCCGTGAG GAAAG	
			CGA_	
GAM1676	FLJ20485	3'	GAAAGGATAAATATGCCTTTC 21125	G CCCAC
			GAAAGG GTATT CCTTTC	
			CTTTCC TATAA GGAAAG	
			G ATA_	
GAM1676	KIAA0937	3'	GAAAGGACCCCTGACCCCTTTC 44015	ATTCCCAC
			GAAAGGGT CCTTTC	
			CTTTCCCCA GGAAAG	
			GTCCCCA_	
GAM1676	LY75	3'	GAAAAGGTGAAAATGTTTATT 8150	AG GG CC C
			CA TGAA G TATT CACC TTTC	
			ACTT T GTAA GTGG AAAG	
			AT TT AA A	
GAM1676	ORCTL3	3'	GAAAGGGTAGAGGTCTTTTCA 10444	GTA CC
			TGAAAGGG TTC ACCCTTTC	

ACTTTTCT GAG TGGGAAAG
 G__ A_
 GAM1676 TRIM4 3' GAAAATTGTGGAATCCCCCCT 26903 AA T CC_
 CA TGA GGGG ATTCCCAC TTTC
 ||| ||| ||||| |||
 ACT CCCC TAAGGGTG AAAG
 CC _ TTA
 GAM1676 LOC127702 3' GAAAGGGCAACCTCCCTTTCA 37182 TATTCCCA
 TGAAAGGGG CCCTTTC
 ||||| |||||
 ACTTTCCT GGGAAAG
 CCAAC__
 GAM1676 LOC143310 5' AAAGGGTGGAAGAACCATC 37603 _ A C
 GG GGT TT CCACCCTTT
 || ||| || |||||
 CT CCA GA GGTGGGAAA
 A A A
 GAM1676 LOC144262 5' GAAAGGATAAATGCTCCTTT 37705 CCCAC
 AAAGGGGTATT CCTTTC
 ||||| |||||
 TTTCCTCGTAA GGAAAG
 ATA__
 GAM1676 LOC144519 5' AAAGGGTGTGGCCCCTT 37754 ATTCC
 AAGGGGT CACCCTTT
 ||||| |||||
 TTCCCCG GTGGGAAA
 GT__
 GAM1676 LOC145790 3' GAAAAGGTGGGAAATATTTTC 37978 GG A C
 GAAAG GT TTCCCACC TTTC
 |||| || ||||| |||
 CTTTT TA AAGGGTGG AAAG
 A_ _ A
 GAM1676 LOC164382 3' GAAAGAGCTATTACCCCTTTC 42165 TTCCCACC
 GAAAGGGGTA CTTTC
 ||||| |||||
 CTTTCCCCAT GAAAG
 TATCGA__
 GAM1676 LOC168346 5' AAAGAGTGGGAATCAGTCA 40241 AAGG AT C
 TGA GGT TCCCAC CTTT
 ||| ||| ||||| |||
 ACT CTA AGGGTG GAAA
 GA__ _ A
 GAM1676 LOC197117 3' GAAAAGGTCACACCCTTTTCA 43195 ATTCCC C
 TGAAAGGGGT ACC TTTC
 ||||| ||| |||
 ACTTTTCCCA TGG AAAG
 CAC__ A
 GAM1676 LOC255645 3' GGTGGGAACCCCTTCCA 46223 A TA
 TG AAGGGG TTCCCACC
 || ||||| |||||

		AC TTCCCC AAGGGTGG	
		C C_	
GAM1677 CYP51	5'	CCTGTGGACGACCATCTGCCAG 6436	C GA
		CTGGCAGATGG CGT GCAGG	
		GACCGTCTACC GCA TGTCC	
		A GG	
GAM1677 DNASE1L1	3'	CCTGCACTCATGCCACCTGCCA 13566	A C _
	GG	TCTGGCAG TGGC GTGA GCAGG	
		GGACCGTC ACCG TACT CGTCC	
		C _ CA	
GAM1677 ELK3	5'	TCCTGCTCTCACACACCAGA 11733	CAGA GCCGT
		TCTGG TG GAGCAGGA	
		AGACC AC CTCGTCCT	
		AC_ AACT	
GAM1677 ENPP3	3'	CCTGATACCATCTGCCAG 11462	CCGTGAG
		CTGGCAGATGG CAGG	
		GACCGTCTACC GTCC	
		ATA_	
GAM1677 GCGR	5'	CCAGTGTGCAGCCCTGCCAGA 5664	AT C A A
		TCTGGCAG GGC GTG GC GG	
		AGACCGTC CCG CGT TG CC	
		C_ A G A	
GAM1677 GRIK3	3'	CCTGCCCTTACCTGCCAGG 6485	ATGGCC _
		TCTGGCAG GTGA GCAGG	
		GGACCGTC CATT CGTCC	
		_ CC	
GAM1677 ICAM1	3'	CCCACCCACATACATTTCTGCC 35442	_ GCC AGCA
	AG	CTGGCAGA TG GTG GG	
		GACCGTCT AC CAC CC	
		TT ATA CCAC	
GAM1677 MNT	3'	CCCAGCACAGCCACCTGCCAGA 21559	A C AGCA
		TCTGGCAG TGGC GTG GG	
		AGACCGTC ACCG CAC CC	
		C A GAC_	
GAM1677 NOS1	3'	CCTGCTCACTCTTCCACAGA 6230	GCA T CC
		TCTG GA GG GTGAGCAGG	
		AGAC CT CT CACTCGTCC	
		AC_ T _	
GAM1677 NPEPPS	3'	CTGCTCACACTCCAGA 12997	C ATGGCC
		TCTGG AG GTGAGCAG	

		AGACC TC CACTCGTC		
		— A —		
GAM1677	NRGN	5' CCCGCCACCGCTGCCGGA	12835	ATGGCC A A
		TCTGGCAG GTG GC GG		
		AGGCCGTC CAC CG CC		
		C — C C		
GAM1677	P53AIP1	3' TCCTGAAATTTGCCATCTGACA	22659	G CGTGAG
		TG CAGATGGC CAGGA		
		AC GTCTACCG GTCCT		
		A TTAAA		
GAM1677	PKHD1	3' CCTGCTCCCTGATCTGTCAGA	28940	— CCGT
		TCTGGCAGAT GG GAGCAGG		
		AGACTGTCTA CC CTCGTCC		
		GT —		
GAM1677	VIPR1	3' TCCTACCCACACCTCTGCCAGA	10995	T CC AGC
		TCTGGCAGA GG GTG AGGA		
		AGACCGTCT CC CAC TCCT		
		— A_ CCA		
GAM1677	APOL6	5' TCACAGCCCCCTGCCAGA	24970	AT C
		TCTGGCAG GGC GTGA		
		AGACCGTC CCG CACT		
		CC A		
GAM1677	FLJ20435	3' CCCACTCAGCACTCTGCCAG	19468	TG CG CA
		CTGGCAGA GC TGAG GG		
		GACCGTCT CG ACTC CC		
		CA — AC		
GAM1677	KIAA0247	3' CCCGCCTTCCCATCTGTCAGA	16373	CCGTGA A
		TCTGGCAGATGG GC GG		
		AGACTGTCTACC CG CC		
		CTTC_ C		
GAM1677	KIAA0368	3' TCTTTTATGGCCATCTGCCA	32490	C
		TGGCAGATGGCCGTGAG AGG		
		ACCGTCTACCGGTATTT TCT		
		—		
GAM1677	MGC11115	3' TCCTGTACTGCTATCCGCCAGA	26099	A C GA
		TCTGGC GATGGC GT GCAGGA		
		AGACCG CTATCG CA TGTCCT		
		C T —		
GAM1677	NXN	3' CCCACTCAGCACTCTGCCAG	22807	TG CG CA
		CTGGCAGA GC TGAG GG		

		GACCGTCT CG ACTC CC		
		CA _ AC		
GAM1677 NXPH3	3'	CCTGAACTGCCATCTGCAGA 32717	G	C GAG
		TCTG CAGATGGC GT CAGG		
		AGAC GTCTACCG CA GTCC		
		_ T A _		
GAM1677 PCBP3	3'	CCCGCGTCACCCACCTGCCAGA 21751	A	CC _ A
		TCTGGCAG TGG GTGA GC GG		
		AGACCGTC ACC CACT CG CC		
		C _ G C		
GAM1677 RAI15	3'	CCTGCCCTAGACCCTGCCAGA 33119	AT	CCGTGA
		TCTGGCAG GG GCAGG		
		AGACCGTC CC CGTCC		
		_ AGATCC		
GAM1677 SFXN5	3'	TCCCGCCCTCCCCCTGCCAGA 29388	AT	CCGTGA A
		TCTGGCAG GG GC GGA		
		AGACCGTC CC CG CCT		
		CC TCC _ C		
GAM1677 SMOC1	3'	TCCTGCTCTCCGGACCCCA 22700	CAGAT	_ T _
		TGG GG CCG GAGCAGGA		
		ACC CC GGC CTCGTCCT		
		C _ A CT		
GAM1677 LOC144519	5'	CCACCCTCACCTGCCAGA 37759	ATGGCC	CA _
		TCTGGCAG GTGAG GG		
		AGACCGTC CACTC CC		
		C _ CCA		
GAM1677 LOC144866	5'	CCTTCAAACCATCTGCCAG 40477	CCG	GC
		CTGGCAGATGG TGA AGG		
		GACCGTCTACC ACT TCC		
		AA _ _		
GAM1677 LOC149302	5'	CTGTGGCTGCCATTGCCAGA 38706	A	C GA
		TCTGGCAG TGGC GT GCAG		
		AGACCGTT ACCG CG TGTC		
		_ T G _		
GAM1677 LOC149373	3'	CCTGCTCACACTGCCAGA 38719	ATGGCC	
		TCTGGCAG GTGAGCAGG		
		AGACCGTC CACTCGTCC		
		A _ _		
GAM1677 LOC150685	5'	CCTGAGCTGCCTGCCACCTGCC 42155	A	C _ AG _
		AGA TCTGGCAG TGGC GTG CAGG		

AGACCGTC ACCG CGT GTCC
 C TC CGA
 GAM1677 LOC152274 3' TCCTGCTCACAGCCTGGCACAG 39235 _ AGAT C
 A TCTG GC GGC GTGAGCAGGA
 |||| || ||| ||||||||
 AGAC CG CCG CACTCGTCCT
 A GT__ A
 GAM1677 LOC163682 5' CCCACCCACAGCCAGCTCTGCC 42089 __ C AGCA
 AGA TCTGGCAGA TGGC GTG GG
 |||||| ||| || ||
 AGACCGTCT ACCG CAC CC
 CG A CCAC
 GAM1677 LOC90906 5' CCTGCTCAACCTGGCAGA 32148 G ATGGCCG
 TCTG CAG TGAGCAGG
 ||| ||| ||||||
 AGAC GTC ACTCGTCC
 G CA____
 GAM1677 LOC91445 3' CCCACTCACCTCTGCCAGG 30367 T CC CA
 TCTGGCAGA GG GTGAG GG
 |||||| || ||| ||
 GGACCGTCT CC CACTC CC
 _ _ AC
 GAM1678 PLA2G4C 5' GACCCAGGCTCAGGAGGACTGA 36342 C _ T A_
 GAA TTC CAGTC TCCTGA TTT GTC
 ||| |||| ||||| ||| |||
 AAG GTCAG AGGACT GGA CAG
 A G C CC
 GAM1678 SEL1L 3' GGACTAAGTGGGAGAAATTAGA 11503 CCAG_ AT
 A TTC TCTCCTG TTTAGTCC
 ||| ||||| ||||||
 AAG AGAGGGT GAATCAGG
 ATTAA ____
 GAM1678 BIRC8 5' ACTGAAAACTGGGAA 27194 CTCCTGA
 TTCCAGT TTTTAGT
 |||||| |||||
 AAGGGTCA AAAGTCA
 A_____
 GAM1678 C1QTNF7 3' GGACATGTGTACAGGAGACCAA 25666 CCA _ TTTA
 GAA TTC GTCTCCTG AT GTCC
 ||| |||||| || |||
 AAG CAGAGGAC TG CAGG
 AAC A TGTA
 GAM1678 DKFZp547I224 3' GACCATCGAGACTAGGAA 21478 C CT TTTA
 TTCC AGTCTC GAT GTC
 ||| ||||| ||| |||
 AAGG TCAGAG CTA CAG
 A _ C____
 GAM1678 FLJ10120 3' GGACCAATGGAAGACTGAGAA 19729 C _ TGATTTTA
 TTC CAGTCT CC GTCC
 ||| ||||| || |||

AAG GTCAGA GG CAGG
 A A TAAC____
 GAM1678 FLJ11783 3' GCCTGATCAGGAGACTG 24365 TTA
 CAGTCTCCTGATT GT
 ||||| ||
 GTCAGAGGACTAG CG
 TC_
 GAM1678 FLJ22174 5' GGA CTAATCCATCGATGACTGG 22467 TCC T__
 CCAGTC TGAT TTAGTCC
 ||||| ||| |||||
 GGTCAG GCTA AATCAGG
 TA_ CCT
 GAM1678 FLJ23499 3' ACTAGTAGAGACTGAGAA 23005 C CTGATT
 TTC CAGTCTC TTAGT
 ||| ||||| |||||
 AAG GTCAGAG GATCA
 A AT____
 GAM1678 IKKE 5' GGCTACCAGGAGGCTAAGAA 15203 CC ATTT
 TTC AGTCTCCTG TAGTC
 ||| ||||| |||||
 AAG TCGGAGGAC ATCGG
 AA C____
 GAM1678 KIAA0323 3' GGA C TGGGAGAGGAATCTAAGA 31695 CC TC GA
 A TTC AG TCCT TTTTAGTCC
 ||| || ||| |||||
 AAG TC AGGA AGGGTCAGG
 AA TA G_
 GAM1678 KIAA1161 5' GGATCAGAAGACAGGAA 39754 CA C
 TTCC GTCT CTGATTT
 |||| ||| |||||
 AAGG CAGA GACTAGG
 A_ A
 GAM1678 KIAA1727 3' GACTAATTGGGAAACGGGGAA 32033 A C TG TT
 TTCCC GT TCC AT TAGTC
 ||||| || ||| ||| |||||
 AAGGG CA AGG TA ATCAG
 G A GT ____
 GAM1678 MGC4415 3' GCTTATCAAAGACTGAGAA 25570 C CC TTT
 TTC CAGTCT TGAT AGT
 ||| ||||| ||||| |||
 AAG GTCAGA ACTA TCG
 A A_ T__
 GAM1678 NTN4 3' GACCTCAGACAGGAAACTGG 31513 C A TA_
 CCAGT TCCTG TTT GTC
 ||||| ||||| ||| |||
 GGTCA AGGAC AGA CAG
 A _ CTC
 GAM1678 RNPC1 3' GGA CTTTAAGAATGACTGAGAA 18958 C TCCTGA TT
 TTC CAGTC TT AGTCC
 ||| ||||| || ||| |||||

		AAG GTCAG	AA TCAGG		
		A	TAAG__ TT		
GAM1678	SS18L1	3'	GGACTAAAATTTCCCACTG	32562	CTCCT
			CAGT GATTTTAGTCC		
			GTCA TTAAAATCAGG		
			CCCT_		
GAM1678	LOC114932	3'	GACTGCTTTGCATAAACTGGG	36005	CTCC ATTT_
		AA	TTCCCACT TG TAGTC		
			AAGGGTCA AC GTCAG		
			AAAT GTTTC		
GAM1678	LOC145497	5'	ACTACCTCCAGGAGATGGAA	37871	CA ATTT
			TTCC GTCTCCTG TAGT		
			AAGG TAGAGGAC ATCA		
			__ CTCC		
GAM1678	LOC145978	3'	GGATTTGGTCAAATAGACTGAG	38033	C CC_ TT
		AA	TTC CAGTCT TGATT AGTCC		
			AAG GTCAGA ACTGG TTAGG		
			A TAA T_		
GAM1678	LOC146429	5'	GACGGCTCAGGAACTGGGAA	40696	C TTTTA
			TTCCCACT TCCTGA GTC		
			AAGGGTCA AGGACT CAG		
			_ CGG__		
GAM1678	LOC149386	3'	TATAATCCAGAGACTGAGAA	40987	C CT T
			TTC CAGTCTC GATT TA		
			AAG GTCAGAG CTAA AT		
			A AC T		
GAM1678	LOC158581	5'	GATTACATCATAAGACTG	42015	CC TT
			CAGTCT TGAT TAGTC		
			GTCAGA ACTA ATTAG		
			AT C_		
GAM1678	LOC202460	5'	GACCTAAATAACTGGGAA	42984	CTCCTG TA
			TTCCCACT ATTT GTC		
			AAGGGTCA TAAA CAG		
			A_____ TC		
GAM1678	LOC219894	3'	ACTAGGGAGATGACTGAGAA	44792	C TC GA
			TTC CAGTC CT TTTTAGT		
			AAG GTCAG GA GGGATCA		
			A TA _		
GAM1678	LOC221751	5'	GGACTAATCCATCGATGACTGG	44190	TCC T__
			CCAGTC TGAT TTAGTCC		

GGTCAG GCTA AATCAGG
TA_ CCT
GAM1678 LOC254268 3' GACTAAAATCAAAATTCTGAGA 45691 C TCTCC
A TTC CAG TGATTTTAGTC
||| ||| |||||
AAG GTC ACTAAAATCAG
A TTAAA
GAM1678 LOC255252 3' GGATCAGGAGACAGGAA 45546 CA
TTCC GTCTCCTGATTT
|||| |||||
AAGG CAGAGGACTAGG
A_
GAM1678 LOC90499 3' AGAGCCAGGAGACCAGGGA 31581 A_ AT
TCCC GTCTCCTG TTT
|||| ||||| |||
AGGG CAGAGGAC AGA
AC CG
GAM1679 CDK5R2 3' GAAAGGCACTCCAACCTCA 10042 ACG
TGAG GGAGTGCCTTTT
|||| |||||
ACTC CCTCACGGAAG
CAA
GAM1679 PACE4 3' GGCAGGCACTCCCATCCA 28720 A C TTTA
TG GA GGGAGTGCCT GTC
|| || ||||| |||
AC CT CCCTCACGGA CGG
_ A _
GAM1679 PACE4 3' GGCAGGCACTCCCATCCA 8431 A C TTTA
TG GA GGGAGTGCCT GTC
|| || ||||| |||
AC CT CCCTCACGGA CGG
_ A _
GAM1679 VANG2 3' GGAAGGACTCCCACCTCA 35483 AC G
TGAG GGGAGT CCTTTT
|||| ||||| |||||
ACTC CCCTCA GGAAGG
CA _
GAM1679 ARL8 3' GACCAGCACTCCCTCCCA 44763 A C CTTTTA
TG GA GGGAGTGC GTC
|| || ||||| |||
AC CT CCCTCACG CAG
C _ AC_
GAM1679 FLJ13659 3' AGAGTGGCACTCCATCTCA 24830 CG _
TGAGA GGAGTGCC TTTT
|||| ||||| |||||
ACTCT CCTCACGG GAGA
A_ T
GAM1679 GNG4 5' GAAGGGCACCCCCGCCTC 10811 A A
GAG CGGG GTGCCTTTT
||| ||| |||||

				CTC GCCC CACGGGAAG			
				C C			
GAM1679	HTCD37	3'	TGACCCAGCAGAGCACTCCCTC	33620	A C		T A
	CCA		TG GA GGGAGTGC CT TT GTCA				
			AC CT CCCTCACG GA GA CAGT				
			C _ A C CC				
GAM1679	KIAA0451	3'	ACTAAAAGGAGCCCATCT	16803	C	AGTG	
			AGA GGG CCTTTTAGT				
			TCT CCC GGAAAATCA				
			A GA_				
GAM1679	MGC2562	3'	GACAGAGCAATACTCCCGTCTC	26163		CCT	A
	A		TGAGACGGGAGTG TTT GTC				
			ACTCTGCCCTCAT GAG CAG				
			AAC A				
GAM1679	TOB2	3'	TGACGGACTCAGCACTCCCGCC	45770	A	CTTTTA	_
	T		AG CGGGAGTGC GTCA				
			TC GCCCTCACG CAGT				
			C ACTCAGG				
GAM1679	LOC149576	5'	AAGAGACTCCCGTCTCA	38775		GC	
			TGAGACGGGAGT CTTTT				
			ACTCTGCCCTCA GAGAA				
			—				
GAM1679	LOC151278	3'	TGAGGGGACACCCAGCCTCA	39097	AC_	A	
			TGAG GGG GTGCCTTTTA				
			ACTC CCC CACGGGGAGT				
			CGA _				
GAM1679	LOC91565	5'	TGACTAAAAGGCTTTGGTTCA	33024	A G	GT	
			TGAG C GGA GCCTTTTAGTCA				
			ACTT G TTT CGGAAAATCAGT				
			_G _				
GAM1680	COL13A1	5'	CGACCCACCTCTGCCCA	28066	AA	A	
			TG CGGAGGTG GGTG				
			AC GTCTCCAC CCAGC				
			CC _				
GAM1680	COL13A1	5'	CGACCCACCTCTGCCCA	28068	AA	A	
			TG CGGAGGTG GGTG				
			AC GTCTCCAC CCAGC				
			CC _				
GAM1680	COL13A1	5'	CGACCCACCTCTGCCCA	28070	AA	A	
			TG CGGAGGTG GGTG				

			AC GTCTCCAC CCAGC			
			CC _			
GAM1680	COL13A1	5'	CGACCCACCTCTGCCCA	28072	AA	A
			TG CGGAGGTG GGTG			
			AC GTCTCCAC CCAGC			
			CC _			
GAM1680	COL13A1	5'	CGACCCACCTCTGCCCA	28074	AA	A
			TG CGGAGGTG GGTG			
			AC GTCTCCAC CCAGC			
			CC _			
GAM1680	COL13A1	5'	CGACCCACCTCTGCCCA	28076	AA	A
			TG CGGAGGTG GGTG			
			AC GTCTCCAC CCAGC			
			CC _			
GAM1680	COL13A1	5'	CGACCCACCTCTGCCCA	11703	AA	A
			TG CGGAGGTG GGTG			
			AC GTCTCCAC CCAGC			
			CC _			
GAM1680	HPCAL1	3'	GTGCATGGCTGCCCCCGTTT	28638		A TGA _
	A		TGAACGG GG GGT TGCAC			
			ACTTGCC CC TCG ACGTG			
			C CCG GT			
GAM1680	HPCAL1	3'	GTGCATGGCTGCCCCCGTTT	7931		A TGA _
	A		TGAACGG GG GGT TGCAC			
			ACTTGCC CC TCG ACGTG			
			C CCG GT			
GAM1680	AMOTL1	3'	CGTGTGCAAATATGACTCAATT	36465		CG GTGAGG
	CA		TGAA GAG TTGCACACG			
			ACTT CTC AACGTGTGC			
			AA AGTATA			
GAM1680	FLJ11110	3'	CAACCTCACCTCCCTCA	20319	AC	
			TGA GGAGGTGAGGTTG			
			ACT CCTCCACTCCAAC			
			C_			
GAM1680	KIAA1910	3'	CACCCCCACCTTCGCTCA	36285	A	A T
			TGA CGGAGGTG GG TG			
			ACT GCTTCCAC CC AC			
			C C C			
GAM1680	MGC10818	5'	GCCACCCTCACCTCCTTCA	24940	C	TT_
			TGAA GGAGGTGAGG GC			

ACTT CCTCCACTCC CG
 _ CAC
 GAM1680 RAB40C 3' CGTGCCTGGAACCACCTCGTCC 22145 A G GA G _
 A TG ACG AGGT GGTT CA CACG
 || ||| ||| || |||
 AC TGC TCCA CCAA GT GTGC
 C _ _ G CC
 GAM1680 SCAMP-4 3' CGTGTGGTCACCCGCCGTCC 27822 _ A T _
 GGA GGTG GGT GC ACACG
 ||| ||| ||| || |||
 CCT CCGC CCA TG TGTGC
 G _ C G
 GAM1680 LOC221288 3' GTGCTTCACCTCCATTTA 44969 C GTT
 TGAA GGAGGTGAG GCAC
 ||| ||| ||| |||
 ATTT CCTCCACTT CGTG
 A _
 GAM1681 CFTR 3' TATGCCTTTTCCCAACTC 6103 AT CAGT
 GAGTT GGA GGGGCATA
 ||| ||| ||| |||
 CTCAA CCT TTCCGTAT
 C _ T _
 GAM1681 STS 3' TCCACTGCCCATGACCCT 5911 A A
 AG GTTATGG CAGTGGG
 || ||| ||| |||
 TC CAGTACC GTCACCT
 C C
 GAM1681 FLJ11286 3' ATATGCCCCACCACGAAACTC 20414 A GACA
 GAGTT TG GTGGGGCATAT
 ||| || ||| ||| |||
 CTCAA GC CACCCCGTATA
 A AC _
 GAM1681 KIAA0747 3' CCCCACTGTCCTCAACCCT 17612 A AT
 AG GTT GGACAGTGGGG
 || ||| ||| ||| |||
 TC CAA CCTGTCACCCC
 C CT
 GAM1681 MGC13061 3' TGTGTCTCACCGCCCACAACCC 26132 A A ACA
 T AG GTT TGG GTGGGGCATAT
 || ||| ||| ||| ||| |||
 TC CAA ACC CACTCTGTGT
 C C CGC
 GAM1681 TLN2 3' ATGTCCTACCCACAACCTC 30897 A ACA
 GAGTT TGG GTGGGGCAT
 ||| ||| ||| ||| |||
 CTCAA ACC CATCCTGTA
 C _
 GAM1681 LOC151361 3' TTCATACCATAACTCT 41334 ACA
 AGAGTTATGG GTGGG
 ||| ||| ||| ||| |||

TCTCAATACC TACTT
 A__
 GAM1681 LOC158314 5' ATATGTGCATGTCTATAACTC 41952 _ GGG
 GAGTTATGGACA GT GCATAT
 ||||| || |||||
 CTCAATATCTGT CG TGTATA
 A ____
 GAM1682 B3GALT3 3' AAGAAATTAATAGGACC 9867 ATCG
 GGTC ATTAATTTCTT
 |||| |||||
 CCAGG TAATTAAAGAA
 A__
 GAM1682 B3GALT3 3' AAGAAATTAATAGGACC 27016 ATCG
 GGTC ATTAATTTCTT
 |||| |||||
 CCAGG TAATTAAAGAA
 A__
 GAM1682 B3GALT3 3' AAGAAATTAATAGGACC 27019 ATCG
 GGTC ATTAATTTCTT
 |||| |||||
 CCAGG TAATTAAAGAA
 A__
 GAM1682 CMG2 3' GAAGAAACAGAGGAACCCA 27720 A GATTAA
 TGGGTT TC TTTCTTC
 ||||| || |||||
 ACCCAAG AG AAAGAAG
 G AC____
 GAM1682 DDX28 5' AAGAAAAGATGACCCA 20406 T GATTAA
 TGGGT CATC TTTCTT
 |||| || |||||
 ACCCA GTAG AAAGAA
 _ A____
 GAM1682 KIAA1323 5' TGAAGAAATTATTTGAAACCCA 31572 CA T
 TGGGTT TCGA TAATTTCTTCA
 |||| ||| |||||
 ACCCAA AGTT ATTAAGAAGT
 _ T
 GAM1682 MGC5306 3' AAGAAATTAGATCCCA 23570 T ATCGAT
 TGGG TC TAATTTCTT
 ||| || |||||
 ACCC AG ATTAAGAA
 T ____
 GAM1682 PRO1386 5' TGAAGAAAGCCAAGAAAACCCA 25292 CA GATTAA
 TGGGTT TC TTTCTTCA
 |||| || |||||
 ACCCAA AG AAAGAAGT
 A_ AACCG_
 GAM1682 TTTY9 5' TGAAGAAGAGGACAACAAGCCC 25681 CATCGA AA
 A
 TGGGTT TT TTTCTTCA
 |||| || |||||

ACCCGA AG GAAGAAGT
 ACAAC_ GA
 GAM1682 LOC143286 5' AAGAAATTAACCCTAACCCA 40351 CATCGA
 TGGGTT TTAATTTCTT
 ||||| |||||
 ACCCAA AATTAAAGAA
 TCCC_
 GAM1682 LOC150519 3' TGAAGAAATCAGAGGGAACGCA 38989 G A_ GATTA
 TG GTTC TC ATTTCTTCA
 || ||| || |||||
 AC CAAG AG TAAAGAAGT
 G GG AC_
 GAM1682 LOC222128 5' TGAAGAAACAAGGAGTAAACCC 44543 CA_ GATTAA
 A TGGGTT TC TTTCTTCA
 ||||| || |||||
 ACCCAA AG AAAGAAGT
 ATG GAAC_
 GAM1682 LOC57795 5' GAAGAAACCAATCGCCC 34360 TTCAT AA
 GGG CGATT TTTCTTC
 || |||| |||||
 CCC GCTAA AAAGAAG
 _____ CC
 GAM1682 LOC85479 5' TGAAGAAATTAAGAAAACCTA 26959 CATCGA
 TGGGTT TTAATTTCTTCA
 ||||| |||||
 ATCCAA AATTAAAGAAGT
 AAG_
 GAM1682 LOC92573 5' TGAAGAAACTCCCCCAACCCA 34602 CATC TTAA
 TGGGTT GA TTTCTTCA
 ||||| || |||||
 ACCCAA CT AAAGAAGT
 CCCC C_
 GAM1682 LOC92973 5' AAGAACGCTGAACCCA 35182 T ATTAAT
 TGGGTTCA CG TTCTT
 ||||| || |||||
 ACCCAAGT GC AAGAA
 C _____
 GAM1683 ARHGEF6 3' TAGTGTGTAAGTTTCTA 33849 C T
 TAGAAAAC TATACA CTG
 ||||| ||||| |||
 ATCTTTTG ATGTGT GAT
 A _
 GAM1683 BIG1 3' CAGATGTAAAGTTTCTA 13137 CTA
 TAGAAAAC TACATCTG
 ||||| |||||
 ATCTTTTG ATGTAGAC
 AA_
 GAM1683 RAF1 3' CAGGAATACAGGTTTCT 39246 A CA
 AGAAAACCT TA TCTG
 ||||| || |||

TCTTTTGGGA AT GGAC
 C AA
 GAM1683 SALL2 3' TGGTGGGTATGGGTCCCCTA 31938 AAA AT TG
 TAG ACCTATAC C CCG
 ||| ||||| | |||
 ATC TGGGTATG G GGT
 CCC _ GT
 GAM1683 CYYR1 3' TCAGCAGAAATAGGGTTTCT 27516 ATACA C
 AGAAAACCT TCTGC GA
 ||||| |||| ||
 TCTTTTGGG AGACG CT
 ATAA_ A
 GAM1683 FLJ13782 3' TCGGCAGACTGGGGCTTC 24439 AA TACA
 GAA CCTA TCTGCCGA
 ||| ||| |||||
 CTT GGGT AGACGGCT
 CG C_
 GAM1683 KIAA0895 3' TCAGCATTGTGTAGTGTCTTCT 44547 _ TC C
 A TAGAAAAC CTATACA TGC GA
 ||||| ||||| ||| ||
 ATCTTTTG GATGTGT ACG CT
 T T_ A
 GAM1683 KIAA1255 3' AGATGTATATGCTTTCTA 33346 ACC
 TAGAAA TATACATCT
 ||||| |||||
 ATCTTT ATATGTAGA
 CGT
 GAM1683 KIAA1387 3' TCAGCACATGTTGAGTTTCTA 35105 CTAT C C
 TAGAAAAC ACAT TGC GA
 ||||| ||||| ||| ||
 ATCTTTTG TGTA ACG CT
 AGT_ C A
 GAM1683 SCYB10 3' TAGATGTATATATTTCTA 7293 A CC
 TAG AAA TATACATCTG
 ||| ||| |||||
 ATC TTT ATATGTAGAT
 C AT
 GAM1683 SLC1A7 3' GTGGAGTCAGGTTTCTA 13490 AT A TG
 TAGAAAACCT AC TC C
 ||||| ||| |
 ATCTTTTGGG TG AG G
 C_ _ GT
 GAM1683 LOC203339 5' TCGGCAGATCTGAATTTTCT 43527 CCTA C
 AGAAAA TA ATCTGCCGA
 ||||| || |||||
 TCTTTT GT TAGACGGCT
 AA_ C
 GAM1683 LOC222234 3' CACATGACAGGTTTCTA 45239 ATA C
 TAGAAAACCT CAT TG
 ||||| ||| ||

		ATCTTTTGGA GTA AC	
		CA_ C	
GAM1684	SNX3	3' TAAATGCATTTCTGATATGCA 9876	TTCCAC
	A	TTGCATATCGG CATTTTA	
		AACGTATAGTC GTAAAAT	
		TTTAC_	
GAM1684	LOC115265	3' AAAATGGTGGCTTATGGAA 36305	G TC C_
		TT CATA GGTT CACCATTTT	
		AA GTAT TCGG GTGGTAAAA	
		G _ TA	
GAM1685	TU3A	3' TCACCAAGCCAATACCA 14035	G ACA
		TGG ATTGGCTTG TGA	
		ACC TAACCGAAC ACT	
		A C_	
GAM1685	LOC257481	3' TGTCTGCCAAGCCAGCCCCA 30631	AT A T
		TGGG TGGCTTG CA GATG	
		ACCC ACCGAAC GT CTGT	
		CG C _	
GAM1686	ABCC12	3' CCACCCCAGTGCCTGAGA 27072	CGA A_ A
		TCTCAGGC GC GG TGG	
		AGAGTCCG TG CC ACC	
		_ AC C	
GAM1686	AXIN1	3' GAGGCCACCCGCAGGGCCCAGA 30518	CA GA A A
		TCT GGCC GC GG TGGCCTC	
		AGA CCGG CG CC ACCGGAG	
		C_ GA C _	
GAM1686	KCNK5	3' CCCTCCTGCCCCGCCTGAGA 9828	C A T
		TCTCAGGC G GCAGGA GG	
		AGAGTCCG C CGTCCT CC	
		_ C C	
GAM1686	L1CAM	3' GAGGCCATCTGGAGAGCCCAGA 6003	CA CGAGCA
		TCT GGC GGATGGCCTC	
		AGA CCG TCTACCGGAG	
		C_ AGAGG_	
GAM1686	L1CAM	3' GAGGCCATCTGGAGAGCCCAGA 23431	CA CGAGCA
		TCT GGC GGATGGCCTC	
		AGA CCG TCTACCGGAG	
		C_ AGAGG_	
GAM1686	MEF2B	5' AGATCATTCCACTCAGCCTGGG 12544	C CA GC
	A	TCTCAGGC GAG GGATG CT	

AGGGTCCG CTC CTTAC GA
 A AC TA
 GAM1686 PEX10 3' ATCTGCATCTCAGCCTGAGA 8479 C CA__
 TCTCAGGC GAG GGAT
 ||||| || ||||
 AGAGTCCG CTC TCTA
 A TACG
 GAM1686 PIK3R1 3' GAGGCAGAAGAACCCTGGCCTG 34036 AGCAGGATG_
 AGA TCTCAGGCCG GCCTC
 ||||| ||||
 AGAGTCCGGT CGGAG
 CCCAAGAAGA
 GAM1686 SHMT1 3' GCTTTCCTGCTCCACCTGAGA 10374 CC T
 TCTCAGG GAGCAGGA GGC
 ||||| ||||| ||||
 AGAGTCC CTCGTCCT TCG
 AC T
 GAM1686 TNFAIP1 3' GAGACTGGAATGCGTCAGCCTG 22113 C _ GGA C
 AGA TCTCAGGC GA GCA TGG CTC
 ||||| || ||||
 AGAGTCCG CT CGT GTC GAG
 A G AAG A
 GAM1686 VANG2 3' GAGACCATCCTGCTGTC 35480 CG C
 GGC AGCAGGATGG CTC
 || ||||| ||||
 CTG TCGTCCTACC GAG
 _ A
 GAM1686 DKFZP434J046 5' AGACCATCCTGGATGCCAGGA 35150 CA CGAG C
 TCT GGC CAGGATGG CT
 || || ||||| ||
 AGG CCG GTCCTACC GA
 AC TAG_ A
 GAM1686 FLJ10385 5' AGCCATCCTGGCTGAGG 19840 G GAGC C
 TCTCAG CC AGGATGGC T
 ||||| || ||||| |
 GGAGTC GG TCCTACCG A
 _ _ A
 GAM1686 FLJ12876 3' GCCACCGCACCCGGCCTGA 22987 A_ A A
 TCAGGCCG GC GG TGGC
 ||||| || ||||
 AGTCCGGC CG CC ACCG
 CCA _ _
 GAM1686 FLJ20375 3' GCCACCCTGCTGTCTTGAGA 19433 CCG A
 TCTCAGG AGCAGG TGGC
 ||||| ||||| ||||
 AGAGTTC TCGTCC ACCG
 CTG C
 GAM1686 FLJ22625 5' GAGGCCGTCCGCCGACTCCAA 24042 CA_ C A A
 GA TCT GG CG GC GGATGGCCTC
 || || || ||||| |||||

AGA TC GC CG CCTGCCGGAG
 ACC A C _
 GAM1686 GR6 5' AGTGCTTCCTGTCCCGGCCTGA 14280 A_ T _
 GA TCTCAGGCCG GCAGGA GGC CT
 ||||| ||||| ||
 AGAGTCCGGC TGTCCT TCG GA
 CC _ T
 GAM1686 KIAA0451 3' GAGGCCATCCCAAGCCGAGA 16807 A CGAGCA
 TCTC GGC GGATGGCCTC
 ||| || |||||
 AGAG CCG CCTACCGGAG
 _ AAC_
 GAM1686 KIAA0544 3' AGGCCCCACTCCAGCCTGAGA 35109 C_ CAGGAT
 TCTCAGGC GAG GGCCT
 ||||| || ||||
 AGAGTCCG CTC CCGGA
 AC AC_
 GAM1686 MGC12435 5' GAGGCCATCTGAAGCCAAAGA 25423 CA CGAGCA
 TCT GGC GGATGGCCTC
 ||| || |||||
 AGA CCG TCTACCGGAG
 AA AAG_
 GAM1686 MGC29643 5' GAGGCGCGGTGCTCGGCCCGGG 29406 A GGA _
 A TCTC GGCCGAGCA TG GCCTC
 ||| ||||| || ||||
 AGGG CCGGCTCGT GC CGGAG
 C G_ G
 GAM1686 OSBPL5 3' GAGGCCATCCTCTCCATCCGAG 35988 A CC_ C
 A TCTC GG GAG AGGATGGCCTC
 |||| || || |||||
 AGAG CC CTC TCCTACCGGAG
 _ TAC _
 GAM1686 TUB 3' AGGCCTCACTCAAGCCTGAGA 9319 C_ CAG T
 TCTCAGGC GAG GA GGCCT
 ||||| || || ||||
 AGAGTCCG CTC CT CCGGA
 AA A_ _
 GAM1686 LOC119188 5' GAAGCCATCCTGCAGCTCTGAG 36613 _ CGA C
 A TCTCAG GC GCAGGATGGC TC
 ||||| || ||||| ||
 AGAGTC CG CGTCCTACCG AG
 T A_ A
 GAM1686 LOC145717 5' AGGCCCTCGGCTCGGCCGAGA 33190 A AG T
 TCTC GGCCGAGC GA GGCCT
 ||| ||||| || ||||
 AGAG CCGGCTCG CT CCGGA
 _ G_ C
 GAM1686 LOC146795 5' GCCCCCTCGCCCAGCCTGAGA 38244 CGA _ AT
 TCTCAGGC GC AGG GGC
 ||||| || ||| ||

	AGAGTCCG CG TCC CCG		
	ACC C CC		
GAM1686 LOC151176 5'	GAGGCCATCATGGGCCTGGAGA 41317	_	GAG G
	TCTC AGGCC CA GATGGCCTC		
	AGAG TCCGG GT CTACCGGAG		
	G ____ A		
GAM1686 LOC152453 5'	GAGGCTGTCTCCAGCCTGAGA 39276		CGAGCAG
	TCTCAGGC GATGGCCTC		
	AGAGTCCG CTGTCCGAG		
	ACCTA__		
GAM1686 LOC155061 5'	GAGAGCCCCGCCGGCCTGAGA 39536		A AGGAT _
	TCTCAGGCCG GC GGC CTC		
	AGAGTCCGGC CG CCG GAG		
	C C____ A		
GAM1686 LOC197342 3'	GGGGCTGTCCCAGCCCAAGA 42488	CA	CGAGCA
	TCT GGC GGATGGCCTC		
	AGA CCG CCTGTCCGGG		
	AC AC____		
GAM1686 LOC201689 3'	AGGCCAGCATTGAGCCTGAGA 33332		C CAGGA
	TCTCAGGC GAG TGGCCT		
	AGAGTCCG CTT ACCGGA		
	A ACG__		
GAM1686 LOC221140 5'	GAGACCAGCATCTCGGCCTGAG 44907		CAGGA C
	CTCAGGCCGAG TGG CTC		
	GAGTCCGGCTC ACC GAG		
	TACG_ A		
GAM1686 LOC222166 3'	CCAGCTGCCAGCCTGAGA 45151	CGA	GA
	TCTCAGGC GCAG TGG		
	AGAGTCCG CGTC ACC		
	AC_ G_		
GAM1686 LOC254431 5'	ATCTGCATCTCAGCCTGAGA 46290		C CA__
	TCTCAGGC GAG GGAT		
	AGAGTCCG CTC TCTA		
	A TACG		
GAM1686 LOC91974 5'	GAGACCATCCTGCCCATCCGAG 33653	A CCGA	C
	CTC GG GCAGGATGG CTC		
	GAG CC CGTCCTACC GAG		
	_ TACC A		
GAM1687 CELSR1 3'	GGGCCAGCACCGCTGA 15516	A	AT
	TCA CGGTGTTG GTTC		

AGT GCCACGAC CGGG
 C _
 GAM1687 SLC7A6 3' CAGAACATATCATCACTG 10125 T _
 CCGTG TGA TGTTCTG
 ||||| ||| |||||
 GTCAC ACT ACAAGAC
 T AT
 GAM1687 LOC120826 5' CGCAGACCTCACAACATC 37223 A T_
 GGTGTTG TG TCTGCG
 ||||| || |||||
 CTACAAC AC AGACGC
 _ TCC
 GAM1687 LOC160717 5' CGCAGAATCATCTCCGTTGA 40007 TGTT _
 TCAACGG GATG TTCTGCG
 ||||| ||| |||||
 AGTTGCC CTAC AAGACGC
 T_ T
 GAM1688 ESPL1 5' ACACTGCCGTCGCTTTTGCTG 14630 T A C
 CAGCG GAGCGACG CAG GT
 ||||| ||||| ||| ||
 GTCGT TTCGCTGC GTC CA
 T C A
 GAM1688 KIAA0515 3' ACGCTGTCGCCAGCCATG 31918 A GA_
 CGTG GC CGACAGCGT
 |||| || |||||
 GTAC CG GCTGTCGCA
 _ ACCC
 GAM1688 LOC255937 3' GACGCTGTGGCTCACACCTGTA 45931 C_ GACG
 TACAG GTGAGC ACAGCGTC
 ||||| ||||| |||||
 ATGTC CACTCG TGTCGCAG
 CA G_
 GAM1689 DGAT1 5' CCTCGGGCGCTACGAACCCGGC 32236 A CG CA_ T
 A TGCC GG CG GCTCG GG
 |||| || || |||||
 ACGG CC GC CGGGC CC
 C AA ATCG T
 GAM1689 PPP2R5A 5' CTTCCACCGTCTGCGCGCC 12910 CTC
 GGCGCGCAG GTGGAAG
 ||||| |||||
 CCGCGCGTC CACCTTC
 TGC
 GAM1689 ROBO1 5' CTTCCACGAGCCAGGGGTGC 28584 GCA_
 GCGC GCTCGTGGAAG
 |||| |||||
 CGTG CGAGCACCTTC
 GGGAC
 GAM1689 SHOX 3' TCCCAGCGCTGGCCGCCTGGCA 6058 _G TCGT
 TGCCAGGCG C CAGC GGA
 ||||| ||| |||

		ACGGTCCGC G GTCG CCT		
		C _ CGAC		
GAM1689	TERF2	3' CATGAGCCACGCGCCTGGCA 12188	CA_	
		TGCCAGGCGCG GCTCGTG		
		ACGGTCCGCGC CGAGTAC		
		CAC		
GAM1689	XRCC3	3' TCCACATGCTGCCTGGCA 11909	C GCTC	
		TGCCAGGCG GCA GTGGA		
		ACGGTCCGT CGT CACCT		
		_ A _		
GAM1689	C21orf4	5' CTTCTGCGCGCGCCTG 12776	A T T	
		CAGGCGCGC GC CG GGAAG		
		GTCCGCGCG CG GT CCTTC		
		_ C _		
GAM1689	Di-Ras2	3' CTTCTGTACCCGCGCTGGCA 19043	CGCAGCT T	
		TGCCAGGCG CG GGAAG		
		ACGGTCCGC GT CCTTC		
		CCACT _ _		
GAM1689	DKFZp761G2113	3' CCAGGGGCCACCCGCGCTGGCA 34640	CGCA G	
		TGCCAGGCG GCTC TGG		
		ACGGTCCGC CGGG ACC		
		CCAC G		
GAM1689	FLJ14251	5' CCGCTGCTGCGCGCCTGGC 24323	TC	
		GCCAGGCGCGCAGC GTGG		
		CGGTCCGCGCGTCG CGCC		
		T _		
GAM1689	MAP1LC3A	5' CCCGGCCTGCGCGCCCAGC 26265	CA CT T	
		GC GCGCGCAG CG GG		
		CG CCGCGCGTC GC CC		
		AC CG _		
GAM1689	RASD2	3' CCCCAGCTGCGCCTGACA 15603	C GC CGT	
		TG CAGGC GCAGCT GG		
		AC GTCCG CGTCGA CC		
		A _ _ CC_		
GAM1689	SIAT8C	5' CTCGGCTGACGCCTGGCA 18027	GC T T	
		TGCCAGGC GCAGC CG GG		
		ACGGTCCG CGTCG GC TC		
		A _ _ _		
GAM1689	LOC124930	3' CCCGGCCTGCGCGCCTGCA 36767	C CT T	
		TGC AGGCGCGCAG CG GG		

		ACG TCCGCGCGTC GC CC	
		CG _	
GAM1689	LOC127534 5'	CTTCCACGTGCAGCACCCAGG 37170	A_ C GCA T
		CC GG GC GC CGTGGAAG	
		GG CC CG CG GCACCTTC	
		AC A A_ T	
GAM1689	LOC129566 5'	CCCGGGCTGCGCCCCAGCA 37279	CA C T
		TGC GG GCGCAGCTCG GG	
		ACG CC CGCGTCGGGC CC	
		AC _ _	
GAM1689	LOC146957 3'	TCCTGCCTCTGCAGGCCTGGCA 38281	GC CTCGT
		TGCCAGGC GCAG GGA	
		ACGGTCCG CGTC CCT	
		GA TCCGT	
GAM1689	LOC147136 5'	CCCCGTTGCAGGCCTGGCA 38301	GC TCGT
		TGCCAGGC GCAGC GG	
		ACGGTCCG CGTTG CC	
		GA CC_	
GAM1689	LOC153480 5'	TCCAACATGGCGCCTGGCA 36089	G GCTCG
		TGCCAGGCGC CA TGGGA	
		ACGGTCCGCG GT ACCT	
		_ ACA_	
GAM1689	LOC161635 5'	TTCACAAACTGCGGCCTGGCA 46187	G CTC
		TGCCAGGC CGCAG GTGGA	
		ACGGTCCG GCGTC CACTT	
		_ AAA	
GAM1689	LOC222865 5'	CCGCGCTGCGCGCCCGG 44622	A T T
		CC GCGCGCAGC CG GG	
		GG CCGCGCGTCG GC CC	
		C C _	
GAM1689	LOC253962 5'	CCACAGCTGCGCCTGG 46225	GC C
		CCAGGC GCAGCT GTGG	
		GGTCCG CGTCGA CACC	
		_ _	
GAM1690	MYH11 3'	AGTTTTGCACCACGGCAAGAAA 8299	ACATCA C
		TTTCTTGCC CA GATT	
		AAAGAACGG GT TTGA	
		CACCAC T	
GAM1690	MYH11 3'	AGTTTTGCACCACGGCAAGAAA 23141	ACATCA C
		TTTCTTGCC CA GATT	

			AAAGAACGG	GT TTGA	
			CACCAC	T	
GAM1690	RPE	3'	TGTGTTATAAATATGGCAAGAA	31159	C C_____
	A		TTTCTTGCCA	AT ACACG	
			AAAGAACGGT	TA TGTGT	
			A	AATAT	
GAM1690	PANK	3'	AAATCTTTGTGCAAGAAA	28713	C TCACAC
			TTTCTTGC	ACA GATTT	
			AAAGAACG	TGT CTAAG	
			_	TT_____	
GAM1690	LOC126755	3'	TTGAGGATGCAGCAAGAAA	36859	CA ACA
			TTTCTTGC	CATC CGA	
			AAAGAACG	GTAG GTT	
			AC	GA_	
GAM1690	LOC164382	3'	TGTGACGGTGGCAAGAAA	42166	A_
			TTTCTTGCCAC	TCACA	
			AAAGAACGGTG	AGTGT	
			GC		
GAM1691	ABH	3'	ATGTTTGCAGAGTATTT	30053	AAGTAC
			AGATACTC	CAAACAT	
			TTTATGAG	GTTTGTA	
			AC_____		
GAM1691	CD244	3'	CATGTTCTATTTAAGTTCTGA	18523	T C CCA
			TCAGA	ACT AAGTA AACATG	
			AGTCT	TGA TTTAT TTGTAC	
			_	A C_	
GAM1691	CPSF4	3'	ATGTTTGGCTGGGCATC	13513	A AGTA
			GAT	CTCA CCAAACAT	
			CTA	GGGT GGTGTGTA	
			C	C_	
GAM1691	ITK	3'	CATGCTTGGAGCATTGGGTATC	12074	_ A A
	TGA		TCAGATACTCAA	GT CCAA CATG	
			AGTCTATGGGTT	CG GGTT GTAC	
			A	A C	
GAM1691	CLSTN2	3'	CATGTTTGTTCGAATGTCTGA	22692	C AAGTAC
			TCAGATA	TC CAAACATG	
			AGTCTGT	AG GTTTGTAC	
			A	CTTT_	
GAM1691	CMG2	3'	ATGTTTGGCGGGCATGTGA	27717	G A AAGTA
			TCA	AT CTC CCAAACAT	

		AGT TA GGG GGT TTGTA	
		G C C_____	
GAM1691	FLJ23186	3' CATGACCTGTACCTGAGTATCT 30296	A CAAA
		AGATACTCA GTAC CATG	
		TCTATGAGT CATG GTAC	
		C TCCA	
GAM1691	KIAA0367	3' ATGTTTGGTAGCTCTCTGA 33416	TACTCA _
		TCAGA AGT ACCAAACAT	
		AGTCT TCG TGGTTTGTA	
		C_____ A	
GAM1691	SLC21A14	3' CATGTTTGAAAGGTGAATTTCT 18890	TAC AGTAC
		GA TCAGA TCA CAAACATG	
		AGTCT AGT GTTTGTAC	
		TTA GAAA	
GAM1691	LOC116411	5' TGGTACCTGAGTTATACCCCTG 36573	AT_____ A
		G TCAG ACTCA GTACCA	
		GGTC TGAGT CATGGT	
		CCCATAT C	
GAM1691	LOC157349	3' CATGCCTGTGTGGGTATCTGA 39587	AGTAC AA
		TCAGATACTCA CA CATG	
		AGTCTATGGGT GT GTAC	
		GT__ CC	
GAM1692	PRKCN	3' CTAGCTCCACTCTGCTGC 12400	C TTTA _ C
		GCAGCA GA GTG AGCTA G	
		CGTCGT CT CAC TCGAT C	
		_ ____ C A	
GAM1692	WASF3	3' TAGCAAATTGTGCTGC 13443	AGTGA
		GCAGCACGATTT GCTA	
		CGTCGTGTAAA CGAT	

GAM1692	CAMKK1	3' AGCTCACTCGTATGTCCTGC 26063	C ATTT
		GCAG ACG AGTGAGCT	
		CGTC TGT TCACTCGA	
		C ATGC	
GAM1693	INPP5D	3' ATGTATTCCATCGTGCTG 40302	A_ _
		CAGCACGAT AAT CGT	
		GTCGTGCTA TTA GTA	
		CC T	
GAM1694	INPP5D	3' ATGTATTCCATCGTGCTG 40302	A_ _
		CAGCACGAT AAT CGT	

GTCGTGCTA TTA GTA
 CC T
 GAM1695 INPP5D 3' ATGTATTCCATCGTGCTG 40302 A_ _
 CAGCACGAT AAT CGT
 ||||| ||||
 GTCGTGCTA TTA GTA
 CC T
 GAM1696 HTR2C 5' GCAGCTCAGCGCACCGACTGC 6534 CA ATTTA _
 GCAG CG G TGAGCTGC
 ||| || | |||||
 CGTC GC C ACTCGACG
 A_ CACG_ G
 GAM1696 ITPR3 3' GTGCAGCTCCCTCCGTGC 7998 ATTT T
 GCACG AG GAGCTGCAC
 |||| || |||||
 CGTGC TC CTCGACGTG
 C_ C
 GAM1696 CAMKK1 3' CAGCTCACTCGTATGTCCTGC 26067 C ATTT
 GCAG ACG AGTGAGCTG
 |||| || |||||
 CGTC TGT TCACTCGAC
 C ATGC
 GAM1696 FLJ21432 3' GTGCAGCTCACTACCAACAGC 23769 ACGATT
 GC TAGTGAGCTGCAC
 || |||||
 CG ATCACTCGACGTG
 ACAACC
 GAM1696 LGP1 5' GTGCAGCCCACTAAATTGCTC 26231 C CG A
 G AGCA ATTTAGTG GCTGCAC
 | ||| ||||| |||||
 C TCGT TAAATCAC CGACGTG
 _ _ C
 GAM1696 MAP2K4 3' CAGAACCAAATCGTGGC 8918 AG A GAG
 GC CACGATTT GT CTG
 || ||||| || |||
 CG GTGCTAAA CA GAC
 _ C A_
 GAM1696 MGC14161 5' CAGCTGCACCGTGCGGC 26718 A ATTTA _
 GC GCACG GTG AGCTG
 || |||| || ||||
 CG CGTGC CAC TCGAC
 G _ G
 GAM1696 LOC115330 3' GCAGCTCAAGGTCCACATCTGC 28810 CAC_ AG
 GCAG GATTT TGAGCTGC
 ||| |||| |||||
 CGTC CTGGA ACTCGACG
 TACAC _
 GAM1696 LOC116437 3' TGCAATTTTAAAACCTGTGCTG 36581 ATTTAGT C
 C GCAGCACG GAG TGCA
 ||||| || |||

			CGTCGTGT	TTT ACGT		
			CCAAAAT	A		
GAM1696	LOC131873	3'	GTA	ACTAAATCTGCTGC	37366	C GA
			GCAGCA	GATTTAGT GC		
			CGTCGT	CTAAATCA TG		
			_	A_		
GAM1696	LOC58489	3'	TGCAGCTCTCTTTCTGC	35907	C TTT T	
			GCA GA	AG GAGCTGCA		
			CGT CT	TC CTCGACGT		
			_	T_ T		
GAM1697	INPP5D	3'	ATGTATTCCATCGTGCTG	40302	A_ _	
			CAGCACGAT	AAT CGT		
			GTCGTGCTA	TTA GTA		
			CC	T		
GAM1698	KIAA1126	3'	ATCATGCTGCAATATGAT	35605	CG C	
			ATTA	TTGCAGCA GAT		
			TAGT	AACGTCGT CTA		
			AT	A		
GAM1699	HPCAL1	3'	AACACAGGCTTGTCGTGC	7926	AT _	
			GCACGATAA	C GTGTT		
			CGTGCTGTT	G CACAA		
			CG	A		
GAM1699	HPCAL1	3'	AACACAGGCTTGTCGTGC	28633	AT _	
			GCACGATAA	C GTGTT		
			CGTGCTGTT	G CACAA		
			CG	A		
GAM1699	INPP5D	3'	AACATGTATTCCATCGTGCTG	40301	A_ _	
			CAGCACGAT	AAT CGTGTT		
			GTCGTGCTA	TTA GTACAA		
			CC	T		
GAM1699	FLJ11712	5'	AACGTAACACGAGCAGCAGGCT	23795	ACGATAAA	
		G	CAGC	TCGTGTTACGTT		
			GTCG	AGCACAATGCAA		
			GACGACG_			
GAM1700	RAD52	3'	AACGTCATTGCGATTTATCTTG	28640	CA TT_	
		CTT	AAGCA	ATAAATCGTG ACGTT		
			TTCGT	TATTTAGCGT TGCAA		
			TC	TAC		
GAM1700	RAD52	3'	AACGTCATTGCGATTTATCTTG	28650	CA TT_	
		CTT	AAGCA	ATAAATCGTG ACGTT		

			TTCGT TATTTAGCGT TGCAA		
			TC TAC		
GAM1700 RAD52	3'	AACGTCATTGCGATTATCTTG 28659	CA TT_		
	CTT	AAGCA ATAAATCGTG ACGTT			
		TTCGT TATTTAGCGT TGCAA			
		TC TAC			
GAM1700 FLJ10583	3'	AACGTTTTTTTTATTTTTGTGCT 19948	T CGTGTT		
	T	AAGCACAA AAAT ACGTT			
		TTCGTGTT TTTA TGCAA			
		_ TTTTT			
GAM1700 FLJ21106	5'	AAGGTTCCAATTTATTGTGC 24732	CG TT G		
		GCACAATAAAT TG AC TT			
		CGTGTTATTTA AC TG AA			
		_ CT G			
GAM1700 KIAA0429	3'	AACAGTAAATTATTGTGCTT 16462	ATCG_		
		AAGCACAAATAA TGTT			
		TTCGTGTTATT ACAA			
		AAATG			
GAM1700 PORIMIN	3'	AACATCAACATTTTTGTGCTT 27489	T C__		
		AAGCACAA AAAT GTGTT			
		TTCGTGTT TTTA TACAA			
		T CAAC			
GAM1701 ALEX2	5'	TGCGCAGCTCGCTGCCGTGC 16635	ATT A		
		GCACG TAGTGAGCTGC CA			
		CGTGC GTCGCTCGACG GT			
		C_ C			
GAM1701 DBY	3'	CAGCTTGCAAATACGTACT 11027	C _ A TG		
		AG ACG ATTT G AGCTG			
		TC TGC TAAA C TCGAC			
		A A _ GT			
GAM1701 ITPR3	3'	TGTGCAGCTCCCTCCGTGC 8000	ATTT T		
		GCACG AG GAGCTGCACA			
		CGTGC TC CTCGACGTGT			
		C_ C			
GAM1701 UBE4A	3'	GTGCAGCTTAATATGCTG 11198	CGATT G		
		CAGCA TA TGAGCTGCAC			
		GTCGT AT ATTCGACGTG			
		_ _ _ A			
GAM1701 BTBD3	5'	GCAGCTCCAGCCCATCTTGCTG 17339	C TTA _		
		CAGCA GAT GT GAGCTGC			

GTCGT CTA CG CTCGACG
 T CC_ AC
 GAM1701 CAMKK1 3' CAGCTCACTCGTATGTCCTG 26066 C ATTT
 CAG ACG AGTGAGCTG
 ||| ||| |||||
 GTC TGT TCACTCGAC
 C ATGC
 GAM1701 DKFZp434C0923 3' GCAGCCCCTGTTCTGCTG 19065 C TT TGA
 CAGCA GA TAG GCTGC
 ||||| || ||| |||||
 GTCGT CT GTC CGACG
 _ T_ CC_
 GAM1701 FLJ10292 3' TGTGCAGTATGAAATCGTATTG 19802 C AGTGA
 CAG ACGATT GCTGCACA
 ||| ||||| |||||
 GTT TGCTAAA TGACGTGT
 A GTA_
 GAM1701 FLJ11730 3' TGTACAGCTCATACTTTCCTGC 22995 C TTTA C
 TG CAGCA GA GTGAGCTG ACA
 ||||| || ||||| |||
 GTCGT CT TACTCGAC TGT
 C TTCA A
 GAM1701 FLJ21432 3' GTGCAGCTCACTACCAACAGC 23768 ACGATT
 GC TAGTGAGCTGCAC
 || |||||
 CG ATCACTCGACGTG
 ACAACC
 GAM1701 KIAA0450 3' TGTGCAGCCTGGAAACCATCGC 16036 ACGA_ TGA
 TG CAGC TTTAG GCTGCACA
 ||| ||||| |||||
 GTCG AGGTC CGACGTGT
 CTACCAA _
 GAM1701 KIAA0544 3' GTGCAGCTCTGGTCTGC 35116 C TAGT
 GCA GATT GAGCTGCAC
 ||| ||||| |||||
 CGT CTGG CTCGACGTG
 _ T_
 GAM1701 MGC12966 3' TGTGCAGCCCTTAGGTTTCCTGC 26420 C _ TGA
 TG CAGCA GA TTTAG GCTGCACA
 ||||| || ||||| |||||
 GTCGT CT GGATT CGACGTGT
 C T CC_
 GAM1701 PDE4DIP 3' TGTGCAGCTACCTATCTGCTG 45710 C TT TG
 CAGCA GA TAG AGCTGCACA
 ||||| || ||| |||||
 GTCGT CT ATC TCGACGTGT
 _ _ CA
 GAM1701 LOC139221 3' AGCTCACTAAATGTGCTG 37332 G
 CAGCAC ATTTAGTGAGCT
 ||||| |||||

GTCGTG TAAATCACTCGA

GAM1701 LOC146287 5' GCACTTATCCAAGTCGTGC 40690 A_ C
GCACGATTT GTGAG TGC
||||||| |||||
CGTGCTGAA TATTC ACG

CC _
GAM1701 LOC149296 5' TGCAGCTCAATCTGC 38696 C TTAG
GCA GAT TGAGCTGCA
||| ||| |||||
CGT CTA ACTCGACGT

_ _
GAM1701 LOC253461 3' CAGCTCTGAATTACCAACGCTG 46072 AC____ GT
CAGC GATTTA GAGCTG
||| ||||| |||||
GTCG TTAAGT CTCGAC
CAACCA _

GAM1701 LOC58489 3' TGCAGCTCTCTTTCTGC 35906 C TTT T
GCA GA AG GAGCTGCA
||| || |||||
CGT CT TC CTCGACGT
_ T_ T

GAM1702 ATP6V1C1 3' TAGCTCACTTGCTATGCTGC 7416 CGATTT
GCAGCA AGTGAGCTA
||||| |||||
CGTCGT TCACTCGAT
ATCGT_

GAM1702 PRKCN 3' TAGCTCCACTCTGCTGC 12401 C TTTA _
GCAGCA GA GTG AGCTA
||||| || |||||
CGTCGT CT CAC TCGAT

_ _ C
GAM1702 WASF3 3' TAGCAAATTGTGCTGC 13444 AGTGA
GCAGCACGATTT GCTA
||||||| |||
CGTCGTGTAAA CGAT

_ _
GAM1702 CAMKK1 3' AGCTCACTCGTATGTCCTGC 26064 C ATTT
GCAG ACG AGTGAGCT
||||| |||||
CGTC TGT TCACTCGA
C ATGC

GAM1702 FLJ12294 3' TGGAGCGCCAATCGTGCTGC 24747 TA AG
GCAGCACGATT GTG CTA
||||||| ||| |||
CGTCGTGCTAA CGC GGT
C_ GA

GAM1702 FLJ23598 5' GAGCCATCCGTGCTGC 45467 ATTTA A A
GCAGCACG GTG GCT C
||||||| ||| |||

			CGTCGTGC	TAC CGA G		
			C_____C			
GAM1702	TBX4	3'	TAGCCCCGGGACCGTGTTC	20547	A	AGTGA
			GCAGCACG TTT	GCTA		
			CGTTGTGC AGG	CGAT		
			C	GCCC_		
GAM1702	LOC148147	3'	CGCAGCTCACTGCAATCTCTGC	38475	CAC	_ A
			GCAG	GATT TAGTGAGCT CG		
			CGTC	CTAA GTCACTCGA GC		
			T__	C C		
GAM1703	RAD52	3'	AACGTCATTGCGATTTATCTTG	28640	C	TT_
	CTT		AAGCA GATAAATCGTG	ACGTT		
			TTCGT CTATTTAGCGT	TGCAA		
			T	TAC		
GAM1703	RAD52	3'	AACGTCATTGCGATTTATCTTG	28650	C	TT_
	CTT		AAGCA GATAAATCGTG	ACGTT		
			TTCGT CTATTTAGCGT	TGCAA		
			T	TAC		
GAM1703	RAD52	3'	AACGTCATTGCGATTTATCTTG	28659	C	TT_
	CTT		AAGCA GATAAATCGTG	ACGTT		
			TTCGT CTATTTAGCGT	TGCAA		
			T	TAC		
GAM1703	SLC2A6	3'	AACGTAGTCATATCATCGCGCT	19030	A	AAATC _
			AGC CGAT	GTG TTACGTT		
			TCG GCTA	TAC GATGCAA		
			C	CTA__ T		
GAM1703	ChGn	5'	AACACGCTTATCAATGTTATCG	20390	AT_____	
	TGC		GCACGATAA	CGTGTT		
			CGTGCTATT	GCACAA		
			GTAACCTATTC			
GAM1704	EFNB2	3'	TGCAGCTCACTGCTGCTGC	10297	CGATT	
			GCAGCA	TAGTGAGCTGCA		
			CGTCGT	GTCACTCGACGT		
			C_____			
GAM1704	EGR1	5'	TGCAGCTCCAGCCCCGGGCTGC	7692	A	ATTTAGT
			GCAGC CG	GAGCTGCA		
			CGTCG GC	CTCGACGT		
			G	CCCGAC_		
GAM1704	FGF2	3'	TGCAGTGAGCCATAATCGTGC	7744	TA_	GA
			GCACGATT	GT GCTGCA		

CGTGCTAA CG TGACGT
 TAC AG
 GAM1704 HTR2C 5' GCAGCTCAGCGCACCGACTGC 6535 CA ATTTA_
 GCAG CG G TGAGCTGC
 |||| || | |||||
 CGTC GC C ACTCGACG
 A_ CACG_ G
 GAM1704 ITPR3 3' TGCAGCTCCCTCCGTGC 7999 ATTT T
 GCACG AG GAGCTGCA
 |||| || |||||
 CGTGC TC CTCGACGT
 C__ C
 GAM1704 PSMB2 3' TGCAGTGAGCCTAGATCGCGC 8673 A _GA
 GC CGATTTAG T GCTGCA
 || ||||| | |||||
 CG GCTAGATC G TGACGT
 C C AG
 GAM1704 CALN1 3' TGCAGCTCACCGCGCATGTGC 25519 ATTTA_
 GCACG GTGAGCTGCA
 |||| |||||
 CGTGT CACTCGACGT
 ACGCGC
 GAM1704 CAMKK1 3' CAGCTCACTCGTATGTCCTGC 26068 C ATTT
 GCAG ACG AGTGAGCTG
 ||| || |||||
 CGTC TGT TCACTCGAC
 C ATGC
 GAM1704 DC-TM4F2 3' TGCAGCTCAAGCATGTCTGC 25199 C ATTTAG
 GCAG ACG TGAGCTGCA
 ||| || |||||
 CGTC TGT ACTCGACGT
 _ ACGA_
 GAM1704 DDX34 3' TGCAGTGAGCCAAGATCGTGC 16169 A_ GA
 GCACGATTT GT GCTGCA
 ||||| || |||||
 CGTGCTAGA CG TGACGT
 AC AG
 GAM1704 DRIL2 3' GCAGCTCTGCTCAACTGC 13188 CACGA T _
 GCAG TT AGT GAGCTGC
 ||| || || |||||
 CGTC AA TCG CTCGACG
 ____ C T
 GAM1704 FLJ12294 3' CAGCTGGAGCGCCAATCGTGCT 24743 TA ____
 GC GCAGCACGATT GTG AGCTG
 ||||| || |||||
 CGTCGTGCTAA CGC TCGAC
 C_ GAGG
 GAM1704 FLJ13456 3' TGCAGTGAGCTAAGATCGTGC 32800 _ GA
 GCACGATTT AGT GCTGCA
 ||||| || |||||

		CGTGCTAGA TCG TGACGT		
		A AG		
GAM1704	FLJ20489	5' TGCAGCTCGGCCTCCGCGCCGC 19507	A A	ATTTAG
		GC GC CG TGAGCTGCA		
		CG CG GC GCTCGACGT		
		C C CTCCG_		
GAM1704	FLJ21551	3' TGCAGTGAGCCAAGATCGTGC 24181	A_	GA
		GCACGATTT GT GCTGCA		
		CGTGCTAGA CG TGACGT		
		AC AG		
GAM1704	FLJ22362	5' GCAGCTCGGCCCGCGCTGC 23105	A	ATTTAG
		GCAGC CG TGAGCTGC		
		CGTCG GC GCTCGACG		
		C CCCG_		
GAM1704	FLJ22692	3' CAGTGAGCCAAGATCGTGC 24644	A_	GA
		GCACGATTT GT GCTG		
		CGTGCTAGA CG TGAC		
		AC AG		
GAM1704	FLJ23598	5' GCAGCCATCCGTGCTGC 45468	ATTTA	A
		GCAGCACG GTG GCTGC		
		CGTCGTGC TAC CGACG		
		C_ _		
GAM1704	KIAA0795	3' TGCAATGAGCTAAGATCGTGC 24588	_	GAGC
		GCACGATTT AGT TGCA		
		CGTGCTAGA TCG ACGT		
		A AGTA		
GAM1704	KIAA1872	3' CAGTGAGCCAAGATCGTGC 31518	A_	GA
		GCACGATTT GT GCTG		
		CGTGCTAGA CG TGAC		
		AC AG		
GAM1704	LGP1	5' TGCAGCCCACTAAATTGCTC 26232	C CG	A
		G AGCA ATTTAGTG GCTGCA		
		C TCGT TAAATCAC CGACGT		
		_ _ C		
GAM1704	MAP2K4	3' CAGAACCAAATCGTGGC 8917	AG	A GAG
		GC CACGATTT GT CTG		
		CG GTGCTAAA CA GAC		
		_ C A_		
GAM1704	MGC29891	3' TGCAGTGAGCCAAGATCGTGC 29438	A_	GA
		GCACGATTT GT GCTGCA		

		CGTGCTAGA CG TGACGT	
		AC AG	
GAM1704 Nup43	3'	TGCAGTGACCCAAGATCGTGC 23937	AGTGA_
		GCACGATTT GCTGCA	
		CGTGCTAGA TGACGT	
		ACCCAG	
GAM1704 NXPH3	3'	CAGCCCATCCGCGTGCTGT 32715	ATTTA A
		GCAGCACG GTG GCTG	
		TGTCGTGC TAC CGAC	
		GCC__ C	
GAM1704 RGS11	3'	GCAGCTCAACGTCCTGC 9925	C ATTTAG
		GCAG ACG TGAGCTGC	
		CGTC TGC ACTCGACG	
		C A_____	
GAM1704 ZAK	3'	CAGCTCACTGTTTTTGGTGC 28606	G C TT
		GCA CA GA TAGTGAGCTG	
		CGT GT TT GTCACTCGAC	
		G _ TT	
GAM1704 LOC115129	3'	TGCAGTGAGCCTAGATCGTGC 36255	_ GA
		GCACGATTTAG T GCTGCA	
		CGTGCTAGATC G TGACGT	
		C AG	
GAM1704 LOC115330	3'	GCAGCTCAAGGTCCACATCTGC 28811	CAC__ AG
		GCAG GATTT TGAGCTGC	
		CGTC CTGGA ACTCGACG	
		TACAC _	
GAM1704 LOC116437	3'	TGCAATTTTAAAACCTGTGCTG 36582	ATTTAGT C
C		GCAGCACG GAG TGCA	
		CGTCGTGT TTT ACGT	
		CCAAAAT A	
GAM1704 LOC145955	5'	CAGCTCACTAGTTAGCTGT 40644	ACGAT
		GCAGC TTAGTGAGCTG	
		TGTCG GATCACTCGAC	
		ATT__	
GAM1704 LOC148147	3'	GCAGCTCACTGCAATCTCTGC 38477	CAC _
		GCAG GATT TAGTGAGCTGC	
		CGTC CTAA GTCACTCGACG	
		T__ C	
GAM1704 LOC149460	3'	TGCAGTCAGCCAAGATCGTGC 40998	A_ GA
		GCACGATTT GT GCTGCA	

		CGTGCTAGA CG TGACGT		
		AC AC		
GAM1704	LOC158819 3'	TGCAGTGAGCCAAGATCGTGC 42029	A_	GA
		GCACGATTT GT GCTGCA		
		CGTGCTAGA CG TGACGT		
		AC AG		
GAM1704	LOC169026 5'	TGCAGCTCACCCACGTGTGCT 40269	ATTTA	
		AGCACG GTGAGCTGCA		
		TCGTGT CACTCGACGT		
		GCACC		
GAM1704	LOC196955 3'	CAGCTGGATCCTGCTGC 37931	C	AGTG
		GCAGCA GATTT AGCTG		
		CGTCGT CTAGG TCGAC		
		C _		
GAM1704	LOC199678 3'	CAGGGACTGAACCGTGCTGC 43227	A	GAG
		GCAGCACG TTTAGT CTG		
		CGTCGTGC AAGTCA GAC		
		C GG_		
GAM1704	LOC58489 3'	TGCAGCTCTCTTTCTGC 35908	C	TTT T
		GCA GA AG GAGCTGCA		
		CGT CT TC CTCGACGT		
		_ T_ T		
GAM1704	LOC90538 3'	TGCAGTGAGCTATAATCGTGC 31659	_	GA
		GCACGATT TAGT GCTGCA		
		CGTGCTAA ATCG TGACGT		
		T AG		
GAM1704	LOC93132 5'	TGCAGTGAGCCAAGATCGTGC 35411	A_	GA
		GCACGATTT GT GCTGCA		
		CGTGCTAGA CG TGACGT		
		AC AG		
GAM1705	CTNS 3'	CATAGCTCTCTCCTGCT 11383	C	TTTA T
		AGCA GA G GAGCTATG		
		TCGT CT C CTCGATAC		
		C _ T		
GAM1705	PRKCN 3'	CATAGCTCCACTCTGCTGC 12398	C	TTTA _
		GCAGCA GA GTG AGCTATG		
		CGTCGT CT CAC TCGATAC		
		_ _ C		
GAM1705	CAMKK1 3'	CACAGCTCACTCGTATGTCCTG 26065	C	ATTT A
	C	GCAG ACG AGTGAGCT TG		

		CGTC TGT TCACTCGA AC	
		C ATGC C	
GAM1705 SYNE-2	3'	GCATAGCTGGCCACAGTGCT 17535	GATTTA G
		AGCAC GT AGCTATGC	
		TCGTG CG TCGATACG	
		ACAC_ G	
GAM1705 ZF	5'	CATAGCTGACCAAGCTGC 22189	ACGAT A G
		GCAGC TT GT AGCTATG	
		CGTCG AA CA TCGATAC	
		_____ C G	
GAM1706 EFNB2	3'	TGCAGCTCACTGCTGCTGC 10297	CGATT
		GCAGCA TAGTGAGCTGCA	
		CGTCGT GTCACTCGACGT	
		C_____	
GAM1706 EGR1	5'	TGCAGCTCCAGCCCCGGGCTGC 7692	A ATTTAGT
		GCAGC CG GAGCTGCA	
		CGTCG GC CTCGACGT	
		G CCCGAC_	
GAM1706 FGF2	3'	TGCAGTGAGCCATAATCGTGC 7744	TA_ GA
		GCACGATT GT GCTGCA	
		CGTGCTAA CG TGACGT	
		TAC AG	
GAM1706 HTR2C	5'	GCAGCTCAGCGCACCGACTGC 6535	CA ATTTA_
		GCAG CG G TGAGCTGC	
		CGTC GC C ACTCGACG	
		A_ CACG_ G	
GAM1706 ITPR3	3'	TGCAGCTCCCTCCGTGC 7999	ATTT T
		GCACG AG GAGCTGCA	
		CGTGC TC CTCGACGT	
		C_ C	
GAM1706 PSMB2	3'	TGCAGTGAGCCTAGATCGCGC 8673	A _ GA
		GC CGATTTAG T GCTGCA	
		CG GCTAGATC G TGACGT	
		C C AG	
GAM1706 CALN1	3'	TGCAGCTCACCGCGCATGTGC 25519	ATTTA_
		GCACG GTGAGCTGCA	
		CGTGT CACTCGACGT	
		ACGCGC	
GAM1706 CAMKK1	3'	CAGCTCACTCGTATGTCCTGC 26068	C ATTT
		GCAG ACG AGTGAGCTG	

		CGTC TGT TCACTCGAC	
		C ATGC	
GAM1706 DC-TM4F2	3'	TGCAGCTCAAGCATGTCTGC 25199	C ATTTAG
		GCAG ACG TGAGCTGCA	
		CGTC TGT ACTCGACGT	
		_ ACGA_	
GAM1706 DDX34	3'	TGCAGTGAGCCAAGATCGTGC 16169	A_ GA
		GCACGATTT GT GCTGCA	
		CGTGCTAGA CG TGACGT	
		AC AG	
GAM1706 DRIL2	3'	GCAGCTCTGCTCAACTGC 13188	CACGA T _
		GCAG TT AGT GAGCTGC	
		CGTC AA TCG CTCGACG	
		_____ C T	
GAM1706 FLJ12294	3'	CAGCTGGAGCGCCAATCGTGCT 24743	TA _____
		GC GCAGCACGATT GTG AGCTG	
		CGTCGTGCTAA CGC TCGAC	
		C_ GAGG	
GAM1706 FLJ13456	3'	TGCAGTGAGCTAAGATCGTGC 32800	_ GA
		GCACGATTT AGT GCTGCA	
		CGTGCTAGA TCG TGACGT	
		A AG	
GAM1706 FLJ20489	5'	TGCAGCTCGGCCTCCGCGCCGC 19507	A A ATTTAG
		GC GC CG TGAGCTGCA	
		CG CG GC GCTCGACGT	
		C C CTCCG_	
GAM1706 FLJ21551	3'	TGCAGTGAGCCAAGATCGTGC 24181	A_ GA
		GCACGATTT GT GCTGCA	
		CGTGCTAGA CG TGACGT	
		AC AG	
GAM1706 FLJ22362	5'	GCAGCTCGGCCCGCGCTGC 23105	A ATTTAG
		GCAGC CG TGAGCTGC	
		CGTCG GC GCTCGACG	
		C CCCG_	
GAM1706 FLJ22692	3'	CAGTGAGCCAAGATCGTGC 24644	A_ GA
		GCACGATTT GT GCTG	
		CGTGCTAGA CG TGAC	
		AC AG	
GAM1706 FLJ23598	5'	GCAGCCATCCGTGCTGC 45468	ATTTA A
		GCAGCACG GTG GCTGC	

CGTCGTGC TAC CGACG
C_____

GAM1706 KIAA0795 3' TGCAATGAGCTAAGATCGTGC 24588 _ GAGC
GCACGATTT AGT TGCA
||||||| ||| |||
CGTGCTAGA TCG ACGT
A AGTA

GAM1706 KIAA1872 3' CAGTGAGCCAAGATCGTGC 31518 A_ GA
GCACGATTT GT GCTG
||||||| || |||
CGTGCTAGA CG TGAC
AC AG

GAM1706 LGP1 5' TGCAGCCCACTAAATTGCTC 26232 C CG A
G AGCA ATTTAGTG GCTGCA
| ||| ||||||| |||||
C TCGT TAAATCAC CGACGT
_ _ C

GAM1706 MAP2K4 3' CAGAACCAAATCGTGGC 8917 AG A GAG
GC CACGATTT GT CTG
|| ||||||| || |||
CG GTGCTAAA CA GAC
_ C A_

GAM1706 MGC29891 3' TGCAGTGAGCCAAGATCGTGC 29438 A_ GA
GCACGATTT GT GCTGCA
||||||| || |||||
CGTGCTAGA CG TGACGT
AC AG

GAM1706 Nup43 3' TGCAGTGACCCAAGATCGTGC 23937 AGTGA_
GCACGATTT GCTGCA
||||||| |||||
CGTGCTAGA TGACGT
ACCCAG

GAM1706 NXPH3 3' CAGCCCATCCGCGTGCTGT 32715 ATTTA A
GCAGCACG GTG GCTG
||||||| ||| |||
TGTCGTGC TAC CGAC
GCC_ C

GAM1706 RGS11 3' GCAGCTCAACGTCCTGC 9925 C ATTTAG
GCAG ACG TGAGCTGC
||| ||| |||||||
CGTC TGC ACTCGACG
C A_____

GAM1706 ZAK 3' CAGCTCACTGTTTTTGGTGC 28606 G C TT
GCA CA GA TAGTGAGCTG
||| ||| |||||||
CGT GT TT GTCACGAC
G _ TT

GAM1706 LOC115129 3' TGCAGTGAGCCTAGATCGTGC 36255 _ GA
GCACGATTTAG T GCTGCA
||||||||| | |||||

	CGTGCTAGATC G TGACGT	
	C AG	
GAM1706 LOC115330 3'	GCAGCTCAAGGTCCACATCTGC 28811	CAC__ AG
	GCAG GATTT TGAGCTGC	
	CGTC CTGGA ACTCGACG	
	TACAC _	
GAM1706 LOC116437 3'	TGCAATTTTAAAACCTGTGCTG 36582	ATTTAGT C
C	GCAGCACG GAG TGCA	
	CGTCGTGT TTT ACGT	
	CCAAAAT A	
GAM1706 LOC145955 5'	CAGCTCACTAGTTAGCTGT 40644	ACGAT
	GCAGC TTAGTGAGCTG	
	TGTCG GATCACTCGAC	
	ATT__	
GAM1706 LOC148147 3'	GCAGCTCACTGCAATCTCTGC 38477	CAC _
	GCAG GATT TAGTGAGCTGC	
	CGTC CTAA GTCACCTCGACG	
	T__ C	
GAM1706 LOC149460 3'	TGCAGTCAGCCAAGATCGTGC 40998	A_ GA
	GCACGATTT GT GCTGCA	
	CGTGCTAGA CG TGACGT	
	AC AC	
GAM1706 LOC158819 3'	TGCAGTGAGCCAAGATCGTGC 42029	A_ GA
	GCACGATTT GT GCTGCA	
	CGTGCTAGA CG TGACGT	
	AC AG	
GAM1706 LOC169026 5'	TGCAGCTCACCCACGTGTGCT 40269	ATTTA
	AGCACG GTGAGCTGCA	
	TCGTGT CACTCGACGT	
	GCACC	
GAM1706 LOC196955 3'	CAGCTGGATCCTGCTGC 37931	C AGTG
	GCAGCA GATTT AGCTG	
	CGTCGT CTAGG TCGAC	
	C _	
GAM1706 LOC199678 3'	CAGGGACTGAACCGTGCTGC 43227	A GAG
	GCAGCACG TTTAGT CTG	
	CGTCGTGC AAGTCA GAC	
	C GG_	
GAM1706 LOC58489 3'	TGCAGCTCTCTTTCTGC 35908	C TTT T
	GCA GA AG GAGCTGCA	

CGT CT TC CTCGACGT
 _ T_ T
 GAM1706 LOC90538 3' TGCAGTGAGCTATAATCGTGC 31659 _ GA
 GCACGATT TAGT GCTGCA
 ||||| ||| |||||
 CGTGCTAA ATCG TGACGT
 T AG
 GAM1706 LOC93132 5' TGCAGTGAGCCAAGATCGTGC 35411 A_ GA
 GCACGATTT GT GCTGCA
 ||||| || |||||
 CGTGCTAGA CG TGACGT
 AC AG
 GAM1707 ACCN2 3' CCACATCCTCTTCCCCA 21296 A AGCG CC
 TG GGAAGA GGG GTGG
 || ||||| ||| |||
 AC CCCTTCT CCT CACC
 _ _ _ A_
 GAM1707 ACHE 3' TCCGGCCCCGCCTCTGCCCTCA 17943 A A T
 TGAGGG AGA GCGGGGCCG GG
 ||||| ||| ||||| ||
 ACTCCC TCT CGCCCCGGC CT
 G C _
 GAM1707 B3GAT1 3' CCACGGCCCCACTGTCC 20717 AGA C
 GGA AG GGGGCCGTGG
 ||| || ||||| |||||
 CCT TC CCCCGGCACC
 G_ A
 GAM1707 B3GAT1 3' CCACGGCCCCACTGTCC 27629 AGA C
 GGA AG GGGGCCGTGG
 ||| || ||||| |||||
 CCT TC CCCCGGCACC
 G_ A
 GAM1707 EPHA8 3' TCCACGGCCCAGGTCTCCTCA 21749 GA AGCG
 TGAGG AGA GGGCCGTGGA
 ||||| ||| ||||| |||||
 ACTCC TCT CCCGGCACCT
 _ GGA_
 GAM1707 GSPT1 5' GCCCCGCCGCCTTCCCTCA 7882 AA_
 TGAGGGAAG GCGGGGC
 ||||| |||||
 ACTCCCTTC CGCCCCG
 CGC
 GAM1707 KCNK4 3' CCCTGGCCCCGGCCCTTCCCTC 18715 AAG T
 A TGAGGGAAG CGGGGCCG GG
 ||||| ||||| ||
 ACTCCCTTC GCCCCGGT CC
 CCG C
 GAM1707 KIP2 3' CCACAGCCCCGCTGTGGTCC 13088 AGA_ C
 GGA AGCGGGGC GTGG
 ||| ||||| |||||

		CCT TCGCCCCG CACC	
		GGTG A	
GAM1707 MEL	3'	CCACTTCCACCTCTTCTCTCA 11844	AGC _ CC
		TGAGGGAAGA GG GG GTGG	
		ACTCTCTTCT CC CC CACC	
		___ A TT	
GAM1707 MMP15	3'	CCACACCTTCTTCCCTC 8262	AGCG CC
		GAGGGAAGA GGG GTGG	
		CTCCCTTCT TCC CACC	
		___ A_	
GAM1707 NRGH	3'	TCCACGGCCCCGCCCCGCCCT 12836	AAGAA
		AGGG GCGGGGCCGTGGA	
		TCCC CGCCCCGGCACCT	
		GCCC_	
GAM1707 NRXN2	3'	CCACGGGCTCCCTGCTCCCCC 17467	AA A _
		GGG GA GCGGGG CCGTGG	
		CCC CT CGTCCC GGCACC	
		C_ _ TCG	
GAM1707 NRXN2	3'	CCACGGGCTCCCTGCTCCCCC 28983	AA A _
		GGG GA GCGGGG CCGTGG	
		CCC CT CGTCCC GGCACC	
		C_ _ TCG	
GAM1707 NRXN2	3'	CCACGGGCTCCCTGCTCCCCC 28989	AA A _
		GGG GA GCGGGG CCGTGG	
		CCC CT CGTCCC GGCACC	
		C_ _ TCG	
GAM1707 RNF26	5'	CTTACCCACTTCTTCTCTCA 25729	G C GCCGT
		TGAGG AAGAAG GGG GG	
		ACTCC TTCTTC CCC TC	
		_ A AT_	
GAM1707 SCD	3'	TCCACAGTGTTGTGCCCTTCA 11496	G AA G C_
	CTCA	TGAG GAAG GCG GGC GTGGA	
		ACTC CTTC CGT TTG CACCT	
		A CC G TGA	
GAM1707 STAU	5'	TCCACGGCCACTCCGCCTCTTC 10944	A _
	CCTC	GAGGGAAGA GCGG GGCCGTGGA	
		CTCCCTTCT CGCC CCGGCACCT	
		C TCA	
GAM1707 STAU	5'	TCCACGGCCACTCCGCCTCTTC 18928	A _
	CCTC	GAGGGAAGA GCGG GGCCGTGGA	

			CTCCCTTCT CGCC CCGGCACCT		
			C TCA		
GAM1707	STAU	5'	TCCACGGCCACTCCGCCTCTTC 18916	A	___
		CCTC	GAGGGAAGA GCGG GGCCGTGGA		
			CTCCCTTCT CGCC CCGGCACCT		
			C TCA		
GAM1707	STAU	5'	TCCACGGCCACTCCGCCTCTTC 18922	A	___
		CCTC	GAGGGAAGA GCGG GGCCGTGGA		
			CTCCCTTCT CGCC CCGGCACCT		
			C TCA		
GAM1707	TCIRG1	5'	TGGCCCCGCCTCCTCCTTCA 12691	A A	
			TGAGGGA GA GCGGGGCCG		
			ACTTCCT CT CGCCCCGGT		
			C C		
GAM1707	TFE3	3'	GGCCCCGCCTTTTCCCCCA 13276	A A	
			TG GGGAAGA GCGGGGCC		
			AC CCCTTTT CGCCCCGG		
			C C		
GAM1707	C1orf2	5'	CCACGCCGACCCCTCCCCTC 13355	AA AGC	C___
			GAGGG GA GGGG CGTGG		
			CTCCC CT CCCC GCACC		
			___ ___ AGCC		
GAM1707	C1orf2	5'	CCACGCCGACCCCTCCCCTC 45395	AA AGC	C___
			GAGGG GA GGGG CGTGG		
			CTCCC CT CCCC GCACC		
			___ ___ AGCC		
GAM1707	C20orf162	5'	CCACAGCTGAGGTCCTTCTCTC 27913	AAGCGG	C
		A	TGAGGGAAG GGC GTGG		
			ACTCTCTTC TCG CACC		
			CTGGAG A		
GAM1707	CENTB5	3'	TGGCCCCGCCTCTTGCCCCA 45726	A _ A	
			TG GGG AAGA GCGGGGCCG		
			AC CCC TTCT CGCCCCGGT		
			_ G C		
GAM1707	CHST3	5'	CCACGGCCCCACCTTTCCC 10479	AAGC	
			GGGAAG GGGGCCGTGG		
			CCCTTT CCCCGGCACC		
			CCA_		
GAM1707	DKFZP586M1120	3'	CCAACACCATTCTTCCCCCA 25319	A	GC GGCCG
			TG GGGAAGAA GG TGG		

AC CCCTTCTT CC ACC
 C A_ ACA_
 GAM1707 FADS1 3' TCACACCCGCTTCCCCCTC 15068 AA GCC
 GAGGG GAAGCGGG GTGG
 |||| ||||| |||
 CTCCC CTTCGCCC CACT
 C_ A_
 GAM1707 FLJ13310 3' CCATCCACCCACTTCCCTCA 24767 AAGC GCC
 TGAGGGAAG GGG GTGG
 ||||| || |||
 ACTCCCTTC CCC TACC
 A__ ACC
 GAM1707 FLJ14251 3' TCCTTTGCCTCCTCTTCCCTCA 24326 A C CGT
 TGAGGGAAGA G GGGGC GGA
 ||||| |||| |||
 ACTCCCTTCT C CTCCG CCT
 __ TTT
 GAM1707 FLJ21839 3' CCACGGCCCCGCTCTGCCCCCT 22406 A_ A
 AGGG AGA GCGGGGCCGTGG
 ||| || |||||
 TCCC TCT CGCCCCGGCACC
 CG _
 GAM1707 HRD1 3' CCTGCCCCGCCCCTCCCCCA 34470 A A AA CGT
 TG GGG AG GCGGGGC GG
 || ||| || ||||| ||
 AC CCC TC CGCCCCG CC
 C C CC T_
 GAM1707 HU-K4 5' CCACAGGCCCGCCCTCCTCC 14590 A A__ _
 C GGGGA GA GCGGGGCC GTGG
 |||| || ||||| |||
 CCCT CT CGCCCCGG CACC
 C CCC A
 GAM1707 KIAA0082 3' CCACAGTGCTGGCTTCTTCCC 44263 G _ C
 GGGAAGAAGC GG GC GTGG
 ||||| || || |||
 CCCTTCTTCG TC TG CACC
 G G A
 GAM1707 KIAA0429 5' CCACGGGTGCAGGCCTTTTCCC 16468 A GGGG_
 TCA TGAGGGAAGA GC CCGTGG
 ||||| || |||||
 ACTCCCTTTT CG GGCACC
 C GACGTG
 GAM1707 KIAA1240 3' TCCTCTGGCCCTCCTTCCCTCA 33142 AAGC T_
 TGAGGGAAG GGGGCCG GGA
 ||||| |||| |||
 ACTCCCTTC TCCCGGT CCT
 C__ CT
 GAM1707 KIAA1719 3' CCACCTGCCCTCTCCCCCA 33817 A A AGCG C_
 TG GGG AGA GGGC GTGG
 || ||| || |||| |||

	AC CCC TCT CCCG CACC	
	_ C _ TC	
GAM1707 KIAA1854 3'	CCTGCACCCGCTTCTTCCC 35528	_ CGT
	GGGAAGAAGCGGG GC GG	
	CCCTTCTTCGCCC CG CC	
	A T_	
GAM1707 KIAA1855 3'	CCAAGCCCACTCTTCCCTCA 44354	AGCG CG
	TGAGGGAAGA GGGC TGG	
	ACTCCCTTCT CCCG ACC	
	CA_ A_	
GAM1707 MGC4796 3'	TCCATGGCCACTCCCTGCCCCC 30834	AAGA C _
	GGG AG GG GGCCGTGGA	
	CCC TC CC CCGGTACCT	
	CCG_ _ TCA	
GAM1707 NET-7 3'	CCACGGCCTCTGCCTCCCC 14735	AA A _
	GGG GA GCGG GGCCGTGG	
	CCC CT CGTC CCGGCACC	
	_ C T	
GAM1707 PRKWNK2 3'	CCACAGCCCGTGGTCCCCCTC 43517	AA A_ G C
	GAGGG GA GCGGG C GTGG	
	CTCCC CT TGCCC G CACC	
	C_ GG _ A	
GAM1707 SEPT3 3'	CCTTTCCTCCTTCCCTCA 21183	AAGC CCGT
	TGAGGGAAG GGGG GG	
	ACTCCCTTC TCCC CC	
	C_ TTT_	
GAM1707 LOC114932 5'	TCCACGGCGATTCTTCCCGCA 36008	A GCGGG
	TG GGGAAGAA GCCGTGGA	
	AC CCCTTCTT CGGCACCT	
	G AG_	
GAM1707 LOC115708 3'	CCACGGCCCTGGCTGCCCC 36404	AAGA _
	GGG AGC GGGGCCGTGG	
	CCC TCG TCCCGGCACC	
	CG_ G	
GAM1707 LOC131034 5'	TCCACTCCACTCCCTCCCTC 28315	AGA C GCC
	GAGGGA AG GGG GTGGA	
	CTCCCT TC CCT CACCT	
	CCC A _	
GAM1707 LOC145082 5'	TCCACGGCCAGGGCTCTCCTCC 40493	A _ GG_
C	GGGA GA AGC GGCCGTGGA	

	CCCT CT TCG CCGGCACCT	
	C C GGA	
GAM1707 LOC145371 3'	CACGACACCCCTCTTCCCTCA 37844	AGC C__
	TGAGGGAAGA GGGG CGTG	
	ACTCCCTTCT CCCC GCAC	
	__ ACA	
GAM1707 LOC146268 3'	CCCTGCTTCCCACCACTTCCCT 38121	_____
CA	TGAGGGAA GAAGCGGGG	
	ACTCCCTT CTTCGTCCC	
	CACCACC	
GAM1707 LOC148530 5'	TCCACCGACACCTGCTTCTTCC 40888	GCC__
CTCA	TGAGGGAAGAAGCGGG GTGGA	
	ACTCCCTTCTTCGTCC CACCT	
	ACAGC	
GAM1707 LOC150538 3'	CCACGGCCCCGCCCCGTT 38990 G AAGAA	
	GA GG GCGGGGCCGTGG	
	TT CC CGCCCCGGCACC	
	G _____	
GAM1707 LOC157922 5'	TCCACGGATGGCTTCTTCCTTC 41891	GGGG
A	TGAGGGAAGAAGC CCGTGGA	
	ACTTCCTTCTTCG GGCACCT	
	GTA_	
GAM1707 LOC158722 5'	TCACTTCCCTCTTCTTCCCTCA 39890	C CC
	TGAGGGAAGAAG GGGG GTGG	
	ACTCCCTTCTTC TCCC CACT	
	_ TT	
GAM1707 LOC162083 5'	TCCACAGCCAGCCTTCCCTC 40048	AA GG C
	GAGGGAAG GC GGC GTGGA	
	CTCCCTTC CG CCG CACCT	
	_ A_ A	
GAM1707 LOC201911 5'	CCACAGCCCGCTTCCCGCA 43390	A AGA G C
	TG GGA AGCGGG C GTGG	
	AC CCCT TCGCCC G CACC	
	G _ _ A	
GAM1707 LOC219653 3'	CCACGGGGCCCCTTCCCTC 43867	GAAGC _
	GAGGGAA GGGGCC GTGG	
	CTCCCTT CCCC GG CACC	
	__ GG	
GAM1707 LOC221399 5'	CCACGCTTCAGACTTCTTCCCT 45048	C__ C
	AGGGAAGAAG GGGGC GTGG	

		TCCCTTCTTC CTTCG CACC	
		AGA _	
GAM1707 LOC90271	5'	TCCACGGCCAGCCCCTCCCTCA 31045	A AA GG
		TGAGGGA G GC GGCCGTGGA	
		I	
		ACTCCCT C CG CCGGCACCT	
		_ CC A_	
GAM1707 LOC90550	3'	CCAGTCGTCAGCTCCTTCCCTC 36177	A GG CG_
A		TGAGGGAAG AGC GGC TGG	
		ACTCCCTTC TCG CTG ACC	
		C A_ CTG	
GAM1708 ADAMTS3	3'	TTTTGTTCTGCATTGACT 15511	GGCC TA
		AGTCAGT GC AACAAAA	
		TCAGTTA CG TTGTTTT	
		_____ TC	
GAM1708 APAF1	3'	TTTTGGAATTA AAAAGCCACTGA 14872	CGCTAAA__
CT		AGTCAGTGGC CAAAA	
		TCAGTCACCG GTTTT	
		AAAATTAAG	
GAM1708 APAF1	3'	TTTTGGAATTA AAAAGCCACTGA 6833	CGCTAAA__
CT		AGTCAGTGGC CAAAA	
		TCAGTCACCG GTTTT	
		AAAATTAAG	
GAM1708 CD2AP	3'	TTTTTTGTTTGTGACCACTAAG 14435	C_ C T
CT		AGT AGTGG CGC AAACAAAAAA	
		TCG TCACC GTG TTTGTTTTTT	
		AA A _	
GAM1708 CDR2	5'	TTTGTTTATTC CGGACCCAC 37429	_ C__
		GTGG CCG TAAACAAA	
		CACC GGC ATTTGTTT	
		CA CTT	
GAM1708 DPYSL2	3'	TTTTTGTAACCACTGTCT 7067	T CCGCTAA
		AG CAGTGG ACAAAAA	
		TC GTCACC TGTTTTT	
		T AA_____	
GAM1708 PDCL	3'	TTTTTGTTTAACAAGGTA ACT 11867	G GC__
		AGT GCC TAAACAAAAA	
		TCA TGG ATTTGTTTTT	
		A AACA	
GAM1708 REQ	3'	TGCTTAGTGGCACTGAC 12953	G A
		GTCAGTG CCGCTAA CA	

CAGTCAC GGTGATT GT
 _ C
 GAM1708 SFPQ 3' TTTTTTGTTTAGATACCA 11505 CCG
 TGG CTAAACAAAAAA
 ||| |||||
 ACC GATTTGTTTTT
 ATA
 GAM1708 SP100 3' TTTTTTGTATAGTTAACCCTA 9086 C CC_ A
 C GT AGTGG GCTA ACAAAAAA
 || |||| ||| |||||
 CA TCACC TGAT TGTTTTTT
 _ AAT A
 GAM1708 C17orf26 3' TTTGTTTGGCCACTGA 29190 CT
 TCAGTGGCCG AAACAAA
 ||||| |||||
 AGTCACCGGT TTTGTTT
 _
 GAM1708 CNM1 3' TTGCCAGCTGACCACTGGC 21614 C_ AAA
 GTCAGTGG C GCT CAA
 ||||| | ||| |||
 CCGTCACC G CGA GTT
 A T CCC
 GAM1708 DKFZp547O146 5' TTTTACTCAAAGGCACTGACT 21487 G GCTAAAC
 AGTCAGTG CC AAAAA
 ||||| || |||||
 TCAGTCAC GG TTTT
 _ AAACCTCA
 GAM1708 DKFZP564J157 3' TTTTGTGTTGTTGCACTAACT 20530 C G C A
 AGT AGTG C GCTAA CAAAA
 ||| |||| | |||| |||||
 TCA TCAC G TGGTT GTTTT
 A _ T _
 GAM1708 DKFZp761K1423 5' TTTTGTTTAAACACACTGCCT 20476 T GCCGC
 AG CAGTG TAAACAAAA
 || |||| |||||
 TC GTCAC ATTTGTTTT
 C ACAA_
 GAM1708 FLJ20511 3' TGCCTAGCAGCCGCTGAC 19531 C AA
 GTCAGTGGC GCTA CA
 ||||| |||| |||
 CAGTCGCCG CGAT GT
 A CC
 GAM1708 KIAA1130 3' TGTGCCTGCCACTGGCT 31290 C_ TAA
 AGTCAGTGGC GC ACA
 ||||| || |||
 TCGGTCACCG CG TGT
 TC _
 GAM1708 KIAA1238 3' TTTTTTGTTAACAAGACACTGA 35219 GCCGCTA
 CT AGTCAGTG AACAAAAA
 ||||| |||||

		TCAGTCAC	TTGTTTTTT		
		AGAACAA			
GAM1708 KIAA1466	5'	TTTTGTTTGC	GGCACCTAC	35604	C TG T
		GT AG	GCCGC AAACAAAA		
		CA TC	CGGCG TTTGTTTT		
		_ CA _			
GAM1708 KIAA1536	3'	TTTCTGTTCCCC	CATTGACT	21926	CCGCTA A
		AGTCAGTGG	AACA AAA		
		TCAGTTACC	TTGT TTT		
		CCC__	C		
GAM1708 KIAA1956	3'	TTTTTTGTCCAGCCTG	GCCGCT	38365	C_ AA
		AGTGGC GCT	ACAAAAAA		
		TCGCCG CGA	TGTTTTTT		
		TC CC			
GAM1708 KOC1	3'	TTTTTTGTTTAGCTACATGATT	43782		G GCC
		AGTCA TG	GCTAAACAAAAAA		
		TTAGT AC	CGATTTGTTTTTT		
		_ AT_			
GAM1708 MGC15619	5'	TTGTTTTATTGCATTGACT	26159		G CGCT
		AGTCAGTG C	AAACAA		
		TCAGTTAC G	TTTGTT		
		_ TTAT			
GAM1708 MGC16824	5'	TGTTTGCAGCCACTGCT	21573		T C T
		AG CAGTGGC GC	AAACA		
		TC GTCACCG CG	TTTGT		
		_ A _			
GAM1708 NET-2	3'	TTTGTTTTATTTCACTGATT	14734		CCGCT
		AGTCAGTGG	AAACAAA		
		TTAGTCACT	TTTGTTT		
		TTAT_			
GAM1708 NY-REN-60	3'	TTTTTTGTCTTTGCCACTAC	33320		C CGCTAA
		GT AGTGGC	ACAAAAAA		
		CA TCACCG	TGTTTTTT		
		_ TTTC__			
GAM1708 RENT2	3'	TTTTTTGTTTTCCCCCACT	17804		CCGCT
		AGTGG	AAACAAAAAA		
		TCACC	TTTGTTTTTT		
		CCCT_			
GAM1708 RENT2	3'	TTTTTTGTTTTCCCCCACT	27910		CCGCT
		AGTGG	AAACAAAAAA		

		TCACC TTTGTTTTTT	
		CCCT_	
GAM1708	LOC145333 3'	TTTTTGCTCCTGGCT 40534	CCGCTAA
		AGTCAGTGG ACAAAAA	
		TCGGTCACC TGTTTTT	
		TC_____	
GAM1708	LOC146839 5'	TTGTTTAACTGCACTGGCT 40757	G CGC
		AGTCAGTG C TAAACAA	
		TCGGTCAC G ATTTGTT	
		_TCA	
GAM1708	LOC153205 3'	TGTGCTGTGGACACTGACT 41583	G TAA
		AGTCAGTG CCGC ACA	
		TCAGTCAC GGTG TGT	
		A TCG	
GAM1708	LOC197125 3'	TTTGTTTAAAGGCCTGGCT 42450	GT GC
		AGTCA GGCC TAAACAAA	
		TCGGT CCGG ATTTGTTT	
		___ AA	
GAM1708	LOC56912 5'	TTTTTGCTAGCGACTGAC 21366	GGC AA
		GTCAGT CGCTA CAAAAA	
		CAGTCA GCGAT GTTTTT	
		___ CC	
GAM1709	CENPF 3'	AAAGTTTGGAAGCACTGA 18469	ATG T
		TCA GCTTCC GGATTTT	
		AGT CGAAGG TTTGAAA	
		CA_ _	
GAM1709	CLECSF5 3'	GAAAATTTAGCAAGCCACTGA 14920	A C
		TCA TGGCTT CTGGATTTTC	
		AGT ACCGAA GATTTAAAAG	
		C C	
GAM1709	CPD 3'	AGAATCCAGAAACATT 6982	GC C
		AATG TTC TGGATTTT	
		TTAC AAG ACCTAAGA	
		A_ _	
GAM1709	EPB41 5'	GAAGAGGGTGAGGAAGCCAT 10722	GG
		ATGGCTTCCT ATTTTCTTC	
		TACCGAAGGA TGGGAGAAG	
		G_	
GAM1709	FUS1 3'	AAGAAAGGAGGGAAAAACCAT 14135	C_ GGA
		ATGG TTCCT TTTTCTT	

			TACC AAGGG GAAAGAA		
			AAA AG_		
GAM1709	IRTA1	3'	AAGAAATAGGAAGCCA 25301	GAT	
			TGGCTTCCTG TTTCTT		
			ACCGAAGGAT AAAGAA		

GAM1709	MSR1	3'	GAAGAAAATCCATTTCATTCA 8285	CTTCC	
			TGG TGGATTTTCTTC		
			ACT ACCTAAAAGAAG		
			TACTT		
GAM1709	TLL1	3'	GAAGAAAATCCATTTCCATGA 14837	A CTTCC	
			TCA TGG TGGATTTTCTTC		
			AGT ACC ACCTAAAAGAAG		
			_ TTT_		
GAM1709	TOX	3'	AAGAAAAGGGAAAGCCAT 16324	_ GGA	
			ATGGCTT CCT TTTTCTT		
			TACCGAA GGG AAAAGAA		
			A _		
GAM1709	TRIM	3'	GAAGAAAAATAAAAGCCAATGA 18531	A CC GA	
			TCA TGGCTT TG TTTTCTTC		
			AGT ACCGAA AT AAAAGAAG		
			A A_ A_		
GAM1709	TRIM9	5'	GAAGAAAGACAAGGAAACCCCT 17516	AT C GGA	
	GA		TCA GG TTCCT TTTTCTTC		
			AGT CC AAGGA GAAAGAAG		
			CC A ACA		
GAM1709	AAK1	5'	AAAATCTAGAAACCATCGG 17142	A C C	
			TC ATGG TTC TGGATTTT		
			GG TACC AAG ATCTAAAA		
			C A _		
GAM1709	ACAA2	5'	GAAGAAAACCCAGGAGGACGCA 44094	AA G A	
	GA		TC TG CTCCTGG TTTTCTTC		
			AG GC GGAGGACC AAAAGAAG		
			AC A C		
GAM1709	DKFZP564D166	3'	AAGAAAACCTTAGCCATGGA 24989	A TCCT A	
			TC ATGGCT GG TTTTCTT		
			AG TACCGA TC AAAAGAA		
			G T_ _		
GAM1709	DKFZP564J102	5'	GAAATGTGCAGAAAGCCATTGA 32848	C G _	
			TCAATGGCTT CTG AT TTTC		

		AGTTACCGAA GAC TG AAAG	
		A G T	
GAM1709	FLJ12488	3' AAGAAATAAAAATAGCCATTGA 25263	TCCTGGAT
		TCAATGGCT TTTCTT	
		AGTTACCGA AAAGAA	
		TAAAAAT_	
GAM1709	FLJ13593	3' GAAGAAAATCCAAGGCT 24150	CC
		GGCTT TGGATTTTCTTC	
		TCGGA ACCTAAAAGAAG	
		—	
GAM1709	FLJ20718	3' AAGAAAATCCAAAGCATTG 19633	G CC
		CAATG CTT TGGATTTTCTT	
		GTTAC GAA ACCTAAAAGAA	
		— —	
GAM1709	FLJ23511	5' AAGAACCAAAAAGCCATTGA 25961	CC ATT
		TCAATGGCTT TGG TTCTT	
		AGTTACCGAA ACC AAGAA	
		A_ —	
GAM1709	KIAA0296	3' GAAAAAGAGGAAGCCATTGG 16221	GGA
		TCAATGGCTTCCT TTTTC	
		GGTTACCGAAGGA AAAAG	
		GA_	
GAM1709	KIAA0869	3' AAAATGCACAGAAACCATTGG 35093	C C_ G
		TCAATGG TTC TG ATTTT	
		GGTTACC AAG AC TAAAA	
		A AC G	
GAM1709	KIAA1054	3' GAGTCCAAGATACCACTGA 33955	A CT C
		TCA TGG TC TGGATTT	
		AGT ACC AG ACCTGAG	
		C AT A	
GAM1709	MGC22014	3' GAAGAAAAATAAAGCCATTG 32219	CC GA
		CAATGGCTT TG TTTTCTTC	
		GTTACCGAA AT AAAAGAAG	
		— A_	
GAM1709	MGC32104	3' GAAGAAAACCCAGGAAATGCCA 29506	— A
	T	ATGGC TTCCTGG TTTTCTTC	
		TACCG AAGGACC AAAAGAAG	
		TA C	
GAM1709	MGC4832	5' GAAAATCAAGAAGGCATTGA 29700	G CTG
		TCAATG CTTC GATTTTC	

		AGTTAC GAAG CTAAAAG		
		G AA_		
GAM1709	MST4	3' GAAGATTTGGAAGAAGCTATT 18608	___	TG
		AATGGCTTC C GATTTTC		
		TTATCGAAG G TTAGAAG		
		AA GT		
GAM1709	PELI2	3' AAGAAAGGAGAAAAGCCATTGG 22226	C	GGA
		TCAATGGCTT CT TTTTCTT		
		GGTTACCGAA GA GAAAGAA		
		A G__		
GAM1709	RASSF2	3' GAAAATCAGAGGAGCCACTGA 16393	A	_ G
		TCA TGGCTTC CTG ATTTTC		
		AGT ACCGAGG GAC TAAAAG		
		C A _		
GAM1709	LOC120939	5' AAGAAGAGGGAAAAGCCATAGA 37509	A	___ GGA
		TC ATGGCT TCCT TTTTCTT		
		AG TACCGA AGGG AGAAGAA		
		A AA ____		
GAM1709	LOC145978	3' GAAAAAATCTGAAGCCA 38032	CT	C
		TGGCTTC GGATTTT TTC		
		ACCGAAG TCTAAAA AAG		
		__ A		
GAM1709	LOC147077	3' GAAAAAGGAAGCCACTG 38290	A	GGA
		CA TGGCTTCCT TTTTC		
		GT ACCGAAGGA AAAAG		
		C ____		
GAM1709	LOC154930	3' AGAATGTAGAAAAGCCATT 39502	C_	G
		AATGGCTT CTG ATTTT		
		TTACCGAA GAT TAAGA		
		AA G		
GAM1709	LOC169270	3' GAAAACCTCTAAAAAGCCATTGA 40275	CC	_
		TCAATGGCTT TGGA TTTTC		
		AGTTACCGAA ATCT AAAAG		
		AA C		
GAM1709	LOC197358	3' GAAAAAATCCAAATGGACATC 42508	CT	___ C
	A	TGG TCC TGGATTTT TTC		
		ACT AGG ACCTAAAA AAG		
		AC TAA A		
GAM1709	LOC199775	3' GAAGAATGTGGAAAAGCCATT 42615	___	TGGATT
		AATGGCT TCC TTCTTC		

		TTACCGA AGG AAGAAG		
		AA TGT___		
GAM1709	LOC199863 5'	GAAAAAGAAGCCATTGA 43255		CTGGA
		TCAATGGCTTC TTTTC		
		AGTTACCGAAG AAAAG		
		A___		
GAM1709	LOC219672 5'	GAAAACAGGAAACCATTGA 43889	C	GA
		TCAATGG TTCCTG TTTTC		
		AGTTACC AAGGAC AAAAG		
		A _		
GAM1709	LOC219894 3'	GAAGAAAAGTTTGAAACCATGA 44796	A C	CTGGA
		TCA TGG TTC TTTCTTC		
		AGT ACC AAG AAAAGAAG		
		_ A TTTG_		
GAM1709	LOC220706 5'	GAAGAAAACACAGAGAAAGCCG 43837		GA
	TTGA	TCAATGGCTT C CTG TTTCTTC		
		AGTTGCCGAA G GAC AAAAGAAG		
		A A AC		
GAM1709	LOC221103 5'	GAAAAAATCCAAGACAAGTTA 44779	_ C	C
		TGGCT TC TGGATTTT TTC		
		ATTGA AG ACCTAAAA AAG		
		AC A A		
GAM1709	LOC222681 5'	GAAGAAAACCTCCAGCAACCA 44616	C C	_
		TGG TT CTGGA TTTCTTC		
		ACC AA GACCT AAAAGAAG		
		_ C C		
GAM1709	LOC257507 5'	GAAGAAAACCTCCAGCAACCA 46682	C C	_
		TGG TT CTGGA TTTCTTC		
		ACC AA GACCT AAAAGAAG		
		_ C C		
GAM1709	LOC257625 5'	GAAGAAAACCTCCAGCAACCA 46738	C C	_
		TGG TT CTGGA TTTCTTC		
		ACC AA GACCT AAAAGAAG		
		_ C C		
GAM1709	LOC90019 3'	GAAGAAGAGAAAGACAGCCA 28872	TC	GGA
		TGGCT CT TTTCTTC		
		ACCGA GA AGAAGAAG		
		CA AAG		
GAM1710	CISH 3'	TGAGAGGAGAGAAATACACGTC 14973	G	AACAGG
	T	AGA GTGTAT TCCTCTCA		

			TCT CACATA	AGGAGAGT		
			G	AAGAG_		
GAM1710	CISH	3'	TGAGAGGAGAGAAATACACGTC	29706	G	AACAGG
	T		AGA GTGTAT	TCCTCTCA		
			TCT CACATA	AGGAGAGT		
			G	AAGAG_		
GAM1710	RALBP1	3'	GAAAGGACCCGTGCATCT	13661	AACA	C
			AGGTGTAT	GGTCCT TC		
			TCTACGTG	CCAGGA AG		
			C_	A		
GAM1710	C20orf162	5'	TGAGAAAGTTGTATACACTC	27919	_	AGGTCC
			GAG GTGTATAAC	TCTCA		
			CTC CATATGTTG	AGAGT		
			A	AA_		
GAM1710	FLJ20297	3'	TGAGAGGACCTGGGAAGCCCCT	19653	T	ATAA
	C		GAGG GT	CAGGTCCTCTCA		
			CTCC CG	GTCCAGGAGAGT		
			C	AAGG		
GAM1710	FLJ20297	3'	TGAGAGGACCTGGGAAGCCCCT	19361	T	ATAA
	C		GAGG GT	CAGGTCCTCTCA		
			CTCC CG	GTCCAGGAGAGT		
			C	AAGG		
GAM1710	MGC16121	5'	AGAAGTCTTTACACCTCT	26505	TAAC	TCC
			AGAGGTGTA	AGG TCT		
			TCTCCACAT	TTC AGA		
			_	TGA		
GAM1710	ZER6	3'	GATCTGTTACACACCTCT	31744	AT_	
			AGAGGTGT	AACAGGTC		
			TCTCCACA	TTGTCTAG		
			CAC			
GAM1710	LOC126661	3'	AGAGGACCTATTCCTTT	36848	T	ATAAC
			AGAGG GT	AGGTCCTCT		
			TTTCC TA	TCCAGGAGA		
			T	_		
GAM1710	LOC144467	3'	GAAAGGAGATACACTTCT	28821	AACAGG	C
			AGAGGTGTAT	TCCT TC		
			TCTTCACATA	AGGA AG		
			G_	A		
GAM1710	LOC149830	3'	TGAGAGATGAACATACACATCT	41095	A	ACAGGTC
	CT		AGAGGTGT TA	CTCTCA		

TCTCTACA AT GAGAGT
 C ACAAGTA
 GAM1710 LOC150776 3' TGAGAGGACCTGGGAAGCCCCT 31679 T ATAA
 C GAGG GT CAGGTCCTCTCA
 |||| || |||||
 CTCC CG GTCCAGGAGAGT
 C AAGG
 GAM1710 LOC152359 3' ATCTGCTACCACACCTCT 41491 A_ A
 AGAGGTGT TA CAGGT
 ||||| || ||||
 TCTCCACA AT GTCTA
 CC C
 GAM1710 LOC154930 3' TGAAATGATCCATACACCTCT 39506 AACA CTC
 AGAGGTGTAT GGTC TCA
 ||||| ||| |||
 TCTCCACATA CTAG AGT
 C__ TAA
 GAM1710 LOC221103 5' AGAGTATGTTATCACCTC 44778 T GGTC
 GAGGTG ATAACA CTCT
 |||| |||| |||
 CTCCAC TATTGT GAGA
 _ AT__
 GAM1710 LOC253120 5' TGAGAAAGATGGCTACACACAC 46076 ATAACA C____
 CT AGGTGT GGTC TCTCA
 |||| ||| ||||
 TCCACA TCGG AGAGT
 CACA__ TAGAA
 GAM1711 ADCY2 3' GGCCGGGTGCAGTGGCTCCTA 32434 _ G AC
 TAGGA TG TGC ACCCGGCC
 |||| || ||| |||||
 ATCCT GT ACG TGGGCCGG
 CG G _
 GAM1711 APOL1 3' GGCCGGGTGTAGTGGCTCA 9733 T _ _
 A GGT GC ACACCCGGCC
 | ||| || |||||
 A TCG TG TGTGGGCCGG
 C G A
 GAM1711 ATF5 3' GGCCGGGTGCAGTGGCTTA 14321 AT G AC
 TAGG G TGC ACCCGGCC
 |||| | ||| |||||
 ATTC T ACG TGGGCCGG
 GG G _
 GAM1711 CHST5 3' GGCCGGGTGCGGTGGCTCA 14440 T _ A_
 A GGT GC CACCCGGCC
 | ||| || |||||
 A TCG TG GTGGGCCGG
 C G GC
 GAM1711 CRY2 3' GCCAGGGAAACCATCTA 35732 GCACA _
 TAGGATGGT CCC GGC
 ||||| ||| |||

		ATCTTACCA	GGG CCG		
		AA___	A		
GAM1711 EGFL5	3'	GGCCGGGTGCGGTGGCTCA	41883	T _ A_	
		A GGT GC CACCCGGCC			
		A TCG TG GTGGGCCGG			
		C G GC			
GAM1711 GFPT2	3'	GGCCAAACTGTTTCATCCTA	11593	T CACCC	
		TAGGATGG GCA GGCC			
		ATCCTACT TGT CCGG			
		_ CAAA_			
GAM1711 GLP1R	3'	GGCCGGGTGGCCAATCC	7826	GGT A	
		GGAT GC CACCCGGCC			
		CCTA CG GTGGGCCGG			
		AC_ _			
GAM1711 IRAK1	3'	GGCCGGGTGCGGTGGCTCA	7300	T _ A_	
		A GGT GC CACCCGGCC			
		A TCG TG GTGGGCCGG			
		C G GC			
GAM1711 KIF3B	3'	GGCCGGGTATGGTGACTCA	11217	T G _	
		A GGT CAC ACCCGGCC			
		A TCA GTG TGGGCCGG			
		C _ GTA			
GAM1711 LEP	3'	GGCCGGGTGCGGTGGCTCA	5740	T _ A_	
		A GGT GC CACCCGGCC			
		A TCG TG GTGGGCCGG			
		C G GC			
GAM1711 LHX1	5'	GGCCGAGTGTGTGTCCT	12093	GGT C	
		AGGAT GCACAC CGGCC			
		TCCTG TGTGTG GCCGG			
		_ A			
GAM1711 LMO2	5'	GGCCGGGCGGGGCGCACACCATC	12102	ACA	
C		GGATGGT GC CCCGGCC			
		CCTACCA CG GGGCCGG			
		CACG GGC			
GAM1711 MOG	3'	GGCCGGGTGCGGTGGCTCA	8279	T _ A_	
		A GGT GC CACCCGGCC			
		A TCG TG GTGGGCCGG			
		C G GC			
GAM1711 PITX3	5'	GGCCGGGTGCCCGGCCCTG	11470	AT _ CA	
		TAGG GGT G CACCCGGCC			

GTCC CCG C GTGGGCCGG
 _ G CC
 GAM1711 ST5 3' GCCGGGTGCTTTCCTG 11889 T TGCA
 TAGGA GG CACCCGGC
 ||||| || |||||
 GTCCT TC GTGGGCCG
 T _
 GAM1711 ST5 3' GCCGGGTGCTTTCCTG 29169 T TGCA
 TAGGA GG CACCCGGC
 ||||| || |||||
 GTCCT TC GTGGGCCG
 T _
 GAM1711 USP14 3' CCACTCTGTGCACCAACCTA 11627 A CCC_
 TAGG TGGTGCACA GG
 ||||| ||||| ||
 ATCC ACCACGTGT CC
 A CTCA
 GAM1711 AGPAT1 3' GCCCTGCTGCACCATCT 26473 _ CCC
 GGATGGTGCA CA GGC
 ||||| || |||||
 TCTACCACGT GT CCG
 C C_
 GAM1711 AKR1D1 3' GGCCGGGTGCGGTGGCTCA 12611 T _ A_
 A GGT GC CACCCGGCC
 | ||| || |||||
 A TCG TG GTGGGCCGG
 C G GC
 GAM1711 C20orf20 3' GGCCACAGTGATACCATCC 20245 _ ACCC
 GGATGGTG CAC GGCC
 ||||| || |||||
 CCTACCAT GTG CCGG
 A ACA_
 GAM1711 FLJ10547 3' GGCCGGGTGCAGTGGCTC 19931 A_ G AC
 GG TG TGC ACCCGGCC
 || || || |||||
 CT GT ACG TGGGCCGG
 CG G _
 GAM1711 FLJ11577 3' GCCGGGTGTAGTGGCTCA 24800 T _ _
 A GGT GC ACACCCGGC
 | ||| || |||||
 A TCG TG TGTGGGCCG
 C G A
 GAM1711 FLJ20079 3' GGCCAGGTGTTGCTTGCCCTC 19174 T _ _ C
 GA GGT GCA CACC GGCC
 || ||| || |||||
 CT CCG CGT GTGG CCGG
 C TT T A
 GAM1711 FLJ20306 3' GGCCGGGTGCGGTGGCTCA 19369 T _ A_
 A GGT GC CACCCGGCC
 | ||| || |||||

A TCG TG GTGGGCCGG
 C G GC
 GAM1711 FLJ22167 3' GGCCGGGTGCGGTGGCTCA 23742 T _ A_
 A GGT GC CACCCGGCC
 | ||| || |||||
 A TCG TG GTGGGCCGG
 C G GC
 GAM1711 FLJ22615 3' GCCTGTCACCCATCCTA 33991 _ C CCC
 TAGGATGG TG ACA GGC
 ||||| || ||| |||
 ATCCTACC AC TGT CCG
 C _ ____
 GAM1711 FLJ22635 3' GCCAGGTGTGCATGGGTCC 24717 G_ C
 GGAT GTGCACACC GGC
 ||| ||||| |||
 CCTG TACGTGTGG CCG
 GG A
 GAM1711 FLJ22814 3' GGCCGGGTGCGGTGGCTCA 24442 T _ A_
 A GGT GC CACCCGGCC
 | ||| || |||||
 A TCG TG GTGGGCCGG
 C G GC
 GAM1711 GPA33 3' GCTGGCGCCCATCCTA 12404 T ACAC
 TAGGATGG GC CCGGC
 ||||| || ||||
 ATCCTACC CG GGTCG
 _ C____
 GAM1711 HSRNAFEV 5' GGCCGGGTACACCAGCC 18969 A CAC
 GG TGGTG ACCCGGCC
 || |||| |||||
 CC ACCAC TGGGCCGG
 G A_
 GAM1711 KIAA0057 3' GGCCGGACGCAGTAGCTTA 14621 A G ACAC
 TAGG TG TGC CCGGCC
 ||| || ||| |||||
 ATTC AT ACG GGCCGG
 G G CA_
 GAM1711 KIAA0284 3' GCCGGGTGCATGGCAGCCCT 31618 A_ G CA
 AGG TG TG CACCCGGC
 ||| || || |||||
 TCC AC GT GTGGGCCG
 CG G AC
 GAM1711 KIAA0710 5' GGCCAGGATGTCCATTCTA 16992 T CA C
 TAGGATGG GCA CC GGCC
 ||||| ||| || ||||
 ATCTTACC TGT GG CCGG
 _ A_ A
 GAM1711 KIAA0716 3' GTCAGTGCACATCCTA 16247 G ACCC
 TAGGATG TGCAC GGC
 ||||| |||| |||

		ATCCTAC ACGTG CTG	
		— A —	
GAM1711 KIAA1228	3'	GGCCGGGTGCGGTGGCTCA 32446	T _ A_
		A GGT GC CACCCGGCC	
		A TCG TG GTGGGCCGG	
		C G GC	
GAM1711 KIAA1969	3'	GGCCGGGTGCGGTGGCTTA 38492	AT G AC
		TAGG G TGC ACCCGGCC	
		ATTC T GCG TGGGCCGG	
		GG G —	
GAM1711 MGC2452	5'	GCCAAGTGGCCATCCTA 26371	GCA CC
		TAGGATGGT CAC GGC	
		ATCCTACCG GTG CCG	
		— AA	
GAM1711 MRP63	3'	GGCCGGGTGCGGTGGCTCA 23456	T _ A_
		A GGT GC CACCCGGCC	
		A TCG TG GTGGGCCGG	
		C G GC	
GAM1711 MRPL20	3'	GGCCAGAGTGATGGCACCATC 19697	A__ CC_
		GATGGTGC CAC GGCC	
		CTACCACG GTG CCGG	
		GTA AGA	
GAM1711 NGEF	5'	GCCGGGGACACACCATCCTG 34277	CACA
		TAGGATGGTG CCCGGC	
		GTCCTACCAC GGGCCG	
		ACAG	
GAM1711 PRO0529	3'	CCCTGTGTGCACCAACCTA 15299	A CC
		TAGG TGGTGCACAC GG	
		ATCC ACCACGTGTG CC	
		A TC	
GAM1711 PTPRU	3'	GCCCCTTGGCACCATCCTG 28401	A CCC
		TAGGATGGTGC CA GGC	
		GTCCTACCACG GT CCG	
		— TCC	
GAM1711 PTPRU	3'	GCCCCTTGGCACCATCCTG 28406	A CCC
		TAGGATGGTGC CA GGC	
		GTCCTACCACG GT CCG	
		— TCC	
GAM1711 PTPRU	3'	GCCCCTTGGCACCATCCTG 12256	A CCC
		TAGGATGGTGC CA GGC	

GTCCTACCACG GT CCG
 _ TCC
 GAM1711 PTR4 5' GGCCGGGCGCGGCCATCCTG 36653 ACA
 TAGGATGGTGC CCCGGCC
 ||||| |||||
 GTCCTACCGCG GGGCCGG
 CGC
 GAM1711 PTRF 3' GCCTCTGTGCTCCATCCTA 31783 T CCC
 TAGGATGG GCACA GGC
 ||||| ||||| |||
 ATCCTACC CGTGT CCG
 T CT_
 GAM1711 SMCR5 3' GGCCGGGTGCAGTGGCTC 29563 A_ G AC
 GG TG TGC ACCCGGCC
 || || || |||||
 CT GT ACG TGGGCCGG
 CG G _
 GAM1711 SMCR5 3' GGCCTGAGCATCCATCCTA 29564 _ A CCC
 TAGGATGG TGC CA GGCC
 ||||| || || |||||
 ATCCTACC ACG GT CCGG
 T A _
 GAM1711 T2BP 5' GGCCGGGTGTCCACCCCATCC 34682 _ C
 TG TAGGAT GGTG ACACCGGCC
 ||||| |||| |||||
 GTCCTA CCAC TGTGGGCCGG
 CCC C
 GAM1711 UBCE7IP5 3' GGCCGGGCATGGTGGCTCATGC 17272 _ _ G A_
 CTA TAGG ATG GT CAC CCCGGCC
 |||| |||| || |||||
 ATCC TAC CG GTG GGGCCGG
 G T _ GTAC
 GAM1711 ZNF212 3' GGCCAGGTCTTCATCCTG 14558 TGCAC C
 TAGGATGG ACC GGCC
 ||||| || |||||
 GTCCTACT TGG CCGG
 TC_ A
 GAM1711 LOC134147 3' GGCCGGGTGCGGTGGCTCA 29032 T _ A_
 A GGT GC CACCCGGCC
 | ||| || |||||
 A TCG TG GTGGGCCGG
 C G GC
 GAM1711 LOC138307 5' GGCCAGGCTGCCGTGCACCATC 37123 A_ C
 CTG TAGGATGGTGCAC CC GGCC
 ||||| || |||||
 GTCCTACCACGTG GG CCGG
 CCGTC A
 GAM1711 LOC145195 3' CCACCTGAGCACCATCCTG 40513 A CCC
 TAGGATGGTGC CA GG
 ||||| || ||

GTCCTACCACG GT CC
 A CCA
 GAM1711 LOC146780 3' GGCCGGGTGCGGTGGCTCA 40743 T _ A_
 A GGT GC CACCCGGCC
 | ||| || |||||
 A TCG TG GTGGGCCGG
 C G GC
 GAM1711 LOC150935 3' GGCCGGGTGCGGTGGCTCA 39020 T _ A_
 A GGT GC CACCCGGCC
 | ||| || |||||
 A TCG TG GTGGGCCGG
 C G GC
 GAM1711 LOC152804 3' GGCCGGGTGCGGTGGCTCA 41556 T _ A_
 A GGT GC CACCCGGCC
 | ||| || |||||
 A TCG TG GTGGGCCGG
 C G GC
 GAM1711 LOC162137 3' GGCTGCTGCACCATCC 42115 CACC
 GGATGGTGCA CGGCC
 ||||| ||||
 CCTACCACGT GTCGG
 C____
 GAM1711 LOC166867 5' GCCGGGTGCGATGGACTCC 40223 TG G ____
 GGA GT CA CACCCGGC
 ||| ||| |||||
 CCT CA GT GTGGGCCG
 ____ G AGC
 GAM1711 LOC197201 3' GGCCGGGTGCGGTGGCTCA 42464 T _ A_
 A GGT GC CACCCGGCC
 | ||| || |||||
 A TCG TG GTGGGCCGG
 C G GC
 GAM1711 LOC199957 3' GGCCAAGGTCACCACCCTG 42675 A CAC C_
 TAGG TGGTG ACC GGCC
 |||| |||| || ||||
 GTCC ACCAC TGG CCGG
 C ____ AA
 GAM1711 LOC202052 3' GGCCGGGTGCACTGGCT 43408 AT AC
 GG GGTGC ACCCGGCC
 || |||| |||||
 TC TCACG TGGGCCGG
 GG ____
 GAM1711 LOC203042 5' GGCCGGGTGTTGGATACCA 43475 C____
 TGGTG ACACCCGGCC
 |||| |||||
 ACCAT TGTGGGCCGG
 AGGT
 GAM1711 LOC219722 3' GCCGGATAGTACGCTTCCTA 44709 T C AC_
 TAGGA GGTG AC CCGGC
 |||| |||| || ||||

		ATCCT TCGC TG GGCCG	
		_ A ATA	
GAM1711	LOC221271 3'	GGCCGGGTGCGGTGGCTCA 44125	T _ A_
		A GGT GC CACCCGGCC	
		A TCG TG GTGGGCCGG	
		C G GC	
GAM1711	LOC221410 3'	GGCCGGGTGTGGTGGTTC 44195	GG G
		GGAT T CACACCCGGCC	
		CTTG G GTGTGGGCCGG	
		GT _	
GAM1711	LOC90509 3'	GGCCAGGAGATCGACACCATCC 31608	CACA__ C
	TG	TAGGATGGTG CC GGCC	
		GTCCTACCAC GG CCGG	
		AGCTAGA A	
GAM1712	EPHB3 3'	AGGACCGTGCAGGGATGCCAAG 10736	AA C A_
	C	GCT GC TTCT CACGGTCCT	
		CGA CG AGGG GTGCCAGGA	
		AC T AC	
GAM1712	HSPA9B 3'	AGAACAATGGGAAACTTAGCTA 10347	CC A CG C
		TAGCTAAG TTCT CA GT CT	
		ATCGATTG AAGG GT CA GA	
		A_ _ AA A	
GAM1712	C1orf24 3'	GACTGTGCAAAGGGCTTAGCTA 27533	CTA
		TAGCTAAGCCTT CACGGTC	
		ATCGATTGCGGA GTGTCAG	
		AAC	
GAM1712	NIBAN 3'	GACTGTGCAAAGGGCTTAGCTA 22630	CTA
		TAGCTAAGCCTT CACGGTC	
		ATCGATTGCGGA GTGTCAG	
		AAC	
GAM1712	ZNF84 5'	GTGTAGAAGACCTAGCTG 9479	AGC
		TAGCTA CTTCTACAC	
		GTCGAT GAAGATGTG	
		CCA	
GAM1712	LOC256310 5'	AGGGCGAGCAGAAGGCTTGC 46093	T ACACG
		GC AAGCCTTCT GTCCT	
		CG TTCGGAAGA CGGGA	
		_ CGAG_	
GAM1713	ATP10C 3'	CCAGTCAAGCAGAAAAACAGGC 23687	CAC_ CATG
	A	TGCCT TTCT TTGACTGG	

ACGGA AAGA AACTGACC
 CAAA CG__
 GAM1713 PHKB 3' CCAGCCAACATGGTGA 5837 TTCT A
 TCAC CATGTTG CTGG
 ||| ||||| |||
 AGTG GTACAAC GACC
 ____ C
 GAM1713 acmsd 5' CCAGTAGAGTGAGGAAGTGAGA 28729 C _ GTTG
 CA TG CTCACTTC TCAT ACTGG
 || ||||| ||| ||||
 AC GAGTGAAG AGTG TGACC
 A G AGA_
 GAM1713 AMOT 3' CCAATCATTTGCAAAGTGAGG 28411 CT TGT C
 CCTCACTT CA TGA TGG
 ||||| || ||| |||
 GGAGTGAA GT ACT ACC
 AC TT_ A
 GAM1713 BTN2A2 3' CCAGTCAAAAAGAAAGTGAG 13858 C ATG
 CTCACTT TC TTGACTGG
 ||||| || |||||
 GAGTGAA AG AACTGACC
 _ AAA
 GAM1713 DKFZP564D0462 3' CCAAGGAATATGAAGTGAGACA 34897 C TC GA _
 TG CTCACT TCATGTT CT GG
 || ||||| ||||| || ||
 AC GAGTGA AGTATAA GA CC
 A _ G_ A
 GAM1713 Kv6.3 3' CCAGATGGTCTGAGAAGTGA 28565 T TT A
 TCACTTCTCA G G CTGG
 ||||| || |||
 AGTGAAGAGT T T GACC
 C GG A
 GAM1713 LOC149153 5' CCAGTCAACATGAATGGG 40964 CTTC
 CTCA TCATGTTGACTGG
 ||| |||||
 GGGT AGTACAACTGACC
 A_
 GAM1713 LOC150759 3' CCAGTCATGGAGTTAAGAAGTG 39012 C CATGT_
 AGTCA TG CTCACTTCT TGACTGG
 || ||||| |||||
 AC GAGTGAAGA ACTGACC
 T ATTGAGGT
 GAM1713 LOC151323 3' CCAGTCATGGAGCTAAGAAGTG 39101 C CAT ____
 AGTCA G CTCACTTCT GT TGACTGG
 | ||||| || |||||
 C GAGTGAAGA CG ACTGACC
 T AT_ AGGT
 GAM1713 LOC200399 3' CCAGTCATGGAGTTAAGAAGTG 42809 C CATGT_
 AGTCA TG CTCACTTCT TGACTGG
 || ||||| |||||

			AC GAGTGAAGA ACTGACC	
			T ATTGAGGT	
GAM1714	GGT2	5'	ACCTGACAACCATGTGTACACC 36486	_ A GCGAT
	A		TGGTGTACACA GG TG GGT	
			ACCACATGTGT CC AC CCA	
			A A AGT__	
GAM1714	GJB3	3'	CATCCCCACCCTGTGTACAC 23436	A C
			GTGTACACAGG TGG GATG	
			CACATGTGTCC ACC CTAC	
			C C	
GAM1714	KCNT1	3'	ACCATCGTCAACGTGCAGACCA 30971	GTA AGGA
			TGGT CAC TGGCGATGGT	
			ACCA GTG ACTGCTACCA	
			GAC CA__	
GAM1714	KIAA0125	5'	ACCATCGCCATCATCATCACCA 16688	TACACAG
			TGGTG GATGGCGATGGT	
			ACCAC CTACCGCTACCA	
			TACTA__	
GAM1714	KIAA0628	3'	ACCACCACCACCTGTGTAAACCA 16672	G A CGA
			TGGT TACACAGG TGG TGGT	
			ACCA ATGTGTCC ACC ACCA	
			_ _ ACC	
GAM1714	SH3BGRL	3'	GCCATCCTGTATACACCA 31026	C
			TGGTGTA ACAGGATGGC	
			ACCACAT TGTCCTACCG	
			A	
GAM1714	LOC124602	3'	CATCGCCCAGTACACCA 36757	ACAGGAT
			TGGTGTAC GGCGATG	
			ACCACATG CCGCTAC	
			AC_____	
GAM1714	LOC149319	5'	ACCTGACAACCATGTGTACACC 38711	_ A GCGAT
	A		TGGTGTACACA GG TG GGT	
			ACCACATGTGT CC AC CCA	
			A A AGT__	
GAM1714	LOC203397	3'	CATCGCCCAGTACACCA 43037	ACAGGAT
			TGGTGTAC GGCGATG	
			ACCACATG CCGCTAC	
			AC_____	
GAM1714	LOC254100	5'	ACCATCGCCACCCAGTAATCA 46126	TAC A_ A
	C		GTG AC GG TGGCGATGGT	

CAC TG CC ACCGCTACCA
TAA AC C
GAM1715 MAP1A 3' CCTCCCTTCCCCAAGGATCCA 8183 A CTAGTCAA
TG GATCCTTG GGAGG
|| ||||| ||||
AC CTAGGAAC CCTCC
_ CCCTTC_
GAM1715 SORCS2 3' CTCCTCTCTGGCAGGGATCTC 21876 TCA
A TGAGATCCTTGCTAG AGGAGG
||||||| |||||
ACTCTAGGGACGGTC TCCTCC
TC_
GAM1715 DEPC-1 5' CCTCCTTAAAGAGAAGGATCT 29191 G AGTC
AGATCCTT CT AAGGAGG
||||| || |||||
TCTAGGAA GA TTCCTCC
_ GAAA
GAM1715 FLJ12891 3' CCTCCTTGAAGAAAGAATTCA 24509 A C G AG
TGAG TC TT CT TCAAGGAGG
||| || || || |||||
ACTT AG AA GA GGTCCTCC
A A _ A_
GAM1715 FLJ21977 3' CTCCCTTCAAGGATCTCA 25939 CT TCAA
TGAGATCCTTG AG GGAG
||||||| || |||
ACTCTAGGAAC TC CCTC
T_ ____
GAM1715 PPP2R3A 3' CCTCCCTGACTGTGGATCTTA 8585 TT T A
TGAGATCC GC AGTCA GGAGG
|||||| || |||| |||||
ATTCTAGG TG TCAGT CCTCC
_ _ C
GAM1715 LOC146108 5' CCTGCTAGCAAGGTTCCCA 38062 A T CA
TG GA CCTTGCTAGT AGG
|| || ||||| |||
AC CT GGAACGATCG TCC
C T _
GAM1715 LOC219529 3' CCTTCCCAGCAAGGATATCA 44671 G AGTC
TGA ATCCTTGCT AAGG
|| ||||| |||
ACT TAGGAACGA TTCC
A CCC_
GAM1716 MCP 3' CGTTCATTGTAAAAAGCCCTT 8205 AAT C
AAGG TTTTTCAC GTGAACG
||| ||||| |||||
TTCC GAAAAATG TACTTGC
C_ T
GAM1716 DKFZP564C196 3' TCACGGCAAAGAGAGCCACCT 34715 AA_ A
AGG TTTTTTT CCGTGA
|| ||||| |||||

		TCC AGAGAAA GGC ACT	
		ACCG C	
GAM1716 FLJ20984	5'	CGTTCACAGCAAACAGGATTCC 23895	_ ACC
	T	AGGAATTTT TTT GTGAACG	
		TCCTTAGGA AAA CACTTGC	
		C CGA	
GAM1716 ZFP95	3'	CACAGTAAAAGAATTCCTT 15918	C
		AAGGAATTTTTTTTAC GTG	
		TTCCTTAAGAAAATG CAC	
		A	
GAM1716 ZFP95	3'	CACAGTAAAAGAATTCCTT 29708	C
		AAGGAATTTTTTTTAC GTG	
		TTCCTTAAGAAAATG CAC	
		A	
GAM1716 LOC126964	3'	ATGGGCAGAAAAATTCCTT 36882	A_
		AAGGAATTTTTTTT CCGT	
		TTCCTTAAAAAGA GGTA	
		CG	
GAM1717 ADARB1	3'	GCGCCCAGCGTGCACGGGA 6777	_
		TCCCGTGCACGCTGG CGC	
		AGGGCACGTGCGACC GCG	
		C	
GAM1717 ADARB1	3'	GCGCCCAGCGTGCACGGGA 17948	_
		TCCCGTGCACGCTGG CGC	
		AGGGCACGTGCGACC GCG	
		C	
GAM1717 EGFL4	3'	CACATGCACATGTGCAC 30964	C GC
		GTGCACG TG GCATGTG	
		CACGTGT AC CGTACAC	
		_ A_	
GAM1717 FLJ14566	5'	CACATGGTGTGCACGGG 26564	TGGCG
		CCCGTGCACGC CATGTG	
		GGGCACGTGTG GTACAC	

GAM1717 KIAA1644	3'	CACATGCGCGCACACACAGG 41200	C CACGC _
		CC GTG TG GCGCATGTG	
		GG CAC AC CGCGTACAC	
		A ACAC_ G	
GAM1717 RoXaN	3'	CACATGTGCACATGCAC 24600	CGC _
		GTGCA TG GCGCATGTG	

CACGT AC CGTGACAC
___ A
GAM1717 LOC128989 3' ACATGTACGTGCACAGG 36939 C CTGGC
CC GTGCACG GCATGT
|| ||||| |||||
GG CACGTGC TGTACA
A A___
GAM1717 LOC147054 5' CACACGCAGGTGTGCAAGG 40788 G G CA
CC TGCACGCT GCG TGTG
|| ||||| ||| ||||
GG ACGTGTGG CGC ACAC
A A ___
GAM1717 LOC149103 3' CATTATTCCAACCTGCACGGGA 38651 CGC CGCAT
TCCCGTGCA TGG GTG
||||||| ||| |||
AGGGCACGT ACC TAC
CA_ TTAT_
GAM1718 AQP1 3' ACTCTGACAAGCTGGCCA 5958 ACGCC C
TGGCCAGC GTCG GGT
||||||| ||| |||
ACCGGTCG CAGT TCA
AA___ C
GAM1718 ATP8A2 3' CTGCTGCATGGCTGGCCA 44919 A CC C
TGGCCAGC CG GT GCGG
||||||| || || |||||
ACCGGTCG GT CG CGTC
_ A_ T
GAM1718 DLK1 5' ACCGCGACCCCGGCCGCC 9928 CA A CC
GGC GC CG GTCGCGGT
||| ||| |||||
CCG CG GC CAGCGCCA
C_ _ CC
GAM1718 HD 3' CCACAGCTGCTGGCCA 7892 C C CGC
TGGCCAGCA GC GT GG
||||||| || || ||
ACCGGTCGT CG CA CC
_ A ___
GAM1718 IL12RB2 3' ACTTTCTTGCTATGCTGGCCA 7278 CG TCGC
TGGCCAGCA CCG GGT
||||||| ||| |||
ACCGGTCGT GGT TCA
AT TCTT
GAM1718 JAG2 3' ACCTCGCGCTTGCTGGCCA 8004 C C T C
TGGCCAGCA GC G CG GGT
||||||| || || |||
ACCGGTCGT CG C GC CCA
T _ _ T
GAM1718 MSX1 5' TGCCCGGCGGCTGGCCA 8286 A TC
TGGCCAGC CGCCG GCG
||||||| ||||| |||

		ACCGGTCG GCGGC CGT	
		— C—	
GAM1718	MTA1L1	5' ACCGCGACGGCTGAGGC 11135	AG C
		GCC CA GCCGTCGCGGT	
		CGG GT CGGCAGCGCCA	
		A— —	
GAM1718	MTMR3	3' TTGTCTGGCTGCTGGCCA 22073	C TC
		TGGCCAGCA GCCG GCGG	
		ACCGGTCGT CGGT TGTT	
		— C—	
GAM1718	PPP2R2C	5' CGGGAGAGCTGCTGGCCA 30939	C CG G
		TGGCCAGCA GC TC CG	
		ACCGGTCGT CG AG GC	
		— AG G	
GAM1718	SLC19A1	3' ACCGCGGACGTGCTGGCC 9020	CCG
		GGCCAGCACG TCGCGGT	
		CCGGTCGTGC GGCGCCA	
		A—	
GAM1718	TRIM9	5' GCCGCCGCCGCTGGCCA 17518	AC CGTC
		TGGCCAGC GC GCGGT	
		ACCGGTCG CG CGCCG	
		C— C—	
GAM1718	TRPV2	5' CCGTGCCGGCTGGCCA 18195	GCAC T
		TGGCCA GCCG CGCGG	
		ACCGGT CGGC GTGCC	
		— C	
GAM1718	USP6	5' ACTGGTGCAGCTGCTGGCCA 43807	C C CG
		TGGCCAGCA GC GT CGGT	
		ACCGGTCGT CG CG GTCA	
		— A TG	
GAM1718	C1QTNF7	3' ATGGTGCGGCGGCTGGCCA 25662	A T G
		TGGCCAGC CGCCG CGC GT	
		ACCGGTCG GCGGC GTG TA	
		— — G	
GAM1718	CBX6	3' ACCGGGGCCCCGCTGGCCA 15572	ACGCC G
		TGGCCAGC GTC CGGT	
		ACCGGTCG CGG GCCA	
		CCC— G	
GAM1718	DKFZP434O047	5' ACTGGTGCAGCTGCTGGCCA 17860	C C CG
		TGGCCAGCA GC GT CGGT	

		ACCGGTCGT CG CG GTCA	
		_ A TG	
GAM1718 DRAP1	5'	ACCGCGACGGGCGGGCGGC 13154	A A _
		GCC GC CGCC GTCGCGGT	
		CGG CG GCGG CAGCGCCA	
		_ G G	
GAM1718 FLJ00001	3'	CTGAGACGTGCTGGCC 39779	GCC G
		GGCCAGCAC GTC CGG	
		CCGGTCGTG CAG GTC	
		___ A	
GAM1718 FLJ21562	5'	ACCGGGAGCGCGGTGGCCA 24761	G A CG G
		TGGCCA C CGC TC CGGT	
		ACCGGT G GCG AG GCCA	
		___ CG G	
GAM1718 KIAA0350	3'	ACCACGACCACCGTGGCCA 30658	AGC CC_ C
		TGGCC ACG GTCG GGT	
		ACCGG TGC CAGC CCA	
		___ CAC A	
GAM1718 KIAA0513	3'	ACCGTGACCATGCTGCCA 16351	C CGCC
		TGGC AGCA GTCGCGGT	
		ACCG TCGT CAGTGCCA	
		_ AC_	
GAM1718 KIAA1297	5'	GCCCGGCTGCTGGCCA 35714	C TC
		TGGCCAGCA GCCG GC	
		ACCGGTCGT CGGC CG	
		_ C_	
GAM1718 KIAA1813	5'	GTGGCGGCGCGCGGGCCA 34813	A A
		TGGCC GC CGCCGTCGC	
		ACCGG CG GCGGCGGTG	
		G C	
GAM1718 KIAA1977	5'	TGCGAGGCGGCTGGCCA 36748	A G
		TGGCCAGC CGCC TCGCG	
		ACCGGTCG GCGG AGCGT	
		- -	
GAM1718 MOT8	5'	ACGGCGGCGGCGCGCCGGCC 20823	A A G
		GGCC GC CGCCGTCGC GT	
		CCGG CG GCGGCGGCG CA	
		C C G	
GAM1718 OBSCN	3'	CTGCCAGGTGCTGGCCA 34990	AC GTC
		TGGCCAGC GCC GCGG	

			ACCGGTCG TGG CGTC		
			___ AC_		
GAM1718	RAI16	3'	ACTGCGGCATGTTGACCA 22968	C C	GTC
			TGG CAGCA GCC GCGGT		
			ACC GTTGT CGG CGTCA		
			A A ___		
GAM1718	RHO6	3'	CGGGGGGCATGCTGGCC 15820	C G G	
			GGCCAGCA GCC TC CG		
			CCGGTCGT CGG GG GC		
			A G _		
GAM1718	LOC125704	5'	ACCAGGGCGGCACGCTGGCC 36796	AC	GC
			GGCCAGC GCCGTC GGT		
			CCGGTCG CGGCGG CCA		
			CA GA		
GAM1718	LOC126917	5'	CGTCGCGGTACAACGTGCTGGC 36869	G_____	TCG
			CA TGGCCAGCAC CCG CG		
			ACCGGTCGTG GGC GC		
			CAACAIIT GCT		
GAM1718	LOC146782	5'	ACTGGTGCAGCTGCTGGCCA 37523	C C	CG
			TGGCCAGCA GC GT CCGT		
			ACCGGTCGT CG CG GTCA		
			_ A TG		
GAM1718	LOC152078	5'	GCGCCGGCTGCTGGCCA 39212	C	T
			TGGCCAGCA GCCG CGC		
			ACCGGTCGT CGGC GCG		
			_ C		
GAM1718	LOC200014	3'	ACCGCACCCGGCTGGCCA 42688	A CC	C
			TGGCCAGC CG GT GCGGT		
			ACCGGTCG GC CA CGCCA		
			_ C_ _		
GAM1718	LOC255397	5'	ACCACGGGCTGCTGGCC 46565	C	GT C
			GGCCAGCA GCC CG GGT		
			CCGGTCGT CGG GC CCA		
			_ _ A		
GAM1718	LOC256158	5'	ACCTGTCCAGTGCTGGCCA 46616	GCCGT	C
			TGGCCAGCAC CG GGT		
			ACCGGTCGTG GT CCA		
			ACCT_ _		
GAM1719	PYGO2	3'	CTGGTGATTAATTAGCAATTCT 31999	TC	CG ATC
			C GAGA TGC G ATCACCAG		

CTCT ACG T TAGTGGTC
 TA AT AAT
 GAM1719 ST7 5' GGTGAATCATCCCGGCAGA 20455 _ CA_
 TCTGCCGG AT TCACC
 ||||| || ||||
 AGACGGCC TA AGTGG
 C CTA
 GAM1719 ST7 5' GGTGAATCATCCCGGCAGA 22431 _ CA_
 TCTGCCGG AT TCACC
 ||||| || ||||
 AGACGGCC TA AGTGG
 C CTA
 GAM1719 TRAF5 3' CTGGTGATGACCATGCACCTT 10966 ATC C_ A
 GAG TGC GG TCATCACCAG
 || || || |||||
 TTC ACG CC AGTAGTGGTC
 C_ TA _
 GAM1719 DKFZp434O0515 5' CTGGCGATGAGGAAGATCTTG 32786 G GGA A
 CGAGATCT CC TCATC CCAG
 ||||| || |||| ||||
 GTTCTAGA GG AGTAG GGTC
 A _ C
 GAM1719 KIAA1161 5' CTGGTGATAGTGAATAGATCTC 39753 CCGG C
 GAGATCTG AT ATCACCAG
 ||||| || |||||
 CTCTAGAT TG TAGTGGTC
 AAG_ A
 GAM1719 MADHIP 5' CTGGTGGTGCAGCAGACATC 14241 GA CGGAT
 GA TCTGC CATCACCAG
 || |||| |||||
 CT AGACG GTGGTGGTC
 AC AC_
 GAM1719 MADHIP 5' CTGGTGGTGCAGCAGACATC 14243 GA CGGAT
 GA TCTGC CATCACCAG
 || |||| |||||
 CT AGACG GTGGTGGTC
 AC AC_
 GAM1719 MADHIP 5' CTGGTGGTGCAGCAGACATC 11220 GA CGGAT
 GA TCTGC CATCACCAG
 || |||| |||||
 CT AGACG GTGGTGGTC
 AC AC_
 GAM1719 NKX2B 3' CTGGTGGCAGATTTCG 8343 GGATCATC
 CGAGATCTGCC ACCAG
 ||||| ||||
 GCTTTAGACGG TGGTC

 GAM1719 LOC124216 3' CTGGTGATTAACAAAGACCTCG 36739 A GCCGGATC
 CGAG TCT ATCACCAG
 ||| || |||||

		GCTC AGA TAGTGGTC	
		C AACAAT__	
GAM1719	LOC147071 5'	CTGGTGACATGGAGCAGATCT 36137	CGGATCA
		AGATCTGC TCACCAG	
		TCTAGACG AGTGGTC	
		AGGTAC_	
GAM1719	LOC201173 5'	CTGGTGACATGGAGCAGATCT 42216	CGGATCA
		AGATCTGC TCACCAG	
		TCTAGACG AGTGGTC	
		AGGTAC_	
GAM1719	LOC201220 5'	CTGGTGACATGGAGCAGATCT 42223	CGGATCA
		AGATCTGC TCACCAG	
		TCTAGACG AGTGGTC	
		AGGTAC_	
GAM1719	LOC203504 3'	CTGGTCCCCCAACAGATCTC 43570	CC ATCATC
		GAGATCTG GG ACCAG	
		CTCTAGAC CC TGGTC	
		AA CCCC__	
GAM1719	LOC256682 5'	CTGGCGTGTCGGCAGA 46593	AT CA
		TCTGCCGG CAT CCAG	
		AGACGGCT GTG GGTC	
		_ C_	
GAM1719	LOC257451 3'	CTGGTGATTAATTAGCAATTCT 45742	TC CG ATC
	C	GAGA TGC G ATCACCAG	
		CTCT ACG T TAGTGGTC	
		TA AT AAT	
GAM1720	ACK1 5'	GCGCAGGGAGGGGCCGG 12360	A G TCC
		CC GCC CTCTTTGC GC	
		GG CGG GAGGGACG CG	
		C G _	
GAM1720	ANK1 3'	CGCACAGCGCGGCTGGGA 30285	TCTTT CC
		TCCCAGCCGC GCT GCG	
		AGGGTCGGCG CGA CGC	
		_ CA	
GAM1720	AXIN1 5'	CGCGGAGCGGGCGGGTGGGA 30515	G TTT
		TCCA CCGCTC GCTCCGCG	
		AGGGT GGCGGG CGAGGCGC	
		G _	
GAM1720	AXUD1 5'	GCGCAGAGCGAGGGCGGCTGG 26920	C
		CCAGCCGCTCTTTGCTC GCGC	

GGTCGGCGGGGAGCGAG CGCG

A

GAM1720 BMP4 5' CGCGGAGCCCGGCCGGA 28387 CA CTCTTT
TCC GCCG GCTCCGCG
||| |||| |||||
AGG CGGC CGAGGCGC
CC C_____

GAM1720 BMP4 5' CGCGGAGCCCGGCCGGA 6866 CA CTCTTT
TCC GCCG GCTCCGCG
||| |||| |||||
AGG CGGC CGAGGCGC
CC C_____

GAM1720 DSCR5 5' GCGCGGAGAACTCAGCGCTGAG 18550 C C CTTTG
A TC CAGC GCT CTCCGCGC
|| ||||| |||||
AG GTCG CGA GAGGCGCG
A _ CTCAA

GAM1720 DYRK2 5' GCGCGAGGGGCGGCCGGA 13209 A TCC
TCCC GCCGCTCTTTGC GC
|||| ||||| ||||| ||
AGGG CGGCGGGGAGCG CG
C _____

GAM1720 DYRK2 5' GCGCGAGGGGCGGCCGGA 9633 A TCC
TCCC GCCGCTCTTTGC GC
|||| ||||| ||||| ||
AGGG CGGCGGGGAGCG CG
C _____

GAM1720 EMP3 5' CGCAGAAGGAGAGCGAGC 7137 _ GC C
GC CGCTCTTT TC GCG
|| ||||| || |||
CG GCGAGAGG AG CGC
A A_ A

GAM1720 EP300 5' GCGCGGAGCGCGGCCGAGG 7152 A CTT
CC GCCGCT TGCTCCGCGC
|| ||||| |||||
GG CGGCGG GCGAGGCGCG
A C_

GAM1720 FZD1 5' CGCAGAACAGGAGCCGGGG 9593 AGCC T C C
CCC GCTCTT G TC GCG
||| ||||| || |||
GGG CGAGGA C AG CGC
GC_ _ A A

GAM1720 GALGT 5' GCGCGGAGCCGAAGCAGCCGC 7212 C _ _
GC GCT CTTTG CTCCGCGC
|| ||| ||||| |||||
CG CGA GAAGC GAGGCGCG
C C C

GAM1720 KCNA6 5' GCGCAGTGGAGAACTGGGA 8017 CCGC TG C
TCCCAG TCTT CT CGC
||||| |||| || |||

		AGGGTC AGAG GA GCG	
		A___ GT C	
GAM1720 MAN2A1	5'	GCGCGGAGGTCGCGCAGCCCGG 8179	A_ C TCTTTG
GA		TCCC GC GC CTCCGCGC	
		AGGG CG CG GAGGCGCG	
		CC A CGCTG_	
GAM1720 PRKAB1	5'	GCACGAGGAAGCGGTTGGGA 12930	_ CTCC
		TCCCAGCCGCT CTTTG GC	
		AGGGTTGGCGA GGAGC CG	
		A A___	
GAM1720 SORCS2	5'	GCGCGGAGCCCGGTGGCGGCGA 21878	CA _ TT
GGA		TCC GCCGCT CT GCTCCGCGC	
		AGG CGGCGG GG CGAGGCGCG	
		AG T CC	
GAM1720 ZNF26	5'	GCGCGGAGCTAAGCGGCTCGGA 36130	C CTTT
		TCC AGCCGCT GCTCCGCGC	
		AGG TCGGCGA CGAGGCGCG	
		C AT___	
GAM1720 C21orf93	5'	GCACGGAGCATGTGGCTGGG 29742	TCTT C
		CCCAGCCGC TGCTCCG GC	
		GGGTCGGTG ACGAGGC CG	
		T___ A	
GAM1720 CARD9	3'	CGCAGGCCTGAGCAGCGGGGA 22748	A C TTT CC
		TCCC GC GCTC GCT GCG	
		AGGG CG CGAG CGG CGC	
		G A TC_ A_	
GAM1720 CASKIN1	3'	GCGCGGCGCGAGCGGCCGGG 21864	A TTT T
		CCC GCCGCTC GC CCGCGC	
		GGG CGGCGAG CG GGCGCG	
		C ___ C	
GAM1720 DED	5'	GCGCGAAGCGGAGTGGACCGGG 14448	AG_ TT C
A		TCCC CCGCTCT GCT CGCGC	
		AGGG GGTGAGG CGA GCGCG	
		CCA _ A	
GAM1720 FLJ00001	3'	CGCAGAGCATGGTCAGGA 39777	CA CTCTT C
		TCC GCCG TGCTC GCG	
		AGG TGGT ACGAG CGC	
		AC _____ A	
GAM1720 FLJ12355	5'	GCGCAGAGCAGCGGGGCTGGGG 24543	G CT C
		TCCCAGCC CT TTGCTC GCGC	

	GGGGTCGG GG GACGAG CGCG	
	_ C_ A	
GAM1720 FLJ12895 5'	GCACGAGGGGGCGGCTGGGA 23405	TTG C_
	TCCCAGCCGCTCT CTC GC	
	AGGGTCGGCGGGG GAG CG	
	___ CA	
GAM1720 FLJ13072 5'	CGTCCTCAAGAGCGGCTGG 43234	TGCTCC
	CCAGCCGCTCTT GCG	
	GGTCGGCGAGAA TGC	
	CTCC__	
GAM1720 FLJ20374 5'	GCGCGGAGCACCCGGCGCCGA 19430	CCA CTCTT
	TC GCCG TGCTCCGCGC	
	AG CGGC ACGAGGCGCG	
	CCG CC__	
GAM1720 FLJ20730 3'	GCAAGTAAAGAGCAACGGGA 19640	AGCC CC
	TCCC GCTCTTTGCT GC	
	AGGG CGAGAAATGA CG	
	CAA_ A_	
GAM1720 FLJ21596 3'	GCGCAGGTCTCAAGGCGGCTGA 24213	C T TGCT _
GA	TC CAGCCGC CTT CC GCGC	
	AG GTCGGCG GAA GG CGCG	
	A _ CTCT A	
GAM1720 HRIHFB2122 5'	GCGCGGCGGCGGGCGGC 13901	TTT _
	GCCGCTC GCT CCGCGC	
	CGGCGGG CGG GGCGCG	
	___ C	
GAM1720 HRIHFB2122 5'	GCGCGGCGGCGGGCGGC 28904	TTT _
	GCCGCTC GCT CCGCGC	
	CGGCGGG CGG GGCGCG	
	___ C	
GAM1720 KIAA0410 3'	GCACATTAAGGAGCAACTGGGA 16620	CC CTCC
	TCCCAG GCTCTTTG GC	
	AGGGTC CGAGGAAT CG	
	AA TACA	
GAM1720 KIAA0844 5'	CGCGGAGGTGCGGCGGGGA 17283	A T TTTG
	TCCC GCCGC C CTCCGC	
	AGGG CGGCG G GAGGCGC	
	G T__	
GAM1720 KIAA1319 5'	CGCGGAGCCCGGCTAGGGA 21867	_ CTCTTT
	TCCC AGCCG GCTCCGCG	

AGGG TCGGC CGAGGCGC
 A C____
 GAM1720 MGC15437 5' GCGCAGAGCTGGGGGCAGCCGG 26689 A C TT C
 GG TCCC GC GCTCT GCTC GCGC
 |||| || |||| ||||
 GGGG CG CGGGG CGAG CGCG
 C A GT A
 GAM1720 MGC2705 5' GCACGAGGAGCGGATGAGA 26417 C G CTCC
 TC CA CCGCTCTTTG GC
 || || |||| || ||
 AG GT GGCGAGGAGC CG
 A A A____
 GAM1720 MOT8 5' CGCGGAGCTCCGGCTGG 20824 CTCTTT
 CCAGCCG GCTCCGCG
 |||| ||||
 GGTCGGC CGAGGCGC
 CT____
 GAM1720 RIN3 5' CCGGAGCAAGGCCAGGA 24231 CA GCTCT C
 TCC GCC TTGCTCCG G
 ||| ||| ||||| |
 AGG CGG AACGAGGC C
 AC _____ A
 GAM1720 RP4-622L5 3' GTCAAAGGGCAGCTGAGA 21202 C C _
 TC CAGC GCTCTTTG C
 || ||| ||||| |
 AG GTCG CGGGAAAC G
 A A T
 GAM1720 SEMA7A 3' GCACGGATGGTGAGGGGCTGAG 9664 C G TTTGC C
 A TC CAGCC CTC TCCG GC
 || |||| || ||||
 AG GTCGG GAG AGGC CG
 A G TGGT_ A
 GAM1720 STX11 5' GCGCGGAGCTCGGGCGGCCGTG 9842 _ TTT
 G CCA GCCGCTC GCTCCGCGC
 ||| ||||| |||||
 GGT CGGCGGG CGAGGCGCG
 GC CT_
 GAM1720 T2BP 5' GCGCGGAGGAGCAGCGGCCGGG 34681 A _ TG
 CCC GCCGCT CTT CTCCGCGC
 ||| ||||| ||| |||||
 GGG CGGCGA GAG GAGGCGCG
 C C _
 GAM1720 TREX2 5' GCGCGAAACATGGCGGGGCAGG 27988 CAG_ CTT CTC
 A TCC CCGCT TG CGCGC
 ||| |||| || ||||
 AGG GGCGG AC GCGCG
 ACGG T_ AAA
 GAM1720 TREX2 5' GCGCGAAACATGGCGGGGCAGG 14069 CAG_ CTT CTC
 A TCC CCGCT TG CGCGC
 ||| |||| || ||||

AGG GCGCG AC GCGCG
 ACGG T__ AAA
 GAM1720 VPS39 3' GCGGGGGGCAAGAACAGCAGG 31471 _ C__ G
 CC GCT TTTGCTCC CGC
 || ||| ||||| |||
 GG CGA GAACGGGG GCG
 A CAA G
 GAM1720 LOC143666 3' GAGATAAAGAGCAGCTGGG 40370 C _
 CCCAGC GCTCTTTG CTC
 ||||| ||||| |||
 GGGTCG CGAGAAAT GAG
 A A
 GAM1720 LOC146138 3' GCACAGAGGGCGGAGCTGG 40656 __ CTCC
 CCAGC CGCTCTTTG GC
 ||||| ||||| ||
 GGTCG GCGGGAGAC CG
 AG A__
 GAM1720 LOC148132 5' CGCAGAGCAAGGGCGGCAAGGA 40869 CA T C
 TCC GCCGC CTTTGCTC GCG
 ||| ||||| ||||| |||
 AGG CGGCG GGAACGAG CGC
 AA _ A
 GAM1720 LOC148229 5' CGCAGAGCAGAGCCTGG 38496 CC TT C
 CCAG GCTCT GCTC GCG
 ||||| ||||| ||| |||
 GGTC CGAGA CGAG CGC
 _ _ A
 GAM1720 LOC150935 3' GCACGTGAGAGCGGCCAGGG 39019 A_ _
 CCC GCCGCTCTT TGC
 ||| ||||| |||
 GGG CGGCGAGAG ACG
 AC TGC
 GAM1720 LOC151174 5' GCGCAGAGCAGGGCTGGCAGG 41311 A _ TT C
 CC GCC GCTCT GCTC GCGC
 || ||| ||||| ||||| |||
 GG CGG CGGGA CGAG CGCG
 A T _ A
 GAM1720 LOC154101 5' CGCGAAAGCCAACGGACAGGA 40237 CAG CTC T C_
 TCC CCG TT GCT CGCG
 ||| ||| || ||| |||||
 AGG GGC AA CGA GCGC
 ACA _ C AA
 GAM1720 LOC202559 5' GCGCGGAGGAGGAGCAGCGCGG 42986 A_ C G
 GA TCCC GC GCTCTTT CTCCGCGC
 ||||| || ||||| ||||| |||||
 AGGG CG CGAGGAG GAGGCGCG
 CG A _
 GAM1720 LOC221876 5' GCGCAGAGGGCTGGCTGGGA 45077 _ TCC
 TCCCAGCC GCTCTTTG GC
 ||||| ||||| ||| |||

AGGGTCGG CGGGAGACG CG
 T _____
 GAM1720 LOC253258 3' GAGATAAAGAGCAGCTGGG 46148 C _
 CCCAGC GCTCTTTG CTC
 ||||| ||||| |||
 GGGTCG CGAGAAAT GAG
 A A
 GAM1720 LOC255146 3' GCACAGGTGGCAGCTGGGA 45756 C _ _
 TCCCAGC GCT CTT TGC
 ||||| ||| ||| |||
 AGGGTCG CGG GGA ACG
 A T C
 GAM1720 LOC257478 5' CGCGGAGTGCGAGTGGGA 36183 GC TCTTT
 TCCCA CGC GCTCCGCG
 |||| ||| |||||
 AGGGT GCG TGAGGCGC
 GA _____
 GAM1721 GPR30 3' CGTCATGTCTCTAAACTG 7250 C CCCA C
 CAGT TGG AGACA GACG
 |||| ||| ||||| |||||
 GTCA ATC TCTGT CTGC
 A _____ A
 GAM1721 FLJ12788 3' TCTGTCTCAGGCCAGAT 22873 CA C
 GTCTGGCC AGACA GA
 ||||| ||||| ||
 TAGACCGG TCTGT CT
 AC _
 GAM1721 HGC6.1.1 3' CGTTACCGGGTCCAGACTGA 15684 _ AAGAC
 TCAGTCTGG CCC ACG
 ||||| ||| |||
 AGTCAGACC GGG TGC
 T CCAT_
 GAM1721 LOC254423 5' GTGTGAGCCAGACTGA 46529 C AAG
 TCAGTCTGGC C ACAC
 ||||| ||| |||
 AGTCAGACCG G TGTG
 A _____
 GAM1722 CORO2B 3' ACTCATCTCCTCCTCCCA 32253 A A C AA
 TG GAG AGG AGAT GAGT
 || ||| ||| ||| |||
 AC CTC TCC TCTA CTCA
 C C _ _
 GAM1722 FOXE3 3' CTTTCATCAACCTTCTCTCA 14471 CA _
 TGAGAGAAGG GAT AAG
 ||||| ||| |||
 ACTCTCTTCC CTA TTC
 AA C
 GAM1722 FOXE3 3' ACCTGGCTGCCTTCTTCA 14468 G ATA A
 TGA AGAAGGCAG AG GT
 ||| ||||| ||| |||

ACT TCTTCCGTC TC CA
 _ GG_ _
 GAM1722 PVT1 3' TACTCCCTGGAGCCTTCTCCCG 32662 A AGATAA
 TG GAGAAGGC GAGTA
 || ||||| ||||
 GC CTCTTCCG CTCAT
 C AGGTCC
 GAM1722 FLJ22002 3' TACTTTTGCCTTCTGCTCA 24247 _ TAAG
 TGAG AGAAGGCAGA AGTA
 ||| ||||| ||||
 ACTC TCTTCCGTTT TCAT
 G _
 GAM1722 FUT10 3' TACCCTGAGCCACCTCTCTCA 26392 A_ AGATA A
 TGAGAGA GGC AG GTA
 ||||| || ||||
 ACTCTCT CCG TC CAT
 CCA AG_ C
 GAM1722 KIAA0014 3' TTTTGTCTGCCTCCCCTCA 16120 AGA
 TGAG AGGCAGATAAGA
 ||| ||||| ||||
 ACTC TCCGTCTGTTTT
 CCC
 GAM1722 KIAA0794 3' CGTACCCTTCTGCCTCCCCCTC 39178 AGA_ TA A
 GAG AGGCAGA AG GTACG
 || ||||| || ||||
 CTC TCCGTCT TC CATGC
 CCCC _ C
 GAM1722 MIL1 3' CGTACTCTCAGCTGCCTCTC 17667 A ATA
 GAGA GGCAG AGAGTACG
 ||| |||| |||||
 CTCT CCGTC TCTCATGC
 _ GAC
 GAM1722 PFDN1 3' CTTTCCCTGCCTTCTCCCA 8482 A AT_
 TG GAGAAGGCAG AAG
 || ||||| ||||
 AC CTCTTCCGTC TTC
 C CCT
 GAM1722 LOC145195 3' TACTCTTACCCTCAACTCT 40516 A_ CAGA
 AGAG AGG TAAGAGTA
 ||| || |||||
 TCTC TCC ATTCTCAT
 AAC C_
 GAM1722 LOC157697 5' TACTCTTACCTGTAGGATCCA 39646 A GAAG A
 TG GA GCAG TAAGAGTA
 || || |||| |||||
 AC CT TGTC ATTCTCAT
 _ AGGA C
 GAM1722 LOC222160 3' CTTATCTCCCTTCTCCCA 45165 A C
 TG GAGAAGG AGATAAG
 || ||||| |||||

AC CTCTTCC TCTATTC
 C C
 GAM1722 LOC257449 3' GCTACCTGCCTTCTTTCA 31426 ATAAG
 TGAGAGAAGGCAG AGT
 ||||| |||
 ACTTTCTTCCGTC TCG
 CA__
 GAM1723 LOC122210 5' GACGTGTGCGGAAATGCACACG 36681 AC A_____ CGTG
 AAGTC TTCGT GC CGA TC
 |||| || ||| ||
 AAGCA CG GCT AG
 CA TAAAGC||| GTGC
 GAM1724 SYNGR3 3' CCCTCGCCCCAAGACTGGGGA 10406 C ATTCTC
 TCCCTAGTCT GG GGG
 ||||| || |||
 AGGGGTCAGA CC CCC
 A CCGCT_
 GAM1724 HSPC195 3' CCCACAGTCCCGAGACTGGG 39420 _ CTC
 CCTAGTCTCGG ATT GGG
 ||||| ||| |||
 GGGTCAGAGCC TGA CCC
 C CA_
 GAM1724 KIAA1677 3' CCCAGCGACACTAGGGA 33290 C GATT C
 TCCCTAGT TCG CT GGG
 ||||| ||| || |||
 AGGGATCA AGC GA CCC
 C ____ _
 GAM1724 LOC221042 3' TGCCTCTGTGCGGAGACTAG 44759 G TCTC
 CTAGTCTC GAT GGGCA
 ||||| ||| |||||
 GATCAGAG CTG TCCGT
 G TC_
 GAM1725 ARF3 3' AGTGGTAACTGCAGTTCCTC 7378 C GCC
 GAGGAACTGT GT TACCACT
 ||||| || |||||
 CTCCTTGACG CA ATGGTGA
 T ____
 GAM1725 PAFAH1B1 3' AGTGGTAATTGAGGAAAACAGT 6008 A CGTG _____
 TCCCCA GGAAGTGT CCT ACCACT
 ||||| ||| |||||
 CCTTGACA GGA TGGTGA
 C AAA_ GTTAA
 GAM1725 FLJ10697 3' AGTAACAGGGGCGAGTTCCT 20014 GTG ACC
 AGGAACTGTC CCT ACT
 ||||| ||| |||
 TCCTTGACGG GGA TGA
 ____ CAA
 GAM1725 FLJ22679 3' GTGGGCACAGCTCCCCA 25953 A ACT C
 TG GGA GT GTGCCTAC
 || ||| || |||||

AC CCT CG CACGGGTG
 C ____ A
 GAM1725 FLJ22679 3' GTGGGCACAGCTCCCCA 19266 A ACT C
 TG GGA GT GTGCCTAC
 || ||| || |||||
 AC CCT CG CACGGGTG
 C ____ A
 GAM1725 KIAA1954 3' AGTGGTAGTCCCAGCTACTCA 38093 GAA TCGTGC
 TGAG CTG CTACCACT
 |||| ||| |||||
 ACTC GAC GATGGTGA
 ATC CCT____
 GAM1725 ST7L 3' GTAGCAGGCAGTTCCCA 28977 A G C
 TG GGAAGTGTG TGC TAC
 || ||||| ||| |||
 AC CCTTGACGG ACG ATG
 - - -
 GAM1725 ST7L 3' GTAGCAGGCAGTTCCCA 19335 A G C
 TG GGAAGTGTG TGC TAC
 || ||||| ||| |||
 AC CCTTGACGG ACG ATG
 - - -
 GAM1725 ST7L 3' GTAGCAGGCAGTTCCCA 29207 A G C
 TG GGAAGTGTG TGC TAC
 || ||||| ||| |||
 AC CCTTGACGG ACG ATG
 - - -
 GAM1725 TSPAN-2 3' AGTGATAATGGGTCAGTTTCTC 12280 TCGT C____
 A TGAGGAACTG GCCTA CACT
 ||||| |||| |||
 ACTCTTTGAC TGGGT GTGA
 _____ AATA
 GAM1725 LOC116028 3' GGCAGGCATGGCGGCCCT 36492 AA A
 AGG CTGTCGTGCCT CC
 ||| ||||| |||
 TCC GGCGGTACGGA GG
 CC C
 GAM1725 LOC150236 5' GCAACCGACGGTTCCCCA 38906 A ____
 TG GGAAGTGTG TGC
 || ||||| |||
 AC CCTTGGCAGC ACG
 C CA
 GAM1726 GPRC5B 3' ATGTTTCAATAAACCTTTTGA 18351 C ____
 TCAAGAGGT TATT AATAT
 ||||| ||| |||||
 AGTTTCCA ATAA TTGTA
 A CT
 GAM1726 KIAA0893 3' TCAATAAAGACCTTTGA 17361 ATTAA
 TCAAGAGGTCT TATTGA
 ||||| |||||

AGTTCTCCAGA ATA ACT
 A____
 GAM1726 KIAA1596 5' ATCAGATAGCAATAGACCTCTA 35118 A AA _
 GA TC AGAGGTCTATT TAT TGAT
 || ||||| || ||||
 AG TCTCCAGATAA ATA ACTA
 A CG G
 GAM1726 MGC14836 3' TATCAACTGAATAGACCTTCT 27236 _ AATA
 AGA GGTCTATT TTGATA
 ||| ||||| |||||
 TCT CCAGATAA AACTAT
 T GTC_
 GAM1726 PRSC 3' ATCAATATTAACACTTGA 13348 AG CTAT
 TCAAG GT TAATATTGAT
 |||| || |||||
 AGTTC CA ATTATAACTA
 A_ ____
 GAM1726 LOC152627 5' TATCAACATTAATAGTACTTT 39297 _ A
 GAGGT CTATTAAT TTGATA
 |||| ||||| |||||
 TTTCA GATAATTA AACTAT
 T C
 GAM1727 ANKTM1 3' AGCTTCATGTTGAAAGAACCTA 14256 A G AG
 TAG TTCTTTTAAAC AT AGCT
 || ||||| || ||||
 ATC AAGAAAGTTG TA TCGA
 C _ CT
 GAM1727 CHI3L1 3' AGCTCTATCACCAAGGAG 6941 TAAC
 TTCTTT GATAGAGCT
 |||| |||||
 GAGGAA CTATCTCGA
 CCA_
 GAM1727 NR2E1 3' GAGCTTTACTAAAAGAA 9278 ACGA
 TTCTTTTA TAGAGCTC
 ||||| |||||
 AAGAAAAT ATTTTCGAG
 C_
 GAM1727 FLJ10392 5' AGCTCGATTAGAAGAATC 19847 CGATA
 GATTCTTTTAA GAGCT
 ||||| |||||
 CTAAGAAGATT CTCGA
 AG_
 GAM1727 FLJ23511 3' AGCTTTCTTAAAGAATC 25963 TAAC T
 GATTCTTT GA AGAGCT
 ||||| || |||||
 CTAAGAAA TT TTTCGA
 ____ C
 GAM1727 KIAA0527 3' GAGCTCTGTGGAAACAGAATC 45847 T AA G
 GATTCT TT C ATAGAGCTC
 ||||| || | |||||

CTAAGA AA G TGTCTCGAG
C AG _

GAM1728 ATP6V1G2 3' ATAATTTTCCTGTGACA 28223 T
TGTCA CAGGAAAATTAT
||||| |||||||||
ACAGT GTCCTTTTAATA

—

GAM1728 ATP6V1G2 3' ATAATTTTCCTGTGACA 28697 T
TGTCA CAGGAAAATTAT
||||| |||||||||
ACAGT GTCCTTTTAATA

—

GAM1728 PRKRA 3' ATGTTGATAATTCTG 9799 AAA
CAGGA TTATCAACAT
||||| |||||||||
GTCTT AATAGTTGTA

—

GAM1728 FLJ11806 5' ATGTTGATGAAGAACTTCCTGA 24215 C AA____
TTACA TGT ATCAGGAA TTATCAACAT
||| ||||||| |||||||||
ACA TAGTCCTT AGTAGTTGTA
T CAAGA

GAM1728 FLJ22055 3' ATGTTGAGAACCCTGATGA 24146 AAAATTA
TCATCAGG TCAACAT
||||||| |||||||
AGTAGTCC AGTTGTA
CAAG____

GAM1728 KIAA0960 3' ATAACCTTTTCCTGGCAACA 44515 CA _
TGT TCAGGAAAA TTAT
||| ||||||||| |||
ACA GGTCTCTTTT AATA
AC C

GAM1728 KIAA1922 3' TGATGCCCCCTGATGGCA 36461 AAAAT
TGTCATCAGG TATCA
||||||| |||
ACGGTAGTCC GTAGT
CC____

GAM1728 MIC2L1 3' TGCTGAGGCCTGATGACA 25492 AAAATTA A
TGTCATCAGG TCA CA
||||||| ||| ||
ACAGTAGTCC AGT GT
GG____ C

GAM1728 PXR2b 3' ATAATTTTCCCAATGTCA 18634 T CA
TG CAT GGAAAATTAT
|| ||| |||||||||
AC GTA CCTTTTAATA
T AC

GAM1728 LOC206426 5' ATGTGGCTTTTTCCTGACGCA 43116 CA TTATCA
TGT TCAGGAAAA ACAT
||| ||||||||| |||

ACG AGTCCTTTT TGTA
 C_ TCGG_
 GAM1728 LOC92935 3' ATGTTGGGTTTCCTGAT 35130 ATTA
 ATCAGGAAA TCAACAT
 ||||| |||||
 TAGTCCTTT GGTGTA
 G_
 GAM1729 MAGEC1 5' CTAGAGCACCACTTAAG 11945 AGGATC
 TTTAAGGTGGT TTCTAG
 ||||| |||||
 GAATTCCACCA GAGATC
 C_
 GAM1729 VCL 3' TCTAAAAGATCCTTTTTTAAA 9405 TGGT C
 TTTAAGG AGGATCTT TAGA
 ||||| ||||| |||||
 AAATTTT TCCTAGAA ATCT
 A
 GAM1729 VCL 3' TCTAAAAGATCCTTTTTTAAA 15194 TGGT C
 TTTAAGG AGGATCTT TAGA
 ||||| ||||| |||||
 AAATTTT TCCTAGAA ATCT
 A
 GAM1729 DKFZP434J193 5' TCCAGAAGGGGTTACCTTAAA 35167 TAGGA A
 TTTAAGGTGG TCTTCT GA
 ||||| ||||| |||||
 AAATTCCACT GGAAGA CT
 TGG_ C
 GAM1729 KIAA1161 3' TCCAAATATCACCTTAAA 39756
 TTTAAGGTGGTA GGA
 ||||| ||||| |||||
 AAATTCCACTAT CCT
 AAA
 GAM1730 CDH18 5' TTTGATTTTCCAAGTGGT 11380 TACTT
 ACCACTTGGAG ATCAAA
 ||||| ||||| |||||
 TGGTGAACCTT TAGTTT
 T_
 GAM1730 COX15 3' TTGACATACCAAGTGGT 27794 A ACTTA
 ACCACTTGG GT TCAA
 ||||| ||||| |||||
 TGGTGAACC TA AGTT
 A C_
 GAM1730 DPYSL3 3' TGGGGAATCCAAGTGGTA 7074 GTA
 TACCACTTGA CTTA
 ||||| ||||| |||||
 ATGGTGAACCT GGGT
 AAG
 GAM1730 ESR1 3' TGATAAGCACTTTTAAATGG 5601 CTT_ A
 CCA GGAGT CTTATCA
 ||||| ||||| |||||

		GGT TTTCA GAATAGT		
		AAATT C		
GAM1730 KL	3'	TTTGTATAAGTATCTGCGG 11204	G _	
		TTG AG TACTTATCAAAA		
		GGC TC ATGAATAGTTTT		
		G T		
GAM1730 MCL1	3'	TAGGACACCCCAAGTGGT 22490	A A_	
		ACCACTTGG GT CTTA		
		TGGTGAACC CA GGAT		
		C CA		
GAM1730 MGAT1	3'	TTTGTATTTTTCCGAGTGG 8229	TACTT	
		CCACTTGGAG ATCAAAA		
		GGTGAGCCTT TAGTTTT		
		TT__		
GAM1730 MGAT2	3'	TTTGTATATTTGTCCAAACAGG 8235	AC_ G CT	
		CC TTGGA TA TATCAAAA		
		GG AACCT GT ATAGTTTT		
		ACA _ TT		
GAM1730 SET	3'	TTGATTTTTATCTCCAAGTGG 8923	TACTT_	
		CCACTTGGAG ATCAA		
		GGTGAACCTC TAGTT		
		TATTTT		
GAM1730 AMOTL1	3'	TTTGTAGTCATTCCAAGTGGTA 36470	_ TAT	
		TACCACTTGGAGT ACT CAAA		
		ATGGTGAACCTTA TGA GTTT		
		C T__		
GAM1730 FLJ10901	3'	TGATGCACACACCAAGTGGTA 20233	A ACT	
		TACCACTTGG GT TATCA		
		ATGGTGAACC CA GTAGT		
		A CAC		
GAM1730 NFX1	3'	TTTGAATATTCCAAGTAGTA 8328	C CTTA	
		TAC ACTTGGAGTA TCAAA		
		ATG TGAACCTTAT AGTTT		
		A A__		
GAM1730 PRO1914	5'	TTTTGTTACAGGTACTTCAA 15330	AT__	
		TTGGAGTACTT CAAAA		
		AACTTCATGGA GTTTT		
		CATT		
GAM1730 PRO2000	5'	TTTGGAGGTACTCCAGT 15338	T A	
		ACT GGAGTACTT TCAAA		

TGA CCTCATGGA GGTTT
 C _
 GAM1730 LOC149722 5' TTTTGATAAATTGTAAGTG 41046 G AC
 CACTTG AGT TTATCAAAA
 ||||| ||| |||||
 GTGAAT TTA AATAGTTTT
 G _
 GAM1730 LOC152992 3' ATGGGCCCACTCTAAGTGG 39349 A_
 CCACTTGGAGT CTTAT
 ||||| ||| |||||
 GGTGAATCTCA GGGTA
 CC
 GAM1730 LOC157663 3' TTTTGATATGCATCAAGTGG 39640 GA CT
 CCACTTG GTA TATCAAAA
 ||||| ||| |||||
 GGTGAAC CGT ATAGTTTT
 TA _
 GAM1730 LOC245771 5' TGATGCACACACCAAGTGGTA 44638 A ACT
 TACCACTTGG GT TATCA
 ||||| || |||||
 ATGGTGAACC CA GTAGT
 A CAC
 GAM1731 F7 3' AGTAGAGGCATGAACACAC 5604 CATCC _ C
 GTG TTCGT CCTC ACT
 ||| |||| ||| |||
 CAC AAGTA GGAG TGA
 AC_ C A
 GAM1731 F7 3' AGTAGAGGCATGAACACAC 21233 CATCC _ C
 GTG TTCGT CCTC ACT
 ||| |||| ||| |||
 CAC AAGTA GGAG TGA
 AC_ C A
 GAM1731 GPR44 3' GGCAGTGGAGTCCGAAGGGGCAC 11175 AT GTC A
 GTGC CCTTC CTCCACT CC
 |||| |||| ||||| ||
 CACG GGAAG GAGGTGA GG
 _ GCT C
 GAM1731 TPK1 3' GTAGTGGGAAAGATACAT 22780 C C GTCCT
 GTG ATC TTC CCACTAC
 ||| ||| ||| |||||
 TAC TAG AAG GGTGATG
 A A _
 GAM1731 DKFZP564M082 5' GGAGACGAAGGACGCAT 15271 A C
 GTGC TCCTTCGTC TCC
 |||| ||||| |||
 TACG AGGAAGCAG AGG
 C _
 GAM1731 FLJ13265 3' GGCTGAGAACGAAGGATCAC 24312 C C CA
 GTG ATCCTTCGT CTC CT
 ||| ||||| ||| ||

CAC TAGGAAGCA GAG GG
_ A TC
GAM1731 HSU79303 3' GGCAGCGAGTGAAGGACGC 14962 A _ _ _
GC TCCTTCG TC CT CC
|| ||||| || || ||
CG AGGAAGT AG GA GG
C G C C
GAM1731 KIAA0472 3' AGTGGAGGAAAGAATGCAT 35574 C CG
GTGCAT CTT TCCTCCACT
||||| ||| |||||
TACGTA GAA AGGAGGTGA
A _
GAM1731 KIAA1237 3' AGAAGAGGCCTGGATGCAC 39216 TTC T CA
GTGCATCC G CCTC CT
||||| | ||| ||
CACGTAGG C GGAG GA
TC_ AA
GAM1731 PALM 3' GGCAGTGGAGGGAGGGACAC 8439 CA GT A
GTG TCCTTC CCTCCACT CC
||| ||||| ||||| ||
CAC AGGGAG GGAGGTGA GG
_ _ C
GAM1731 LOC152445 5' TGGGGTCAAAGGATGCAC 41512 CGT T
GTGCATCCTT CC CCA
||||||| || |||
CACGTAGGAA GG GGT
ACT _
GAM1731 LOC157247 5' TGGTGGTAAAGGATGTAC 39578 CGT T
GTGCATCCTT CC CCA
||||||| || |||
CATGTAGGAA GG GGT
AT_ T
GAM1731 LOC219333 3' GAGTGGAAAGTGGATGCAC 44934 TTCGTCC A
GTGCATCC TCCACT C
||||| ||||| |
CACGTAGG AGGTGA G
TGA_ C
GAM1731 LOC58489 3' GGTAATGGAATAAAGGATGCAT 35904 CG CC C
GTGCATCCTT T TCCA TACC
||||||| | ||| ||||
TACGTAGGAA A AGGT ATGG
AT_ A
GAM1732 PMX1 3' AGAAGAAATATTTTTCACCT 13776 GATA C
AGG GAAAATAT TCTTCT
||| ||||| |||||
TCC TTTTATA AGAAGA
AC_ A
GAM1732 PMX1 3' AGAAGAAATATTTTTCACCT 22911 GATA C
AGG GAAAATAT TCTTCT
||| ||||| |||||

TCC TTTTATA AGAAGA
 AC__ A
 GAM1732 C9orf14 5' AGAGCATCTCTCCATCCCTCA 41909 A AAT _
 TGAGGGAT GAA AT CTCT
 ||||| || |||||
 ACTCCCTA CTT TA GAGA
 C CTC C
 GAM1732 CDIPT 3' GATATTTTCTACCCTCA 13008 A
 TGAGGG TAGAAAATATC
 ||||| |||||
 ACTCCC ATCTTTTATAG
 -
 GAM1732 DJ328E19.C1.1 3' AGAAGAGATATTTTCGGTT 17682 A
 GAT GAAAATATCTCTTCT
 || |||||
 TTG CTTTTATAGAGAAGA
 G
 GAM1732 KIAA0408 3' AGAACATTTTCTTTCCCTCA 16229 T TATC
 TGAGGGA AGAAAA TCT
 ||||| ||||| |||||
 ACTCCCT TCTTTT AGA
 T TACA
 GAM1732 KIAA1005 3' AAGAAATACTTTTATGTTATCC 35776 ____ A C
 CT AGGGATA GAAA TAT TCTT
 ||||| ||||| |||||
 TCCCTAT TTTT ATA AGAA
 TGTA C A
 GAM1732 KIAA1255 3' AGAAGAGATCCCCCGTCCCCCA 33344 A AGAAAAT
 TG GGGAT ATCTCTTCT
 || ||||| |||||
 AC CCCTG TAGAGAAGA
 C CCCCC__
 GAM1732 NBR2 5' AGAAGAGGTCCCAATCCCCCA 12423 A AGAAAAT
 TG GGGAT ATCTCTTCT
 || ||||| |||||
 AC CCCTA TGGAGAAGA
 C ACCC__
 GAM1732 RAB14 3' AGAAAAGATAATTTATCCTCA 18446 G AAA C
 TGAGG ATAGA TATCT TTCT
 ||||| ||||| ||||| |||||
 ACTCC TATTT ATAGA AAGA
 _ A__ A
 GAM1732 LOC137362 3' AGAAGTACCGACACTCCCTATC 37105 AAAATATCT__
 CTTCA TGAGGGATAG CTTCT
 ||||| |||||
 ACTTCCTATC GAAGA
 CCTCACAGCCAT
 GAM1732 LOC203025 3' AGAAGTACCGACACTCCCTATC 43000 AAAATATCT__
 CTTCA TGAGGGATAG CTTCT
 ||||| |||||

ACTTCCTATC GAAGA
 CCTCACAGCCAT
 GAM1732 LOC90643 3' AGAAGAGGACCTCCTTTCCCCC 31850 A T AAAATA
 A TG GGA AG TCTCTTCT
 || ||| || |||||
 AC CCCT TC GGAGAAGA
 C T CTCCA_

GAM1733 DR1 5' GCTGGGGAGTTTTTA 29857 GTCGTTG
 TAAAAACT CCCCGGT
 ||||| |||||
 ATTTTGA GGGGTCTG

GAM1733 IHPK3 3' CCAGGGGCAATGTTTACA 27656 AACTGT _
 TGTAAG CGTTGCCCC GG
 ||||| ||||| ||
 ACATTT GTAACGGGG CC
 A

GAM1733 LOC123036 5' ACCGGAGTCACAGTTCCCGCA 36716 AAA CGTT C
 TGT AACTGT GC CCGGT
 || ||||| || |||||
 ACG TTGACA TG GGCCA
 CCC C__ A

GAM1733 LOC144962 5' ACCAGGGGGCGGCGCAGCTCCC 37790 AAAAA T _
 ACA TGT CTG CGTTGCCCC GGT
 || || ||||| || |||
 ACA GAC GCGGCGGGG CCA
 CCCTC _ GA

GAM1734 ACADSB 3' TTGAATACTGTTTCTTCAGTCA 7317 C TAAT C
 TGAC GG AACAGTAT CAA
 |||| || ||||| |||
 ACTG CT TTGTCATA GTT
 A TCT_ A

GAM1734 FLJ20331 3' GTTGAATACTGTTCTTTGGCA 19385 A TAAT C
 TG CCGG AACAGTAT CAAC
 || ||| ||||| |||||
 AC GGTT TTGTCATA GTTG
 _ TC_ A

GAM1735 MSTP032 3' AACTTCAATAATGTAATA 24904 _
 TATTACATTGT GAAGTT
 ||||||| |||||
 ATAATGTAATA CTTCAA
 A

GAM1735 SGKL 3' GTTTTATTACAATGTAA 14927 AGT
 TTACATTGTGA TAAAC
 ||||||| |||||
 AATGTAACATT ATTTTG

GAM1735 LOC149401 5' AGCTTCCCTTACAATGTAAT 38736 _
 ATTACATTGT GAAGTT
 ||||||| |||||

			TAATGTAACA	CTTCGA		
			TTCC			
GAM1736	FBXL3A	3'	GAATTTTTTTTAATGTGG	14455	GGCAA	
			CCACA	TAAAAAAATTC		
			GGTGT	ATTTTTTTTAAG		
			A	_____		
GAM1736	GLP1R	3'	TTTTCTTTATTGCTGTG	7829	G	A
			CACAG	CAATAAA AAAA		
			GTGTC	GTTATTT TTTT		
			—	C		
GAM1736	TCF8	3'	TTTTCTTATTGCTGTGGA	25039	G	A
			TCCACAG	CAATAA AAAA		
			AGGTGTC	GTTATT TTTT		
			—	C		
GAM1736	GRSF1	3'	TTTTTTTTTTTGCCTGTG	7881	T	
			CACAGGCAA	AAAAAAAAA		
			GTGTCCGTT	TTTTTTTTT		
			T			
GAM1736	KIAA0416	3'	TTTTTAATTGCCTGTAGA	17840	C	A
			TC	ACAGGCAAT AAAAA		
			AG	TGTCCGTTA TTTTT		
			A	A		
GAM1736	SCDGF-B	3'	ATTTTTTCTTATTGCCTTG	24878	C	—
			CA	AGGCAATAA AAAAAAT		
			GT	TCCGTTATT TTTTTTA		
			—	C		
GAM1736	SCDGF-B	3'	ATTTTTTCTTATTGCCTTG	26980	C	—
			CA	AGGCAATAA AAAAAAT		
			GT	TCCGTTATT TTTTTTA		
			—	C		
GAM1736	LOC143943	5'	GTTGTTTTTCATTGCCTGCAGA	40383	CA	A A
			TC	CAGGCAAT AAAAA AAT		
			AG	GTCCGTTA TTTT TTG		
			AC	C G		
GAM1737	CNTNAP2	3'	CACATTATACCCTGCTCTTA	15417	ATA	TT
			TAAGAGCAG	GT TGTG		
			ATTCTCGTC	TA ACAC		
			CCA	TT		
GAM1737	FBXL11	3'	ATCGCATGTCCTACAATCTGCT	14678	A	TT__
			CTTA	TAAGAGCAGAT GT TGTGCGAT		

ATTCTCGTCTA CA GTACGCTA
 A TCCT
 GAM1737 PACSIN1 3' CACAACATCTGCTCTT 44314 A TT
 AAGAGCAGAT GT TGTG
 ||||| || |||
 TTCTCGTCTA CA ACAC

 — —
 GAM1737 FLJ11850 3' ATCGCACAGAACACCACCCTC 22947 CAGATA
 GAG GTTTTGTGCGAT
 || |||||
 CTC CAAGACACGCTA
 CCACCA
 GAM1737 KIAA0255 3' CACAAACATTTGCTCTTA 16415 A T
 TAAGAGCAGAT GTTT GTG
 ||||| ||| |||
 ATTCTCGTTTA CAAA CAC

 — —
 GAM1737 RANBP6 5' ATCACATGCAGCTTCTGCTCTT 30884 T T C
 A TAAGAGCAGA AGTT TGTG GAT
 ||||| ||| ||| |||
 ATTCTCGTCT TCGA GTAC CTA
 — C A
 GAM1737 LOC157798 5' ATCTTCATAACTTCCTGCTCTT 41847 AT T TGC
 A TAAGAGCAG AGTT TG GAT
 ||||| ||| || |||
 ATTCTCGTC TCAA AC CTA
 CT T TT_
 GAM1737 LOC221715 3' CACTTTTCCTATCTGTCTTA 45016 G TTTT_
 TAAGA CAGATAG GTG
 |||| ||||| |||
 ATTCT GTCTATC CAC
 — CTTT
 GAM1737 LOC254659 5' TCAGCAGCATCTGCTC 45600 A TTTG _
 GAGCAGAT GT TGC GA
 ||||| || ||| |||
 CTCGTCTA CG ACG CT
 — — A
 GAM1738 ECM2 3' CAGTATATTAAGATTACCTTC 7086 C _
 GGAGGTAATCT AA GTATTG
 ||||| || |||||
 CTTCCATTAGA TT TATGAC
 A A
 GAM1738 EPN2 3' ACTAATATTACCTCC 17344 ATCTCAA
 GGAGGTA GTATTGGT
 ||||| |||||
 CCTCCAT TATAATCA

 — —
 GAM1738 RAB39 3' AATCTTTTTCTTGAAATTACCT 37643 C TATT_
 CC GGAGGTAAT TCAAG GGT
 ||||| ||||| |||

			CCTCCATTA AGTTC	CTAA	
			A	TTTTT	
GAM1738	LOC151473	3'	ATACTTAATTACCTCC	39118	CTC
			GGAGGTAAT AAGTAT		
			CCTCCATTA TTCATA		
			TAA		
GAM1739	ARF4L	3'	CTGCACACTTGGACAGCAGGGT	34603	AT TTA A
	G		CACCCT CT TAAGT TGCAG		
			GTGGGA GA GTTCA ACGTC		
			C_ CAG C		
GAM1739	CPNE3	3'	GCATTAAGATAGGGTG	9993	TATAAGT
			CACCCTATCTT ATGC		
			GTGGGATAGAA TACG		
			T_____		
GAM1739	FLNB	3'	CTGCATTGACAATAAAGATGGG	31143	AAGT_
			CCTATCTTTAT ATGCAG		
			GGGTAGAAATA TACGTC		
			ACAGT		
GAM1739	SMURF1	3'	CTGTTCTACAAAAAGTAGGGTG	44413	T ATAA T_
			CACCCTA CTTT GTA GCAG		
			GTGGGAT GAAA CAT TGTC		
			_ AA_ CT		
GAM1739	FOXJ1	5'	CATACTTATTCGGAGGAGG	7188	A_ TT
			CCT TCT ATAAGTATG		
			GGA AGG TATTCATAC		
			GG CT		
GAM1739	GRO3	3'	CTTGATAAATGACAGGGTG	31334	A _ _
			CACCCT TC TTTAT AAG		
			GTGGGA AG AAATA TTC		
			C T G		
GAM1739	HPCAL4	3'	CATACTTACTCCGGTTGGGTG	18386	T TTTA
			CACCC ATC TAAGTATG		
			GTGGG TGG ATTCATAC		
			T CCTC		
GAM1739	HSPB7	3'	CATACAGAAGCAGGGTG	15779	AT ATAA
			CACCCT CTTT GTATG		
			GTGGGA GAAG CATAC		
			C_ A_		
GAM1739	HSPC144	5'	CATACTGAGATAGGG	15462	TATA
			CCCTATCTT AGTATG		

GGGATAGAG TCATAC

GAM1739 KIAA0433 3' TACTTATAAAAATAGTGTG 17550 C C
CAC CTAT TTTATAAGTA
||| ||| |||||
GTG GATA AAATATTCAT
T A

GAM1739 KIAA1084 3' CTGCATACTTATACCTGGATGG 17137 T__
CTATCT TATAAGTATGCAG
||||| |||||
GGTAGG ATATTCATACGTC
TCC

GAM1739 LOC90750 3' CATACTAGGTTAAAGATAAAGT 31965 CC TA__
G CAC TATCTTTA AGTATG
||| ||||| |||||
GTG ATAGAAAT TCATAC
AA TGGA

GAM1740 CLN5 3' TTTAAGTATTTGATGATC 13233 TG C
GATCAT GAT ACTTAAA
||||| ||| |||||
CTAGTA TTA TGAATTT
GT _

GAM1740 COX11 3' TTTAAGTGAGTATTTGTTCCAA 10597 T TTGGA
TTGGA CA TCACTTAAA
||||| || |||||
AACCT GT AGTGAATTT
T TTATG

GAM1740 SON 3' TTTAAGTGGCTAACATCCAA 29043 CA A
TTGGAT TTGG TCACTTAAA
||||| ||| |||||
AACCTA AATC GGTGAATTT
C_ _

GAM1740 SON 3' TTTAAGTGGCTAACATCCAA 27747 CA A
TTGGAT TTGG TCACTTAAA
||||| ||| |||||
AACCTA AATC GGTGAATTT
C_ _

GAM1740 SON 3' TTTAAGTGGCTAACATCCAA 29047 CA A
TTGGAT TTGG TCACTTAAA
||||| ||| |||||
AACCTA AATC GGTGAATTT
C_ _

GAM1740 TRIM9 3' TAAGTGATGCTATTCCAA 27550 TCAT _
TTGGA TGG ATCACTTA
||||| ||| |||||
AACCT ATC TAGTGAAT
T__ G

GAM1740 XBP1 3' TAAGGAATGATCCAA 11532 TGGA A
TTGGATCAT TC CTTA
||||| || |||

AACCTAGTA AG GAAT

GAM1740 DJ37E16.5 3' AAGTGATAGTGACCCAG 21574 A GG
TTGG TCATT ATCACTT
|||| |||| |||||
GACC AGTGA TAGTGAA
C _

GAM1740 KIAA1456 3' TTTAAGTGACCATCAATTCAA 33266 CAT A
TTGGAT TGG TCACTTAAA
||||| ||| |||||
AACTTA ACC AGTGAATTT
ACT _

GAM1740 TUCAN 3' TTTAAGTGATGACAAGTTCCAA 17321 TCA G_
TTGGA TTG ATCACTTAAA
|||| | |||||
AACCT AAC TAGTGAATTT
TG_ AG

GAM1740 LOC158310 5' TTAAGTGATCCACCCA 41950 ATCAT
TGG TGGATCACTTAA
||| |||||
ACC ACCTAGTGAATT
C_

GAM1741 AGPAT2 3' CCCTTCTGTCACTGGCCTCA 32744 ATATCCC A A
TGAGGTCA CA AAG GG
||||| || |||
ACTCCGGT GT TTC CC
CACT_ C _

GAM1741 ENTPD3 3' TTGAAGAATTGACCTCA 6922 A CC
TGAGGTCAAT TC CAA
||||||| || |||
ACTCCAGTTA AG GTT
_ AA

GAM1741 MAPRE2 3' CTCCTTGTCATTGACCTTA 15548 ATCCC AA
TGAGGTCAAT CAA GAG
||||||| ||| |||
ATTCCAGTTA GTT CTC
CT_ C_

GAM1741 SNTB2 3' CCTCCCTTGATCTGACCTTA 28379 ATATCC AA
TGAGGTCA CCAA GAGG
||||| ||| |||
ATTCCAGT GGTT CTCC
CTA_ CC

GAM1741 ASB13 3' CCTCTTTTACGGACCATCCTCA 24013 TCAATA CC
TGAGG TCC AAAAGAGG
|||| | |||||
ACTCC AGG TTTTCTCC
TACC_ CA

GAM1741 BIRC1 5' GGCCCCGGGTATTGACCCCA 10887 A _____
TG GGTCAATATCC CC
|| ||||| ||

		AC CCAGTTATGGG	GG		
		C	CCCCIII		
GAM1741	CLIPR-59	3'	CCTTTGGGGGACCCCA	17787	A AATAT A A
			TG GGTC CCCCCAA G G		
			AC CCAG GGGGTTT C C		
			C _____ C		
GAM1741	KIAA1084	3'	CCTCTCTCGGCACCAGTTGACC	17135	ATCC_ AAA
	T		AGGTCAAT CC AGAGG		
			TCCAGTTG GG TCTCC		
			ACCAC CTC		
GAM1741	OBTP	3'	TTGAGTGACATTGACCTCA	19082	A CC_
			TGAGGTCAAT TC CAA		
			ACTCCAGTTA AG GTT		
			C TGA		
GAM1741	Rpo1-2	3'	CCTGTCTTGAAGACCCTGACCT	25932	ATA CC AAG
	CA		TGAGGTCA TC CAA AGG		
			ACTCCAGT AG GTT TCC		
			CCC AA CTG		
GAM1741	SPBPBP	5'	CCTCTTTCTCCTTACTGACTTC	13509	A TCCCCA
	A		TGAGGTCA TA AAAGAGG		
			ACTTCAGT AT TTTCTCC		
			C TCCTC_		
GAM1741	TTY9	3'	CCTCCTTTACAATTGATCTCA	25678	ATCCCC A
			TGAGGTCAAT AAA GAGG		
			ACTCTAGTTA TTT CTCC		
			ACA_ C		
GAM1741	LOC145216	3'	CCTCTCCTGCCTTTGACCTC	40505	TATCCC AA
			GAGGTCAA CA AGAGG		
			CTCCAGTT GT TCTCC		
			TCC_ CC		
GAM1741	LOC152457	3'	CCTCTCCCAGACTGTGACCTTA	39279	ATA CCCAAA
			TGAGGTCA TC AGAGG		
			ATTCCAGT AG TCTCC		
			GTC ACCC_		
GAM1741	LOC221421	3'	CTCCTTTGGGGATGGCC	44323	ATA A
			GGTCA TCCCCAAA GAG		
			CCGGT AGGGGTTT CTC		
			_ C		
GAM1742	COX10	5'	CAGCCAGTCCCTTCCGAT	6980	TTT G A
			ATCGGAAGG GA TG CTG		

TAGCCTTCC CT AC GAC
 ____ G C
 GAM1742 FLJ22055 3' TCAATCACTCAGCCCCTCC 24147 A T C
 GGA GG TTGAGTGA TGA
 ||| || ||||| |||
 CCT CC GACTCACT ACT
 C C A
 GAM1742 KIAA0802 3' TCAGTCACCCGGAGACCCGA 31352 AAGG A
 TCGG TTTG GTGACTGA
 ||| ||| |||||
 AGCC AGGC CACTGACT
 CAG_ C
 GAM1742 LOC115574 3' TCAGTCACTCCACGCTCCCC 36367 AA TT_
 GG GGT GAGTGACTGA
 || ||| |||||
 CC TCG CTCACTGACT
 CC CAC
 GAM1742 LOC221968 3' TTCAGTCACTACAGCTCCGA 44471 AG TG
 TCGGA GTT AGTGACTGAA
 |||| ||| |||||
 AGCCT CGA TCACTGACTT
 ____ CA
 GAM1742 LOC256021 3' CAGCTTTCAAATCTTCC 46164 TGA
 GGAAGGTTTGAG CTG
 ||||| |||
 CCTTCTAAACTT GAC
 TC_
 GAM1743 ADAM19 3' GCAAACCCTCAGCAGTCCT 27097 T G AAA
 GGG ATTG CT GGTTCG
 ||| ||| || |||||
 TCC TGAC GA CCAAACG
 _ _ CTC
 GAM1743 NUMA1 3' AACAGTAGCCAAACCCCT 44879 A AAG
 AGGGGT TTGGCTA GTT
 ||||| ||||| |||
 TCCCCA AACCGAT CAA
 _ GA_
 GAM1743 ATIP1 3' GCAAACCTTCTACCTCCT 21861 TAT CTA
 AGGGG TGG AAGGTTTGC
 |||| ||| |||||
 TCCTC ATC TTCCAAACG
 C_ _
 GAM1743 KIAA0295 3' GCACAGCAGCCATACCCCT 33783 T AAAG _
 AGGGGTAT GGCT GTT TGC
 ||||| ||| ||| |||
 TCCCCATA CCGA CGA ACG
 _ _ _ C
 GAM1743 RNF24 3' AGCAAACCTTCCCAGCAGCCCT 14084 A_ CTA
 GGGGT TTGG AAGGTTTGCT
 |||| ||| |||||

TCCCG GACC TTCCAAACGA
 AC C__
 GAM1743 VIT1 5' GCAAACCTAAATACCACC 20766 _ GGCTAA
 GG GGTATT AGGTTTGC
 || ||||| |||||
 CC CCATAA TCCAAACG
 A A____
 GAM1743 LOC118786 5' AGCAAACCCAGAATACTCC 37197 GG AAA
 GGGGTATT CT GGTTTGCT
 ||||| || |||||
 CCTCATAA GA CCAAACGA
 _ C_
 GAM1743 LOC121441 3' CAAACCTTTAGCTCACT 36659 ATT
 GGT GGCTAAAGGTTTG
 || |||||
 TCA TCGATTTCCTAAAC
 C_
 GAM1744 ABCC5 3' GTGTAGCTATATCTATAT 12249 C ATTG
 ATG AGATATAG GCGC
 || ||||| ||
 TAT TCTATATC TGTG
 A GA_
 GAM1744 FLJ21736 3' GCACCAATCCACACTCTGTAT 24460 TATA_ C
 ATGCAGA GATTGG GC
 ||||| ||||| ||
 TATGTCT CTAACC CG
 CACAC A
 GAM1744 GIT2 3' GCACCATGGAGCAGCCTGCATG 29213 ATATAGAT_ C
 TGA TCACATGCAG TGG GC
 ||||| || ||
 AGTGTACGTC ACC CG
 CGACGAGGT A
 GAM1744 KIAA1128 3' GCACCAATCTACAACCTATGT 33968 CAGATA C
 ACATG TAGATTGG GC
 |||| ||||| ||
 TGTAT ATCTAACC CG
 CAAC_ A
 GAM1744 KIAA1384 3' GCATTGTAGTCTACCTGCATGT 32260 ATA ____
 GA TCACATGCAG TAGATTG GC
 ||||| ||||| ||
 AGTGTACGTC ATCTGAT CG
 C_ GTTA
 GAM1744 KIAA1958 3' GCACCTTTCATATCTGCTGT 39831 T A TT C
 ACA GCAGATAT GA GG GC
 || ||||| || ||
 TGT CGTCTATA CT CC CG
 _ _ TT A
 GAM1744 LOC143915 3' GCATCATATTTGCAT 40378 A TG
 ATGCAGATAT GAT GC
 ||||| || ||

TACGTTTATA CTA CG

GAM1744 LOC200558 3' GCATTTATATGTGCAT 42819 G TG
ATGCA ATATAGAT GC
||||| ||||| ||
TACGT TATATTTA CG

GAM1744 LOC202934 3' CAGTGGTATAGTCTGCATATGA 43455 C _ G_
TCA ATGCAGAT ATA ATTG
||| ||||| ||| ||||
AGT TACGTCTG TAT TGAC

GAM1745 PRKCN 3' AGTACTGGATTCCAGCATT 12397 _ ACGA
AATGCTGGAA CCG TACT
||||||| ||| ||||
TTACGACCTT GGT ATGA

GAM1745 KIAA1432 5' AGTGTGCTCCAGCATTA 33147 ACCGACG
TTAATGCTGGA ATACT
||||||| ||||
AATTACGACCT TGTGA

GAM1745 MO25 3' AGTATCACAGCATTA 18414 GAACCGAC
TTAATGCTG GATACT
||||||| ||||
AATTACGAC CTATGA

GAM1746 SNL 3' GACTGGAAGCAGAAAATG 9062 ACA T
TATTTTC GTTT CCAGTC
||||| ||| |||||
GTAAAAG CGAA GGTCAG

GAM1746 TGFBR2 3' ACTGGTAGTGAGAATATCA 9236 AGTTTT
TGATATTTTCAC CCAGT
||||||| ||||
ACTATAAGAGTG GGTC

GAM1746 TPK1 3' GACTGAAAACTGTTGGTTCAT 22778 ATTT _ C
C GAT TCA CAGTTTT CAGTC
||| ||| ||||| |||||
CTA GGT GTCAAAA GTCAG

GAM1746 KIAA0528 3' ACTGGGATAAAAATGTCA 35839 CACAGTT
TGATATTTT TTCCAGT
||||||| |||||
ACTGTAAAA AGGGTCA

GAM1746 KIAA1128 3' AAAACTGCAAGAATATCA 33963 CA
TGATATTTT CAGTTTT
||||||| |||||

ACTATAAGA GTCAAAA
 AC
 GAM1746 ZNF387 3' GACTGGAAAGGAATGGAAAATA 16176 A GT__
 T ATATTTTC CA TTTCCAGTC
 ||||| || |||||
 TATAAAAG GT AAAGGTCAG
 _ AAGG
 GAM1746 LOC197317 5' AACTGTGGGAAAATATCA 43205 _
 TGATATTTTC ACAGTT
 ||||| |||||
 ACTATAAAAG TGTCAA
 GG
 GAM1746 LOC199926 5' ACTGTTTACTAACCTGTGAAAA 43259 A T TC____
 TACCA TG TATTTTCACAG TT CAGT
 || ||||| || |||||
 AC ATAAAAGTGTC AA GTCA
 C C TCATT
 GAM1746 LOC202025 3' GACTGACATTCCTGGAAAATAT 43403 A TTTTC_
 CA TGATATTTTC CAG CAGTC
 ||||| || |||||
 ACTATAAAAG GTC GTCAG
 _ CTTACA
 GAM1746 LOC202316 5' ACTGTTTACTAACCTGTGAAAA 43423 A T TC____
 TACCA TG TATTTTCACAG TT CAGT
 || ||||| || |||||
 AC ATAAAAGTGTC AA GTCA
 C C TCATT
 GAM1746 LOC90494 5' GAGTAACTGCCAAAATATCA 31577 CA _
 TGATATTTT CAGTT TTC
 ||||| |||||
 ACTATAAAA GTCAA GAG
 CC T
 GAM1747 MGC4342 3' CTAAAAATATCTGTGAA 23623 TCTTA
 TTCACGG GTATTTT TAG
 ||||| |||||
 AAGTGTC TATAAAAATC

 GAM1748 FLJ11210 3' ATGGTCTTGGGCAAACATA 29971 T _
 TAT TTTGT GAGACCAT
 || ||||| |||||
 ATA AAACG TTCTGGTA
 C GG
 GAM1748 HTCD37 3' CGATGGTCTCCATGTATT 33618 TTT T
 AATAT TG GAGACCATCG
 |||| || |||||
 TTATG AC CTCTGGTAGC
 T__ _
 GAM1749 FLJ13614 3' CTATCATTTTGAATACAGTA 29148 TT__
 TACTGT AGATGATAG
 ||||| |||||

	ATGACA TTTACTATC		
	TAAGT		
GAM1749 FLJ20508 3'	CTATCATCGATACATACTGTT 19517	TAC	TTA
	AACA TGT GATGATAG		
	TTGT ACA CTACTATC		
	CAT TAG		
GAM1749 KIAA1189 3'	CTATTATCACCAAACAATATGT 35650	C	A__
T	AACATA TGTTT GATGATAG		
	TTGTAT ACAA CTATTATC		
	A CCA		
GAM1749 MGC10955 3'	CATCCAGAACACCAGATGTTGT 26397	AC__	A_
A	TACAACAT TGTTT GATG		
	ATGTTGTA ACAAG CTAC		
	GACC AC		
GAM1749 PRO1163 5'	CATCTGGACACCATGTTGTA 20653	AC	
	TACAACAT TGTTTAGATG		
	ATGTTGTA ACAGGTCTAC		
	CC		
GAM1749 LOC118706 5'	TCAAACAGATGTTGTA 36596	A	A
	TACAACAT CTGTTT GA		
	ATGTTGTA GACAAA CT		
	- -		
GAM1749 LOC143158 5'	TCAAACAGATGTTGTA 37591	A	A
	TACAACAT CTGTTT GA		
	ATGTTGTA GACAAA CT		
	- -		
GAM1749 LOC150862 5'	CTATCATCCAAGCTTTGTG 39016	CT	A
	CATA GTTT GATGATAG		
	GTGT CGAA CTACTATC		
	TT C		
GAM1749 LOC151826 3'	TTTATACAGCATGTTGTA 39167	A	T
	TACAACAT CTGT TAGA		
	ATGTTGTA GACA ATTT		
	C T		
GAM1749 LOC158267 5'	CTATCACCCTGGATGGTAT 39793	A_	
	ATACTGTTTAG TGATAG		
	TATGGTAGGTC ACTATC		
	CC		
GAM1749 LOC220466 5'	TCAAACAGATGTTGTA 36610	A	A
	TACAACAT CTGTTT GA		

ATGTTGTA GACAAA CT

GAM1750 LOC152078 3' GGCCTCAAAAAATATTA 39213 G A
TAATATTTTT TGAG CC
||||||| ||| ||
ATTATAAAAA ACTC GG

— C
GAM1751 LOC152078 3' GGCCTCAAAAAATATTA 39213 G A
TAATATTTTT TGAG CC
||||||| ||| ||
ATTATAAAAA ACTC GG

— C
GAM1752 C11orf23 3' ACATCATAGTTGATAAATTGAT 20298 — CCA
GTTAT ATAACATCGAT TC TATGATGT
||||||| || |||||
TATTGTAGTTA AG ATACTACA
AAT TTG

GAM1752 LOC160646 3' ACATTAATTGGGAATCATATGT 40000 C_ TA
ACAT GATTCCCA TGATGT
||| ||||| |||||
TGTA CTAAGGGT ATTACA
TA TA

GAM1752 LOC201475 5' ACATCATATATTTTGATGTTAT 42576 TTCCC
ATAACATCGA ATATGATGT
||||||| |||||
TATTGTAGTT TATACTACA
TTA_

GAM1753 EFG1 3' TGTCTATCTCAACTCTATT 45397 ATC TC
AATAGAGTT GAT AGACA
||||||| ||| |||||
TTATCTCAA CTA TCTGT
CT_ —

GAM1753 SLC6A3 3' TGTCTGTTGACCAATCTCTATT 6713 TTA_ TT
CA TGAATAGAG TCGA CAGACA
||||||| ||| |||||
ACTTATCTC AGTT GTCTGT
TAACC —

GAM1753 H2AV 3' TGCCTGACAATTAGCTCTATTC 28912 TCGAT A
A TGAATAGAGTTA TCAG CA
||||||| ||| ||
ACTTATCTCGAT AGTC GT
TAAC_ C

GAM1753 HMP19 3' GTCTGAACCGATATTTCT 42273 T A
AGAG TATCG TTCAGAC
||| ||||| |||||
TCTT ATAGC AAGTCTG
T C

GAM1754 CAV1 3' TCGGTGTTTCTGACTCTGA 7489 CA T
TCAGAG AGAAACAC GCA
||||| ||||| |||

			AGTCTC TCTTTGTG CGT		
			AG _		
GAM1754	ICOS	3'	ACTAGGTATTCTTGCTC 14384	AC	GC
			GAGCAAGAA ACT AGT		
			CTCGTTCTT TGG TCA		
			A_ A_		
GAM1754	ITGA11	3'	GCTGCAGCCCCTTGCTCT 14513	AAACA	
			AGAGCAAG CTGCAGT		
			TCTCGTTC GACGTCG		
			CCC__		
GAM1754	MEF2A	3'	TACTGCAGTGACCTGCCCT 12116	A	A AAA
			AG GCA G CACTGCAGTA		
			TC CGT C GTGACGTCAT		
			C _ CA_		
GAM1754	MID1	5'	CGGTGTTTCCGCTCTGA 5955	AA	
			TCAGAGC GAAACACTG		
			AGTCTCG CTTTGTGGC		
			C_		
GAM1754	MUC3B	3'	TACTGCCTGTTTCTTACTTTGA 45257	C	CT
			TCAGAG AAGAAACA GCAGTA		
			AGTTTC TTCTTTGT CGTCAT		
			A C_		
GAM1754	NEU3	3'	TACTGCAGTGGAAGAGCACTG 13457	A	AAGAAA
	A		TCAG GC CACTGCAGTA		
			AGTC CG GTGACGTCAT		
			A AGAAAG		
GAM1754	PLS3	3'	TGTTATTTCTTGCTCTG 11473	CACT	
			CAGAGCAAGAAA GCA		
			GTCTCGTTCTTT TGT		
			AT__		
GAM1754	SPS2	3'	TACTGGCTCTTTCCTGCTCTGG 14555	A	CACT _
			TCAGAGCA GAAA GC AGTA		
			GGTCTCGT CTTT CG TCAT		
			C CT__ G		
GAM1754	TRAP240	3'	ACTGCCTTCTTGCTTT 11604	ACACT	
			AGAGCAAGAA GCAGT		
			TTTCGTTCTT CGTCA		
			C__		
GAM1754	AKAP11	3'	ACTGTATTCCTGCTCTGA 18365	A	ACAC
			TCAGAGCA GAA TGCAGT		

AGTCTCGT CTT ATGTCA
 C _____
 GAM1754 CAP 3' ACTGCTTCTCTGCTCTGA 13056 _ AACT
 TCAGAGCA AGAA GCAGT
 ||||| ||| ||||
 AGTCTCGT TCTT CGTCA
 C _____
 GAM1754 CGI-01 5' ACTGCAGTGTCCCGGAGCCTG 18054 A AAGAA_
 CAG GC AACTGCAGT
 ||| || |||||
 GTC CG TGTGACGTCA
 _ AGGCC
 GAM1754 DKFZP434D1335 3' TACTAGTTCTACTTGCTCTGA 32467 AAAC GC
 TCAGAGCAAG ACT AGTA
 ||||| ||| ||||
 AGTCTCGTTC TGA TCAT
 ATCT _
 GAM1754 FLJ10498 3' GTTTGTGTCCTTGCTCTGA 19887 AA T_
 TCAGAGCAAG ACAC GC
 ||||| ||| ||
 AGTCTCGTTC TGTG TG
 C_ TT
 GAM1754 FLJ10901 3' GCTATGCTTCTGCTCTGA 20231 A A CT
 TCAGAGCA GAA CA GC
 ||||| ||| || ||
 AGTCTCGT CTT GT CG
 _ C AT
 GAM1754 FLJ14547 3' TACTAAGTGGTTTTCTTGCTC 26561 _ GC
 GAGCAAGAAA CACT AGTA
 ||||| ||| ||||
 CTCGTTCTTT GTGA TCAT
 TG A_
 GAM1754 FLJ22693 3' CTGCCTGTTGCTCTGA 22973 AGAA CT
 TCAGAGCA ACA GCAG
 ||||| ||| ||||
 AGTCTCGT TGT CGTC
 _____ C_
 GAM1754 HBP1 3' GCTGCTTTTGCTCTGA 14562 AACACT
 TCAGAGCAAGA GCAGT
 ||||| ||| ||||
 AGTCTCGTTTT CGTCG

 GAM1754 HCA3 5' TGCTGCGGTCCTCTCCGA 28952 A CA AAC
 TC GAG AGA ACTGCAGTA
 || ||| ||| |||||
 AG CTC TCT TGGCGTCGT
 C _ CC_
 GAM1754 HCNGP 3' GCCTGTTTCTTCTCTGA 14930 C CT
 TCAGAG AAGAAACA GC
 ||||| ||||| ||

		AGTCTC TTCTTTGT CG	
		_ C_	
GAM1754	MGC15429	3' GCTTGTTTCCTGCTCTGA 26485	A CT
		TCAGAGCA GAAACA GC	
		AGTCTCGT CTTTGT CG	
		C T_	
GAM1754	NUDT11	3' ACTGACTCTTGCTCTGG 30138	AACACTG
		TCAGAGCAAGA CAGT	
		GGTCTCGTTCT GTCA	
		CA_____	
GAM1754	P5-1	3' ACTGCAGTGGCCACTTCTGA 13493	CAAGAAA
		TCAGAG CACTGCAGT	
		AGTCTT GTGACGTCA	
		CACCG_	
GAM1754	PARVA	3' ACTAAGTGCTCTGCTCTGA 20144	A AA GC
		TCAGAGCA GA CACT AGT	
		AGTCTCGT CT GTGA TCA	
		_ C_ A_	
GAM1754	PPP1R16B	3' CAGGTTATCCCTTGCTCTG 30768	A_ A
		CAGAGCAAG AAC CTG	
		GTCTCGTTC TTG GAC	
		CCTA _	
GAM1754	PRO0245	5' CTGCCATGCCCTGCTCTGA 15377	A AAA CT
		TCAGAGCA G CA GCAG	
		AGTCTCGT C GT CGTC	
		_ CC_ AC	
GAM1754	LOC139174	5' TACTACAGTTCCCATGCTCTGA 37328	AGAAAC C
		TCAGAGCA ACTG AGTA	
		AGTCTCGT TGAC TCAT	
		ACCCT_ A	
GAM1754	LOC148738	3' TACTGCAGATTTACCCTT 29789	CAA CA
		GAG GAAA CTGCAGTA	
		TTC CTTT GACGTCAT	
		CCA A_	
GAM1754	LOC152059	3' ACTGCTTCTCTGCTCTGA 39205	_ AACT
		TCAGAGCA AGAA GCAGT	
		AGTCTCGT TCTT CGTCA	
		C _____	
GAM1754	LOC154881	3' TACTGCATTTCTTCTTGCTCT 39500	ACAC_
	G	CAGAGCAAGAA TGCAGTA	

GTCTCGTTCTT ACGTCAT
 CCTTT
 GAM1754 LOC196759 3' ACTGCAGTTCTCCTCTGA 42291 CA AAC
 TCAGAG AGA ACTGCAGT
 ||||| || |||||
 AGTCTC TCT TGACGTCA
 C_ ____
 GAM1754 LOC220486 5' TACTGCAGTGAATGAGCTTCTG 43616 _ AAGAAA
 A TCAGA GC CACTGCAGTA
 ||||| || |||||
 AGTCT CG GTGACGTCAT
 T AGTAA_
 GAM1754 LOC257273 5' ACTGCAGTTTCTACCTGA 45745 AGCA AC
 TCAG AGAA ACTGCAGT
 ||| ||| |||||
 AGTC TCTT TGACGTCA
 CA_ ____
 GAM1754 LOC92573 5' ACCGCGGACTTGCCCTGA 34592 A AAACA A
 TCAG GCAAG CTGC GT
 ||| |||| ||| ||
 AGTC CGTTC GGCG CA
 C A_ _ C
 GAM1754 LOC96597 3' ACTGCAGTGCAGGCAGTCTGA 33227 _ AAGAAA
 TCAGA GC CACTGCAGT
 ||||| || |||||
 AGTCT CG GTGACGTCA
 GA GAC_ _
 GAM1755 MAOB 3' GTATTGTTACAGCTGAA 30147 C CGTTG
 TTCA GC TGTAACAATAT
 ||||| || |||||
 AAGT CG ACATTGTTATG
 _ _ _
 GAM1756 NESG1 5' CCAGAGACCATCCAGCTCATCA 14733 T _ TTATA
 TGATG AG TGG GTCTCTGG
 ||||| || ||| |||||
 ACTAC TC ACC CAGAGACC
 _ G TAC_ _
 GAM1756 LOC148638 5' CCAATCACTACAACCACTA 38569 A CTC
 TAGTGGTT TAGT TGG
 ||||| |||| |||
 ATCACCAA ATCA ACC
 C CTA
 GAM1756 LOC152359 3' CCAGAGAGCCACCACTACA 41492 TATAG
 TGTAGTGGT TCTCTGG
 ||||| |||||
 ACATCACCA AGAGACC
 CACCG
 GAM1757 MEIS2 3' AAAGAATGACTGTTTTGGTT 21344 TGTTGC A
 GACC ACA TCATTCTTT
 ||| ||| |||||

TTGG TGT AGTAAGAAA
 TTT___ C
 GAM1757 BS69 5' AGAAGTAAACAGGTCA 13405 GC AATCA
 TGACCTGTT AC TTCT
 ||||| || |||
 ACTGGACAA TG AAGA
 A_ _____
 GAM1757 CXorf1 3' AATGATTGTGCAAAAAGTCA 11053 CTG
 TGAC TTGCACAATCATT
 ||| |||||
 ACTG AACGTGTTAGTAA
 AAA
 GAM1757 FLJ21791 3' AAAGCCAGGTTACGCAACAGGC 30807 A AC ATT
 A TG CCTGTTGC AATC CTTT
 || ||||| ||| |||
 AC GGACAACG TTGG GAAA
 _ CA ACC
 GAM1757 LANO 3' AAAGAATGATCATCAGTAACA 24804 ACA__
 TGTTGC ATCATTCTTT
 ||||| |||||
 ACAATG TAGTAAGAAA
 ACTAC
 GAM1757 PSMF1 3' AAAGAATGATGGTTCAAGGCCA 13686 A GTT A A
 TG CCT GC CA TCATTCTTT
 || ||| || |||||
 AC GGA TG GT AGTAAGAAA
 C ACT _ _
 GAM1757 LOC115129 3' AAAGAATGATAAAATAGGCCA 36249 A GCACA
 TG CCTGTT ATCATTCTTT
 || ||||| |||||
 AC GGATAA TAGTAAGAAA
 C AA__
 GAM1758 LOC152078 3' GGCCTCAAAAAATATTA 39213 G A
 TAATATTTTT TGAG CC
 ||||| ||| ||
 ATTATAAAAA ACTC GG
 _ C
 GAM1759 ADG-90 3' CCTCCAATGTGGACATTT 26934 _ TAGT
 AAGTG CT GCATTGGAGG
 |||| || |||||
 TTTAC GG TGTAACCTCC
 A _____
 GAM1759 NEU4 5' ACCCCCGTGTCTCAGCAC 28026 T TG T A
 GTGCT AG CAT GG GGT
 |||| || ||| |||
 CACGA TC GTG CC CCA
 C CT C _
 GAM1759 LOC149535 5' ACCTCCGCACCTAAGCACT 38771 _ ATT
 AGTGCTTAG TGC GGAGGT
 ||||| ||| |||||

		TCACGAATC ACG CCTCCA		
		C ____		
GAM1759	LOC200301 5'	ACCTCCAACCCTTAAGCA 42779	TGCA	
		TGCTTAG TTGGAGGT		
		ACGAATT AACCTCCA		
		CCC_		
GAM1760	CRTAC1 3'	CACTTGGCACAAAACCTGGCA 19826	A C	A__
		TGCCA G TTTTGT GAGTG		
		ACGGT C AAAACA TTCAC		
		_C CGG		
GAM1760	DKFZP434J193 3'	ACGGCACCACAGAAGCCTGGCA 35160	A	AGA
		TGCCA GCTTTTGT GTGCTGT		
		ACGGT CGAAGACA CACGGCA		
		C C__		
GAM1760	MTHFD2 3'	ACAGCACTCCAGGCCAGCT 13430	__	TA
		AGCT TTTG GAGTGCTGT		
		TCGA GGAC CTCACGACA		
		CC __		
GAM1760	SMC1L1 3'	ACAGCACCCCTGAGCTGGGCA 35616	A	TTGTAGA
		TGCC AGCTT GTGCTGT		
		ACGG TCGAG CACGACA		
		G TCCC__		
GAM1760	LOC145483 3'	CAGCACTCCAGCCTGGGCA 37881	AA_	TTTGTA
		TGCC GCT GAGTGCTG		
		ACGG CGA CTCACGAC		
		GTC C_____		
GAM1760	LOC158476 5'	AGTTTCAACAAAAGCTTAGCA 41996	C	A T
		TGC AAGCTTTTGT GAG GCT		
		ACG TTCGAAAACA CTT TGA		
		A A _		
GAM1760	LOC161823 3'	CAGCACTCCAGCCTGGGCA 40032	AA_	TTTGTA
		TGCC GCT GAGTGCTG		
		ACGG CGA CTCACGAC		
		GTC C_____		
GAM1760	LOC164295 5'	CAGCACTGGGAACTTAGCA 40140	C C	G TAG
		TGC AAG TTTT AGTGCTG		
		ACG TTC AGGG TCACGAC		
		A A ____		
GAM1760	LOC92661 3'	GGCCTCCACAAAGGCCTGGCA 34725	A	A T
		TGCCA GCTTTTGT GAG GCT		

ACGGT CGGAAACA CTC CGG
C C _

GAM1761 AIM1 3' GGACAATGCTGATGGAAGACCA 44115 CCA GT CA_
TGG CT CATCAGCAT CC
||| || ||||| ||
ACC GA GTAGTCGTA GG
A_ AG ACA

GAM1761 CHST6 3' GAGCGATGCTGGTGGTCA 22247 T A A
TGGCCACTG CATC GC TC
||||| ||| || ||
ACTGGTGGT GTAG CG AG
C _ _

GAM1761 EGFR 3' GGTGCGAATGACAGTAGC 11725 C CA
GC ACTGTCAT GCATC
|| ||||| ||||
CG TGACAGTA CGTGG
A AG

GAM1761 GRB14 5' GAGCAATGCCAGTGGCC 10829 T CA A
GGCCACTG CAT GC TC
||||| ||| || ||
CCGGTGAC GTA CG AG
C A _ _

GAM1761 IRTA2 3' TGATAACTGCACAGTGGC 25300 CAT C_
GCCACTGT CAG ATCA
||||| ||| ||||
CGGTGACA GTC TAGT
C_ AA

GAM1761 PML 3' GGTGATGCTGGCTACAGCC 27078 CAC CA
GGC TGT TCAGCATCACC
||| ||| ||||| |||||
CCG ACA GGTCGTAGTGG
_ TC

GAM1761 PNUTL2 3' GGACAATGCTGGTACGTACCCA 27834 CC T C CA_
TGG AC GT ATCAGCAT CC
||| ||| ||||| ||
ACC TG CA TGGTCGTA GG
CA _ _ ACA

GAM1761 PNUTL2 3' GGACAATGCTGGTACGTACCCA 27838 CC T C CA_
TGG AC GT ATCAGCAT CC
||| ||| ||||| ||
ACC TG CA TGGTCGTA GG
CA _ _ ACA

GAM1761 SPK 5' GAGCTGCGCTGACAGCAGCCA 11235 CA T_ A
TGGC CTGTCA CAGC TC
|||| |||| ||| ||
ACCG GACAGT GTCG AG
AC CGC _

GAM1761 TNF 3' ATGCTGATTTGGTGACCA 43770 C TC
TGG CACTG ATCAGCAT
||| |||| |||||

ACC GTGGT TAGTCGTA
 A T_
 GAM1761 TRIM8 3' TGCCAATGATAGTGACCA 25182 C CA
 TGG CACTGTCAT GCA
 ||| ||||| |||
 ACC GTGATAGTA CGT
 A AC
 GAM1761 TRPM6 5' GATGTCTGTGATGACAGTGGCC 19200 ____
 A TGGCCACTGTCATCA GCATC
 ||||| |||||
 ACCGGTGACAGTAGT TGTA
 GTC
 GAM1761 USP6 5' GGTGTTGATGCCAATAACCA 43811 CCAC T
 TGG TG CATCAGCATC
 ||| || |||||
 ACC AC GTAGTTGTGG
 AATA C
 GAM1761 DKFZP434L0718 3' TGATGCTGAGCGTGAACA 25822 GC T CA
 TG CAC GT TCAGCATCA
 || ||| || |||||
 AC GTG CG AGTCGTAGT
 AA _ _
 GAM1761 FLJ14596 3' TGATGCTGGGTGTGGCC 26572 TGTC
 GGCCAC TCAGCATCA
 ||||| |||||
 CCGGTG GGTCGTAGT
 TG____
 GAM1761 FLJ21276 3' TGACGCTGATGATCACACCA 23905 CCACT A
 TGG GTCATCAGC TCA
 ||| ||||| |||
 ACC TAGTAGTCG AGT
 ACAC_ C
 GAM1761 HSH2 3' GTGACGCTGATGGTTTGGGGC 26654 A _ A
 GCC CTG TCATCAGC TCAC
 ||| ||| ||||| |||||
 CGG GGT GGTCGTAGT AGTG
 _ TT C
 GAM1761 KR18 3' ATGTAGTGACAGTGGCCA 27114 CA
 TGGCCACTGTCAT GCAT
 ||||| ||||| |||
 ACCGGTGACAGTG TGTA
 A_
 GAM1761 MAP2K4 3' GGTGATGCCATTACAGAACCA 8919 CCA C CA
 TGG CTGT AT GCATCACC
 ||| ||| || |||||
 ACC GACA TA CGTAGTGG
 AA_ T C_
 GAM1761 NPD009 3' GTAATCTGTTGACAGTGCCA 45563 C T C C
 TGGC ACTGTCA CAG AT AC
 |||| ||||| ||| |||

		ACCG TGACAGT GTC TA TG		
		— T — A		
GAM1761	TIX1	3' GATGTGGGATGGCAGCAGCCA 30929	CA	A_
		TGGC CTGTCATC GCATC		
		ACCG GACGGTAG TGTAG		
		AC GG		
GAM1761	LOC129198	5' GGTGATGCTGACTCGATGGCC 37464	C	TCA
		GGCCA TG TCAGCATCACC		
		CCGGT GC AGTCGTAGTGG		
		A TC_		
GAM1761	LOC143310	5' GGGTGATGCTTCCAAGCTGACC 37609	C	_ GTCATC
	A	TGG CA CT AGCATCACCC		
		ACC GT GA TCGTAGTGGG		
		A C ACCT_		
GAM1761	LOC145453	3' GCATGATGACAATGACCA 37837	C C	_
		TGG CA TGTCATCA GC		
		ACC GT ACAGTAGT CG		
		A A A		
GAM1761	LOC150159	3' GATGTGATGACAGTAGC 29181	C	G
		GC ACTGTCATCA CATC		
		CG TGACAGTAGT GTAG		
		A _		
GAM1761	LOC150967	3' GGTAAATGACAGTTGCCA 39037	C	CAGCATC
		TGGC ACTGTCAT ACC		
		ACCG TGACAGTA TGG		
		T AAT_		
GAM1761	LOC152345	3' GGGTGCACCAGATGACAGGACC 39267	CCA	AGCAT
	A	TGG CTGTCATC CACCC		
		ACC GACAGTAG GTGGG		
		AG_ ACCAC		
GAM1761	LOC168576	5' GGCAACGCTGGCTGGTGGCC 40253	TCA	ATCA
		GGCCACTG TCAGC CC		
		CCGGTGGT GGTCG GG		
		C_ CAAC		
GAM1761	LOC200312	3' GGGCTGAGACTACAGTGGCCA 43291	CA_	A
		TGGCCACTGT TCAGC TC		
		ACCGGTGACA AGTCG GG		
		TCAG _		
GAM1761	LOC203350	3' GGACCGTGAATTAACAGTGGCC 43535	CATCAG	CA_
	A	TGGCCACTGT CAT CC		

ACCGGTGACA GTG GG
 ATTA_ CCA
 GAM1761 LOC220776 3' GGGTGATGATAAACTGTGGCCA 33936 T CATCAG
 TGGCCAC GT CATCACCC
 ||||| || |||||
 ACCGGTG CA GTAGTGGG
 T AATA_
 GAM1761 LOC257551 3' ATGCTGATTTGGTGACCA 46644 C TC
 TGG CACTG ATCAGCAT
 || |||| |||||
 ACC GTGGT TAGTCGTA
 A T_
 GAM1761 LOC257601 3' ATGCTGATTTGGTGACCA 46695 C TC
 TGG CACTG ATCAGCAT
 || |||| |||||
 ACC GTGGT TAGTCGTA
 A T_
 GAM1761 LOC91585 5' TGAGAGTCTGAAAGTGGCCA 33077 GTCA _A_
 TGGCCACT TCAG C TCA
 ||||| |||| |||
 ACCGGTGA AGTC G AGT
 A_ T AG
 GAM1761 LOC93624 5' GGGTGATGCTCAGACAGTGTGC 36016 _ ATC
 CA TGGC CACTGTC AGCATCACCC
 ||| ||||| |||||
 ACCG GTGACAG TCGTAGTGGG
 T AC_
 GAM1762 ADRB3 3' GCAAAGAGAGCTCCCCTGGTTC 5460 C ATT A C
 CA TGG AT GG AGC CTCTTTGC
 ||| || |||| |||||
 ACC TG CC TCG GAGAAACG
 T GTC C A
 GAM1762 CNTNAP2 3' GCAAAGAGAACCTATTATTTGC 15419 TAT A CC_
 CA TGGCA TGG AG CTCTTTGC
 |||| |||| |||||
 ACCGT ATT TC GAGAAACG
 TT_ A CAA
 GAM1762 FLJ22746 3' GCAAAGAGGACCTCAGAACCCA 24165 CATA AAGC
 TGG TTGG CCTCTTTGC
 || |||| |||||
 ACC GACT GGAGAAACG
 CAA_ CCA_
 GAM1762 SQV7L 5' GCAAAGAGAACTACCTCATATG 34933 T_ A CC
 C GCATAT GG AG CTCTTTGC
 |||| || |||||
 CGTATA CC TC GAGAAACG
 CT A AA
 GAM1762 ZNF237 3' CAAAGAAGGCTAATGTCA 15505 ATTGGA C
 TGGCAT AGCC TCTTTG
 |||| |||| |||||

		ACTGTA	TCGG AGAAAC		
		A_____	A		
GAM1762	LOC153688	3'	CAAAGAAAACATTCAATATCCA	41653	C AGCCC
			TGG ATATTGGA	TCTTTG	
			ACC TATAACTT	AGAAAC	
			_____	ACAAA	
GAM1762	LOC220846	3'	GCAAAGAGAGCTCCCCTGGTTC	43662	C ATT A C
		CA	TGG AT	GG AGC CTCTTTGC	
			ACC TG	CC TCG GAGAAACG	
			T GTC	C A	
GAM1763	CRHR2	3'	TCCCCTGCCCTACTCATGGAG	7613	CAT AAA
			TTCCATGAGTA	CA GGA	
			GAGGTACTCAT	GT CCT	
			CCC	CC_	
GAM1763	DUSP6	3'	TCCTTTTGCATCTGGAA	32810	T GTACAT
			TTCCA GA	CAAAAGGA	
			AAGGT CT	GTTTTCCT	
			_____	AC_____	
GAM1763	LRP8	3'	CCTTCGTGCCTCATGGAAT	27130	_ ATCAA
			ATTCCATGAG TAC	AAGG	
			TAAGGTACTC GTG	TTCC	
			C	C_____	
GAM1763	LRP8	3'	CCTTCGTGCCTCATGGAAT	11006	_ ATCAA
			ATTCCATGAG TAC	AAGG	
			TAAGGTACTC GTG	TTCC	
			C	C_____	
GAM1763	PTTG1IP	3'	TCCTTCTGCCTCATGGGA	10537	TACAT A
			TTCCATGAG	CA AAGGA	
			AGGGTACTC	GT TTCCT	
			C_____	C	
GAM1763	CHL1	3'	TTCCTATTTTATACTCATGGAA	13398	CATCAAA
			TTCCATGAGTA	AGGAA	
			AAGGTACTCAT	TCCTT	
			ATTTTA_		
GAM1763	DJ167A19.1	3'	TCCTTTTCACCCATGGA	21051	A ACATC
			TCCATG GT	AAAAGGA	
			AGGTAC CA	TTTTCCT	
			C	C_____	
GAM1763	FLJ22054	3'	TTCCTTTTAGTATTCATG	45318	ATC
			CATGAGTAC	AAAAGGAA	

GTACTTATG TTTTCCTT
 A__
 GAM1763 GFR 3' TCCTTGCCCACACTATGGAAT 14643 G ACATCAA
 ATTCCAT AGT AAGGA
 ||||| ||| |||||
 TAAGGTA TCA TTCCT
 _ CACCCG_
 GAM1763 HDAC11 3' TCCCCTTGGTCATGGGAT 24218 GTACA AA
 ATTCCATGA TCAA GGA
 ||||| ||| |||
 TAGGGTACT GGTT CCT
 _____ CC
 GAM1763 KIAA0415 3' CCTTTTGATGCCCTTGAAT 44475 CAT TA
 ATTC GAG CATCAAAAGG
 ||| ||| |||||
 TAAG TTC GTAGTTTTCC
 ____ CC
 GAM1763 KIAA0978 3' TCCTTTTGACGTACTTTTG 34888 T A
 CA GAGTAC TCAAAAGGA
 || ||||| |||||
 GT TTCATG AGTTTTCT
 T C
 GAM1763 KIAA1042 3' TTCCTTTTGAGAAGCACTGAA 17354 CA AGTACA
 TTC TG TCAAAAGGAA
 ||| || |||||
 AAG AC AGTTTTCTT
 TC GAAG_
 GAM1763 KIAA1045 3' TCCTTCCTAAGTACTCATCAA 35201 CC ATCAA
 T ATT ATGAGTAC AAGGA
 ||| ||||| |||||
 TAA TACTCATG TTCCT
 AC AATCC
 GAM1763 MGC12760 3' TCCTTTTGTGCCTCGGAA 26451 AT TA T
 TTCC GAG CA CAAAAGGA
 ||| ||| || |||||
 AAGG CTC GT GTTTTCCT
 ____ C_ _
 GAM1763 PRO0800 3' TTCCTCTGTTAATTCATGGAAT 20672 ACAT AA
 ATTCCATGAGT CA AGGAA
 ||||| || |||||
 TAAGGTACTTA GT TCCTT
 ATT_ C_
 GAM1763 SQV7L 5' TTCCTTTTGATGGCTGCAT 34934 _ A
 ATG AGT CATCAAAAGGAA
 ||| ||| |||||
 TAC TCG GTAGTTTTCTT
 G _
 GAM1763 LOC170082 3' TTCCTTAAAAAACTCATGGAAT 40171 ACATCAA
 ATTCCATGAGT AAGGAA
 ||||| |||||

			TAAGGTA	CTCA		TTCCTT	
			AAAAA	___			
GAM1763	LOC221687	3'	TCCTTTCG	TATTCATGGA	44308		ATCA
			TCCATGAG	TAC AAAGGA			
			AGGTACTT	TATG TTCCT			
			C	___			
GAM1763	LOC255862	3'	TTCCTTTT	GGTCTTCATGGA	45343		TAC
			TCCATGAG	ATCAAAAGGAA			
			AGGTACTT	TGGTTTTCCTT			
			C	___			
GAM1764	EGFL5	3'	ACCACTGAA	ATCATTCTA	41877	C	ACAA
			TAG AATGAT	TCAGTGGT			
			ATC T	TACTA AGTCACCA			
			-	A	___		
GAM1764	PCDHB16	5'	TACCACTG	ATTGCAATTTTGC	21948		TGATA
			GCAA	CAATCAGTGGTA			
			CGTT	GTTAGTCACCAT			
			TTAAC				
GAM1764	TRIM14	3'	TACTGCTG	TATCATGC	16669	A	AT
			GCA TGATA	CA CAGTG			
			CGT ACTATGT	GTCAT			
			-	C	___		
GAM1764	CCNE2	3'	ACCACTAAT	TGTGTACAT	11048	-	C
			ATG ATACA	AT AGTGGT			
			TAC TGTGT	TTCACCA			
			A	A			
GAM1764	CCNE2	3'	ACCACTAAT	TGTGTACAT	27709	-	C
			ATG ATACA	AT AGTGGT			
			TAC TGTGT	TTCACCA			
			A	A			
GAM1764	DAPK2	3'	TACCACAGA	ATATCACTGT	15638	A	CAA A
			GCA TGATA	TC GTGGTA			
			TGT ACTAT	AG CACCAT			
			C	A	___	A	
GAM1764	DKFZP566F2124	3'	TATTGCATT	TATCATTGC	17889	C	-
			GCAATGATA	AAT CAGTG			
			CGTTACTAT	TTA GTTAT			
			A	C			
GAM1764	EVI5	3'	TACCACTG	ATTACCATTGC	12214	A	C
			GCAATG	TA AATCAGTGGTA			

			CGTTAC AT TTAGTCACCAT		
			C _		
GAM1764 KIAA0368	3'	TACCACTCCAAGTAAATCATTG	32489	___	AATC
		C	GCAATGA TAC AGTGGTA		
			CGTTACT ATG TCACCAT		
			AA AACC		
GAM1764 KIAA1508	3'	TACCAGATTCGTGTCACTGC	30996	A _	AG
			GCA TGATAC AATC TGGTA		
			CGT ACTGTG TTAG ACCAT		
			C C _		
GAM1764 KIAA1535	3'	TGCCACTGCCATCACTGC	38768	A	ACAAT
			GCA TGAT CAGTGGTA		
			CGT ACTA GTCACCGT		
			C CC_		
GAM1764 MFN2	3'	TACTCCTGTATCATTGCT	17012		ATC
			AGCAATGATACA AGTG		
			TCGTTACTATGT TCAT		
			CC_		
GAM1764 NR6A1	3'	ACCACCATCATTGTCTA	7230	_	ACAATCA
			TAG CAATGAT GTGGT		
			ATC GTTACTA CACCA		
			T C_		
GAM1764 NR6A1	3'	ACCACCATCATTGTCTA	27178	_	ACAATCA
			TAG CAATGAT GTGGT		
			ATC GTTACTA CACCA		
			T C_		
GAM1764 NR6A1	3'	ACCACCATCATTGTCTA	27184	_	ACAATCA
			TAG CAATGAT GTGGT		
			ATC GTTACTA CACCA		
			T C_		
GAM1764 NUDT11	3'	ACCACTGACTCTTGCT	30137	T	TACAA
			AGCAA GA TCAGTGGT		
			TCGTT CT AGTCACCA		
			_ C_		
GAM1764 NY-REN-60	3'	TACAGGTTACATCATTGC	33319	AC	A
			GCAATGAT AATC GTG		
			CGTTACTA TTGG CAT		
			CA A		
GAM1764 PEG10	3'	TACCACTGAACCCCATTCG	17431		ATACAA
			GCAATG TCAGTGGTA		

			CGTTAC	AGTCACCAT		
			CCCA__			
GAM1764	PELI2	3'	CATCGATCGTATCACTGCT	22228	A	A A
			AGCA TGATAC ATC GTG			
			TCGT ACTATG TAG TAC			
			C C C			
GAM1764	PRO2133	3'	CCACTGATCATACCACTGC	20691	A A	CA
			GCA TG TA ATCAGTGG			
			CGT AC AT TAGTCACC			
			C C AC			
GAM1764	SULT1C2	3'	ATCCTGGTATCATTGC	13352	AAT	T
			GCAATGATAC CAG GGT			
			CGTTACTATG GTC CTA			
			— —			
GAM1764	LOC143879	3'	TACTTTTTATGTATCATTGCTA	37661		ATCAGT
			TAGCAATGATACA GGTA			
			ATCGTTACTATGT TCAT			
			ATTTT_			
GAM1764	LOC154007	3'	CATTTTATAGTATCACTGCTA	39453	A	AATC_
			TAGCA TGATAC AGTG			
			ATCGT ACTATG TTAC			
			C ATATT			
GAM1764	LOC203636	3'	ACCGCATGTCACTGCTA	43076	A	CAATCA
			TAGCA TGATA GTGGT			
			ATCGT ACTGT CGCCA			
			C A_____			
GAM1764	LOC221477	3'	CACTGGTCATGCCATTGC	44252	A	CA
			GCAATG TA ATCAGTG			
			CGTTAC GT TGGTCAC			
			C AC			
GAM1764	LOC51336	5'	CACATTTTGATCATTGCTA	18756	A	TCA
			TAGCAATGAT CAA GTG			
			ATCGTTACTA GTT CAC			
			_ TTA			
GAM1765	CCND1	3'	AAGAAAAAACCACACA	27597	T	CC
			TGT GTGGTTTT TCTT			
			ACA CACCAAAA AGAA			
			_ AA			
GAM1765	LOC157280	5'	CCAATTTAAAGGTGGCCCAACA	36591	T	TT C
			TGTTG GGTT CCT TTAATTGG			

		ACAAC CCGG GGA AATTAACC	
		_ T_ A	
GAM1765	LOC255448 5'	CCAATTTAAAGGTGACCCAACA 45401	T TT C
		TGTTG GGTT CCT TTAATTGG	
		ACAAC CCAG GGA AATTAACC	
		_ T_ A	
GAM1765	LOC92661 3'	CCAACCACAGGTAAACCACAAC 34720	T CTAA
	A	TGTTGTGGTTT CCT TTGG	
		ACAACACCAAA GGA AACC	
		T CACC_	
GAM1766	SRRM1 3'	GAAAGGATCCTTCAGTTACATA 12451	CACAC AGTA
	CA	TGT ACT GATCCTTTC	
		ACA TGA CTAGGAAAG	
		TACAT CTTC	
GAM1766	STK38 5'	AAAAGATATATATGTGTGAC 14133	CTA G C
		GTCACACA GTA ATC TTT	
		CAGTGTGT TAT TAG AAA	
		A_ A A	
GAM1766	ARHU 3'	GAAAGAAGTTTTATGCGTGTGA 22183	ACTA TC_
	CA	TGTCACAC GTAGA CTTTC	
		ACAGTGTG TATTT GAAAG	
		CG_ TGAA	
GAM1766	THEA 3'	GAAGGCTTAGTGTGCAAC 32951	CA TAGAT
		GT CACACTAG CCTTT	
		CA GTGTGATT GGAAG	
		AC C_	
GAM1766	ZNF347 3'	ATGTACTGTGTGTGACA 26318	T G
		TGTCACACAC AGTA AT	
		ACAGTGTGTG TCAT TA	
		_ G	
GAM1766	LOC131873 5'	GAAAGGATTTGAGTACAGGACA 37364	ACAC AG
		TGTC ACT TAGATCCTTTC	
		ACAG TGA GTTTAGGAAAG	
		GACA _	
GAM1766	LOC143465 5'	AAAGGATAGAGTGTGTGCA 40359	T AGTAG
		TG CACACACT ATCCTTT	
		AC GTGTGTGA TAGGAAA	
		_ GA_	
GAM1766	LOC158927 3'	GAAAGGATATAGATGATGACA 42041	_ CA GTAG
		TGTCA CA CTA ATCCTTTC	

		ACAGT GT GAT TAGGAAAG	
		A A_ A__	
GAM1766	LOC221495 5'	AAAGGAGAATGTGTGATA 45054	CTAGTAGA
		TGTCACACA TCCTTT	
		ATAGTGTGT AGGAAA	
		AAG_____	
GAM1766	LOC257319 3'	GAAAAATCATCTAGTGTGTGAC 45832	TA CC
		GTCACACACTAG GAT TTTC	
		CAGTGTGTGATC CTA AAAG	
		TA A_	
GAM1766	LOC51031 3'	GAAAGGAATGAGTGTGTGAC 18153	AGTAGA
		GTCACACACT TCCTTTC	
		CAGTGTGTGA AGGAAAG	
		GTA_____	
GAM1767	CFTR 3'	GGAATTGGAGCTCGTGGA 6102	A CA CC
		TTCCACGA GT TCGA TCC	
		AAGGTGCT CG GGTT AGG	
		_ A_ A_	
GAM1767	EXTL3 5'	GAGATCGTTTTGTGGAATA 7167	TCAT C
		TATTCCACGAAG CGA CTC	
		ATAAGGTGTTTT GCT GAG	
		_____ A	
GAM1767	GNAI3 3'	GGAAATGAGACCTGGTGGAATA 13241	GAA A ACC
		TATTCCAC GTC TCG TCC	
		ATAAGGTG CAG AGT AGG	
		GTC _ AA_	
GAM1767	FNBP3 3'	GAAGTATTGACTTCGTGG 39074	TCG C
		CCACGAAGTCA AC TC	
		GGTGCTTCAGT TG AG	
		TA_ A	
GAM1767	KIAA0781 3'	TTGATGATTTCGTGAAATA 33501	C
		TATT CACGAAGTCATCGA	
		ATAA GTGCTTTAGTAGTT	
		A	
GAM1767	KIAA1715 3'	GGAAACTGAACTCTGTGGAAT 33793	A CA ACC
	A	TATTCCACG AGT TCG TCC	
		ATAAGGTGT TCA AGT AGG	
		C A_ CAA	
GAM1767	PIP3-E 3'	GAAGTGTGCCTCGTGGA 33179	A T CG C
		TTCCACGA G CAT AC TC	

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AAGGTGCT C GTG TG AG
      C _ _ A
GAM1767 SFRS5 5' GGAGGTCGACGACTCCGT 13805 A A
      ACG AGTC TCGACCTCC
      ||| ||| |||||
      TGC TCAG AGCTGGAGG
      C C
GAM1767 LOC160414 5' GGCCATGACTTCGTGGA 42104 CGA
      TCCACGAAGTCAT CC
      ||||| ||
      AGGTGCTTCAGTA GG
      CC_
GAM1767 LOC170217 5' GGAGGTTGAGCTTCCAGAA 40179 CAC CA
      TTC GAAGT TCGACCTCC
      ||| ||| |||||
      AAG CTTCTG AGTTGGAGG
      AC_ _
GAM1767 LOC170218 5' GGAGGTTGAGCTTCCAGAA 40181 CAC CA
      TTC GAAGT TCGACCTCC
      ||| ||| |||||
      AAG CTTCTG AGTTGGAGG
      AC_ _
GAM1767 LOC206887 5' GGAAGTGGCTTCTTGGAA 43125 C CGA
      TTCCA GAAGTCAT CC
      |||| ||||| ||
      AAGGTCTTCGGTG GG
      T AA_
GAM1768 LOC93538 3' AACTACTCAATGAAAACA 35921 CA C
      TGT TCAT GAGTAGTT
      ||| ||| |||||
      ACA AGTA CTCATCAA
      AA A
GAM1769 COL4A5 3' TCTATTATTTTCTACTAAAGA 6110 CC TAGAA
      TCT GGTAGAAG AATAGA
      ||| ||||| |||||
      AGA TCATCTTT TTATCT
      AA TTA_
GAM1769 COL4A5 3' TCTATTATTTTCTACTAAAGA 27213 CC TAGAA
      TCT GGTAGAAG AATAGA
      ||| ||||| |||||
      AGA TCATCTTT TTATCT
      AA TTA_
GAM1769 COL4A5 3' TCTATTATTTTCTACTAAAGA 27216 CC TAGAA
      TCT GGTAGAAG AATAGA
      ||| ||||| |||||
      AGA TCATCTTT TTATCT
      AA TTA_
GAM1769 DAAM2 3' TCTATCTCCCCCGACTTCTACC 44334 C AGAAA_
      AGGGA TCTC GGTAGAAGT ATAGA
      |||| ||||| ||||

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AGGG CCATCTTCA TATCT
 A GCCCCCTC
 GAM1769 SIP 3' TCCATTTCTACTGGAGG 15758 _ A
 TCTCCGGTAG AAGT GA
 ||||| ||| ||
 GGAGGTCATC TTTA CT
 C C
 GAM1769 CDH26 3' TCTACCTTCTACTTCCGAGA 22372 C__ _
 TCTC GGTAGAAG TAGA
 ||| ||||| |||
 AGAG TCATCTTC ATCT
 CCT C
 GAM1769 FLJ12604 5' TCTATTTTCTATGACCAGAGA 32193 C AGAA
 TCTC GGT GTAGAAAATAGA
 ||| ||| |||||
 AGAG CCA TATCTTTTATCT
 A G__
 GAM1769 HIC2 3' TTAACTTTCTACCAGGA 32534 _ _ A
 TCC GGTAGAA GT GAA
 ||| ||||| |||
 AGG CCATCTT CA TTT
 A T A
 GAM1769 KIAA1255 3' TCCATTTTCTATTACCTGGA 33348 _ GAA A
 TCC GGTA GTAGAAAAT GA
 ||| ||| ||||| ||
 AGG CCAT TATCTTTTA CT
 T _ C
 GAM1769 MGC11257 3' TCTATTTTCTACCGGGA 26140 T _
 TC CCGGTAGAA GTAGA
 || ||||| |||||
 AG GGCCATCTT TATCT
 _ TT
 GAM1769 OSBPL3 3' TCTATTTTGTGCTACCAGATGA 17818 _ C AAGTA
 TC TC GGTA GAAAATAGA
 || ||||| |||||
 AG AG CCATC TTTTATCT
 T A G__
 GAM1769 LOC113763 3' TCTATTTCCAGACTACTGGA 28806 _____
 TCCGGTA GAAGTAGA
 ||||| |||||
 AGGTCAT CTTTATCT
 CAGAC
 GAM1769 LOC130595 5' CTATTTTCCACCCTGCAGAG 37300 CG AA A
 CTC GTAG GT GAAAATAG
 ||| ||| || |||||
 GAG CGTC CA CTTTATC
 A_ C_ C
 GAM1769 LOC199796 5' CATTCTCTGCACTGGAGA 36809 AGAA A A
 TCTCCGGT GTAGA AAT G
 ||||| ||||| ||| |


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AGAGGTCA CGTCT TTA C
      C C
GAM1770 ATRX 5' ATTTGATTCCTTGTGCACAT 28682 ACT TG C
      ATGTG G AGGAA CAAAT
      |||| | |||| ||||
      TACAC T TCCTT GTTTA
      G__GT A
GAM1770 C1orf6 3' GGTTCTTCTGTCAATC 21330 G TGT
      GAT TGAC GAGGAACC
      ||| ||| |||||
      CTA ACTG CTTCTTGG
      _ T_
GAM1770 FBLN1 3' TTGGCTCAGAAGTCACCTC 13213 T G_ GAA
      GA GTGACT TGAG CCAA
      || ||||| ||| |||
      CT CACTGA ACTC GGTT
      C AG _
GAM1770 KCNA6 3' TTGGGTCCACAGTCACTCT 8020 T GA A
      AGA GTGACTGT GGA CCAA
      ||| ||||| ||| |||
      TCT CACTGACA CCT GGTT
      _ _ G
GAM1770 SCNN1G 3' TTCATACCACATTACATCT 6705 C AG__
      AGATGTGA TGTG GAA
      ||||| ||| |||
      TCTACACT ACAC CTT
      T CATA
GAM1770 C20orf121 3' TGGTTCTTACACATCT 23637 ACTGTG
      AGATGTG AGGAACCA
      ||||| |||||
      TCTACAC TTCTTGGT
      A__
GAM1770 FKBP9 3' ATTTGATTCCTCATTTGCCACA 45143 ACT_ C
      T ATGTG GTGAGGAA CAAAT
      |||| ||||| ||||
      TACAC TACTCCTT GTTTA
      CGTT A
GAM1770 FLJ10661 3' TTGGTTCCTCACAAAGC 19998 GAC
      GT TGTGAGGAACCAA
      || ||||| ||||
      CG ACACTCCTTGGTT
      AA_
GAM1770 FLJ10661 3' TTGGTTCCTCACAAAGC 19999 GAC
      GT TGTGAGGAACCAA
      || ||||| ||||
      CG ACACTCCTTGGTT
      AA_
GAM1770 FLJ21162 5' TTCCTATCCACAGTCACTTCT 24308 T _
      AGA GTGACTGTG AGGAA
      ||| ||||| |||

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		TCT CACTGACAC TCCTT		
		T CTA		
GAM1770	ICK	5' ATTTGGGAGACAGTCACGTC	18593	GAGGAA
		GATGTGACTGT CCAAAT		
		CTGCACTGACA GGTTTA		
		GAG__		
GAM1770	ICK	5' ATTTGGGAGACAGTCACGTC	17193	GAGGAA
		GATGTGACTGT CCAAAT		
		CTGCACTGACA GGTTTA		
		GAG__		
GAM1770	KIAA0319	3' ATTTGATCCTTATAATCA	16758	C AC
		TGA TGTGAGGA CAAAT		
		ACT ATATTCCT GTTTA		
		A A_		
GAM1770	KIAA0892	3' TCCTTCCACAGCCGCATCT	35173	A _
		AGATGTG CTGTG AGGA		
		TCTACGC GACAC TCCT		
		C CT		
GAM1770	LHFP	3' TTTAGTTCCTCAACATAT	12357	ACTG C
		ATGTG TGAGGAAC AAA		
		TATAC ACTCCTTG TTT		
		A__ A		
GAM1770	MAC30	5' ATTTGGCCCCTCTTCTCACATC	31401	CTGT AA
		GATGTGA GAGG CCAAAT		
		CTACACT CTCC GGTTTA		
		CTT_ CC		
GAM1770	P2RX5	3' ATTTGGTTCCAGCCCACTC	8409	T ACT GA
		GA GTG GT GGAACCAAAT		
		CT CAC CG CCTTG GTTTA		
		_ C_ A_		
GAM1770	LOC149577	3' TCCATATACAGTCACATC	41026	A__
		GATGTGACTGTG GGA		
		CTACACTGACAT CCT		
		ATA		
GAM1770	LOC153196	5' TGGTTCCTACCTTCACATCT	41594	CT G
		AGATGTGA GT AGGAACCA		
		TCTACACT CA TCCTTG GT		
		TC _		
GAM1771	FABP2	3' AGCTCTCTTCCCTGGGGGCAGA	5622	A ____
	TA	TATCTGCC CCCA AGAGGGCT		

			ATAGACGG GGGT TCTCTCGA		
			— CCCT		
GAM1771	LUZP1	3'	GCCTGGGGGCAGATA 27354	A	AGAG
			TATCTGCC CCCA GGC		
			ATAGACGG GGGT CCG		
			— ———		
GAM1771	SIX2	3'	AGCCGGGTAGGGCAGATA 18849	—	AAGAG
			TATCTGCC ACCC GGCT		
			ATAGACGG TGGG CCGA		
			GA ———		
GAM1771	STAM	3'	TCCTCTTGGTGGCAGATA 9541	C	
			TATCTGCCACC AAGAGGG		
			ATAGACGGTGG TTCTCCT		
			—		
GAM1771	FLJ10724	3'	GTTCCCAAGTGGTAGATA 20053	CCAAGA	CT
			TATCTGCCAC GGG AC		
			ATAGATGGTG CCC TG		
			AA—— T—		
GAM1771	FLJ13072	5'	AGTGCTTGGGTGGGAGA 43232	G	AGG
			TCT CCACCCAAG GCT		
			AGA GGTGGGTTC TGA		
			G G—		
GAM1771	GENX-3414	3'	AGTCACTATCTTGGGTAACA 10058	CC	G CT
			TG ACCCAAGA GG ACT		
			AC TGGGTTCT TC TGA		
			AA A AC		
GAM1771	KIAA0430	3'	GGTTCTTTGGGCAACAGA 21150	CCA	A
			TCTG CCCA GAGGGCT		
			AGAC GGGT TTCTTGG		
			AAC —		
GAM1771	KIAA0992	3'	AGCACCGGGTGGCAGATG 18157	AAGA	—
			TATCTGCCACCC GG GCT		
			GTAGACGGTGGG CC CGA		
			—— A		
GAM1771	KIAA1466	3'	AGTAGCCCCCCTGAAGTTAGA 35601	CC CCA	A—
			TCTG AC AG GGGCTACT		
			AGAT TG TC CCCGATGA		
			— AAG CC		
GAM1771	KIAA1500	3'	TAGCTTTGAGTGGCAGA 32069	C	GAG
			TCTGCCAC CAA GGCTA		

		AGACGGTG GTT TCGAT	
		A ____	
GAM1771 KIAA1613	3'	TAGCCTGGTGGCAGATG 32360	CAAGA
		TATCTGCCACC GGGCTA	
		GTAGACGGTGG TCCGAT	

GAM1771 KIAA1977	5'	GTCCAGGGTGGCAGATA 36747	AAGA
		TATCTGCCACCC GGGC	
		ATAGACGGTGGG CCTG	
		A ____	
GAM1771 LAK-4P	5'	AGCCCCCTGGATGGCAG 14131	C A A
		CTGCCA CCA G GGGCT	
		GACGGT GGT C CCCGA	
		A _ C	
GAM1771 MGC35558	3'	AGCAATTTTTTAAAGGGCAGAT 29612	ACCC__ GG
	A	TATCTGCC AAGA GCT	
		ATAGACGG TTTT CGA	
		GAAATT AA	
GAM1771 MKRN1	3'	AGCCTTGTGTGGCAGATA 15112	C AGA
		TATCTGCCAC CA GGGCT	
		ATAGACGGTG GT TCCGA	
		T ____	
GAM1771 PACSIN2	3'	AGCCTCAGGTGGCAGATG 14095	CAA G
		TATCTGCCACC GAGG CT	
		GTAGACGGTGG CTCC GA	
		A__ _	
GAM1771 RRP4	3'	AGCCTGGGTGGCAGATG 15560	AGAG
		TATCTGCCACCCA GGCT	
		GTAGACGGTGGGT CCGA	

GAM1771 SIMRP7	3'	AGTAACCCTGGACAGAGTGGCA 44368	____ AGA C
	GG	TCTGCCAC CCA GGG TACT	
		GGACGGTG GGT CCC ATGA	
		AGACA ____ A	
GAM1771 LOC145783	3'	AGATTTTCTTGAATGGCAG 37976	CC _
		CTGCCA CAAGAGGG CT	
		GACGGT GTTCTTTT GA	
		AA A	
GAM1771 LOC220514	3'	AGCCTCAGGTGGCAGATG 30320	CAA G
		TATCTGCCACC GAGG CT	

		GTAGACGGTGG CTCC GA		
		A__ _		
GAM1771	LOC220930	3' AGTCCTTAGGAACAGATA 44732	CCA CAA	
		TATCTG CC GAGGGCT		
		ATAGAC GG TTCCTGA		
		AA_ A__		
GAM1772	MHC2TA	3' AAACAGCTAATGGGACACTAA 5775	_ ACATTA C	
		TTAG GT CA TAGCTGTTT		
		AATC CA GT ATCGACAAA		
		A GG__ A		
GAM1772	ARHGEF3	3' AACAGCTAAGTACCTAG 21208	ATTACAC	
		TTAGGTAC TAGCTGTT		
		GATCCATG ATCGACAA		
		A_____		
GAM1772	SEMA3C	3' AAACAGATATTGTACCATGTAC 13071	__ C G	
	CTAA	TTAGGTACAT TACA TA CTGTTT		
		AATCCATGTA ATGT AT GACAAA		
		CC T A		
GAM1773	PAX4	3' TGCATATGTATTTTGTATTTGC 12865	CCTA_	
		GCGAATACAAAA GTGCA		
		CGTTTATGTTTT TACGT		
		ATGTA		
GAM1773	ABCA5	5' TGCACTAGGCTTTTGTACTGT 20746	AAT _	
		GCG ACAAAA CCTAGTGCA		
		TGT TGTTTT GGATCACGT		
		CAT C		
GAM1773	PSMD12	3' CACTAGGCTCTTTGTGTA 8680	TACAAAA	
		TACGCGAA CCTAGTG		
		ATGTGTTT GGATCAC		
		CTC_____		
GAM1773	TAF2	3' TGCACCATTTTTGTATTAACGT 9161	CG CCTA	
	A	TACG AATACAAAA GTGCA		
		ATGC TTATGTTTT CACGT		
		AA TAC_		
GAM1774	MLLT3	3' GAACAGCTCATCTTCAAAGT 10867	CA _ G	
		ACT TGAAGATG GTTG TC		
		TGA ACTTCTAC CGAC AG		
		A_ T A		
GAM1774	PDE4D	3' AAGGTGGACATCTTCACGA 36425	A G G T	
		TC TGAAGATG TT G CCTT		

AG ACTTCTAC AG T GGAA
 C _ G _
 GAM1774 PTHLH 3' GCTAGTGACCATCTTCAT 8685 ____
 ATGAAGATGGTT GGT
 ||||| ||
 TACTTCTACCAG TCG
 TGA
 GAM1774 ARHGEF3 3' GACCAACTCATGAAGT 21210 _ AGATG
 ACT CATGA GTTGGTC
 ||| ||| |||||
 TGA GTACT CAACCAG
 A ____
 GAM1774 DKFZP434I0714 5' AAGGACCAGAATCCTCAGA 41528 A A GG
 TC TGA GAT TTGGTCCTT
 || ||| |||||
 AG ACT CTA GACCAGGAA
 _ C A_
 GAM1774 DKFZP586F1524 3' AAGGCTGGCCTCCTCATAAG 17851 C A T TG T
 CT ATGA GA GGT G CCTT
 || ||| || ||| | |||
 GA TACT CT CCG C GGAA
 A C _ GT _
 GAM1774 FLJ10815 5' GCTCCATTTTCATGAGT 20173 A TT
 ACTCATGA GATGG GGT
 ||||| |||| ||
 TGAGTACT TTACC TCG
 _ _
 GAM1774 FLJ22415 3' AAGAGCTTTCCATCTTCATGA 43983 TT TC
 TCATGAAGATGG GG CTT
 ||||| || |||
 AGTACTTCTACC TC GAA
 TT GA
 GAM1774 KIAA0820 3' AAGGACCAGATGATTCACATG 34214 AA G _
 CATG GAT GT TGGTCCTT
 ||| ||| || |||||
 GTAC TTA TA ACCAGGAA
 AC G G
 GAM1774 KIAA1863 3' AAGGACCAACCAGTTTGGGT 32379 TGAAGA
 ACTCA TGGTTGGTCCTT
 |||| |||||
 TGGGT ACCAACCAGGAA
 TTG____
 GAM1774 LIG-1 3' GCTAACCATCTTATGAGT 31952 A
 ACTCATGA GATGGTTGGT
 ||||| |||||
 TGAGTATT CTACCAATCG
 _
 GAM1774 NCE2 3' GAAGACCATCTTCATGA 27971 GG
 TCATGAAGATGGTT TC
 ||||| ||

AGTACTTCTACCAG AG
 A_
 GAM1774 PCDH19 3' AAGGATGTCATTTTCATGAGT 31857 A TTG
 ACTCATGA GATGG GTCCTT
 ||||| ||| |||||
 TGAGTACT TTACT TAGGAA
 _ G_
 GAM1774 RNAC 3' AAGGACTCACCTCCTTGAG 12343 TGAA T T
 CTCA GA GGT GGTCTT
 ||| || ||| |||||
 GAGT CT CCA TCAGGAA
 TC_ _ C
 GAM1774 STRIN 3' ACTTCATCATCTTGATAAGT 18394 C G T_
 ACT AT AAGATGGT GGT
 ||| || ||||| |||
 TGA TA TTCTACTA TCA
 A G CT
 GAM1774 TREX1 5' AAGGACAAGCTCTTCATGA 27343 TG G
 TCATGAAGA GTT GTCCTT
 ||||| ||| |||||
 AGTACTTCT CGA CAGGAA
 _ A
 GAM1774 TREX1 5' AAGGACAAGCTCTTCATGA 27334 TG G
 TCATGAAGA GTT GTCCTT
 ||||| ||| |||||
 AGTACTTCT CGA CAGGAA
 _ A
 GAM1774 ZNF282 3' AAGGGTAACACCTTCATGA 42991 A GTTG
 TCATGAAG TG GTCCTT
 ||||| || |||||
 AGTACTTC AC TGGGAA
 C AA_
 GAM1774 LOC124602 5' AAGGACCAGCAACTCATGG 36755 A ATG
 TCATGA G GTTGGTCCTT
 ||||| | |||||
 GGTACT C CGACCAGGAA
 _ AA_
 GAM1774 LOC163397 5' AAGGACCGTAAGCCCCATGAG 42081 AAGAT ____
 CTCATG GGT TGGTCCTT
 ||||| ||| |||||
 GAGTAC CCG GCCAGGAA
 C_ AAT
 GAM1774 LOC203397 5' AAGGACCAGCAACTCATGG 43035 A ATG
 TCATGA G GTTGGTCCTT
 ||||| | |||||
 GGTACT C CGACCAGGAA
 _ AA_
 GAM1774 LOC90499 3' AAGGCTGGCATCTTCGTGAGT 31580 G TG T
 ACTCATGAAGATG T G CCTT
 ||||| ||||| | |||||

			TGAGTGCTTCTAC G C GGAA		
			_ GT _		
GAM1774	LOC91445	3'	GACCACCATCCTCAGAAG 30368	CA A T	
			CT TGA GATGGT GGTC		
			GA ACT CTACCA CCAG		
			AG C _		
GAM1775	ABCD3	3'	GTGGCAGATTTCTTTAGCTGC 8753	CT T	
			GCAGC AAGA AGTCTGCCAC		
			CGTCG TTCT TTAGACGGTG		
			AT _		
GAM1775	ARF3	3'	GTAGTATCCCTGGCTGCTA 7381	TAA GT	
			TAGCAGCC GATA CTGC		
			ATCGTCGG CTAT GATG		
			TCC _		
GAM1775	B3GAT1	3'	GTGGCAAAGGGGTAGGCTCTA 20720	C AGATAGTC	
			TAG AGCCTA TGCCAC		
			ATC TCGGAT ACGGTG		
			_ GGGGAA_		
GAM1775	B3GAT1	3'	GTGGCAAAGGGGTAGGCTCTA 27633	C AGATAGTC	
			TAG AGCCTA TGCCAC		
			ATC TCGGAT ACGGTG		
			_ GGGGAA_		
GAM1775	HNRPA1	3'	TGGCAGGGCCTAGCTGCTA 25248	CTAAGA _	
			TAGCAGC TAG TCTGCCA		
			ATCGTCG ATC GGACGGT		
			_ CG		
GAM1775	LZTS1	3'	GTGGCAGATGTCTTCCCTGGGC 22009	_ G	
	TGC		GCAGCCTA AGATA TCTGCCAC		
			CGTCGGGT TCTGT AGACGGTG		
			CCCT _		
GAM1775	PEA15	3'	TGGCAGAATCAAATTGCTA 9852	CCTAA AG	
			TAGCAG GAT TCTGCCA		
			ATCGTT CTA AGACGGT		
			AAA_ _		
GAM1775	PXN	3'	GTAGCTCTCCCTAGGCTGC 8756	A_ T T	
			GCAGCCTA GA AG CTGC		
			CGTCGGAT CT TC GATG		
			CC C _		
GAM1775	TCF7	3'	TGACAGTGCTCTAGGCTGC 9195	A TAGT C	
			GCAGCCTA GA CTG CA		

	CGTCGGAT CT GAC GT		
	_ CGT_ A		
GAM1775 C1QTNF6 3'	GCTTCTATCTTGGCTGC 25658	T	TCT
	GCAGCC AAGATAG GC		
	CGTCGG TTCTATC CG		
	_ TT_		
GAM1775 DKFZp761D0614 3'	GTGGCAGATTGTACACTGCTA 42311		CCTAAG
	TAGCAG ATAGTCTGCCAC		
	ATCGTC TGTTAGACGGTG		
	ACA__		
GAM1775 FLJ10508 3'	CAGACATTATTTTAAGCTGCTA 19891	C	_
	TAGCAGC TAAGATA GTCTG		
	ATCGTCG ATTTTAT CAGAC		
	A TA		
GAM1775 FLJ14297 3'	GTGGCAGATACTTCAGGCT 24393	_	ATA
	AGCCT AAG GTCTGCCAC		
	TCGGA TTC TAGACGGTG		
	C A__		
GAM1775 MGC11115 3'	GCGGCTTGTCGCCAGGCTGCTG 26096	AA	T
	TAGCAGCCT GATAG CTGC		
	GTCGTCGGA CTGTT GGCG		
	CC C		
GAM1775 RAB22A 5'	GCGGCGTCCCGGCTGCTA 30111	TAA	A T
	TAGCAGCC GAT G CTGC		
	ATCGTCGG CTG C GGCG		
	CC_ _ _		
GAM1775 LOC115110 3'	CAGCCGGTCTCAGGCTGCTG 35506	A	AGT
	TAGCAGCCT AGAT CTG		
	GTCGTCGGA TCTG GAC		
	C GCC		
GAM1775 LOC130162 3'	TGGCAAAGCTTAGGCTTCTA 36985	C	ATAGTC
	TAG AGCCTAAG TGCCA		
	ATC TCGGATTC ACGGT		
	T GAA__		
GAM1775 LOC146375 5'	GCAACAGCTAGGCTGCTG 38140	A	ATA C
	TAGCAGCCTA G GT TGC		
	GTCGTCGGAT C CA ACG		
	_ GA_ _		
GAM1775 LOC151249 3'	TGGCAGGGCCTAGCTGCTA 30163	CTAAGA	_
	TAGCAGC TAG TCTGCCA		

		ATCGTCG	ATC	GGACGGT		
		_____	CG			
GAM1775	LOC153817	3'	TGGCAGGGCCTAGCTGCTA	30599	CTAAGA	___
			TAGCAGC	TAG	TCTGCCA	
			ATCGTCG	ATC	GGACGGT	
			_____	CG		
GAM1775	LOC199858	5'	GCAACAGGTCCAGGCTGCTG	42638	AA	AGTC
			TAGCAGCCT	GAT	TGC	
			GTCGTCGGA	CTG	ACG	
			C_	GACA		
GAM1775	LOC203378	5'	TGGTGTTTTCCCCAGGCTGCTA	43560	AA_	TAGTCT
			TAGCAGCCT	GA	GCCA	
			ATCGTCGGA	CT	TGGT	
			CCC	TTTG_		
GAM1775	LOC220840	3'	TGGCAGGGCCTAGCTGCTA	43659	CTAAGA	___
			TAGCAGC	TAG	TCTGCCA	
			ATCGTCG	ATC	GGACGGT	
			_____	CG		
GAM1775	LOC253943	3'	TGGCAAAGCAACCTTAAGCTCT	45985	C	C ATA C_
	A		TAG	AGC	TAAG	GT TGCCA
			ATC	TCG	ATTC	CG ACGGT
			_	A	CAA	AA
GAM1776	EXTL1	3'	GCACTACCAAGGCCGAC	10753	AT	A
			GTC	GCCTTGGTAG	TGC	
			CAG	CGGAACCATC	ACG	
			C_	_		
GAM1776	MLLT4	3'	CGCTGTTACCAAGAATGACT	35886	GC	AT
			AGTCAT	CTTGGTAG	GCG	
			TCAGTA	GAACCATT	CGC	
			A_	GT		
GAM1776	EREG	3'	GTGGATACCAAGGTACAAC	7156	CA	GA
			AGT	TGCCTTGGTA	TGC	
			TCA	ATGGAACCAT	GTG	
			AC	AG		
GAM1776	KIAA0057	3'	TGTCCCAAGGCATAACT	14627	C	TA
			AGT	ATGCCTTGG	GATG	
			TCA	TACGGAACC	CTGT	
			A	_		
GAM1776	KIAA1500	3'	CGCTTTACAAAGGCATGACT	32064	G	T
			AGTCATGCCTT	GTAGA	GCG	

TCAGTACGGAA CATTTCGC

A _

GAM1776 PRPF8 3' GTGAAGGCCAAGGCTGACT 30686 T AGATG

AGTCA GCCTTGGT CGC

||||| ||||| ||

TCAGT CGGAACCG GTG

_ GAA _

GAM1776 SLC2A12 3' GCCTACCAAGACACTACT 29737 CA C AT

AGT TG CTTGGTAG GC

||| || ||||| ||

TCA AC GAACCATC CG

TC A _

GAM1776 LOC153572 5' GCGCACACCACCGGCATGAC 41640 T_ AGA

GTCATGCC TGGT TGCGC

|||||| ||| ||||

CAGTACGG ACCA ACGCG

CC C _

GAM1777 GLUD1 3' CCCAGAAAAAACCCTTGG 11773 A CC_ CC

CCAGGT GT TTTC GGG

||||| || ||| |||

GGTTCA CA AAAG CCC

C AAA A _

GAM1777 RAD52 3' TCTGGACAAAGACTACCTG 28648 C TC

CAGGTAGTC TT CCGGG

||||||| || ||||

GTCCATCAG AA GGTCT

A CA

GAM1777 RAD52 3' TCTGGACAAAGACTACCTG 28656 C TC

CAGGTAGTC TT CCGGG

||||||| || ||||

GTCCATCAG AA GGTCT

A CA

GAM1777 SLC4A7 3' AACTGAAAACCTACCTGG 9668 CC CCG

CCAGGTAGT TTTC GGTT

||||||| ||| ||||

GGTCCATCA AAAG TCAA

_ _

GAM1777 DKFZP434O047 5' GGAACCCGGAACCTGACCCCC 17867 TA CT C

GG GTC TTCC GGGTTCC

|| ||| ||| |||||

CC CAG AAGG CCAAGG

CC TC _

GAM1777 EPB41L1 3' GGAACCTGAGGAGCCACCTG 34942 A CCTT _

CAGGT GT TCC CGGGTTCC

||||| || ||| |||||

GTCCA CG AGG GTCCAAGG

C _ A

GAM1777 FLJ14126 3' GAACCCAGGAGAGCCACTCTGG 24282 _ AGTC C

CCAG GT CTTTCC GGGTTC

|||| || ||||| |||||

			GGTC CA GAGAGG CCCAAG		
			T CC_ A		
GAM1777	GPR107	3'	GGAACCTTGAAAACCTG 21950	CC	CC
			CAGGTAGT TTTC GGGTTCC		
			GTCCATCA AAAG TCCAAGG		
			_ T_		
GAM1777	HSGP25L2G	3'	GGAGAAAGGACCTCCTGG 31134	TA	_
			CCAGG GTCCTTTC CC		
			GGTCC CAGGAAAG GG		
			TC A		
GAM1777	NMU2R	3'	AACCCAAGACTGCCTG 21384	C	TCCC
			CAGGTAGTC TT GGGTT		
			GTCCGTCAG AA CCCAA		
			- - - - -		
GAM1777	NYD-SP11	5'	GACCCAAAGAACTGCCTG 25691	C	CCC
			CAGGTAGT CTTT GGGTT		
			GTCCGTCA GAAA CCCAG		
			A - - - - -		
GAM1777	SQV7L	5'	CTGGGAGAAGACCACCTG 34932	A	C
			CAGGT GTC TTTCCCGG		
			GTCCA CAG AGAGGGTC		
			C A		
GAM1777	ZER6	3'	AACCCAGAAAGACCTGG 31739	AGTC	CC
			CCAGGT CTTTC GGGTT		
			GGTCCA GAAAG CCCAA		
			- - - - - A_		
GAM1777	LOC158434	3'	GAACCCAGAATAAACCACTGG 41985	GTA	CCT CC
			CCAG GT TTC GGGTTC		
			GGTC CA AAG CCCAAG		
			AC_ AAT A_		
GAM1777	LOC165741	3'	AACCCGGAAGGAAGCT 42189	AG	C
			GGT TCCTTT CCGGGTT		
			TCG AGGAAA GGCCCAA		
			A_ A		
GAM1777	LOC90342	5'	CCCGAAAAAGACTACCTGG 31249	C	CC
			CCAGGTAGTC TTT CGGG		
			GGTCCATCAG AAA GCCC		
			- AA		
GAM1777	LOC92689	3'	AATCTGGAAAAAATTACCTG 34780	CC	C
			CAGGTAGT TTT CCGGGTT		

			GTCCATTA AAA GGTCTAA		
			AA A		
GAM1778	DNAJB1	3'	GCAATACCTCTCGTTCCA 12788	_	C C
			TGGAACG GAGG AT GC		
			ACCTTGC CTCC TA CG		
			T A A		
GAM1778	GPR75	5'	CGATGGCGATGATGCCTCT 13669	___	
			GGAGGCA TCGCCATCG		
			TCTCCGT AGCGGTAGC		
			AGT		
GAM1778	HPS1	3'	CGATGGCACCTCCGTCCCA 5693	A	CATC
			TGG ACGGAGG GCCATCG		
			ACC TGCCTCC CGGTAGC		
			C A___		
GAM1778	HS3ST3A1	5'	GATGTGGCCTCCGTCCA 12676	A	ATCGC
			TGGA CGGAGGC CATC		
			ACCT GCCTCCG GTAG		
			_ GT___		
GAM1778	RALBP1	3'	GGCATGCCTCCCTTCCA 13664	C	C
			TGGAA GGAGGCAT GCC		
			ACCTT CCTCCGTA CGG		
			C _		
GAM1778	TRPV1	3'	ATGGCACATGCTTCCACTCCA 27999	AC	C_
			TGGA GGAGGCAT GCCAT		
			ACCT CCTTCGTA CGGTA		
			CA CA		
GAM1778	TRPV1	3'	ATGGCACATGCTTCCACTCCA 28007	AC	C_
			TGGA GGAGGCAT GCCAT		
			ACCT CCTTCGTA CGGTA		
			CA CA		
GAM1778	TRPV1	3'	ATGGCACATGCTTCCACTCCA 20811	AC	C_
			TGGA GGAGGCAT GCCAT		
			ACCT CCTTCGTA CGGTA		
			CA CA		
GAM1778	TRPV1	3'	ATGGCACATGCTTCCACTCCA 27991	AC	C_
			TGGA GGAGGCAT GCCAT		
			ACCT CCTTCGTA CGGTA		
			CA CA		
GAM1778	FLJ20273	3'	ATGGTTCGTGCCTTCATTCCA 21114	C	C_
			TGGAA GGAGGCAT GCCAT		

		ACCTT CTTCCGTG TGGTA		
		A CT		
GAM1778	LOC219649	3' TGGAGATGCCTCCCTCCA 44669	AC	G
		TGGA GGAGGCATC CCA		
		ACCT CCTCCGTAG GGT		
		C_ A		
GAM1778	LOC91828	5' CGAGCCGCTGCCTCCGCTCC 33408	A	T CCA
		GGA CGGAGGCA CG TCG		
		CCT GCCTCCGT GC AGC		
		C C CG_		
GAM1779	CEACAM6	3' CTAATGCTTTAAGATTTGGTCA 8309		CCCAGTCT
		TGACCGAA GCATTAG		
		ACTGGTTT CGTAATC		
		AGAATTT_		
GAM1779	TRPS1	3' CTAAAGCAGTACTGGACTGGCC 15351	A AAC	_ A
	A	TG CCG CCAGT CTGC TTAG		
		AC GGT GGTCA GACG AATC		
		C CA_ T A		
GAM1779	ARPC5	3' CTAATACTGAGAGATTTGGTCA 12272	CC__	CTGC
		TGACCGAA CAGT ATTAG		
		ACTGGTTT GTCA TAATC		
		AGAGA ____		
GAM1779	FLJ23056	3' GCTGACTAGGTTGGGTCA 23808	G C T	
		TGACC AACC AGTC GC		
		ACTGG TTGG TCAG CG		
		G A T		
GAM1779	LOC51141	3' GCTTTAGCTGGGTTTCAGTCA 34048	C	CT__
		TGAC GAACCCAGT GC		
		ACTG CTTGGGTCG CG		
		A ATTT		
GAM1780	LZTS1	3' CAGGACGAAAAAGAGGCATAC 22005	G C	
		GTATGC TTC TTTTCGTCCTG		
		CATACG GAG AAAAGCAGGAC		
		_ A		
GAM1781	CEP2	5' CCGTAGCCTCACAGCCAG 13650	TGT C	
		CTGGTTGTGAG GC ACGG		
		GACCGACACTC CG TGCC		
		__ A		
GAM1781	CERD4	3' CACACGTGTCACAGCCAG 14344	__	
		CTGGTTGTGA GTGTG		

			GACCGACACT CACAC		
			GTG		
GAM1781	GCK	5'	CCACAGCTCAACACAACCAG 5670	AG T CAC	
			CTGGTTGTG TG GC GG		
			GACCAACAC AC CG CC		
			A_ T ACA		
GAM1781	GRLF1	3'	CGTAGCTGCTCACACCAG 38413	T T C	
			CTGGT GTGAGTG GC ACG		
			GACCA CACTCGT CG TGC		
			_ _ A		
GAM1781	HIVEP3	5'	CCGAGTCCACTCACAGCCAG 23698	TG CA	
			CTGGTTGTGAGTG C CGG		
			GACCGACACTCAC G GCC		
			CT A_		
GAM1781	PTGFR	5'	CCATGGCACACCGAGCGG 6661	G TGA C	
			CTG TTG GTGTGCCA GG		
			GGC AGC CACACGGT CC		
			G _ A		
GAM1781	SCD	5'	CCGCGGCTAGCGCCGACAACCA 11489	GA _ A	
	G		CTGGTTGT GTGT GCC CGG		
			GACCAACA CGCG CGG GCC		
			GC AT C		
GAM1781	TM4SF6	3'	CCATGGCACATGTATACC 9284	T A C	
			GGT GTG GTGTGCCA GG		
			CCA TAT TACACGGT CC		
			_ G A		
GAM1781	13CDNA73	5'	CCGCGCTGACATCACAACC 23321	_ GT CA	
			GGTTGTGA GT GC CGG		
			CCAACACT CA CG GCC		
			A GT C_		
GAM1781	C17orf31	5'	CCGTGGCACACTCCTGTCC 19002	TTGT	
			GG GAGTGTGCCACGG		
			CC CTCACACGGTGCC		
			TGTC		
GAM1781	FLJ13241	3'	CCGCAGCACACTGGCCA 24706	GTG CA	
			TGGTT AGTGTGC CGG		
			ACCGG TCACACG GCC		
			_ AC		
GAM1781	FLJ14743	5'	CCGCGAGTTCAACCGCAACCAG 33762	AG T CA_	
			CTGGTTGTG TG GC CGG		

		GACCAACGC AC TG GCC	
		CA T AGC	
GAM1781	GMPPB	5' CCGCACCGCCTCACAACC 45811	T CCA
		GGTTGTGAG GTG CGG	
		CCAACACTC CGC GCC	
		_ CAC	
GAM1781	KIAA0445	5' CCACAGCCATAGACAACTAG 16146	GA T CAC
		CTGGTTGT GTG GC GG	
		GATCAACA TAC CG CC	
		GA _ ACA	
GAM1781	KIAA0478	3' CCATGGCACACTCAGCAG 16976	_ C
		TTG TGAGTGTGCCA GG	
		GAC ACTCACACGGT CC	
		G A	
GAM1781	KIAA1018	3' CCATGACTACATCACAGCCAG 17356	G C_ C
		CTGGTTGTGA TGTG CA GG	
		GACCGACACT ACAT GT CC	
		_ CA A	
GAM1781	MGC2477	5' CCATGGCCGCCTGCACAGCCAG 23541	A__ T C
		CTGGTTGTG GTG GCCA GG	
		GACCGACAC CGC CGGT CC	
		GTC _ A	
GAM1781	PTPNS1	3' CCGTGATGAGCACAGCCA 28052	AG GC
		TGGTTGTG TGT CACGG	
		ACCGACAC GTA GTGCC	
		GA _	
GAM1781	TIGD5	5' CCTGCGCCACCACAACCAG 26667	A T _ C
		CTGGTTGTG GTG GC CA GG	
		GACCAACAC CAC CG GT CC	
		_ _ C _	
GAM1781	TRIP13	3' CCATGGAGAACACACAACCAG 10435	A GTG C
		CTGGTTGTG GT CCA GG	
		GACCAACAC CA GGT CC	
		A AGA A	
GAM1781	LOC115110	3' CCGTGGAGTAACACAGCCAG 35508	AG TG
		CTGGTTGTG TG CCACGG	
		GACCGACAC AT GGTGCC	
		A_ GA	
GAM1781	LOC149579	5' CCACAGCCATAGACAACTAG 35242	GA T CAC
		CTGGTTGT GTG GC GG	

			GATCAACA TAC CG CC		
			GA _ ACA		
GAM1781	LOC154386	5'	CCGTAATGCTCACAAC 39471	GCC	
			GTTGTGAGTGT ACGG		
			CAAACTCGTA TGCC		
			A__		
GAM1781	LOC256158	5'	CCGTGGCAGAGAGCAACGAG 46624	G	GAGTG
			CT GTTGT TGCCACGG		
			GA CAACG ACGGTGCC		
			G AGAG_		
GAM1782	BRCA1	3'	CGGCACTCCAGCCTGGGTGACA 14164	A G G	A
			TGT CA T CGGGCTGGA TGCCG		
			ACA GT G GTCCGACCT ACGGC		
			_ _ G C		
GAM1782	BRCA1	3'	CGGCACTCCAGCCTGGGTGACA 14201	A G G	A
			TGT CA T CGGGCTGGA TGCCG		
			ACA GT G GTCCGACCT ACGGC		
			_ _ G C		
GAM1782	BRCA1	3'	CGGCACTCCAGCCTGGGTGACA 14189	A G G	A
			TGT CA T CGGGCTGGA TGCCG		
			ACA GT G GTCCGACCT ACGGC		
			_ _ G C		
GAM1782	BRCA1	3'	CGGCACTCCAGCCTGGGTGACA 14209	A G G	A
			TGT CA T CGGGCTGGA TGCCG		
			ACA GT G GTCCGACCT ACGGC		
			_ _ G C		
GAM1782	BRCA1	3'	CGGCACTCCAGCCTGGGTGACA 14221	A G G	A
			TGT CA T CGGGCTGGA TGCCG		
			ACA GT G GTCCGACCT ACGGC		
			_ _ G C		
GAM1782	BRCA1	3'	CGGCACTCCAGCCTGGGTGACA 14195	A G G	A
			TGT CA T CGGGCTGGA TGCCG		
			ACA GT G GTCCGACCT ACGGC		
			_ _ G C		
GAM1782	BRCA1	3'	CGGCACTCCAGCCTGGGTGACA 14170	A G G	A
			TGT CA T CGGGCTGGA TGCCG		
			ACA GT G GTCCGACCT ACGGC		
			_ _ G C		
GAM1782	BRCA1	3'	CGGCACTCCAGCCTGGGTGACA 14182	A G G	A
			TGT CA T CGGGCTGGA TGCCG		

			ACA GT G GTCCGACCT ACGGC			
			— _ G C			
GAM1782	BRCA1	3'	CGGCACTCCAGCCTGGGTGACA 14215	A G G		A
			TGT CA T CGGGCTGGA TGCCG			
			ACA GT G GTCCGACCT ACGGC			
			— _ G C			
GAM1782	BRCA1	3'	CGGCACTCCAGCCTGGGTGACA 14176	A G G		A
			TGT CA T CGGGCTGGA TGCCG			
			ACA GT G GTCCGACCT ACGGC			
			— _ G C			
GAM1782	FOXE1	3'	GCACTCCAGTCCCATCA 10783	A C		A
			C GTG GGGCTGGA TGC			
			A TAC CCTGACCT ACG			
			C _ C			
GAM1782	HSPA5	3'	CGGCACTCCAGCCTGGC 11820	G		A
			GT CGGGCTGGA TGCCG			
			CG GTCCGACCT ACGGC			
			— C			
GAM1782	PTGIS	3'	CGGCACTCCAGCCTGGGC 6669	G		A
			GT CGGGCTGGA TGCCG			
			CG GTCCGACCT ACGGC			
			G C			
GAM1782	FLJ10781	3'	CGGCACTCCAGCCTGGGC 20134	G		A
			GT CGGGCTGGA TGCCG			
			CG GTCCGACCT ACGGC			
			G C			
GAM1782	FLJ14397	3'	GCACTCCAGCCTGGGTGACA 26522	A G G		A
			TGT CA T CGGGCTGGA TGC			
			ACA GT G GTCCGACCT ACG			
			— _ G C			
GAM1782	KIAA1582	5'	GCATTCCAACAGTGACA 32589	A G	CGGGC	
			TGT CA TG TGGAATGC			
			ACA GT AC ACCTTACG			
			_ G A _ _ _			
GAM1782	MGC9564	3'	TTCCAGCCCCAACTGCACA 27961	A	GC	
			TGT CAGT GGGCTGGAA			
			ACA GTCA CCCGACCTT			
			C AA			
GAM1782	SLC26A6	5'	GCAGGAGCAGCCCGCACCGGAC 23217	ACA		GAA_
			TGT GTGCGGGCTG TGC			

			ACA CACGCCCGAC ACG		
			GGC GAGG		
GAM1782	SLC26A6	5'	GCAGGAGCAGCCCGCACCGGAC	28666	ACA GAA_
	A		TGT GTGCGGGCTG TGC		
			ACA CACGCCCGAC ACG		
			GGC GAGG		
GAM1782	SLC26A6	5'	GCAGGAGCAGCCCGCACCGGAC	28612	ACA GAA_
	A		TGT GTGCGGGCTG TGC		
			ACA CACGCCCGAC ACG		
			GGC GAGG		
GAM1782	LOC148479	5'	GCATCCCAGCTCCTGCACT	38541	_ _ A
			AGTGC GG GCTGG ATGC		
			TCACG CC CGACC TACG		
			T T C		
GAM1782	LOC150299	3'	CGGCACTCCAGCCTGGC	41182	G A
			GT CGGGCTGGA TGCCG		
			CG GTCCGACCT ACGGC		
			_ C		
GAM1782	LOC220538	3'	CATGACAACCCCACTGTACA	43626	C C GA
			TGTACAGTG GGG TG ATG		
			ACATGTCAC CCC AC TAC		
			_ A AG		
GAM1783	TM7SF1	3'	ACATTAAAAATGTAGCTGACTT	9286	A AGAA
	A		TAAGT AGCTACATT GATGT		
			ATTCA TCGATGTAA TTACA		
			G AAA_		
GAM1783	ANKT	3'	TTCTAACATTGCTTACTTA	18499	TACA
			TAAGTAAGC TTAGAA		
			ATTCATTCTG AATCTT		
			TTAC		
GAM1783	LOC153077	3'	ACATTTTAAACACGCTTACTTA	41567	TACATTA
			TAAGTAAGC GAAGATGT		
			ATTCATTCTG TTTTACA		
			CACAA_		
GAM1783	LOC91286	5'	ACATCGAATGTAGCTTAC	32620	AGAA
			GTAAGCTACATT GATGT		
			CATTCGATGTAA CTACA		
			G_		
GAM1784	CCRL1	3'	ATGACACAGAACTATATACA	18631	_ A
			TG ATATAGTTCTGT TCAT		

			AC TATATCAAGACA AGTA		
			A C		
GAM1784	OXTR	3'	ATGACACAGTTTTGTATATAGA 6618	A TT A	
	A		TTCTATG TATAG CTGT TCAT		
			AAGATAT ATGTT GACA AGTA		
			_ TT C		
GAM1784	FLJ10702	3'	ATGATACAGAGATGTC 20025	AG	
			GATAT TTCTGTATCAT		
			CTGTA GAGACATAGTA		
			—		
GAM1784	KIAA1013	3'	ATGATACAGAAAGTATC 42856	AG	
			GATAT TTCTGTATCAT		
			CTATG AAGACATAGTA		
			A_		
GAM1784	SOX7	3'	GCTAACTATATCACAGAA 25451	A CT	
			TTCT TGATATAGTT GT		
			AAGA ACTATATCAA CG		
			C T_		
GAM1784	LOC115297	3'	ATGGAACTATACATAGAA 36069	A	
			TTCTATG TATAGTTCTGT		
			AAGATAC ATATCAAGGTA		
			—		
GAM1784	LOC221288	5'	ACAGGACCTACCTCATAGAA 44966	TA _	
			TTCTATGA TAG TTCTGT		
			AAGATACT ATC AGGACA		
			CC C		
GAM1784	LOC90643	3'	ACTGAACTATATCAAGAA 31849	A T	
			TTCT TGATATAGTTC GT		
			AAGA ACTATATCAAG CA		
			_ T		
GAM1785	ACTR2	3'	CTTAATAAAACAAGCAGGTA 12274	—	
			TACTTGCTT TATTAAG		
			ATGGACGAA ATAATTC		
			CAAA		
GAM1785	FLJ20189	3'	AGAGCAAGTAACATATTA 19279	CT	
			TAATA TTACTTGCTTT		
			ATTAT AATGAACGAGA		
			AC		
GAM1785	My015	3'	CTTTAGAAAGCATGTAAAGTA 33107	T ATT	
			TACTTTAC TGCTTT AAG		

		ATGAAATG ACGAAA TTC	
		T GAT	
GAM1786	MGC16175 3'	TCAAGTATATACTCATGTTATT 26513	ATTAT_
		TTG TAAAATAACA TATACTTGA	
		GTTTTATTGT ATATGAACT	
		ACTCAT	
GAM1786	LOC119548 3'	TCAGGTATAATAATCATTGTT 36617	CA
		AATAA ATTATTATACTTGA	
		TTGTT TAATAATATGGACT	
		AC	
GAM1787	BLAME 3'	ATGCAGAAGACTTACCTTA 21304	T
		TAAGGTAAGTTTTCT TAT	
		ATTCCATTTCAGAAGA GTA	
		C	
GAM1787	RBM3 3'	TAAACATAAAAAAATTAGCCT 34895	A C
		AGGT AGTTTT TTTATGTTTA	
		TCCG TTAAAA AAATACAAAT	
		A _	
GAM1787	LOC152002 3'	CATAAGAAACTTATCT 39193	T
		AGGTAAGTTTTCTT ATG	
		TCTATTCAAAGAA TAC	
		_	
GAM1787	LOC92979 5'	AAAGATTTGAAAACCTACC 28763	TTT G
		GGTAAGTTTTTC AT TTT	
		CCATTCAAAAG TA AAA	
		TT_ G	
GAM1788	CSMD1 3'	TTGGTGGGGACCGACAT 36196	A AT
		ATGTC GTT CCTACCAA	
		TACAG CAG GGGTGGTT	
		C _	
GAM1788	PRO2389 5'	TTGGTAGTTGGCATA 31881	TTATC
		TATGTCAG CTACCAA	
		ATACGGTT GATGGTT	

GAM1789	NDP 3'	CGGGCATCATTCTCTAATA 5807	AA A AT
		TATTAGAGAAT GA TG CG	
		ATAATCTCTTA CT AC GC	
		_ _ GG	
GAM1789	DKFZp761F2014 3'	TGCGATCACTGACTTCTCTA 21463	TA_ AA
		TAGAGAA AG TGATCGCA	

	ATCTCTT TC ACTAGCGT		
	CAG _		
GAM1789 FLJ23590 3'	GTCTCTCCCATTCTCTAGTA 23941	AA	AT
	TATTAGAGAAT GA GAT		
	ATGATCTCTTA CT CTG		
	CC CT		
GAM1789 KIAA0016 3'	TGGGACCTCTTATTCTCAAATA 16535	A	ATGA G
	TATT GAGAATAAGA TC CA		
	ATAA CTCTTATTCT AG GT		
	A CC_ G		
GAM1789 LOC145566 5'	TGCAGGTTCTCTCTCATTCTCT 37901	A	AT _ _
A	TAGAGAAT AGA GA TC GCA		
	ATCTCTTA TCT CT GG CGT		
	C CT T A		
GAM1790 PPARGC1 3'	AAAGACTATTAAGAGCAATA 14931	A_	ATAT
	TATT TCTTA ATAGTCTTT		
	ATAA AGAAT TATCAGAAA		
	CG _		
GAM1790 PRO1575 5'	TAAAGACTGCAATTGAAGATAA 15312	AATATA	
	TTATCTT TAGTCTTTA		
	AATAGAA GTCAGAAAT		
	GTTAAC		
GAM1790 LOC90141 3'	TAAAGACTTCTCTAAGATAATG 30881	ATATAT	
	TATTATCTTA AGTCTTTA		
	GTAATAGAAT TCAGAAAT		
	CTCT_		
GAM1791 B3GALT5 5'	AGCCACACTCCTGGCATCC 27026	G	CGGC
	GGA GCT GGAGTGTGGCT		
	CCT CGG CCTCACACCGA		
	A T_		
GAM1791 B3GALT5 5'	AGCCACACTCCTGGCATCC 27036	G	CGGC
	GGA GCT GGAGTGTGGCT		
	CCT CGG CCTCACACCGA		
	A T_		
GAM1791 B3GALT5 5'	AGCCACACTCCTGGCATCC 27031	G	CGGC
	GGA GCT GGAGTGTGGCT		
	CCT CGG CCTCACACCGA		
	A T_		
GAM1791 B3GALT5 5'	AGCCACACTCCTGGCATCC 12698	G	CGGC
	GGA GCT GGAGTGTGGCT		

			CCT CGG CCTCACACCGA		
			A T__		
GAM1791	DNASE1L1	3'	AGCCACACTCGCACCTCCTG 13564	CTCG	G
			CAGGAGG GCG AGTGTGGCT		
			GTCCTCC CGC TCACACCGA		
			A__ _		
GAM1791	GJB3	3'	CCACACTCCCTCCTCT 23437	CTC	C
			GGAGG GG GGAGTGTGG		
			TCTCC TC CCTCACACC		
			__ _		
GAM1791	GRLF1	3'	AGCCACGTCCCAAGCCACCTG 38408	A	CGGC AG
			CAGG GGCT GG TGTGGCT		
			GTCC CCGA CC GCACCGA		
			A A__ CT		
GAM1791	MNT	3'	GCCACTGCCAAGCTTCCTG 21565	C	GAGT
			CAGGAGGCT GGCG GTGGC		
			GTCCTTCGA CCGT CACCG		
			A ____		
GAM1791	MTA1L1	5'	AGCCCTGCCCCGCGAGCCTCC 11136	G	A_ T
			GGAGGCTCG CGG GTG GGCT		
			CCTCCGAGC GCC CGT CCGA		
			_ CC C		
GAM1791	PML	3'	AGCCTCACAGCGAGCCTCCTG 27079	G	GGA T
			CAGGAGGCTCG C GTG GGCT		
			GTCCTCCGAGC G CAC CCGA		
			_ A_ T		
GAM1791	PML	3'	AGCCTCACAGCGAGCCTCCTG 27083	G	GGA T
			CAGGAGGCTCG C GTG GGCT		
			GTCCTCCGAGC G CAC CCGA		
			_ A_ T		
GAM1791	TRAF5	5'	AGCCCGCGCGCCGAGCCCC 10965	A	GA T
			GG GGCTCGGCG GTG GGCT		
			CC CCGAGCCGC CGC CCGA		
			_ G_ _		
GAM1791	C20orf112	3'	GCCACACTCCAAGCACCTG 27931	AG	CGGC
			CAGG GCT GGAGTGTGGC		
			GTCC CGA CCTCACACCG		
			A_ A__		
GAM1791	FLJ12488	3'	AGCCACACTCATCCACATCCTG 25264	GGCTC	CG
			CAGGA GG GAGTGTGGCT		

		GTCCT CC CTCACACCGA	
		ACA__ TA	
GAM1791	FLJ23392 3'	AGCCACCATGCCAGCCTCCT 24159	C GAGT
		AGGAGGCT GGCG GTGGCT	
		TCCTCCGA CCGT CACCGA	
		C AC__	
GAM1791	KIAA0153 3'	ACCTTCACCAGCAAACCTCCTG 17495	__ C C T
		CAGGAG GCT GG GGAG GT	
		GTCCTC CGA CC CTTC CA	
		CAAA _ A _	
GAM1791	KIAA0555 3'	AGCCACTGTGCCCGGCCTCCTG 16678	C G GT
		CAGGAGGCT GGCG AGT GGCT	
		GTCCTCCGG CCGT TCA CCGA	
		C G _	
GAM1791	KIAA1204 5'	ACCCACCGCAGCCCCCTG 34313	A _ C A
		CAGG GGCT CGG GG GT	
		GTCC CCGA GCC CC CA	
		C C A _	
GAM1791	KIAA1755 3'	ACCTCCCCACCAAGCCTCC 30746	C C__ T
		GGAGGCT GG GGAG GT	
		CCTCCGA CC CCTC CA	
		A ACC _	
GAM1791	KIAA1908 5'	CCACAGCGAGCCTCC 36330	G GGAG
		GGAGGCTCG C TGTGG	
		CCTCCGAGC G ACACC	

GAM1791	MYH10 3'	GCCACATCAAGTCTCCT 34264	C GCGGA
		AGGAGGCT G GTGTGGC	
		TCCTCTGA C TACACCG	
		A _____	
GAM1791	TOLLIP 3'	AGCCACACTCAGAGGCCTCACT 21090	_ CGGCG
	G	CAG GAGGCT GAGTGTGGCT	
		GTC CTCCGG CTCACACCGA	
		A AGA__	
GAM1791	LOC143451 3'	GCCACACCTCAGCCTCC 37620	CGGC GA
		GGAGGCT G GTGTGGC	
		CCTCCGA C CACACCG	
		_____ TC	
GAM1791	LOC145125 3'	GCCACACCTCAGCCTCC 37797	CGGC GA
		GGAGGCT G GTGTGGC	

		CCTCCGA C CACACCG		
		____ TC		
GAM1791	LOC147495 5'	CCGCCTCCGCCAGGCCTCCTG 40839	TC	T
		CAGGAGGC GGCGGAG GTGG		
		GTCCTCCG CCGCCTC CGCC		
		GA _		
GAM1791	LOC158158 5'	AGCCAAACTCGCCGGGCCTCC 39733	G	G
		GGAGGCTCGGCG AGT TGGCT		
		CCTCCGGGCCGC TCA ACCGA		
		_ A		
GAM1791	LOC254440 3'	GCCACACCTCAGCCTCC 46374	CGGC	GA
		GGAGGCT G GTGTGGC		
		CCTCCGA C CACACCG		
		____ TC		
GAM1791	LOC256310 5'	AGCTCATGTCCACCGAGCCTCT 46092	C	G _
		GGAGGCTCGG GGA TGTG GCT		
		TCTCCGAGCC CCT GTAC CGA		
		A _ T		
GAM1791	LOC93356 5'	AGCCATGTCTCCAAGCCTCC 35671	C	C G
		GGAGGCT GG GGA TGTGGCT		
		CCTCCGA CC CCT GTACCGA		
		A T _		
GAM1791	LOC93496 3'	AGCCACATTTGCCAGGCCTCC 35865	TC	G
		GGAGGC GGC GAGTGTGGCT		
		CCTCCG CCG TTTACACCGA		
		GA G		
GAM1792	MYH11 3'	CAAACCTTTCCAACCTTCTCACG 8300	TTCTC__	AA
	TCA	TGACGTGG GAAA GTTTG		
		ACTGCACT CTTT CAAAC		
		CTTCAAC C_		
GAM1792	MYH11 3'	CAAACCTTTCCAACCTTCTCACG 23142	TTCTC__	AA
	TCA	TGACGTGG GAAA GTTTG		
		ACTGCACT CTTT CAAAC		
		CTTCAAC C_		
GAM1792	RPE65 3'	AAACTTTTTCTCAAACCA 5870	CTC	
		TGGTT GAAAAAGTTT		
		ACCAA CTTTTTCAAA		
		ACT		
GAM1792	CAMKK2 3'	TTTTCAGAACCACGTCA 13316	C	
		TGACGTGGTTCT GAAAA		

ACTGCACCAAGA CTTTT

GAM1792 FLJ32894 3' CAAACTTCCCCGCCTCCACGT 29485 TTCT AAA
ACGTGG CG AAGTTTG
||||| || |||||
TGCACC GC TTCAAAC
TCC_ CCC

GAM1793 AREG 5' CCTGGGTGCCAGCGCCCA 7376 A A_
TG GGTGCTGGCGC AGG
|| ||||| |||
AC CCGCGACCGTG TCC
C GG

GAM1793 ARHGAP6 5' CGTCCTTCTCCACACCCA 6843 A C CGC
TG GGTG TGG AAGGACG
|| ||| || |||||
AC CCAC ACC TTCCTGC
_ _ TC_

GAM1793 CALM3 3' CGTCCTGGTCCGCCAGCACCTC 11684 CA_
GAGGTGCTGGCG AGGACG
||||||| |||||
CTCCACGACCGC TCCTGC
CTGG

GAM1793 DNAJB9 5' CGTCAGGGTCGCCAGCGCCTCA 14718 _ AAG
TGAGGTGCTGGCG C GACG
||||||| | |||
ACTCCGCGACCGC G CTGC
T GGA

GAM1793 EPHA8 3' CGCCAGGTCCAGCACCCA 21746 A C AA A
TG GGTGCTGG GC GG CG
|| ||||| || |||
AC CCACGACC TG CC GC
_ _ GA _

GAM1793 EVC 3' CGCCTGCACCAACAGCCTCA 15882 GC_ C A A
TGAGGT TGG GCA GG CG
||||| ||| ||| |||
ACTCCG ACC CGT CC GC
ACA A _ _

GAM1793 GNA15 5' CCCTGTTCCCAGCACTCA 30103 G C_ A
TGAG TGCTGG GCA GG
||| ||||| ||| |||
ACTC ACGACC TGT CC
_ CT C

GAM1793 HTR1D 3' CGCCCGCCTCAGCATCCA 6530 A C AA A
TG GGTGCTGG GC GG CG
|| ||||| || |||
AC CTACGACT CG CC GC
C C C_ _

GAM1793 IER3 3' TCCTCCAGCATCTCA 9980 CGCA
TGAGGTGCTGG AGGA
||||||| |||

ACTCTACGACC TCCT

GAM1793 IER3 3' TCCTCCAGCATCTCA 27400 CGCA
TGAGGTGCTGG AGGA
||||||| |||
ACTCTACGACC TCCT

GAM1793 KCNAB2 3' CCTCAGTGCAGGCACCTC 9706 G A_
GAGGTGCT GCGC AGG
||||||| ||| |||
CTCCACGG CGTG TCC
A AC

GAM1793 MUC3B 5' CGTCTGTGGGCACCAGCACTTC 45253 C AA_
A TGAGGTGCTGG GC GGACG
||||||| || |||||
ACTTCACGACC CG TCTGC
A GGTG

GAM1793 MYLK2 3' TCCTGCTAGCACCTC 26966 GCA
GAGGTGCTGGC AGGA
||||||| |||
CTCCACGATCG TCCT

GAM1793 MYOG 3' TCCTTGCGAGCCCCCA 29848 A T GG
TG GG GCT CGCAAGGA
|| ||| |||||
AC CC CGA GCGTTCCT
C C _

GAM1793 NRG1 5' CCGCGCAGCGCGAGCGCCTCA 10834 G AA_
TGAGGTGCT GCGC GG
||||||| ||| ||
ACTCCGCGA CGCG CC
G ACGCG

GAM1793 NRG1 5' CCGCGCAGCGCGAGCGCCTCA 15137 G AA_
TGAGGTGCT GCGC GG
||||||| ||| ||
ACTCCGCGA CGCG CC
G ACGCG

GAM1793 NRG1 5' CCGCGCAGCGCGAGCGCCTCA 15138 G AA_
TGAGGTGCT GCGC GG
||||||| ||| ||
ACTCCGCGA CGCG CC
G ACGCG

GAM1793 NRG1 5' CCGCGCAGCGCGAGCGCCTCA 15141 G AA_
TGAGGTGCT GCGC GG
||||||| ||| ||
ACTCCGCGA CGCG CC
G ACGCG

GAM1793 OLFM1 5' CGCCGGCCGGCCAGCACCCA 15558 A _ AA A
TG GGTGCTGGC GC GG CG
|| ||||| || |||

			AC CCACGACCG CG CC GC		
			GC G_ _		
GAM1793	OLFM1	5'	CGCCGGCCGGCCAGCACCCA 13034	A	___ AA A
			TG GGTGCTGGC GC GG CG		
			AC CCACGACCG CG CC GC		
			GC G_ _		
GAM1793	OLFM1	5'	CGCCGGCCGGCCAGCACCCA 27761	A	___ AA A
			TG GGTGCTGGC GC GG CG		
			AC CCACGACCG CG CC GC		
			GC G_ _		
GAM1793	RUNX1	3'	CGCCGGCCCCAGCACCCA 7497	A	C AA A
			TG GGTGCTGG GC GG CG		
			AC CCACGACC CG CC GC		
			C G_ _		
GAM1793	SCA7	5'	CGTCCTCACCGGGCACCCA 5884	A	CGCA
			TG GGTGCTGG AGGACG		
			AC CCACGGCC TCCTGC		
			CAC_		
GAM1793	SNL	3'	CGTCCCCAACATGCATCTCA 9060		_ GCGCAA
			TGAGGTGC TG GGACG		
			ACTCTACG AC CCTGC		
			T AACC_		
GAM1793	APEG1	3'	CGCCCCTGTCTCAGGCACCTC 35693		_ C A A
			GAGGTGC TGG GCA GG CG		
			CTCCACG ACT TGT CC GC		
			G C C C		
GAM1793	CECR7	5'	TCAGCTGCCACCAGCACTCA 38879	G	C_ AG_
			TGAG TGCTGG GCA GA		
			ACTC ACGACC CGT CT		
			AC CGA		
GAM1793	CPLX1	3'	CGCCCCTGCCAGCACCTC 13449		C A A
			GAGGTGCTGG GCA GG CG		
			CTCCACGACC CGT CC GC		
			C C		
GAM1793	DKFZP434B205	3'	CGTCCTCCAGGCACCTC 37125		_ CGCA
			GAGGTGC TGG AGGACG		
			CTCCACG ACC TCCTGC		
			G _		
GAM1793	DKFZP586J1624	3'	TCCCTGCTTACTTAGACCTCA 17799	G	C_ A
			TGAGGT CTGG GCA GGA		

		ACTCCA GATT CGT CCT		
		_ CATT C		
GAM1793	FLJ10342	5' CGTCCCCGACCCACCCG	19835	A CT _ CAA
		TG GGTG GG CG GGACG		
		GC CCAC CC GC CCTGC		
		_ C_ A C_		
GAM1793	FLJ10759	5' CGTCCCCGCGCCAGCCCTC	20101	T _ AA
		GAGG GCTGG CGC GGACG		
		CTCC CGACC GCG CCTGC		
		_ C CC		
GAM1793	FLJ13052	3' CCTCGTCTGGGCACCTCA	23283	_ CA
		TGAGGTGCT GGCG AGG		
		ACTCCACGG CTGC TCC		
		GT _		
GAM1793	FLJ23511	5' TCCTCTGTCAGCACTTCA	25967	CA
		TGAGGTGCTGGCG AGGA		
		ACTTCACGACTGT TCCT		
		C_		
GAM1793	HSPC154	5' CGTTTTTGCCTAACACCCCA	15463	A C C
		TG GGTG TGG GCAAGGACG		
		AC CCAC ATC CGTTTTTGC		
		C A _		
GAM1793	HSU79274	5' TCCTTGCGCCACGTGCTTC	14959	TG _
		GAGG C TGGCGCAAGGA		
		CTTC G ACCGCGTTCCT		
		GT C		
GAM1793	KIAA0217	3' CGCTGGCCGCCAGCAGCTCA	33280	G CAA A
		TGAG TGCTGGCG GG CG		
		ACTC ACGACCGC TC GC		
		G CGG _		
GAM1793	KIAA0848	3' TCTTTGTGACACTTCA	17214	CTGG
		TGAGGTG CGCAAGGA		
		ACTTCAC GTGTTTCT		
		A_		
GAM1793	KIAA1467	3' TCCCTGAGTGCACCTCA	35457	TG G A
		TGAGGTGC GC CA GGA		
		ACTCCACG TG GT CCT		
		_ A C		
GAM1793	KIAA1582	5' CGCCCCCGCACCAGGCCGGTAC	32587	G _ AA A
	TCA	TGAG TGCTGGC GC GG CG		

			ACTC ATGGCCG	CG	CC	GC	
			— GACCA	CC	C		
GAM1793	KIAA1784	3'	CGTCCTCCTCAGCACTCA	32484	G	CGCA	
			— TGAG	TGCTGG	AGGACG		
			ACTC	ACGACT	TCCTGC		
			— CC	—			
GAM1793	KIAA1908	3'	CCCTGGGTCAGTACCTCA	36333	G	A	
			— TGAGGT	TGCTGGC	CA	GG	
			ACTCCATGACTG	GT	CC		
			G	C			
GAM1793	KLK15	3'	CGTCCCTTGTGACAACACC	28863	C	G	—
			— GGTG	TG	CGCAAGG	ACG	
			CCAC	AC	GTGTTCC	TGC	
			A	A	C		
GAM1793	KLK15	3'	CGTCCCTTGTGACAACACC	23265	C	G	—
			— GGTG	TG	CGCAAGG	ACG	
			CCAC	AC	GTGTTCC	TGC	
			A	A	C		
GAM1793	LYPLA3	3'	CCCTGGCCAGCACCCA	14699	A	G	A
			— TG	GGTGCTGGC	CA	GG	
			AC	CCACGACCG	GT	CC	
			—	—	C		
GAM1793	MIG	3'	TCTTGTCCCAACACCCCA	8248	A	C	C_
			— TG	GGTG	TGG	GCAAGG	
			AC	CCAC	ACC	TGTTCT	
			C	A	CC		
GAM1793	NEU4	5'	CCGTGTCCTCAGCACCCCA	28027	A	_C	A
			— TG	GGTGCTG	G	GCA	GG
			AC	CCACGAC	C	TGT	CC
			C	T	C	G	
GAM1793	PCANAP7	5'	CGCCCAGTGAGCCAGCCCCCA	44837	A	T	G A_ A
			— TG	GG	GCTGGC	CA	GG
			AC	CC	CGACCG	GT	CC
			C	_	A	GA	C
GAM1793	SAST	5'	TCCTGACCAGCACTTCA	31543	CGCA		
			— TGAGGT	TGCTGG	AGGA		
			ACTTCACGACC	TCCT			
			AG	—			
GAM1793	SLC26A9	3'	CCGTGCCCAGCACCCG	28631	A	C	A
			— TG	GGTGCTGG	GCA	GG	

[illegible]

AC CCACGACC CG TTC
 _ A G
 GAM1793 LOC202284 5' CGTCCCTTCCAGCACCCCA 43418 A CGCAA
 TG GGTGCTGG GGACG
 || ||||| ||||
 AC CCACGACC CCTGC
 C TTC__
 GAM1793 LOC222183 5' CGGCCCGCCAGCACCTC 45184 CAA A
 GAGGTGCTGGCG GG CG
 ||||| || ||
 CTCCACGACCGC CC GC
 ____ G
 GAM1793 LOC90120 5' CGCCCCAGCCGCGCGCCCA 30852 A _ GCAA A
 TG GGTGC TGGC GG CG
 || |||| || || ||
 AC CCGCG GCCG CC GC
 C C ACCC _
 GAM1793 LOC90499 3' TCCTGGAGCAGCACCTCA 31584 G GCA
 TGAGGTGCTG C AGGA
 ||||| | ||||
 ACTCCACGAC G TCCT
 _ AGG
 GAM1793 LOC96652 3' CCCTGCACCTGCACCTCA 32627 T C A
 TGAGGTGC GG GCA GG
 ||||| || || ||
 ACTCCACG CC CGT CC
 T A C
 GAM1794 ALPI 3' CCATGCGGCTGCCTGCACCCCA 7343 A CA C CC
 TG GG CA GGCAGCCGT TGG
 || || || ||||| ||||
 AC CC GT CCGTCGGCG ACC
 C AC _ T_
 GAM1794 ALPP 3' CCTGTGGCTGCCTGCACCCCA 34138 A CA C TCCT
 TG GG CA GGCAGCCG GG
 || || || ||||| ||
 AC CC GT CCGTCGGT CC
 C AC _ GT_
 GAM1794 MAN2A2 3' CCAGGACGCACAGAAGCGCCTC 12765 ACACGGCA C
 A TGAGGC GC GTCCTGG
 |||| | |||||
 ACTCCG CG CAGGACC
 CGAAGACA _
 GAM1794 PARK2 3' CCAGGGCGGCCGGGCGCCCA 15151 A ACA AGC
 TG GGC CGGC CGTCCTGG
 || || || |||||
 AC CCG GCCG GCGGGACC
 C CGG ____
 GAM1794 PARK2 3' CCAGGGCGGCCGGGCGCCCA 15158 A ACA AGC
 TG GGC CGGC CGTCCTGG
 || || || |||||

		AC CCG GCCG GCGGGACC	
		C CGG ____	
GAM1794	PARK2	3' CCAGGGCGGCCGCGGCCCA 10904	A ACA AGC
		TG GGC CGGC CGTCCTGG	
		AC CCG GCCG GCGGGACC	
		C CGG ____	
GAM1794	PGD	3' CCAGGACATTCCATGTGCCTCA 38523	C C CC
		TGAGGCACA GG AG GTCCTGG	
		ACTCCGTGT CC TT CAGGACC	
		A _ A_	
GAM1794	FLJ10352	3' CAGAACATAGTGTGCTTCA 25824	GGCAGCC C
		TGAGGCACAC GT CTG	
		ACTTCGTGTG CA GAC	
		ATA____ A	
GAM1794	KIAA0935	3' CCAGACGCCACCTGTGCCTCA 36010	C CAGC C
		TGAGGCACA GG CGTC TGG	
		ACTCCGTGT CC GCAG ACC	
		_ ACCC _	
GAM1794	KIAA1061	3' CCAGAACAAGTTCTGTGTGCCT 35265	C C_ C
	C	GAGGCACACGG AGC GT CTGG	
		CTCCGTGTGTC TTG CA GACC	
		_ AA A	
GAM1794	KIAA1750	3' CCAGGACGACCAAGTGCATCCTC 33873	CA_ _ CAGC
	A	TGAGG CAC GG CGTCCTGG	
		ACTCC GTG CC GCAGGACC	
		TAC A A____	
GAM1794	KIAA1881	3' CCAGGGGTCAACCGTGTGCACCA 45654	AG CA GT
		TG GCACACGG GCC CCTGG	
		AC CGTGTGCC TGG GGACC	
		CA AC ____	
GAM1794	MAPKAPK2	3' CCTGGTGCTGCCGTGCCCA 11148	A CA CGT T
		TG GG CACGGCAGC CC GG	
		AC CC GTGCCGTCG GG CC	
		_ CC T__ T	
GAM1794	SLC39A3	3' AGGACACGGTGCCTCA 29354	A GCAGCC
		TGAGGCAC CG GTCCT	
		ACTCCGTG GC CAGGA	
		_ A____	
GAM1794	SLC39A3	3' CAGGACGGCCCCGTCCC 29355	CAC CA
		GG ACGG GCCGTCCTG	

		CC TGCC CGGCAGGAC	
		C__ C_	
GAM1794	LOC159199 5'	CCAGGACGACTGGGAGGGCGGC 39980	ACACGG__ C
		CTCA TGAGGC CAG CGTCCTGG	
		ACTCCG GTC GCAGGACC	
		GCGGGAGG A	
GAM1794	LOC51134 3'	CCAAAACACTTGAATGTGCCTC 18209	CGG CC CC
		A TGAGGCACA CAG GT TGG	
		ACTCCGTGT GTT CA ACC	
		AA_ CA AA	
GAM1795	LOC157663 3'	CAAGATAGTAGTATTATTA 39638	G
		TAA AGTACTACTATCTTG	
		ATT TTATGATGATAGAAC	
		A	
GAM1795	LOC254228 3'	CAAAATAGTAGTAACAAATATA 45919	TAAGAG C
		TA TATAT TACTACTAT TTG	
		ATATA ATGATGATA AAC	
		TAAACA A	
GAM1796	C9orf9 3'	CGCCCACCACCCACCTGGCT 21027	_ AACAA A
		AGTT GGTGG GT GGCG	
		TCGG CCACC CA CCGC	
		T CCAC C	
GAM1796	KIAA0472 3'	CTTTTGACTCCATCAACTT 35577	A_ T
		AAGTTGGTGGA CAG AG	
		TTCAACTACCT GTT TC	
		CA T	
GAM1796	LOC158402 5'	CCTACTGTAACCTTAA 41975	GGTGGA
		TTAAAGTT ACAGTAGG	
		AATTTCAA TGTCATCC	
GAM1797	ANKTM1 3'	CCTGTGATTATTGTATGA 14258	CA T
		TCA ATAATAGTT CAGG	
		AGT TGTTATTAG GTCC	
		A_ T	
GAM1797	CPNE3 3'	GTCCTGAATTCTACATTATT 9996	_ T_
		AATAA TAG TTCAGGAC	
		TTATT ATC AAGTCCTG	
		AC TT	
GAM1797	DUSP5 3'	CCTGAAATGTTGTGTAGA 10684	_ AATA
		TCT CACAAT GTTTCAGG	

AGA GTGTTG TAAAGTCC
 T ____
 GAM1797 GUCY1B2 5' TCCTGAAACTCTTTGGAGA 10336 A TAAT
 TCTC CAA AGTTTCAGGA
 |||| ||| |||||
 AGAG GTT TCAAAGTCCT
 _ TC_
 GAM1797 NEURL 3' GTCCATGTGGCACCTTTGTGAG 10414 TAATA TT _
 A TCTCACAA GT CA GGAC
 ||||| || || ||||
 AGAGTGTT CG GT CCTG
 TCCA_ GT A
 GAM1797 RAB6A 3' TCTTTACTAGTTATTGTGAGA 8778 _ TTC
 TCTCACAATAAT AGT AGGA
 ||||| ||| |||
 AGAGTGTTATTG TCA TTCT
 A T_
 GAM1797 RGS5 3' GTCCTATGATGCTATTATCATA 9679 CACA T _
 GA TCT ATAATAGT TCA GGAC
 || ||||| || |||
 AGA TATTATCG AGT CCTG
 TAC_ T AT
 GAM1797 SNAP23 3' TCCTGAAAAGTGTTATGA 9921 C ATAG
 TCA AATA TTTCAGGA
 || ||| |||||
 AGT TTGT AAAGTCCT
 A GA_
 GAM1797 SNAP23 3' TCCTGAAAAGTGTTATGA 28286 C ATAG
 TCA AATA TTTCAGGA
 || ||| |||||
 AGT TTGT AAAGTCCT
 A GA_
 GAM1797 ZNF175 3' CCTGTTTATTGTGGGA 13998 TAGTTT
 TCTCACAATAA CAGG
 ||||| |||
 AGGGTGTTATT GTCC
 T____
 GAM1797 ZNF264 3' GTCCTGAACATGATTGTGGA 9457 T AATAGT
 TC CACAAT TTCAGGAC
 || |||| |||||
 AG GTGTTA AAGTCCTG
 _ GTAC_
 GAM1797 ACTR1A 3' CCAAGAGCTATTACAGAGA 31531 ACAA CA
 TCTC TAATAGTTT GG
 ||| ||||| ||
 AGAG ATTATCGAG CC
 AC_ AA
 GAM1797 ATF3 3' CCTGAAGCCATTGGAGA 10243 A AATA
 TCTC CAAT GTTTCAGG
 ||| ||| |||||

AGAG GTTA CGAAGTCC
 _ C_
 GAM1797 BANK 3' CCTGAAAACATTATTATTGA 19626 C _
 TCA AATAAGT TTCAGG
 ||| ||||| |||||
 AGT TTATTATTA AAGTCC
 _ CAA
 GAM1797 C8orf2 3' GTCTTTCTATTATTGTAGAGA 14023 _ TTTC
 TCTC ACAATAATAG AGGAC
 ||| ||||| |||||
 AGAG TGTTATTATC TTCTG
 A T_
 GAM1797 CHL1 3' CCTGATTTTAATTGTGA 13393 AA TT
 TCACAAT TAG TCAGG
 ||||| ||| |||||
 AGTGTTA ATT AGTCC
 _ TT
 GAM1797 COE2 3' GTCCTGAAATGGATTGGAGA 32130 A AATA
 TCTC CAAT GTTTCAGGAC
 ||| ||| |||||
 AGAG GTTA TAAAGTCCTG
 _ GG_
 GAM1797 DAPK2 3' GTCCTGAGCACTTTGCAAGA 15636 CA TAAT _
 TCT CAA AGT TTCAGGAC
 ||| ||| ||| |||||
 AGA GTT TCA GAGTCCTG
 AC _ C
 GAM1797 ERAP140 3' GTCCATGATACTATAATTGTGA 37087 A T _
 GA TCTCACAAT ATAGT TCA GGAC
 ||||| ||||| ||| |||||
 AGAGTGTTA TATCA AGT CCTG
 A T A
 GAM1797 FLJ10201 5' TTGAGACTATTATCAAAGA 19764 CACA
 TCT ATAATAGTTTCAG
 ||| |||||
 AGA TATTATCAGAGTT
 AAC_
 GAM1797 FLJ30567 3' TCCTGTGATATTGTGA 29633 AATA T
 TCACAAT GTT CAGGA
 ||||| ||| |||||
 AGTGTTA TAG GTCCT
 _ T
 GAM1797 GPT2 3' GTCCCAAATGGGATTGGAGA 28526 A AATA CA
 TCTC CAAT GTTT GGAC
 ||| ||| ||| |||||
 AGAG GTTA TAAA CCTG
 _ GGG_ AC
 GAM1797 HIC 3' TCCTGAATACACTATTTTG 33495 T _
 CAA AATAGT TTCAGGA
 ||| ||||| |||||

		GTT TTATCA AAGTCCT	
		— CAT	
GAM1797	HMGH4	3' GTCCTGAACTGATTTTGTGA 13048	T _ T
		TCACAA AAT AGTT CAGGAC	
		AGTGTT TTA TCAA GTCCTG	
		T G _	
GAM1797	HSPC039	3' GTCTCAGACCATTCTGTGAGA 18181	TAATA CA
		TCTCACAA GTTT GGAC	
		AGAGTGTT CAGA TCTG	
		CTAC_ C_	
GAM1797	KIAA0637	5' TCCTGAAAGATGGAATTATGAC 16861	_ C AA G_
	GA	TC TCA AAT TA TTTTCAGGA	
		AG AGT TTA GT AAAGTCCT	
		C A AG AG	
GAM1797	KIAA1136	3' TCCTAAACTATTATCTGA 43885	CA C
		TCA ATAATAGTTT AGGA	
		AGT TATTATCAAA TCCT	
		C_ A	
GAM1797	KIAA1464	3' GTCCTGAAACCGAATGGCAGA 33885	CA ATAATA
		TCT CA GTTTCAGGAC	
		AGA GT CAAAGTCCTG	
		CG AAGC__	
GAM1797	KIAA1948	3' CCTGAAACTACGTAGAGA 40082	_ AATAA
		TCTC AC TAGTTTCAGG	
		AGAG TG ATCAAAGTCC	
		A C__	
GAM1797	LBP-9	3' GTCCCACTGCTGATTATTGAGA 15879	CA _ TTCA
		TCTCA ATAAT AGT GGAC	
		AGAGT TATTA TCG CCTG	
		_ G TCAC	
GAM1797	MacGAP	3' GTCCTGAATAAGTCTACTGGAA 27288	CA A ATAGT_
	GA	TCT CA TA TTCAGGAC	
		AGA GT AT AAGTCCTG	
		AG C CTGAAT	
GAM1797	MGC5242	5' CCTGACTTTTCTTTGTGAGA 23463	TAAT TT
		TCTCACAA AG TCAGG	
		AGAGTGTT TT AGTCC	
		TCT_ TC	
GAM1797	N4BP2	3' GTCCTAAAAGTCTTTTGTGAGA 20004	TAATAG C
		TCTCACAA TTT AGGAC	

		AGAGTGTT	AAA TCCTG		
		TTCTGA	_		
GAM1797	OLFM3	3'	CCTGAGGAGTTATTGGCAAGA	39960	CA_ AG
			TCT CAATAAT TTTCAGG		
			AGA GTTATTG GGAGTCC		
			ACG A_		
GAM1797	PRO2133	3'	CCTGGGCCATATTGTGAGA	20692	ATA T
			TCTCACAATA GTT CAGG		
			AGAGTGTTAT CGG GTCC		
			AC_ _		
GAM1797	RAB6C	3'	TCTTTACTAGTTATTGTGAGA	25835	_ TTC
			TCTCACAATAAT AGT AGGA		
			AGAGTGTTATTG TCA TTCT		
			A T_		
GAM1797	RPS6KC1	3'	GTCCCAGATTATTTCTGTAAGA	14801	C AT CA
			TCT ACA AATAGTTT GGAC		
			AGA TGT TTATTAGA CCTG		
			A CT C_		
GAM1797	SE57-1	3'	CTGGACTACCATTGTGAGA	24889	AA T
			TCTCACAAT TAGTT CAG		
			AGAGTGTTA ATCAG GTC		
			CC _		
GAM1797	TED	3'	GTCCCAGACTGATTACATGAGA	17921	CAA _ CA
			TCTCA TAAT AGTTT GGAC		
			AGAGT ATTA TCAGA CCTG		
			AC_ G C_		
GAM1797	TTY7	3'	GTCCTGAAGTTGGATTGT	25673	AA GT
			ACAAT TA TTCAGGAC		
			TGTTA GT AAGTCCTG		
			G_ TG		
GAM1797	WNT16	3'	TCCTGAAACATGCGGGA	18172	A ATAATA
			TCTC CA GTTTCAGGA		
			AGGG GT CAAAGTCCT		
			C A_____		
GAM1797	WNT16	3'	TCCTGAAACATGCGGGA	27676	A ATAATA
			TCTC CA GTTTCAGGA		
			AGGG GT CAAAGTCCT		
			C A_____		
GAM1797	ZNF212	3'	GTCCTGAAAACCCTGTGGA	14559	T ATAATAG
			TC CACA TTTCAGGAC		

		AG GTGT AAAGTCCTG		
		— CCCA—		
GAM1797	ZNF347	3' TCCTGAAGCTCTTACTCTAAGA 26319	CACAA	T
		TCT TAA AGTTTCAGGA		
		AGA ATT TCGAAGTCCT		
		ATCTC C		
GAM1797	LOC153516	3' CCTGGAAACTACCATTGTGAGG 28842	AA	—
		TCTCACAAT TAGTTTC AGG		
		GGAGTGTTA ATCAAAG TCC		
		CC G		
GAM1797	LOC160646	3' CCTGGCAACATTGTGAGA 40001	AATA	—
		TCTCACAAT GTT TCAGG		
		AGAGTGTTA CAA GGTCC		
		— C		
GAM1797	LOC200609	5' TCCAAC TATTACTGTAGA 43334	C A	TCA
		TCT ACA TAATAGTT GGA		
		AGA TGT ATTATCAA CCT		
		— C —		
GAM1797	LOC221069	3' TCCTGAGGAAATTATCCGAGA 44768	ACA	AG
		TCTC ATAAT TTTCAGGA		
		AGAG TATTA GGAGTCCT		
		CC_ AA		
GAM1797	LOC255461	5' GGAAC TATCATTGGAGA 46466	A	A
		TCTC CAAT ATAGTTTC		
		AGAG GTTA TATCAAGG		
		— C		
GAM1797	LOC255516	5' GGAAC TATCATTGGAGA 46472	A	A
		TCTC CAAT ATAGTTTC		
		AGAG GTTA TATCAAGG		
		— C		
GAM1797	LOC51020	3' TCTTGAGACCTTTATTGT 18138	TA	
		ACAATAA GTTTCAGGA		
		TGTTATT CAGAGTTCT		
		TC		
GAM1798	SNAP25	3' CTGTCGGGCAAGATAGCTCCTT 9054	A	— A_ —
	CA	TGAA GAGT ATCTT CT ATAG		
		ACTT CTCG TAGAA GG TGTC		
		C A CG C		
GAM1798	SNAP25	3' CTGTCGGGCAAGATAGCTCCTT 28317	A	— A_ —
	CA	TGAA GAGT ATCTT CT ATAG		

ACTT CTCG TAGAA GG TGTC
 C A CG C
 GAM1798 NSG-X 3' CTACTATAGTAACTCTT 15753 ATC
 AAGAGT TTACTATAGTAG
 ||||| |||||
 TTCTCA AATGATATCATC

 GAM1798 LOC158332 3' CTACTTGTGTGAGATACTCTTC 39823 A TAT
 CA TG AAGAGTATCTTAC AGTAG
 || ||||| |||||
 AC TTCTCATAGAGTG TCATC
 C TGT
 GAM1798 LOC84549 3' CTACTATAAGCAACAGCTCCTT 26259 A ATCTTAC
 CA TGAA GAGT TATAGTAG
 ||| ||| |||||
 ACTT CTCG ATATCATC
 C ACAACGA
 GAM1799 CCNF 3' ATCCGCCCACTTCGGTCTC 7523 C A CAC
 GA GAT CGA GGGCGGAT
 || ||| |||||
 CT CTG GCT CCCGCCTA
 _ _ TCA
 GAM1799 LOC200574 3' CCTTGTCAAATCGTCTTA 42821 AC C
 TAAGACGAT GACA GG
 ||||| ||| ||
 ATTCTGCTA CTGT CC
 AA T
 GAM1800 CCND2 3' GAGCAGCCAGCAAGTAAGCTAG 7516 _ GTA A
 CTAGTTTA GC GCT CTC
 ||||| || ||| |||
 GATCGAAT CG CGA GAG
 GAA AC_ C
 GAM1800 CYP4A11 3' AGCAGATGCTAAACCGTC 6418 TA A_
 GAC GTTTAGCGT GCT
 || ||||| |||
 CTG CAAATCGTA CGA
 C_ GA
 GAM1800 LILRB1 3' AGTAGCTGAGAAACTAAGTC 13485 _ AGCG
 GACT AGTTT TAGCTACT
 ||| |||| |||||
 CTGA TCAAA GTCGATGA
 A AGA_
 GAM1800 VDR 3' AGTTGCTAAACGAGTC 5943 A TA
 GACT GTTTAGCG GCT
 ||| ||||| |||
 CTGA CAAATCGT TGA
 G _
 GAM1800 ZNF217 3' TAGCAATACAACTAGTTG 13278 AGC A
 CGACTAGTTT GT GCTA
 ||||| || |||

GTTGATCAAA TA CGAT
 CA_ A
 GAM1800 ATP10B 3' AGCAACTGGTACAAGTGGTC 31733 _ G_ A
 GACTAGTT TA C GT GCT
 ||||| || || ||
 CTGGTCAA AT G CA CGA
 C G T A
 GAM1800 FLJ10246 3' AGTTACCAAAGTAGTC 19784 AGC
 GACTAGTTT GTAGCT
 ||||| ||||
 CTGATCAAA CATTGA
 C_
 GAM1800 KIAA0532 3' AGTAGCTACGACTGCAAGC 35021 _ _
 GTT TAG CGTAGCTACT
 || || |||||
 CGA GTC GCATCGATGA
 AC A
 GAM1800 LAK-4P 5' GCCACGCTGAACCAGCCG 14132 A A A
 CG CT GTTTAGCGT GC
 || || ||||| ||
 GC GA CAAGTCGCA CG
 C C C
 GAM1800 LOC146517 3' GAGTAAAGATAACCTAGTCG 38182 T GCGTAGC
 CGACTAG TTA TACTC
 ||||| || ||||
 GCTGATC AAT ATGAG
 C AGAA_
 GAM1800 LOC149842 3' AGCAGCAGCAACTAGTC 41089 TA _ A
 GACTAGTT GC GT GCT
 ||||| || || ||
 CTGATCAA CG CG CGA
 _ A A
 GAM1800 LOC254243 3' GAGCAGCTACGTAACCTG 46513 T G A
 TAG TTA CGTAGCT CTC
 || || ||||| ||
 GTC AAT GCATCGA GAG
 C _ C
 GAM1800 LOC254413 5' GAATAGCTACAAACAAGTGGTC 46402 TAGC C
 GACTAGTT GTAGCTA TC
 ||||| ||||| ||
 CTGGTCAA CATCGAT AG
 CAAA A
 GAM1800 LOC90038 3' GAGCAGCTACGTAACCTG 30650 T G A
 TAG TTA CGTAGCT CTC
 || || ||||| ||
 GTC AAT GCATCGA GAG
 C _ C
 GAM1801 COAS3 3' TACAAATGGATACACTAACGGA 29121 CG_ TCGC
 TCCGTTAG GTCT TGTA
 ||||| || || ||

AGGCAATC TAGG ACAT
 ACA TAA_
 GAM1802 MGC11061 3' AAATGTTTTCTCCAGCATC 26115 ATC TAC
 GAT GGAGAAAG CGTTT
 ||| ||||| ||||
 CTA CCTCTTTT GTAAA
 CGA ____
 GAM1803 C20orf177 3' GACTATTTTAACCAATATTGTC 31128 AACTGTCC
 A TGACGATATT GTAGTC
 ||||| ||||
 ACTGTTATAA TATCAG
 CCAATT_
 GAM1804 CCR2 3' TCAACCCAATAGTTGTTGATTG 6310 TCCG_ AA_
 GC GCCAATCA TAT GTTGA
 ||||| ||| ||||
 CGGTTAGT ATA CAACT
 TGTTG ACC
 GAM1804 MBL2 3' TCAACTTATGCAGAACTGGC 5764 ATCA C
 GCCA TC GTATAAGTTGA
 ||| || |||||
 CGGT AG CGTATTCAACT
 CA_ A
 GAM1804 PDAP1 3' CAACTTGTATATTTGGC 44419 TCATCC
 GCCAA GTATAAGTTG
 |||| |||||
 CGGTT TATGTTCAAC
 TA____
 GAM1804 KIAA1668 3' CAACCTGATTCTGATGACTGCG 33026 CAA CGT AA_
 G CCGC TCATC AT GTTG
 ||| |||| || ||||
 GGCG AGTAG TA CAAC
 TC_ TCT GTC
 GAM1805 ADH1B 3' ATTCAAGTGAGAAGTAAAT 35960 CC _
 ATTTAT TC CACTTGAAT
 |||| || |||||
 TAAATG AG GTGAACTTA
 A_ A
 GAM1805 CBFA2T1 3' CAAGAAGATGAATGGCGT 10542 A CTCCA
 AC CCATTTATC CTTG
 || ||||| |||
 TG GGTAAGTAG GAAC
 C AA____
 GAM1805 DMRT1 3' ATTCAAGTGAAGCCATTTGTGT 22480 _ TTTATC C
 G CAC CA CT CACTTGAAT
 ||| || || |||||
 GTG GT GA GTGAACTTA
 T TTACC_ A
 GAM1805 EGR3 3' TTTTGGTGGTGGATAAAT 29961 T T
 ATTTATCC CCACT GAA
 ||||| |||| |||

		TAAATAGG GGTGG TTT	
		T T	
GAM1805 MEOX2	3'	TCAAGTGGATAAAAAGTGT 12552	CA TCC
		ACAC TTTA TCCAATTGA	
		TGTG AAAT AGGTGAACT	
		AA ____	
GAM1805 PDE4D	3'	TCTTGGTGAGAGAATGAATGGT 36436	C _ T_
GT		ACACCATTTAT CTC CACT GA	
		TGTGGTAAGTA GAG GTGG CT	
		A A TT	
GAM1805 PLAG1	3'	ATTCAAGTGCCATTAGATG 8518	TCCTC
		CATTTA CACTTGAAT	
		GTAGAT GTGAACTTA	
		TACC_	
GAM1805 PTP4A2	5'	ATTCAAGTGGATTCTAAAT 9549	TCC
		ATTTA TCCAATTGAAT	
		TAAAT AGGTGAACTTA	
		CTT	
GAM1805 PTP4A2	5'	ATTCAAGTGGATTCTAAAT 27829	TCC
		ATTTA TCCAATTGAAT	
		TAAAT AGGTGAACTTA	
		CTT	
GAM1805 TPK1	3'	TAGGTGGAAAGAGAAATGATGT 22782	C A C_
		ACA CATTT TC TCCAATTG	
		TGT GTAAA AG AGGTGGAT	
		A G AA	
GAM1805 TRAM	3'	ATTCAGGTGGATAAATAGT 15590	C TCC
		AC ATTTA TCCAATTGAAT	
		TG TAAAT AGGTGGACTTA	
		A ____	
GAM1805 CNOT8	3'	TCAAGTGAATGAATGGT 11181	CCTC
		ACCATTTAT CACTTGA	
		TGGTAAGTA GTGAACT	
		A____	
GAM1805 FYCO1	3'	TCAAGAATAAATGGTGT 23713	CCTCCA
		ACACCATTTAT CTTGA	
		TGTGGTAAATA GAACT	
		A_____	
GAM1805 KCNS1	5'	CAAGTGGAGGTGGGAGCGG 8041	A AT_
		CC TTT CCTCCTTG	

GG GAG GGAGGTGAAC
C GGT
GAM1805 KIAA1237 3' TTCAGAGAGGATAAAT 39221 CAC
ATTTATCCTC TTGAA
||||||| ||||
TAAATAGGAG GACTT
A__
GAM1805 KIAA1254 3' ATTCAAGTGGAGAGGGTTA 34696 C ATTTATC
A ACC CTCCACTTGAAT
| || | |||||
A TGG GAGGTGAACTTA
T GA____
GAM1805 KIAA1287 3' ATTCAAGTGAAAACAGATGTGT 38325 _ ATCCTC
G CAC CATT CACTTGAAT
|| | |||||
GTG GTAGA GTGAACTTA
T CAAAA_
GAM1805 MGC14161 5' ATTCAAGTGGTCTAATGG 26717 TATCCT
CCATT CCACTTGAAT
|||| | |||||
GGTAA GGTGAACTTA
TCT____
GAM1805 MGC33182 3' TATTCAAGTAGAAAAGTTAACT 37234 TCC_____ C |||
AAATGGT TTA TC ACTTGAAT A
|| | ||||| |
AAT AG TGA ACTTA T
CAATTGAAA A |||
GAM1805 PRO1992 5' AGTGAAAAGGATAAATGG 15331 C__
CCATTTATCCT CACT
||||||| |||
GGTAAATAGGA GTGA
AAA
GAM1805 RABEX5 3' GTTCAAGAAAATTAAATGGT 15839 TCCTCCA
ACCATTTA CTTGAAT
|||||| | |||||
TGGTAAAT GAACTTG
TAAAA_
GAM1805 LOC118611 5' TCTCTGCAGGAAGACAATGGTG 37189 TA__ C CTT
T ACACCATT TCCT CA GA
|||||| | ||| || ||
TGTGGTAA AGGA GT CT
CAGA C CT_
GAM1805 LOC152715 5' ATTCTCACCAAAATAGATGGTG 39303 CCTCCACTT
T ACACCATT TAT GAAT
||||||| |||
TGTGGTAGATA CTTA
AAACCACT_
GAM1805 LOC220143 5' TTCAAGTGGCATCAATG 44956 T CCT
CATT AT CCACTTGAA
||| || |||||

			GTAA TA GGTGAACTT		
			C C__		
GAM1806	CARKL	3'	TTTCAAGCAGTGCTTGTTGTG 14941	ACA	GA C
			TACAACAA CAC CT GAAA		
			GTGTTGTT GTG GA CTTT		
			C__ AC A		
GAM1806	PRDM2	3'	TTTTAGCAGTAGTTTGTGTA 18008	AC	GA C
			TACAACAAAC AC CT GAA		
			ATGTTGTTTG TG GA TTT		
			A_ AC T		
GAM1806	RAB18	3'	TGAATAGTGTGTTTATTGTA 22223	C	GAC
			TACAA AAACACAC TCG		
			ATGTT TTTGTGTG AGT		
			A ATA		
GAM1806	TNFRSF11A	3'	AGTGTGTGTTTCATTGTA 9931	CA	G
			TACAA AACACAC ACT		
			ATGTT TTGTGTG TGA		
			AC _		
GAM1806	ZNF192	5'	TTCGAGTCTGTTTATCCGTTG 12992	AAAC__	C
			CAAC ACA GACTCGAA		
			GTTG TGT CTGAGCTT		
			CCTATT _		
GAM1806	AP3D1	3'	TCAGTCGTGTGTACTGTA 10048	ACAA	C
			TACA ACACACGACT GA		
			ATGT TGTGTGCTGA CT		
			CA__ _		
GAM1806	CNOT8	3'	TTTTGGGTCATGTCTGTTGTA 11183	A	CAC
			TACAACA ACA GACTCGAAA		
			ATGTTGT TGT CTGGGTTTT		
			C A__		
GAM1806	FLJ10260	5'	TTTGTGTTGTGTGTTTGT 19787	CT	
			ACAAACACACGA CGAA		
			TGTTTGTGTGTT GTTT		
			T_		
GAM1806	FLJ12568	3'	GGGTTGATTTTGTGTA 24553	CACA	
			TACAACAAA CGACTC		
			ATGTTGTTT GTTGGG		
			TA__		
GAM1806	ITGB5	3'	TCCTGTCCGTGTTTGTGTTA 29923	C	AC TC
			A AACAAACAC GAC GA		

A TTGTTTGTG CTG CT
 T C_ TC
 GAM1806 KIAA1434 3' TTTTGTATGTGCGTGTGTT 34493 _ T__
 AACACACG AC CGAAA
 ||||| || ||||
 TTGTGTGC TG GTTTT
 G TAT
 GAM1806 KIAA1751 3' GGTGCGTGTGTTGTGTA 35498 A A G
 TACA CAAACAC C ACT
 ||| ||||| | |||
 ATGT GTTTGTG G TGG
 _ C_
 GAM1806 KIAA1854 3' TTCTCAAGTGGTTTGTGTA 35539 A GACTC
 TACAACAAAC CAC GAA
 ||||| ||| |||
 ATGTTGTTTG GTG CTT
 _ AACT_
 GAM1806 MAWBP 3' TTTTCAAGTCATTAAGAGTGT 22683 C AC_____ C
 TGTTTA AACAAACAC GACT GAAAA
 ||||| ||| ||||
 TTGTTTGTG CTGA CTTTT
 T AGAATTA A
 GAM1806 PPM1A 3' TTTCAAGTCATGTTGTGTTTG 22000 C__ C
 CAAACACA GACT GAAA
 ||||| ||| ||||
 GTTTGTGT CTGA CTTT
 TGTA A
 GAM1806 STIP-1 3' TTGAGAATGTTTGTGTA 34528 CACGA
 TACAACAAACA CTCGA
 ||||| ||||
 ATGTTGTTTGT GAGTT
 AA__
 GAM1806 TEB4 3' TTTTCATGTGTCTGTGTTTGT 30430 C TC__
 ACAACACA GAC GAAAA
 ||||| ||| ||||
 TGTTTGTGT CTG CTTTT
 _ TGTA
 GAM1806 ZWINT 3' TCAGTTGTGTATTTGTTCA 26876 C C C
 A AACAAA ACACGACT GA
 | |||| ||||| ||
 A TTGTTT TGTGTTGA CT
 C A _
 GAM1806 ZWINT 3' TCAGTTGTGTATTTGTTCA 13923 C C C
 A AACAAA ACACGACT GA
 | |||| ||||| ||
 A TTGTTT TGTGTTGA CT
 C A _
 GAM1806 LOC152348 3' TTTTGAATGTGTTTGT 41489 CGAC
 AACAAACACA TCGAAA
 ||||| ||||

	TTGTTTGTGT AGTTT		
	A__		
GAM1806 LOC220573	3' TTTGATCTGTGTTTGT 34485	C C	
	AACAAACACA GA TCGAA		
	TTGTTTGTGT CT AGTTT		
	- -		
GAM1806 LOC256073	3' TCAGGGCGCACGTGTTTGTTC 46230	C	A__ A _
	A AACAAACAC CG CTC GA		
	A TTGTTTGTG GC GGG CT		
	C CAC _ A		
GAM1806 LOC92606	3' TTTCTTTATGTGTTTGCTGTA 34680	A	CG CTC
	TACA CAAACACA A GAAA		
	ATGT GTTTGTGT T CTTT		
	C AT T__		
GAM1807 KIAA1013	3' GTGTAAATGTTTTTTAGGATA 42860		TGTCG
	TATCCTAAGA TTACAC		
	ATAGGATTTT AATGTG		
	TTGTA		
GAM1807 MGC13007	3' TAACAATGTTTAGGATATTG 26122	A C	
	TAATATCCTA GATGT GTTA		
	GTTATAGGAT TTGTA CAAT		
	- A		
GAM1807 PTD012	3' GTGTTATTACCTGCAGGATATT 15269	A_ AT C T	
A	TAATATCCT AG GT GT ACAC		
	ATTATAGGA TC CA TA TGTG		
	CG _ T T		
GAM1807 SGK2	3' TGTAACAAGCTCATAGGGTAT 18399	A T C_	
	ATATCCTA GA GT GTTACA		
	TATGGGAT CT CG CAATGT		
	A _ AA		
GAM1807 LOC152559	3' GTGCAACAGTAGTAGGATAT 39286	AGA_ C T	
	ATATCCTA TGT GT AC		
	TATAGGAT ACA CG TG		
	GATG A _		
GAM1807 LOC90509	3' GTGAGTCATTTTAGAATATTA 31609	C	TCG
	TAATAT CTAAGATG TTAC		
	ATTATA GATTTTAC AGTG		
	A TG_		
GAM1808 ATRX	3' CTCAACATGGCAGAACCA 28684	CA	T
	TGG TCTGCCATGTT AG		

		ACC AGACGGTACAA TC		
		A_ C		
GAM1808	ATRX	3' CTCAACATGGCAGAACCA 6095	CA	T
		TGG TCTGCCATGTT AG		
		ACC AGACGGTACAA TC		
		A_ C		
GAM1808	DMD	5' TCCTCAAAAACAGATGCCA 10197	CCATG	T
		TGGCATCTG TT AGGA		
		ACCGTAGAC AA TCCT		
		AAA_ C		
GAM1808	DMD	5' TCCTCAAAAACAGATGCCA 10224	CCATG	T
		TGGCATCTG TT AGGA		
		ACCGTAGAC AA TCCT		
		AAA_ C		
GAM1808	DMD	5' TCCTCAAAAACAGATGCCA 10236	CCATG	T
		TGGCATCTG TT AGGA		
		ACCGTAGAC AA TCCT		
		AAA_ C		
GAM1808	MMP15	3' AGCCCTGAGGACAGATGCC 8261	_ ATGT	A
		GGCATCTG CC TTAGG CT		
		CCGTAGAC GG AGTCC GA		
		A _ C		
GAM1808	POLH	3' AGCCTGGCCAACATGGCAAAAC 13247	CATC	_ A
	CA	TGG TGCCATGTT TAGG CT		
		ACC ACGGTACAA GTCC GA		
		AAA_ CCG _		
GAM1808	PTGFRN	5' CCCAGCACAGATGCCA 33362	CCA	TA
		TGGCATCTG TGTT GG		
		ACCGTAGAC ACGA CC		
		_ CC		
GAM1808	SLC20A1	5' CCCAGACAACAGATGCC 29873	CCA	A
		GGCATCTG TGTTT GG		
		CCGTAGAC ACAGA CC		
		A_ C		
GAM1808	SLC6A6	3' AGCCCTCATTAAGATGCCA 9003	GCC	TTT A
		TGGCATCT ATG AGG CT		
		ACCGTAGA TAC TCC GA		
		AAT _ C		
GAM1808	TRPM8	3' AGCCTGGCCAACATGGCAAAAC 23513	CATC	_ A
	CA	TGG TGCCATGTT TAGG CT		

		ACC ACGGTACAA GTCC GA	
		AAA_ CCG _	
GAM1808	C20orf80 5'	AGTCTGGCCTCATGAAGATGCC 32537	GC TTTA_
	A	TGGCATCT CATG GGA CT	
		ACCGTAGA GTAC TCTGA	
		A_ TCCGG	
GAM1808	C5orf4 3'	TCATGACATACCAGATGCCA 26184	CC TAG
		TGGCATCTG ATGTT GA	
		ACCGTAGAC TACAG CT	
		CA TA_	
GAM1808	C5orf4 3'	TCATGACATACCAGATGCCA 18476	CC TAG
		TGGCATCTG ATGTT GA	
		ACCGTAGAC TACAG CT	
		CA TA_	
GAM1808	ELOVL2 3'	AGCCTAGGTTATACAGATGCCA 19387	CCAT TT A
		TGGCATCTG G TAGG CT	
		ACCGTAGAC T ATCC GA	
		ATAT GG _	
GAM1808	FLJ13352 3'	TGAGCATGGCAGTGCCA 23828	T
		TGGCA CTGCCATGTTTA	
		ACCGT GACGGTACGAGT	
		-	
GAM1808	FLJ14346 3'	GTGCCACACAGATGCCA 24622	CCA TTA _
		TGGCATCTG TGT GG AC	
		ACCGTAGAC ACA CC TG	
		_ _ G	
GAM1808	FLJ20073 3'	AGTCCCTCATCCAGAAGATGCC 19162	GCC_ TTTA
	A	TGGCATCT ATG GGA CT	
		ACCGTAGA TAC CCTGA	
		AGACC TC_	
GAM1808	FLJ22378 3'	AGTCCTTGGGGACGTGGCAGAT 24678	_
	GCCA	TGGCATCTGCCATGTTT AGGACT	
		ACCGTAGACGGTGCAGG TCCTGA	
		GGT	
GAM1808	JDD1 3'	AGCCTGGGTGATGGAGATGCCA 31670	G _ TT A
		TGGCATCT CCAT G TAGG CT	
		ACCGTAGA GGTA T GTCC GA	
		_ G GG _	
GAM1808	KCNT1 3'	AGGACTACATGGCGGACGCCA 30972	A TT GA
		TGGC TCTGCCATGT AG CT	

		ACCG AGGCGGTACA TC GA	
		C _ AG	
GAM1808 KIAA0285	5'	AGCCCTGGGACCAGCAGCCACC 16746	CAT CATG A
	A	TGG CTGC TTTAGG CT	
		ACC GACG GGGTCC GA	
		ACC ACCA C	
GAM1808 KIAA1764	5'	CCTACAGCAGATGCC 34353	CA TT
		GGCATCTGC TGT AGG	
		CCGTAGACG ACA TCC	
		— —	
GAM1808 MGC2941	3'	GCCAAGATGGAGATGCCA 23577	G G TA A
		TGGCATCT CCAT TT GG C	
		ACCGTAGA GGTA AA CC G	
		— G — —	
GAM1808 moblak	3'	CCCGGACGGCAGATGCC 28305	AT TA
		GGCATCTGCC GTT GG	
		CCGTAGACGG CAG CC	
		— GC	
GAM1808 MSP	3'	AGCCCAGTGTGGGCAGATGCCA 25760	ATGT A A
		TGGCATCTGCC TT GG CT	
		ACCGTAGACGG GA CC GA	
		GTGT C _	
GAM1808 MYH10	3'	AGCCTCCAGAACAGATGCCA 34260	CCA TTT A
		TGGCATCTG TG AGG CT	
		ACCGTAGAC AC TCC GA	
		AAG C _ _	
GAM1808 SLC5A7	3'	AGTCCTAAAGTGAAGAAGCCA 22387	A GC G
		TGGC TCT CAT TTTAGGACT	
		ACCG AGA GTG AAATCCTGA	
		A A _ _	
GAM1808 LOC147514	3'	AGCCCTAAACACTGATGTCA 33548	TGCCA A
		TGGCATC TGTTTAGG CT	
		ACTGTAG ACAAATCC GA	
		TC _ C	
GAM1808 LOC157657	3'	TTTGGACATGGCAGAAACCA 39629	CA
		TGG TCTGCCATGTTTAGG	
		ACC AGACGGTACAGGTTT	
		AA	
GAM1808 LOC219347	5'	AGTCCTCCAAGAAGATGCCA 44677	GCCA TTT
		TGGCATCT TG AGGACT	

ACCGTAGA AC TCCTGA
 AGA_ C_
 GAM1808 LOC221692 3' AACAGGGCACAGAGATGCCA 44295 ____ A
 TGGCATCT GCC TGTT
 ||||| ||| |||
 ACCGTAGA CGG ACAA
 GACA G
 GAM1808 LOC63923 3' AGTCCTCGCAGGAGACACCA 33322 CA G A TT
 TGG TCT CC TGT AGGACT
 ||| ||| ||| |||||
 ACC AGA GG ACG TCCTGA
 AC _ _ C_
 GAM1808 LOC90342 5' GTCTGACTGCAGATGCCA 31255 CAT TA
 TGGCATCTGC GTT GGAC
 ||||| ||| |||
 ACCGTAGACG CAG TCTG
 T_ _
 GAM1808 LOC92465 5' AGCCTGGCCAACATGGCAAATC 34392 C C ____ A
 CCA TGG AT TGCCATGTT TAGG CT
 ||| ||| ||||| ||| |||
 ACC TA ACGGTACAA GTCC GA
 C A CCG _
 GAM1809 TEP1 3' AAAATGAAGTGTCAAAAAATCT 13975 A _ GA
 CA TGAGAT TTTT ACGCT CATTTT
 ||||| ||| ||||| |||||
 ACTCTA AAAA TGTGA GTAAAA
 A C A_
 GAM1809 ZNF265 3' AAAATGAAAGCAAAATATCTTA 11937 AC GA
 TGAGATATTTT GCT CATTTT
 ||||| ||| |||||
 ATTCTATAAAA CGA GTAAAA
 _ AA
 GAM1809 LOC147837 3' TCATGAAATATCTCA 38395 CGC
 TGAGATATTTTA TGA
 ||||| |||
 ACTCTATAAAGT ACT
 _
 GAM1809 LOC221656 3' CAGTTTAATAATATCTCA 44293 _ C
 TGAGATATT TTA GCTG
 ||||| ||| |||
 ACTCTATAA AAT TGAC
 T T
 GAM1810 IHPK1 3' CCTTGGTAAGTATGGACTCA 45823 GAATCA C
 TGAGTCCAT TGCCA AGG
 ||||| ||| |||
 ACTCAGGTA ATGGT TCC
 GTCA_ _
 GAM1810 RNF26 3' CTGTGGCACCCAGCTCA 25728 CCA AATCA
 TGAGT TG TGCCACAG
 |||| ||| |||||

ACTCG AC ACGGTGTC
 ___ CCC___
 GAM1810 FLJ10898 5' CTGTGGTCCAGAGACTCA 29892 CA AATCAT
 TGAGTC TG GCCACAG
 ||||| || |||||
 ACTCAG AC TGGTGTC
 AG C___
 GAM1810 KIAA1550 3' CTGACATACACTCATGGACTCA 33070 ATC_ CCA
 TGAGTCCATGA ATG CAG
 ||||| || ||
 ACTCAGGTACT TAC GTC
 CACA A___
 GAM1810 UHRF1 3' CCCGTGGCATGGCGTGGCTCA 14951 T AA A
 TGAG CCATG TCATGCCAC GG
 ||| |||| ||||| ||
 ACTC GGTGC GGTACGGTG CC
 _ _ C
 GAM1810 USP20 3' CCTGCAGACTGAAGACTCTGGA 13502 T A___ TGCCA
 CTCA TGAGTCCA GA TCA CAGG
 ||||| || ||| ||||
 ACTCAGGT CT AGT GTCC
 _ CAGA CAGAC
 GAM1810 LOC147299 3' CCTGTTTCTGGACTCAGTGGAC 38331 _ A ATGCC
 TCA TGAGTCCA TGA TC ACAGG
 ||||| ||| || ||||
 ACTCAGGT ACT AG TGTCC
 G C GTCTT
 GAM1810 LOC255189 5' CCTATGGCATGATGAACTT 46193 CCATGA C
 GAGT ATCATGCCA AGG
 ||| ||||| |||
 TTCA TAGTACGGT TCC
 AG___ A
 GAM1810 LOC257476 3' CCTTGGTAACTGATGGACTCA 30715 GAATCA C
 TGAGTCCAT TGCCA AGG
 ||||| ||||| |||
 ACTCAGGTA ATGGT TCC
 GTCA_ _
 GAM1810 LOC90917 3' GCAGGAGGTTTCATGGCCCA 32167 A T A___
 TG G CCATGAATC TGC
 || ||||| |||
 AC C GGTACTTGG ACG
 C_ AGG
 GAM1811 C7 3' GAGTGAAAACATCTGCACA 6190 CT G
 TGTGCAGA TTTTCA TTC
 ||||| ||||| |||
 ACACGTCT AAAAGT GAG
 AC _
 GAM1811 CCKAR 5' GGCTGAAAAAGCCCACA 6389 CAGA
 TGTG CTTTTTCAGTT
 ||| |||||

		ACAC	GAAAAAGTCGG		
		CC__			
GAM1811	IFNW1	5'	AAGAACTGAAAGTACA 7936	AGACTT	C
			TGTGC TTTCAGTT CTT		
			ACATG AAAGTCAA GAA		
			_____ A		
GAM1811	LARGE	3'	GAAGGAACTACTTCAGTGCACA 11129	AG	TTTTC
			TGTGC ACT AGTTCCTTC		
			ACACG TGA TCAAGGAAG		
			___ CTTCA		
GAM1811	LARGE	3'	GAAGGAACTACTTCAGTGCACA 28601	AG	TTTTC
			TGTGC ACT AGTTCCTTC		
			ACACG TGA TCAAGGAAG		
			___ CTTCA		
GAM1811	UBE2V1	3'	AAGGAACCCGGTGTGCACA 22516	G	TTTTC
			TGTGCA ACT GTTCCTT		
			ACACGT TGG CAAGGAA		
			G CC__		
GAM1811	UBE2V1	3'	AAGGAACCCGGTGTGCACA 22763	G	TTTTC
			TGTGCA ACT GTTCCTT		
			ACACGT TGG CAAGGAA		
			G CC__		
GAM1811	UBE2V1	3'	AAGGAACCCGGTGTGCACA 9364	G	TTTTC
			TGTGCA ACT GTTCCTT		
			ACACGT TGG CAAGGAA		
			G CC__		
GAM1811	CALN1	5'	AAGGAATAAATTCCGCACA 25510	A C	TTCA
			TGTGC GA TTT GTTCCTT		
			ACACG CT AAA TAAGGAA		
			C T ____		
GAM1811	CDC14A	3'	GAAAAAACTGAAAAAGATGCTG 9764	A__	CC
	C		GCAG CTTTTTCAGTT TTC		
			CGTC GAAAAAGTCAA AAG		
			GTA AA		
GAM1811	DNAJC5	3'	AAGGAACTGGCATGCACA 30810	GACTTTT	
			TGTGCA TCAGTTCCTT		
			ACACGT GGTCAAGGAA		
			AC__		
GAM1811	KIAA0367	3'	GAAAGAACAGAAATTTGCACA 33420	CTT A	C
			TGTGCAGA TTTC GTTC TTC		

ACACGTTT AAAG CAAG AAG
 ____ A A
 GAM1811 MGC12538 3' GAAGGACATTGAAAAAATGTAC 26481 GAC _
 A TGTGCA TTTTTCAGT TCCTTC
 ||||| ||||| |||||
 ACATGT AAAAAGTTA AGGAAG
 A__ C
 GAM1811 PCDH10 3' AACTGGGTGTCTGTACA 26766 TTT
 TGTGCAGAC TTCAGTT
 ||||| |||||
 ACATGTCTG GGGTCAA
 T__
 GAM1811 PDE1C 3' GAGGCCTGAAAAAAGCCACACA 11460 CAGAC TT
 TGTG TTTTTCAG CCTT
 ||| ||||| |||
 ACAC AAAAAGTC GGAG
 ACCGA C_
 GAM1811 STATI2 3' AAGGAACCAAGCTGACACA 45368 _ A TTTCA
 TGTG CAG CTT GTTCCTT
 ||| ||| ||| |||||
 ACAC GTC GAA CAAGGAA
 A _ C____
 GAM1811 STATI2 3' AAGGAACCAAGCTGACACA 9957 _ A TTTCA
 TGTG CAG CTT GTTCCTT
 ||| ||| ||| |||||
 ACAC GTC GAA CAAGGAA
 A _ C____
 GAM1811 LOC143173 5' AAGGAAGCTAAATTTGCACA 30268 CTT C _
 TGTGCAGA TTT AGTT CCTT
 ||||| ||| ||| |||
 ACACGTTT AAA TCGA GGAA
 ____ _ A
 GAM1811 LOC152059 5' GAACTGAGTGGACTCTGCCA 39207 T C _
 TG GCAGA TTT TTCAGTTC
 || ||||| ||| |||||
 AC CGTCT AGG GAGTCAAG
 _ C T
 GAM1811 LOC157507 5' GAAAGAAGCTGTAAAGTCTGCA 39605 T C
 TGCAGACTTTT CAGTTC TTC
 ||||| ||||| |||
 ACGTCTGAAAA GTCAAG AAG
 T A
 GAM1811 LOC157697 5' GATCTGAAAAGGCTACACA 39645 C A T
 TGTG AG CTTTTTCAG TC
 ||| || ||||| |||
 ACAC TC GGAAAAGTC AG
 A _ T
 GAM1811 LOC201252 3' GAGCTCCAGAAATCTGCACA 42556 C TC
 TGTGCAGA TTTT AGTTC
 ||||| ||| |||

ACACGTCT AAGA TCGAG
 A CC
 GAM1812 BRCA1 3' GATCCCCCAGGCGCACTACTG 14202 ____ T TT
 CAGTA GCTGTGG GG TC
 |||| ||||| || ||
 GTCAT CGACACC CC AG
 CAC _ CT
 GAM1812 GNAO1 3' AGAAGGCCACAGGCCACTGC 43718 A _ GG
 GCAGT GC TGTGGT TTT
 ||||| || ||||| |||
 CGTCA CG ACACCG AGA
 C G GA
 GAM1812 PPP1R12B 5' GAGACTACCACAAACTACTAC 25796 C____
 GTAG TGTGGTGGTTTC
 |||| |||||
 CATC ACACCATCAGAG
 ACAA
 GAM1812 PPP1R12B 5' GAGACTACCACAAACTACTAC 25794 C____
 GTAG TGTGGTGGTTTC
 |||| |||||
 CATC ACACCATCAGAG
 ACAA
 GAM1812 PTGER4 5' AAATCGACAGCCACTGAGA 6660 G A GG
 TC CAGT GCTGT TGGTTT
 || |||| |||||
 AG GTCA CGACA GCTAAA
 A C _
 GAM1812 FLJ10922 3' GAAACCACCCTCGCCACCAAGA 20255 GCA A TGT
 TC GT GC GGTGGTTTC
 || |||| |||||
 AG CA CG CCACCAAAG
 AAC C CTC
 GAM1812 FLJ12876 3' AAGTCAGTCACAGACCACTGC 22986 AG_ _ GT
 GCAGT CTGTGG TG TT
 |||| ||||| || ||
 CGTCA GACACT AC AA
 CCA G TG
 GAM1812 KIAA1582 5' ACCACCACCACTACCACGA 32579 CA CT
 TCG GTAG GTGGTGGT
 ||| |||| |||||
 AGC CATC CACCACCA
 AC AC
 GAM1812 NFAT5 5' CGGAAACTTTTAGCTCCACGA 28953 CAGT TGGT
 TCG AGCTG GGTTCG
 ||| |||| |||||
 AGC TCGAT TCAAAGGC
 ACC_ TT_
 GAM1812 LOC151568 5' GAAACCACCTAGGGACCACG 28837 CA AG T
 CG GT CTG GGTGGTTTC
 || || |||||

		GC CA GAT CCACCAAAG		
		AC GG _		
GAM1812	LOC199986 3'	GAAAGACTCAGCCACTGGA	43271	G A T GG
		TC CAGT GCTG GGT TTT		
		AG GTCA CGAC TCA AAG		
		_ C _ GA		
GAM1812	LOC255057 3'	AGACCAGCTACCGCGA	45660	A TGTGG
		TCGC GTAGC TGGTTT		
		AGCG CATCG ACCAGA		
		C _ _ _ _		
GAM1812	LOC91801 3'	GAATTCTGCAAAGCTACTACGA	29009	C GTG TG T_
		TCG AGTAGCT G G TTC		
		AGC TCATCGA C C AAG		
		A AA_ GT TT		
GAM1813	MAPK14 5'	GGGGTCGCGGCAGCCGCACC	7003	A
		GGT CGGCTGCCGCGATCTC		
		CCA GCCGACGGCGCTGGGG		
		C		
GAM1813	MAPK14 5'	GGGGTCGCGGCAGCCGCACC	29107	A
		GGT CGGCTGCCGCGATCTC		
		CCA GCCGACGGCGCTGGGG		
		C		
GAM1813	MAPK14 5'	GGGGTCGCGGCAGCCGCACC	29110	A
		GGT CGGCTGCCGCGATCTC		
		CCA GCCGACGGCGCTGGGG		
		C		
GAM1813	MAPK14 5'	GGGGTCGCGGCAGCCGCACC	29114	A
		GGT CGGCTGCCGCGATCTC		
		CCA GCCGACGGCGCTGGGG		
		C		
GAM1813	DKFZP434M154 5'	CCTGGCGGCGGCAGCCGCAC	35807	A GATC
		GT CGGCTGCCGC TCAGG		
		CA GCCGACGGCG GGTCC		
		C GC_		
GAM1813	KIAA1110 3'	CCAGAGACCACAGGAGCCGTAC	30982	G GCGA_ A
	CA	TGGTACGGCT CC TCTC GG		
		ACCATGCCGA GG AGAG CC		
		_ ACACC A		
GAM1813	LOC146315 5'	CTGACAGGCAGCTGCACCA	30533	A GCGATC
		TGGT CGGCTGCC TCAG		

ACCA GTCGACGG AGTC
 C AC____
 GAM1813 LOC256158 5' CCCAAGATCACGTGGCACCG 46621 C ____ CA
 CGG TGCCGC GATCT GG
 ||| ||||| |||| ||
 GCC ACGGTG CTAGA CC
 _ CA AC
 GAM1814 KHDRBS1 3' ATCCACTTTGTACATAAGTTA 13327 CATCTAT
 TAGCTTA GGGTGGAT
 ||||| |||||
 ATTGAAT TTCACCTA
 ACATGT_
 GAM1814 MGC3222 3' AGATCCACCCACACCTAAGT 23641 CATCTA
 GCTTA TGGGTGGATCT
 |||| |||||
 TGAAT ACCCACCTAGA
 CCAC_
 GAM1814 PRO2198 3' AGCTCCACAAATGTGAGCTA 20694 CTATGG T
 TAGCTTACAT GTGGA CT
 ||||| |||| ||
 ATCGAGTGTA CACCT GA
 AA____ C
 GAM1814 LOC200339 3' TACCTAAATGTAAGCTA 43299 CTA
 TAGCTTACAT TGGGTG
 ||||| ||||
 ATCGAATGTA ATCCAT
 A_
 GAM1815 EN1 5' CCCACGGGCCGCTGGC 7139 A AGATT
 GCCGGCG CT CGTGGG
 ||||| || ||||
 CGGTCGC GG GCACCC
 C ____
 GAM1815 MAN2A1 5' CCCCTTCCCAGTTGCCGGCGA 8178 AGATTCGT
 TCGCCGGCGACT GGGG
 ||||| ||||
 AGCGGCCGTTGA CCCC
 CCCTT_
 GAM1815 NTN4 5' CCCCTGGCTCCCAGCTGCCGGC 31511 A A_ TT T
 GA TCGCCGGCG CT GA CG GGGG
 ||||| || || ||||
 AGCGGCCGT GA CT GT CCCC
 C CC CG _
 GAM1815 Rabip4R 3' CCCCACGAAGTAGATGCC 19716 A A
 GGCG CTAG TTCGTGGGG
 ||| ||| |||||
 CCGT GATC AAGCACCCC
 A _
 GAM1815 LOC143384 5' CCCATTCTGCCGCCGGCGA 37614 AC ATTC
 TCGCCGGCG TAG GTGGG
 ||||| || ||||

			AGCGGCCGC GTC TACCC		
			C_ CT__		
GAM1816 FHL1	3'	TTTCTACATTCTGTCATTAG	7181	_	T
		CTAATGGCA AATGTA AAA			
		GATTACTGT TTACAT TTT			
		C C			
GAM1816 GRM1	3'	GTTTTATACATCATTGTCAT	6498	—	
		ATGGCAA ATGTATAAAAC			
		TACTGTT TACATATTTTG			
		AC			
GAM1816 PKP2	3'	TTTGCAAGTTTGCCACCAGT	10915	AA	GTA
		ACT TGGCAAAT TAAA			
		TGA ACCGTTTG GTTT			
		CC AAC			
GAM1816 RCN1	3'	TTTTTTATATTTGCCACTGTTA	29996	TAA	T
		TAAC TGGCAAATGTA AAAA			
		ATTG ACCGTTTATAT TTTT			
		TC_ T			
GAM1816 RCN1	3'	TTTTTATATTTGCCACTGTTA	8804	TAA	T
		TAAC TGGCAAATGTA AAA			
		ATTG ACCGTTTATAT TTT			
		TC_ T			
GAM1816 SCN8A	3'	TGCATTCTTACATTAGTTA	15475	GCA_	
		TAAC TAATG AATGTA			
		ATTGATTAC TTACGT			
		ATTC			
GAM1816 TEM6	3'	TTTATGATAATTTGCCATTG	22967	G_	
		TAATGGCAAAT TATAAA			
		GTTACCGTTTA GTATTT			
		ATA			
GAM1816 BTBD3	3'	GTTTTAATCACTCTTGCCATTA	17340	AT A_	
		TAATGGCAA GT TAAAAC			
		ATTACCGTT CA ATTTTG			
		CT CTA			
GAM1816 SSR3	3'	ATACATGTTATTAGTTG	13969	AA	
		TAAC TAATGGCA TGTAT			
		GTTGATTATTGT ACATA			
		—			
GAM1816 SUN1	3'	TTTCTACAGACTGCCATTG	24794	AA_	T
		TAATGGCA TGTA AAA			

			GTTACCGT ACAT TTT		
			CAG C		
GAM1816	LOC125228	3'	TTTAAGAATTTGCCATCAGT 36794	A	GTA
			ACT ATGGCAAAT TAAA		
			TGA TACCGTTTA ATTT		
			C AGA		
GAM1816	LOC158563	3'	TTTATACATTTTCACTTAG 39871	_	C
			CTAA TGG AAATGTATAAA		
			GATT ACT TTTACATATTT		
			C _		
GAM1816	LOC161635	5'	TTTTATACACAGAGCCATTA 46188	AAA_	
			TAATGGC TGTATAAAA		
			ATTACCG ACATATTTT		
			AGAC		
GAM1816	LOC257206	3'	TTTTATTTTGCCATCAGTTA 46386	A	TGT
			TAACT ATGGCAAA ATAAAA		
			ATTGA TACCGTTT TATTTT		
			C _		
GAM1817	COL4A4	3'	TAGTTATTCACAAAATTGACT 5554	C	A
	C		GAG TAATTTTGT AATAACTA		
			CTC GTTAAAAACA TTATTGAT		
			A C		
GAM1817	CDC14B	3'	TAGTTATTTACAACCTTTTGCTC 27172	TAATTT	
	A		TGAGC TTGTAAATAACTA		
			ACTCG AACATTTATTGAT		
			TTTTC_		
GAM1817	FLJ23120	3'	TTTACAAAAACCAGCTCA 41267	AA	
			TGAGCT TTTTGTAAA		
			ACTCGA AAAAACATTT		
			CC		
GAM1817	KIAA0738	3'	ATTTTAAAAATTAGCCA 16277	A	T
			TG GCTAATTTTGT AAAT		
			AC CGATTAAAAAT TTTA		
			_ T		
GAM1817	KIAA1239	3'	TAGTTCTACAAAATCAGCT 35341	A	AAT
			AGCT ATTTTGTGTA AACTA		
			TCGA TAAAAACAT TTGAT		
			C C_		
GAM1818	OSRF	3'	ATAGTGAATAATTTGATCAA 29941	AATA	
			TTGGT AAATTATTCATAT		

AACTA TTTAATAAGTGATA
 G____
 GAM1818 POPX1 3' AGTGAATAATTTCTTACCAA 17116 TA
 TTTGGTAA AAATTATTCACT
 ||||| |||||
 AAACCATT TTTAATAAGTGA
 C_
 GAM1818 LOC124045 3' ATAGTGAATAAGATGCCTCCCA 37439 TAATAAAA
 AA TTTGG TTATTCACTAT
 |||| |||||
 AAACC AATAAGTGATA
 CTCCGTAG
 GAM1818 LOC150848 5' ATAATGAATAATTTTGGCTGAG 41253 TG AA C
 TT GT TAAAATTATTCA TAT
 || || ||||| ||
 GA CG GTTTTAATAAGT ATA
 GT _ A
 GAM1819 TMPRSS3 3' CGATCCTCCCCTGGACTC 23451 A AA
 GAGT CCAG GAGGATCG
 ||| ||| |||||
 CTCA GGTC CTCCTAGC
 _ CC
 GAM1819 TMPRSS3 3' CGATCCTCCCCTGGACTC 26187 A AA
 GAGT CCAG GAGGATCG
 ||| ||| |||||
 CTCA GGTC CTCCTAGC
 _ CC
 GAM1819 TMPRSS3 3' CGATCCTCCCCTGGACTC 26189 A AA
 GAGT CCAG GAGGATCG
 ||| ||| |||||
 CTCA GGTC CTCCTAGC
 _ CC
 GAM1819 C20orf130 3' CCACTCTGGTACTATCA 30937 CG A A
 TGA AGTACCAGA G GG
 || ||||| ||
 ACT TCATGGTCT C CC
 A_ _A
 GAM1819 KIAA0757 3' TCAATCCTCTTCTCTTC 12673 TACC C
 GAG AGAAGAGGAT GA
 || ||||| ||
 CTT TCTTCTCCTA CT
 C_ A
 GAM1819 KIAA0828 3' CGATCCTTTTAACTCTCA 39512 C ACCA
 TGA GAGT GAAGAGGATCG
 ||| ||| |||||
 ACT CTCA TTTTTCCTAGC
 _ CAA_
 GAM1819 LOC51133 3' TCATTTTCTGATTCTCATCA 18206 C TAC G
 TGA GAG CAGAAGA GA
 ||| ||| ||||| ||

		ACT CTC GTCTTTT CT	
		A TTA A	
GAM1820	ESRRBL1	3' GCAGATGCTGCTGCTGTCA 19743	AGT A __
		TGACAGCA GCA GC CTGC	
		ACTGTCGT CGT CG GACG	
		__ _ TA	
GAM1820	FEZ1	3' GCCCTGGTACTTGCTGTCATA 22878	AA__
		TATGACAGCAAGTGC GC	
		ATACTGTCGTTTCATG CG	
		GTCC	
GAM1820	HGF	3' CAGGCTTTTGCTTGCTATC 45220 C C	
		GA AGCAAGTG AAGCCTG	
		CT TCGTTCGT TTCGGAC	
		A T	
GAM1820	HOXD4	3' GCAGGCCGGGCCTGCTGTCA 15982	A T AA_
		TGACAGCA G GC GCCTGC	
		ACTGTCGT C CG CGGACG	
		__ GGC	
GAM1820	NKX3A	3' GCAGGCTTACTGAGCTGTC 12827	A_ CA
		GACAGC AGTG AGCCTGC	
		CTGTCTG TCAT TCGGACG	
		AG __	
GAM1820	SCD	3' GCAGTGATGACTTGCTGTC 11491	G AGC
		GACAGCAAGT CA CTGC	
		CTGTCGTTCA GT GACG	
		_ AGT	
GAM1820	SMT3H1	3' CAGACTGTCACTTGCTGTTA 30124	CA C
		TGACAGCAAGTG AG CTG	
		ATTGTCGTTTAC TC GAC	
		TG A	
GAM1820	CBX3	3' GCAGTTTAGGACCTGCTGTCAT 14141	A GCAAGC
	A	TATGACAGCA GT CTGC	
		ATACTGTCGT CA GACG	
		C GGATTT	
GAM1820	CBX3	3' GCAGTTTAGGACCTGCTGTCAT 18661	A GCAAGC
	A	TATGACAGCA GT CTGC	
		ATACTGTCGT CA GACG	
		C GGATTT	
GAM1820	CGI-127	3' GCACTATGTGCATTTGCTGTCA 18136	AGCC_
		TGACAGCAAGTGCA TGC	

		ACTGTCGTTTACGT	ACG	
		GTATC		
GAM1820	CYorf14	3'	GCAGGCTTGCAAGCCATG	20613 ACAG AG
			TATG CA TGCAAGCCTGC	
			GTAC GT ACGTTCGGACG	
			CGA_ G_	
GAM1820	DKFZP434I092	3'	GCAGGCTTGCAACCTCTCA	33675 C CAAG
			TGA AG TGCAAGCCTGC	
			ACT TC ACGTTCGGACG	
			C CA_	
GAM1820	FLJ14827	5'	GCAGAGCACACCTGCTGTCA	26642 A CAA _
			TGACAGCA GTG GC CTGC	
			ACTGTCGT CAC CG GACG	
			C A_ A	
GAM1820	KIAA0247	3'	CAGACTTGTTGCTGTC	16371 AGT C
			GACAGCA GCAAG CTG	
			CTGTCGT TGTTC GAC	
			_ A	
GAM1820	KIAA0367	3'	CAAACCTGTTTTTGTACTGTC	33417 _ T CC
			GACAG CAAG GCAAG TG	
			CTGTC GTTT TGTTC AC	
			AT T AA	
GAM1820	KIAA1040	3'	GCAGTGAACCTGCTGTCA	35741 G AGC
			TGACAGCAAGT CA CTGC	
			ACTGTCGTTCA GT GACG	
			A _	
GAM1820	PDE7B	5'	GCAGGCTCGGCTCTGTC	21011 CA GCA
			GACAG AGT AGCCTGC	
			CTGTC TCG TCGGACG	
			_ GC_	
GAM1820	LOC145134	5'	GCAGAACTGTACACCCCTGTCA	40502 CAA_ AGC
	TA		TATGACAG GTGCA CTGC	
			ATACTGTC CATGT GACG	
			CCCA CAA	
GAM1820	LOC90246	5'	GCAGGCTTCTCTCCCTGCCA	31000 A CA TGC
			TG CAG AG AAGCCTGC	
			AC GTC TC TTCGGACG	
			C CC TC_	
GAM1820	LOC93097	5'	GCAAGCCTGCTCACTGTTCATG	35355 CAAGT A C
			TATGACAG GCA GC TGC	

GTACTGTC CGT CG ACG
 ACT__ C A
 GAM1821 B4GALT5 3' GCCCAGGTGCACTGCTCACA 11170 C CG_ T
 TG GAGCAG ATTT GGC
 || ||||| |||||
 AC CTCGTC TGGG CCG
 A ACG C
 GAM1821 BAK1 3' GCCAAGGTCCTGCTCAACTCTA 44175 ATGC C
 TAGA GAGCAG GATTTTGGC
 ||| ||||| |||||
 ATCT CTCGTC CTGGAACCG
 CAA_ _
 GAM1821 FOXO1A 3' GCCAAAATCACTGTAAAATCT 7758 ATGCG C
 AGA AGCAG GATTTTGGC
 ||| ||||| |||||
 TCT TTGTC CTAAAACCG
 AAAA_ A
 GAM1821 AMOTL2 3' CCAGGATTGCTGCCGCATTG 18293 A
 GAATGCG GCAGCGATTTTGG
 ||||| |||||
 CTTACGC CGTCGTTAGGACC
 _
 GAM1821 FUSIP1 3' CCAAATCACGCCACTGCA 27624 G CA _
 TGC AG GC GATTTTGG
 ||| || |||||
 ACG TC CG CTAAAACC
 _ AC CA
 GAM1821 MGC10999 3' CAGTCACGCCACTGCATTCTA 26090 G CA ATT
 TAGAATGC AG GCG TTG
 ||||| || |||
 ATCTTACG TC CGC GAC
 _ AC ACT
 GAM1821 LOC153259 5' CCAAATCAAGCGACATTTTA 41600 CGA AGC
 TAGAATG GC GATTTTGG
 ||||| || |||||
 ATTTTAC CG CTAAAACC
 AG_ AA_
 GAM1822 MEP50 3' CAGTTAGGAGTCATGGAT 23548 AAC A
 ATCCA GA TCCTAACTG
 |||| || |||||
 TAGGT CT AGGATTGAC
 A_ G
 GAM1822 LOC139197 5' AGTGCTCATTGGATTGCA 37329 C ATCCTA
 TGTAATCCAAA GA ACT
 ||||| || |||
 ACGTTAGGTTT CT TGA
 A CG____
 GAM1823 KIAA0547 3' AACGCAATAATGATGAGA 16693 CC GA
 TCTCATCATTG TG CGTT
 ||||| || |||

			AGAGTAGTAAT AC GCAA		
			A_ _		
GAM1823	NDP52	3'	TCAGAATAATGAGACA 12446	C GC	
			TGTCTCAT ATT CTGG		
			ACAGAGTA TAA GACT		
			A _		
GAM1823	OSBPL2	3'	AACATCCAGAGGTGAGAC 16847	ATTGC C	
			GTCTCATC CTGGA GTT		
			CAGAGTGG GACCT CAA		
			A _ A		
GAM1823	OSBPL2	3'	AACATCCAGAGGTGAGAC 29315	ATTGC C	
			GTCTCATC CTGGA GTT		
			CAGAGTGG GACCT CAA		
			A _ A		
GAM1823	LOC124152	3'	CCAACAAGATGAGACA 36736	A CC	
			TGTCTCATC TTG TGG		
			ACAGAGTAG AAC ACC		
			_ A _		
GAM1823	LOC197358	3'	GAACATCGCCAATAATGGGACA 42509	C CCTG C	
			TGTCTCAT ATTG GA GTTC		
			ACAGGGTA TAAC CT CAAG		
			A CG_ A		
GAM1823	LOC200317	3'	GAACTTAATAATAATGAGACA 42803	C CCTG C	
			TGTCTCAT ATTG GA GTTC		
			ACAGAGTA TAAT TT CAAG		
			A AA_ _		
GAM1824	FLJ21032	5'	ACAGACGCCGCGCCGC 24395	T CAA	
			GCGGCCGG CGTT TGT		
			CGCCGGCC GCAG ACA		
			_ _		
GAM1824	KIAA0258	3'	ATACATTGGCAGCTGCTA 16642	CG CGTT	
			TAGCGGC GT CAATGTAT		
			ATCGTCG CG GTTACATA		
			A_ _		
GAM1825	RASA1	3'	TGTCCAACATGGTAATTCA 22907	ATAT A	
			TGAGTTA TCATGTTG ACA		
			ACTTAAT GGTACAAC TGT		
			_ C		
GAM1825	SEPP1	3'	ATGTCATAGAAATATTGACTCA 11878	CA T A	
			TGAGTTAATATT TGT GA CAT		

		ACTCAGTTATAA ATA CT GTA		
		AG _ _		
GAM1825 SEPP1	3'	ATGTCATAGAAATATTGACTCA 30185	CA	T A
		TGAGTTAATATT TGT GA CAT		
		ACTCAGTTATAA ATA CT GTA		
		AG _ _		
GAM1825 ENPP4	3'	GTTCTCAAAATATTA ACTC 17240	CA	TT
		GAGTTAATATT TG GAAC		
		CTCAATTATAA AC CTTG		
		A _ T _		
GAM1825 FADS1	3'	ATGGCAGCATGAATTCCA ACTC 15067	AAT	AA
A		TGAGTT ATTCATGTTG CAT		
		ACTCAA TAAGTACGAC GTA		
		CCT G _		
GAM1825 GENX-3414	3'	CAGCAAATATTA ACTTA 10059	CA	
		TGAGTTAATATT TGTTG		
		ATTCAATTATAA ACGAC		
		—		
GAM1825 MGC3048	3'	AGCATGAATGTTAACCCA 23488	A	
		TG GTTAATATTCATGTT		
		AC CAATTGTAAGTACGA		
		C		
GAM1825 YME1L1	3'	CAGATGAATATTTAACTCA 29293	_	G
		TGAGTTAA TATTCAT TTG		
		ACTCAATT ATAAGTA GAC		
		T _		
GAM1825 YME1L1	3'	CAGATGAATATTTAACTCA 15537	_	G
		TGAGTTAA TATTCAT TTG		
		ACTCAATT ATAAGTA GAC		
		T _		
GAM1825 LOC51696	3'	ATGTTGGGGGAAAATTA ACTCA 18308	A	ATGT G
		TGAGTTAAT TTC T AACAT		
		ACTCAATTA AAG G TTGTA		
		A GG _ G		
GAM1826 CCND2	3'	CCAGAGGAGCTCTCCCCCTTG 7512	ATA	
		CAAG GAGAGCTCCTTTGG		
		GTTC CTCTCGAGGAGACC		
		CCC		
GAM1826 HAS2	3'	CACCAAAGGAGACATATC 11801	GAGAG	
		GATA CTCCTTTGGTG		

CTAT GAGGAAACCAC
 ACA__
 GAM1826 ITGBL1 3' TCACCAAAGAAGATTCTCTTA 11201 T _ C
 A AGAGAG CT CTTTGGTGA
 | ||||| || |||||
 A TCTCTT GA GAAACCACT
 T A A
 GAM1826 NEFH 3' CCAGAGCTCTCTATTCTG 22046 AG CTT
 CA ATAGAGAGCTC TGG
 || ||||| ||
 GT TATCTCTCGAG ACC
 CT ____
 GAM1826 C22orf5 3' TCACCAAGCTGTCTCTC 14585 T G CCTT
 GA AGA AGCT TGGTGA
 || ||| |||||
 CT TCT TCGA ACCACT
 C G ____
 GAM1826 CENTB5 3' CACTTTGCAGCCCTCATCTCA 45723 A A A CCTTT
 C AGAT GAG GCT GGTG
 | ||| ||| |||
 A TCTA CTC CGA TCAC
 C _ C CGTT_
 GAM1826 FLJ00026 5' CTGAAAGAGCCCTCTCCTTG 32427 AT A C TG
 CAAG AGAG GCTC TT G
 ||| ||| ||| || |
 GTTC TCTC CGAG AA C
 C_ C A GT
 GAM1826 FLJ10718 3' CACCACACCCAGCTCTCTTTCT 20048 T CCTT_
 TG CAAGA AGAGAGCT TGGTG
 |||| ||||| ||||
 GTTCT TCTCTCGA ACCAC
 T CCCAC
 GAM1826 FLJ10743 3' TCACCAAGTCACCTCCCTCCTT 20081 AT A CTCC
 G CAAG AG GAG TTTGGTGA
 ||| ||| |||||
 GTTC TC CTC GAACCACT
 C_ C CACT
 GAM1826 FLJ14260 5' TCATCTGGAGCTCTTACCTT 24618 ATA TTT
 AAG GAGAGCTCC GGTGA
 || ||||| ||||
 TTC TTCTCGAGG CTA CT
 CA_ T_
 GAM1826 FLJ14800 3' CACCAAGCCCTCTATCTCC 26620 A A CCTT
 C AGATAGAG GCT TGGTG
 | ||||| ||| ||||
 C TCTATCTC CGA ACCAC
 C C ____
 GAM1826 FLJ14810 3' CACCTGCTCTCTGTCTCA 26631 A TCCTTT
 C AGATAGAGAGC GGTG
 | ||||| ||| |||

A TCTGTCTCTCG CCAC
 C T____
 GAM1826 FLJ20079 3' CTAGTGAGAGCTCTCTTCCT 19172 AT CT_
 AG AGAGAGCTC TTGG
 || ||||| |||
 TC TCTCTCGAG GATC
 CT AGT
 GAM1826 FLJ30294 3' CCAGCAAGCCTCTATCTTG 29449 A CCT
 CAAGATAGAG GCT TTGG
 ||||| ||| |||
 GTTCTATCTC CGA GACC
 _ AC_
 GAM1826 KIAA0430 3' TCACCAAACCCCTTTCCCAT 21152 A_ CTCC_
 CTTG CAAGAT GAGAG TTTGGTGA
 |||| ||| |||||
 GTTCTA CTTTC AAACCACT
 CC CCCCCA
 GAM1826 KIAA0564 3' CACCAAATGCTCCTATC 32900 A TCC
 GATAG GAGC TTTGGTG
 |||| ||| |||||
 CTATC CTCG AAACCAC
 _ TA_
 GAM1826 MGC15882 5' TCACCAAAGAGCACTCGATCCT 26706 A A A C
 G CA GAT GAG GCTC TTTGGTGA
 || ||| ||| |||||
 GT CTA CTC CGAG AAACCACT
 C G A _
 GAM1826 SEMA4F 3' TCATCCCTGGCCCCCTATCTTG 10460 AGA CCTTT
 CAAGATAG GCT GGTGA
 ||||| ||| |||||
 GTTCTATC CGG CTACT
 CCC TCC__
 GAM1826 SIAT4A 3' CACCAGAGGCTCCTA 8978 A TC
 TAG GAGC CTTTGGTG
 ||| ||| |||||
 ATC CTCG GAGACCAC
 _ _
 GAM1826 VEZATIN 3' CATCAAATCCCTATCTCA 19068 A A GCTCC
 C AGATAG GA TTTGGTG
 | |||| || |||||
 A TCTATC CT AAACCTAC
 C C ____
 GAM1826 LOC120087 5' CAAAAGCTCTCTCCCTT 37208 AT CC
 AAG AGAGAGCT TTG
 ||| ||||| |||
 TTC TCTCTCGA AAAC
 CC _
 GAM1826 LOC138128 5' CCGAGAGGAGCCCTCTACCTTG 37393 A A _
 CAAG TAGAG GCTCCTTT GG
 ||| |||| ||||| ||

		GTTC ATCTC CGAGGAGA CC		
		C C G		
GAM1826	LOC148930 3'	ACCAACCTCTGTCTTG 38616	AGCTCCT	
		CAAGATAGAG TTGGT		
		GTTCTGTCTC AACCA		
		C_____		
GAM1826	LOC150372 5'	CACCAAGGCTTTCCCATCTTG 38936	A_ CCT	
		CAAGAT GAGAGCT TTGGTG		
		GTTCTA CTTTCGG AACCAC		
		CC _____		
GAM1826	LOC151877 3'	CCAAAGCTCGCCATCTTG 41393	AGA CCT	
		CAAGAT GAGCT TTGG		
		GTTCTA CTCGA AACC		
		CCG _____		
GAM1826	LOC154761 3'	CACCAAAGCTCATCCCTCTCC 39483	A TA _ CCT	
		C AGA GA GAGCT TTGGTG		
		CTCT CTCTCGA AACCAC		
		C CC A _____		
GAM1826	LOC163882 3'	TCACCTCTTGGGTCTCTATCCT 39973	A G CTTT	
	G	CA GATAGAGA CTC GGTGA		
		GTCTATCTCT GGG CCACT		
		C _ TTCT		
GAM1827	SE57-1 3'	AGCACTTTACTTGTATTA 24886	_____	
		TAATACAAGTAA TGTT		
		ATTATGTTTCATT ACGA		
		TC		
GAM1828	TBL1X 3'	GACATGAAGACACAATCT 12184	CA AC	
		AGATTGTGTC TAT GTC		
		TCTAACACAG GTA CAG		
		AA _____		
GAM1828	CXorf1 3'	GTATGAACACAATTGCTA 11056	A C	
		TAGCAG TTGTGT CATAT		
		ATCGTT AACACA GTATG		
		_ A		
GAM1829	DKFZP564L0864 3'	CACTATGGTTAAATAAGGTCTT 35918	A CA T	
	A	TAAGA CTTA TGA CCATAGTG		
		ATTCT GAAT ATT GGTATCAC		
		G AA _		
GAM1829	KIAA1596 3'	CACCATGATTGTAAGTTC 35119	TGATC A	
		GAAC TTACA CAT GTG		

CTTGAATGT GTA CAC
 TA__ C
 GAM1829 LOC90246 3' GTGGGTCACACAAGCCCTTA 31002 AA ACA
 TAAG CTT TGATCCAT
 ||| ||| |||||
 ATTC GAA ACTGGGTG
 CC CAC
 GAM1830 FLJ12270 3' AGTGGGTAGGAATTTTCATCAAC 24953 GTA ____
 AAA TTTG ATGAAAT TATTCAT
 ||| ||||| |||||
 AAAC TACTTTA ATGGGTGA
 AAC AGG
 GAM1830 OSRF 3' ATAGTGAATAATTTGATCAA 29941 AATG
 TTGGT AAATTATTCAT
 ||| |||||
 AACTA TTTAATAAGTGATA
 G__
 GAM1830 POPX1 3' AGTGAATAATTTCTTACCAA 17116 T
 TTTGGTAA GAAATTATTCAT
 ||||| |||||
 AAACCATT CTTAATAAGTGA
 -
 GAM1830 LOC124045 3' ATAGTGAATAAGATGCCTCCCA 37439 TAATGAAA
 AA TTTGG TTATTCAT
 ||| |||||
 AAACC AATAAGTGATA
 CTCCGTAG
 GAM1830 LOC51279 3' ATAGTGAACCCCATCTCCAAA 18614 TA AAATTA
 TTTGG ATG TTCAT
 ||| ||| |||||
 AAACC TAC AAGTGATA
 TC CCCA__
 GAM1831 B4GALT5 3' GCCCAGGTGCACTGCTCACA 11170 C CG_ T
 TG GAGCAG ATTT GGC
 || ||||| ||| |||
 AC CTCGTC TGGA CCG
 A ACG C
 GAM1831 BAK1 3' GCCAAGGTCCTGCTCAACTCTA 44175 ATGC C
 TAGA GAGCAG GATTTTGGC
 ||| ||||| |||||
 ATCT CTCGTC CTGGAACCG
 CAA_ _
 GAM1831 FOXO1A 3' GCCAAAATCACTGTAAAATCT 7758 ATGCG C
 AGA AGCAG GATTTTGGC
 ||| ||||| |||||
 TCT TTGTC CTAAAACCG
 AAAA_ A
 GAM1831 AMOTL2 3' CCAGGATTGCTGCCGCATTC 18293 A
 GAATGCG GCAGCGATTTTGG
 ||||| |||||

CTTACGC CGTCGTTAGGACC

GAM1831 FUSIP1 3' CCAAATCACGCCACTGCA 27624 G CA _
TGC AG GC GATTTTGG
||| || || |||||
ACG TC CG CTAAAACC
_ AC CA

GAM1831 MGC10999 3' CAGTCACGCCACTGCATTCTA 26090 G CA ATT
TAGAATGC AG GCG TTG
||||||| || ||| |||
ATCTTACG TC CGC GAC
_ AC ACT

GAM1831 LOC153259 5' CCAAATCAAGCGACATTTTA 41600 CGA AGC
TAGAATG GC GATTTTGG
||||||| || |||||
ATTTTAC CG CTAAAACC
AG_ AA_

GAM1832 GA 5' TGTCTCGCTCGCTCCGCCC 14936 _ _
GGGCGGAGC CGA ACA
||||||| ||| |||
CCCGCCTCG GCT TGT
CTC C

GAM1832 KIAA0753 3' TGGAGAAGGGATGGCACCACCC 16737 C A AACA
GGG GG GCCG TTCTCCA
||| ||| |||||
CCC CC CGGT AAGAGGT
A A AGGG

GAM1832 KIAA1130 3' TGGGAGCCCAGGCTCCGCCC 31289 GAACA T
GGGCGGAGCC TTC CCA
||||||| ||| |||
CCCGCCTCGG GAG GGT
ACCC_ _

GAM1832 RPL36 5' GAGCCGGTACTCACCTCCGCCC 17715 CC _ ATT
GGGCGGAG GA AC CTC
||||||| || || |||
CCCGCCTC CT TG GAG
CA CA GCC

GAM1832 LOC56920 3' AGAGCTGCAGCCAGCTCTGCCC 21381 CGAA_ _
GGGCGGAGC CA TTCT
||||||| || |||
CCCGTCTCG GT GAGA
ACCGAC C

GAM1833 CA12 3' GATGTCAAATCGTGGTTTA 6881 A _ T
TAAACCAC ATTTG C TC
||||||| ||||| |||
ATTTGGTG TAAAC G AG
C T T

GAM1833 CLASP2 3' TGGAAAAATTGTGTTTACA 32270 C GC
TGTAAC ACAATTT TTCCG
||||||| ||||| |||||

ACATTTG TGTTAAA AAGGT

GAM1833 GPR48 3' GCAGACTGTAAATTGTGGTTT 20549 _ T_ C
ATA TGTAACCACAATTTG C TC GC

|||||
ATATTTGGTGTAAAT G AG CG
T TC A

GAM1833 LAD1 3' AAGCTGTGGTTTACA 12083 ATTT
TGTAACCACA GCTT
|||||
ACATTTGGTGT CGAA

GAM1833 PIGA 3' GCAGCCAGTTGTGGTTTACA 21710 T TCC
TGTAACCACAATT GCT GC
|||||
ACATTTGGTGTGA CGA CG
C

GAM1833 PIGA 3' GCAGCCAGTTGTGGTTTACA 21717 T TCC
TGTAACCACAATT GCT GC
|||||
ACATTTGGTGTGA CGA CG
C

GAM1833 SFRS7 3' AGTAAATTTGGCTTACA 29898 A C
TGTAACCA AATTTGCT
|||||
ACATT GGT TTAAATGA
C

GAM1833 XPO1 3' AGCAAAATAAACTTGGTTTACA 9436 CAA____
TGTAACCA TTTGCT
|||||
ACATTTGGT AAACGA
TCAAATA

GAM1833 KIAA0368 3' AGCAGAAGACTGGTTTACA 32487 CAA_
TGTAACCA TTTGCT
|||||
ACATTTGGT AGACGA
CAGA

GAM1833 KIAA1018 3' GCGGAAGTAGCACAGTTTCCA 17358 T CACAAT
TG AAAC TTGCTTCGC
|| |||
AC TTTG GATGAAGGCG
C ACAC__

GAM1833 KIAA1576 3' AGCAAATTATGTTTACA 32769 CAC
TGTAAC AATTTGCT
|||||
ACATTTG TTAAACGA
TA_

GAM1833 TOMM70A 3' GAATTATAATTATGGTTTACA 16791 C TGC_
TGTAACCA AATT TTC
|||||

ACATTTGGT TTAA AAG
 A TATT
 GAM1833 LOC158527 5' GCGGAAGCAGGAATGCCTTACA 39862 AC CAA
 TGTA CA TTTGCTTCCGC
 |||| || ||||||||
 ACATT GT GGACGAAGGCG
 CC AA_

GAM1834 E2F3 3' TCCAAGAGAGTATCATGA 7670 GAA
 TCATGATATT TTGGA
 |||||||| ||||
 AGTACTATGA AACCT
 GAG

GAM1834 HOXB3 5' TTTTCCAAACACACATGACA 7924 ATAT AA
 TGTCATG TG TTGGAAAA
 |||||| || ||||||
 ACAGTAC AC AACCTTTT
 AC_ A_

GAM1834 NR1I2 5' TTTCCAATATCCTCATGACA 9975 TATT _
 TGTCATGA GA ATTGGAAA
 |||||| || ||||||
 ACAGTACT CT TAACCTTT
 C_ A

GAM1834 NRL 3' TTTTCAAGATTTCAATATCCAA 12840 CAT _
 CA TGT GATATTGAA TTGGAAA
 || |||||||| ||||||
 ACA CTATAACTT AACTTTT
 AC_ TAG

GAM1834 PKHD1 3' TTTTCCAACTCAATGAATGAC 28947 GA A
 A TGTCAT TATTGA TTGGAAAAA
 |||||| |||||| ||||||||
 ACAGTA GTAACCT AACCTTTTT
 A_ C

GAM1834 SLC1A4 3' TTTTCCAAATTACCTGCTGACA 9000 TGATATTG
 TGTCA AATTGGAAAAA
 |||| ||||||||
 ACAGT TTAACCTTTTT
 CGTCCA_

GAM1834 BCMP1 3' TTTTGGCTGTCAATATCATAAC 25460 C A_ TG
 GT ATGATATTGA T GAA
 || |||||||| | |||
 CA TACTATAACT G TTT
 A GTC GT

GAM1834 DIM1 3' CAATTCAATCCATGACA 13525 AT
 TGTCATG ATTGAATTG
 |||||| ||||||||
 ACAGTAC TAACTTAAC
 C_

GAM1834 FLJ10738 3' TTTTCCCAATTCAACTTCAT 20071 TA _
 ATGA TTGAATTGG AAAA
 |||| |||||||| ||||

		TACT AACTTAACC TTTT		
		TC C		
GAM1834 KIAA0040	3'	TTTTCTTGTAACATGACA 16101	TA	AATT
		TGTCATGA TTG GGAAAA		
		ACAGTACT AAT TCTTTT		
		C_ GT__		
GAM1834 KIAA0261	3'	CCATATTCAATATCATACCA 33831	TC	_
		TG ATGATATTGAAT TGG		
		AC TACTATAACTTA ACC		
		CA T		
GAM1834 KIAA0261	3'	TTTTATAGATTTAATATCATAA 33837	C	GG_
	CA	TGT ATGATATTGAATT AAAA		
		ACA TACTATAATTTAG TTTT		
		A ATA		
GAM1834 KIAA1922	3'	TCAGTGGAATATCATACA 36459	C	GA
		TGT ATGATATT ATTGG		
		ACA TACTATAA TGA CT		
		_ GG		
GAM1834 LOC149842	3'	TCCAGGTTCCAATATCAAACA 41093	CA	AA__
		TGT TGATATTG TTGGA		
		ACA ACTATAAC GACCT		
		A_ CTTG		
GAM1834 LOC150967	3'	TCATAATTCAACCCATGACA 39038	ATA	_
		TGTCATG TTGAATTG GA		
		ACAGTAC AACTTAAT CT		
		CC_ A		
GAM1834 LOC152503	3'	TTTCCAACAATGGTCATGAC 41520	_	AATT
		GTCATGAT ATTG GGAAA		
		CAGTACTG TAAC CCTTT		
		G AAC_		
GAM1834 LOC221495	3'	TTTTCCAACCCAAAAGCAGAC 45063	A ATA	AA
		GTC TG TTG TTGGAAAA		
		CAG AC AAC AACCTTTT		
		_ GAA CC		
GAM1834 LOC221935	3'	TTTTCGATACAACATCATGACA 44504	A	A
		TGTCATGAT TTG ATTGGAAA		
		ACAGTACTA AAC TAGCTTTT		
		C A		
GAM1834 LOC254100	3'	TCCAATTTACTCCTCATGACA 46129	TAT_	
		TGTCATGA TGAATTGGA		

		ACAGTACT	ATTTAACCT		
		CCTC			
GAM1835	DPYSL3	3'	AATGGTACACCGATATTT	7068	C
			GAATATCGG	GTATCGTT	
			TTTATAGCC	CATGGTAA	
			A		
GAM1836	KIAA1856	3'	TAAAACTGTGAAAAATAGCTAT	44526	ATCTA
			ATAGCTATTTTT	TTTTA	
			TATCGATAAAAA	AAAAT	
			GTGTC		
GAM1837	CNTNAP2	3'	AGGTATTACTTCTGCACTTA	15413	CAA A
			TAAG	AGAAGTAA	ATCT
			ATTC	TCTTCATT	TGGA
			ACG	A	
GAM1837	GPR65	5'	GAGACAAGACTTCTCTGTTTA	30051	A AAAA
			TAAGCA	AGAAGT	TCTT
			ATTTGT	TCTTCA	AGAG
			C	GAAC	
GAM1837	NRXN1	3'	ACAAAGACTCAGCTACTTCTTT	28992	C AAA__ C
			TCTTA	TAAG AAAGAAGTA	TCTT GT
			ATTC	TTTCTTCAT	AGAA CA
			T	CGACTC	A
GAM1837	NRXN1	3'	ACAAAGACTCAGCTACTTCTTT	11221	C AAA__ C
			TCTTA	TAAG AAAGAAGTA	TCTT GT
			ATTC	TTTCTTCAT	AGAA CA
			T	CGACTC	A
GAM1837	C3F	5'	ACGAGGGGTTACCCCTTTGCTT	12329	AA AA
			AAGCAAAG	GTA	ATCTTCGT
			TTCGTTTC	CAT	TGGGAGCA
			CC	__	
GAM1837	ENPP4	3'	AGGGTTTTACTTCCTTGTT	17239	A
			AGCAA	GAAGTAAAATCTT	
			TTGTT	CTTCATTTTGGGA	
			C		
GAM1837	LOC148824	3'	GTTTTACCTTTTTGCTTA	40909	A
			TAAGCAAAGA	GTAAAAT	
			ATTCGTTTTT	CATTTTG	
			C		
GAM1837	LOC153711	3'	ACGAAAACAGCCAGCATCTTTG	41665	A AAAATC__
			CTTA	TAAGCAAAGA	GT TTCGT

		ATTCGTTTCT CG	AAGCA	
		A ACCGACAA		
GAM1837	LOC253664 5'	ACGAAGATCCTGAGACGCTTA	45446	AAAGA TAAA
		TAAGC AG ATCTTCGT		
		ATTCG TC TAGAAGCA		
		CAGAG C__		
GAM1838	AGL 3'	CCTAATAAAATAATGGTATTT	5466	ATT
		GAATA TTATTTTATTAGG		
		TTTAT AATAAAATAATCC		
		GGT		
GAM1838	AGL 3'	CCTAATAAAATAATGGTATTT	6305	ATT
		GAATA TTATTTTATTAGG		
		TTTAT AATAAAATAATCC		
		GGT		
GAM1838	AGL 3'	CCTAATAAAATAATGGTATTT	6298	ATT
		GAATA TTATTTTATTAGG		
		TTTAT AATAAAATAATCC		
		GGT		
GAM1838	AGL 3'	CCTAATAAAATAATGGTATTT	6293	ATT
		GAATA TTATTTTATTAGG		
		TTTAT AATAAAATAATCC		
		GGT		
GAM1838	AGL 3'	CCTAATAAAATAATGGTATTT	6288	ATT
		GAATA TTATTTTATTAGG		
		TTTAT AATAAAATAATCC		
		GGT		
GAM1838	AGL 3'	CCTAATAAAATAATGGTATTT	6283	ATT
		GAATA TTATTTTATTAGG		
		TTTAT AATAAAATAATCC		
		GGT		
GAM1838	MGC27382 3'	GCCTAATAAAATAAATGGTTGA	29523	ATAAT
		TCGA TTTATTTTATTAGGC		
		AGTT AAATAAAATAATCCG		
		GGT__		
GAM1838	SNTG1 3'	CCTAATAAGATTTATTATC	21039	A TTT
		GA TAAT ATTTTATTAGG		
		CT ATTA TAGAATAATCC		
		_ TT_		
GAM1838	LOC133686 3'	CCTATGTGAATAAAATTACTC	37052	A TAT
		GA TAATTTTATTT TAGG		

		CT ATTAAATAAG ATCC		
		C TGT		
GAM1838	LOC91301	5' GCCTAATAAATGCTCGTTACTT 32649	A	TTTAT
	GA	TCGA TAAT TTTATTAGGC		
		AGTT ATTG AAATAATCCG		
		C CTCGT		
GAM1839	FLJ20051	3' CAATGTTTTCTTGATTACATCT 21163	C	TAT G
		AGATGTAA CGAG GC ATTG		
		TCTACATT GTTC TG TAAC		
		A TTT _		
GAM1840	TES	3' GATTGCACTTGCCTGCCATGAT 35632	_	AACA
		ATCATGGCAGG AGG CAATC		
		TAGTACCGTCC TTC GTTAG		
		G AC_		
GAM1840	C6orf37	3' ATTGCATTCCCTCTATGATG 33509	GGCA	CA
		TATCAT GGAGGAA CAAT		
		GTAGTA TCTCCTT GTTA		
		_ AC		
GAM1840	SYNE-2	3' GATTGTGTTCCCTCCCCAGGA 17534	A	CA
		TC TGG GGAGGAACACAATC		
		AG ACC CCTCCTTGTGTTAG		
		G _		
GAM1840	LOC121838	5' ATTGTGTTCCCTCAAATTCAT 37417	CAG_	
		ATGG GAGGAACACAAT		
		TACT CTCCTTGTGTTA		
		TAAA		
GAM1840	LOC158337	3' GATTGCATCAAGAGCCATGGTA 41960	AGGAG	ACA
		TATCATGGC GA CAATC		
		ATGGTACCG CT GTTAG		
		AGAA_ AC_		
GAM1841	ANKRD3	3' CCCAGGCGTGGAAGCAT 21797	GA	A
		ATGCT TCACGCCT GG		
		TACGA GGTGCGGA CC		
		A_ C		
GAM1841	DBN1	3' CCTAGGCGCGGTTTCAGGTCA 10638	ATG	_ A
		TGAC CTGA TC CGCCTAGG		
		ACTG GACT GG GCGGATCC		
		_ T C		
GAM1841	DBN1	3' CCTAGGCGCGGTTTCAGGTCA 28121	ATG	_ A
		TGAC CTGA TC CGCCTAGG		

		ACTG GACT GG GCGGATCC		
		___ T C		
GAM1841	ST7	3' GTCCTAGTTGTTTCAGCATG 22432	TC	C
		CATGCTGA ACG CTAGGAC		
		GTACGACT TGT GATCCTG		
		___ T		
GAM1841	THBD	5' CCTGGCCGATCCGCATGTCA 5918	T	AC T
		TGACATGC GATC GCC AGG		
		ACTGTACG CTAG CGG TCC		
		C C_ _		
GAM1841	DKFZP727M111	5' GGCATGATCAGCACATCA 17800	CA	C
		TGA TGCTGATCA GCC		
		ACT ACGACTAGT CGG		
		AC A		
GAM1841	KIAA0700	3' CCTAGGCGTATGTGTAT 35659	TG	C
		ATGC AT ACGCCTAGG		
		TATG TA TGCGGATCC		
		TG _		
GAM1841	LOC116166	3' CCCAGAAGATTAGCATGCCA 30060	A	ACGC A
		TG CATGCTGATC CT GG		
		AC GTACGATTAG GA CC		
		C AA_ C		
GAM1841	LOC158987	3' CTTGCTAATCAGCATATCA 42048	C	CAC CT
		TGA ATGCTGAT GC AG		
		ACT TACGACTA CG TC		
		A AT_ CT		
GAM1841	LOC165904	3' TCAGCAATCAGCATGTC 40195	CAC	CTAG
		GACATGCTGAT GC GA		
		CTGTACGACTA CG CT		
		A_ A_		
GAM1841	LOC90678	3' TCCTAAGCTCCAAGCATGTC 28747	GATCAC	C
		GACATGCT GC TAGGA		
		CTGTACGA CG ATCCT		
		ACCT_ A		
GAM1841	LOC91807	5' CCTGCACCAGCATGTCA 33384	ATCAC	CT
		TGACATGCTG GC AGG		
		ACTGTACGAC CG TCC		
		CA_ _		
GAM1842	MPZ	3' GACAAGTGATCGCCACCCCCC 6130	A TA T T	C
	A	TG GG GT GT GATCACT GTC		

		AC CC CA CG CTAGTGA CAG	
		C CC C _ A	
GAM1842	LOC147080 5'	ACAAGTGATCAAACCT 40796	AGTTG C
		AGGT TTGATCACT GT	
		TCCA AACTAGTGA CA	
		_____ A	
GAM1843	CYP4F3 3'	CTGTTCCACAGTCCTGTATTCC 6591	TA AA_____
	A	TGGGATACG GGC AACAG	
		ACCTTATGT CTG TTGTC	
		C_ ACACC	
GAM1843	DMD 3'	CTGCTTTACTGTGTATCTCA 5570	GC A
		TGGGATACGTAG AAA CAG	
		ACTCTATGTGTC TTT GTC	
		A_ C	
GAM1843	DMD 3'	CTGCTTTACTGTGTATCTCA 10155	GC A
		TGGGATACGTAG AAA CAG	
		ACTCTATGTGTC TTT GTC	
		A_ C	
GAM1843	DMD 3'	CTGCTTTACTGTGTATCTCA 10161	GC A
		TGGGATACGTAG AAA CAG	
		ACTCTATGTGTC TTT GTC	
		A_ C	
GAM1843	DMD 3'	CTGCTTTACTGTGTATCTCA 10168	GC A
		TGGGATACGTAG AAA CAG	
		ACTCTATGTGTC TTT GTC	
		A_ C	
GAM1843	DMD 3'	CTGCTTTACTGTGTATCTCA 10175	GC A
		TGGGATACGTAG AAA CAG	
		ACTCTATGTGTC TTT GTC	
		A_ C	
GAM1843	DMD 3'	CTGCTTTACTGTGTATCTCA 10181	GC A
		TGGGATACGTAG AAA CAG	
		ACTCTATGTGTC TTT GTC	
		A_ C	
GAM1843	DMD 3'	CTGCTTTACTGTGTATCTCA 10186	GC A
		TGGGATACGTAG AAA CAG	
		ACTCTATGTGTC TTT GTC	
		A_ C	
GAM1843	DMD 3'	CTGCTTTACTGTGTATCTCA 10193	GC A
		TGGGATACGTAG AAA CAG	

		ACTCTATGTGTC TTT GTC	
		A_ C	
GAM1843 DMD	3'	CTGCTTTACTGTGTATCTCA 10203	GC A
		TGGGATACGTAG AAA CAG	
		ACTCTATGTGTC TTT GTC	
		A_ C	
GAM1843 DMD	3'	CTGCTTTACTGTGTATCTCA 10208	GC A
		TGGGATACGTAG AAA CAG	
		ACTCTATGTGTC TTT GTC	
		A_ C	
GAM1843 DMD	3'	CTGCTTTACTGTGTATCTCA 10213	GC A
		TGGGATACGTAG AAA CAG	
		ACTCTATGTGTC TTT GTC	
		A_ C	
GAM1843 DMD	3'	CTGCTTTACTGTGTATCTCA 10220	GC A
		TGGGATACGTAG AAA CAG	
		ACTCTATGTGTC TTT GTC	
		A_ C	
GAM1843 DMD	3'	CTGCTTTACTGTGTATCTCA 10232	GC A
		TGGGATACGTAG AAA CAG	
		ACTCTATGTGTC TTT GTC	
		A_ C	
GAM1843 FGFR1	3'	CTGTTTTGCCTTCACCCA 17978	ATACGT
		TGGG AGGCAAAACAG	
		ACCC TCCGTTTTGTC	
		ACT__	
GAM1843 FGFR1	3'	CTGTTTTGCCTTCACCCA 23372	ATACGT
		TGGG AGGCAAAACAG	
		ACCC TCCGTTTTGTC	
		ACT__	
GAM1843 FGFR1	3'	CTGTTTTGCCTTCACCCA 6207	ATACGT
		TGGG AGGCAAAACAG	
		ACCC TCCGTTTTGTC	
		ACT__	
GAM1843 NPY2R	3'	CTGTTTTGCTCCTACCCA 6611	A CGTA
		TGGG TA GGCAAAACAG	
		ACCC AT TCGTTTTGTC	
		_ CC_	
GAM1843 NRAS	3'	CTGTTTTGGGGCTTTCCCA 8361	TAC AGG
		TGGGA GT CAAAACAG	

		ACCCT CG GTTTTGTC	
		TT_ GG_	
GAM1843	PIK3C2B	3' GTTTTGCTGACTCATTCCA 8508	AC A
		TGGGAT GT GGCAAAAC	
		ACCTTA CA TCGTTTTG	
		CT G	
GAM1843	RGS16	3' CTGTTTTGCCTGTTGCTCA 8833	ATACG
		TGGG TAGGCAAAACAG	
		ACTC GTCCGTTTTGTC	
		GTT_	
GAM1843	SELPLG	3' CTGTTTTGGCAAGACCCCA 30019	ATAC AG_ _
		TGGG GT GC AAAACAG	
		ACCC CA CG TTTTGTC	
		___ GAA G	
GAM1843	SGT	3' GTTTCTGTCTGTGTCCCA 8942	GT _
		TGGGATAC AGGCA AAAC	
		ACCCTGTG TCTGT TTTG	
		_ C	
GAM1843	SLC7A6	3' CTGTTTTGTGATGCCCCCA 10130	ATA AG
		TGGG CGT GCAAAACAG	
		ACCC GTA TGTTTTGTC	
		CC_ G_	
GAM1843	TYRP1	3' TGCTCTATAAATAGTATTCCA 35797	_____ _
		TGGGATAC GTAG GCA	
		ACCTTATG TATC CGT	
		ATAAA T	
GAM1843	CYP4F2	3' CTGTTCCACAGTCCTGTATTCC 6742	TA AA_
	A	TGGGATACG GGC AACAG	
		ACCTTATGT CTG TTGTC	
		C_ ACACC	
GAM1843	DDX34	3' CTGTCCTGTATGTATCC 16161	AG AA
		GGATACGT GCA ACAG	
		CCTATGTA TGT TGTC	
		_ CC	
GAM1843	DJ971N18.2	3' CTGTTTTGTTTTCATCTCA 22135	ACGT
		TGGGAT AGGCAAAACAG	
		ACTCTA TTTGTTTTGTC	
		CT_	
GAM1843	DKFZp547M072	3' CTGTTTCCTCCGCCCCCA 30615	ATA T CA
		TGGG CG AGG AACAG	

ACCC GC TCC TTTGTC
 CC_ C _
 GAM1843 DKFZP586M1120 3' CTGTTTTGTGTGCGTTCCCA 25322 T G
 TGGGA ACGTA GCAAAACAG
 |||| |||| |||||
 ACCCT TGC GT TGT TTTGTC
 _ G
 GAM1843 FLJ10751 3' CTGTTTCATTCTGCTCGTATCCC 20092 TA A____
 A TGGGATACG GGCA AACAG
 ||||| ||| ||||
 ACCCTATGC TCGT TTGTC
 _ CTTAC
 GAM1843 FLJ10751 3' CTGTTTCATTCTGCTCGTATCCC 20191 TA A____
 A TGGGATACG GGCA AACAG
 ||||| ||| ||||
 ACCCTATGC TCGT TTGTC
 _ CTTAC
 GAM1843 FLJ12581 3' CTGTTTTGCTATATCCC 24300 CGTA
 GGGATA GGCAAAACAG
 |||| |||||
 CCCTAT TCGTTTTGTC
 A____
 GAM1843 KIAA0342 5' CTGTTTTGGTCCAACCCCA 34959 ATAC A ____
 TGGG GT GG CAAACAG
 ||| || |||||
 ACCC CA CC GTTTTGTC
 ____ A TG
 GAM1843 KIAA0478 3' CTGTTCTGCTTGTATCCCA 16978 TA A
 TGGGATACG GGCA AACAG
 ||||| ||| ||||
 ACCCTATGT TCGT TTGTC
 _ C
 GAM1843 KIAA1332 3' CTGCCTTGTCTGCCCCCA 35256 ATAC AA
 TGGG GTAGGCAA CAG
 ||| ||||| |||
 ACCC CGTCTGTT GTC
 C____ CC
 GAM1843 KIAA1529 5' TTTTGCCCGCGTATCTCA 34951 TA
 TGGGATACG GGCAAAA
 ||||| |||||
 ACTCTATGC CCGTTTT
 GC
 GAM1843 KIAA1674 3' CTGTCTTCTGTTGTGTCCCA 34112 TA C A
 TGGGATACG GG AA ACAG
 ||||| || |||
 ACCCTGTGT TC TT TGTC
 TG _ C
 GAM1843 KIAA1679 3' CTGTTCTCTTATGTGTCCCA 34751 CAA
 TGGGATACGTAGG AACAG
 ||||| ||||

		ACCCTGTGTATTC	TTGTC		
		TC_			
GAM1843	KIAA1878	3'	CTGTCCTGTCTGTGCTCCCA	44075	TA AA
			TGGGA CGTAGGCA ACAG		
			ACCCT GTGTCTGT TGTC		
			C_ CC		
GAM1843	STK38L	3'	CTGTTTTGCTACAACCCA	34290	ATAC G
			TGGG GTAG CAAAACAG		
			ACCC CATC GTTTTGTC		
			AA_ _		
GAM1843	LOC139248	5'	CTGGAGCTCCACGCATCCTA	37335	A A_ AAAA
			TGGGAT CGT GGC CAG		
			ATCCTA GCA TCG GTC		
			C CC AG_		
GAM1843	LOC145225	3'	CTGCTCCATCTAGGTGTCCCA	40526	G CAAAA
			TGGGATAC TAGG CAG		
			ACCCTGTG ATCT GTC		
			G ACCTC		
GAM1843	LOC146756	3'	CTGTTTTGCTCCATCCC	40736	ACGTA
			GGGAT GGCAAAACAG		
			CCCTA TCGTTTTGTC		
			CC_		
GAM1843	LOC148229	5'	CTGTCTTGCCTGCTGTCC	38497	C A
			GGATA GTAGGCAA ACAG		
			CCTGT CGTCCGTT TGTC		
			_ C		
GAM1843	LOC166867	5'	CTGTTTTGCTGAGTTCCCA	40222	T GTA
			TGGGA AC GGCAAAACAG		
			ACCCT TG TCGTTTTGTC		
			_ AG_		
GAM1843	LOC196510	3'	CTGTCCTGCTTTTGCTTCCCA	42395	TA T AA
			TGGGA CG AGGCA ACAG		
			ACCCT GT TTCGT TGTC		
			TC T CC		
GAM1843	LOC200220	3'	CTGTCCTGCTTTTGCTTCCCA	42744	TA T AA
			TGGGA CG AGGCA ACAG		
			ACCCT GT TTCGT TGTC		
			TC T CC		
GAM1843	LOC200310	3'	CTGTTTTGAGGACGATACCC	32708	_ A AGG
			GGG AT CGT CAAAACAG		

CCC TA GCA GTTTTGTC
 A _ GGA
 GAM1843 LOC201952 3' CTGTTTTGCAGCAGATCTCCA 43394 _ AC AG
 TGG GAT GT GCAAAACAG
 ||| ||| || |||||
 ACC CTA CG CGTTTTGTC
 T GA A_
 GAM1843 LOC202934 5' CTGCTTTTGCTGTATCCCA 43459 GTA _
 TGGGATAC GGCAAAA CAG
 ||||| ||||| |||
 ACCCTATG TCGTTTT GTC
 _ C
 GAM1843 LOC219627 3' CTGCTTTGTTGCATGTATCCTA 44274 A_ A
 TGGGATACGT GGCAAA CAG
 ||||| ||||| |||
 ATCCTATGTA TTGTTT GTC
 CG C
 GAM1843 LOC219848 3' CTGTTTTGCCCTTACTCTCA 43986 TAC _
 TGGGA GTA GGCAAAACAG
 |||| ||| |||||
 ACTCT CAT CCGTTTTGTC
 _ TC
 GAM1843 LOC222066 5' CTGTTTTGTGAAGCATCCCA 44556 AC AG_
 TGGGAT GT GCAAAACAG
 |||| || |||||
 ACCCTA CG TGTTTTGTC
 _ AAG
 GAM1843 LOC222962 3' CTGTTTCACCCCTGCTGTGTCC 44629 _ CA_
 CA TGGGATAC GTAGG AAACAG
 ||||| |||| |||||
 ACCCTGTG CGTCC TTTGTC
 T CCAC
 GAM1843 LOC254015 3' CTGTTTTGCTCCATCCC 46244 ACGTA
 GGGAT GGCAAAACAG
 |||| |||||
 CCCTA TCGTTTTGTC
 CC_
 GAM1843 LOC254778 3' CTGCTTTGCCTACTCTC 45977 TAC A
 GGGA GTAGGCAAA CAG
 ||| ||||| |||
 CTCT CATCCGTTT GTC
 _ C
 GAM1843 LOC255465 5' CTGCTTTTGCTGTATCCCA 46452 GTA _
 TGGGATAC GGCAAAA CAG
 ||||| ||||| |||
 ACCCTATG TCGTTTT GTC
 _ C
 GAM1844 AMACR 3' AGACTCTGATTCTACAGTGA 34014 A C A
 TCACTGTA AATTA GA TCT
 ||||| |||| || |||

			AGTGACAT TTAGT CT AGA		
			C _ C		
GAM1844	KIAA1305	3'	GAGATCACCTTGCAGTGA 24683		AATTAC A
			TCACTGTAA GA TCTC		
			AGTGACGTT CT AGAG		
			CCCA__ _		
GAM1844	LOC145547	3'	GAGATCACCTTGCAGTGA 37894		AATTAC A
			TCACTGTAA GA TCTC		
			AGTGACGTT CT AGAG		
			CCCA__ _		
GAM1845	CD3Z	3'	GCGGGAGCCTCCCTGCCTCA 6391		T AA__
			TGAGGCAGG GA CCCGT		
			ACTCCGTCC CT GGGCG		
			_ CCGA		
GAM1845	CXCL16	3'	ACGGGTTGGTTTCACCTCCTCA 22596	C	_____
			TGAGG AGGTGAA ACCCGT		
			ACTCC TCCACTT TGGGCA		
			_ TGGT		
GAM1845	HAP1	3'	CGAGTGCTCACCTGCCCA 10074	A	A_ C
			TG GGCAGGTGA AC CG		
			AC CCGTCCACT TG GC		
			C CG A		
GAM1845	PIGR	3'	CACCATTCTCCTGCCTCA 35936	T	ACCC
			TGAGGCAGG GAA GTG		
			ACTCCGTCC CTT CAC		
			T AC__		
GAM1845	PRG2	5'	ATCATCACCTGCCCA 8592	A	AACCCG
			TG GGCAGGTGA TGAT		
			AC CCGTCCACT ACTA		
			C _____		
GAM1845	PSD	5'	GCACTGCCTACCCACCTGCCCC 8670	A	AAACCC GA
	A		TG GGCAGGTG GT TGC		
			AC CCGTCCAC CG ACG		
			C CCATC_ TC		
GAM1845	PTGIS	3'	CACCATTCTCCTGCCTCA 6666	T	ACCC
			TGAGGCAGG GAA GTG		
			ACTCCGTCC CTT CAC		
			T AC__		
GAM1845	SLC22A12	3'	CACCCGTCCACCTGCCCA 29403	A	AA CC
			TG GGCAGGTG AC GTG		

		AC CCGTCCAC TG CAC		
		— C_ CC		
GAM1845 UNC13	3'	TGGGAGTCTCCCTGCCTCA 13069	T_ AA	
		TGAGGCAGG GA CCCG		
		ACTCCGTCC CT GGGT		
		CT GA		
GAM1845 YES1	3'	CACCATTCTCCTGCCTCA 11911	T ACCC	
		TGAGGCAGG GAA GTG		
		ACTCCGTCC CTT CAC		
		T AC__		
GAM1845 ZNF137	3'	CACCTGTGGTCCCAGCTGCCTC 9492	G AA _ _	
A		TGAGGCAG TG ACC C GTG		
		ACTCCGTC AC TGG G CAC		
		G CC TTC		
GAM1845 APCL	3'	GCATTACCTACCCGGCCCCA 12501	A A_ AACCC	
		TG GGC GGTGA GTGATGC		
		AC CCG CCACT CATTACG		
		C GC C__		
GAM1845 C11orf17	3'	CACCATTCTCCTGCCTCA 21806	T ACCC	
		TGAGGCAGG GAA GTG		
		ACTCCGTCC CTT CAC		
		T AC__		
GAM1845 CEACAM8	3'	CACCATTCTCCTGCCTCA 7560	T ACCC	
		TGAGGCAGG GAA GTG		
		ACTCCGTCC CTT CAC		
		T AC__		
GAM1845 DKFZP434P0111	3'	GCCTCAGCCCCACACCTGCCTCA 33456	AAACCCG T	
		TGAGGCAGGTG TGA GC		
		ACTCCGTCCAC ACT CG		
		ACCCG_ C		
GAM1845 DKFZP566G1424	5'	CATCTGGCCCCACCTGCTCA 41113	G AAAC T	
		TGAG CAGGTG CCG GATG		
		ACTC GTCCAC GGT CTAC		
		_ CCC_ _		
GAM1845 FLJ14442	3'	GCGATTCCCCTGCCTCA 26538	T ACC	
		TGAGGCAGG GAA CGT		
		ACTCCGTCC CTT GCG		
		C A__		
GAM1845 FLJ20291	3'	ACCTATTTCACTGCCTCA 19340	G CCC	
		TGAGGCAG TGAAA GT		

			ACTCCGTC ACTTT CA		
			— ATC		
GAM1845	FLJ23556	3'	CACCATTCTCCTGCCTCA 24319	T	ACCC
			TGAGGCAGG GAA GTG		
			ACTCCGTCC CTT CAC		
			T AC__		
GAM1845	KIAA0720	3'	GTACCACCCACCTGCCCA 31236	A	AAACCC A
			TG GGCAGGTG GTG TGC		
			AC CCGTCCAC CAC ATG		
			— CC__ C		
GAM1845	KIAA1615	3'	GCGATTCCCCTGCCTCA 34087	T	ACC
			TGAGGCAGG GAA CGT		
			ACTCCGTCC CTT GCG		
			C A__		
GAM1845	KIAA1727	3'	GCTTCAGAGTTTCACCTGCCCA 32035	A	CCG T
			TG GGCAGGTGAAAC TGA GC		
			AC CCGTCCACTTTG ACT CG		
			— AG_ T		
GAM1845	KIAA1877	3'	CACCATTCTCCTGCCTCA 32880	T	ACCC
			TGAGGCAGG GAA GTG		
			ACTCCGTCC CTT CAC		
			T AC__		
GAM1845	KIAA1924	3'	CACCATTCTCCTGCCTCA 36472	T	ACCC
			TGAGGCAGG GAA GTG		
			ACTCCGTCC CTT CAC		
			T AC__		
GAM1845	Nup43	3'	TCATGATCCACCTGCCTCA 23935		AAACC
			TGAGGCAGGTG CGTGA		
			ACTCCGTCCAC GTACT		
			CTA__		
GAM1845	PHYHIP	5'	GCTCTTGCGTGTACCTGCCCC 16510	A	AAC T T
	A		TG GGCAGGTGA CCG GA GC		
			AC CCGTCCACT GGT CT CG		
			C GTC T _		
GAM1845	PRO1992	3'	GCGATTCCCCTGCCTCA 15334	T	ACC
			TGAGGCAGG GAA CGT		
			ACTCCGTCC CTT GCG		
			C A__		
GAM1845	RAP140	3'	CACCATTCTCCTGCCTCA 17552	T	ACCC
			TGAGGCAGG GAA GTG		

	ACTCCGTCC CTT CAC		
	T AC__		
GAM1845 LOC121504 3'	GCGATTCACCTGCCTCA 36670	ACC	
	TGAGGCAGGTGAA CGT		
	ACTCCGTCCACTT GCG		
	A__		
GAM1845 LOC128077 3'	CACCATTCTCCTGCCTCA 36915	T ACCC	
	TGAGGCAGG GAA GTG		
	ACTCCGTCC CTT CAC		
	T AC__		
GAM1845 LOC146909 3'	CACCATTCTCCTGCCTCA 38265	T ACCC	
	TGAGGCAGG GAA GTG		
	ACTCCGTCC CTT CAC		
	T AC__		
GAM1845 LOC147080 5'	CACCATTCTCCTGCCTCA 40797	T AACCC A	
	TGAGGCAGG GA GTG TG		
	ACTCCGTCC CT TAC AC		
	T ____ C		
GAM1845 LOC147299 3'	CATGGCCTCACCTGCTCA 38329	G AAC	
	TGAG CAGGTGA CCGTG		
	ACTC GTCCACT GGTAC		
	_ CC_		
GAM1845 LOC151701 3'	CAGAGCCTCACCTGCCTCA 41384	AACCC GA	
	TGAGGCAGGTGA GT TG		
	ACTCCGTCCACT CG AC		
	C__ AG		
GAM1845 LOC154877 3'	CACCATTCTCCTGCCTCA 41739	T ACCC	
	TGAGGCAGG GAA GTG		
	ACTCCGTCC CTT CAC		
	T AC__		
GAM1845 LOC220002 3'	CATTGCTTCACCTGGCCCCA 44047	A _ ACCC TG	
	TG GGC AGGTGAA G ATG		
	AC CCG TCCACTT C TAC		
	C G ____ GT		
GAM1845 LOC91115 3'	CACCATTCTCCTGCCTCA 32393	T ACCC	
	TGAGGCAGG GAA GTG		
	ACTCCGTCC CTT CAC		
	T AC__		
GAM1846 FLJ10713 3'	AGGCCACATCTATGGTAATTAA 20039	GCTCT	
	TTAGTTACCG TGTGGCCT		

AATTAATGGT ACACCGGA
 ATCT_
 GAM1846 FLJ22794 5' GAGACCCAAGAGCCACAATA 44031 ACC T C
 TTAGTT GGCTCTTG GG CTC
 ||||| ||||| || |||
 AATCAA CCGAGAAC CC GAG
 CA_ _ A
 GAM1846 LOC152271 3' GAGGCCACAAGAAGAAAATA 39239 ACCGGC
 TTAGTT TCTTGTGGCCTC
 ||||| |||||
 AGTCAA AGAACACCGGAG
 AAGA_
 GAM1847 AIM1 3' ACTTACTCATCGTTTCAA 44113 CCATC C
 TTGAA ACGGTGAG AAGT
 ||||| ||||| |||||
 AACTT TGCTACTC TTCA
 _ _ A
 GAM1847 KIAA1301 3' CTTACCCTTGAACGTGGTTCAA 32976 _ C_
 TTGAACCA TCA GGTGAG
 ||||| || |||||
 AACTTGGT AGT CCATTC
 GCA TC
 GAM1847 LOC157681 5' CTCAGTGATGGTCTAA 39644 A GG
 TTG ACCATCAC TGAG
 || ||||| |||||
 AAT TGGTAGTG ACTC
 C _
 GAM1847 LOC92391 3' ACCTGCTCACTGTTCTGTCTCA 34271 AC TC A
 A TTGA CA ACGGTGAGCA GT
 |||| || ||||| |||||
 AACT GT TGCTACTCGT CA
 CT CT C
 GAM1848 SLC9A6 3' AGTTTGAACGTCAGTGTAC 13052 CA
 GTGACAC ACGTTCGAATT
 ||||| |||||
 CACTGTG TGCAAGTTTGA
 AC
 GAM1848 SPF30 3' AGCAATTCATTGGAACAC 12489 ACA CGTTC
 GTG CCAA GAATTGCT
 || ||||| |||||
 CAC GGTT CTTAACGA
 AA_ A_
 GAM1848 FLJ10035 3' AGCAATTTTGGCTTAATGGCAC 19706 ACA AC_ TC
 A TGTG CCA GT GAATTGCT
 |||| || || |||||
 ACAC GGT CG TTTAACGA
 _ AATT GT
 GAM1848 PELI1 3' AGCATGGTAACGATGGTGTAC 21813 A CGAAT
 A TGTGACACCA CGTT TGCT
 ||||| ||||| |||||

		ACACTGTGGT GCAA ACGA	
		A TGGT_	
GAM1848	LOC145786 5'	CAATTCAGATCGTGTCACA 40590	CAAC TC
		TGTGACAC GT GAATTG	
		ACACTGTG TA CTTAAC	
		C__ GA	
GAM1849	ATP11B 3'	GATAGTGGCAAGCACCAAGT 39147	T G TG_
		ACTTGGTG CT TGCC ATC	
		TGAACCAC GA ACGG TAG	
		_ _ TGA	
GAM1849	PIK3C2B 5'	ATCAGGCGCCCAGACACCATGT 8505	T _
		AC TGGTGTCT GTGCCTGAT	
		TG ACCACAGA CGCGGACTA	
		T CC	
GAM1849	CDCA7 3'	CAGGCACAAGGTTCAAGTT 25687	TGTC
		AACTTGG TGTGCCTG	
		TTGAACT ACACGGAC	
		TGGA	
GAM1849	HABP2 3'	ATCAAACATACCCCAAGTTA 10342	T C GCC
		TA ACTTGG GT TGT TGAT	
		ATTGAACC CA ACA ACTA	
		C T A__	
GAM1849	KIAA0523 3'	GACCAGCCACACCAAGT 33642	CT T C A
		ACTTGGTGT G GC TG TC	
		TGAACCACA C CG AC AG	
		_ _ _ C	
GAM1849	LOC122618 5'	ATCAGGATAGACACCAAG 29014	G
		CTTGGTGTCTGT CCTGAT	
		GAACCACAGATA GGACTA	
		_	
GAM1849	LOC154739 5'	GGATCAGGCAGCTCCAA 41720	T CTG
		TTGG GT TGCCTGATCC	
		AACC CG ACGGACTAGG	
		T _	
GAM1849	LOC203276 3'	GGATCAGGCAGCTCCAA 43489	T CTG
		TTGG GT TGCCTGATCC	
		AACC CG ACGGACTAGG	
		T _	
GAM1849	LOC203305 3'	GGATCAGGCAGCTCCAA 43513	T CTG
		TTGG GT TGCCTGATCC	

		AACC CG ACGGACTAGG			
		T ____			
GAM1849	LOC204970 3'	GGATCAGGCAGCACCCAG	43071	T CTG	
		CT GGTGT TGCCTGATCC			
		GA CCACG ACGGACTAGG			
		C ____			
GAM1849	LOC206324 5'	GACCAAGGCACAGAAAGCTGA	43612	TG G_ A	
		T GT TCTGTGCCTG TC			
		A CG AGACACGGAC AG			
		GT AA C			
GAM1849	LOC219894 3'	GGA CTCAGCAGACACCAA	44797	TGC _	
		TTGGTGTCTG CTGA TCC			
		AACCACAGAC GACT AGG			
		____ C			
GAM1849	LOC254243 3'	GGATCAGGCAGCTCCAA	46515	T CTG	
		TTGG GT TGCCTGATCC			
		AACC CG ACGGACTAGG			
		T ____			
GAM1849	LOC90038 3'	GGATCAGGCAGCTCCAA	30652	T CTG	
		TTGG GT TGCCTGATCC			
		AACC CG ACGGACTAGG			
		T ____			
GAM1849	LOC91796 3'	GGATCAAACACAAAGGGCATCA	33373	____ CC	
		TGGTGTCT GTG TGATCC			
		ACTACGGG CAC ACTAGG			
		AAA AA			
GAM1850	BCRP2 3'	TCACCCTGTTTACATGCCATA	31276	A T TTAAC	
		TATGGCAT TA AT GGTGA			
		ATACCGTA AT TG CCACT			
		C T TC____			
GAM1850	NCAM2 3'	TCACCATTAAATATAATTGGCT	10891	ATA_ C	
	A	TGGC TATATTTAA GGTGA			
		ATCG ATATAAATT CCACT			
		GTTA A			
GAM1850	Di-Ras2 3'	TCACAAACATGTATATGCCA	19045	TTAACG	
		TGGCATATATAT GTGA			
		ACCGTATATGTA CACT			
		CAAA____			
GAM1851	APPBP2 3'	ATGCAAGATGCTCTGAT	13079	T TC	
		ATCAGAGC TCT TGCAT			

				TAGTCTCG AGA ACGTA		
				T _		
GAM1851	LMAN1	3'	ATGATGCAGCCTCTGA	12097	CTTCTT	
			TCAGAG CTGCATCAT			
			AGTCTC GACGTAGTA			
			C _			
GAM1851	RNF14	3'	ATGTGCCCAAAGCTCTGA	10502	CTTCT T	
			TCAGAGCTT GCA CAT			
			AGTCTCGAA CGT GTA			
			ACC _ _			
GAM1851	SCN1A	5'	ATGTGGAAATAGCTCTGATG	42830	TC TG	
			CATCAGAGCT TTC CAT			
			GTAGTCTCGA AAG GTA			
			TA GT			
GAM1851	FLJ20274	3'	TATGATGCAAAAAAGGTTTTG	31386	C C	
			CAGAGCTT TT TGCATCATA			
			GTTTTGGA AA ACGTAGTAT			
			A A			
GAM1851	FLJ21617	5'	ATGACACAGAAGAGCGCTG	25165	A T CA	
			CAG GCT CTTCTG TCAT			
			GTC CGA GAAGAC AGTA			
			G _ AC			
GAM1851	KATII	5'	TGAAGAAGAAGCTTGATG	18343	G G	
			CATCA AGCTTCTTCT CA			
			GTAGT TCGAAGAAGA GT			
			_ A			
GAM1851	KIAA0090	3'	ATGATGCAGAAAGGATC	42650	G C	
			GA CTT TTCTGCATCAT			
			CT GGA AAGACGTAGTA			
			A _			
GAM1851	NYD-SP16	3'	ATGTCTAAGAAGCTCCCATG	25693	CA CT	
			CAT GAGCTTCTT GCAT			
			GTA CTCGAAGAA TGTA			
			CC TC			
GAM1851	LOC203378	5'	TATGGGAGAGAAGAAGCTATGA	43557	G GCA	
			TCA AGCTTCTTCT TCATA			
			AGT TCGAAGAAGA GGTAT			
			A GAG			
GAM1852	ABCB4	5'	ATGGAAGAAATAACAGTATGT	6029	ATGCAGC	
			GCATACT TCTCCAT			

			TGTATGA	AGAAGGTA		
			CAATAA_			
GAM1852	ABCB4	5'	ATGGAAGAAATAACAGTATGT	20834	ATGCAGC	
			GCATACT	TCTTCCAT		
			TGTATGA	AGAAGGTA		
			CAATAA_			
GAM1852	GRM6	3'	GAAGAGCTTCTGTATAGTA	6509	___	
			TACTATGCA	GCTCTTC		
			ATGATATGT	CGAGAAG		
			CTT			
GAM1852	HTR2C	3'	ATGGTGTCTGCATGTATGC	6532	T	CTCTT
			GCATAC	ATGCAG	CCAT	
			CGTATG	TACGTC	GGTA	
			_	CTGT_		
GAM1852	CGGBP1	3'	TGGAAGAACTGCCCTGCT	9743	TACTAT	C
			AGCA	GCAG	TCTTCCA	
			TCGT	CGTC	AGAAGGT	
			CC___	A		
GAM1852	DKFZP434G1411	3'	GAGCTCCTGCATAGTATGC	44231	___	
			GCATACTATGCA	GCTC		
			CGTATGATACGT	CGAG		
			CCT			
GAM1852	FLJ10154	3'	ATGGAAAACTTTGTATGGTA	19744	CTC___	
			TACTATGCAG	TTCCAT		
			ATGGTATGTT	AAGGTA		
			TCAAA			
GAM1852	FLJ14281	5'	ATGGAAGAGCTGGTTATAG	24451	___	
			CTATG	CAGCTCTTCCAT		
			GATAT	GTCGAGAAGGTA		
			TG			
GAM1852	FLJ20457	3'	GAAGAGTTTTAAGTAGC	19497	A	A C
			GC	TACT TG AGCTCTTC		
			CG	ATGA AT TTGAGAAG		
			_	_	T	
GAM1852	GMFB	3'	AAGTTCTGCATAGCATCTA	10327	C A	CT
			TAG	AT CTATGCAG	CTT	
			ATC	TA GATACGTC	GAA	
			_	C	TT	
GAM1853	CDH17	3'	GTGCTATTTTCAGCAA	10270	ATCT	
			TTGC	TGAAATAGCAC		

AACG ACTTTATCGTG

GAM1853 CPNE3 3' GGTGCCCAGGATAGATGTAATA 9995 TGAAATA
TATTGCATCT GCACC
||||||| ||||
ATAATGTAGA CGTGG
TAGGACC

GAM1853 CUL3 3' TGCAATCTAAAGATGCAATA 9646 GAA A
TATTGCATCTT AT GCA
||||||| ||||
ATAACGTAGAA TA CGT
ATC A

GAM1853 FSTL1 3' GGTGCTATTTCTCTGTAA 13953 TCTT
TTGCA GAAATAGCACC
|||| | |||||
AATGT CTTTATCGTGG
CT__

GAM1853 GPM6A 3' GTGCTTGCAAAATGTAATA 11779 C AAAT
TATTGCAT TTG AGCAC
||||| || | ||||
ATAATGTA AAC TCGTG
A GT__

GAM1853 IL8 3' GTGCCAGATGCAATA 45339 T AAATA _
TATTGCATCT G GCA C
||||||| | |||
ATAACGTAGA C CGT G
_ T

GAM1853 UMPS 3' GGTGCTATAGGCATGCA 5941 _ GAA
TGCAT CTT ATAGCACC
|||| | |||||
ACGTA GGA TATCGTGG
C _

GAM1853 CLDN1 3' TGCTATTTCACTTGAGCAA 22084 A T__
TTGC TC TGAAATAGCA
||| || |||||
AACG AG ACTTTATCGT
_ TTC

GAM1853 DKFZp434E2220 5' TGCTATTTCAAAGCAATA 19112 ATC
TATTGC TTGAAATAGCA
|||| | |||||
ATAACG AACTTTATCGT
A__

GAM1853 FLJ12409 3' TGCTATGAAAGATGCAA 24755 GAA
TTGCATCTT ATAGCA
|||||| | ||||
AACGTAGAA TATCGT
AG_

GAM1853 FLJ20274 3' TGCTGGGGCAAGATGCAGTA 31387 AAA
TATTGCATCTTG TAGCA
||||||| ||||

		ATGACGTAGAAC	GTCGT		
		GGG			
GAM1853	FLJ22056	3'	GTTTAATCAAATGCAATG	22870	C AAT
			TATTGCAT TTGA AGC		
			GTAACGTA AACT TTG		
			A AAT		
GAM1853	FLJ23598	3'	GCATGTGGTCAAGATGCA	24156	A_ _
			TGCATCTTGA ATA GC		
			ACGTAGA AACT TGT CG		
			GG A		
GAM1853	HIC	3'	GTGCTATTTTTGTAA	33493	TCTT
			TTGCA GAAATAGCAC		
			AATGT TTTTATCGTG		
			T_		
GAM1853	KIAA1500	3'	GGCACTATTCCTGGTGCAGTA	32068	TT A CA
			TATTGCATC GAA TAG CC		
			ATGACGTGG CTT ATC GG		
			TC _ AC		
GAM1853	MYH10	3'	TGCTATTTTCAGTGAGCAA	34266	A _
			TTGC TC TTGAAATAGCA		
			AACG AG GACTTTATCGT		
			_ T		
GAM1853	PRO0082	3'	GGTGCTATATTAATTCAATA	20670	CATC A
			TATTG TTGA ATAGCACC		
			ATAAC AATT TATCGTGG		
			TT_ A		
GAM1853	SLC6A14	3'	GGTGCTATTTAAGGTGTGCAAT	14102	_ G
			ATTGCAT CTT AAATAGCACC		
			TAACGTG GGA TTTATCGTGG		
			T A		
GAM1853	LOC256733	5'	TGCTATAGGATGCTATA	46369	T GAA
			TAT GCATCTT ATAGCA		
			ATACGTAGGA TATCGT		
			T _		
GAM1853	LOC83690	3'	CTATTCCAAATGCAATA	25484	C A
			TATTGCAT TTG AATAG		
			ATAACGTA AAC TTATC		
			_ C		
GAM1854	TEAD3	3'	TCCGGGGCGCTGACCCACCATC	9214	ATTAAAC T
	A		TGAT CAGT GTCTCGGA		

ACTA GTCG CGGGGCCT
 CCACCCA _
 GAM1854 FLJ14442 3' CCGAGTGTGATTTTAATATCA 26535 C_ TTGT
 TGATATTAAA CAG CTCGG
 ||||| ||| ||||
 ACTATAATTT GTT GAGCC
 TA GT_
 GAM1854 LOC150998 3' CCGAAGCCATTAGTTTAATAGC 41286 A C T TC
 A TG TATTAAAC AGT G TCGG
 || ||||| ||| ||||
 AC ATAATTTG TTA C AGCC
 G A C GA
 GAM1854 LOC256096 5' CCAAAACAATATTACAAGTTTA 46419 CA_____ CTC
 ATATCA GATATTAAAC GTTGT GG
 ||||| |||| ||
 CTATAATTTG TAACA CC
 AACATTA AAA
 GAM1855 COL15A1 3' GACAAAATCTGATCCATATA 7587 A G_
 TATAT GATCAGGTT GTT
 |||| ||||| |||
 ATATA CTAGTCTAA CAG
 C AA
 GAM1855 MYO1C 3' GACCAACCTGACCTACATG 30697 A A
 TAT TAG TCAGGTTGGTT
 ||| ||| |||||
 GTA ATC AGTCCAACCAG
 C C
 GAM1855 DKFZp564I1922 3' AACCAGAGTGACTGATATATAT 17721 G GT____
 A TATATA ATCAG TGGTT
 ||||| |||| |||||
 ATATAT TAGTC ACCAA
 A AGTGAG
 GAM1855 KIAA1579 3' AATCAAATTGCACTGATCTATG 20116 _ TGG
 TA TATATAGATCAG GT TTGATT
 ||||| ||| |||||
 ATGTATCTAGTC CG AACTAA
 A TTA
 GAM1855 LOC219686 3' AACCCCTGATTTATATA 43671 TT
 TATATAGATCAGG GGTT
 ||||| |||| |||||
 ATATATTTAGTCC CCAA
 _
 GAM1856 UC28 3' ATTATTATCTATTATCTCA 22279 A TT
 TGAGATAATA ATA ATGAT
 ||||| ||| |||||
 ACTCTATTAT TAT TATTA
 C _
 GAM1856 KIAA1463 3' CATGATATTCTTCATCTCA 35770 AATA
 TGAGAT AATATTATG
 ||||| |||||

		ACTCTA TTATAGTAC		
		CTTC		
GAM1856	OBTP	5' CATGAGTATTCATTATCTC 19077	A	_
		GAGATAAT AATA TTATG		
		CTCTATTA TTAT AGTAC		
		C G		
GAM1856	PCDH20	3' CAGAATGTTTATTACCTCA 23135	A	A
		TGAG TAATAAATATT TG		
		ACTC ATTATTTGTAA AC		
		C G		
GAM1856	LOC153020	3' ATCAAAGATATTTATTTCTCA 39353	AT	A_
		TGAG AATAAATATT TGAT		
		ACTC TTATTTATAG ACTA		
		CT AA		
GAM1857	ADH1B	3' CTCTAAATGTGACATGCAA 35961	GA	AA
		TTGCATGTC GCA TTAGAG		
		AACGTACAG TGT AATCTC		
		_ A_		
GAM1857	SCAMP1	3' CTCTAATTTGCATGGGCA 11290	GA_	
		TGTC GCAAATTAGAG		
		ACGG CGTTTAATCTC		
		GTA		
GAM1857	SLC10A2	3' CTAATTTGCTAGTGGA 6063	G	GTCG
		TT CAT AGCAAATTAG		
		AG GTG TCGTTTAATC		
		G A__		
GAM1857	FLJ20457	3' CTCTAACAACTGGCATGCAA 19496	G	CAAA
		TTGCATGTC AG TTAGAG		
		AACGTACGG TC AATCTC		
		_ AAC_		
GAM1857	KIAA1223	3' CTCTAATTTCTATTACATGTAA 35247	CG_	C
		TTGCATGT AG AAATTAGAG		
		AATGTACA TC TTTAATCTC		
		TTA _		
GAM1857	YME1L1	3' CTCTACTAAACATGCAA 29294	CG	CAAAT
		TTGCATGT AG TAGAG		
		AACGTACA TC ATCTC		
		AA _____		
GAM1857	YME1L1	3' CTCTACTAAACATGCAA 15538	CG	CAAAT
		TTGCATGT AG TAGAG		

		AACGTACA TC ATCTC		
		AA _____		
GAM1857	LOC154881 3'	CTTGTTTGCTCAAATGCAA 39498	GTC	T
		TTGCAT GAGCAAAT AG		
		AACGTA CTCGTTTG TC		
		AA_ T		
GAM1857	LOC256925 5'	CTCTGACACTGCTGCAACATGC 46611	CG_	AA_
	AA	TTGCATGT AGCA TTAGAG		
		AACGTACA TCGT AGTCTC		
		ACG CAC		
GAM1858	GCNT2 5'	GCTGTAATATCGGCACAGGGA 7239	CACAAAT	
		TCCCTG TGTTGCAGC		
		AGGGAC ATAATGTCTG		
		ACGGCT_		
GAM1858	LDHB 5'	TGTACTTTGTGCAGGGA 8091	TTGT	
		TCCCTGCACAAA TGCA		
		AGGGACGTGTTT ATGT		
		C_		
GAM1858	NPEPPS 3'	CTGCTTCGCTGCAGGGATA 12998	CAAAT	TT
		TATCCCTGCA TG GCAG		
		ATAGGGACGT GC CGTC		
		C_ TT		
GAM1858	PTPRK 3'	CTGTTACACTTGTGCAG 8733	AT	T
		CTGCACAA TGT GCAG		
		GACGTGTT ACA TGTC		
		C_ T		
GAM1858	PTPRO 3'	CTGCAGCATGCTGGGA 8739	T	CAAAT
		TCCC GCA TGTTGCAG		
		AGGG CGT ACGACGTC		
		T _____		
GAM1858	PTPRO 3'	CTGCAGCATGCTGGGA 25004	T	CAAAT
		TCCC GCA TGTTGCAG		
		AGGG CGT ACGACGTC		
		T _____		
GAM1858	PTPRO 3'	CTGCAGCATGCTGGGA 25012	T	CAAAT
		TCCC GCA TGTTGCAG		
		AGGG CGT ACGACGTC		
		T _____		
GAM1858	PTPRO 3'	CTGCAGCATGCTGGGA 25021	T	CAAAT
		TCCC GCA TGTTGCAG		

			AGGG CGT	ACGACGTC		
			T	_____		
GAM1858	PTPRO	3'	CTGCAGCATGCTGGGA	25031	T	CAAAT
			TCCC GCA	TGTTGCAG		
			AGGG CGT	ACGACGTC		
			T	_____		
GAM1858	SMARCD2	3'	GCCACTTTTTTTGTACAGGGGT	9051	C	TT__ T
	A		TATCCCTG ACAA	GT GC		
			ATGGGGAC TGTTT	CA CG		
			A	TTTT C		
GAM1858	VIPR1	3'	CTGCAACAGGCTTGTGCA	10991	A_	
			TGCACAA TTGTTGCAG			
			ACGTGTT GACAACGTC			
			CG			
GAM1858	C22orf19	3'	CAAAATCTGTGCAGGGA	9774	A	G
			TCCCTGCACA ATT TTG			
			AGGGACGTGT TAA AAC			
			C	_		
GAM1858	DKFZp547D155	3'	CTGCAAAGCTGTGCAGGG	34869		AATTG
			CCCTGCACA TTGCAG			
			GGGACGTGT AACGTC			
			CGA__			
GAM1858	ELF2	3'	GCCTTGGCATTTGTGCAG	13744	T	CA
			CTGCACAAAT GTTG GC			
			GACGTGTTTA CGGT CG			
			_	TC		
GAM1858	FLJ10648	3'	TGCCTGTGTAGGGATA	19985		AATTGTT
			TATCCCTGCACA GCA			
			ATAGGGATGTGT CGT			
			C_____			
GAM1858	FLJ20432	5'	ACAATTTTGCAGAGATA	19466	C	C
			TATC CTGCA AAATTGT			
			ATAG GACGT TTTAACA			
			A	_		
GAM1858	GOLGA1	5'	GCTCGTCATCTGTGCAGG	7862	AAT	T C
			CCTGCACA TG TG AGC			
			GGACGTGT AC GC TCG			
			CT_ T _			
GAM1858	KIAA0193	3'	GCTGAGCATGCTTGTGCAG	16543	AT_	G
			CTGCACAA TGTT CAGC			

		GACGTGTT ACGA GTCG		
		CGT _		
GAM1858 KIAA0746	3'	CTGCGTGAGTCTGTACAGGGAT 34414	C A GT	
A		TATCCCTG ACA ATT TGCAG		
		ATAGGGAC TGT TGA GCGTC		
		A C GT		
GAM1858 KIAA1041	3'	GCTGCAAGCAGTTTATATAAAG 17264	CCTGCAC	_
ATA		TATC AAATTGTT GCAGC		
		ATAG TTTGACGA CGTCG		
		AAATATA A		
GAM1858 KIAA1219	3'	GCTACTTTTCTGCAGGGATA 30758	C TT T	
		TATCCCTGCA AAA GT GC		
		ATAGGGACGT TTT CA CG		
		C T_ T		
GAM1858 LRRFIP1	3'	CTGCAGTATTTGAGCAGGGA 11120	A TGT	
		TCCCTGC CAAAT TGCAG		
		AGGGACG GTTTA ACGTC		
		A TG_		
GAM1858 NIR3	3'	GCTATTTATTTTGTGCAGAGA 32929	C T TT_	
		TC CTGCACAAA TG GC		
		AG GACGTGTTT AT CG		
		A T TTAT		
GAM1858 PAK6	3'	TTGATATTTGCACAGGGATA 21392	CA TGTTG	
		TATCCCTG CAAAT CAG		
		ATAGGGAC GTTTA GTT		
		AC TA_		
GAM1858 SNPH	3'	GCCACAAGCGCAGGGGTA 16296	ACAAA T	
		TATCCCTGC TTGT GC		
		ATGGGGACG AACA CG		
		CG_ C		
GAM1858 TP53TG3	3'	CTGCCTCAGCTCCGTGCAGGG 17671	AAA_ TT	
		CCCTGCAC TTG GCAG		
		GGGACGTG GAC CGTC		
		CCTC TC		
GAM1858 USP24	3'	GCTGGCGATGATCCCACTGGG 43818	TGCACAA TG _	
ATA		TATCCC AT TTGC AGC		
		ATAGGG TA AGCG TCG		
		TCACACC GT G		
GAM1858 LOC151571	5'	CTGTATCAGTGCAGGGA 41372	AAAT T	
		TCCCTGCAC TG TGCAG		

AGGGACGTG AC ATGTC
 _____ T
 GAM1858 LOC196337 5' GCTGCAACAACTGCTGCA 42359 _ AA
 TGCA CA TTGTTGCAGC
 ||||| || |||||
 ACGT GT AACACGTCG
 C C_

GAM1858 LOC221341 5' CTGGGACCCGTGCGGGGA 44619 AAATT G
 TCCCTGCAC GTT CAG
 ||||| || |||||
 AGGGGCGTG CAG GTC
 CC_ G

GAM1858 LOC54505 5' GCTGCAACATGGGCGG 33695 A AAT
 CTGC CA TGTTGCAGC
 ||||| || |||||
 GGCG GT ACAACGTCG
 G _

GAM1858 LOC54516 3' CATTAAC TTGAACAGGGATA 21123 CA A T
 TATCCCTG CAA TTG TG
 ||||| || |||||
 ATAGGGAC GTT AAT AC
 AA C T

GAM1858 LOC90917 3' GCTGCAAAGCAGATGTGCAGGG 32170 AA _
 A
 TCCCTGCACA TTGT TGCAGC
 ||||| || |||||
 AGGGACGTGT GACG ACGTCG
 A_ AA

GAM1859 HDAC4 3' TATGTGGAACAGTGTTTTA 12669 ATAAA
 TAAACATTG TACATA
 ||||| |||||
 ATTTTGTGAC GTGTAT
 AAAG_

GAM1859 HMGA2 3' TATGTATTTTCTATGTTTT 9570 T T
 AAAACAT GA AAATACATA
 ||||| || |||||
 TTTTGTA CT TTTATGTAT
 T T

GAM1859 PDE4D 3' ATGTATTTATTGCAATGT 36428 _
 ACATTG ATAAATACAT
 ||||| |||||
 TGTAAC TATTTATGTA
 GT

GAM1859 ADMP 3' ATGTATTTGTTGAGTTTTG 29655 A TG
 TAAAAC T ATAAATACAT
 ||||| | |||||
 GTTTTG A TGTTTATGTA
 _ GT

GAM1859 DKFZP586N0721 3' TATGTATTTATAGTGTTTTA 17710 A
 TAAACATTG TAAATACATA
 ||||| |||||

ATTTTGTGAT ATTTATGTAT

GAM1859	FLJ13096	3'	TATGTATTTATATGTGTTT	24568	TG
			AAACAT ATAAATACATA		
			TTTGTG TATTTATGTAT		
			TA		
GAM1859	FLJ22794	3'	TATGTATTTCTCATTGTTTTA	44035	T T
			TAAAACA TGA AAATACATA		
			ATTTTGT ACT TTTATGTAT		
			T C		
GAM1859	KIAA0232	3'	TATGTATTTATTTGTTTT	36038	TT
			AAAACA GATAAATACATA		
			TTTTGT TTATTTATGTAT		
GAM1859	MAPK8IP3	3'	TGTATTTTCAGTGTTTTA	27223	T
			TAAAACATTGA AAATACA		
			ATTTTGTGACT TTTATGT		
GAM1859	TESK2	3'	TATGTATTTATCAACATGT	31653	—
			ACAT TGATAAATACATA		
			TGTA ACTATTTATGTAT		
			CA		
GAM1859	LOC150225	5'	TGTAAATCAATGTTTTG	41194	AAA
			TAAAACATTGAT TACA		
			GTTTTGTAACTA ATGT		
			A—		
GAM1859	LOC221814	5'	GTGTGTATCCAATGTTTTA	45094	ATAA
			TAAAACATTG ATACAT		
			ATTTTGTAAAC TGTGTG		
			CTA—		
GAM1860	BACE2	3'	CCAGATGCCTTCTAGATTCA	29093	A TATA C—
			TGAG TCTAGAA GC CTGG		
			ACTT AGATCTT CG GACC		
			— C— TA		
GAM1860	BACE2	3'	CCAGATGCCTTCTAGATTCA	29091	A TATA C—
			TGAG TCTAGAA GC CTGG		
			ACTT AGATCTT CG GACC		
			— C— TA		
GAM1860	BACE2	3'	CCAGATGCCTTCTAGATTCA	14423	A TATA C—
			TGAG TCTAGAA GC CTGG		

			ACTT AGATCTT CG GACC		
			— C___ TA		
GAM1860	CHST6	3'	CCAGGGCTCACCCAGATTCA 22245	A	AGAATAT
			TGAG TCT AGCCCTGG		
			ACTT AGA TCGGGACC		
			— CCCAC__		
GAM1860	SCNN1A	3'	CCAGGGCTCCTCTAGCCTCA 6703	AT	ATAT
			TGAG CTAGA AGCCCTGG		
			ACTC GATCT TCGGGACC		
			C_ CC__		
GAM1860	SPON1	3'	CCAGGGCTGCACTCTAGATTCC 31300	AG	ATA
	A		TG ATCTAGA TAGCCCTGG		
			AC TAGATCT GTCGGGACC		
			CT CAC		
GAM1860	SUFU	3'	CCAGTACTGCAGATCTCA 18252	AGAATA	CC
			TGAGATCT TAG CTGG		
			ACTCTAGA GTC GACC		
			C___ AT		
GAM1860	AKAP11	3'	TCCAAAGATGTTCTAGATCT 18373		AGCCC
			AGATCTAGAATAT TGGA		
			TCTAGATCTTGTA ACCT		
			GAA__		
GAM1860	CHFR	3'	CCAGGGCTGGAGGCAGGTCCCA 20147	A	AGAATA
			TG GATCT TAGCCCTGG		
			AC CTGGA GTCGGGACC		
			C CGGAG_		
GAM1860	FLJ10724	3'	TCCAAGACTGGATGCTGGATCT 20055		AATA CCC
	CA		TGAGATCTAG TAG TGGA		
			ACTCTAGGTC GTC ACCT		
			GTAG AGA		
GAM1860	HRH4	3'	TCCAGATTTTATATTCCTAATC 22264	A	CTA CC_
	CCA		TG GAT GAATATAG CTGGA		
			AC CTA CTTATATT GACCT		
			C ATC TTA		
GAM1860	KIAA0152	3'	CCAGGTTTTTATAGATCCCA 16333	A	TATAGC
			TG GATCTAGAA CCTGG		
			AC CTAGATTTT GGACC		
			C T_____		
GAM1860	KIAA1871	3'	TCCAGGGCAGCTCAGACCTCA 30706	A	A ATATA
			TGAG TCT GA GCCCTGGA		

		ACTC AGA CT CGGGACCT	
		C _ CGA__	
GAM1860	MGC32043 3'	CCAGGGCTTGCTAAATCCA 29391	A C AATAT
		TG GAT TAG AGCCCTGG	
		AC CTA ATC TCGGGACC	
		_ A GT__	
GAM1860	MGC32104 3'	CCAAAGGCTCCTAGATCT 29504	AATAT C_
		AGATCTAG AGCC TGG	
		TCTAGATC TCGG ACC	
		C____ AA	
GAM1860	PPP1R16B 3'	CCAGGGCTACTAAAGACTTCA 30771	A AGAATA
		TGAG TCT TAGCCCTGG	
		ACTT AGA ATCGGGACC	
		C AATC__	
GAM1860	RAB1B 3'	TCCAGGGCCCTGGGCTGGACCT 25245	A AA TA
	CA	TGAG TCTAG TA GCCCTGGA	
		ACTC AGGTC GT CGGGACCT	
		C GG CC	
GAM1860	SMT3H2 3'	TCCAAAAGTTTCTCTAGGTCCC 13820	A ATAT CC_
	A	TG GATCTAGA AGC TGGA	
		AC CTGGATCT TTG ACCT	
		C CT__ AAA	
GAM1860	TP53TG3 3'	CCAGGCTGCTTCCCAGGCCTCA 17670	AT A_ TA C
		TGAG CT GAA TAGCC TGG	
		ACTC GA CTT GTCGG ACC	
		CG CC C_ _	
GAM1860	LOC158581 5'	TCCAGGGCATGGCCTTAAATCT 42016	CT_ AA A
	CA	TGAGAT AG TAT GCCCTGGA	
		ACTCTA TC GTA CGGGACCT	
		AAT CG _	
GAM1860	LOC166713 5'	TCCAGGGCAGACCTAGACTCA 42196	A AATATA
		TGAG TCTAG GCCCTGGA	
		ACTC AGATC CGGGACCT	
		_ CAGA__	
GAM1860	LOC196074 5'	CCAGGAGTTACACAGATCTCA 42321	AGAATA _
		TGAGATCT TAGC CCTGG	
		ACTCTAGA ATTG GGACC	
		CAC__ A	
GAM1861	FLJ12838 3'	CACATGAGAAAATATCTGA 23922	CC ACCG
		TTAGATAT TC TTATGTG	

AGTCTATA AG AGTACAC
 AA ____
 GAM1861 LOC253971 3' CACAAGTGAGGATACGTAA 45986 GA CGTTA
 TTA TATCCTCAC TGTG
 ||| ||||| |||
 AAT ATAGGAGTG ACAC
 GC A____
 GAM1862 BACH2 3' TGAGGTTTTTCTGCCAGTG 22382 ____
 CACTGGCAGA ATCTCA
 ||||| |||||
 GTGACCGTCT TGGAGT
 TTT
 GAM1862 CLECSF12 3' TGAATTTTCATTCTGCCATTGA 37686 C CTC_
 TCA TGGCAGAAT ATTCA
 ||| ||||| |||||
 AGT ACCGTCTTA TAAGT
 T CTTT
 GAM1862 CLTCL1 3' TGAATGAGACCCAGCTGA 31839 _ CAGAA
 TCA CTGG TCTCATTCA
 ||| ||| |||||
 AGT GACC AGAGTAAGT
 C C____
 GAM1862 HS2ST1 3' AATGAGATGGCATGTGA 14572 _ G GAA
 TCAC TG CA TCTCATT
 ||| || ||| |||||
 AGTG AC GT AGAGTAA
 T G ____
 GAM1862 KCNAB2 3' TGAGCCTCATGCCAGTGA 9709 _ AT
 TCACTGGCA GA CTCA
 ||||| || |||
 AGTGACCGT CT GAGT
 A CC
 GAM1862 TCFL4 3' TGAATGAGATGTCACCAGGA 31771 A CAGA
 TC CTGG ATCTCATTCA
 || ||| |||||
 AG GACC TAGAGTAAGT
 _ ACTG
 GAM1862 THRB 5' GAAGGAGATGTCAGTGA 6077 GAA A
 TCACTGGCA TCTC TTC
 ||||| ||| |||
 AGTGACTGT AGAG AAG
 ____ G
 GAM1862 TTC3 5' TGAAGTAGTTGCCAGTGA 9317 AAT CA
 TCACTGGCAG CT TTCA
 ||||| || |||
 AGTGACCGTT GA AAGT
 ____ TC
 GAM1862 ZNF124 3' TGAATGAGATGTTTTAGGA 9482 A CAGA
 TC CTGG ATCTCATTCA
 || ||| |||||

AG GATT TAGAGTAAGT
 _ TTG_
 GAM1862 AKAP11 3' TGAATGAGACCTCTGATAG 18376 G A_
 CTG CAGA TCTCATTCA
 ||| ||| |||||
 GAT GTCT AGAGTAAGT
 A CC
 GAM1862 C1QTNF2 3' TGAATGAGATACACCAGGA 25652 A CAGA
 TC CTGG ATCTCATTCA
 || ||| |||||
 AG GACC TAGAGTAAGT
 _ ACA_
 GAM1862 C21orf108 3' TGAATAAGTTAATTTCTGCCAG 42773 T___ C
 TG CACTGGCAGAA CT ATTCA
 ||||| || |||
 GTGACCGTCTT GA TAAGT
 TAATT A
 GAM1862 COL12A1 3' TGAATGAGACAAAAGCAGTGG 27937 GCAGAA
 TCACTG TCTCATTCA
 |||| |||||
 GGTGAC AGAGTAAGT
 GAAAAC
 GAM1862 COL12A1 3' TGAATGAGACAAAAGCAGTGG 10590 GCAGAA
 TCACTG TCTCATTCA
 |||| |||||
 GGTGAC AGAGTAAGT
 GAAAAC
 GAM1862 DKFZP564I0422 3' TGAACATAGATTTTCTGCCA 25438 ___ CA_
 TGGCAGA ATCT TTCA
 ||||| ||| |||
 ACCGTCT TAGA AAGT
 TT TAC
 GAM1862 DKFZP667O116 3' TGAATGGCCTCTTCTGCCAG 45266 TC___
 CTGGCAGAA TCATTCA
 ||||| |||||
 GACCGTCTT GGTAAGT
 CTCC
 GAM1862 FLJ10687 3' TGAATGAGATAAAAAGTGA 20011 GGCAGA
 TCACT ATCTCATTCA
 |||| |||||
 AGTGA TAGAGTAAGT
 AAAA_
 GAM1862 FLJ14260 3' TGAATGAGATGACTAACGG 24619 GC A_
 CTG AG ATCTCATTCA
 ||| || |||||
 GGC TC TAGAGTAAGT
 AA AG
 GAM1862 FLJ20445 3' AATGAGATTTTGTGGTG 19476 G
 CACTG CAGAATCTCATT
 |||| |||||

GTGGT GTTTTAGAGTAA

GAM1862 FLJ20972 3' TGAATGAGATCCTGAAAATGA 24628 CTGG A
TCA CAG ATCTCATTCA
||| ||| |||||
AGT GTC TAGAGTAAGT
AAAA C

GAM1862 FLJ21432 3' AATGAGATTCTGACGTG 23763 TGG
CAC CAGAATCTCATT
||| |||||
GTG GTCTTAGAGTAA
CA_

GAM1862 HU-K4 5' TGAATGAGATTGAGGCGTGG 14591 TG AG_
TCAC GC AATCTCATTCA
||| || |||||
GGTG CG TTAGAGTAAGT
_ GAG

GAM1862 HZFW1 3' AATGAGATCTCAGTGG 24914 GC A
TCACTG AGA TCTCATT
||||| ||| |||||
GGTGAC TCT AGAGTAA

GAM1862 KIAA0237 3' GAAGGAGCTCTGCCAGTGG 16448 AT A
TCACTGGCAGA CTC TTC
||||||| ||| |||
GGTGACCGTCT GAG AAG
C_ G

GAM1862 KIAA0322 3' TGACATTTTCTGGCCAGTGA 44563 _ C
TCACTGGC AGAAT TCA
||||| ||| |||
AGTGACCG TTTTA AGT
GTCC C

GAM1862 KIAA1775 3' TGGAGGAGACCCCGCCAGTGG 26946 AGAA A
TCACTGGC TCTC TTCA
||||| ||| |||
GGTGACCG AGAG AGGT
CCCC G

GAM1862 KIAA1948 3' AATGAGATCAGCCAGATGA 40075 _ A A
TCA CTGGC GA TCTCATT
||| ||| || |||||
AGT GACCG CT AGAGTAA
A A _

GAM1862 NCBP2 3' TGAGAGCTCTGTCAAGTGA 14294 A_
TCACTGGCAGA TCTCA
||||||| |||
AGTGA CTGTCT AGAGT
CG

GAM1862 PNPASE 3' AATGAGATTCTAACTAGGA 35100 A C_
TC CTGG AGAATCTCATT
|| ||| |||||

			AG GATC TCTTAGAGTAA		
			— AA		
GAM1862	SBI31	3'	TGAGATTTTCTCAGCCAGTGA 15267	_____	
			TC ACTGGC AGAATCTCA		
			AGTGACCG TTTTAGAGT		
			ACTC		
GAM1862	TXI1	5'	TGAATGAGGACTGCAATGA 20493	CTG AA	
			TCA GCAG TCTCATTCA		
			AGT CGTC GGAGTAAGT		
			AA_ A_		
GAM1862	ZNF17	3'	TGAATAAAATTCTGTTAGT 40069	CTC	
			ACTGGCAGAAT ATTCA		
			TGATTGTCTTA TAAGT		
			AAA		
GAM1862	LOC120114	3'	TGAAAATTCTGCCGGCGA 37215	A C_	
			TC CTGGCAGAAT TCA		
			AG GGCCGTCTTA AGT		
			C AA		
GAM1862	LOC122553	3'	TGAAGGGACATTCTGCCATGA 36691	C C A_	
			TCA TGGCAGAAT TC TTCA		
			AGT ACCGTCTTA AG AAGT		
			_ C GG		
GAM1862	LOC123242	5'	TGAAGAGTTTTCTGCCAATGA 37246	C T_ A	
			TCA TGGCAGAA CTC TTCA		
			AGT ACCGTCTT GAG AAGT		
			A TT _		
GAM1862	LOC145815	5'	GAATGGCTTGCCAGTGG 40605	AATC	
			TC ACTGGCAG TCATTC		
			GGTGACCGTT GGTAAG		
			C_		
GAM1862	LOC149448	3'	TGAATTTCTTCTGCCAGT 40991	TCTC	
			ACTGGCAGAA ATTCA		
			TGACCGTCTT TAAGT		
			CTT_		
GAM1862	LOC153146	3'	TGAATGAGACCTGAGTG 41578	GG AA	
			CACT CAG TCTCATTCA		
			GTGA GTC AGAGTAAGT		
			_ C_		
GAM1862	LOC153768	5'	TGAATGAGATCATGCGCA 28844	_ GA	
			TG GCA ATCTCATTCA		

AC CGT TAGAGTAAGT
 G AC
 GAM1862 LOC157627 3' AATGAGGTGTCCGAGTGA 39618 _ CAGA
 TCACT GG ATCTCATT
 ||||| || |||||
 AGTGA CC TGGAGTAA
 G TG__
 GAM1862 LOC196955 5' TGAAGAGTTTTCTGCCAATGA 37938 C T_ A
 TCA TGGCAGAA CTC TTCA
 ||| ||||| ||| ||||
 AGT ACCGTCTT GAG AAGT
 A TT _
 GAM1862 LOC201824 3' TGAATGCAGAACTTGCCAGT 42920 AA _
 ACTGGCAG TCT CATTCA
 ||||| ||| |||||
 TGACCGTT AGA GTAAGT
 CA C
 GAM1862 LOC219654 3' AGTGACCTTGCCAGTGA 43871 AATC
 TCACTGGCAG TCATT
 ||||| ||||
 AGTGACCGTT AGTGA
 CC__
 GAM1862 LOC222803 5' TGAATGTGCTGCCAGTGA 45305 AATCT
 TCACTGGCAG CATTCA
 ||||| ||||
 AGTGACCGTC GTAAGT
 GT__
 GAM1862 LOC257438 3' TGAGGCTGCTTCGCCAGTGA 45109 A ____
 TCACTGGC GAA TCTCA
 ||||| ||| ||||
 AGTGACCG CTT GGAGT
 _ CGTC
 GAM1862 LOC90906 3' TGAATGGGGATCCCAG 32155 CA A
 CTGG GA TCTCATTCA
 ||| || |||||
 GACC CT GGGGTAAGT
 _ A
 GAM1863 ASGR1 5' CAAGCTTCAGCCCCCTC 7384 ACTAA G C
 GAGGGG GT GAGGC TG
 ||||| || ||||| ||
 CTCCCC CG CTTCG AC
 _ A A
 GAM1863 ATP2B4 5' CTTCCACTCAGTTCCCCCA 34826 A A
 TG GGGGACT AGTGGAGG
 || ||||| |||||
 AC CCCTTGA TCACCTTC
 C C
 GAM1863 GNAZ 3' CAGACCTCCAGCCACTCA 7845 G A AAGT C
 TGAG GG CT GGAGG CTG
 ||| || ||| |||

ACTC CC GA CCTCC GAC
 A _ _ _ _ A
 GAM1863 KCNJ10 3' TCAGGATACCCAGTTCCTCA 8028 AAGT AGG
 TGAGGGGACT GG CCTGA
 ||||| || ||||
 ACTCCCTTGA CC GGA CT
 C _ _ ATA
 GAM1863 PAK4 3' CAGGCCTCCCACTCCTCCC 12505 CTA _
 GGA AGTGG AGGCCTG
 ||| |||| |||||
 CCCT TCACC TCCGGAC
 CC _ C
 GAM1863 PKD2L1 5' TCAAACCCCCACCTTCCAGTTC 18193 AA _ _ A CC
 CCTCA TGAGGGGACT GTGG GG TGA
 ||||| ||| || |||
 ACTCCCTTGA CACC CC ACT
 CCTTC C AA
 GAM1863 RERE 3' CAGGCCCCACCTTCTC 14404 ACTAA A
 GAGGGG GTGG GGCCTG
 |||| ||| |||||
 CTCTTC CACC CCGGAC
 _ _ C
 GAM1863 SELL 3' TCAGGCCTCCCTCAACCCC 6317 ACTA T
 GGGG AG GGAGGCCTGA
 ||| || |||||
 CCCC TC CCTCCGACT
 AAC _ _
 GAM1863 SNAI1 3' TCAGGGGACCCCACTCCCCTCA 12608 CTAA A _
 TGAGGGGA GTGG GG CCTGA
 ||||| ||| || ||||
 ACTCCCCT CACC CC GGA CT
 _ _ _ AGG
 GAM1863 SRGAP2 3' CAAGTCTCAGTCCCCTCA 36878 AAGTG C
 TGAGGGGACT GAGGC TG
 ||||| ||| ||
 ACTCCCCTGA CTCTG AC
 _ _ _ A
 GAM1863 C1orf8 5' TTCCACCCAGTCCCCCA 11300 A AA
 TG GGGGACT GTGGAG
 || ||||| |||||
 AC CCCCTGA CACCTT
 C CC
 GAM1863 CNOT8 5' CAGGCCTCCCACTCCCC 11179 CTAA
 GGGGA GTGGAGGCCTG
 ||| |||||
 CCCCT CACCTCCGGAC
 _ _ _
 GAM1863 COPS7B 3' CAGACCTGCCCGTCCCCTCA 22931 TAAGT _ C
 TGAGGGGAC GG AGG CTG
 ||||| || ||| |||

		ACTCCCCTG CC TCC GAC	
		C____ G A	
GAM1863	DDR1	5' TCAGCTATGACTCAGTCCCCT 15179	A GGA C
		AGGGGACT AGT GGC TGA	
		TCCCCTGA TCA TCG ACT	
		C GTA _	
GAM1863	DDR1	5' TCAGCTATGACTCAGTCCCCT 15181	A GGA C
		AGGGGACT AGT GGC TGA	
		TCCCCTGA TCA TCG ACT	
		C GTA _	
GAM1863	DDR1	5' TCAGCTATGACTCAGTCCCCT 7678	A GGA C
		AGGGGACT AGT GGC TGA	
		TCCCCTGA TCA TCG ACT	
		C GTA _	
GAM1863	DKFZP667O116	5' CAGGCCTCAGGCCCTCA 45263	A AAGTG
		TGAGGGG CT GAGGCCTG	
		ACTCCCC GG CTCCGGAC	
		C A____	
GAM1863	FHX	5' TCAGGGGACCCAGTTCCCCTCA 20463	CTA G AGG_
		TGAGGGGA A TGG CCTGA	
		ACTCCCCT T ACC GGA CT	
		____ G CAGG	
GAM1863	FLJ13241	3' TCAGGCCTCCCCGGGCCCCCA 24710	A A AAGT
		TG GGGG CT GGAGGCCTGA	
		AC CCCC GG CCTCCGGACT	
		C _ GCC_	
GAM1863	FLJ14107	5' CTTCCACCCAGTCCCCTC 24617	AA
		GAGGGGACT GTGGAGG	
		CTCCCCTGA CACCTTC	
		CC	
GAM1863	FLJ22644	3' CAGGCCTCCACCTCCAGCCC 24741	A AA__
		GGG CT GTGGAGGCCTG	
		CCC GA CACCTCCGGAC	
		_ CCTC	
GAM1863	HXCP2	3' CAAACCCCCACTTCCCTCA 26313	ACTA A CC
		TGAGGGG AGTGG GG TG	
		ACTCCCT TCACC CC AC	
		____ C AA	
GAM1863	KIAA0275	3' CCTGCCACCCAGCCCCTC 16551	A AA _
		GAGGGG CT GTGG AGG	

CTCCCC GA CACC TCC
 _ CC G
 GAM1863 KIAA0537 5' CAGGCCTCCCTGCCCCCTC 16864 ACTA T
 GAGGGG AG GGAGGCCTG
 ||||| || |||||
 CTCCCC TC CCTCCGGAC
 CG__ _
 GAM1863 KIAA1393 3' TCAGCATAGACTTAATCCCCTT 35689 C GGAG C
 A TGAGGGGA TAAGT GC TGA
 ||||| ||||| || |||
 ATTCCCCT ATTCA CG ACT
 A GATA _
 GAM1863 LIECG3 3' CAGGCCTCTGGCGCCCCCA 42247 A ACTAAGT
 TG GGGG GGAGGCCTG
 || |||| |||||
 AC CCCC TCTCCGGAC
 _ GCGG__
 GAM1863 MGC4504 3' CAGGCCTCCACCTCCCC 23559 CTAA
 GGGGA GTGGAGGCCTG
 |||| |||||
 CCCCT CACCTCCGGAC
 C__
 GAM1863 PL6 3' CAAGCCCCCCTTGACATCCTCT 13883 C__ T A C
 CA TGAGGGGA TAAG GG GGC TG
 ||||| ||| || || ||
 ACTCTCCT GTTC CC CCG AC
 ACA _ C A
 GAM1863 SEMA6C 5' AGGTTTCCTATCCCCCTCA 25183 ACTAAGT
 TGAGGGG GGAGGCCT
 ||||| |||||
 ACTCCCC CCTTTGGA
 CTAT__
 GAM1863 TP53TG3 3' TCAGGCCTCTTGGGATCGCCTC 17672 G _ AAGT
 A TGAGG GA CT GGAGGCCTGA
 |||| || || |||||
 ACTCC CT GG TCTCCGGA
 G A GT__
 GAM1863 LOC116113 3' CAGGCCTCCACCCCCACCCCC 44283 ACTAA_
 GGGG GTGGAGGCCTG
 ||| |||||
 CCCC CACCTCCGGAC
 CACCCC
 GAM1863 LOC145757 5' CAGCCCCTCCCAGTCCCCTCA 37970 AAGT C_
 TGAGGGGACT GGAGG CTG
 ||||| |||| |||
 ACTCCCCTGA CCTCC GAC
 C__ CC
 GAM1863 LOC146988 5' CAGGCCTCCTCTCCCCC 40777 ACTA T
 GGGG AG GGAGGCCTG
 ||| || |||||

		CCCC TC CCTCCGGAC	
		C___ T	
GAM1863	LOC148029 5'	CAGGCCCCCAGTCCCCTC 38443	AAGT A
		GAGGGGACT GG GGCCTG	
		CTCCCCTGA CC CCGGAC	
		___ C	
GAM1863	LOC148114 5'	CCTCCACCCAAGCCCCCA 38466	A A AA_
		TG GGGG CT GTGGAGG	
		AC CCCC GA CACCTCC	
		C _ ACC	
GAM1863	LOC157450 3'	CAAGTCCCTAGCTCCCTCA 35145	GA AGT A C
		TGAGGG CTA GG GGC TG	
		ACTCCC GAT CC CTG AC	
		TC ___ _ A	
GAM1863	LOC157923 5'	AGACCCCATCCCCTCA 39684	CTAAG A C
		TGAGGGGA TGG GG CT	
		ACTCCCCT ACC CC GA	
		___ _ A	
GAM1863	LOC199986 5'	AGAACTCCAGTCCCCTCA 43269	AAGT GC
		TGAGGGGACT GGAG CT	
		ACTCCCCTGA CCTC GA	
		___ AA	
GAM1863	LOC203043 5'	AGCCTAGTCTCCTCA 43615	AAGTGG C
		TGAGGGGACT AGGC T	
		ACTCCTCTGA TCCG A	
		___ A	
GAM1863	LOC221749 3'	CAGGCCTCCCCCGCCTCA 44179	_ ACTAAGT
		TGAGG GG GGAGGCCTG	
		ACTCC CC CCTCCGGAC	
		G C___	
GAM1864	ADCY8 5'	GCCACCCCCGCCCCGTTCCGG 6788	A C__ AA
	GG	CCCC GAACC CC GGGGTGGC	
		GGGG CTTGG GG CCCACCG	
		C CCC C_	
GAM1864	ATBF1 5'	GCCACCTCCGAGTCCTGGGG 13748	A CCCCAA
		CCCCAG AC GGGGTGGC	
		GGGGTC TG CTCCACCG	
		C AGC___	
GAM1864	BCL2L2 3'	GCCTCAGGAGTCCTTGGGGA 10262	A_ C CAA
		TCCCCAG AC CC GGGGT	

AGGGGTT TG GG CTCCG
 CC A A__
 GAM1864 DVL1 3' GCCACAGGGAGGGAGGTCTTGG 29842 GA _ AAGGG
 GGA TCCCCA ACC CCC GTGGC
 ||||| ||| ||| |||||
 AGGGGT TGG GGG CACCG
 TC A AGGGA
 GAM1864 EIF4EBP2 3' GCCTGGCTGGGAAGTCTGGGGA 10302 ACC AG_
 TCCCCAGA CCCA GGGT
 ||||| ||| |||
 AGGGGTCT GGGT TCCG
 GAA CGG
 GAM1864 EN2 3' GCCACCTCAAGGCCTTGGGGA 7145 AA CCCAA
 TCCCCAG CC GGGGTGGC
 ||||| || |||||
 AGGGGTT GG CTCCACCG
 CC AA__
 GAM1864 GPR85 3' CTTGTAAGTTCTGGGGA 21043 CCC
 TCCCCAGAAC CAAGG
 ||||| |||
 AGGGGTCTTG GTTCC
 AAT
 GAM1864 GPX3 3' GCCACCCCTGCTCCTTCGGAGG 7879 _ A CCCCCA
 A TCC CC GAA AGGGGTGGC
 ||| ||| |||||
 AGG GG CTT TCCCCACCG
 A _ CCTCG_
 GAM1864 HMGB2 5' GCTCTGCGGGACTCTGAGGA 7907 C AC CAA
 TCC CAGA CCC GGGGT
 ||| ||| ||| |||||
 AGG GTCT GGG TCTCG
 A CA CG_
 GAM1864 ITPKB 3' CCACCCCGGGGTCTCTGGGGA 7981 AC AA
 TCCCCAGA CCCC GGGGTGG
 ||||| ||| |||||
 AGGGGTCT GGGG CCCCACC
 CT _
 GAM1864 KCNE1L 3' GCTCCAGGGGCTGCCAGGGA 14615 _ AA CAA
 TCCC CAG CCCC GGGGT
 ||| ||| ||| |||||
 AGGG GTC GGGG CCTCG
 ACC _ A_
 GAM1864 LAPTM5 3' GCCACGGAGGCAGGGTCTCTGG 13616 _ _ AAGGG
 GGA TCCCCAGA ACCC CC GTGGC
 ||||| ||| ||| |||||
 AGGGGTCT TGGG GG CACCG
 C AC AGG_
 GAM1864 LRP4 3' TCCTGGGATTCTGGGGA 32203 CC A
 TCCCCAGAA CCCA GGG
 ||||| ||| |||

		AGGGGTCTT GGGT CCT	
		A_ _	
GAM1864 NEURL	3'	CCCTTGAAGGTTTGGGGA 10411	A CC
		TCCCCAGA CC CAAGGG	
		AGGGGTTT GG GTTCCC	
		_ AA	
GAM1864 NTSR1	5'	TCCTCGGGGGCCTGGGGA 8371	AA A
		TCCCCAG CCCCC AGGG	
		AGGGGTC GGGGG TCCT	
		C_ C	
GAM1864 PIK3R1	3'	GCCACCCTGAGGCCTCTGG 34037	AC CCAA
		CCAGA CC GGGGTGGC	
		GGTCT GG TCCCACCG	
		CC AG_	
GAM1864 PLAC1	5'	GCCACCCCTCTTCAGTTCCGGT 22353	C A CCCCCA
GA		TC CC GAAC AGGGGTGGC	
		AG GG CTTG TCCCACCG	
		T C ACTTC	
GAM1864 POU4F1	3'	ACCCGAGCAGGGGTTTAAAGGA 12896	CC CAAG_
		TCC AGAACCCC GGGT	
		AGG TTTTGGGG CCCA	
		AA ACGAG	
GAM1864 RBM8A	3'	GCCATTTTGCAGGGACTCTG 11580	AC CAA
		CAGA CCC GGGGTGGC	
		GTCT GGG TTTTACCG	
		CA ACG	
GAM1864 ROR2	3'	TTTTTTGGGAATTCAAGGGA 10899	CA CC
		TCCC GAA CCCAAGGGG	
		AGGG CTT GGGTTTTTT	
		AA AA	
GAM1864 SLC1A5	3'	ACTCCCAGGGACTCTGGGGA 12140	AC CAA
		TCCCCAGA CCC GGGGT	
		AGGGGTCT GGG CCTCA	
		CA AC_	
GAM1864 SLC1A5	3'	ACTCCCAGGGACTCTGGGGA 38400	AC CAA
		TCCCCAGA CCC GGGGT	
		AGGGGTCT GGG CCTCA	
		CA AC_	
GAM1864 SLC30A3	5'	GCCCTGCGGGGATCCCGGGGG 9526	A_ A CAA
		TCCCC GA CCCC GGGGT	

			GGGGG CT GGGG TCCCG		
			CC A CG_		
GAM1864	SLC9A6	3'	TTCCTTGGAACCTAGGGA 13055	C AACC	
			TCCC AG CCCAAGGGG		
			AGGG TC GGGTTCCTT		
			A CAA_		
GAM1864	SPON1	3'	CTTTTGGGGGTTTCAGAGGA 31301	CCA	
			TCC GAACCCCCAAGGG		
			AGG CTTGGGGGTTTTTC		
			AGA		
GAM1864	TGM2	3'	GCTCCAGGGGCCCTTGGA 10956	C AA CAA	
			TCCC AG CCCC GGGGT		
			AGGG TC GGGG CCTCG		
			T CC A_		
GAM1864	VEGF	3'	GCTCTGACCAGGAGTTTGGGGA 9409	AC CCAA_	
			TCCCCAGA CC GGGGT		
			AGGGGTTT GG TCTCG		
			GA ACCAG		
GAM1864	ZNF144	3'	GCTGTTTTTGGGGGTGCCTGGA 13991	C A_ G TG	
	GA		TC CCAG ACCCCCAAGG G GC		
			AG GGTC TGGGGGTTTT T CG		
			A CG _GT		
GAM1864	13CDNA73	5'	GCCTCCGAGGGCTGCAGGGA 23322	_ AACC AA _	
			TCCC CAG CCC GG GGT		
			AGGG GTC GGG CC CCG		
			AC _ AG T		
GAM1864	B3GNT6	3'	GCCTTCAAGGGTTCTGGAGG 13745	_ CCAA	
			CC CCAGAACCC GGGGT		
			GG GGTCTTGGG TTCCG		
			A AAC_		
GAM1864	CAMKK1	3'	CCTGGGGGTTTCGGGGA 26069	A A	
			TCCCC GAACCCCCA GG		
			AGGGG CTTGGGGGT CC		
			- -		
GAM1864	CLDN4	3'	CCCTTGGAAGTCCTGGGG 6987	A CC	
			CCCCAG AC CCAAGGG		
			GGGGTC TG GGTTC		
			C AA		
GAM1864	CLIPR-59	3'	GCCCCATTCTAGGACTCTGGGG 17790	AC CCAA_	
	A		TCCCCAGA CC GGGGT		

AGGGGTCT GG CCCCCG
 CA ATCTTA
 GAM1864 DKFZP434C131 3' GCCACTTCTGAAGGGTTCTG 34244 CCA
 CAGAACCC AGGGGTGGC
 ||||| |||||
 GTCTTGGG TCTTCACCG
 AAG
 GAM1864 DKFZP434N1511 5' CTAGGCCGGGGGTTTGAGG 43935 CA AA GG
 CC GAACCCCC GG TGG
 || ||||| || |||
 GG TTTGGGGG CC ATC
 AG _ GG
 GAM1864 DKFZp547D155 3' CATGTTTGGGGGTCTG 34866 A G G
 CAGA CCCCCAA G GTG
 ||| ||||| | |||
 GTCT GGGGGTT T TAC
 _ _ G
 GAM1864 DKFZP727C091 3' CAAACTGGGGGTTGTGGG 32902 G AG GG
 CCCA AACCCCCA G TG
 ||| ||||| | ||
 GGGT TTGGGGGT C AC
 G _ AA
 GAM1864 DKFZp762P2111 3' GCTAGTCTCAGGTGTTCTGGGG 41757 C CAA G
 A TCCCCAGAAC CC GGG TGGC
 ||||| || ||| |||
 AGGGGTCTTG GG TCT ATCG
 T AC_ G
 GAM1864 DZIP1 5' CAGCTGGGGTTCTAGGGA 17232 C CAAG G
 TCCC AGAACCCC GG TG
 ||| ||||| || ||
 AGGG TCTTGGGG TC AC
 A _ G
 GAM1864 EPB41L1 3' CACCAGGGTTTGGGGA 34939 A CCAAGG
 TCCCCAGA CCC GGTG
 ||||| || |||
 AGGGGTTT GGG CCAC
 _ A _
 GAM1864 ETR101 3' GCCACCCCCCTCCATCCTGGGG 35831 AACCCCCAA
 G TCCCCAG GGGGTGGC
 ||||| |||||
 GGGGGTC CCCCACCG
 CTACCTCC_
 GAM1864 FBXO21 3' ACCCTTTGGAACCCCTGGGG 27319 AACCC
 CCCCAG CCAAGGGGT
 ||||| |||||
 GGGGTC GGTTTCCCA
 CCAAA
 GAM1864 FLJ12541 3' GCCAGCAGGGGTTCTGGAGA 22758 C CAAGG
 TC CCAGAACCCC GGT
 || ||||| |||

		AG GGTCTTGGGG CCG	
		A ACGA_	
GAM1864	FLJ12816 3'	GCCGTTTCAGGGGTTCTGGG 22604	CAA GG
		CCCAGAACCCC GG TGGC	
		GGGTCTTGGGG CT GCCG	
		A_ TT	
GAM1864	FLJ13189 3'	CCACCTCTGCAGTCCTGGAGA 24329	C A CCCCCA
		TC CCAG AC AGGGGTGG	
		AG GGTC TG TCTCCACC	
		A C ACG_	
GAM1864	FLJ14803 3'	GCTATTTCAAAAGTTACTGAGG 26626	C _ CCCCAG GG
	A	TCC CAG AAC G GTGGC	
		AGG GTC TTG C TATCG	
		A A AAAA_ TT	
GAM1864	FLJ20249 3'	CCACCCCTTAGTTGAGGGA 38773	_ AACCCCC
		TCCC CAG AAGGGGTGG	
		AGGG GTT TTCCCCACC	
		A GA_	
GAM1864	FLJ20695 5'	ATCCCGGAGCCTCTGGGGA 19610	ACCC AA
		TCCCCAGA CC GGGGT	
		AGGGGTCT GG CCCTA	
		CCGA _	
GAM1864	FLJ20886 5'	GCCCCTTGGGGGTTTCAGGGA 45596	CA
		TCCC GAACCCCCAAGGGGT	
		AGGG CTTGGGGGTTCCCCG	
		A_	
GAM1864	FLJ21313 3'	CCATCTCTGGAGGTCTCAGGA 23407	CC A C A
		TCC AGA CC CCA GGGGTGG	
		AGG TCT GG GGT CTCTACC	
		AC _ A _	
GAM1864	FLJ23024 3'	GCCTCTCTGGAGACTTGGGGA 24473	AACCC _
		TCCCCAG CCA AGGGGT	
		AGGGGT GGT TCTCCG	
		CAGA_ C	
GAM1864	FLJ23441 5'	CTTTTGGGAGTTCTGTGGA 23988	C C
		TCC CAGAAC CCAAGGG	
		AGG GTCTTG GGGTTTTC	
		T A	
GAM1864	FOXJ1 5'	GCCGTGTAAACGGGAGTCTGGGG 7189	AC CAAGGGG
	A	TCCCCAGA CCC TGGC	

			AGGGGTCT GGG GCCG	
			GA CAATGT_	
GAM1864	HYA22	3'	GCCTCTGAGGGTTCTGG 12388	CCA
			CCAGAACCC AGGGGT	
			GGTCTTGGG TCTCCG	
			AG_	
GAM1864	IDI2	3'	GCTGATCCTGAAAGTCTTGGGG 27092	GA CCCCCA GG
	A		TCCCCA AC AGG TGGC	
			AGGGGT TG TCC GTCG	
			TC AAAG_ TA	
GAM1864	KCNJ9	5'	GCCACCCCCCAGGGGTCTCTG 11431	_ CAA
			CAGA ACCCC GGGGTGGC	
			GTCT TGGGG CCCCACCG	
			C ACC	
GAM1864	KIAA0513	3'	TCTCTTGGGAACGCTGGAGA 16363	C AACC
			TC CCAG CCAAGGGG	
			AG GGTC GGGTTCTCT	
			A GCAA	
GAM1864	KIAA0515	3'	GCCACTTCTAGGGACACTGGGG 31925	AACC A
	A		TCCCCAG CCC AGGGGTGGC	
			AGGGGTC GGG TCTTCACCG	
			ACA_ A	
GAM1864	KIAA0545	3'	TTTCTTGGGGGCCTGAGGA 31637	C AA GG
			TCC CAG CCCCCAAG G	
			AGG GTC GGGGGTTC T	
			A C_ TT	
GAM1864	KIAA0792	3'	TCCTGGGGATTCTGGGGA 16214	C A
			TCCCCAGAA CCCCAGG	
			AGGGGTCTT GGGGT CCT	
			A _	
GAM1864	KIAA0937	3'	CATTAGATTGGGGGTTCTGGG 44014	GG_
			CCCAGAACCCCAA GTTG	
			GGGTCTTGGGGGTT TTAC	
			AGA	
GAM1864	KIAA1126	3'	CCACCCCTTGCCTGAGG 35606	C AACCCC
			CC CAG CAAGGGGTGG	
			GG GTC GTTCCCCACC	
			A C_____	
GAM1864	KIAA1257	3'	GCCACCTCAGGAAACTCAGGGG 31435	A ACCC AA
	A		TCCCC GA CC GGGGTGGC	

AGGGG CT GG CTCCACCG
 A CAAA A_
 GAM1864 KIAA1363 3' CTTTTAGGGGCTGCGGA 34333 C AA C
 TCC CAG CCCC AAGGG
 ||| ||| ||| ||||
 AGG GTC GGGG TTTTC
 C _ A
 GAM1864 KIAA1377 5' GCCATGAGGGAGGTTCTGGGGG 33360 _ AAGGG
 TCCCCAGAACC CCC GTGGC
 ||||| ||| ||||
 GGGGGTCTTGG GGG TACCG
 A AG_
 GAM1864 KIAA1509 3' CCAGGGGGTTTGGGGA 30874 A AA
 TCCCCAGA CCCCC GG
 ||||| ||| ||
 AGGGGTTT GGGGG CC
 _ A_
 GAM1864 KIAA1750 3' GCCATAGTAGGGGTTCTGGG 33876 CAAGGG
 CCCAGAACCCC GTGGC
 ||||| ||| ||||
 GGGTCTTGGGG TACCG
 ATGA_
 GAM1864 LASP1 3' GCGATTTGGGGGCTCGGGGA 12800 A A GG
 TCCCC GA CCCCCAAG GT
 |||| || ||||| ||
 AGGGG CT GGGGGTTT CG
 _ C AG
 GAM1864 LMOD1 3' GCCACCCCTTGGA CACTGTGGA 14446 C AACCC
 TCC CAG CCAAGGGGTGGC
 ||| ||| ||||| ||||
 AGG GTC GGTCCCCACCG
 T AC_
 GAM1864 MAPK13 3' CCCTTTGAAGGCTCTGGGGA 8632 A CC
 TCCCCAGA CC CAAGGGG
 ||||| || |||||
 AGGGGTCT GG GTTTCCC
 C AA
 GAM1864 MEP50 3' ACCATAGGGGAAAGTTTGGGGA 23546 AC_ AAGG
 TCCCCAGA CCCC GGT
 ||||| ||| |||
 AGGGGTTT GGGG CCA
 GAAA ATA_
 GAM1864 PDEF 5' GCCACCCCTTGAGGGTGGCCAG 14747 CCAGA C
 G CC ACCC CAAGGGGTGGC
 || ||| ||||| ||||
 GG TGGG GTTCCCCACCG
 ACCGG A
 GAM1864 PHF7 5' GCCACCCCTCAGATGTTTTG 18581 CCCCCA
 CAGAAC AGGGGTGGC
 ||||| |||||

			GTTTTG TCCCCACCG		
			TAGAC		
GAM1864	PPI5PIV	3'	CCTTTCGGGGATCCGAGGGA	21275	CA_ A C
			TCCC GA CCCC AAGGG		
			AGGG CT GGGG TTTCC		
			AGC A C		
GAM1864	PRSS25	5'	CCGCAGGGGCTCTTGGA	14908	C A CAAGGG
			TCCC AGA CCCC GTGG		
			AGGG TCT GGGG CGCC		
			T C A_____		
GAM1864	PRSS25	5'	CCGCAGGGGCTCTTGGA	29707	C A CAAGGG
			TCCC AGA CCCC GTGG		
			AGGG TCT GGGG CGCC		
			T C A_____		
GAM1864	RAB17	3'	GCCACTCCTGGGGGCTGTGGGG	22786	GAA A
	A		TCCCCA CCCCCA GGGGTGGC		
			AGGGGT GGGGT CCTCACCG		
			GTC _		
GAM1864	SARM	3'	CAGATCAGGGGCTCTGGGA	17454	A CAA GG
			TCCCCAGA CCCC GG TG		
			AGGGGTCT GGGG CT AC		
			C A_ AG		
GAM1864	SDC3	5'	CCTGGAGGGCTCTGGGA	16080	A _ A
			TCCCCAGA CCC CCA GG		
			AGGGGTCT GGG GGT CC		
			C A _		
GAM1864	SKIP	3'	ACCCTCTAGGGGCTTTGGGA	18596	A CAA
			TCCCCAGA CCCC GGGGT		
			AGGGGTTT GGGG TCCCA		
			C ATC		
GAM1864	SKIP	3'	ACCCTCTAGGGGCTTTGGGA	28259	A CAA
			TCCCCAGA CCCC GGGGT		
			AGGGGTTT GGGG TCCCA		
			C ATC		
GAM1864	TBC1D2	5'	GCCATTATTGGAAATTTCTAAG	20466	CC CCC_ GG
	GA		TCC AGAA CCAA GGTGGC		
			AGG TCTT GGTT TTACCG		
			AA TAAA A_		
GAM1864	TED	3'	CACCCGGCTTTGGGA	17912	A CCCAAG
			TCCCCAGA CC GGGTG		

AGGGGTTT GG CCCAC
 C _____
 GAM1864 TOMM70A 3' GCCACTTATTTTGAAGATGCT 16792 _ AACCCC ____
 GAGG CC CAG CAAGG GGTGGC
 || ||| |||| |||||
 GG GTC GTTTT TCACCG
 A GTAGAA TAT
 GAM1864 ZNF313 3' CCACCCCTGGTCTGTTCTG 20753 CC_ A
 CAGAAC CCA GGGGTGG
 ||||| ||| |||||
 GTCTTG GGT CCCCACC
 TCT _
 GAM1864 LOC124044 3' GCCCCAGGTCAAGGGCTCTTGG 37432 C A ____ AA
 GA TCCC AGA CCC CC GGGGT
 |||| ||| || |||||
 AGGG TCT GGG GG CCCCCG
 T C AACT A_
 GAM1864 LOC124997 5' ACCCCTGAGGGCCTGGAGA 36786 C AAC CA
 TC CCAG CCC AGGGGT
 || |||| ||| |||||
 AG GGTC GGG TCCCCA
 A C__ AG
 GAM1864 LOC126006 5' CATGAGCTGGGGATTTGGGGA 36801 AC AGGG
 TCCCCAGA CCCCCA GTG
 ||||| |||| |||
 AGGGGTTT GGGGT TAC
 A_ CGAG
 GAM1864 LOC130813 3' GCTCTTTTAGGAGTATCTGGGG 37312 _ _ CC
 A TCCCCAGA AC CC AAGGGGT
 ||||| || || |||||
 AGGGGTCT TG GG TTTCTCG
 A A AT
 GAM1864 LOC145371 3' ACCCTAGGGGTTTCTGG 37841 CAA
 CCAGAACCCC GGGGT
 ||||| |||||
 GGTCTTGGGG TCCCCA
 A_
 GAM1864 LOC145438 5' GCCACCCCTCTAGGGACCCAGG 40535 CCAGAA CCA
 A TCC CCC AGGGGTGGC
 || ||| |||||
 AGG GGG TCCCCACCG
 ACCCA_ ATC
 GAM1864 LOC146728 5' GCCAGGTCCCCGGGGGGTTC 40724 AA ____
 GAACCCCC GGGG TGGC
 ||||| ||| |||
 CTTGGGGG CCCC ACCG
 G_ TGG
 GAM1864 LOC148397 3' CCAAGCTGGGAGTCTGGGGA 38526 AC CAA GG
 TCCCCAGA CCC GG TGG
 ||||| ||| || |||

	AGGGGTCT GGG TC ACC	
	GA ____ GA	
GAM1864 LOC149171 5'	GCTCCTGGAGGCCCTGGGGA 38667	AA C A
	TCCCCAG CC CCA GGGGT	
	AGGGGTC GG GGT CCTCG	
	CC A _	
GAM1864 LOC149706 5'	CCAAGGGATGGGGGTTTGGGGA 41058	A AGGGG
	TCCCCAGA CCCCCA TGG	
	AGGGGTTT GGGGT ACC	
	_ AGGGA	
GAM1864 LOC152805 5'	GCCAAGTGAGGCGGTTCTGGGG 39323	_ _ AGGGG
A	TCCCCAGAACC CC CA TGGC	
	AGGGGTCTTGG GG GT ACCG	
	C A GA__	
GAM1864 LOC153577 3'	GCCCCTTGCTGGAGGGTTCTGG 41646	- _
GGA	TCCCCAGAACCC CCA AGGGGT	
	AGGGGTCTTGGG GGT TCCCCG	
	A CGT	
GAM1864 LOC157349 5'	GCCCCGGAACCAGAGGTCTGGG 39598	A CCCAA__
GA	TCCCCAGA CC GGGGT	
	AGGGGTCT GG CCCCCG	
	_ AGACCAAGG	
GAM1864 LOC157858 3'	CCACGGGAGCTCTGGGGA 41865	ACC AAGGG
	TCCCCAGA CCC GTGG	
	AGGGGTCT GGG CACC	
	CGA ____	
GAM1864 LOC164382 3'	ACCAAGGAGGGATTTGGGGA 42160	A _ AAGG
	TCCCCAGA CCC CC GGT	
	AGGGGTTT GGG GG CCA	
	A A AA__	
GAM1864 LOC166042 5'	CTTTTGGGATTCCGGGGA 40200	A CC
	TCCCC GAA CCCAAGGG	
	AGGGG CTT GGGTTTTC	
	C A_	
GAM1864 LOC196707 3'	GCCAGTGGGGATCCTGGGGG 42297	AAC AGG
	TCCCCAG CCCCCA GGT	
	GGGGGTC GGGGT CCG	
	CTA GA_	
GAM1864 LOC199923 5'	GCCATTCTGCTGGGGTTCTGGA 42670	C CAA
GA	TC CCAGAACCCC GGGGTGGC	

	AG GGTCTTGGGG TCTTACCG	
	A TCG	
GAM1864 LOC200470 5'	GCCCCAAGGCTCTGGGGA 43306	A CCCAA
	TCCCCAGA CC GGGGT	
	AGGGGTCT GG CCCCG	
	C AA__	
GAM1864 LOC201617 3'	CCACCCCCTCCTTTGGGGA 43380	ACCCCCAA
	TCCCCAGA GGGGTGG	
	AGGGGTTT CCCCACC	
	CCTC__	
GAM1864 LOC202126 3'	ACTCCAGGAGTTCTTGGGA 43410	C C CAA
	TCCC AGAAC CC GGGGT	
	AGGG TCTTG GG CCTCA	
	T A A__	
GAM1864 LOC203504 5'	GCCCAAGGGTAGGGAATCTGGG 43572	A_ __ AAG
GA	TCCCCAGA CCC CC GGGT	
	AGGGGTCT GGG GG CCCG	
	AA AT GAA	
GAM1864 LOC204161 5'	CCCTGGAGGCCTTGGGGA 43579	AA C A
	TCCCCAG CC CCA GGG	
	AGGGGTT GG GGT CCC	
	CC A _	
GAM1864 LOC204161 5'	CCTTGGGGATTCTGGAGGA 43580	_ A C
	TCC CC GAA CCCCAGG	
	AGG GG CTT GGGGTTCC	
	A _ A	
GAM1864 LOC205143 5'	GCTCCCCTGAGGATCCCAGGA 43586	CCA A CCCA T
	TCC GA CC AGGGG GGC	
	AGG CT GG TCCCC TCG	
	ACC A AG__ _	
GAM1864 LOC221463 3'	ACCTTCTGGCAGCTCTGGGGA 44199	ACCC AG
	TCCCCAGA CCA GGGT	
	AGGGGTCT GGT TCCA	
	CGAC CT	
GAM1864 LOC221490 5'	GCTTCTTGAGCCTCTGGGGA 44987	ACCC
	TCCCCAGA CCAAGGGGT	
	AGGGGTCT GGTCTTCG	
	CCGA	
GAM1864 LOC253675 5'	CATTTCGGTGGGCTCTGGGGA 46263	A _ AA GG
	TCCCCAGA CCC CC G GTG	

	AGGGGTCT GGG GG C TAC	
	C T C_ TT	
GAM1864 LOC253891 3'	GCCACCCCAGAGCCCTGGGGG 45323	AACCCCCAA
	TCCCCAG GGGGTGGC	
	GGGGGTC CCCCACCG	
	CCGAGA__	
GAM1864 LOC254228 3'	CCTTGGCTAAAGGTCTGGGGA 45920	A C__
	TCCCCAGA CC CCAAGG	
	AGGGGTCT GG GGTTC	
	_ AAATC	
GAM1864 LOC255189 5'	GCTCCAGGGA CTCTTGGGGA 46194	_ AC CAA
	TCCCCA GA CCC GGGGT	
	AGGGGT CT GGG CCTCG	
	T CA A__	
GAM1864 LOC256502 3'	GCCCTTTATCCGACGGTTCTGG 45367	CCC__
	CCAGAACC AAGGGGT	
	GGTCTTGG TTTCCCG	
	CAGCCTA	
GAM1864 LOC256581 5'	ACCTCTAAGTGGCTCTGGGGA 46591	A CCCA
	TCCCCAGA CC AGGGGT	
	AGGGGTCT GG TCTCCA	
	C TGAA	
GAM1864 LOC257447 5'	CCCTGGAGGATCTGGAGA 40568	C A C A
	TC CCAGA CC CCA GGG	
	AG GGTCT GG GGT CCC	
	A A A _	
GAM1864 LOC51152 3'	GCTAAATCTAGTGGGTTCTGAG 18284	C CCA GG
GA	TCC CAGAACCC AGG TGGC	
	AGG GTCTTGGG TCT ATCG	
	A TGA AA	
GAM1864 LOC90141 3'	CTTTTGGTAACTCTGGGGA 30880	ACCC
	TCCCCAGA CCAAGGG	
	AGGGGTCT GGTTTTC	
	CAAT	
GAM1864 LOC92568 3'	GCCACCTCTGAGTGCTCTGAGG 34579	C ACCCCCA
A	TCC CAGA AGGGGTGGC	
	AGG GTCT TCTCCACCG	
	A CGTGAG_	
GAM1864 LOC93268 5'	TCTTGGGGGTCTGCAGGA 35588	C_
	TCC CAGAACCCCCAAGG	

		AGG GTCTTGGGGGTTCT		
		AC		
GAM1865 E2F3	3'	ACTCCAGGTAGATTTCACA 7665	C	C__
		TGTGGAAA CTGCC AGT		
		ACACCTTT GATGG TCA		
		A ACC		
GAM1865 PTPRA	5'	ATTGGGCAGCTTCCACA 8714	AC	
		TGTGGAA CTGCCCAGT		
		ACACCTT GACGGGTTA		
		C_		
GAM1865 SH3GL1	3'	TCCCTGAGCAGGACCCACA 8964	AAA	C T
		TGTGG CCTGC CAG GA		
		ACACC GGACG GTC CT		
		CCA A C		
GAM1865 SLC1A4	3'	ACAGGACAGGTTTCACA 8993	G	C A
		TGTG AAACCTG CC GT		
		ACAC TTTGGAC GG CA		
		_ A A		
GAM1865 SLC21A9	3'	GACCCTGGGTAGACTCCCACA 14125	AAAC	TGAC
		TGTGG CTGCCCAG GTC		
		ACACC GATGGGTC CAG		
		CTCA C__		
GAM1865 TNFAIP2	3'	CGTGACAGGTTTCCACA 12982	GCCCA	G
		TGTGGAAACCT GT ACG		
		ACACCTTTGGA CA TGC		
		_____ G		
GAM1865 C1QTNF7	3'	ACATCACATACAAGGTTTCCAC 25661	GCCCA	C
		GTGGAAACCT GTGA GT		
		CACCTTTGGA CACT CA		
		ACATA A		
GAM1865 KIAA1979	3'	GCAGCAGGCAGACCTTCCACA 42591	AC_	CAG AC
		TGTGGAA CTGCC TG GT		
		ACACCTT GACGG AC CG		
		CCA ____ GA		
GAM1865 STAF65(gamma)	3'	GACGTCACCAAACAAGGTTGCA 16926	GA	GCCCA_
T		GTG AACCT GTGACGTC		
		TAC TTGGA CACTGCAG		
		G_ ACAAAC		
GAM1865 LOC146856	3'	ACTCCAGGTAGATTTCACA 40298	C	C__
		TGTGGAAA CTGCC AGT		

ACACCTTT GATGG TCA
 A ACC
 GAM1866 BRF1 3' AGACCCCCCTACCCCCGCCCA 7254 _ A CCGAAT
 TGGG GG GGT GGGGGTCT
 |||| |||||
 ACCC CC CCA CCCCCAGA
 G C TC____
 GAM1866 HHLA1 5' AGACCCCCACTCCTGCCCGCCA 12264 _ _ TCCGAA
 TGG GGG AGG TGGGGGTCT
 ||| ||| |||||
 ACC CCC TCC ACCCCCAGA
 G G TC____
 GAM1866 NGFR 3' GACCCCCACCCCTTCCCCA 8333 TCCGAA
 TGGGGGAGG TGGGGGTC
 ||||| |||||
 ACCCCTTCC ACCCCCAG
 CC____
 GAM1866 PTPN18 3' AGACCCCAGCCAGACCCCCGCC 15702 _ A CGAATG
 A TGG GGG GGTC GGGGTCT
 ||| ||| |||||
 ACC CCC CCAG CCCCAGA
 G _ ACCGA_
 GAM1866 VDR 3' AGACCCCCACTCTCATTCCCC 5942 GTCC A
 GGGGAG GA TGGGGGTCT
 ||||| |||||
 CCCCTT CT ACCCCCAGA
 ACT_ C
 GAM1866 A2BP1 5' AGACCCCCACCCAGTGGCCGCC 20802 A T AA____
 GG GG CCG TGGGGGTCT
 || ||| |||||
 CC CC GGT ACCCCCAGA
 G _ GACCC
 GAM1866 BRD4 3' AGACCCCCCGACCCTCCCCCA 27773 TC AAT
 TGGGGGAGG CG GGGGGTCT
 ||||| |||||
 ACCCCCTCC GC CCCCCAGA
 CA ____
 GAM1866 DKFZP564B1162 3' CCCACTCAAACCTCTCCCA 25336 CC A
 TGGGGGAGGT GA TGGG
 ||||| |||||
 ACCCTCTCCA CT ACCC
 AA C
 GAM1866 KIAA1607 3' ACCCCCAGGGCCTCCTTCCCCA 31913 ____ GAA
 TGGGG GAGGTCC TGGGGGT
 |||| ||||| |||||
 ACCCC CTCCGGG ACCCCCA
 TTC ____
 GAM1866 KIAA1987 3' ACCCCCGGTATCCCCCCA 42491 A TCCGAA
 TGGGGG GG TGGGGGT
 ||||| |||||

ACCCCC CC GCCCCCA
 _ TATG_
 GAM1866 LOC116113 3' AGACCCCTCCTCAGACCCTCCC 44282 GA C AT
 CA TGGGG GGTC GA GGGGGTCT
 |||| | || | |||||
 ACCCC CCAG CT TCCCCAGA
 TC A CC
 GAM1866 LOC162333 5' GGGCACCCAGCCTCCCCCA 42132 CCGAA G
 TGGGGGAGGT TGGG GTCT
 ||||||| ||| |||
 ACCCCTCCG ACCC CGGG
 A
 GAM1866 LOC221495 3' AGACCCCCACCCCCCGACCCCC 45055 A CGAA_
 C GGGG GGTC TGGGGGTCT
 ||| ||| |||||
 CCCC CCAG ACCCCCAGA
 _ CCCCC
 GAM1866 LOC257479 5' GACCTTCCAACCTCCCCCA 46053 CCGAA _
 TGGGGGAGGT TGGG GGTC
 ||||||| ||| |||
 ACCCCTCCA ACCT CCAG
 T
 GAM1867 AGL 5' AAGAAACTGGGTCTCA 6301 C GC
 TGAGACCC AG TTCTT
 |||||| | ||||
 ACTCTGGG TC AAGAA
 A_
 GAM1867 ARHC 5' AAGGGAAAAGGGGTTTCA 11661 AGGCTTC
 TGAGACCCC TTCCCTT
 ||||||| |||||
 ACTTTGGGG AAGGGAA
 AA_
 GAM1867 DAZL 3' AAGGGAAAAGTTGTATCA 33797 G CCCA C
 TGA AC GGCTT TTCCCTT
 || | |||| | |||||
 ACT TG TTGAA AAGGGAA
 A A
 GAM1867 FOSB 3' AAGGGGCTGGAATCTCA 13579 CC G
 TGAGA CCAG CTTCTT
 |||| | |||||
 ACTCT GGTC GGGGAA
 AA _
 GAM1867 HMGCR 3' AAGGGAAGAAACACTCTTA 6521 CCCCAGGC
 TGAGA TTCTTCCCTT
 |||| |||||
 ATTCT AAGAAGGGAA
 CACA_
 GAM1867 LRAT 3' AGGAAGCCTGGAATTCA 30181 ACC
 TGAG CCAGGCTTCTT
 ||| |||||

ACTT GGTCCGAAGGA
 AA_
 GAM1867 MTMR8 3' AAGAAAACCTTAGGGTCTCA 17742 C_ GC
 TGAGACCC AG TTCTT
 ||||| || ||||
 ACTCTGGG TC AAGAA
 AT AA
 GAM1867 NCALD 3' AAGGGAGGCCCAAATTCTCA 25742 CCCCCA TCT
 TGAGA GGCT TCCCTT
 |||| ||| |||||
 ACTCT CCGG AGGGAA
 TAAAC ____
 GAM1867 PACE 3' AAGGAAAGGGGGTCCCA 8421 A AGGCTT C
 TG GACCCC CTT CCTT
 || ||||| ||| ||||
 AC CTGGGG GAA GGAA
 C _____ A
 GAM1867 PTPN7 3' AAGAAAGAAGCCCAGGTGTC 8708 _ CA CC
 GAC CC GGCTTCTT CTT
 ||| || ||||| |||
 CTG GG CCGAAGAA GAA
 T AC A_
 GAM1867 PTPN7 3' AAGAAAGAAGCCCAGGTGTC 27886 _ CA CC
 GAC CC GGCTTCTT CTT
 ||| || ||||| |||
 CTG GG CCGAAGAA GAA
 T AC A_
 GAM1867 PTPN7 3' AAGAAAGAAGCCCAGGTGTC 27889 _ CA CC
 GAC CC GGCTTCTT CTT
 ||| || ||||| |||
 CTG GG CCGAAGAA GAA
 T AC A_
 GAM1867 SFRP5 3' TAAGGGAAAGGTGGAGGGGCTC 8940 A AG_ C
 A TGAG CCCC GCTT TTCCCTTA
 |||| ||| ||||| |||||
 ACTC GGGG TGA AAGGGAAT
 _ AGG _
 GAM1867 DKFZp434F054 5' TAAGGGAAGCTAGGAAGTC 26002 C_ A TCT
 GAC CC GGCT TCCCTTA
 ||| || |||| |||||
 CTG GG TCGA AGGGAAT
 AA A ____
 GAM1867 FACTP140 3' AAGGGGGGAGGGGTCCCG 14045 A AGGCT
 TG GACCCC TCTTCCCTT
 || ||||| ||||| |||||
 GC CTGGGG AGGGGGGAA
 C _____
 GAM1867 FLJ11099 3' AAGGGAAGCCTTGGGGCCTCA 20312 A CTT
 TGAG CCCCAGG CTTCCCTT
 |||| ||||| |||||

ACTC GGGGTTC GAAGGGAA
 C C__
 GAM1867 FLJ20436 5' GACAGAGCTGGGGTCTCA 19474 G CT
 TGAGACCCAG CTT TC
 ||||| || ||
 ACTCTGGGGTC GAG AG
 _ AC
 GAM1867 FLJ21977 3' AAGGGGCCTGAGGCCTCA 25938 A C
 TGAG CC CAGGCTTCTT
 ||| || |||||
 ACTC GG GTCCGGGGAA
 C A
 GAM1867 HCA127 3' TAAGGGAAGGGCAAAAGGCTCA 20758 A CCAG T
 TGAG CC GCT CTTCCCTTA
 ||| || || |||||
 ACTC GG CGG GAAGGGAAT
 _ AAAA _
 GAM1867 KIAA0493 5' GAGACGCCTGGGGTCCCA 32141 A T
 TG GACCCAGGC TCTT
 || ||||| |||
 AC CTGGGGTCCG AGAG
 C C
 GAM1867 KIAA0618 3' TAAGGGAATCCGGGATC 16838 C A CTTC
 GA CCC GG TTCCCTTA
 || ||| || |||||
 CT GGG CC AAGGGAAT
 A _ T__
 GAM1867 MGC20235 5' GAGGAGCCTGGGATCCCA 29667 A C
 TG GA CCCAGGCTTCTT
 || || |||||
 AC CT GGGTCCGAGGAG
 C A
 GAM1867 MGC23280 3' TAAGGGAAGCCCTAGGGTCTC 29500 C TTCT
 A TGAGACCC AGGC TCCCTTA
 ||||| ||| |||||
 ACTCTGGG TCCG AGGGAAT
 A CTC_
 GAM1867 MGC4771 3' GGAAGAAGCCCGGATCCCG 26395 A C A
 TG GA CCC GGCTTCTTCC
 || || || |||||
 GC CT GGG CCGAAGAAGG
 C A C
 GAM1867 MGC5149 3' AAGCAGCCAGGGTCTCA 35781 CA T
 TGAGACCC GGCT CTT
 ||||| ||| |||
 ACTCTGGG CCGA GAA
 A_ C
 GAM1867 PCBP4 3' AAGGAGACTCCACCCTGGGGTC 26893 A CTTCT_ _
 CCA TG GACCCAGG TC CCTT
 || ||||| || |||

			AC CTGGGGTCC	AG GGAA		
			C	CACCTC A		
GAM1867	PCBP4	3'	AAGGAGACTCCACCCTGGGGTC	26895	A	CTTCT_ _
	CCA		TG GACCCCAGG	TC CCTT		
			AC CTGGGGTCC	AG GGAA		
			C	CACCTC A		
GAM1867	PCBP4	3'	AAGGAGACTCCACCCTGGGGTC	21677	A	CTTCT_ _
	CCA		TG GACCCCAGG	TC CCTT		
			AC CTGGGGTCC	AG GGAA		
			C	CACCTC A		
GAM1867	SLC26A9	3'	TAAAGGATGAGCCTGGGGTC	27495		CT C
			GACCCCAGGCTT	TCC TTA		
			CTGGGGTCCGAG	AGG AAT		
			T_ A			
GAM1867	LOC129566	5'	AGGGAAGCCCGGGGTCT	37278	A	TCT
			AGACCCC	GGCT TCCCT		
			TCTGGGG	CCGA AGGGA		
			C	___		
GAM1867	LOC130595	5'	AAGGGAGCGACTGCCTGGGGTC	37298		T_ _
			GACCCCAGGC	TC TTCCCTT		
			CTGGGGTCCG	AG GAGGGAA		
			TC C			
GAM1867	LOC143286	5'	AAGGGAAAGGGAGTGTCA	40352	G	_ AGGCTTC
			TGA AC CCC	TTCCCTT		
			ACT TG GGG	AAGGGAA		
			G A A	_____		
GAM1867	LOC144438	3'	AAGTAGGCCTGGAGCCTCA	37733	ACC	_
			TGAG	CCAGGCTT CTT		
			ACTC	GGTCCGGA GAA		
			CGA	T		
GAM1867	LOC147077	5'	AAGGGAAGGCAAAGTCCA	38289	A	CCCAG TT
			TG GAC	GC CTTCCCTT		
			AC CTG	CG GAAGGGAA		
			_ AAA_ _			
GAM1867	LOC152765	3'	AAAGGAAGGAGGGTATCA	39309	G	CAGGC C
			TGA ACCC	TTCTTCC TT		
			ACT TGGG	AGGAAGG AA		
			A	_____ A		
GAM1867	LOC152765	3'	AAAGGAAGGAGGGTATCA	39310	G	CAGGC C
			TGA ACCC	TTCTTCC TT		

		ACT TGGG AGGAAGG AA		
		A _____ A		
GAM1867	LOC152845 5'	GGAGAGAAGCTGAGGCCTCA 30257	A CCA	TC
		TGAG CC GGCTTCT CC		
		ACTC GG TCGAAGA GG		
		C AG_ GA		
GAM1867	LOC153577 5'	AGGAAGCCTGGATCCCA 41642	A CC	
		TG GA CCAGGCTTCTT		
		AC CT GTCCGAAGGA		
		C A_		
GAM1867	LOC90936 5'	GAAGAAGCCTGGGGCCTCA 32189	A	
		TGAG CCCCAGGCTTCTTC		
		ACTC GGGGTCCGAAGAAG		
		C		
GAM1867	LOC92218 5'	AAGGGAAGGAAGAGGTCCCA 33986	A CCAGGC	
		TG GACC TTCTTCCCTT		
		AC CTGG AGGAAGGGAA		
		C AGA_		
GAM1867	LOC92305 3'	AGGGAAGGCCGAGGTCTCA 28757	CCA TT	
		TGAGACC GGC CTTCCT		
		ACTCTGG CCG GAAGGGA		
		AG_ _		
GAM1868	AKT1 3'	GCTGTCTGTCACCAGCTA 11653	A AA	
		TAGCTG TGACAGACA GC		
		ATCGAC ACTGTCTGT CG		
		C _		
GAM1868	ESRRG 3'	TGTGTATCTATCATTAGCTA 33000	C CAAA	
		TAGCTGATGA AGA GCA		
		ATCGATTACT TCT TGT		
		A ATG_		
GAM1868	PCDHB9 3'	ACATGCTTGTAATCCCAGCTA 21204	AT CAG A	
		TAGCTG GA ACAA GCATGT		
		ATCGAC CT TGTT CGTACA		
		C_ AA_ _		
GAM1868	SIAT8E 5'	ACGGCCCGCCTATCATTAGC 30089	C ACAA A	
		GCTGATGA AG GC TGT		
		CGATTACT TC CG GCA		
		A CGCC_ _		
GAM1868	TRAF1 3'	ACATCCTGTGCCTCCATCAGCT 12197	AC A A C	
	A	TAGCTGATG AG CA AG ATGT		

	ATCGACTAC TC GT TC TACA	
	C_ C G C	
GAM1868 DKFZP434G1411 3'	CTTTACCTGTCATCAGTTA 44230	AC
	TAGCTGATGACAG AAAG	
	ATTGACTACTGTC TTTC	
	CA	
GAM1868 FLJ10956 3'	GCTTTCGTCTGTCATCAG 20276	_
	CTGATGACAGAC AAAGC	
	GACTACTGTCTG TTTCG	
	C	
GAM1868 FLJ12787 3'	CATGCCCTGCTTCAGCTG 25889	TGA ACAA
	TAGCTGA CAG GCATG	
	GTCGACT GTC CGTAC	
	TC_ C__	
GAM1868 OSBPL11 3'	ACATACCTGTTGTTTATCAGC 23045	CA AAGC
	GCTGATGA GACA ATGT	
	CGACTATT TTGT TACA	
	TG CCA_	
GAM1868 PSR 3'	ACATGCTTTGTTTATTCCTGC 32495	T_ TGAC
	GC GA AGACAAAGCATGT	
	CG CT TTTGTTTCGTACA	
	TC TA__	
GAM1868 RA-GEF-2 3'	ACACACTTATTCCATCAGCTA 18460	ACA CA CA
	TAGCTGATG GA AAG TGT	
	ATCGACTAC CT TTC ACA	
	__ TA AC	
GAM1868 LOC149401 5'	ACATGCCCTGCCTGTTTC 38735	T A AA
	GA GACAG CA GCATGT	
	CT TTGTC GT CGTACA	
	_ C CC	
GAM1868 LOC157860 5'	GCTCGTCGTCTGACATCAGCTA 41860	A AA__
	TAGCTGATG CAGAC AGC	
	ATCGACTAC GTCTG TCG	
	A CTGC	
GAM1868 LOC158927 3'	ACATGCTTCAAATAAATCAGCT 42040	GACAGACA
	AGCTGAT AAGCATGT	
	TCGACTA TTCGTACA	
	AATAAAC_	
GAM1868 LOC165552 3'	ATGTTGTCCTTCATCAGC 40132	CA AA
	GCTGATGA GACA GCAT	

			CGACTACT CTGT TGTA		
			TC _		
GAM1868	LOC92370	3'	ACATACAGTCTCTGTCATAACT 34258	CTG	CAAAGC
	A		TAG ATGACAGA ATGT		
			ATC TACTGTCT TACA		
			AA_ CTGACA		
GAM1869	CDS2	5'	CGGGCGGGGCGGGGCCGGCC 9908	G	GAGG
			GGCCGG C CGCCCCGCCCG		
			CCGGCC G GCGGGGCGGGC		
			GG		
GAM1869	DYSF	5'	CGAGCCGGCCTCGCCAGCCA 9585	C	GCC C C
			TGGC GGGCGAGGC C GC CG		
			ACCG CCCGCTCCG G CG GC		
			A _ C A		
GAM1869	FGF18	5'	CGAGCTTCCCCGCACCGGCCA 9955	_ A C_ CC	
			TGGCCGG GCG GG GC CG		
			ACCGGCC CGC CC CG GC		
			A C TT A_		
GAM1869	FGF18	5'	CGAGCTTCCCCGCACCGGCCA 27383	_ A C_ CC	
			TGGCCGG GCG GG GC CG		
			ACCGGCC CGC CC CG GC		
			A C TT A_		
GAM1869	ITGAM	3'	GGCACACGCCACCTCGCCCGGC 35564	C_ CCC_	
	C		GGCCGGGCGAGG GC GCC		
			CCGGCCCCGCTCC CG CGG		
			AC CACA		
GAM1869	LENG4	3'	GGACGGGGCGCCCGCGC 23585	CGG A C	
			GC GCG GGCGCCCCG CC		
			CG CGC CCGCGGGGC GG		
			_ _ A		
GAM1869	LYN	5'	GGGCGGGGCGGCCGCGCC 8153	A _	
			GGCG GGC GCCCCGCC		
			CCGC CCG CGGGGCGGG		
			G G		
GAM1869	MMP25	3'	GCCCCGCCCGCCTGGCCA 22822	A CCCC	
			TGGCCGGGCG GGCG GC		
			ACCGGTCCGC CCGC CG		
			C CC_		
GAM1869	PLA2G10	5'	GGCGTGAGTCACCGCGCCCGGC 9619	A C_ CC_	
	CA		TGGCCGGGCG GG GC CGCC		

ACCGGCCCCG CC TG GCGG
 G AC AGT
 GAM1869 SCRT1 3' GGGGCCTCCCCAGCCA 25346 C C G
 TGGC GGG GAGGC CCC
 |||| ||| ||||| |||
 ACCG CCC CTCCG GGG
 A C _
 GAM1869 SLC14A2 5' GGC GTGGGCCGCCGACCCGGC 14011 CGA _ _
 CA TGGCCGGG GGCG CCC CGCC
 ||||| ||| ||| |||
 ACCGGCCC CCGC GGG GCGG
 ACG C T
 GAM1869 SMN1 5' GCGGTCCTCCCGGCCA 23151 CG CGCC
 TGGCCGGG AGG CCGC
 ||||| ||| |||
 ACCGGCCC TCC GGCG
 _ T _
 GAM1869 SMN1 5' GCGGTCCTCCCGGCCA 5895 CG CGCC
 TGGCCGGG AGG CCGC
 ||||| ||| |||
 ACCGGCCC TCC GGCG
 _ T _
 GAM1869 WNT3A 3' GGCGGGGCGCCCCAAGAGCCC 26974 GA____
 GGGC GGCGCCCCGCC
 ||| |||||
 CCGG CCGCGGGGCGG
 AGAACC
 GAM1869 CENTB5 3' CGGGCAGCTGCCACCCCGCCCG 45724 A____ _ CCC
 GCC GGCCGGGCG GGC GC GCCCG
 ||||| ||| ||| |||
 CCGGCCCGC CCG CG CGGGC
 CCCA T A _
 GAM1869 DKFZP434F0318 3' GGCATGAGCCACCTCGCCTGGC 25142 C_ CCC_
 CA TGGCCGGGCGAGG GC GCC
 ||||| ||| |||
 ACCGGTCCGCTCC CG CGG
 AC AGTA
 GAM1869 DKFZp761O0113 5' GCGGTGAGCCACGCGCCCGGC 20447 A C_ CC_
 C GGCCGGGCG GG GC CGCC
 ||||| ||| ||| |||
 CCGGCCCGC CC CG GCGG
 G AC AGT
 GAM1869 FLJ10297 3' CGGGACTGGCCCTGCCAGCCA 19804 C G C CCG
 TGGC GGGC AGG GCC CCCG
 ||| ||| ||| ||| |||
 ACCG CCCG TCC CGG GGGC
 A _ _ TCA
 GAM1869 FLJ10297 3' GGCATGAGCCGCCACCCGGC 19806 CGA _ CCC_
 CA TGGCCGGG GGCG C GCC
 ||||| ||| | |||

		ACCGGCCC CCGC G CGG	
		ACA C AGTA	
GAM1869	FLJ10560 3'	GGCGCCCGCCACCACGCCCGGC 19937	A___ CCC
	CA	TGGCCGGGCG GGCG CGCC	
		ACCGGCCCGC CCGC GCGG	
		ACCA CC_	
GAM1869	FLJ12387 3'	CGGGCACCGCCCAACGAGCCA 23102	_ GCGA CCCC
		TGGC CGG GGCG GCCCG	
		ACCG GCC CCGC CGGGC	
		A AC__ CA__	
GAM1869	FLJ12581 3'	GGCGCCCGCCACCTCGCCCGGC 24301	C_ CC_
	TA	TGGCCGGGCGAGG GC CGCC	
		ATCGGCCCGCTCC CG GCGG	
		AC CCC	
GAM1869	FLJ14810 3'	GGCACCTCTGCCCTGCCCGGC 26636	A CCCC__
	CA	TGGCCGGGCG GGCG GCC	
		ACCGGCCCGT CCGT CGG	
		C CTCCA	
GAM1869	FLJ14834 5'	GGCAGGGCGCCCGGCC 26643	GAGGC C
		GGCCGGGC GCCC GCC	
		CCGGCCCG CGGG CGG	
		_____ A	
GAM1869	FLJ21032 5'	CGGGCGCCACCTCGCCCAGCC 24397	C CGCCC
		GGC GGGCGAGG CGCCCG	
		CCG CCGCTCC GCGGGC	
		A ACCC_	
GAM1869	FLJ22479 5'	CGAGCGAGCGGCGCCCAGCCC 24385	GA C__ C
		GGGC GGCGCC CGC CG	
		CCCG CCGCGG GCG GC	
		AC CGA A	
GAM1869	HCA4 3'	GGCATGAGCCACCTCGCCCAGC 38023	C C_ CCC_
	C	GGC GGGCGAGG GC GCC	
		CCG CCGCTCC CG CGG	
		A AC AGTA	
GAM1869	KIAA0089 5'	CGGGCGGGGGTGGCCGCGACCA 34665	C _ GAG G
		TGG CG GGC GC CCGCGCCG	
		ACC GC CCG TG GGGGCGGGC	
		A G G__ _	
GAM1869	KIAA0557 3'	GGCGTGAGCCACCGCGCCCGGC 38208	A C_ CC_
	C	GGCCGGGCG GG GC CGCC	

		CCGGCCCCGC CC CG GCGG	
		G AC AGT	
GAM1869 KIAA1210	3'	GGCGTGAGCCACCGCGCCCGGC 46087	A C_ CC_
	C	GGCCGGGCG GG GC CGCC	
		CCGGCCCCGC CC CG GCGG	
		G AC AGT	
GAM1869 KIAA1668	3'	GGCGTGAGCCACGACCGCCCGGC 33028	A___ GCCC
	C	GGCCGGGCG GGC CGCC	
		CCGGCCCCGC CCG GCGG	
		ACCA AGT_	
GAM1869 SARM	3'	GGCAAGAGCCTCCACGCCCCGC 17462	___ GCCC
	CA	TGGCCGGGC GAGGC GCC	
		ACCGGCCCG CTCCG CGG	
		CAC AGAA_	
GAM1869 SNFT	5'	CGGGCGGGGCGGGGCGGGCCGG 20743	G GAGG_
	GCCA	TGGCC GGC CGCCCCGCCCCG	
		ACCGG CCG GCGGGGCGGGC	
		G GCGGG	
GAM1869 UHRF2	5'	GGGCGGGGCGCGGCGCCC 36356	AG
		GGGCG GCGCCCCGCCC	
		CCCGC CGCGGGGCGGG	
		GG	
GAM1869 LOC134121	5'	CGGGCGGGACGGACCGCGGCCA 37063	_ CGAGG C
		TGGCCG GG CG CCCGCCCCG	
		ACCGGC CC GC GGGCGGGC	
		G AG___ A	
GAM1869 LOC150630	5'	GGCGTGAGCCACCGCGCCCGGC 41241	A C_ CC_
	C	GGCCGGGCG GG GC CGCC	
		CCGGCCCCGC CC CG GCGG	
		G AC AGT	
GAM1869 LOC155382	5'	CGGGCGGGGCCGGAGCCCGGC 41765	GAGGC
		GCCGGGC GCCCGCCCCG	
		CGGCCCG CGGGGCGGGC	
		AGGC_	
GAM1869 LOC203369	3'	GGCGTGAGCCACGACCGCCCGGC 43032	A___ GCCC
	C	GGCCGGGCG GGC CGCC	
		CCGGCCCCGC CCG GCGG	
		ACCA AGT_	
GAM1869 LOC203427	5'	CGGGCGGGGCCTGGGGCCCGCC 43044	C GA_ C
	A	TGGC GGGC GG GCCCGCCCCG	

		ACCG CCCG TC CGGGGCGGGC		
		— GGG —		
GAM1869	LOC221431 5'	GGCATGAGCCACCGCACCCGGC 44224	— A_	GCCCC
	CA	TGGCCGG GCG GGC GCC		
		ACCGGCC CGC CCG CGG		
		CA CA AGTA_		
GAM1869	LOC254057 5'	CGAGCGGAAGCTTCCCGCCCGG 46343	—	GCC C
	CC	GGCCGGGC GAGGC CCGC CG		
		CCGGCCCG CTTCG GGCG GC		
		CC AA_ A		
GAM1869	LOC257486 3'	GGCGTGAGCCACCGCGCCCGGC 34325	A C_ CC_	
	C	GGCCGGGCG GG GC CGCC		
		CCGGCCCGC CC CG GCGG		
		G AC AGT		
GAM1869	LOC91300 5'	GCTGCCACCTCGCCCAGCCA 29006	C	C_ CCC
		TGGC GGGCGAGG GC GC		
		ACCG CCCGCTCC CG CG		
		A AC T_		
GAM1869	LOC91300 5'	GCTGCCACCTCGCCCAGCCA 45387	C	C_ CCC
		TGGC GGGCGAGG GC GC		
		ACCG CCCGCTCC CG CG		
		A AC T_		
GAM1869	LOC91301 5'	GGGGCGCCCCGCCCTGGCCA 32652	_	A
		TGGCC GGGCG GGCGCCCC		
		ACCGG CCCGC CCGCGGGG		
		T C		
GAM1869	LOC92697 5'	GGCATGAGCCACCGCACCCGGC 34804	— A_	GCCCC
	CA	TGGCCGG GCG GGC GCC		
		ACCGGCC CGC CCG CGG		
		CA CA AGTA_		
GAM1870	ZNF261 3'	AATGAAAGCGATGAG 11561		CGA
		TTCATCGTT TTCATT		
		GAGTAGCGA AAGTAA		
		—		
GAM1870	HTEX4 5'	AATAGTGGAAATGATGAA 44213		CGA
		TTCATCGTT TTCATTATT		
		AAGTAGTAA AGGTGATAA		
		—		
GAM1870	HTEX4 5'	AATAGTGGAAATGATGAA 46718		CGA
		TTCATCGTT TTCATTATT		

AAGTAGTAA AGGTGATAA

GAM1870 HTEX4 5' AATAGTGGAAATGATGAA 46649 CGA
TTCATCGTT TTCATTATT
||||||| |||||||
AAGTAGTAA AGGTGATAA

GAM1870 LOC90355 3' AATAATGTTATTGAGCAATGAA 27061 C T_
TTCAT GTTCGAT CATTATT
||||| ||||||| |||||||
AAGTA CGAGTTA GTAATAA
A TT

GAM1871 AFAP 3' ACCAAGACATGAAAAGCTG 22288 A A_
CAGCTTTT CAT TTTGGT
||||||| ||| |||||||
GTCGAAAA GTA GAACCA
_ CA

GAM1871 ARP3BETA 3' ACCATTGTAATAAAAGCTGTTA 21686 CATATT
TAACAGCTTTTA TGGT
||||||| |||
ATTGTCGAAAAT ACCA
AATGTT

GAM1871 MSTP032 3' ACCAAATATGTATCTGT 24905 CTTT
ACAG TACATATTTGGT
||| |||||||||
TGTC ATGTATAAACCA
T__

GAM1871 PLEKHA3 3' TATGCAAAAAGCTGCTGTA 21168 A A
TATA CAGCTTTT CATA
||| ||||||| |||
ATGT GTCGAAAA GTAT
C C

GAM1871 PRO2133 3' ATGTGATATAAAAAGCTGT 20690 _
ACAGCTTTTA CATAT
||||||| |||
TGTCGAAAAT GTGTA
ATA

GAM1872 PPP1R3A 3' ATTTTACTGAGAATATCGAA 8566 AACAA
TTTGATATTT AGTAAAAAT
||||||| |||||||
AAGCTATAAG TCATTTTTA
AG__

GAM1872 PRSS16 3' TTTTGAATGTTAAATGTCAAA 12483 AAG
TTTGATATTTAACA TAAAA
||||||| |||
AAACTGTAAATTGT GTTTT
AA_

GAM1872 FLJ13576 3' ATTTTGTAAAAATCAAA 22861 A
TTTGAT TTAAACAAAGT
||||| |||||||||

		AAACTA AAATTGTTT		
		A		
GAM1872	KIAA0372	3' TTTTCTTTTGTTAAAAATCAAA 16038	A	T
		TTTGAT TTTAACAAAG AAAA		
		AAACTA AAATTGTTTT TTTT		
		A C		
GAM1872	KIAA1361	3' TTTTACTTTGTTTGTACAAA 31173	A	TT
		TTTG TAT AACAAAGTAAAA		
		AAAC ATG TTGTTTCATTTT		
		_ T_		
GAM1872	LOC222060	5' TACTTTGT CATATCAGA 45161	TTA	
		TTTGATAT ACAAAGTA		
		AGACTATA TGTTTCAT		
		C_		
GAM1873	ELMO1	3' GTCTAACATTTTTTGCC 28204	AT	T_
		GGCAAAAA ATGTT AC		
		CCGTTTTT TACAA TG		
		_ TC		
GAM1873	ENC1	3' AGTTGTGAATACATTCTTTGCT 9697	A	A
		GGCAAA AAT TGTTTACAACT		
		TCGTTT TTA ATAAGTGTTGA		
		C C		
GAM1873	HPSE	3' AGGGGTACACACTTTTTGCTTA 13475	ATA	T AA
		TAGGCAAAAA TGT TAC CT		
		ATTCGTTTTT ACA ATG GA		
		C_ C GG		
GAM1873	RAB3B	3' AGTTGCTGCTATTCTTTGCCTG 8771	A	T TTA
		TAGGCAAA AATA GT CAACT		
		GTCCGTTT TTAT CG GTTGA		
		C _ TC_		
GAM1873	SLC16A1	3' TGTAATATTTTTTTAACCTA 9012	CA	T
		TAGG AAAAA ATGTTTACA		
		ATCC TTTT TATAAATGT		
		AA T		
GAM1873	ZNF268	5' GTTGTAGTTTTTTTGCCT 31500	TATGT	
		AGGCAAAAAA TTACAAC		
		TCCGTTTTT GATGTTG		
		T_		
GAM1873	ARHE	3' GTTGTGTGATTTTTTGCC 11668	ATGTT	
		GGCAAAAAAT TACAAC		

		CCGTTTTTTA GTGTTG		
		GT___		
GAM1873	FLJ12934	3' AGTTGTAAACTCTCTTGCC 23175	AAAATAT	
		GGCAA GTTTACAACT		
		CCGTT CAAATGTTGA		
		CTCT___		
GAM1873	HCA4	3' TTGTAAATATGTTTTCTGCCT 38030	A	
		AGGCA AAAATATGTTTACAA		
		TCCGT TTTTGTATAAATGTT		
		C		
GAM1873	KIAA0427	3' AGACATACTGTTTGCCTA 16571	AAA	
		TAGGCAAA TATGTTT		
		ATCCGTTT ATACAGA		
		GTC		
GAM1873	LOC116228	3' AGTTGTAGTCATTTTTTTCCC 36533	C T T	
		GG AAAAAA ATG TTACAACT		
		CC TTTTTT TAC GATGTTGA		
		C _ T		
GAM1873	LOC221540	3' AGTTGCACATGTTTTCCCCTA 45044	CAA TTA	
		TAGG AAAATATGT CAACT		
		ATCC TTTTGTACA GTTGA		
		CC_ C_		
GAM1873	LOC257545	3' AGTTGCACATGTTTTCCCCTA 46692	CAA TTA	
		TAGG AAAATATGT CAACT		
		ATCC TTTTGTACA GTTGA		
		CC_ C_		
GAM1873	LOC257598	3' AGTTGCACATGTTTTCCCCTA 46749	CAA TTA	
		TAGG AAAATATGT CAACT		
		ATCC TTTTGTACA GTTGA		
		CC_ C_		
GAM1874	CEACAM6	3' AACCCAGCCATGCAATGCCA 8307	A T A	
		TGGCAT TG CG GGCTGGGT		
		ACCGTA AC GT CCGACCCAA		
		_ _ A		
GAM1874	MMP19	5' ACCCAGTCCCATGCCAGA 23072	ATGTCGA	
		TCTGGCAT GGCTGGGT		
		AGACCGTA CTGACCCA		
		CC_____		
GAM1874	MMP19	5' ACCCAGTCCCATGCCAGA 23081	ATGTCGA	
		TCTGGCAT GGCTGGGT		

		AGACCGTA	CTGACCCA	
		CC_____		
GAM1874	PODXL	3' AACCCAGCCCTCCACTGCCA	11868	TAT C _
		TGGCA GT GAGG CTGGGTT		
		ACCGT CA CTCC GACCCAA		
		___ C C		
GAM1874	DREV1	3' AACCCAGCCTCATTGAGATACA	18106	GCATA TC_
	GA	TCTG TG GAGGCTGGGTT		
		AGAC AC CTCCGACCCAA		
		ATAG_ TTA		
GAM1874	KCNE4	3' AACCCAGCCCATTGTCACA	27967	_ T TCGA
		TG GCA ATG GGCTGGGTT		
		AC CGT TAC CCGACCCAA		
		A T _____		
GAM1874	PLSCR4	3' AACCCAGTAAACATATACA	21619	GC CGAG
		TG ATATGT GCTGGGTT		
		AC TATACA TGACCCAA		
		A_ AA_		
GAM1874	LOC163033	5' AACCCAGCCCCAGCGACCAGG	40072	CATA CGA
		TCTGG TGT GGCTGGGTT		
		GGACC GCG CCGACCCAA		
		A_ ACC		
GAM1874	LOC219920	5' AACCCAGCCCCGGGTCA	44801	ATATG A
		TGGC TCG GGCTGGGTT		
		ACTG GGC CCGACCCAA		
		_____ C		
GAM1874	LOC253598	5' CAGTCCGCATATGCCAGA	46609	T A
		TCTGGCATATG CG GGCTG		
		AGACCGTATAC GC CTGAC		

GAM1874	LOC254173	3' AACCCAGCCCTGCACACCA	46285	CATA _ A
		TGG TGT CG GGCTGGGTT		
		ACC ACA GT CCGACCCAA		
		_____ C C		
GAM1875	CDH13	3' ATCTGTATGTATATATAC	6925	GACC
		GTATATATA ACAGAT		
		CATATATAT TGTCTA		
		GTA_		
GAM1875	F13A1	3' TGGTCTATATAACCACA	43774	A A
		TGT GT TATATAGACCA		

			ACA CA ATATATCTGGT		
			C _		
GAM1875 HPSE	3'	TGGTACATATATACCACA	13482	A	AG
		TGT GTATATAT ACCA			
		ACA CATATATA TGGT			
		C CA			
GAM1875 PPT2	3'	TATCTGTGGCCTATGAGGC	28965	ATA	A
		GT TATAG CCACAGATA			
		CG GTATC GGTGTCTAT			
		GA_ C			
GAM1875 PPT2	3'	TATCTGTGGCCTATGAGGC	11634	ATA	A
		GT TATAG CCACAGATA			
		CG GTATC GGTGTCTAT			
		GA_ C			
GAM1875 SIM1	3'	TGTGCATATATACTACA	11513		AGAC
		TGTAGTATATAT CACA			
		ACATCATATATA GTGT			
		C__			
GAM1875 KIAA0836	3'	TATCTGTGACCTATATCAAGTA	32247		AC
		C GTAT ATATAG CACAGATA			
		CATG TATATC GTGTCTAT			
		AAC CA			
GAM1875 KIAA0953	3'	CTGTGGTCCCAGGTA	33168	T	ATATA
		TG AGTAT GACCACAG			
		AC TCATG CTGGTGTC			
		_ GACC_			
GAM1875 PRO2958	5'	ATCTGTGGTAGTTTGATACTAC	20624		ATATAG
		A TGTAGTAT ACCACAGAT			
		ACATCATA TGGTGTCTA			
		GTTTGA			
GAM1875 SDCCAG1	3'	ATCTAATATATATATTACA	11070		GACCAC
		TGTAGTATATATA AGAT			
		ACATTATATATAT TCTA			
		AA__			
GAM1875 SNTG1	3'	ATCTGTGAAATATACTACA	21037		ATAGAC
		TGTAGTATAT CACAGAT			
		ACATCATATA GTGTCTA			
		AA__			
GAM1875 LOC120856	3'	TATCTATGCAGTTTATATAAAC	36642	A	__ C
		TACA TGTAGT TATATAGAC CA AGATA			

ACATCA ATATATTTG GT TCTAT
 A AC A
 GAM1875 LOC131744 3' GTGTCTAGCACATACTACA 37358 ATA_ C
 TGTAGTAT TAGAC AC
 ||||| |||||
 ACATCATA ATCTG TG
 CACG _
 GAM1875 LOC147172 3' TATCTGTGACTGTCATACTA 38313 AT AC
 TAGTAT ATAG CACAGATA
 ||||| ||| |||||
 ATCATA TGTC GTGTCTAT
 C_ A_
 GAM1875 LOC152195 3' TTGTGTATATATACCACA 41435 A GAC
 TGT GTATATATA CACAG
 || ||||| |||||
 ACA CATATATAT GTGTT
 C _
 GAM1875 LOC153454 3' TATCCGTGTATGTATATATACA 39375 A GAC_ A
 CA TGT GTATATATA CAC GATA
 || ||||| || |||||
 ACA CATATATAT GTG CTAT
 _ GTAT C
 GAM1876 C7 3' CTATTTCTATCCTGAGTAGTA 6188 A T
 TATTACTCAG ATAGA ATAG
 ||||| ||||| |||||
 ATGATGAGTC TATCT TATC
 C T
 GAM1876 CALU 3' CTATATCTTTGTGGATAATA 6884 CT G T
 TATTA CA AA AGATATAG
 ||||| || || |||||
 ATAAT GT TT TCTATATC
 AG G _
 GAM1876 HPSE 3' CTATAATTGTCTCTGAGTAA 13478 _ A
 TTAATCAGA ATAG TATAG
 ||||| ||||| |||||
 AATGAGTCT TGTT ATATC
 C A
 GAM1876 PTGFR 3' CTATGTTATCTGAGTA 6662 ATA
 TACTCAGA GATATAG
 ||||| |||||
 ATGAGTCT TTGTATC
 A_
 GAM1876 RAB18 3' CTATTCAATTTCTGAGTAATA 22220 TAGAT
 TATTACTCAGAA ATAG
 ||||| ||||| |||||
 ATAATGAGTCTT TATC
 TAACT
 GAM1876 C1QTNF7 3' CTATTAAATGCCCTGAGTGATA 25664 AA GAT_
 TATTACTCAG TA ATAG
 ||||| || |||||

		ATAGTGAGTC GT TATC	
		CC AAAT	
GAM1876	FLJ13340	3' TATCTTGCTCTGAGTAGTA 27708	AT_
		TATTACTCAGA AGATA	
		ATGATGAGTCT TCTAT	
		CGT	
GAM1876	FLJ14621	3' CTATTACAGCCTGAGTAATA 26579	_____
		TATTACTCAG AATAG	
		ATAATGAGTC TTATC	
		CGACA	
GAM1876	TBDN100	3' TATCTTGCTCTGAGTAGTA 24699	AT_
		TATTACTCAGA AGATA	
		ATGATGAGTCT TCTAT	
		CGT	
GAM1877	AKAP11	3' TATACACATGTGTAGTGT 18372	CC A
		ACGCTAC TATG TGTATA	
		TGTGATG GTAC ACATAT	
		T_ _	
GAM1877	CG012	3' TTATACATTAAAAATAGTGT 40490	CCCTA
		ACGCTA TGATGTATAA	
		TGTGAT ATTACATATT	
		AAAA_	
GAM1877	KIAA0565	3' TTATACATTTTAGGGGTAG 33222	AT_
		CTACCCT GATGTATAA	
		GATGGGG TTACATATT	
		ATT	
GAM1877	METAP1	3' TTGTGCATAGGGAAGC 35959	A TGA
		GCT CCCTA TGTATAA	
		CGA GGGAT ACGTGTT	
		A _	
GAM1877	PTD002	3' ATGTATCAAGGAGCGT 18228	AC A
		ACGCT CCT TGATGTAT	
		TGCGA GGA ACTATGTA	
		_ _	
GAM1877	RAB40A	5' ATACACAGCATAGGGTACGT 39928	C A_
		ACG TACCCTATG TGTAT	
		TGC ATGGGATAC ACATA	
		_ GAC	
GAM1877	LOC146723	3' ATACATTGGGTACAGTGT 38228	_ TAT
		ACGCT ACCC GATGTAT	

	TGTGA TGGG TTACATA	
	CA ____	
GAM1877 LOC147341 3'	CATTAAACAGGGGTAGCGT 40826	A____
	ACGCTACCCT TGATG	
	TGCGATGGGG ATTAC	
	ACAA	
GAM1877 LOC196528 3'	TTATACATTCCAGGAGTAGC 42408	_ AT
	GCTAC CCT GATGTATAA	
	CGATG GGA TTACATATT	
	A CC	
GAM1877 LOC203276 3'	TTATACATATTTGTAGGGTA 43491	TG ____
	TACCCTA A TGTATAA	
	ATGGGAT T ACATATT	
	GT TAT	
GAM1877 LOC203305 3'	TTATACATATTTGTAGGGTA 43515	TG ____
	TACCCTA A TGTATAA	
	ATGGGAT T ACATATT	
	GT TAT	
GAM1877 LOC221662 3'	TTATACTCCAGGTAGTGT 44391	CTA AT
	ACGCTACC TG GTATAA	
	TGTGATGG AC CATATT	
	____ CT	
GAM1877 LOC254243 3'	TTATACATATTTGTAGGGTA 46517	TG ____
	TACCCTA A TGTATAA	
	ATGGGAT T ACATATT	
	GT TAT	
GAM1877 LOC90038 3'	TTATACATATTTGTAGGGTA 30654	TG ____
	TACCCTA A TGTATAA	
	ATGGGAT T ACATATT	
	GT TAT	
GAM1878 DKFZp434J1015 3'	CAGAAAAATCCATCCGCCA 44505	A AC_
	TGGCGGAT GA TTTTG	
	ACCGCCTA CT AAGAC	
	C AAA	
GAM1878 FHOD2 5'	TACATTCAAAAGCTCAAAGGCT 36554	GGATA A
A	TGGC GA CTTTTGAATGTA	
	ATCG CT GAAAACTTACAT	
	GAAA_ C	
GAM1878 FLJ32784 3'	AACTCAAGGCCGCTGCCCGCC 29441	A AAC A
A	TGGCGG TAG TTTTGA TGT	

ACCGCC GTC GGAAC T ACA
 C GCC C
 GAM1878 LOC146520 5' ACATTCAGTCTATCACCA 38184 CG AACTTT
 TGG GATAG TGAATGT
 ||| ||||| |||||
 ACC CTATC ACTTACA
 A_ GTC__
 GAM1878 LOC149711 3' TACATTCATGTTTCCACCCACC 41073 C ATA CTTT
 GG GG GAA TGAATGTA
 || || ||| |||||
 CC CC CTT ACTTACAT
 A CAC TGT_
 GAM1878 LOC150113 5' TACACCCAAGCACATCCGTCA 42170 AGAACT AA
 TGGCGGAT TTTG TGTA
 ||||| ||| |||
 ACTGCCTA GAAC ACAT
 CAC__ CC
 GAM1878 LOC90288 3' TACATGGCTCAAGTTCCATCTG 31115 A TTGA_
 CCA TGGCGGAT GAACTT ATGTA
 ||||| ||||| |||||
 ACCGTCTA CTTGAA TACAT
 C CTCGG
 GAM1879 PSMD12 3' CTAACAAACATATTCCAATAAT 8682 A G _
 A TATTAT TGGAG TGTGTT GTTAG
 ||||| ||||| ||||| |||||
 ATAATA ACCTT ATACAA CAATC
 _ _ A
 GAM1880 CYP1A1 3' CCATTGATTTAATGTAATA 6113 CATAT _
 TATTACATTA AATCA TGG
 ||||| ||||| |||
 ATAATGTAAT TTAGT ACC
 _ _ T
 GAM1880 FLJ10781 3' ACCATGACTAGTAAATGTAA 20132 ACATA A
 TTACATT TA TCATGGT
 ||||| || |||||
 AATGTAA AT AGTACCA
 ATG_ C
 GAM1880 LOC51580 3' CCACGTGTGTAATGTTATA 18013 T AATCA
 TAT ACATTACATAT TGG
 ||| ||||| |||
 ATA TGTAATGTGTG ACC
 T C__
 GAM1881 HLF 3' AAAATGGATTTTAGTCA 7900 GA
 TGAATAAAAT CATTTT
 ||||| |||||
 ACTGATTTTA GTAAAA
 G_
 GAM1881 HLF 3' AAGGTGTTTCAATTTGTCA 7901 T _
 TGAC AAAATGA CATTTT
 ||| ||||| |||||

			ACTG TTTTACT GTGGAA		
			— T		
GAM1881	FLJ14686	3'	AAAAAATGTTAAGTCATA 26598	AAAA	
			TATGACT TGACATTTTTT		
			ATACTGA ATTGTAAAAAA		
			—		
GAM1881	KIAA0594	3'	TAAATTATGTATCATTTTAGCA 32389	A — TT	
			TA TATG CTAAAATGA CAT TTTA		
			ATAC GATTTTACT GTA AAAT		
			— AT TT		
GAM1881	KIAA1040	3'	AAAAATGTCCTTTGTCATA 35736	TA T	
			TATGAC AAA GACATTTTT		
			ATACTG TTT CTGTAAAAA		
			— C		
GAM1882	CAV1	3'	TTAGTCCCTCATGCAAATCAAT 7490	AATATTTA	
			TA TAATTGATTTG GCTAA		
			ATTAATAAAC TGATT		
			GTA CTCCC		
GAM1882	FLJ30294	3'	TTAGTTGCTATTCAAATTAAT 29452	TT	
			ATTGATTTGAATA TAGCTAA		
			TAATTAACTTAT GTTGATT		
			C_		
GAM1882	KIAA1571	3'	TTAAATATTCAAATAATTA 30567	A	
			TAATTG TTTGAATATTTAG		
			ATTAAT AAAC TTATAAATT		
			—		
GAM1882	LOC201965	3'	AGCTAAATAGTTTGAATTA 42931	TG _	
			TGATT AAT ATTTAGCT		
			ATTAA TTG TAAATCGA		
			GT A		
GAM1882	LOC257017	5'	CTAAATATTGAAATCAATTA 46494	G	
			TAATTGATTT AATATTTAG		
			ATTAATAAA TTATAAATC		
			G		
GAM1883	GLS	3'	TCTGCTGATATGCATTTAT 17109	T _	
			ATAAAT GCATATCA CGGG		
			TATTTA CGTATAGT GTCT		
			— C		
GAM1883	MMP8	3'	ATATCTTCTACATGCAATTTA 8257	ATCAC	
			TAAATTGCAT GGGATAT		

		ATTTAACGTA TTCTATA		
		CATC_		
GAM1883	SELL	3' CCTGTAACATGCAATTTTG	6314	T ATC
		A AAATTGCAT ACGGG		
		G TTTAACGTA TGTCC		
		T CAA		
GAM1883	DKFZP564D206	3' ATATCCATGAATGCAATTTG	44427	A CG
		TAAATTGCAT TCA GGATAT		
		GTTTAACGTA AGT CCTATA		
		_ A_		
GAM1883	DKFZP564I0422	3' ATCCTTGTTAATGCAATTTAT	25433	AT_ C
		ATAAATTGCAT CA GGGAT		
		TATTTAACGTA GT TCCTA		
		ATT _		
GAM1883	FLJ23189	3' ATCCTTCACCATGCAATTAATG	24655	A ATCAC
		CAT AATTGCAT GGGAT		
		GTA TTAACGTA TCCTA		
		A CCACT		
GAM1883	P37NB	3' ATCTGGTGATATGCAATT	12433	G
		AATTGCATATCAC GGAT		
		TTAACGTATAGTG TCTA		
		G		
GAM1883	VMP	3' ATATCCAACCCCAGCAATTTAT	28016	ATATCACG
		ATAAATTGC GGATAT		
		TATTTAACG CCTATA		
		ACCCCAA_		
GAM1883	LOC170063	3' CTGTAATATGCAATTTTA	42187	T C
		A AAATTGCATAT ACGG		
		A TTTAACGTATA TGTC		
		T A		
GAM1884	MTRR	3' AAGTATGAAAATGATTTAT	23444	C T
		ATAA ATCATTTTCAT CTT		
		TATT TAGTAAAAGTA GAA		
		_ T		
GAM1884	MTRR	3' AAGTATGAAAATGATTTAT	8290	C T
		ATAA ATCATTTTCAT CTT		
		TATT TAGTAAAAGTA GAA		
		_ T		
GAM1884	PDGFRA	3' AAGATAAAATGATGTTAT	12878	CAT
		ATAACATCATTTT TCTT		

			TATTGTAGTAAAA AGAA		
			T__		
GAM1884	PRKAR1A	3'	AATTAAAAATGAAAATTATGTT 8605	C	C
			AACAT ATTTTCATT TTAATT		
			TTGTA TAAAAGTAA AATTAA		
			T A		
GAM1884	PRKCN	3'	AATTAGGGACAAATGATGTTA 12395		TCA
			TAACATCATTT TTCTTAATT		
			ATTGTAGTAAA AGGGATTAA		
			C__		
GAM1884	RINZF	3'	AATGAAGAATGATGTTAT 23411		_
			ATAACATCATTTT CATT		
			TATTGTAGTAAGA GTAA		
			A		
GAM1884	LOC143692	5'	ATTAAGAATGAAGCTGAT 37630	T	
			ATCA TTTCATTCTTAAT		
			TAGT GAAGTAAGAATTA		
			C		
GAM1884	LOC158549	3'	AATTAAGAATGAAGAGGG 42004	A	
			TC TTTTCATTCTTAATT		
			GG AGAAGTAAGAATTAA		
			G		
GAM1885	BCL11A	3'	AAACAGACCCACATTG 28851		CTTCAT
			CAATGTGG TCTGTTT		
			GTTACACC AGACAAA		
			C_____		
GAM1885	BCL11A	3'	AAACAGACCCACATTG 19751		CTTCAT
			CAATGTGG TCTGTTT		
			GTTACACC AGACAAA		
			C_____		
GAM1885	BCL11B	3'	GAAACTAACAAAGCCACATT 23163		CATTCT
			AATGTGGCTT GTTTC		
			TTACACCGAA CAAAG		
			ACAAT_		
GAM1885	BTG2	3'	AAGTGGAAGCTACACTG 13620	A	CAT TG
			CA TGTGGCTT TC TTT		
			GT ACATCGAA AG GAA		
			C ____ GT		
GAM1885	CELSR2	3'	GGAAAGGACAAAGCCACA 7108	CA	GT
			TGTGGCTT TTCT TTCC		

ACACCGAA AGGA AAGG
 AC ____
 GAM1885 CETN1 3' GGAAACAGGGTGGCCAC 45639 TT _
 GTGGC CATTCTGTTT CC
 |||| ||||| ||
 CACCG GTGGGACAAA GG
 ____ A
 GAM1885 LMO4 5' GGGAATATACAAAGTGAAGCCA 13643 C ____
 CATTG CAATGTGGCTTCATT TGT TTCCC
 ||||| ||||| ||
 GTTACACCGAAGTGA ACA AAGGG
 A TAT
 GAM1885 MAP3K1 3' AAACCTGTGGGGAACACATTG 33680 _ TCT
 CAATGTGG CTTCAT GTTT
 ||||| ||||| ||||
 GTTACACC GGGGTG CAAA
 AA TT_
 GAM1885 MNT 3' GGAGCATAGAAGCCACAT 21566 ATTC
 ATGTGGCTTC TGTTTC
 ||||| |||||
 TACACCGAAG ACGAGG
 AT_
 GAM1885 MPP5 3' AAACAAAATGGTGCCACTTTG 22839 T T C
 CAA GTGGC TCATT TGTTT
 || |||| |||| ||||
 GTT CACCG GGTA ACAA
 T T A
 GAM1885 NPEPPS 3' GGAAACATCTTTTCATAGCCACA 12999 TCATTC_
 TT AATGTGGCT TGTTTC
 ||||| |||||
 TTACACCGA ACAAAGG
 TACTTTCT
 GAM1885 RNTRE 3' GAAACCACGTGAAACCTACATT 16188 _ C TCT
 G CAATGT GG TTCAT GTTTC
 ||||| || ||||| |||||
 GTTACA CC AAGTG CAAAG
 T A CAC
 GAM1885 SCN3A 5' AAACCTGAAGCCAAGCCACATCA 13795 A CA_ T
 C ATGTGGCTT TTC GTTT
 | ||||| || |||||
 A TACACCGAA AAG CAAA
 C CCG T
 GAM1885 SLC4A4 3' GAAGCAGAATGAAACCACATT 9837 C
 AATGTGG TTCATTCTGTTTC
 ||||| ||||| |||||
 TTACACC AAGTAAGACGAAG
 A
 GAM1885 SORBS1 3' GAAACAGAGATTTCCAATTG 17687 G CTTCA
 CAAT TGG TTCTGTTTC
 |||| || |||||

			GTTA ACC GAGACAAAG		
			_ TTTA_		
GAM1885	TIMP3	3'	GGAAACAGAGCTGCCAATTG 5932	G	TTCA
			CAAT TGGC TTCTGTTTCC		
			GTTA ACCG GAGACAAAGG		
			_ TC_		
GAM1885	CMG2	3'	GAAACAGAGGAACCCATCA 27719	T	C A
			A GTGG TTC TTCTGTTTC		
			A TACC AAG GAGACAAAG		
			C C _		
GAM1885	DNAJC6	3'	GGAAAACAGAGGCCAC 16662	TCAT	_
			GTGGCT TCTGTTT CC		
			CACCGG AGACAAA GG		
			_____ A		
GAM1885	FLJ20291	3'	GGTAATAGAACCACATTG 19342	CTTCA	T
			CAATGTGG TTCTGTT CC		
			GTTACACC AAGATAA GG		
			_____ T		
GAM1885	FLJ21870	3'	AAACTGTAATGAACTACATTG 23278	C	CT_
			CAATGTGG TTCATT GTTT		
			GTTACATC AAGTAA CAAA		
			A TGT		
GAM1885	IMP-2	3'	GGAAAACAGGAACCCAC 13306	C	ATT _
			GTGG TTC CTGTTT CC		
			CACC AAG GACAAA GG		
			C _ A		
GAM1885	KIAA0628	3'	GGAAAACAGATGAGCAACCCAC 16675	C_	T _
			GTGG TTCAT CTGTTT CC		
			CACC GAGTA GACAAA GG		
			CAAC _ A		
GAM1885	KIAA0737	3'	AAACAGACTAGAGAAGCCAC 16816	AT_	
			GTGGCTTC TCTGTTT		
			CACCGAAG AGACAAA		
			AGATC		
GAM1885	KIAA0820	3'	GGAAACAGCCAGAAGCCA 34219	ATT	
			TGGCTTC CTGTTTCC		
			ACCGAAG GACAAAGG		
			ACC		
GAM1885	KIAA1128	3'	GGAAAATAATAAGCCACA 33970	C	CTG
			TGTGGCTT ATT TTTCC		

ACACCGAA TAA AAAGG
 A TCA
 GAM1885 KIAA1450 3' AAGCAAAGAAAGCCACATTG 32747 CA C
 CAATGTGGCTT TT TGTTT
 ||||| || ||||
 GTTACACCGAA AA ACGAA
 AG _
 GAM1885 KIAA1641 3' AAACAGGATGACCAAATTG 39098 G CT
 CAAT TGG TCATTCTGTTT
 ||| ||| |||||
 GTTA ACC AGTAGGACAAA
 A _
 GAM1885 KIAA1713 5' GGAAACACAGTCCACATCA 35810 A CTTC C
 C ATGTGG ATT TGTTTCC
 | |||| ||| |||||
 A TACACC TGA ACAAAGG
 C _ C
 GAM1885 KIAA1944 3' AAACAGGGCCACTTG 37224 T TCATT
 CAA GTGGCT CTGTTT
 ||| ||||| |||||
 GTT CACCGG GACAAA
 _ _
 GAM1885 MGC26954 3' GAAAAGTGAAGCCCACTG 29638 A T CTG
 CA TG GGCTTCATT TTTC
 || ||| ||||| |||||
 GT AC CCGAAGTGA AAAG
 C _ _
 GAM1885 MRP63 3' GGAAAGCTGCAATAAAGCCACA 23455 C CT_ _
 TGTGGCTT ATT GTTT CC
 ||||| ||| ||| ||
 ACACCGAA TAA CGAA GG
 A CGT A
 GAM1885 PLAC3 5' GGGAGGCATAGAAGCCACACTG 34367 A ATTC
 CA TGTGGCTTC TGTTTCCC
 || ||||| |||||
 GT ACACCGAAG ACGGAGGG
 C AT_
 GAM1885 PLSCR2 5' GGGAAACAGGCTGACCAC 21631 CT TT
 GTGG TCA CTGTTTCCC
 ||| ||| |||||
 CACC AGT GACAAAGGG
 _ CG
 GAM1885 PTD002 3' GGAAACAAAAGTGAATACCATA 18229 C_ C_
 TTG CAATGTGG TTCATT TGTTTCC
 ||||| ||||| |||||
 GTTATACC AAGTGA ACAAAGG
 AT AA
 GAM1885 RAP140 3' GAGAAGGCCCTGAAATCACATT 17558 GC TT_ G
 G CAATGTG TTCA CT TTTC
 ||||| ||| ||| |||

		GTTACAC AAGT GG AGAG	
		TA CCC A	
GAM1885	RNO2	5' GGGAAACAAGTAAACCA 27126	C C C
		TGG TT ATT TGTTTCCC	
		ACC AA TGA ACAAAGGG	
		_ A _	
GAM1885	TACTILE	3' GGAAACAGAATACTTTGCACA 12413	G TTC__
		TGTG C ATTCTGTTTCC	
		ACAC G TAAGACAAAGG	
		_ TTTCA	
GAM1885	LOC115073	3' GGAAACAGAAACACATT 36241	GCTTCA
		AATGTG TTCTGTTTCC	
		TTACAC AAGACAAAGG	
		A_____	
GAM1885	LOC116123	5' GGAAAACAGAATAGAAGCACA 29013	G _ _
		TGTG CTTC ATTCTGTTT CC	
		ACAC GAAG TAAGACAAA GG	
		_ A A	
GAM1885	LOC125929	3' AAACAGAAGCCACACTG 37267	A TCAT
		CA TGTGGCT TCTGTTT	
		GT ACACCGA AGACAAA	
		C _____	
GAM1885	LOC142927	3' GAAAATTTGTAAAGCCACAT 37568	C TCTG
		ATGTGGCTT AT TTTC	
		TACACCGAA TG AAAG	
		A TTTA	
GAM1885	LOC144893	5' GAGACTCCATGAAGCCACA 40460	TCT
		TGTGGCTTCAT GTTTC	
		ACACCGAAGTA CAGAG	
		CCT	
GAM1885	LOC145622	3' AGACTGGATAAAGCCACA 37904	C T
		TGTGGCTT ATTC GTTT	
		ACACCGAA TAGG CAGA	
		A T	
GAM1885	LOC148811	3' GAAACTTTTGATCAAAACCACA 38599	CT____ TTCT
	TTG	CAATGTGG TCA GTTTC	
		GTTACACC AGT CAAAG	
		AAAAC TTT_	
GAM1885	LOC158156	3' GGAAACATGTAAAGCCACAT 39742	C TC
		ATGTGGCTT AT TGTTTCC	

		TACACCGAA TG ACAAAGG	
		A T_	
GAM1885	LOC50999	3' AACTGAATGAAGCCATATT 18114	T
		AATGTGGCTTCATTC GTT	
		TTATACCGAAGTAAG CAA	
		T	
GAM1885	LOC91151	5' GGAAGGGGAGAAGCCACATTG 27054	AT G
		CAATGTGGCTTC TCT TTTCC	
		GTTACACCGAAG AGG GAAGG	
		_ G	
GAM1886	CDH23	3' AATGTCAATGAACAAGCA 22668	CCATCAA
		TGCTTGTTCA GCATT	
		ACGAACAAGT TGTA	
		AAC_	
GAM1886	TRAF1	3' TTGGAGGTGAACAAGCAA 12200	AT
		TTGCTTGTTCAACC CAA	
		AACGAACAAGTGG GTT	
		AG	
GAM1886	KIAA0893	3' CAACACTTGATGGTACAGTAA 17360	T TC CA
		TTGCT GT ACCATCAAG TTG	
		AATGA CA TGGTAGTTC AAC	
		_ _ AC	
GAM1886	LOC203350	3' CAATGCCTAGAACAAATAAGCA 43531	CACCATCAA
	A	TTGCTTGTT GCATTG	
		AACGAATAA CGTAAC	
		ACAAGATC_	
GAM1886	LOC254413	5' AATGCTTAGTTAACAAG 46395	C CATC
		CTTGTT AC AAGCATT	
		GAACAA TG TTCGTAA	
		T A_	
GAM1886	LOC93017	3' CAATGCTTGATGTCATCAAGCA 35253	TTCAC
		TGCTTG CATCAAGCATTG	
		ACGAAC GTAGTTCGTAAC	
		TACT_	
GAM1887	GATA2	3' CCGCTGAGAGGCTGCCTC 7802	A GTGG
		GAGGTA CCTC TCAGCGG	
		CTCCGT GGAG AGTCGCC	
		C _	
GAM1887	MGC2306	3' CCGCTGAGAGGCTGCCTC 26351	A GTGG
		GAGGTA CCTC TCAGCGG	

CTCCGT GGAG AGTCGCC
C ____

GAM1888 CD69 3' AGACCTAGAATAATACTAGTCT 7538 AA_ _ C
TATA TATAAGAC TATTGT CTAGG CT
||||| |||| ||||| ||
ATATTCTG ATAATA GATCC GA
ATC A A

GAM1888 CAT56 3' AGACCCATGACATGTCTTATA 24931 ATAT TA_ C
TATAAGACA TGTC GG CT
||||| ||| || ||
ATATTCTGT ACAG CC GA
____ TAC A

GAM1888 FLJ20527 3' GCCTAAATAGTATTTTATA 19541 GAC C
TATAA AATATTGT TAGGC
|||| ||||| ||||
ATATT TTATGATA ATCCG
____ A

GAM1888 GPR105 5' AGGCCTAGACGCAGGATCTTTA 17021 T CAATAT
A AAGA TGTCTAGGCCT
| ||| ||||| |||||
A TTCT GCAGATCCGGA
T AGGAC_

GAM1888 LOC144893 3' TCTGAACAATATTGTCTT 40463 C
AAGACAATATTGT TAGG
||||||| ||||
TTCTGTTATAACA GTCT
A

GAM1888 LOC170261 5' GCCTAGGCATCTTCTTATA 40184 CAATAT
TATAAGA TGTCTAGGC
||||| ||||| |||||
ATATTCT ACGGATCCG
TCT__

GAM1888 LOC257051 5' GCCTAGGCATCTTCTTATA 46084 CAATAT
TATAAGA TGTCTAGGC
||||| ||||| |||||
ATATTCT ACGGATCCG
TCT__

GAM1889 PLXNA2 3' AGAAGGTGGTTCTTCAAGCCGA 24813 CACTC TTCA
TCG GAGA CACCTTCT
||| ||| ||||| |||||
AGC TTCT GTGGAAGA
CGAAC TG__

GAM1889 SLC7A8 5' AGAAAGTGTGAATGCGGAGTAG 14550 GC GAG C
GA TC ACTC ATTCACAC TTCT
|| ||| ||||| |||||
AG TGAG TAAGTGTG AAGA
GA GCG A

GAM1889 DKFZP434F091 3' AAGGTGTGAATGTAATGTGA 17736 CTCGAG
TCGCA ATTCACACCTT
|||| ||||| |||||

AGTGT TAAGTGTGGAA
 AATG__
 GAM1889 FLJ13111 3' AGAAGGTGTGAGTGTGAGTG 24684 AG
 CACTCG ATTCACACCTTCT
 ||||| |||||
 GTGAGT TGAGTGTGGAAGA
 G_
 GAM1889 FLJ20312 3' AGAAAATGTGAATTTTTCGT 19373 TC CC
 AC GAGATTCACA TTCT
 || ||||| ||||
 TG TTTTAAGTGT AAGA
 CT AA
 GAM1889 KIAA0776 3' AAGATGTGAATTTTGT 32362 CTC C
 GCA GAGATTCACA CTT
 ||| ||||| ||||
 TGT TTTTAAGTGT GAA
 ____ A
 GAM1889 KIAA1040 3' AGAAAAGTGCTCTTGAGT 35738 TT ACC
 ACTCGAGA CAC TTCT
 ||||| ||| ||||
 TGAGTTCT GTG AAGA
 C_ AA_
 GAM1889 KIAA1956 3' AGAAGGGCCTCTTGAGTGCGA 38361 TTCACA
 TCGCACTCGAGA CCTTCT
 ||||| ||||| |||||
 AGCGTGAGTTCT GGAAGA
 CCG____
 GAM1889 MAP3K2 3' AGAAGATATGAATCTCTGAG 13384 _ CAC
 CTC GAGATTCA CTTCT
 ||| ||||| |||||
 GAG CTCTAAGT GAAGA
 T ATA
 GAM1889 PLA2G12 3' GAAGGTGATGTGAATGCGA 25151 C AGATT _
 TCGCA TCG CA CACCTTC
 ||||| ||| || |||||
 AGCGT AGT GT GTGGAAG
 A ____ A
 GAM1890 PRKR 5' AGCATAGAAACATCCTA 8645 _ CACAC
 TAGGATG TCTGT GCT
 ||||| ||||| |||
 ATCCTAC AGATA CGA
 AA ____
 GAM1890 FLJ14117 3' CAGCCTGGGCAACAGACATCCT 23048 CA__ C
 G TAGGATGTCTGT CA GCTG
 ||||| ||||| || |||||
 GTCCTACAGACA GT CGAC
 ACGG C
 GAM1890 KIAA1464 3' CAGCTGCAACAGACATCCT 33880 CA C
 AGGATGTCTGT CA GCTG
 ||||| ||||| || |||||

		TCCTACAGACA GT CGAC		
		AC _		
GAM1890 NR1I3	5'	GGAGTCTGTGACAGCCACCC 11606	A T	C G
		GG TG CTGTCACA GCT CC		
		CC AC GACAGTGT TGA GG		
		C C C _		
GAM1890 NY-REN-25	5'	GGCAGCGTAACACGCCCTA 30418	AT C	CAC
		TAGG GT TGT ACGCTGCC		
		ATCC CG ACA TGCGACGG		
		_ C A _		
GAM1890 LOC199858	3'	CAGCTTGCAGACATCCTA 42632	T	CAC
		TAGGATGTCTG CA GCTG		
		ATCCTACAGAC GT CGAC		
		_ T _		
GAM1891 ATP10C	3'	AGGGCAGAGCACATGGCCCCC 23686	ATAATC	A
		GG TG TGCTCTGCCCT		
		CC AC ACGAGACGGGA		
		CCCGGT _		
GAM1891 COL13A1	5'	AGAGCCGGTCAGATTCCCCTA 28065	AT	_
		TAGG AATCTGAT GCTCT		
		ATCC TTAGACTG CGAGA		
		CC GC		
GAM1891 COL13A1	5'	AGAGCCGGTCAGATTCCCCTA 28067	AT	_
		TAGG AATCTGAT GCTCT		
		ATCC TTAGACTG CGAGA		
		CC GC		
GAM1891 COL13A1	5'	AGAGCCGGTCAGATTCCCCTA 28069	AT	_
		TAGG AATCTGAT GCTCT		
		ATCC TTAGACTG CGAGA		
		CC GC		
GAM1891 COL13A1	5'	AGAGCCGGTCAGATTCCCCTA 28071	AT	_
		TAGG AATCTGAT GCTCT		
		ATCC TTAGACTG CGAGA		
		CC GC		
GAM1891 COL13A1	5'	AGAGCCGGTCAGATTCCCCTA 28073	AT	_
		TAGG AATCTGAT GCTCT		
		ATCC TTAGACTG CGAGA		
		CC GC		
GAM1891 COL13A1	5'	AGAGCCGGTCAGATTCCCCTA 28075	AT	_
		TAGG AATCTGAT GCTCT		

		ATCC TTAGACTG CGAGA		
		CC GC		
GAM1891 COL13A1	5'	AGAGCCGGTCAGATTCCCCTA	11702	AT ____
		TAGG AATCTGAT GCTCT		
		ATCC TTAGACTG CGAGA		
		CC GC		
GAM1891 MYBL1	3'	GAGCATTAAATTATCCTA	32044	C
		TAGGATAAT TGATGCTC		
		ATCCTATTA ATTACGAG		
		A		
GAM1891 KIAA0157	3'	AGATAATCAAATTGTCCTA	25896	C GC
		TAGGATAAT TGAT TCT		
		ATCCTGTTA ACTA AGA		
		A AT		
GAM1891 KIAA1193	3'	GGGCAGAGCCGGCCACCTA	33584	ATAAT AT
		TAGG CTG GCTCTGCCC		
		ATCC GGC CGAGACGGG		
		ACC__ _		
GAM1891 MGC3248	3'	AGGACAAAGCATCAGCTGTCC	26235	AT C C
		GGATA CTGATGCT TG CCT		
		CCTGT GACTACGA AC GGA		
		C_ A A		
GAM1891 PGCP	5'	AGAGCCGCCCTATCAGATTATC	18220	_____
TTA		TAGGATAATCTGAT GCTCT		
		ATTCTATTAGACTA CGAGA		
		TCCCGC		
GAM1891 PRO0529	3'	AGGGCAGAGCAAGGACAACCCC	15297	ATAA_ GA
		GG TCT TGCTCTGCCCT		
		CC AGG ACGAGACGGGA		
		CCAAC A_		
GAM1891 LOC149706	5'	AGGGCAGAGCCTGGCTGTCC	41057	AT TGAT
		GGATA C GCTCTGCCCT		
		CCTGT G CGAGACGGGA		
		CG TC__		
GAM1891 LOC152373	5'	GCAGAGTTGACGGATTATCC	39271	AT_
		GGATAATCTG GCTCTGC		
		CCTATTAGGC TGAGACG		
		AGT		
GAM1891 LOC221477	3'	GGCAGAGCTTATCCT	44256	TCTGAT
		AGGATAA GCTCTGCC		

TCCTATT CGAGACGG

GAM1891 LOC90167 3' GCAGAGCATGGCCCTCCTA 30905 TAAT G
TAGGA CTATGCTCTGC
||||| |||||
ATCCT GG TACGAGACG
CCC_ _

GAM1892 APAF1 3' GCATTTTCCCTTGCTGTA 6828 A A TG
TACAG AAGG GA GGATGC
||||| ||||| || |||||
ATGTC TTCC CT TTTACG
G _ _

GAM1892 APAF1 3' GCATTTTCCCTTGCTGTA 14867 A A TG
TACAG AAGG GA GGATGC
||||| ||||| || |||||
ATGTC TTCC CT TTTACG
G _ _

GAM1892 AQP6 3' TGTCCCATTCCTCTCTGTA 7362 A AG
TACAGA AGG ATGGGATG
||||| |||||
ATGTCT TCC TACCCTGT
C CT

GAM1892 AQP6 3' TGTCCCATTCCTCTCTGTA 27620 A AG
TACAGA AGG ATGGGATG
||||| |||||
ATGTCT TCC TACCCTGT
C CT

GAM1892 ITGA11 3' AAGGCATCAGTCCCCCTGTG 14511 AAA A GG
TACAG GG GAT GATGCCTT
||||| |||||
GTGTC CC CTG CTACGGAA
C_ _ A_

GAM1892 NOV 3' AAGACACATTGACTCCTTTC 8345 A GA C
GAAAGGAG TGG TG CTT
||||| ||||| |||||
CTTTCCTC GTT AC GAA
A AC A

GAM1892 SORCS1 3' GCTCCCTCCCATCTGTA 27486 AA A T T
TACAGA GG GA GGGA GC
||||| ||||| |||||
ATGTCT CC CT CCCT CG
A_ _ _

GAM1892 ZIC3 3' GGATGCCTTAAGACTCTCCTTT 9451 T_____ ATG
CT AGAAAGGAGA GGG CC
||||| ||||| |||||
TCTTTCCTCT TCC GG
CAGAAIIT GTA

GAM1892 D21S2056E 3' AGACATTTCTCCTTTC 9789 TGG C
GAAAGGAGA GATG CT
||||| ||||| |||||

CTTTCCTCT TTAC GA
 ____ A
 GAM1892 FLJ12154 5' AAGGCACCTGTCTCCCTTCTG 22463 A A
 CAGAA GGAGATGGG TGCCTT
 |||| ||||| ||||
 GTCTT CCTCTGTCC ACGGAA
 C _
 GAM1892 SDC3 3' GTGTCCCTCCCTCCTGTG 16089 AA A T
 TACAG AGG GA GGGATGC
 |||| ||| || |||||
 GTGTC TCC CT CCCTGTG
 C _ _ _
 GAM1892 SEMA4C 3' AAGGCATCTTCCTCCTCTCTGT 19420 A AT
 G TACAGA AGGAG GGGATGCCTT
 |||| |||| |||||
 GTGTCT TCCTC TTCTACGGAA
 C C_
 GAM1892 LOC130074 3' AAGGCATCCCTCACCTCTG 37469 AA A T
 CAGA GG GA GGGATGCCTT
 ||| || |||||
 GTCT CC CT CCCTACGGAA
 _ A _
 GAM1892 LOC144681 5' AAGTGCGGCCCATCTCCTCTC 40453 A A A_ _
 CGT AC GA AGGAGATGGG TGC CTT
 || || ||||| ||| |||
 TG CT TCCTCTACCC GCG GAA
 C C CG T
 GAM1892 LOC148438 3' AAGGATCACCTCACTTCCTG 40883 A GA T _ G
 CAG AAG GA GG GAT CCTT
 ||| || || || |||
 GTC TTC CT CC CTA GGAA
 C A_ _ A _
 GAM1892 LOC203276 3' TTACACCTTCTTTCTGTA 43490 A GG
 TACAGAAAGGAG TG A
 ||||| ||| ||
 ATGTCTTTCTTC AC T
 C AT
 GAM1892 LOC203305 3' TTACACCTTCTTTCTGTA 43514 A GG
 TACAGAAAGGAG TG A
 ||||| ||| ||
 ATGTCTTTCTTC AC T
 C AT
 GAM1892 LOC254243 3' TTACACCTTCTTTCTGTA 46516 A GG
 TACAGAAAGGAG TG A
 ||||| ||| ||
 ATGTCTTTCTTC AC T
 C AT
 GAM1892 LOC254887 5' AAGCCGACCCATCTCCCCTC 46071 AA A C
 GA GGAGATGGG TG CTT
 || ||||| || |||

		CT CCTCTACCC GC GAA		
		CC A C		
GAM1892	LOC90038	3' TTACACCTTCTTTCTGTA	30653	A GG
		TACAGAAAGGAG TG A		
		ATGTCTTTCTTC AC T		
		C AT		
GAM1892	LOC92078	5' AGGCAAGGCCCTTTCTGTA	33741	AGATGGGA
		TACAGAAAGG TGCCT		
		ATGTCTTTCC ACGGA		
		CGGA__		
GAM1893	AMD1	3' TGATCCAAAGCAGAATCA	7349	GC _
		TG TCTGCTTTG ATCG		
		AC AGACGAAAC TAGT		
		TA C		
GAM1893	COL4A6	5' CTCCAAGCATCAGCAGAGCC	27359	T_ ATC
		GGCTCTGCT TG GGAG		
		CCGAGACGA AC CCTC		
		CT GAA		
GAM1893	CORO2B	3' CCCCAGAGACAGAGCCA	32254	_ ATC
		TGGCTCTG CTTTG GG		
		ACCGAGAC GAGAC CC		
		A C__		
GAM1893	FAT2	3' GTCCCCGGGGCAAAGCC	7175	C TTGA A
		GGCT TGCT TCGG GAC		
		CCGA ACGG GGCC CTG		
		A __ C		
GAM1893	NTSR1	3' CCCCAGGGAAACAGGGCCA	8366	__ ATC
		TGGCTCTG CTTTG GG		
		ACCGGGAC GGGAC CC		
		AAA C__		
GAM1893	P4HB	3' TGGCCTGTTCAAGGCAGAACCA	6630	C T AGA
		TGG TCTGCTTTGA CGG CCA		
		ACC AGACGGA ACT GTC GGT		
		A T C__		
GAM1893	PIM2	3' TGGCCCCCAATGGTCAGAAGAG	30134	GC __ AGA
	CCA	TGGCTCT TTTGATC GG CCA		
		ACCGAGA AGACTGG CC GGT		
		__ TAA CCC		
GAM1893	SHOX	3' TGGTCTCCGATGAAAATGCCA	6059	TCTGC G
		TGGC TTT ATCGGAGACCA		

	ACCG	AAA	TAGCCTCTGGT		
		TA	G		
GAM1893	C20orf39	3'	CTGAGAAGCAGAGCCA	24368	GA
			TGGCTCTGCTTT	TCGG	
			ACCGAGACGAAG	AGTC	
GAM1893	C20orf45	3'	CCAGAACAGAGCAGAGCCA	18122	A
			TGGCTCTGCTTTG	TC GG	
			ACCGAGACGAGAC	AG CC	
			A	A	
GAM1893	CLONE24945	3'	TCTGGGAGAAACAGAGCCA	17907	C GA
			TGGCTCTG	TTT TCGGA	
			ACCGAGAC	AAG GGTCT	
			A	AG	
GAM1893	FLJ11320	3'	TTCTGAAAGCAGAGCCA	20429	TGA
			TGGCTCTGCTT	TCGGAG	
			ACCGAGACGAA	AGTCTT	
GAM1893	FLJ23112	3'	CCCCTCAAAGCAGAGCCA	24466	TC
			TGGCTCTGCTTTGA	GG	
			ACCGAGACGAAACT	CC	
			CC		
GAM1893	GIT1	3'	TCCCCACCCCAACAGAGCCA	15259	CT ATC_ A
			TGGCTCTG	TTG GG GA	
			ACCGAGAC	AAC CC CT	
				CCCA C	
GAM1893	KIAA1203	3'	TGGTGGGTTCTCAAAGCAGTAC	35473	CT TCGGAG
	CA		TGG	CTGCTTTGA ACCA	
			ACC	GACGAAACT TGGT	
			AT	CTTGGG	
GAM1893	KIAA1538	3'	TGGCCTCCATGAGGGGCAGGGC	35434	GATC A
	CA		TGGCTCTGCTTT	GGAG CCA	
			ACCGGGACGGGG	CCTC GGT	
			AGTA	C	
GAM1893	KIAA1655	5'	CTCCCAAACCAGAGCCA	33088	C ATC
			TGGCTCTG	TTTG GGAG	
			ACCGAGAC	AAAC CCTC	
			C		
GAM1893	KIAA1937	3'	CTCTAAATAGAGCCA	36483	C GATC
			TGGCTCTG	TTT GGAG	

ACCGAGAT AAA TCTC

GAM1893 NDRG4 3' CGGCCCAGAAACCAGAGCCA 21698 C__ A_
TGGCTCTG TTTG TCG
||||||| ||| |||
ACCGAGAC AGAC GGC
CAA CC

GAM1893 NDRG4 3' CGGCCCAGAAACCAGAGCCA 23213 C__ A_
TGGCTCTG TTTG TCG
||||||| ||| |||
ACCGAGAC AGAC GGC
CAA CC

GAM1893 TRIP-Br2 3' CTTCCAAAGCCAGAGCCA 16488 _ ATC
TGGCTCTG CTTTG GGAG
||||||| |||| |||
ACCGAGAC GAAAC CTTC
C _

GAM1893 UHRF1 3' TGGCCCCCAAGGTCAGAGC 14954 _ ATC AGA
GCTCTG CTTTG GG CCA
||||||| |||| || |||
CGAGAC GGAAC CC GGT
T C__ C__

GAM1893 YME1L1 3' GTCTCGGAAACACAGAGCCA 15539 CTTTGA G
TGGCTCTG TC GAGAC
||||||| || |||||
ACCGAGAC AG CTCTG
ACAA__ G

GAM1893 YME1L1 3' GTCTCGGAAACACAGAGCCA 29295 CTTTGA G
TGGCTCTG TC GAGAC
||||||| || |||||
ACCGAGAC AG CTCTG
ACAA__ G

GAM1893 LOC148894 5' GTCTCCTGGAAGCAGAGC 40920 GATC
GCTCTGCTTT GGAGAC
||||||| |||||
CGAGACGAAG CCTCTG
GT__

GAM1893 LOC165405 5' GTCTCCGGGGCAAGCCA 40130 C TTGA
TGGCT TGCT TCGGAGAC
|||| |||| |||||
ACCGA ACGG GGCCTCTG

GAM1893 LOC202908 5' GGTCTCCAACCACAGGGCCA 42997 CTT ATC
TGGCTCTG TG GGAGACC
||||||| || |||||
ACCGGGAC AC CCTCTGG
__ CAA

GAM1893 LOC91149 3' CTACCTATCAAAGCTGAACCA 32457 C T C _
TGG TC GCTTTGAT GG AG
||| || ||||| || ||

ACC AG CGAAACTA CC TC
 A T T A
 GAM1893 LOC93276 5' GGTCTCCAACCACAGGGCCA 35590 CTT ATC
 TGGCTCTG TG GGAGACC
 ||||| || |||||
 ACCGGGAC AC CCTCTGG
 ____ CAA
 GAM1894 LSS 5' TAGTCTGTGGCCCAGCAAAGCC 8140 AA T_ ____
 AC GT CTTTGCTG CTA ACTA
 || ||||| || ||||
 CA GAAACGAC GGT TGAT
 CC CC GTC
 GAM1894 CHODL 3' TAGTTGCAAAGTTAGTCTA 24492 G TGT
 TAGA TAACTTTGC CTA
 ||| ||||| |||
 ATCT ATTGAAACG GAT
 G TT_
 GAM1894 FLJ12057 5' AGTCAGACAGCAGCTCTG 24124 AACTT A
 TAGAGT TGCTGTCT ACT
 |||| | ||||| |||
 GTCTCG ACGACAGA TGA
 ____ C
 GAM1894 FLJ23360 3' TAGTTAGAGGTTATAAATTGCT 23337 CTTT__ G
 CTA TAGAGTAA GCT TCTAACTA
 ||||| || |||||
 ATCTCGTT TGG AGATTGAT
 AAATAT _
 GAM1894 MRPL10 3' TAGGAGCAAAGTCTCTC 29771 TA G
 GAG ACTTTGCT TCTA
 || | ||||| ||||
 CTC TGAAACGA GGAT
 TC _
 GAM1894 LOC143680 5' GGCTCAGCAAAGTGACCCTA 40375 A A T_
 TAG GT ACTTTGCTG CT
 ||| || ||||| ||
 ATC CA TGAAACGAC GG
 C G TC
 GAM1894 LOC256433 5' TAGCCAGAAGCAAAGCCACTGT 46553 G AA G AA
 A TA AGT CTTTGCT TCT CTA
 || ||| ||||| || |||
 AT TCA GAAACGA AGA GAT
 G CC _ CC
 GAM1895 DKFZP434E2135 3' TATTTTCTTTGTTCCCA 25118 A TCTTT
 TG GGAAC GAGAAAAATA
 || |||| | |||||
 AC CCTTG TTCTTTTAT
 _ T____
 GAM1895 KIAA0563 5' TTTCTCAAGCTCCTCA 16846 A CTT
 TGAGGA CT TGAGAAA
 ||||| || |||||

ACTCCT GA ACTCTTT
 C ____
 GAM1895 KIAA1503 5' TTAGCACAGAGTTCCTCA 33918 T AG
 TGAGGAACTCT TG AA
 ||||| || ||
 ACTCCTTGAGA AC TT
 C GA
 GAM1895 KIAA1958 3' TCTTGTAGGCAGTGTTCCTCA 39832 ____ T
 TGAGGAAC TCT TGAGA
 ||||| || |||||
 ACTCCTTG GGA GTTCT
 TGAC T
 GAM1895 LOC112609 3' CTATTTTTTTTAAAGCTCGTCA 36057 G ACT
 TGA GA CTTTGAGAAAAATAG
 || || |||||
 ACT CT GAAATTTTTTTTATC
 G C__
 GAM1895 LOC147071 5' TTTCTCAAGCTCCTCA 36140 A CTT
 TGAGGA CT TGAGAAA
 ||||| || |||||
 ACTCCT GA ACTCTTT
 C ____
 GAM1895 LOC149271 5' ATTTTCTCAGGGCCCTC 38677 AACT
 GAGG CTTTGAGAAAAAT
 ||| |||||
 CTCC GGGACTCTTTTA
 C__
 GAM1895 LOC221092 5' TTTTCTCAGAGAAGTTCC 44775 _
 GGAAC TTTTGAGAAAA
 ||||| |||||
 CCTGA GAGACTCTTTT
 A
 GAM1895 LOC255328 3' TATCCTTCTCGAGTTCCCA 46180 A TTT AA
 TG GGAAC TC GAGAA ATA
 || ||||| ||||| |||
 AC CCTTGAG CTCTT TAT
 _ _ CC
 GAM1895 LOC92719 3' CTATTCCTTCTCAGACCCTCA 34849 AACTC A
 TGAGG TTTGAGAA AATAG
 ||||| ||||| |||||
 ACTCC AGACTCTT TTATC
 C__ C
 GAM1896 PPP1CB 3' GAGCTTTACAGACATTCACCAA 8558 CTA TTGA
 TTGGTGAATG TGTA CTC
 ||||| ||||| |||
 AACC ACTTAC ACAT GAG
 AG_ TTC_
 GAM1896 BY55 3' CAGAACAGCTTTACACCAA 29845 T AT A
 TTGGTGAA GCT GT TTG
 ||||| ||||| ||| |||

AACCACTT CGA CA GAC
 T _ A
 GAM1896 KIAA1042 3' TCAACACAATTTTATTTCACTAA 17353 CTA_ A
 TTGGTGAATG TGT TTGA
 ||||| |||||
 AATCACTTAT ACA AACT
 TTTA C
 GAM1896 MAWBP 3' TCAATAATTCACCAG 22681 GCTATG
 TTGGTGAAT TATTGA
 ||||| |||||
 GACCACTTA ATA ACT

 GAM1896 MEGF10 3' AGTCAATACACAAATGTGCCAG 26209 A GCTA
 TTGGTG AT TGTATTGACT
 ||||| || |||||
 GACCGT TA ACATAACTGA
 G AAC_
 GAM1896 LOC151361 5' TCAATACATGCCCAA 41333 TGAAT T
 TTGG GC ATGTATTGA
 ||| || |||||
 AACC CG TACATAACT
 C _ _
 GAM1896 LOC162333 5' GAATCAGACAGCATTACCAA 42130 AT A C
 TTGGTGAATGCT GT TTGA TC
 ||||| || |||||
 AACCACTTACGA CA GACT AG
 _ _ A
 GAM1896 LOC201725 3' GGGTCACACAACATTCACTAA 42905 CTA AT
 TTGGTGAATG TGT TGA CTC
 ||||| || |||||
 AATCACTTAC ACA ACTGGG
 A _ C_
 GAM1897 MFAP3 5' CTCAAGCAGTGCGAAAAGCAGA 12555 CA A _
 TTA TAA TGCTTTTC CGTT TTTGAG
 || ||||| |||||
 ATT ACGAAAAG GTGA GAACTC
 AG C C
 GAM1897 PMCHL1 3' TCAAAAATTAAGCATGT 25631 TTCAC
 ACATGCTT GTTTTGA
 ||||| |||||
 TGTACGAA TAAAACT
 T _ _
 GAM1897 CBARA1 3' CTCAAAAACATGAACAAGT 12723 _ C
 GCTT TTCA GTTTTGA
 ||| ||||| |||||
 TGAA AAGT CAAAACTC
 C A
 GAM1897 FLJ10704 3' CTCAAAAACGTGAGCGT 20033 TTT
 ATGC TCACGTTTTTGA
 ||| |||||

TGCG AGTGCAAAAACCTC

GAM1897 FLJ13456 3' CTCAAAAAAAAAAAAAGCAT 32798 CACG
ATGCTTTT TTTTGTAG
||||||| |||||||
TACGAAAA AAAAACTC
AAAA

GAM1897 KIAA1013 3' CTCAAAAACATGAAAGGGCAT 42857 _ C
ATGCT TTTCA GTTTTGTAG
||||| ||||| |||||||
TACGG AAAGT CAAAACTC
G A

GAM1897 MGC32104 3' CTCAAAGACATAAAAGCA 29505 CAC
TGCTTTT GTTTTGTAG
||||||| |||||||
ACGAAAA CAGAACTC
TA_

GAM1897 SPTLC2 3' CTCAAAAAAAAAAAAAGTCATGT 11277 _ CACG
TA TAACATG CTTT TTTTGTAG
||||||| ||||| |||||||
ATTGTAC GAAAA AAAAACTC
T AAA_

GAM1897 UBP1 3' CTCACCTTTGAAAAGTATG 15846 CGTTTT
CATGCTTTTCA TGAG
||||||| |||||
GTATGAAAAGT ACTC
TTC__

GAM1897 LOC144348 5' CTCAAAAACGCAAAGGTTTG 37721 T CA
CA GCTTTT CGTTTTGTAG
|| ||||| |||||||
GT TGGAAA GCAAAAACCTC
T C_

GAM1897 LOC196418 5' CTCAAAAACGCAAAGGTTTG 42369 T CA
CA GCTTTT CGTTTTGTAG
|| ||||| |||||||
GT TGGAAA GCAAAAACCTC
T C_

GAM1897 LOC221362 3' CTCAAAAAGTGCAAAAGCA 45020 _ G
TGCTTTT CAC TTTTGTAG
||||||| ||| |||||||
ACGAAAA GTG AAAAACTC
C _

GAM1897 LOC254672 3' TCAAAAATTAAGCATGT 45398 TTCAC
ACATGCTT GTTTTGA
||||||| |||||||
TGTACGAA TAAAACT
T__

GAM1898 ZFP91 3' ATCGAAGGCTTACCCTATT 27571 ACAATC
AATGGG GCTTTCGAT
||||| |||||||

		TTATCC CGGAAGCTA		
		CATT__		
GAM1899 FBN1	3'	TGTCATAAATGTCACAATA 32183	CA	GT
		TAT TGATATTTATG G		
		ATA ACTGTAAATAC T		
		AC TG		
GAM1899 GNAS	3'	CCACCATAGGGCATGAT 18678	ATAT	
		ATCATG TTATGGTGG		
		TAGTAC GATACCACC		
		GG__		
GAM1899 TMOD	3'	TTCAGCAAATCTCATGATA 9295	T TA G	
		TATCATGA ATT TG TGGA		
		ATAGTACT TAA AC ACTT		
		C __ G		
GAM1899 ABCA8	3'	ATCCACAGGTAACACCATGATG 14013	ATAT G_	
		TATCATG TTAT GTGGAT		
		GTAGTAC AATG CACCTA		
		CAC_ GA		
GAM1899 BIRC1	3'	CCATTCGAAATTCATGATA 10884	T AT	
		TATCATGA ATTT GGTGG		
		ATAGTACT TAAA TTACC		
		_ GC		
GAM1899 FLJ10508	3'	CCACAGATACCATGATA 19893	A ATG	
		TATCATG TATTT GTGG		
		ATAGTAC ATAGA CACC		
		C ____		
GAM1899 FLJ12747	3'	CCCTGTAAATACATGATA 25878	A T	
		TATCATG TATTTATGG GG		
		ATAGTAC ATAAATGTC CC		
		- -		
GAM1899 KIAA0527	3'	TTATAAATAGTCATGATA 45850	-	
		TATCATGAT ATTTATGG		
		ATAGTACTG TAAATATT		
		A		
GAM1899 KIAA1948	3'	ATCCACCAAGATACCAGA 40077	A A A	
		TC TG TATTT TGGTGGAT		
		AG AC ATAGA ACCACCTA		
		_ C _		
GAM1899 NESHBP	3'	CCACCATAAATGTTACAATA 17728	CA	
		TAT TGATATTTATGGTGG		

		ATA ATTGTAAATACCACC		
		AC		
GAM1899	P311	3' GTCTACAAAATCATGATA	11161	ATTTATG
		TATCATGAT	GTGGAT	
		ATAGTACTA	CATCTG	
		AAA_____		
GAM1899	PHIP	5' ACCATGAAATACCATGATA	19622	A _
		TATCATG TATT TATGGT		
		ATAGTAC ATAA GTACCA		
		C A		
GAM1899	SPTLC2	3' ATCGTAAACATTCATGATA	11273	TA_
		TATCATGA TTTATGGT		
		ATAGTACT AAATGCTA		
		TAC		
GAM1899	LOC144747	5' ATTGTAAATACCATGATG	37783	A TG
		TATCATG TATTTA GT		
		GTAGTAC ATAAAT TA		
		C GT		
GAM1899	LOC149372	5' ATCCACCATCGAATTCCAT	38723	AT _
		ATG ATTT ATGGTGGAT		
		TAC TAAG TACCACCTA		
		CT C		
GAM1899	LOC257463	3' ATCCACCACTGTAATATCAT	35206	TA__
		ATGATATT TGGTGGAT		
		TACTATAA ACCACCTA		
		TGTC		
GAM1900	ADCY2	3' TCCAAAAACAGTGATT	32435	TAGT
		AATCACT TTTTTGGA		
		TTAGTGA AAAAAACCT		
		C_____		
GAM1900	EGFL5	3' TCCAAAAGCTAAATGATTAA	41886	C T
		TTGAATCA TTAGTTTTT GGA		
		AATTTAGT AATCGAAAA CCT		
		A _		
GAM1900	IFI16	5' TCAGCTAACTAAGTGACTCAA	35282	A TT
		TTGA TCACTTAGTT TTGG		
		AACT AGTGAATCAA GACT		
		C TC		
GAM1900	C12orf22	3' CCAGATTCCAAAGGATTCAA	25124	A AGTTT
		TTGAATC CTT TTTGG		

			AACTTAG GAA AGACC	
			_ ACCTT	
GAM1900	CAPS2	3'	GAAAAAATAAGTGATTCAA 34953	G
			TTGAATCACTTA TTTTTT	
			AACTTAGTGAAT AAAAAG	
			A	
GAM1900	CTPS2	3'	TCCAAAAAACTCAGGAATCAA 21264	A A T
			TTGA TC CT AGTTTTTTGGA	
			AACT AG GA TCAAAAAACCT	
			A _ C	
GAM1900	FLJ10300	5'	TCCAAAGAGAAAAGTAATTCA 19811	C AG
			TGAAT ACTT TTTTTTGGA	
			ACTTA TGAA GAGAAACCT	
			A AA	
GAM1900	SCYA28	3'	TCCATATCCTAATGATTCAA 21251	C TTTTT
			TTGAATCA TTAG TGGA	
			AACTTAGT AATC ACCT	
			_ CTAT_	
GAM1900	STHM	3'	CCAGATGCTAAAGTGATTCAA 13177	_ TT
			TTGAATCACTT AGT TTTGG	
			AACTTAGTGAA TCG AGACC	
			A T_	
GAM1900	LOC151429	3'	TCCAAAAATTGTACAGATGATT 41344	_ TAGT_
	CAA		TTGAATCA CT TTTTTGGA	
			AACTTAGT GA AAAAACCT	
			A CATGTT	
GAM1900	LOC153454	5'	TCGGAAAATTAAGCGACCCAA 39376	AA A
			TTG TC CTTAGTTTTTTGG	
			AAC AG GAATTAAGGCT	
			CC C	
GAM1900	LOC203504	3'	TCCAGGGACAGAGTGATCCAA 43573	A A T
			TTG ATCACTT GTTTTT GGA	
			AAC TAGTGAG CAGGGA CCT	
			C A _	
GAM1901	CLECSF5	3'	ACAACAGAAAGGAAATCCTA 14915	A GGTAGC
			TAGGA TTT TCTGTTGT	
			ATCCT AAG AGACAACA	
			A GAA_	
GAM1901	ESRRG	3'	ACAACAGAAAATACAACCTCTG 32993	ATTTG GC_
	G		CTAGGA GTA TCTGTTGT	

			GGTCCT CAT AGACAACA		
			CAA__ AAA		
GAM1901	FBXW1B	3'	ACGTGGCTACCAAATGCCTA 27362	A	C
			TAGG ATTTGGTAGCT TGT		
			ATCC TAAACCATCGG GCA		
			G T		
GAM1901	FBXW1B	3'	ACGTGGCTACCAAATGCCTA 27372	A	C
			TAGG ATTTGGTAGCT TGT		
			ATCC TAAACCATCGG GCA		
			G T		
GAM1901	FBXW1B	3'	ACGTGGCTACCAAATGCCTA 14660	A	C
			TAGG ATTTGGTAGCT TGT		
			ATCC TAAACCATCGG GCA		
			G T		
GAM1901	KAL1	3'	ACAACAGAACTCAGTTTTCC 5713	T_	GT C
			GGAA TTG AG TCTGTTGT		
			CCTT GAC TC AGACAACA		
			TT __ A		
GAM1901	SMA3	3'	ACAACAGAGGAGATAATCTCC 13653	AT	GTAG
			GGA TTG CTCTGTTGT		
			CCT AAT GAGACAACA		
			CT AGAG		
GAM1901	LOC151056	3'	ACAAACCAGTCACCAAATTCCC 39046	A	AG CTG
	AG		CT GGAATTTGGT CT TTGT		
			GA CCTTAAACCA GA AACA		
			C CT CCA		
GAM1901	LOC157247	5'	CAACAGAGTCATTTCCCTA 39572	TT	GTA
			TAGGAA TG GCTCTGTTG		
			ATCCTT AC TGAGACAAC		
			T_ __		
GAM1901	LOC222066	3'	CAACAAAAAAATTCCTAG 44553		GGTAGCTC
			CTAGGAATTT TGTG		
			GATCCTTAAA ACAAC		
			AAA_____		
GAM1901	LOC254504	5'	ACAACAGGTACAAAGTCCTA 46437	A	GTA T
			TAGGA TTTG GC CTGTTGT		
			ATCCT AAAC TG GACAACA		
			G A__ _		
GAM1901	LOC90520	3'	ACAACAGGTACAAAGCCCTA 31629	AA	GTA T
			TAGG TTTG GC CTGTTGT		

ATCC AAAC TG GACAACA
 CG A__ _
 GAM1902 PRO2015 5' ATTTCCATTCTACTTA 20585 C A
 TAAGTAATGA TG AAAT
 ||||| || ||||
 ATTCATTACT AC TTTA
 T C
 GAM1903 MUC3B 5' CTCTCACCCCTTCGTCTGTGG 45254 AAA AC_ T
 TCACAGAC AAG TGA AG
 ||||| || ||||
 GGTGTCTG TTC ACT TC
 C__ CCC C
 GAM1903 RELN 3' CTGCCATTTTTTGTCTGTGA 45282 AC A
 TCACAGACAAAAAG TG TAG
 ||||| || ||||
 AGTGTCTGTTTTT AC GTC
 _ C
 GAM1903 SELL 3' CTGTAGCCTCGCCGTCTGTGA 6315 AAAA A G
 TCACAGAC AG CT ATAG
 ||||| || ||||
 AGTGTCTG TC GA TGTC
 CCGC C _
 GAM1903 WWOX 3' GTTAATCCCTTTGTCTGT 18505 AA C
 ACAGACAAA GA TGAT
 ||||| || ||||
 TGTCTGTTT CT ATTG
 CC A
 GAM1903 DKFZP434C131 3' ACCCACCAGTCTTTCTGGGA 34242 A CAAA ATA
 TC CAGA AAGACTG GGT
 || |||| ||||| ||
 AG GTCT TTCTGAC CCA
 G _ CAC
 GAM1903 DKFZP564K0322 5' CTGGACCGTCTTTGTCTGCGA 25739 A AA TGA_
 TC CAGACAA AGAC TAG
 || ||||| |||| ||
 AG GTCTGTT TCTG GTC
 C _ CCAG
 GAM1903 FBXO21 3' CTGTGTGTCTTTTTACCCTG 27322 AC_ TG
 CAG AAAAAGAC ATAG
 || ||||| ||||
 GTC TTTTCTG TGTC
 CCA TG
 GAM1903 FLJ30927 5' ACCTATCAGCCCTTGAAATTCT 29509 CAAA_ A_
 AGA AAG CTGATAGGT
 || || |||||
 TCT TTC GACTATCCA
 TAAAG CC
 GAM1903 KIAA1866 3' ACCTATCAGCCCTTCGGTCTCA 30553 C AAA A_
 A AGAC AAG CTGATAGGT
 |||| || |||||

A TCTG TTC GACTATCCA
 C GC_ CC
 GAM1903 KIAA1954 3' ATTAGTCTCTCCTCTGTGA 38094 CAAAA
 TCACAGA AGACTGAT
 ||||| |||||
 AGTGTCT TCTGATTA
 CCTC_
 GAM1903 MGC21675 5' ACCTCCAGTCTTTCCCCTGTGA 27442 ACAA AT
 TCACAG AAAGACTG AGGT
 ||||| ||||| |||
 AGTGTC TTTCTGAC TCCA
 CCC_ C_
 GAM1903 TBDN100 3' TCATCTTTTTGCCTTTGA 24700 C A C
 TCA AG CAAAAAGA TGA
 ||| || ||||| |||
 AGT TC GTTTTTCT ACT
 T C _
 GAM1903 LOC145815 3' ACCTCTGGGTATCCCTTTGTCT 40601 A AAG_ GAT
 GGGA TC CAGACAAA ACT AGGT
 || ||||| || |||
 AG GTCTGTTT TGG TCCA
 G CCCTA GTC
 GAM1903 LOC164382 3' ACCCTCAGTCTCCCTGTCTGTG 42162 AAA TA
 G TCACAGACA AGACTGA GGT
 ||||| ||||| |||
 GGTGTCTGT TCTGACT CCA
 CCC C_
 GAM1903 LOC200169 3' ACCTGGGTGCTTTCCGTTTGTG 43282 AA _ GA
 A TCACAGAC AAAG ACT TAGGT
 ||||| ||||| ||| |||||
 AGTGTTTG TTTC TGG GTCCA
 CC G _
 GAM1904 FLJ20034 3' CACTCAATCCTAAGCTCCTCA 19130 T TA A
 TG GG AGC TTAGGATTGAGTG
 || || || ||||| |||||
 AC CC TCG AATCCTAACTCAC
 T _ _
 GAM1904 KIAA0534 3' ATCCTAATACTGACCACA 35379 A C
 TGTGGT AG ATTAGGAT
 ||||| || |||||
 ACACCA TC TAATCCTA
 G A
 GAM1905 CKN1 3' ATAGTAGTTGAAATGGTAACAT 5530 CTC G
 CA TGATGTTGCCA CAA TGCTAT
 ||||| || |||||
 ACTACAATGGT GTT ATGATA
 AAA G
 GAM1905 P2RY6 3' TGGCACAGCAACATCA 10356 CACTCCAA
 TGATGTTGC GTGCTA
 ||||| |||||

			ACTACAACG	CACGGT		
			A_____			
GAM1905	TMEM2	3'	AGTTTAAAGTGGCAACTCA	15040	T	CCAAGT
			TGA GTTGCCACT	GCT		
			ACT CAACGGTGA	TGA		
			_____	ATTT_____		
GAM1905	C13orf1	3'	GCTTCTCAGACCGGCAACATCA	21692		AC CA T_
			TGATGTTGCC	TC AG GC		
			ACTACAACGG	AG TC CG		
			CC AC TT			
GAM1905	FLJ22390	3'	CACTTGAAGCATGGTGTTTCA	22956	TGT	___ C
			TGA TGCCA	CT CAAGTG		
			ACT GTGGT	GA GTTCAC		
			TT_	AC A		
GAM1905	KIAA0748	3'	AGCATGGCAACATCA	16699		CTCCAAG
			TGATGTTGCCA	TGCT		
			ACTACAACGGT	ACGA		

GAM1905	KIAA1317	3'	TAGCACATGGCAATACCA	41628	A	CTCCAA
			TG TGTTGCCA	GTGCTA		
			AC ATAACGGT	CACGAT		
			C	A_____		
GAM1905	LOC122792	3'	CTTGAAGAGCAACATCA	29762		CA C
			TGATGTTGC	CT CAAG		
			ACTACAACG	GA GTTC		
			A_	A		
GAM1905	LOC148697	5'	ATAGCACTCAAAGCTTATCA	38571		TT CACTCCA
			TGATG GC	AGTGCTAT		
			ACTAT CG	TCACGATA		
			T_	AAAC_____		
GAM1905	LOC221964	3'	AGCTTCTCCAAAGTGACTAACA	45112		C_ CCA_ T_
			TCA	TGATGTTG CACT	AG GCT	
			ACTACAAT	GTGA TC CGA		
			CA	AACC TT		
GAM1905	LOC51134	3'	GCAGGAGGAACAACATCA	18210		CCA AAG
			TGATGTTG	CTCC TGC		
			ACTACAAC	GAGG ACG		
			AAG	_____		
GAM1906	GPC4	3'	TAGGTAGAGCTGAGAATACTA	7178		AAC
			TAGTATTCTCA	CTATCTA		

	ATCATAAGAGT GATGGAT	
	CGA	
GAM1906 LOC221540 3'	AGACACTGGAAAGAGAATACTA 45042	AAA TA__
	TAGTATTCTC CC TCT	
	ATCATAAGAG GG AGA	
	AAA TCAC	
GAM1906 LOC257545 3'	AGACACTGGAAAGAGAATACTA 46690	AAA TA__
	TAGTATTCTC CC TCT	
	ATCATAAGAG GG AGA	
	AAA TCAC	
GAM1906 LOC257598 3'	AGACACTGGAAAGAGAATACTA 46747	AAA TA__
	TAGTATTCTC CC TCT	
	ATCATAAGAG GG AGA	
	AAA TCAC	
GAM1907 KIAA0471 3'	CATCAGATAATACTTTTCT 16910	TCATT C
	AGA GGTATTATC GATG	
	TCT TCATAATAG CTAC	
	TT__ A	
GAM1908 SLC29A1 3'	TGGTTTGACCTGATATACTC 11401	ATA T
	GAGTATGTCAG CAG GCCA	
	CTCATATAGTC GTT TGGT	
	CA_ _	
GAM1908 STS 3'	TGGCACTGGGGAAACATAACTC 5912	_ CAGATA
	GAGT ATGT CAGTGCCA	
	CTCA TACA GTCACGGT	
	A AAGGG_	
GAM1908 KIAA0543 3'	TGGCACTGCTAGGTTACACCCC 34179	TA C A_ _
TC	GAG TGT AG TA CAGTGCCA	
	CTC ACA TT AT GTCACGGT	
	CC C GG C	
GAM1908 UMP-CMPK 3'	GCTTTAGTCTGACATAATCTA 18427	G ACAGT
	TAGA TATGTCAGAT GC	
	ATCT ATACAGTCTG CG	
	A ATTT_	
GAM1908 LOC152441 5'	TGGCATACTCTAACATACTC 41507	C TACA
	GAGTATGT AGA GTGCCA	
	CTCATACA TCT TACGGT	
	A CA__	
GAM1908 LOC51313 3'	GCACTGTATGCATACTT 18721	CAG
	GAGTATGT ATACAGTGC	

TTCATACG TATGTCACG

GAM1909 HMGA2 3' ACCCTCCAAGTCTGTACCTC 9560 A CT_
GGG GT GACTTGAGGGT
||| || |||||
CTC CA CTGAACCTCCCA
_ TGT

GAM1909 MPZ 3' CCAGATCAGACTCTCCTT 6129 _ C
AAGG GAGTCTGA TTGG
|||| ||||| |||
TTCC CTCAGACT GACC
T A

GAM1909 NUP98 3' ACCCTCCATCTACCCCTT 18438 A CT CT
AAGGG GT GA TGGAGGGT
|||| || || |||||
TTCCC CA CT ACCTCCCA
_ T_ _

GAM1909 FLJ20232 5' ACCCTTCCCACAGACTCCT 21081 ACTT
GGGAGTCTG GGAGGGT
||||| |||||
TCCTCAGAC CTTCCCA
ACC_

GAM1909 FLJ32389 3' ACCCTCGCTCTCACACCCCT 29433 A C CTTG
AGGG GT TGA GAGGGT
||| || ||| |||||
TCCC CA ACT CTCCCA
C C CTCG

GAM1909 KIAA1855 3' ACCCCTTTCCAGCCAAAGTCCC 44351 GTC A T ____
GGGA TG CT GGA GGGT
||| || || ||| |||
CCCT AC GA CCT CCCA
GAA C _ TTC

GAM1909 LOC144231 5' CCCCAACAACTCCTCT 40391 _ C AC A
AG GGAGT TG TTGG GG
|| |||| || ||| ||
TC CCTCA AC AACC CC
T A _ _

GAM1909 LOC161823 3' CTTTAATCAGACTCCCTT 40034 C
AAGGGAGTCTGA TTGGAG
||||||| |||||
TTCCCTCAGACT AATTTC

GAM1909 LOC201191 3' CCAAGCCAGGACTCCCTT 43214 GA_
AAGGGAGTCT CTTGG
||||||| |||||
TTCCCTCAGG GAACC
ACC

GAM1909 LOC220776 3' CCCTCACAACCTCCCTTTA 33931 TC ACTTG
TAAAGGGAG TG GAGGG
||||||| || |||||

		ATTTCCTC AC CTCCC	
		CA A__	
GAM1909	LOC91409	3' ACCCTCCAAGGCAGGCTTCCCT 32802	_ A
		TTA TAAAGGGA GTCTG CTTGGAGGGT	
		ATTTCCT CGGAC GAACCTCCCA	
		T G	
GAM1910	FLRT2	3' GTTCAAATCATATATCAGGTTG 14884	T A ATA
		A ACC GGTATAT ATTTGAAC	
		G TGG CTATATA TAACTTG	
		T A C__	
GAM1910	FOLR1	5' CAAAGGATCACCTGGTAT 18783	ATAT AA
		ATACCAGGT AT TTTG	
		TATGGTCCA TA AAAC	
		C__ GG	
GAM1910	LPIN1	3' CAAATATGTATACCTGG 33464	A
		CCAGGTATATATA TTTG	
		GGTCCATATGTAT AAAC	
		—	
GAM1910	PITPNB	3' TTCAATATATATACCTGG 14765	AT
		CCAGGTATATATA TTGAA	
		GGTCCATATATAT AACTT	
		—	
GAM1910	EDR1	3' CAGGTTATAACCTGGTA 10701	ATA
		TACCAGGT TATAATTTG	
		ATGGTCCA ATATTGGAC	
		—	
GAM1910	FLJ10201	3' TCAAATAGTCTATACCTG 19763	T A
		CAGGTATA AT ATTTGA	
		GTCCATAT TG TAACT	
		C A	
GAM1910	KIAA1350	3' CAGGTGATACATAGCCTGGTA 35999	_ A A
		TACCAGGT AT TAT ATTTG	
		ATGGTCCG TA ATA TGGAC	
		A C G	
GAM1911	BRCA1	3' TTGTACAAAATACGTTTTGTAA 14166	TG TC
		TTGCA GC TATTTTGTACAA	
		AATGT TG ATAAAACATGTT	
		TT C_	
GAM1911	BRCA1	3' TTGTACAAAATACGTTTTGTAA 14172	TG TC
		TTGCA GC TATTTTGTACAA	

		AATGT TG ATAAAACATGTT TT C_	
GAM1911 BRCA1	3'	TTGTACAAAATACGTTTTGTAA 14178 TTGCA GC TATTTTGTACAA AATGT TG ATAAAACATGTT TT C_	TG TC
GAM1911 BRCA1	3'	TTGTACAAAATACGTTTTGTAA 14185 TTGCA GC TATTTTGTACAA AATGT TG ATAAAACATGTT TT C_	TG TC
GAM1911 BRCA1	3'	TTGTACAAAATACGTTTTGTAA 14191 TTGCA GC TATTTTGTACAA AATGT TG ATAAAACATGTT TT C_	TG TC
GAM1911 BRCA1	3'	TTGTACAAAATACGTTTTGTAA 14197 TTGCA GC TATTTTGTACAA AATGT TG ATAAAACATGTT TT C_	TG TC
GAM1911 BRCA1	3'	TTGTACAAAATACGTTTTGTAA 14205 TTGCA GC TATTTTGTACAA AATGT TG ATAAAACATGTT TT C_	TG TC
GAM1911 BRCA1	3'	TTGTACAAAATACGTTTTGTAA 14211 TTGCA GC TATTTTGTACAA AATGT TG ATAAAACATGTT TT C_	TG TC
GAM1911 BRCA1	3'	TTGTACAAAATACGTTTTGTAA 14217 TTGCA GC TATTTTGTACAA AATGT TG ATAAAACATGTT TT C_	TG TC
GAM1911 BRCA1	3'	TTGTACAAAATACGTTTTGTAA 14223 TTGCA GC TATTTTGTACAA AATGT TG ATAAAACATGTT TT C_	TG TC
GAM1911 C10orf2	3'	GTTGCTTGGTCATAGAGCCAT 22404 ATGGCTCTAT TTG CAAC TACCGAGATA GGT GTTG CT TC	T_ TA
GAM1911 CA3	5'	TGACCTAATAAGGCCATGCAA 11680 TTGCATGGC TATT GT CA 	TC TT A

			AACGTACCG ATAA CA GT		
			GA TC _		
GAM1911 IL16	3'	TGCAAAGTCATGCAA	10841	CTATT	
		TTGCATGGCT TTGTA			
		AACGTACTGA AACGT			

GAM1911 MGEA5	3'	TGTAAGACCATGCAA	14520	C ATTTTG	
		TTGCATGG TCT TACA			
		AACGTACC AGA ATGT			
		_ AA _____			
GAM1911 CCR6	5'	TGCAAATTGAAAACCATGCAA	25375	C__ TAT	
		TTGCATGG TC TTTGTA			
		AACGTACC AG AAACGT			
		AAA TT_			
GAM1911 DJ167A19.1	3'	TGAAATAGAACCATGGAA	21052	G C	
		TT CATGG TCTATTTTG			
		AA GTACC AGATAAAGT			
		G A			
GAM1911 FLJ10579	3'	TACACATGGGTAGAGCCTGCAA	19946	T	_____
		TTGCA GGCTCTATTT TGTA			
		AACGT CCGAGATGGG ACAT			
		_ TAC			
GAM1911 FLJ10829	3'	GTCACCATAGAGCCTGCAA	20181	T	TT T
		TTGCA GGCTCTAT TG AC			
		AACGT CCGAGATA AC TG			
		_ CC _			
GAM1911 FLJ23462	3'	GTTGTAGAGATAGAGCCAT	24267	G	
		ATGGCTCTATTTT TACAAC			
		TACCGAGATAGAG ATGTTG			

GAM1911 KIAA0285	3'	TGTGATGATGGAGCCACGCAA	16756	A	TTG
		TTGC TGGCTCTATT TACA			
		AACG ACCGAGGTAG GTGT			
		C TA_			
GAM1911 SEC15B	3'	TATGATGGTAGAGCCTCGCAA	33129	AT	_ TG
		TTGC GGCTCTATT T TA			
		AACG CCGAGATGG A AT			
		CT T GT			
GAM1911 LOC197131	3'	TGCAGAAACCATGCAA	42449	CTCTA	
		TTGCATGG TTTTGTA			

AACGTACC AAGACGT
 A____
 GAM1912 CDKN1A 3' TGGGCATTTTATTTTATGAAA 27783 C CATTACC
 TA TAT TCAT AAATGCCCA
 ||| ||| |||||
 ATA AGTA TTTACGGGT
 A TTTTATT
 GAM1912 CHC1L 3' TGGACAGCATTAACAAGAATGA 6930 CA ACCA ____
 GATA TATCTCAT TT AATGC CCA
 ||||| || ||| |||
 ATAGAGTA AA TTACG GGT
 AG CAA_ ACA
 GAM1912 EFEMP1 3' TGGGCATTTAATATGTAAAGAT 10318 CAT TACC
 ATCT CAT AAATGCCCA
 ||| ||| |||||
 TAGA GTA TTTACGGGT
 AAT TAA_
 GAM1912 EFEMP1 3' TGGGCATTTAATATGTAAAGAT 20838 CAT TACC
 ATCT CAT AAATGCCCA
 ||| ||| |||||
 TAGA GTA TTTACGGGT
 AAT TAA_
 GAM1912 IL17R 3' GGGCATTGGGATACCAAGATA 15659 CATCATTA
 TATCT CCAAATGCCC
 ||| |||||
 ATAGA GGTTCACGGG
 ACCATAG_
 GAM1912 KCNAB1 3' GGCATTTGCTAACTCAAAGA 30548 CATCA
 TCT TTACCAAATGCC
 ||| |||||
 AGA AATGGTTTACGG
 AACTC
 GAM1912 RECQL5 3' GGGCACCTGGCAGTGAGGGA 10450 A A AA
 TCTC TCATT CCA TGCCC
 ||| ||| ||| |||
 AGGG AGTGA GGT ACGGG
 _ C CC
 GAM1912 SLC4A10 3' TGGAATAATGATGTGATA 22595 T ____
 TATC CATCATTA CCA
 ||| ||||| |||
 ATAG GTAGTAAT GGT
 T AA
 GAM1912 VIPR1 3' GGCATTTGACTGAAGATG 10993 A C_
 CATC TTA CAAATGCC
 ||| ||| |||||
 GTAG AGT GTTTACGG
 A CA
 GAM1912 C6orf37 3' TGGGCATATTGCAATGATGA 33515 AC _
 TCATCATT CAA ATGCCCA
 ||||| ||| |||||

AGTAGTAA GTT TACGGGT
 C_ A
 GAM1912 COQ7 3' TGGGCATTTGTTTGAAATTAGA 18224 CA__ TTAC
 TA TATCT TCA CAAATGCCCA
 ||||| ||| |||||
 ATAGA AGT GTTTACGGGT
 TTAA TT__
 GAM1912 DKFZP434B172 3' TGGGCATTCAGTATTCTGAGA 34703 TCAT CA
 TCTCA TAC AATGCCCA
 ||||| ||| |||||
 AGAGT ATG TTACGGGT
 CTT_ AC
 GAM1912 DKFZP564D0462 3' GGCTCCAGCAGATGATGAGATA 34898 ACCAAAT
 TATCTCATCATT GCC
 ||||| ||| |||||
 ATAGAGTAGTAG CGG
 ACGACCT
 GAM1912 FLJ12707 5' GGACATTTGGTTCAGAACGAG 22610 A_ ATT C
 CTC TC ACCAAATG CC
 ||| || ||||| ||
 GAG AG TGGTTTAC GG
 CA ACT A
 GAM1912 FLJ20081 3' GGGCATTATAACGAGAT 19181 ATCA CCA
 ATCTC TTA AATGCCC
 ||||| ||| |||||
 TAGAG AAT TTACGGG
 C__ A__
 GAM1912 FLJ23499 3' GGGCATTACTGAGAGATA 23006 A TTACCA
 TATCTC TCA AATGCCC
 ||||| ||| |||||
 ATAGAG AGT TTACGGG
 _ CA__
 GAM1912 KIAA0759 3' GGCATGCATATGTGAGATA 33442 T TACCAA
 TATCTCA CAT ATGCC
 ||||| ||| |||||
 ATAGAGT GTA TACGG
 _ TACG__
 GAM1912 KIAA1908 3' GCCTTTTGGTAGTGATGAAATA 36337 C T_
 TAT TCATCATTACCAAA GC
 ||| ||||| ||||| ||
 ATA AGTAGTGATGGTTT CG
 A TC
 GAM1912 MAP3K2 3' GGCATTTGGCAATTCTTAGAGA 13385 ATC__ A
 TCTC ATT CCAAATGCC
 ||||| ||| |||||
 AGAG TAA GGTTTACGG
 ATTCT C
 GAM1912 PP1665 5' TGGGCACGAGTATGGTGAGA 25094 T CAAA
 TCTCATCAT AC TGCCCA
 ||||| || |||||

		AGAGTGGTA TG ACGGGT	
		_ AGC_	
GAM1912 PRO1728	3'	TGAACATTTGGGTAATGA 20571	_ CC
		TCATTACC AAATG CA	
		AGTAATGG TTTAC GT	
		G AA	
GAM1912 LOC134266	3'	TGGGCATTGTGAACAGTGTGA 37073	T AC_
		TCA CATT CAAATGCCCA	
		AGT GTGA GTTTACGGGT	
		_ CAA	
GAM1912 LOC158314	3'	TGGGCATTCTCTTGAGAGA 41955	A TTACCA
		TCTC TCA AATGCCCA	
		AGAG AGT TTACGGGT	
		_ TCTC_	
GAM1912 LOC90643	3'	TGGACACTTGCCAATGATGA 31856	AC A C
		TCATCATT CAA TG CCA	
		AGTAGTAA GTT AC GGT	
		CC C A	
GAM1913 MEOX2	3'	CTATCAAGAATAAACCATGAA 12549	C CCTGG
		TTCAT GTTT TCTTGATAG	
		AAGTA CAAA AGAACTATC	
		C TA_	
GAM1913 MEOX2	3'	CTATCAAGAGCAAACATGAA 12550	C TCC G
		TTCAT GTT TG TCTTGATAG	
		AAGTA CAA AC AGAACTATC	
		T _ G	
GAM1913 FLJ13231	3'	CTATCAAGGCTAAAC 23328	TCC
		GTT TGGTCTTGATAG	
		CAA ATCGGAACATC	
		_	
GAM1913 KIAA0971	3'	AAGTGCCAGGAACAATGAA 17224	C T _
		TTCAT GTT CCTGGT CTT	
		AAGTA CAA GGACCG GAA	
		A _ T	
GAM1913 LOC158435	3'	CAAAACCAAGATGGTGA 28845	CC C
		TCATCGTTT TGGT TTG	
		AGTGGTAGA ACCA AAC	
		_ A	
GAM1913 LOC220827	3'	CAAAACCAAGATGGTGA 43843	CC C
		TCATCGTTT TGGT TTG	

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AGTGGTAGA ACCA AAC
      _ A
GAM1914 CRTAP 3' AGGAAACACAGATTCTT 13060 CACAT
      AAGAATCTGTGT TTCCT
      ||||| |||
      TTCTTAGACACA AAGGA

      _
GAM1914 ITGA5 3' TAGGAAATCCATTCACAGTTCT 30724 T TCAC_
      T AAGAA CTGTG ATTCCTA
      |||| ||| |||||
      TTCTT GACAC TAAAGGAT
      _ TTACC
GAM1914 LEP 3' GGAAAATGTGACCCAGATCCT 5739 A T _
      AG ATCTG GTCACATTT CC
      || ||| ||||| ||
      TC TAGAC CAGTGTAAGG
      C C A
GAM1914 SOX4 3' TAGGAAATGACCCGAGA 9076 _T CA
      TCT G GTCA TTTCCTA
      ||| ||| |||||
      AGA C CAGT AAAGGAT
      G C _
GAM1914 TLX1 3' AGGGGTGACACAGACTC 12043 A ATT
      GA TCTGTGTCAC TCCT
      || ||||| |||
      CT AGACACAGTG GGGA
      C _
GAM1914 TRHDE 3' GAAAATGGCCAGATTTT 15033 T CA
      AGAATCTG GTCA TTTC
      ||||| ||| |||
      TTTTAGAC CGGT AAAG
      _ A_
GAM1914 ATP9A 3' AGATGTGACTCAGATCCT 31074 A T
      AG ATCTG GTCACATTT
      || ||| |||||
      TC TAGAC CAGTGTAAG
      C T
GAM1914 AUTL1 3' GAAAGATGTCACTAGATTCT 26648 _ T CA
      AGAATCT GTG CA TTTC
      ||||| ||| |||
      TCTTAGA CAC GT AAAG
      T T AG
GAM1914 C6orf33 3' AGGAAATGCTTGGATTC 28491 TGTCA
      GAATCTG CATTCCT
      ||||| |||||
      CTTAGGT GTAAAGGA
      TC__
GAM1914 DKFZP586N0721 5' TAGCACTGGGACACAGATCCTT 17709 A A TTTC
      AAG ATCTGTGTC CA CTA
      || ||||| || |||

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TTC TAGACACAG GT GAT
 C G CAC_
 GAM1914 FLJ10450 3' AGGAAATGTAACCTTTGGTTTT 19862 TGT C
 AGAATC GT ACATTTCT
 ||||| || |||||
 TTTTGG CA TGTAAGGA
 TTT A
 GAM1914 GFRA4 3' TAGGAAATTGTATCAGCCTC 22701 AT TGT C
 GA CTG CA ATTTCTA
 || ||| || |||||
 CT GAC GT TAAAGGAT
 CC TAT _
 GAM1914 KIAA0599 3' AGGGACCCAGATTCTT 37852 T ACATTT
 AAGAATCTG GTC CCT
 ||||| || |||
 TTCTTAGAC CAG GGA
 C _
 GAM1914 KIAA0831 3' GAAATGCAGCGCAGATCCTT 17207 A CA
 AAG ATCTGTGT CATTTC
 || ||||| |||||
 TTC TAGACGCG GTAAAG
 C AC
 GAM1914 KIAA1493 3' TTAGGGGTAAACACAACACAGAT 32095 A CACAT_
 ACTT AAG ATCTGTGT TTCCTAA
 || ||||| |||||
 TTC TAGACACA GGGGATT
 A ACACAAT
 GAM1914 KIAA1598 3' TTAGGAAATGTGCATACCACTC 20332 ATC_ T
 GA TGTG CACATTTCTAA
 || ||| |||||
 CT ATAC GTGTAAAGGATT
 CACC _
 GAM1914 MacGAP 3' TTAGGAAAACTACACATTCT 27291 TC CACA
 AGAA TGTGT TTCCTAA
 ||| |||| |||||
 TCTT ACACA AAAGGATT
 _ TCAA
 GAM1914 PDZD2 5' GAAAATGGCCCAGATTCT 39392 T CA
 AGAATCTG GTCA TTTC
 ||||| |||| |||
 TCTTAGAC CGGT AAAG
 C A_
 GAM1914 PRO1728 3' TTAGGAAACACGACACAAACGC 20572 AATC ACA
 T AG TGTGTC TTCCTAA
 || |||| |||||
 TC ACACAG AAAGGATT
 GCAA CAC
 GAM1914 RAB11B 3' TAGAGAAACACAGATTCTT 36588 CACAT _
 AAGAATCTGTGT TTC CTA
 ||||| || |||

		TTCTTAGACACA	AAG GAT		
		_____ A			
GAM1914	LOC150271 3'	TAGGAAATGTCATTGCTCCTT	41173	AATCT TC	
		AAG GTG ACATTTCTA			
		TTC TAC TGTAAGGAT			
		CTCGT ____			
GAM1914	LOC152048 3'	TAGTGGAAGACACAGATTC	41428	ACA _	
		GAATCTGTGTC TTTC CTA			
		CTTAGACACAG AAGG GAT			
		_____ T			
GAM1914	LOC153883 5'	TTAGAAAATGTGAACTGTTCT	39433	CT G C	
	T	AAGAAT GT TCACATTT CTAA			
		TTCTTG CA AGTGTAAGG GATT			
		T_ A A			
GAM1914	LOC157869 3'	AGGAACACAGGTCCTT	39675	A CACATT	
		AAG ATCTGTGT TCCT			
		TTC TGGACACA AGGA			
		C _____			
GAM1914	LOC196074 5'	AGGAGTTACACAGATCT	42320	A C ATT	
		AGA TCTGTGT AC TCCT			
		TCT AGACACA TG AGGA			
		_ T ____			
GAM1914	LOC201292 3'	AGGGGGAGACAGATTC	42561	G ACAT	
		GAATCTGT TC TTCCT			
		CTTAGACA AG GGGGA			
		G _____			
GAM1914	LOC221763 3'	AGGAAATGTAATAAATTC	45035	C GTC	
		GAAT TGT ACATTTCT			
		CTTA ATA TGTAAGGA			
		A A_			
GAM1914	LOC89231 3'	ATGTGATAACACAGATCTT	44549	A ____	
		AAGA TCTGTG TCACAT			
		TTCT AGACAC AGTGTA			
		_ AAT			
GAM1915	ADARB1 3'	TGGCTCTTTTCTTCTCA	17949	TAAAAA	
		TGAGA AAGAAGAGCTA			
		ACTCT TTTTCTCGGT			
		TCC_			
GAM1915	B29 3'	GTTCCCCTGTTTATCTCA	25683	AA AA	
		TGAGATAAAA AG GAGC			

		ACTCTATTTT TC CTTG		
		G_ CC		
GAM1915 BCL11B	3'	TTTTTTTTTTCCTATCTCA 23172	AA	
		TGAGATA AAAAGAAGAG		
		ACTCTAT TTTTTTTTTT		
		CC		
GAM1915 CALU	3'	ATTAGCTCTTTACTCTTTTCTCA 6883	TAAAAAAA	
		TGAGA GAAGAGCTAAT		
		ACTCT TTTCTCGATTA		
		TTCTCA__		
GAM1915 CLASP2	3'	AGTTTTTCTGTCTCA 32267	AAAAAA	
		TGAGAT AGAAGAGCT		
		ACTCTG TCTTTTTGA		

GAM1915 DUT	3'	GGTTTTTCTGTCTCA 7663	AAAAAA	
		TGAGAT AGAAGAGCT		
		ACTCTG TCTTTTTGG		

GAM1915 FGR	3'	CTCTCCTTTTATCTCA 11757	AAA A	
		TGAGATAAA AG AGAG		
		ACTCTATTT TC TCTC		
		__ C		
GAM1915 MPO	3'	TGGCTCCCCTTTTCTTCCTCA 5787	ATAA AA	
		TGAG AAAAAG GAGCTA		
		ACTC TTTTTC CTCGGT		
		CTTC CC		
GAM1915 MTMR8	3'	TTCTTCTCTTTTGTCTCA 17750	A	
		TGAGATAAAAA AGAAGAG		
		ACTCTGTTTTT TCTTCTT		
		C		
GAM1915 NFRKB	5'	GGCTCTTCTTCCTTCATCTCA 12821	A AA	
		TGAGAT AA AAGAAGAGCT		
		ACTCTA TT TTCTTCTCGG		
		C CC		
GAM1915 OAS2	3'	ATTAGCTCCTCCTTTTTCCTTC 18805	AG TA A A	
CA		TG A AAAAA GA GAGCTAAT		
		AC T TTTTT CT CTCGATTA		
		CT CC C C		
GAM1915 PSMB9	3'	CTCTTTCTTCTTTTGTCCCA 8675	A A _	
		TG GATAAAA AAGAA GAG		

			AC CTGTTTT TTCTT CTC		
			C C T		
GAM1915	PTPRO	3'	CTGTCTTTCTTTGTCTCA 25032	A	AG
			TGAGATAAA AAAGA AG		
			ACTCTGTTT TTTCT TC		
			C G_		
GAM1915	RTN1	3'	AGCTCTCTTCTTACTCA 22108	A	AAA A
			TGAG TAA AAGA GAGCT		
			ACTC ATT TTCT CTCGA		
			_ C_ _		
GAM1915	RUNX1	3'	AGTTCTTTCTTTTCTCA 7494	TAAA	_
			TGAGA AAAAGAA GAGCT		
			ACTCT TTTTCTT CTTGA		
			_ _ T		
GAM1915	TTC3	5'	TTCTTCTGTTATCTCA 9318	AAAA	
			TGAGATAA AGAAGAG		
			ACTCTATT TCTTCTT		
			G_		
GAM1915	ZIC3	3'	CTCTCCTTTCTTTATCTC 9450	A	A
			GAGATAAA AAAG AGAG		
			CTCTATTT TTTC TCTC		
			C C		
GAM1915	C1orf19	3'	CTGCTTCATCTTTTATCTCA 33840	AAA	_
			TGAGATAAAA GAAG AG		
			ACTCTATTTT CTTC TC		
			CTA G		
GAM1915	DKFZP564I0422	3'	AGCTTGCTTTTATCTC 25432	AAGAA	
			GAGATAAAAA GAGCT		
			CTCTATTTT TTCGA		
			CG_		
GAM1915	FACTP140	3'	TCTTCTTTTTTTTCTCA 14047	T	
			TGAGA AAAAAAAGAAGA		
			ACTCT TTTTTTTCTTCT		
			_		
GAM1915	FLJ12644	3'	GCCTTCCTTTTTATCCA 23330	A	A A
			TG GATAAAAAA GAAG GC		
			AC CTATTTTTT CTTC CG		
			_ C _		
GAM1915	FLJ12806	3'	ATTAGCTGTTCTTCTACATC 23109	AAAAA	G
			GAT AAGAA AGCTAAT		

		CTA TTCTT TCGATTA		
		CATC_ G		
GAM1915	FLJ22329	3' TTTTCTTTTTTTCCTCA 23960	AT	
		TGAG AAAAAAAGAAGAG		
		ACTC TTTTTTCTTTT		
		C_		
GAM1915	FLJ23045	3' TTTTCTTTTTTCCCTCA 24021	AT	
		TGAG AAAAAAAGAAGAG		
		ACTC TTTTTTCTTTT		
		CC		
GAM1915	GMFB	3' CTTTCCCTCCTTTTTATCTC 10329	A_____	
		GAGATAAAAA GAAGAG		
		CTCTATTTTT CTCTTC		
		CCTCC		
GAM1915	GOLGIN-67	3' TTTTCTTTTTTCATTTCA 45538	A	
		TGAGAT AAAAAAGAAGAG		
		ACTTTA TTTTTCTTTT		
		C		
GAM1915	KIAA0766	3' GCCTTTTTTTTCATCTCA 16741	AA A	
		TGAGAT AAAAAGAAG GC		
		ACTCTA TTTTTTTC CG		
		C_ _		
GAM1915	KIAA0855	3' TTTTCTTTTTTCATTTCA 17379	A	
		TGAGAT AAAAAAGAAGAG		
		ACTTTA TTTTTCTTTT		
		C		
GAM1915	KIAA0993	3' ATTAACCTCTTTTCTTGCATC 32076	A_ _ A C	
	TCA	TGAGAT AA AAAAGA GAG TAAT		
		ACTCTA TT TTTTCT CTC ATTA		
		CG C _ A		
GAM1915	KIAA1323	3' TTTTCTCCTTTTATCTC 31574	AA	
		GAGATAAAA AGAAGAG		
		CTCTATTTT TCTTTT		
		CC		
GAM1915	PEX11B	3' GCCTTCTTTTTTCTCA 9943	TAA A	
		TGAGA AAAAAGAAG GC		
		ACTCT TTTTCTTC CG		
		— —		
GAM1915	PRO1992	5' TTCTTCTTTTTCTCA 15336	TAAA	
		TGAGA AAAAGAAGAG		

ACTCT TTTTCTTCTT

GAM1915 RABEX5 3' TAGAACCTTTTCTTATCTCA 15841 A AAGAG
TGAGATAA AAAAG CTA
||||| ||| ||
ACTCTATT TTTTC GAT
C CAA__

GAM1915 RBBP4 3' CTCCCCTTTTTCTTCTCA 12131 TA AA
TGAGA AAAAAAG GAG
|||| ||||| ||
ACTCT TTTTTTC CTC
TC CC

GAM1915 RNF24 3' AGCTGCCACTTCTTTTGCCTCA 14085 ATAAA ____
TGAG AAAAGAAG AGCT
||| ||||| |||
ACTC TTTTCTTC TCGA
CG__ ACCG

GAM1915 SLC26A10 5' ATTTTCTCTGCCTTCCTTATCT 28558 AAA A_ CT
CA TGAGATAA AAG AGAG AAT
||||| || ||| |||
ACTCTATT TTC TCTC TTA
CC_ CG TT

GAM1915 THEA 3' AGCCTTCCTCTTATCTCA 32946 AAAAA A
TGAGATAA GAAG GCT
||||| ||| |||
ACTCTATT CTTC CGA
CTC__ _

GAM1915 UPLC1 3' TGGCGGTTCTTTTCTTATCTCA 19286 AAA GA
TGAGATA AAAGAA GCTA
||||| ||||| |||
ACTCTAT TTTCTT CGGT
CC_ GG

GAM1915 LOC145988 3' TTTTCTTTTTTTCATTTCA 38044 A
TGAGAT AAAAAAGAAGAG
||||| ||||| |||||
ACTTTA TTTTTTCTTTTT
C

GAM1915 LOC146880 3' AGCTTTCTCCCTTTGTCTCA 38257 AAA A
TGAGATAAA AGA GAGCT
||||| || |||||
ACTCTGTTT TCT TTCGA
CCC _

GAM1915 LOC150519 3' TCTTCTTTCTCTGTCTCA 38988 AAA
TGAGATA AAAGAAGA
||||| ||||| |||
ACTCTGT TTTCTTCT
CTC

GAM1915 LOC152373 5' AGCTCTTCTTTGTTTCATCT 39269 A A
AGAT AA AAAGAAGAGCT
||| || ||||| |||||

	TCTA TT TTTCTTCTCGA		
	C G		
GAM1915 LOC158969 5'	AGCTCCTTTTTTTTTCACCTCA 39917	ATA	A
	TGAG AAAAAAGA GAGCT		
	ACTC TTTTTTTT CTCGA		
	CAC C		
GAM1915 LOC220980 3'	TTAGTATTCTTTTTTTTCTCA 44742	T	GA
	TGAGA AAAAAAGAA GCTAA		
	ACTCT TTTTTTTCTT TGATT		
	_ A_		
GAM1915 LOC222999 5'	AGCTCCTTCTTTTGCCATCCCA 45312	A AAA	_
	TG GAT AAAAGAAG AGCT		
	AC CTA TTTTCTTC TCGA		
	C CCG C		
GAM1915 LOC51267 3'	TTAGCTCTCTTCTTCTCA 18592	TAAAA	A
	TGAGA AAAGA GAGCTAA		
	ACTCT TTTCT CTCGATT		
	TC__ _		
GAM1915 LOC90268 3'	TTAGCTTTCTCCCATACCTCA 31044	A AAAA	A
	TGAG TAA AGA GAGCTAA		
	ACTC ATT TCT TTCGATT		
	C ACCC _		
GAM1915 LOC91145 3'	AGCTCCTGTTTCTTTTCATCTC 32449	AAA	_____
	GAGAT AAAAGAA GAGCT		
	CTCTA TTTTCTT CTCGA		
	C_ TGTC		
GAM1915 LOC91963 3'	CTTTTCCTGTTTATCTCA 33627	AAA	
	TGAGATAAAA GAAGAG		
	ACTCTATTTT CTTTTC		
	GTC		
GAM1916 AAT1 3'	AGCATCAGGATTCCAGGAGGAT 39227	ATTT	C
	ATCCTCCTG TCC GATGCT		
	TAGGAGGAC AGG CTACGA		
	CTT_ A		
GAM1916 AMOTL1 3'	AGCATCGAGGGCGAGGGGA 36462	C ATTT	_
	TCCTC TG TCC CGATGCT		
	AGGGG GC GGG GCTACGA		
	A ____ A		
GAM1916 DKFZP564C196 3'	CATCGGATAAAAGAGGAT 34711	CTGA	TC
	ATCCTC TTT CCGATG		

			TAGGAG	AAA	GGCTAC		
			A		TA		
GAM1916	EST-YD1	5'	AGCACCAGG	AAAAATCAACAG	22186	CC	CGA
			CT	TGATTTTCC	TGCT		
			GA	ACTAAAAGG	ACGA		
			CA		ACC		
GAM1916	MGC4832	5'	AGCAAGATTG	AAAAATCAAGAA	29699	_C	CGA__
			GG	CCTC	TGATTTTCC	TGCT	
			GGA	GACTAAAAGG	ACGA		
			AA		TTAGA		
GAM1916	SH3KBP1	5'	CATCAGGAAGG	GAGGATG	32981	GATTT	C
			TATCCTCCT	TCC	GATG		
			GTAGGAGGA	AGG	CTAC		
					A		
GAM1917	ADRB3	3'	AGCTACAAAAATCTGTATTA	5458	AT	T	
			TAATACA	TTTTTG	TGCT		
			ATTATGT	AAAAACAT	GA		
			CT		C		
GAM1917	FCMD	3'	AGAAAAAAAAAATTGTAT	13570	GTG		
			ATACAATTTTTT	TCT			
			TATGTTAAAAAA	AGA			
					AAA		
GAM1917	KLK3	3'	AGCAGACACAGGTGTA	7350	ATTT	A	
			TACA	TTTGTGTCT	CT		
			ATGT	GGACACAGA	GA		
					C		
GAM1917	LPP	3'	AGAGAGAAAAAGATTGTATTA	12105	GTG	A	
			TAATACAATTTTTT	TCTCT			
			ATTATGTTAGAAAA	AGA	GA		
					AG_ _		
GAM1917	RAB11A	3'	TAGTAAACACAAAAGATTGTTA	11035	T	C	
			AACAATTTTTTGTGT	TACTA			
			A	TGTTAGAAAACACA	ATGAT		
			T		A		
GAM1917	HCC-4	3'	TAGTAGACAGCCATTAAATT	28899	TT	_	
			AATTT	TG	TGTCTACTA		
			TTAAA	AC	ACAGATGAT		
			TT	CG			
GAM1917	IBTK	5'	AGTGCCAAAAAATTGTAT	33517	T	CT	
			ATACAATTTTTTG	GTACT			

TATGTTAAAAAAC CG TGA

GAM1917 KIAA1641 3' AGACAATAAAATTGTATTA 39099 TTG
TAATACAATTTT TGTCT
||||||| ||||
ATTATGTTAAAA ACAGA
TA_

GAM1917 LOC220846 3' AGCTACAAAAATCTGTATTA 43660 AT T
TAATACA TTTTGTG CT
||||| ||||| ||
ATTATGT AAAACAT GA
CT C

GAM1918 KIAA1036 3' CCTCCATGGAGAAAACAGC 17124 AC_ G
GC TTTC TTCATGGAGG
|| ||| |||||
CG AAAG AGGTACCTCC
ACA _

GAM1918 LOC146713 3' TCCCCCATGGATGAGCCCAA 40716 CACT A
TTTGG TTCGTCATGG GGA
|||| ||||| |||
AAACC GAGTAGGTACC CCT
C_ C

GAM1919 SLC6A8 3' CCCCCTGCCACCTCTCCA 12147 AT AAAC TT
TGGA AGGT GC GGGGG
||| ||| || ||||
ACCT TCCA CG CCCCC
C_ CC_ T_

GAM1919 TERF1 3' CCCCCAAATCCTGTTCCA 18953 TAAACGC
TGGAATAGG TTGGGGG
||||| |||||
ACCTTGTC AACCCCC
TA_

GAM1919 MACF1 3' CCCCCAAGCCACTATCCA 14376 A GTAAAC
TGGA TAG GCTTGGGGG
||| ||| |||||
ACCT ATC CGAACCCCC
_ AC_

GAM1919 TESK2 3' CCCC GTTCTTTCCCCACCCCA 31652 AATA T C_ T
TGG GG AAA GCT GGGG
||| ||| ||| |||
ACC CC TTT TGG CCCC
CCAC C CT _

GAM1919 LOC146488 3' CCCCCTGCCACCTCTCCA 35043 AT AAAC TT
TGGA AGGT GC GGGGG
||| ||| || ||||
ACCT TCCA CG CCCCC
C_ CC_ T_

GAM1919 LOC152620 3' CCCCCAAATCCTGTTCCA 30175 TAAACGC
TGGAATAGG TTGGGGG
||||| |||||

ACCTTGTCC AACCCCC
 TA____
 GAM1919 LOC158668 3' CCCCCAAATCCTGTTCCA 34378 TAAACGC
 TGG AATAGG TTGGGGG
 ||||| |||||
 ACCTTGTCC AACCCCC
 TA____
 GAM1919 LOC257000 3' CCCCCAAATACCTCCCCA 46273 AAT AACGC
 TGG AGGTA TTGGGGG
 || |||| |||||
 ACC TCCAT AACCCCC
 CC_ A____
 GAM1920 IL22RA2 3' ACAGAAAGCTGCCTTCTTCACT 27520 _ TGTCC C
 TGA TCAAGTGA GA GCT TCTGT
 ||||| || |||||
 AGTTCACCT CT CGA AGACA
 T TCCGT A
 GAM1920 DKFZp566D133 5' ACAGAGAACTGGAATCTCACTT 35542 G C_
 AAGTGAGAT TCCG TCTCTGT
 ||||| ||||| |||||
 TTTCACTCTA AGGT AGAGACA
 _ CA
 GAM1920 FLJ11160 3' ACAGAGAGCAGAGCACACTCG 20350 A_ _ C
 TGAG TG TC GCTCTCTGT
 |||| || |||||
 GCTC AC AG CGAGAGACA
 AC G A
 GAM1920 FLJ14936 3' CAGAGAGCAGCACTTA 26668 A CC
 TGAG TGT GCTCTCTG
 |||| || |||||
 ATTTC ACG CGAGAGAC
 _ A_
 GAM1920 KIAA1522 3' AGCAGGACACCTCACCTGA 32415 A A _
 TCA GTGAG TGTCC GCT
 || |||| ||||| |||
 AGT CACTC ACAGG CGA
 C C A
 GAM1920 PTRF 3' ACAGAGAGGTCAGCCCCACCCG 31781 AA AGA_ T GC
 A TC GTG TG CC TCTCTGT
 || ||| || |||||
 AG CAC AC GG AGAGACA
 CC CCG T ____
 GAM1920 LOC253959 5' ACAGAGAACTGGAATCTCACTT 45508 G C_
 AAGTGAGAT TCCG TCTCTGT
 ||||| ||||| |||||
 TTTCACTCTA AGGT AGAGACA
 _ CA
 GAM1921 C20orf108 3' AACTTTGCCAGCAAAAATCAGG 28080 CC_ ACAT
 CCTGAT TG GCAAAGTT
 ||||| || |||||

GGACTA AC CGTTTCAA
AAA GAC_
GAM1921 FLJ10891 3' AACCTTGCATGTCATCA 20225 TCC A
TGA TGACATGCAA GTT
||| |||||
ACT ACTGTACGTT CAA
____ C
GAM1921 FLJ12985 3' AACCTTGCATGTCATCA 24463 TCC A
TGA TGACATGCAA GTT
||| |||||
ACT ACTGTACGTT CAA
____ C
GAM1921 FLJ25416 3' AACTTTGGGAGCTTCAGGATCA 29624 CATG_
TGATCCTGA CAAAGTT
||||| |||||
ACTAGGACT GTTTCAA
TCGAGG
GAM1921 KCNJ2 5' AACTCTGCATGTGACAGTAGACAG 6589 A _ A
CTG TC CTGACATGCA AGTT
||| |||||
GAC AG GACTGTACGT TCAA
_ AT C
GAM1921 KIAA0798 3' AACTTTAAAAAGGATCAGG 16064 GACATGC
CCTGATCCT AAAGTT
||||| |||||
GGACTAGGA TTTCAA
AAAA_
GAM1921 LOC145813 3' AACTTGTTTACCAGGATCAG 40596 ACAT A
CTGATCCTG GCAA GTT
||||| |||||
GACTAGGAC TGTT CAA
CATT _
GAM1921 LOC255624 3' AACCTTGCATGTCATCA 45351 TCC A
TGA TGACATGCAA GTT
||| |||||
ACT ACTGTACGTT CAA
____ C
GAM1921 LOC64116 3' AACTCTATGGTAGGATCA 22712 A CAA
TGATCCTG CATG AGTT
||||| |||||
ACTAGGAT GTAT TCAA
G C_
GAM1922 NAP1L4 3' GGATCTGGAACCTCTC 12591 TCAC
GAGGGGTTCTA ATCC
||||| |||||
CTCTCCAAGGT TAGG
C_
GAM1922 NDRG2 3' GGATGTGATAAAAACATCC 18379 _ C_
GGG GTT TATCACATCC
||| |||||

			CCT CAA ATAGTGTAGG		
			A AA		
GAM1922	PLS3	3'	ATGTAATAGAAGCTTTTCTTA 11472	_	C
			TAAGAGGGGTT CTAT ACAT		
			ATTCTTTTCGA GATA TGTA		
			A A		
GAM1922	RHO	3'	GGGATGTGTGCCCTC 6139	TCTAT	
			GAGGGGT CACATCCC		
			CTCCCCG GTGTAGGG		
			T____		
GAM1922	CSMD1	3'	GATGTGATGCCCTT 36192	TCT	
			GAGGGGT ATCACATC		
			TTCCCCG TAGTGTAG		

GAM1922	MKP-7	3'	GATGCTAGAATCCCCCT 33006	A _	TCA
			AG GGGG TTCTA CATC		
			TC CCCC AAGAT GTAG		
			C T C__		
GAM1922	MMP28	3'	GGGGCAGAACCCCTCTTA 26763	ATCACA	
			TAAGAGGGGTTCT TCCC		
			ATTCTCCCCAAGA GGGG		
			C_____		
GAM1922	MMP28	3'	GGGGCAGAACCCCTCTTA 23594	ATCACA	
			TAAGAGGGGTTCT TCCC		
			ATTCTCCCCAAGA GGGG		
			C_____		
GAM1923	BAZ2A	3'	GTGTGTGTGACCCTGTATTGTT 15121	TG _____	
			TGAT CGAG ATGC TCATATATAC		
			GTTT TATG AGTGTGTGTG		
			GT TCCC		
GAM1923	BCL2L2	3'	TTTGCATGGGTGTTACTTGTCT 10266	T	ATATAC
			G TAG CGAGTGATGCTCAT		
			GTC GTTCATTGTGGGTA		
			T CGTTTG		
GAM1923	CCND2	3'	GTATATGCGAACAGTTATTGTT 7519	TG _ _____	AC
			TGATTA AG ATG CT CATATAT		
			TT TAT GA GTATATG		
			GT T CAAGC C		
GAM1923	CDK2AP1	3'	GTATGTATTTATTACTTGAT 11016	CTC	
			GTCGAGTGATG ATATATAC		

			TAGTTCATTAT TATGTATG		
			T__		
GAM1923	CELSR1	3'	GTATATATATTGCATTCGTGCT 15517	_	ATGCTC
	G		TAGT CGAGTG ATATATAC		
			GTCG GCTTAC TATATATG		
			T GTTA__		
GAM1923	CHC1L	3'	TGTATGATGAGCTATGTTTGGC 6931	TGAT	A
	TG		TAGTCGAG GCTCAT TATAC		
			GTCGGTTT CGAGTA GTATG		
			GTAT _ TA		
GAM1923	CLECSF11	5'	GTGTGCCACCATGCTTGGCTA 28200	G	CT__
			TAGTCGAGT ATG CATAT		
			ATCGGTTTCG TAC GTGTG		
			_ CACC		
GAM1923	CYP1B1	3'	GTGTGAAATATATTACTTAACT 5565	CG	C__ ATAC
	G		AGT AGTGATG TCATAT		
			TCA TCATTAT AGTGTG		
			AT ATAA C		
GAM1923	CYP24	3'	GTGTGTGTGGGTTCTAATGG 6428	AGT	T
			TCG GA GCTCATATATAC		
			GGT CT TGGGTGTGTGTG		
			AAT _		
GAM1923	DMD	5'	GTATAGGTTTTGTTGCGACTG 5572	TG	T TC
			TAGTCGAG A GC ATAT		
			GTCAGCTT T TG TATG		
			GT T GA		
GAM1923	DNMT2	3'	GTATCTACCAGTGTCATTCAAT 10672	C	CA T
	TA		TAGT GAGTGATGCT TA ATAC		
			ATTA CTTACTGTGA AT TATG		
			A CC C		
GAM1923	DPH2L2	3'	ATGCGTGTTGTTTGGCTG 7058	TG	T
			TAGTCGAG ATGC CAT		
			GTCGGTTT TGTG GTA		
			GT C		
GAM1923	EGFR	3'	GTATATGTGAGGATTTTATTG 11726	GT__	G
			CGA GAT CTCATATATAC		
			GTT TTA GAGTGTATATG		
			ATTT G		
GAM1923	F2RL3	3'	GTGTGTGTGCACGCATGGCTG 10084	A	A T
			TAGTCG GTG TGC CATATAT		

			GTCGGT CGC ACG GTGTGTG		
			A _ T		
GAM1923	FACL4	3'	GTGTATGTGAGTATTCTC 23254	T	
			GAG GATGCTCATATATAC		
			CTC TTATGAGTGTATGTG		
			—		
GAM1923	FACL4	3'	GTGTATGTGAGTATTCTC 10764	T	
			GAG GATGCTCATATATAC		
			CTC TTATGAGTGTATGTG		
			—		
GAM1923	GCH1	3'	GTGTGTGTGCGTTGGTTG 5669	G T	
			CGA TGATGC CATATAT		
			GTT GTTGCG GTGTGTG		
			G T		
GAM1923	GPR48	3'	GTATACATAGGCATTACTTTAT 20551	C TC A	
	TA		TAGT GAGTGATGC AT TATAC		
			ATTA TTCATTACG TA ATATG		
			T GA C		
GAM1923	HDAC7A	3'	GTGTGTGTGAGCGTGTGTGTGA 17713	G AGTG_	
	GTG		TA TCG ATGCTCATATATAC		
			GT AGT TGCGAGTGTGTGTG		
			G GTGTG		
GAM1923	HDAC7A	3'	GTGTGTGTGAGCGTGTGTGTGA 18683	G AGTG_	
	GTG		TA TCG ATGCTCATATATAC		
			GT AGT TGCGAGTGTGTGTG		
			G GTGTG		
GAM1923	HHEX	3'	GTGTATATAGAATTGTTCACTG 8594	C TG G C	
			TAGT GAG AT CT ATATATAC		
			GTCA CTT TA GA TATATGTG		
			_ GT A _		
GAM1923	HIF1A	3'	GTATGTGGCATTATTATTGG 7268	_ T	
			TCGAGTGA TGC CATATAT		
			GGTTTATT ACG GTGTATG		
			T _		
GAM1923	HUNK	3'	GTGTGTGTGAGCACCTGAC 15952	G TGA	
			GTC AG TGCTCATATATAC		
			CAG TC ACGAGTGTGTGTG		
			_ C_		
GAM1923	IL8RA	3'	GTGTGTGCAGCATTGTTGGCTG 6267	G TG _	
			TAGTC AG ATGCT CATATAT		

			GTCGG TT TACGA GTGTGTG	
			_ GT C	
GAM1923	IMPA1	3'	GTATGTGTGATACTAAGGTTTG 12058	TGATGC__
	ACTG		AGTCGAG TCATATATAC	
			TCAGTTT AGTGTGTATG	
			GGAATCAT	
GAM1923	INSM1	3'	TATGATATTATTTGATTG 7952	C
			TAGTCGAGTGATG TCATA	
			GTTAGTTTATTAT AGTAT	
			-	
GAM1923	MADH7	3'	GTGTGTGTGAGTGTGAGTGTGC 12525	AGTG__
	GGCTG		TCG ATGCTCATATATAC	
			GGC TGTGAGTGTGTGTG	
			GTGTGAG	
GAM1923	MAX	5'	GTGTGTGTGGGGGGGACTCGGC 8201	GATG
	T		AGTCGAGT CTCATATATAC	
			TCGGCTCA GGGTGTGTGTG	
			GGGG	
GAM1923	MAX	5'	GTGTGTGTGGGGGGGACTCGGC 29718	GATG
	T		AGTCGAGT CTCATATATAC	
			TCGGCTCA GGGTGTGTGTG	
			GGGG	
GAM1923	MAX	5'	GTGTGTGTGGGGGGGACTCGGC 29720	GATG
	T		AGTCGAGT CTCATATATAC	
			TCGGCTCA GGGTGTGTGTG	
			GGGG	
GAM1923	MAX	5'	GTGTGTGTGGGGGGGACTCGGC 29723	GATG
	T		AGTCGAGT CTCATATATAC	
			TCGGCTCA GGGTGTGTGTG	
			GGGG	
GAM1923	MTMR6	3'	GTATAAGCACATTTGACTG 44938	A C
			TAGTCGAGTG TGCT ATAT	
			GTCAGTTTAC ACGA TATG	
			- A	
GAM1923	NHLH1	5'	TGTGTGTGAGTGTGGCTGG 12126	G G
			C AGT ATGCTCATATATA	
			G TCG TGTGAGTGTGTGT	
			G G	
GAM1923	NHP2L1	3'	GTGTTCTGTGAGGTTGTTCGGC 11445	TG G T_
	TA		TAGTCGAG AT CTCATA ATAC	

			ATCGGCTT TG GAGTGT TGTG		
			GT _ CT		
GAM1923 NR3C2	3'	GTGTAGTTTCTGGTATCGTTCG 6598	T	CATA__	
CT		AG CGAGTGATGCT TATAC			
		TC GCTTGCTATGG ATGTG			
		_ TCTTTG			
GAM1923 PER2	3'	GTGTGAAGCGTTGTTTGGC 23093	TG _		
		GTCGAG ATGCT CATAT			
		CGGTTT TGCGA GTGTG			
		GT A			
GAM1923 RAB11A	3'	GTATGTGTGGGCTTGCTTAGAT 11034	_ TG T		
TA		TAGTC GAG A GCTCATATATAC			
		ATTAG TTC T CGGGTGTGTATG			
		A GT_			
GAM1923 RAB6A	3'	GTATGAGTATGGCTTGGTTA 8777	GT G		
		TA CGAGT ATGCTCATAT			
		AT GTTCG TATGAGTATG			
		TG G			
GAM1923 RERE	3'	GTGTACACACACTTGATTG 14409	A_ CT		
		TAGTCGAGTG TG CAT			
		GTTAGTTCAC AC GTG			
		AC AT			
GAM1923 SCN4A	3'	GTGTGTGTTCAAGTGCGTGA CT 5891	A A_ CT AC		
G		TAGTCG GTG TG CATATAT			
		GTCAGT CGT AC GTGTGTG			
		G GA TT			
GAM1923 SLC1A4	3'	GTGTGTAGTTACTTGAC 8998	GCT		
		GTCGAGTGAT CATAT			
		CAGTTCATTG GTGTG			
		AT_			
GAM1923 SNAP23	3'	GTGTGTCACCACGCTCGGCTA 9920	A CT__		
		TAGTCGAGTG TG CATAT			
		ATCGGCTCGC AC GTGTG			
		_ CACT			
GAM1923 SNAP23	3'	GTGTGTCACCACGCTCGGCTA 28285	A CT__		
		TAGTCGAGTG TG CATAT			
		ATCGGCTCGC AC GTGTG			
		_ CACT			
GAM1923 STXBP1	3'	GTGTGTATTACTTGTCTA 9140	T T		
		TAG CGAGTGATGC CAT			

ATC GTTCATTATG GTG
 T T
 GAM1923 SYT1 3' GTGTGTGTGCACATTTG 12170 A T
 CGAGTG TGC CATATAT
 ||||| ||| |||||
 GTTTAC ACG GTGTGTG
 _ T
 GAM1923 TCF8 3' GTGTGTGTGCGCGTGCATTGAT 25038 G _ T
 TA TAGTC AGTG ATGC CATATATAC
 ||||| ||||| ||||| |||||
 ATTAG TTAC TGCG GTGTGTGTG
 _ G C
 GAM1923 TNFSF9 3' GTGTGCCACCACACTTGGCTA 9902 AT__ T
 TAGTCGAGTG GC CAT
 ||||| || |||
 ATCGGTTTAC CG GTG
 ACCAC T
 GAM1923 VSX1 3' GTGTTTTCTTGAGTGTCACTTG 15956 TAT__
 AT GTCGAGTGATGCTCA ATAC
 ||||| ||||| |||||
 TAGTTCAGTGTGAGT TGTG
 TCTTT
 GAM1923 WSX1 5' TGTGTGTGTGTATGGTTG 11256 G G T
 CGA T ATGC CATATATA
 ||| ||||| |||||
 GTT G TATG GTGTGTGT
 _ G T
 GAM1923 YWHAH 3' ATGGGCATTGCTGGACTG 9439 G TG
 TAGTC AG ATGCTCAT
 ||||| || |||||
 GTCAG TC TACGGGTA
 G GT
 GAM1923 AKAP11 3' CGTATGTGTGGGTGTGTGTGTA 18369 ____
 TTTGGGTG AGTG ATGCTCATATATAC G
 ||||| ||||| ||||| |||
 TTAT TGTGGGTGTGTATG C
 GTGTG
 GAM1923 AP1S3 3' GTGTGTGCCACCATACTTGGCT 36987 AT__ T ATAC
 A AGTCGAGTG GC CATAT
 ||||| || |||||
 TCGGTTTCA T CG GTGTG
 ACCAC T C
 GAM1923 ARPP-19 3' TGTGTAGAGTTTTTGATTA 13426 TGAT A
 TAGTCGAG GCTC TATATA
 ||||| ||||| |||||
 ATTAGTTT TGAG ATGTGT
 T__ _
 GAM1923 ATP6V1B2 3' GTATGCCTGTATTGCTGGGCTG 7415 G TG T__
 TAGTC AG ATGC CATAT
 ||||| || ||||| |||||

GTCGG TC TATG GTATG
 G GT TCC
 GAM1923 BLP2 3' GTATATATGAAAATTTGA 24780 GATGC
 TCGAGT TCATATATAC
 ||||| |||||
 AGTTTA AGTATATATG
 AA__
 GAM1923 BLP2 3' GTATATATGAAAATTTGA 27800 GATGC
 TCGAGT TCATATATAC
 ||||| |||||
 AGTTTA AGTATATATG
 AA__
 GAM1923 C1QR1 3' GTGTGTATTTCAAATTTGTTTG 14336 TG TGCTC__
 ACTA AGTCGAG A ATATATAC
 ||||| | |||||
 TCAGTTT T TATGTGTG
 GT TAACTT
 GAM1923 C20orf108 3' GTAGCAGTGGCATCGCTTGGTT 28088 GT T ATA
 A CGAGTGATGC CAT TAC
 | ||||| || |||
 T GTTCGCTACG GTG ATG
 TG _ ACG
 GAM1923 C20orf140 3' GTGTGTATCTTCATCTGGCTG 29443 AG TGCTC
 TAGTCG TGA ATATATAC
 ||||| || |||||
 GTCGGT ACT TATGTGTG
 CT TC__
 GAM1923 C20orf3 3' GTGTGTATGAAAAGCTTG 33766 GATGC
 CGAGT TCATATATAC
 ||||| |||||
 GTTCG AGTATGTGTG
 AAA__
 GAM1923 C20orf81 5' GTGGGCAGCCTCACTTGGCTG 23004 ____
 TAGTCGAGTGA TGCTCAT
 ||||| |||||
 GTCGGTTCACT ACGGGTG
 CCG
 GAM1923 CDW92 3' GTATTTTTGTATACTTGATTG 27868 G TCAT
 TAGTCGAGT ATGC ATAT
 ||||| || |||
 GTTAGTTCA TATG TATG
 A TTTT
 GAM1923 CED-6 3' GTATATATGAGCCTTCTTGTTT 18433 T TGAT
 A TAG CGAG GCTCATATATAC
 || ||| |||||
 ATT GTTC CGAGTATATATG
 T TTC_
 GAM1923 CHCR 3' GTATATGTGTGGTGTGTTGATT 20422 GTG _
 AGTCGA ATGCT CATATATAC
 ||||| ||||| |||||

		TTAGTT TGTGG GTGTATATG	
		____ T	
GAM1923 DCOHM	3'	GTGTATGGGTGATTATTTGAT 25848	_ AC
		GTCGAGTGAT GCTCATATAT	
		TAGTTTATTA TGGGTATGTG	
		G	
GAM1923 DKFZP434C131	3'	GTGTAAAGAGTATCATTC 34245	ATA
		GAGTGATGCTC TATAC	
		CTTACTATGAG ATGTG	
		AA_	
GAM1923 DKFZp761G0313	3'	GTATATGTGTATATTTGCATTG 32742	_ TG TGCT_
		ATTA AGTCGA G A CATATATAC	
		TTAGTT C T GTGTATATG	
		A GT TATAT	
GAM1923 DKFZp762M136	3'	GTATGTGTGAGGAATTTGG 32304	GATG
		TCGAGT CTCATATATAC	
		GGTTTA GAGTGTGTATG	
		AG_	
GAM1923 EDR2	3'	GTGTGTATGACTGTGTGACT 30340	G _
		AGT ATGC TCATATATAC	
		TCA TGTG AGTATGTGTG	
		G TC	
GAM1923 EFA6R	3'	GTATATATAGTGGTATTGTTTT 17626	C TG C_
		ATTA AGT GAG ATGCT ATATATAC	
		TTA TTT TATGG TATATATG	
		T GT TGA	
GAM1923 ESDN	3'	GTATATATGTCTTGCTCAGATT 28154	_ TG TGCT
		A TAGTC GAG A CATATATAC	
		ATTAG CTC T GTATATATG	
		A GT CT_	
GAM1923 FLJ00007	3'	GTGTCTGGTTTGCTTGGCTG 35312	TG T T T
		TAGTCGAG A GC CA ATAT	
		GTCGGTTC T TG GT TGTG	
		GT _ _ C	
GAM1923 FLJ12587	3'	GTGTGAACACTGCTTGGCTG 22852	GA C
		TAGTCGAGT TG TCATAT	
		GTCGGTTCG AC AGTGTG	
		TC A	
GAM1923 FLJ13055	3'	GTGTGCCCCGTCCTCGATTG 22945	T CT_
		TAGTCGAG GATG CATAT	

			GT	T	AT_ C
GAM1923	FLJ13315	3'	TTATTGGGTGGCATTATTTGGT	24577	
		TA	TA CGAGTGATGC CAT	ATA	
			AT GTTTATTACG GTG	TAT	
			TG _ GGT	TG	
GAM1923	FLJ13962	3'	GTGAAGTATGGTTTGGCTG	24299	TG _
			TAGTCGAG ATGCT CAT		
			GTCGGTTT TATGA GTG		
			GG A		
GAM1923	FLJ14084	3'	GTGTGTGTTTTTCATTTGATT	22286	TGCT AC
			AGTCGAGTGA CATATAT		
			TTAGTTTACT GTGTGTG		
			TTTT		
GAM1923	FLJ20312	3'	GTATGTATGTTATACTTGATT	19376	ATGCT
			AGTCGAGTG CATATATAC		
			TTAGTTCAT GTATGTATG		
			ATT_		
GAM1923	FLJ20445	3'	TATGTATGATTTTGGCTA	19483	TGATGC
			TAGTCGAG TCATATATA		
			ATCGGTTT AGTATGTAT		
			T_		
GAM1923	FLJ22794	5'	GTGTAAGGGTGACATTTGGTTA	44034	GT A A
			TA CGAGTG TGCTC TATAT		
			AT GTTTAC GTGGG ATGTG		
			TG A A		
GAM1923	FLJ32783	3'	GTGTAGCATTGTTCTTGATTA	29584	T_ _
			TAGTCGAG GATGCT CAT		
			ATTAGTTC TTACGA GTG		
			TTG T		
GAM1923	GL004	3'	GTATATTCTGTCACTCAGCTG	32828	C CTC
			TAGT GAGTGATG ATATAT		
			GTCG CTCACTGT TATATG		
			A CT_		
GAM1923	HSJ1	3'	GTGTGTGTGGTGGGGCTTGGC	13588	GA T
			GTCGAGT TGC CATATATAC		
			CGGTTTCG GTG GTGTGTGTG		
			GG _		
GAM1923	IBTK	3'	GTATGTGTTGTTGCTTGACT	33518	TG GCT
			AGTCGAG AT CATATAT		

		TCAGTTC TG GTGTATG		
		GT TT_		
GAM1923	KIAA0016	3' GTATGAGCTGGGTGTCACCTTGG 16533		TA_
	CT	AGTCGAGTGATGCTCA TATAC		
		TCGGTTCACCTGTGGGT GTATG		
		CGA		
GAM1923	KIAA0090	3' GTGTGTGTGTGTCAGTGCTCAGCT 42653	C	GA CT
	A	TAGT GAGT TG CATATATAC		
		ATCG CTCG AC GTGTGTGTG		
		A TG T_		
GAM1923	KIAA0152	3' GTATGTGTCAAGAATTACTC 16338	G	C_
		GAGTGAT CT ATATATAC		
		CTCATTA GA TGTGTATG		
		A AC		
GAM1923	KIAA0285	3' ATGGCTATCATTTGGTTG 16748	GT	_ T
		TA CGAGTGAT GC CAT		
		GT GTTACTA CG GTA		
		TG T _		
GAM1923	KIAA0459	3' GTGTGTGCCACCATGCTTGGCT 30577	G	CT__ AC
	A	TAGTCGAGT ATG CATATAT		
		ATCGGTTCG TAC GTGTGTG		
		_ CACC		
GAM1923	KIAA0495	3' GTGTGCCACCACGCTCGGCTA 31361	AT__	T
		TAGTCGAGTG GC CAT		
		ATCGGCTCGC CG GTG		
		ACCAC T		
GAM1923	KIAA0574	3' GTGTCTGAGCTCACTTGATTG 34346	T	T
		TAGTCGAGTGA GCTCA ATAT		
		GTTAGTTCACCT CGAGT TGTG		
		_ C		
GAM1923	KIAA0680	3' GTGTGTGACTCAGCTTGGCTG 16285	GATGC	
		TAGTCGAGT TCATATAT		
		GTCGGTTCG AGTGTGTG		
		ACTC_		
GAM1923	KIAA0800	5' GTGTGTGTGAGTGAGAGTGAG 16238	G	AGTGA
	TG	TA TCG TGCTCATATATAC		
		GT AGT GTGAGTGTGTGTG		
		G GAGAG		
GAM1923	KIAA0871	5' GTGTGTGTGAGTGTGTGTGTGT 17333	T	AGTG_
	CTG	TAG CG ATGCTCATATATAC		

GTC GT TGTGAGTGTGTGTG
 T GTGTG
 GAM1923 KIAA1096 3' GTGAGCAGTGTGGCTA 33997 GT A
 TAGTCGA G TGCTCAT
 ||||| | |||||
 ATCGGTT T ACGAGTG
 TG G
 GAM1923 KIAA1145 3' TGTGTGTGAGCGGGACTT 32683 GA
 GAGT TGCTCATATATA
 ||| |||||
 TTCA GCGAGTGTGTGT
 GG
 GAM1923 KIAA1198 3' GTATATGTGGGTCTATGAT 31713 _ TGAT
 GTCG AG GCTCATATATAC
 ||| || |||||
 TAGT TC TGGGTGTATATG
 A ____
 GAM1923 KIAA1203 3' GTGTGTGTGAGTGTATGCG 35471 AGTG
 CG ATGCTCATATATAC
 || |||||
 GC TGTGAGTGTGTGTG
 GTA_
 GAM1923 KIAA1209 3' GTGTGTGTAAGTGCATTTGTAT 30472 _ A C
 TA TAGT CGAGTG TGCT ATATATAC
 ||| ||||| ||| |||||
 ATTA GTTTAC GTGA TGTGTGTG
 T _ A
 GAM1923 KIAA1277 3' GTGTGTGTGGGTGGGGACTA 32206 GAGTGA
 TAGTC TGCTCATATATAC
 |||| |||||
 ATCAG GTGGGTGTGTGTG
 GG____
 GAM1923 KIAA1301 3' GTATGTGTGTAATTATGGCTA 32979 GA GCT
 TAGTC GTGAT CATATATAC
 |||| |||| |||||
 ATCGG TATTA GTGTGTATG
 _ AT_
 GAM1923 KIAA1497 5' GTATGTATGAGTGTGTGCATTT 33530 ____
 G CGAGTG ATGCTCATATATAC
 |||| |||||
 GTTTAC TGTGAGTATGTATG
 GTG
 GAM1923 KIAA1677 3' TATATGTGGGTGTAGGTC 33293 GTG
 GA ATGCTCATATATA
 || |||||
 CT TGTGGGTGTATAT
 GGA
 GAM1923 KIAA1679 3' GTGTGTGTAATTGCTGGACTA 34753 G TG GCT
 TAGTC AG AT CATATAT
 |||| || || |||||

ATCAG TC TA GTGTGTG
 G GT AT_
 GAM1923 KIAA1701 3' GTGTGTCCATTAGACATTTGGC 33686 ____ CT ATAC
 TA GTCGAGTG ATG CATAT
 ||||| || ||||
 CGGTTTAC TAC GTGTG
 AGAT CT C
 GAM1923 KIAA1750 3' GTATGTGTGGACATGTGTTTAC 33878 C GT _ CT
 TG TAGT GA G ATG CATATATAC
 ||| || | || |||||
 GTCA CT T TAC GTGTGTATG
 _ TG G AG
 GAM1923 KIAA1753 3' GTATGTATGTATATGTATATGA 32381 A _ CT
 TTA TAGTCG GTG ATG CATATATAC
 ||||| ||| ||| |||||
 ATTAGT TAT TAT GTATGTATG
 A G AT
 GAM1923 LCP 5' GTGTGGGCATTGTTGGTTA 15615 GT G TG
 TA C AG ATGCTCATAT
 || || |||||
 AT G TT TACGGGTGTG
 TG _ GT
 GAM1923 LNIR 3' GTGTGTGTCATGTGGCTG 25187 A T
 TAGTCG GTGATGC CAT
 ||||| ||||| |||
 GTCGGT TACTGTG GTG
 G T
 GAM1923 LRRN3 5' GTATATATTTTGTACACTTTGT 34400 TC A TC_
 TA TAG GAGTG TGC ATATATAC
 || ||||| ||| |||||
 ATT TTCAC ATG TATATATG
 GT _ TTT
 GAM1923 MAPK11 3' GTGTGTGTGGGCACGTGTGG 8629 AG A
 TCG TG TGCTCATATATAC
 ||| || |||||
 GGT GC ACGGGTGTGTGTG
 GT _
 GAM1923 MASA 3' GTATATATGTGTATGCTCAGAT 32373 _ G T
 TA TAGTC GAGT ATGC CATATATAC
 ||||| ||| ||| |||||
 ATTAG CTCG TATG GTATATATG
 A _ T
 GAM1923 MGC26655 5' GTGTGTGTGGAGCTCGGGTG 28703 G GA T
 TA TCGAGT TGC CATAT
 || ||||| ||| |||||
 GT GGCTCG GTG GTGTG
 G AG T
 GAM1923 MGC4677 5' GTGTATTGTGATTATTTGAT 27453 TGC _
 GTCGAGTGA TCATA TATAC
 ||||| ||||| |||||

				TAGTTTATT AGTGT ATGTG		
				____ T		
GAM1923	MRPL10	3'	GTGTGTTTGTCACTTGGTT	29770	GT	CT
			A CGAGTGATG CATAT			
			T GTTCACTGT GTGTG			
			TG TT			
GAM1923	MSTP028	3'	GTGTATGTGAGAACTTTTGT	25696	TG TG	____
	G		CGAG A CTCATATATAC			
			GTTT T GAGTGTATGTG			
			GT TTCAA			
GAM1923	PDE3A	3'	GTATGGATGTCACTCAACTA	6632	C	CT
			TAGT GAGTGATG CATAT			
			ATCA CTCCTGT GTATG			
			A AG			
GAM1923	PPFIA4	3'	GTGTGTGTGGGTGGGTGTGAGT	34821	G	AGTGA
	G		TA TCG TGCTCATATATAC			
			GT AGT GTGGGTGTGTGTG			
			G GTGG_			
GAM1923	PRDM12	3'	ATATATTATTATTGATTG	22254		CTC
			TAGTCGAGTGATG ATATAT			
			GTTAGTTTATTAT TATATA			

GAM1923	RAB6C	3'	GTATGAGTATGGCTTGGTTA	25834	GT	G
			TA CGAGT ATGCTCATAT			
			AT GTTCG TATGAGTATG			
			TG G			
GAM1923	SFXN2	3'	TGTGTATGAGTTTTGTCTG	36606	T	TGAT
			TAG CGAG GCTCATATATA			
			GTC GTTT TGAGTATGTGT			
			T _____			
GAM1923	SRF	3'	GTGTGTGTGGGTGTGTGCGCCT	9104	T	AGTG
	G		TAG CG ATGCTCATATATAC			
			GTC GC TGTGGGTGTGTGTG			
			C GTG_			
GAM1923	SS18L1	3'	GTATGTGTTTCATATTCGAT	32563	A	CT
			GTCGAGTG TG CATATAT			
			TAGCTTAT AC GTGTATG			
			_ TT			
GAM1923	STARD7	3'	GTGTGAACGATACTTGGCTA	29262	A	C
			TAGTCGAGTG TG TCATAT			

		ATCGGTTTCAT GC AGTGTG		
		A A		
GAM1923	STARD7	3' GTGTGAACGATACTTGGCTA 21360	A C	
		TAGTCGAGTG TG TCATAT		
		ATCGGTTTCAT GC AGTGTG		
		A A		
GAM1923	TACTILE	3' GTATGCTTATCCTTGA CTG 12414	T CT	
		TAGTCGAG GATG CATAT		
		GTCAGTTC CTAT GTATG		
		_ TC		
GAM1923	TUSP	3' GTGTGCCTGTATCATTTGGC 21533	T__	
		GTCGAGTGATGC CATAT		
		CGGTTTACTATG GTGTG		
		TCC		
GAM1923	WBSCR17	3' GTGTGTGTGTGTCTGGCTG 39548	AGT T	
		TAGTCG GATGC CATATAT		
		GTCGGT CTGTG GTGTGTG		
		___ T		
GAM1923	ZFR	3' GTGTTAGGTATTATTTGA 18188	CAT	
		TCGAGTGATGCT ATAT		
		AGTTTATTATGG TGTG		
		AT_		
GAM1923	LOC115286	3' TGTATGTGGGTGTTTCTC 36315	T	
		GAG GATGCTCATATATA		
		CTC TTGTGGGTGTATGT		
		T		
GAM1923	LOC122830	3' GTAGCATGGGTTCACTTGGCTA 36708	T ATA	
		TAGTCGAGTGA GCTCAT TAC		
		ATCGGTTCACT TGGGTA ATG		
		_ CG_		
GAM1923	LOC126669	3' GTGTGTATTGGTTCATTTACTA 37158	C T C	
		TAGT GAGTGA GCT ATATATAC		
		ATCA TTTACT TGG TATGTGTG		
		_ _ T		
GAM1923	LOC130639	5' GTATGACCCATCATTTGAT 37002	C_	
		GTCGAGTGATG TCATAT		
		TAGTTTACTAC AGTATG		
		CC		
GAM1923	LOC143888	3' GTATGCTATAGGCATCATTC 37671	TC _	
		GAGTGATGC ATA TATAC		

		CTTACTACG TAT GTATG		
		GA C		
GAM1923	LOC145009 5'	ATGGGCGTCCTTTGACTG 30263	T	
		TAGTCGAG GATGCTCAT		
		GTCAGTTT CTGCGGGTA		
		C		
GAM1923	LOC145581 5'	GTGTGTGTGAGTGTGAGC 37902	G_	
		GT ATGCTCATATATAC		
		CG TGTGAGTGTGTGTG		
		AG		
GAM1923	LOC145820 3'	GTATATAAATAAAATCATTCTGA 37991	GCTCA_	
	C	GTCGAGTGAT TATATAC		
		CAGCTTACTA ATATATG		
		AAATAA		
GAM1923	LOC146712 5'	GTGACAGCATCATTTGAGTG 40712	G	—
		TA TCGAGTGATGC TCAT		
		GT AGTTTACTACG AGTG		
		G AC		
GAM1923	LOC147136 3'	TATGGTGTGCTTGGCTA 38306	T	
		TAGTCGAGTGATGC CATA		
		ATCGGTTGCTGTG GTAT		
		—		
GAM1923	LOC147976 3'	GTGTGGACCATTGCTTGA 38427	TG C A	
		TCGAG ATG TC TATAT		
		AGTTC TAC AG GTGTG		
		GT C _		
GAM1923	LOC149401 5'	TATGTGGGCATATTTGGTTG 38738	GT A	
		TA CGAGTG TGCTCATATA		
		GT GTTTAT ACGGGTGTAT		
		TG _		
GAM1923	LOC149721 5'	GTGTGTGTGTCCTCATGTGGCT 38811	A TGCT	
	G	TAGTCG GTGA CATATATAC		
		GTCGGT TACT GTGTGTGTG		
		G CCT_		
GAM1923	LOC151475 3'	GTGTGTGTGAGTGGGTATGAT 41359	AGTGA	
		GTCG TGCTCATATATAC		
		TAGT GTGAGTGTGTGTG		
		ATGG_		
GAM1923	LOC153346 3'	GTAGGGGGCATTATTTATTA 41618	C ATA	
		TAGT GAGTGATGCTC TAT		

	ATTA TTTATTACGGG	ATG	
	— GG—		
GAM1923 LOC153592 3'	TAATATTGAGTGTCAACTTGAT	41649	— T AC
TTG	TAGTCGAGT GATGCTCA ATAT		
	GTTAGTTCA CTGTGAGT TATA		
	A — ATT		
GAM1923 LOC157922 3'	TATATATCGTGTTCGAC	41890	GTG TC
	GTCGA ATGC ATATATA		
	CAGCT TGTG TATATAT		
	— C—		
GAM1923 LOC158476 3'	GTGTATGTGAGTCTCAGTGGAC	42000	GAG T
TA	TAGTC TGA GCTCATATATAC		
	ATCAG ACT TGAGTGTATGTG		
	GTG C		
GAM1923 LOC158709 3'	GTGTGTGTTTCTGGTTGGCTG	39883	G _ T T
	TAGTCGA T GA GC CATAT		
	GTCGGTT G CT TG GTGTG		
	G T T T		
GAM1923 LOC160418 5'	GTGTGTATGAAGTGTTTATTG	39997	GT —
	CGA GATGCT CATATATAC		
	GTT TTGTGA GTATGTGTG		
	AT A		
GAM1923 LOC196027 3'	GTGTGTATGTCCTGCTTCATT	42306	T T—
	AGTGA GC CATATATAC		
	TTACT CG GTATGTGTG		
	T TCCT		
GAM1923 LOC196955 5'	TTAATACTGAGTGTCAACTTGA	37941	— TATATAC
TTG	TAGTCGAGT GATGCTCA		
	GTTAGTTCA CTGTGAGT		
	A CATAATTG		
GAM1923 LOC199858 3'	TTAATACTGAGTGTCAACTTGA	42646	— TATATAC
TTG	TAGTCGAGT GATGCTCA		
	GTTAGTTCA CTGTGAGT		
	A CATAATTG		
GAM1923 LOC199957 3'	GTATAATATTAGCTTATTTGAC	42676	T C —
TA	TAGTCGAGTGA GCT ATAT ATAC		
	ATCAGTTTATT CGA TATA TATG		
	— T A		
GAM1923 LOC219722 5'	GTATGTATGGCGCTTTGGTTGA	44712	G T —
	TCGA TGA GC TCATATATAC		

		AGTT GTT CG GGTATGTATG	
		G T C	
GAM1923	LOC219735 3'	GTATATAGATTATTTTCGATTA 44721	T C A
		TAGTCGAG GATG TC TATATAC	
		ATTAGCTT TTAT AG ATATATG	
		_ T _	
GAM1923	LOC220038 5'	GTATCAGTGCTACTCGGCTA 44080	AT C
		TAGTCGAGTG GCT ATAT	
		ATCGGCTCAT TGA TATG	
		CG C	
GAM1923	LOC256087 5'	GTGTATGTGAGCGGGGAGCT 45602	GA__
		AGT TGCTCATATATAC	
		TCG GCGAGTGTATGTG	
		AGGG	
GAM1923	LOC51706 3'	GTATGTGTGAGTATAAGTTGA 34817	GTG
		TCGA ATGCTCATATATAC	
		AGTT TATGAGTGTGTATG	
		GAA	
GAM1923	LOC90075 5'	GTGTATGGACAGCTTACTCGAC 30739	T CA_
		GTCGAGTGA GCT TATATAC	
		CAGCTCATT CGA GTATGTG	
		_ CAG	
GAM1923	LOC91380 3'	GTATGGTTTTGGGGTTATTTGG 32757	GT G TA__
	TTG	A CGAGTGAT CTCA TATAC	
		T GTTTATTG GGGT GTATG	
		TG _ TTTG	
GAM1923	LOC91496 5'	GTGTTGTATTACTTGTTTA 32918	T T_
		TAG CGAGTGATGC CAT	
		ATT GTTCATTATG GTG	
		T TT	
GAM1923	LOC92912 3'	GTATTCTTGTTCACTTGATTA 35085	T TCAT
		TAGTCGAGTGA GC ATAT	
		ATTAGTTCACT TG TATG	
		_ TTCT	
GAM1924	ABCD3 3'	TCTGTGAATCTTGAATAACTTT 8754	G TG GCT
	T	AAAAGT ATT GGATT TAGG	
		TTTTCA TAA TCTAA GTCT	
		A GT GT_	
GAM1924	ABCD4 3'	CCTACAAATGATTTTCAGATCAT 21587	GG CT__
		GTGATTTG ATTG TAGG	

			TACTAGAC TAGT ATCC	
			TT AAAC	
GAM1924 ABCD4	3'	CCTACAAATGATTTTCAGATCAT 21589		GG CT__
		GTGATTTG ATTG TAGG		
		TACTAGAC TAGT ATCC		
		TT AAAC		
GAM1924 ABCD4	3'	CCTACAAATGATTTTCAGATCAT 21582		GG CT__
		GTGATTTG ATTG TAGG		
		TACTAGAC TAGT ATCC		
		TT AAAC		
GAM1924 ABCD4	3'	CCTACAAATGATTTTCAGATCAT 21584		GG CT__
		GTGATTTG ATTG TAGG		
		TACTAGAC TAGT ATCC		
		TT AAAC		
GAM1924 ABCE1	3'	TAGGTATTTTTTAAATTGTTTTT 29940	TG	T
		AAAAG ATTTGGGA TGCTTA		
		TTTTT TAAATTTT ATGGAT		
		GT T		
GAM1924 ACADSB	3'	CTTAGGCACAGGAGATCCACTT 7313		AT GGGAT
TT		AAAAGTG TT TGCTTAGG		
		TTTTCAC AG ACGGATTC		
		CT AGGAC		
GAM1924 ANGPT1	3'	CTTAGGCAATTTTTTAATT 6814	TG	
		GATT GGATTGCTTAGG		
		TTAA TTTAACGGATTC		
		TT		
GAM1924 AOC3	3'	TCTGGCTTTCCCGAATCTTTTT 9825	T	TT T
		AAAAG GATTTGGGA GCT AGG		
		TTTTT CTAAGCCCT CGG TCT		
		TT _		
GAM1924 AOX1	3'	CTTAAGCAATCTATAAATCATT 6826		_
TT		AAAGTGATTTG GGATTGCTTAGG		
		TTTTACTAAAT TCTAACGAATTC		
		A		
GAM1924 ARHGEF7	3'	CTTGAGTTTTACAAGTTATTTT 9983		GG TT
T		AAAAGTGATTTG A GCTTAGG		
		TTTTTATTGAAC T TGAGTTC		
		AT T_		
GAM1924 AS3	3'	CCTGAAGTTCTTGGATTACTTT 18049	TG	TT _
		AAAGTGATT GGA GCT TAGG		

		TTTCATTAG TCT TGA GTCC	
		GT _ A	
GAM1924 AS3	3'	TCAAACCAATTTCAAATTATTT 18052	GG C AGG
T		AAAGTGATTG ATTG TT	
		TTTTATTAAAC TAAC AA	
		TT C ACTT	
GAM1924 ASGR1	5'	CCTGAGCAATCCCAGGTCCAGC 7386	_
		GT GATTGTTGGATTGCTTAGG	
		CG CTGGACCCTAACGAGTCC	
		AC	
GAM1924 BCRP2	3'	TAAGCCCAAGTCATTTT 31275	GATT
		AAAGTGATTGTTGG GCTTA	
		TTTTACTGAACC CGAAT	
GAM1924 BHLHB3	3'	CTTATGCTGTCTTAAATTATTT 25044	T T
T		AAAGTGATTGTTGGGAT GC TAGG	
		TTTTATTAAATTCTG CG ATTC	
		T T	
GAM1924 BLTR2	5'	CTTGGGCAATCTATACTTTT 21243	ATTG
		AAAAGTG GGATTGCTTAGG	
		TTTTCAT TCTAACGGGTTT	
		A_	
GAM1924 BRIP1	3'	CTTGAGTTTTTGGGTTTCTTTT 25754	T TG TT
		AAAAG GATT GGA GCTTAGG	
		TTTTTCTTG TTT TGAGTTC	
		T GT _	
GAM1924 BTG2	3'	CCTACTGTCCTAAGCTGCTTTT 13625	GA TGCT
		AAAAGT TTTGGGAT TAGG	
		TTTTCG GAATCCTG ATCC	
		TC TC_	
GAM1924 CANX	3'	TAAAAAAGTGATCTTAGGTTTG 42276	TG_ TG AGG
TTTTT		AAAG A TTTGGGAT CTT	
		TTTT TGGATTCTA GAA	
		GT T GT AAAATT	
GAM1924 CAPZA1	3'	TTTGGGTAATTCTGCCACATTT 35953	ATT
		AAGTG TGGGATTGCTTAGG	
		TTTAC GTCTTAATGGGTTT	
		ACC	
GAM1924 CARD4	5'	TCTGGGAAGACAAGTTGCT 12741	TG GGA G
		AG ATTTG TTCTTAGG	

			TC TGAAC AA GGGTCT		
			GT AG_ _		
GAM1924	CBFA2T2	3'	TCTGGGTAGTTCTAGAGGAT 11553	GA	
			GT TTTGGGATTGCTTAGG		
			TA AGATCTTGATGGGTCT		
			GG		
GAM1924	CBFB	3'	CTTAAGCTACCAGATTGCTTTT 23148	TG	GATT
			AAAAG ATTTGG GCTTAGG		
			TTTTC TAGACC CGAATTC		
			GT AT_ _		
GAM1924	CBFB	3'	CTTAAGCTACCAGATTGCTTTT 7507	TG	GATT
			AAAAG ATTTGG GCTTAGG		
			TTTTC TAGACC CGAATTC		
			GT AT_ _		
GAM1924	CD59	3'	TCTGCAGCCCTCAGATTATTTT 6213	_ AT	TTAGG
	T		AAAAGTGATTTG GG TGC		
			TTTTTATTAGAC CC ACG		
			T CG TCT		
GAM1924	CDH6	3'	TCTGGCAGATTCAAATCGTTT 11376	A	T
			AAGTGATTTGGG TTGCT AGG		
			TTTGCTAAACTT GACGG TCT		
			A _		
GAM1924	CENTD1	3'	TTAGGTGGTCAGTCCTTTT 17564	T	TGG TG
			AAAAG GATT GAT CTTAG		
			TTTTC CTGA CTG GGATT		
			_ _ GT		
GAM1924	CENTD1	3'	TTAGGTGGTCAGTCCTTTT 29202	T	TGG TG
			AAAAG GATT GAT CTTAG		
			TTTTC CTGA CTG GGATT		
			_ _ GT		
GAM1924	CERD4	3'	CCTAGCCTTCAAGTTGCTTTT 14345	TG	ATT T
			AAAAG ATTTGGG GCT AGG		
			TTTTC TGAAGTT CGA TCC		
			GT C_ _		
GAM1924	CHAC	3'	CTTGGTTTACCCAAGTCAT 27140	ATT	T G
			GTGATTTGGG GCT AG		
			TACTGAACCC TGG TC		
			ATT T		
GAM1924	CKTSF1B1	3'	CCTGGAAGTCTGTAAGTTGTTT 15024	TG	_ GC
	TT		AAAAG ATTTG GGATT TTAGG		

		TTTTT TGAAT TCTGA GGTCC	
		GT G A_	
GAM1924 CLN2	3'	CTTAAGTAAAAAATCATTTTT 5966	GGA
		AAAAGTGATTT TTGCTTAGG	
		TTTTTACTAAA AATGAATTC	
		A__	
GAM1924 CTNS	5'	CCTGGGGGCGCTCAGATTGCTT 11384	TG ATTG
T		AAAG ATTTGGG CTTAGG	
		TTTC TAGACTC GGGTCC	
		GT GCGG	
GAM1924 CYP2B6	3'	TTTAGGTGGTCTTGAACCTCCT 6417	T _ TG TG
		AG GA TT GGAT CTTAGG	
		TC CT AA TCTG GGATTT	
		_ C GT GT	
GAM1924 DAG1	3'	TCTGAAGCGTTATTTTGGGTAC 10637	G TG _ _
TTTT		AAGT ATT GGAT TGCT TAGG	
		TTCA TGG TTTA GCGA GTCT	
		_ GT TT A	
GAM1924 DGKB	3'	TCTGAGCAGTCTTGTAATATT 44451	ATT
		AGTG TGGGATTGCTTAGG	
		TTAT GTTCTGACGAGTCT	
		AAT	
GAM1924 DISC1	3'	TTTGGGCAGGTGAGTCAT 20742	GGA
		GTGATTT TTGCTTAGG	
		TACTGAG GACGGGTTT	
		TG__	
GAM1924 DNMT3B	3'	TTTAAGGGCCCAGGATCGTTTT 13766	_ ATTG
T		AAAAGTGATT TGGG CTTAGG	
		TTTTTGCTAG ACCC GAATTT	
		G GG__	
GAM1924 DTR	3'	CCTAGGCGATTTTGTCTACCAT 7660	ATT__ GG
TT		AAGTG T GATTGCTTAGG	
		TTTAC G TTAGCGGATCC	
		CATCT TT	
GAM1924 DXS1283E	3'	CTTAGGTGATAAGGAATCATTT 35066	GGG TG
TT		AAAAGTGATTT AT CTTAGG	
		TTTTTACTAAG TA GGATTC	
		GAA GT	
GAM1924 DXS1283E	3'	TCTGAGTAGTTGTCCATCACTT 35068	TT _
T		AAAGTGA TGG GATTGCTTAGG	

		TTTCACT ACC TTGATGAGTCT	
		___ TG	
GAM1924	DYRK1A	3' TCTGTTCATCCTGAACATTTTT 28165	A TG T CT
		AAAAGTG TT GGAT G TAGG	
		TTTTTAC AA CCTA C GTCT	
		_ GT _ TT	
GAM1924	DYRK1A	3' TCTGTTCATCCTGAACATTTTT 28189	A TG T CT
		AAAAGTG TT GGAT G TAGG	
		TTTTTAC AA CCTA C GTCT	
		_ GT _ TT	
GAM1924	DYRK1A	3' TCTGTTCATCCTGAACATTTTT 7094	A TG T CT
		AAAAGTG TT GGAT G TAGG	
		TTTTTAC AA CCTA C GTCT	
		_ GT _ TT	
GAM1924	EDN1	5' CTTGGGCTGAAGGATCGCTTT 7679	GGGATT
		AAAGTGATTT GCTTAGG	
		TTTCGCTAGG CGGGTTC	
		AAGT__	
GAM1924	EDNRA	3' TGGGCTCAAGTCACTTTT 32059	GATT
		AAAAGTGATTTGG GCTTA	
		TTTTCACTGAACT CGGGT	

GAM1924	EDNRB	5' GGCGCGCAAACCTTGAGTTACTT 10148	TG A TTAGG
	TT	AAAAGTGATT GG TTGC	
		TTTTCATTGA TC AACG	
		GT A CGCGGT	
GAM1924	FABP2	3' CCTCAGCCTCTCAAGTTGTTTT 5624	TG TT T
	T	AAAAG ATTTGGGA GCT AGG	
		TTTTT TGAACCTC CGA TCC	
		GT C_ C	
GAM1924	FBLN5	3' CCTGGGAGTAGCTAGTTTGCTT 13023	TG T G_ G
	TT	AAAAG A TTGG ATT CTTAGG	
		TTTTC T GATC TGA GGGTCC	
		GT T GA _	
GAM1924	FBXL7	3' CTTAAGCAGGCTGATCGCT 14671	TG A
		AGTGATT GG TTGCTTAGG	
		TCGCTAG TC GACGAATTC	
		___ G	
GAM1924	FCRH1	3' TCTATTTATTTTGAGTCACT 27500	TG TGCT
		AGTGATT GGAT TAGG	

			TC	ACTGA	TTTA	ATCT		
			GT	TTT				
GAM1924	FZD8	3'	CTTAGGCATGGAGAAAATTACT	25623		GGGAT		
	T		AAGTGATTT	TGCTTAGG				
			TTCATTAAA	ACGGATTC				
			AGAGGT					
GAM1924	GALNT3	3'	CTTAAGTCTTCCTTAAATGACT	10803	G		TT	
	TTT		AAAAGT ATTTG	GGA	GCTTAGG			
			TTTTCA	TAAAT CCT	TGAATTC			
			G	T	TC			
GAM1924	GALNT3	3'	CTTGCGAAATTTTAAAACATTT	10804	A		T G	
	TT		AAAAGTG TTTGGGATT	GCT AG				
			TTTTTAC	AAATTTTAA	CGG TC			
			A	A	T			
GAM1924	GALNT7	5'	CCTGAGCAGAATGGAATCATT	27650		GGGA		
			AGTGATTT	TTGCTTAGG				
			TTACTAAG	GACGAGTCC				
			GTAA					
GAM1924	GLUL	3'	TCTAGGTAATTTTTACAGAATT	7837	TG			
	GCTT		G ATTT	GGGATTGCTTAGG				
			C	TAAG	TTTAAATGGATCT			
			GT	ACAT				
GAM1924	GNB1	3'	CTTGGGTAGCGGGATAAGTCAC	7851		GGA		
	T		AGTGATTTG	TTGCTTAGG				
			TC	ACTGAAT	GATGGGTTC			
			AGGGC					
GAM1924	GRM4	3'	CTTGGGTCCCACCAAGTGTC	ACT 6505			GATT	
	TTT		AAAAGTGAT TTGG	GCTTAGG				
			TTTTCACTG	GACC	TGGGTTC			
			T	ACCC				
GAM1924	HGF	3'	CTTAGTTTTCTTGAGTGATTTT	45223	G	TG	TT	T G
	T		AAAAGT ATT	GGA	GCT AG			
			TTTTTA	TGA	TCT	TGA	TC	
			G	GT	TT	T		
GAM1924	HOXB3	5'	TCTAGGCAGTCTTGAAAGGC	7922		GA	TG	
			GT	TT	GGATTGCTTAGG			
			CG	AA	TCTGACGGATCT			
			GA	GT				
GAM1924	HSPA8	5'	TAGTCTCGAGTTTTTTTTT	13371		T		
			AAAAG	GATTTGGGATTG				

		TTTTT TTGAGCTCTGAT		
		T		
GAM1924 ID4	3'	GCATCTAGATTATTTTT 7272	AT	
		AAAAGTGATTTGGG TGC		
		TTTTTATTAGATCT ACG		
GAM1924 IL10RA	3'	CTTGCTGCTGGGGTCATTTTT 29997	G ATT TT	
		AAAAGTGATTT GG GC AG		
		TTTTTACTGGG TC CG TC		
		G GT_ T_		
GAM1924 IL8	3'	GCTGGAAATCCTGGATTTTTTT 45338	T TG GC G	
		AAAG GATT GGATT TTAG		
		TTTT TTAG CCTAA GGTC		
		T GT A_ GA		
GAM1924 IMPA1	3'	CCTCATAGTCAATCCAGTTGC 12057	TG T _ T_	
	TTTT	AAG ATT GGGATTG CT AGG		
		TTC TGA CCCTAAC GA TCC		
		GT _ T TAC		
GAM1924 INHBB	3'	TTTAAGCGAATGATTGCTTTT 7949	TG TGGGA	
		AAAAG ATT TTGCTTAGG		
		TTTTC TAG AGCGAATTT		
		GT TA__		
GAM1924 JRKL	3'	CCTGGGGAACCTTAGGTTATTT 9855	GA G	
		AAGTGATTTGG TT CTTAGG		
		TTTATTGGATT AA GGGTCC		
		TC G		
GAM1924 KCNA3	3'	AATCCCAAATGCATTTTT 8013	_	
		AAAAGTG ATTTGGGATT		
		TTTTTAC TAAACCCTAA		
		G		
GAM1924 KCNJ16	3'	CCTGGGAGTAATAAAGTTACTT 20728	GGG_ G	
	TT	AAAAGTGATTT ATT CTTAGG		
		TTTTCATTGAA TGA GGGTCC		
		ATAA _		
GAM1924 KMO	3'	TTGAGCTGATTTAAGTTGTTTT 9782	TG ATT G	
	T	AAAAG ATTTGGG GCTTAG		
		TTTTT TGAATTT CGAGTT		
		GT AGT		
GAM1924 LARGE	3'	TTTAGGATGTTCTGGATGCTTT 11130	G TG TG	
	T	AAAAGT ATT GGAT CTTAGG		

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          TTTTCG TAG CTTG GGATTT
            _ GT TA
GAM1924 LARGE 3' TTTAGGATGTTCTGGATGCTTT 28602   G TG TG
      T          AAAAGT ATT GGAT CTTAGG
          ||||| ||| ||| |||||
          TTTTCG TAG CTTG GGATTT
            _ GT TA
GAM1924 M6PR 3' CTTGCTTTCCAGTTTGCTTTT 8165   TG T TT TT
          AAAAG A TTGGGA GC AG
          |||| | ||||| || ||
          TTTTC T GACCTT CG TC
            GT T T_ T_
GAM1924 MBD1 3' GTCTAAGCTGTTCTATTTTAAA 8202   _____ T
      ATTATTTTT          ATT TGGGAT GCTTAGG T
          ||| ||||| ||||| |
          TAA ATCTTG CGAATCT G
          AATTTT T
GAM1924 MBD1 3' GTCTAAGCTGTTCTATTTTAAA 17972   _____ T
      ATTATTTTT          ATT TGGGAT GCTTAGG T
          ||| ||||| ||||| |
          TAA ATCTTG CGAATCT G
          AATTTT T
GAM1924 MBD1 3' GTCTAAGCTGTTCTATTTTAAA 17973   _____ T
      ATTATTTTT          ATT TGGGAT GCTTAGG T
          ||| ||||| ||||| |
          TAA ATCTTG CGAATCT G
          AATTTT T
GAM1924 MBD1 3' GTCTAAGCTGTTCTATTTTAAA 17974   _____ T
      ATTATTTTT          ATT TGGGAT GCTTAGG T
          ||| ||||| ||||| |
          TAA ATCTTG CGAATCT G
          AATTTT T
GAM1924 MEF2C 3' TTGCAACACCCTAAATTGTTTT 8216   TG A__ TTAGG
      T          AAAAG ATTTGGG TTGC
          |||| ||||| |||
          TTTTT TAAATCC AACG
            GT CAC TT
GAM1924 MEN1 5' TAATTCCTAGTCATTTTT 44845   T
          AAAAGTGATT GGGATTG
          ||||| |||||
          TTTTACTGA CCTTAAT
            T
GAM1924 MTM1 3' TTTAAGTAATTGCCAGCTTTT 5792   GATT _
          AAAAGT TGG GATTGCTTAGG
          |||| | ||||| |||
          TTTTCG ACC TTAATGAATTT
            _____ G
GAM1924 MTR 3' CCTAAGTAATCCCAGAACA 5796 A
          TG TTTGGGATTGCTTAGG
          || ||||| |||||

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			AC AGACCCTAATGAATCC		
			A		
GAM1924 MYCN	3'	CCTGGGTAATGAGAGGTGGCTT 11860	G GGG		
TT		AAAAGT ATTT ATTGCTTAGG			
		TTTTCG TGGA TAATGGGTCC			
		G GAG			
GAM1924 MYD88	3'	CCTGAGCAGCTTGGGCTGCTTT 8297	GA TG A		
T		AAAAGT TT GG TTGCTTAGG			
		TTTTCG GG TC GACGAGTCC			
		TC GT _			
GAM1924 NEU3	3'	TCTGGGTTTCTCTCAAGTTTGT 13458	TG_ TT_		
TTTT		AAAG A TTTGGGA GCTTAGG			
		TTTT T GAACTCT TGGGTCT			
		GT T CTT			
GAM1924 NEURL	3'	GCCCCCTCAGATGGCTTTT 10413	G ATT		
		AAAAGT ATTTGGG GC			
		TTTTCG TAGACTC CG			
		G CCC			
GAM1924 NEUROD1	3'	TTTGAGCAATTCATTTCACTTT 8324	TTTG		
		AAAGTGA GGATTGCTTAGG			
		TTTCACT CTTAACGAGTTT			
		TTA_			
GAM1924 NPEPPS	3'	TCAGTGCATAATTCCAAGTGGC 13001	G _ TTAGG		
TTTT		AAAGT ATTTGGGAT TGC			
		TTTTCG TGAACCTTA ACG			
		G AT TGA CT			
GAM1924 NRIP1	3'	CCTGCCATCCAGTTTTTGATCT 30119	T TG CT__		
TTTT		AAG GATT GGATTG TAGG			
		TTT CTAG TTTGAC GTCC			
		_ GT CTACC			
GAM1924 OAT	3'	TTTAACATTCCCTAAATTGTTTT 5816	TG T C		
		AAAG ATTTGGGA TG TTAGG			
		TTTT TAAATCCT AC AATTT			
		GT T _			
GAM1924 OPHN1	3'	CCTAGGTCTATTTGGATTATT 8400	TG ATT		
		AGTGATT GG GCTTAGG			
		TTATTAG TT TGGATCC			
		GT ATC			
GAM1924 OSM	3'	CTGGGGCAGGTCACTTT 21755	GGATTG		
		AAAGTGATTTG CTTAG			

			TTTCACTGGAC	GGGTC		
			G_____			
GAM1924	PCDHB12	3'	TTTGAGATATTTTAAATTGCTT	21004	TG	TG
	T		AAAG ATTTGGGAT CTTAGG			
			TTTC TAAATTTTA GAGTTT			
			GT TA			
GAM1924	PCDHB7	3'	CCTGCTTTTCTGGGTCAATTTT	21006	G	TG TT TT
			AAAA TGATT GGA GC AGG			
			TTTT ACTGG CTT CG TCC			
			A GT TT _			
GAM1924	PCDHB7	3'	TTTGAGATATTTTAAATTGCTT	21010	TG	TG
	T		AAAG ATTTGGGAT CTTAGG			
			TTTC TAAATTTTA GAGTTT			
			GT TA			
GAM1924	PCSK1	3'	TTTGAGCAATTTTTCGAACATT	6025	A	GG _
			AGTG TTTG A TTGCTTAGG			
			TTAC AAGC T AACGAGTTT			
			_ TT T			
GAM1924	PEA15	3'	CCTGAGTACCAGCAGGTCCCTT	9847	T	_ AT
	TT		AAAAG GATTTG GG TGCTTAGG			
			TTTTCTGGAC CC ATGAGTCC			
			C GA _			
GAM1924	PHLDA3	3'	CTGCTGCTTAGGTCCTTTT	14759	T	ATT TT
			AAAAG GATTTGGG GC AG			
			TTTTCTGGATTC CG TC			
			_ GT_ _			
GAM1924	PPP1R8	3'	TAGGTCTCCCACTTTCTAGGAT	15341	_____	TTGCTTAGG
	CATTTT		ATT TGGGA			
			TAG ACCCT			
			GATCTTTC CT GGATT			
GAM1924	PPP1R8	3'	TAGGTCTCCCACTTTCTAGGAT	8571	_____	TTGCTTAGG
	CATTTT		ATT TGGGA			
			TAG ACCCT			
			GATCTTTC CT GGATT			
GAM1924	PPP1R8	3'	TAGGTCTCCCACTTTCTAGGAT	28857	_____	TTGCTTAGG
	CATTTT		ATT TGGGA			
			TAG ACCCT			
			GATCTTTC CT GGATT			
GAM1924	PRKACB	3'	GGAAATTTCAAGCACTTTT	8603	A	GG G
			AAAAGTG TTTG ATT CT			

		TTTTCAC GAAC TAA GG	
		_ TT A	
GAM1924 PRKAR1A	3'	CAATTCTGAAATACTTTT 8606	A TG
		AAAAGTG TT GGATTG	
		TTTTCAT AA CTTAAC	
		A GT	
GAM1924 PRPS2	3'	GTATTTCTGGATCATTTT 8656	TG T
		AAAAGTGATT GGA TGC	
		TTTTTACTAG CTT ATG	
		GT T	
GAM1924 PSA	3'	CCTAGAAGTTCTTGATTCATTT 27739	T TG TTGC
TT		AAAAGTGA T GGA TTAGG	
		TTTTTACT A TCT GATCC	
		T GT TGAA	
GAM1924 PSA	3'	CCTAGAAGTTCTTGATTCATTT 22130	T TG TTGC
TT		AAAAGTGA T GGA TTAGG	
		TTTTTACT A TCT GATCC	
		T GT TGAA	
GAM1924 PSCDBP	3'	TTTATGCTTCTTAAATCATTTT 10501	TT T
T		AAAAGTGATTTGGGA GC TAGG	
		TTTTTACTAAATTCT CG ATTT	
		T_ T	
GAM1924 PTER	3'	CCTAAGCGGAGTTGTTGTTTTT 24996	TG TTGGGA
		AAAAG AT TTGCTTAGG	
		TTTTT TG GGCGAATCC	
		GT TTGA__	
GAM1924 PTER	3'	CTTGAGCGATCTAATGTTTCTT 24997	T TTG
		AAG GAT GGATTGCTTAGG	
		TTC TTG TCTAGCGAGTTC	
		T TAA	
GAM1924 PTP4A2	3'	CTTAAGCCCACCTGGGCACTTT 9552	A TG ATT
T		AAAAGTG TT GG GCTTAGG	
		TTTTCAC GG CC CGAATTC	
		_ GT ACC	
GAM1924 PTPRG	5'	GCGTTCCCGGTCACTTTT 8727	T T
		AAAAGTGATT GGGA TGC	
		TTTTCACTGG CCCT GCG	
		_ T	
GAM1924 PTPRO	3'	CTTGCTTCCAGATTGTTTT 8740	TG TT TT
		AAAG ATTTGGGA GC AG	

			TTTT TAGACCTT CG TC		
			GT __ T_		
GAM1924	PTPRO	3'	CTTGCTTCCAGATTGTTTT 25005	TG	TT TT
			AAAG ATTTGGGA GC AG		
			TTTT TAGACCTT CG TC		
			GT __ T_		
GAM1924	PTPRO	3'	CTTGCTTCCAGATTGTTTT 25013	TG	TT TT
			AAAG ATTTGGGA GC AG		
			TTTT TAGACCTT CG TC		
			GT __ T_		
GAM1924	PTPRO	3'	CTTGCTTCCAGATTGTTTT 25022	TG	TT TT
			AAAG ATTTGGGA GC AG		
			TTTT TAGACCTT CG TC		
			GT __ T_		
GAM1924	PTPRO	3'	CTTGCTTCCAGATTGTTTT 25033	TG	TT TT
			AAAG ATTTGGGA GC AG		
			TTTT TAGACCTT CG TC		
			GT __ T_		
GAM1924	RAB11A	3'	TTTGTAATTCTTGTGTCACCTT 11036	TT_	TTAGG
	T		AAAAGTGAT GGGATTGC		
			TTTTCACTG TCTTAATG		
			TGT TTT		
GAM1924	RGL	3'	CCTGGGAAGTTGAGGTCACCTT 17506	G	ATTG
	T		AAAAGTGATTT GG CTTAGG		
			TTTTCACTGGA TT GGGTCC		
			G GAA_		
GAM1924	RNASE1	5'	CTGACAGGATTTTAGGTCACTT 31944	GC_	G
	T		AAAGTGATTTGGGATT TTAG		
			TTTCACTGGATTTTAG AGTC		
			GAC		
GAM1924	RNF14	3'	CCTAACTTTCTGAATTATTTTT 10504	TG	TTGC
			AAAAGTGATT GGA TTAGG		
			TTTTTATTAA CTT AATCC		
			GT TC__		
GAM1924	RS1	3'	CATTTCCGAGTTACTTTT 5874	T	
			AAAAGTGATTTGGGA TG		
			TTTTCATTGAGCCTT AC		
			T		
GAM1924	RTN1	3'	CTTAGGATATTTGAGTCACTT 22109	TG	ATTG
			AAGTGATT GG CTTAGG		

TTCACTGA TT GGATTC
 GT ATA_
 GAM1924 RUNX1 3' CTACAGCTTTGGGTCATTTTT 7498 TG ATT _
 AAAAGTGATT GG GCT TAG
 ||||| || |||
 TTTTACTGG TT CGA ATC
 GT _ C
 GAM1924 RUNX3 3' CCTAGGTGGTCTCATAATTCCA 10549 ATT__ TG
 TTT AGTG TGGGAT CTTAGG
 ||| ||||| |||||
 TTAC ACTCTG GGATCC
 CTTAAT GT
 GAM1924 SAR1 3' TCTGTAGCTTTTCCAGGTTTTT 21353 T TT _
 TTT AAAAG GATTTGGGA GCT TAGG
 |||| ||||| ||| |||
 TTTT TTGGACCTT CGA GTCT
 T TT T
 GAM1924 SDC4 3' TCTAGGCTCTTTCAAGTGACTT 8893 G GG TT
 TT AAAAGT ATTTG A GCTTAGG
 |||| |||| | |||||
 TTTTCA TGAAC T CGGATCT
 G TT CT
 GAM1924 SERPINB13 3' CCTAGGCACCACTGAGTTGTTT 14762 TG TG GAT
 T AAAG ATT G TGCTTAGG
 ||| || | |||||
 TTTT TGA C ACGGATCC
 GT GT ACC
 GAM1924 SF1 3' GCAAAGCAGCCTGAGTTATTTT 11002 TG A AGG
 T AAAAGTGATT GG TTGCTT
 ||||| || |||||
 TTTTATTGA CC GACGAA
 GT _ ACGG
 GAM1924 SH3GL2 3' GTAATTCCAAATTATTTTT 8968
 AAAAGTGATTTGGGATTGC
 |||||
 TTTTATTAAACCTTAATG

 GAM1924 SLC29A1 3' CCTGAGTGGTCTGGCGGTTTT 11398 G ATTTG TG
 AAAA TG GGAT CTTAGG
 ||| || ||| |||||
 TTTT GC TCTG GAGTCC
 G GG__ GT
 GAM1924 SNRPN 5' CCTGGTAACATTTTCATATTGCT 23083 TG T GG _ T
 TTT AAAG AT TG AT TGCT AGG
 ||| ||| || ||| |||
 TTTC TA AC TA ATGG TCC
 GT T TT CA _
 GAM1924 SNRPN 5' CCTGGTAACATTTTCATATTGCT 23085 TG T GG _ T
 TTT AAAG AT TG AT TGCT AGG
 ||| ||| || ||| |||

			TTTC TA AC TA ATGG TCC		
			GT T TT CA _		
GAM1924	SOCS4	3'	CCTAAGTAGTTTTTCATTATTT 28109	TT	
	T		AAAGTGAT GGGATTGCTTAGG		
			TTTTATTA TTTTGATGAATCC		
			CT		
GAM1924	SPOCK	3'	CCTAGTAAATTCTGAATGCTTT 31456	G TG GC	
	T		AAAAGT ATT GGATT TTAGG		
			TTTTCG TAA CTAA GATCC		
			_ GT AT		
GAM1924	ST3GALVI	5'	CCTGGGCCTCGGCGGGTCACT 12746	GGATT	
			AGTGATTTG GCTTAGG		
			TCACTGGGC CGGGTCC		
			GGCTC		
GAM1924	STAT3	3'	CTTTGTGGTTCCAGATTTTTTT 9123	T TG TT G	
	T		AAAAG GATTTGGGAT C AG		
			TTTTT TTAGACCTTG G TC		
			T GT TT		
GAM1924	STAT3	3'	TTTGAGCAATCTGGGCACTTTT 9124	AT G	
			AAAAGTG TT GGATTGCTTAGG		
			TTTTCAC GG TCTAACGAGTTT		
			_ G		
GAM1924	STAT3	3'	CTTTGTGGTTCCAGATTTTTTT 29270	T TG TT G	
	T		AAAAG GATTTGGGAT C AG		
			TTTTT TTAGACCTTG G TC		
			T GT TT		
GAM1924	STAT3	3'	TTTGAGCAATCTGGGCACTTTT 29271	AT G	
			AAAAGTG TT GGATTGCTTAGG		
			TTTTCAC GG TCTAACGAGTTT		
			_ G		
GAM1924	TR2	3'	AAGTACTTGAATTGCTTTT 35792	TG TG AT	
			AAAAG ATT GG TGCTT		
			TTTTC TAA TC ATGAA		
			GT GT _		
GAM1924	TRPM6	3'	GCCTGGGTTTGAAAAATTCCAA 19202	T _____	
			CTTATTTTT A TTGGGATT GCTTAGG C		
			T AACCTTAA TGGGTCC G		
			C AAAGTT		
GAM1924	TSN	3'	TTTAGTATACCGGAATTACTTT 10989	G AT TAGG	
	T		AAAAGTGATTT GG TGCT		

			TTTTCATTAAG CC ATGA	
			G AT TTT	
GAM1924	TTC3	5'	CTTGGGCATAGGTTCCAAGTAT 9315	G ____
		TTTT	AAGT ATTTGGGAT TGCTTAGG	
			TTTA TGAACCTTG ACGGGTTC	
			_ GAT	
GAM1924	UPF3B	3'	TTTGGGTGGAGCAGAGTCGCTT 27935	GGGA TG
		T	AAAGTGATTT T CTTAGG	
			TTTCGCTGAG G GGGTTT	
			ACGA GT	
GAM1924	UPF3B	3'	TTTGGGTGGAGCAGAGTCGCTT 23274	GGGA TG
		T	AAAGTGATTT T CTTAGG	
			TTTCGCTGAG G GGGTTT	
			ACGA GT	
GAM1924	VPS26	3'	TCTGGGTAATTTTCATGTTTATT 11328	TT_ GG
			AGTGA TG ATTGCTTAGG	
			TTATT AC TAATGGGTCT	
			TGT TT	
GAM1924	YWHAG	3'	TTTAAGCAGCTTGAATGGTTTT 14859	TG TG A
		T	AAAAG ATT GG TTGCTTAGG	
			TTTTT TAA TC GACGAATTT	
			GG GT _	
GAM1924	YWHAZ	3'	TTTTGTGCTTCCAAATCACTTT 9446	TT TTAGG
		T	AAAAGTGATTTGGGA GC	
			TTTTCACTAAACCTT TG	
			CG TTTT	
GAM1924	YY1	3'	TTTAAACCCATTTTAGTCACTT 9438	____ A CTTAGG
		TT	AAGTGATT TGGG TTG	
			TTCACTGA ACCC AAT	
			TTTT A TT G	
GAM1924	ZFP103	5'	CCTGGGCGGATCTGAGTTATTT 12219	TG A
		TT	AAAAGTGATT GG TTGCTTAGG	
			TTTTTATTGA CT GGCGGGTCC	
			GT A	
GAM1924	ZNF135	3'	TTTAGTTATCCCTGCATTATTT 9491	TT_ T TAGG
		TT	AAAAGTGAT GGGAT GCT	
			TTTTTATTA CCCTA TGA	
			CGT T TTT	
GAM1924	ZNF264	3'	GCATCCTAGGGTGCTTTT 9456	GA T
			AAAAGT TTTGGGAT GC	

TTTTCG GGATCCTA CG
 TG _
 GAM1924 AF311304 3' TGTAAGGGATCTTGAGTTGTT 25261 TG TG G AGG
 TT AAAG ATT GGATT CTT
 |||| ||| ||||| |||
 TTTT TGA TCTAG GAA
 GT GT G ATGTC
 GAM1924 AKAP11 3' CTAGGATAAATCACTTTT 18370 GGATTG
 AAAAGTGATTTG CTTAG
 ||||| ||||| |||||
 TTTTCACTAAAT GGATC
 A_____
 GAM1924 AKAP5 5' TTTGAGTAATCTCAAATAATCT 11266 TG_
 AG ATTTGGGATTGCTTAGG
 || ||||| ||||| |||||
 TC TAAACTCTAATGAGTTT
 TAA
 GAM1924 ALS2CR3 3' GCATATTCCAATTCACCTTTT 17413 T _
 AAAAGTGA TTGGGAT TGC
 ||||| ||||| |||||
 TTTTCACT AACCTTA ACG
 T T
 GAM1924 ARAP3 5' CCTAAGTAGAGAGCCATTGCT 22855 TG TT GA_
 AG A TGG TTGCTTAGG
 || | ||| ||||| |||||
 TC T ACC GATGAATCC
 GT__ GAGA
 GAM1924 ARTS-1 3' TTTAGCATCTTCAAATTTCTTT 18563 T AT TAGG
 T AAAAG GATTTGGG TGCT
 ||||| ||||| |||||
 TTTTC TTAAACTT ACGA
 T CT TTT
 GAM1924 ATP1B4 3' TCTGGTAGCACCTGAATTCTTT 14326 T TG AT _
 T AAAAG GATT GG TGCT TAGG
 ||||| ||||| ||| ||||| |||||
 TTTTC TTAA CC ACGA GTCT
 _ GT _ TG
 GAM1924 ATP9A 3' CTTGGGTTTTC AAGTTGCTT 31082 TG GG TT
 AAG ATTTG A GCTTAGG
 ||| ||||| | ||||| |||||
 TTC TGAAC T TGGGTTT
 GT TT_
 GAM1924 BCAA 3' CTTGGCACTTAAGTGCACTTTT 18511 _ AT T
 AAAAGTG ATTTGGG TGCT AG
 ||||| ||||| ||||| ||||| |||||
 TTTTCAC TGAATTC ACGG TC
 G _ T
 GAM1924 BIVM 3' CTTAAGCATGAAGTGACTTTT 19254 G GGGAT
 AAAAGT ATTT TGCTTAGG
 ||||| ||||| ||||| ||||| |||||

		TTTTCA TGAA ACGAATTC	
		G GT__	
GAM1924 BS69	3'	TTTCAGCAAATTTTAAACATT 13408	A _ TAGG
	TTT	AAAAGTG TTTGGGATT GCT	
		TTTTTAC AAATTTTAA CGA	
		A A CTTT	
GAM1924 C11orf25	5'	TTTGTTGCTCTGATCTTAAGTT 25403	T __ TTAGG
	TCTTTT	AG GATTTGGGATT GC	
		TC TTGAATTCTAG CG	
		T TCT TTGTTT	
GAM1924 C1orf16	3'	CTGTAGGATTTCAAATTAC 16856	GG G _ G
		GTGATTTG ATT CT TAG	
		CATTAAAC TAG GA GTC	
		TT _ T	
GAM1924 C1orf24	3'	CCTGCCTCCTTGAGTCACTTT 27530	TG ATT TT
		AAAGTGATT GG GC AGG	
		TTTCACTGA TC CG TCC	
		GT CTC _	
GAM1924 C1QTNF6	3'	TCTAGAATTCTCCCAACATTAT 25659	_ TTGC_
	TTTT	AAAGTGAT TTGGGA TTAGG	
		TTTTATTA AACCT GATCT	
		C CTAA	
GAM1924 C20orf142	3'	TGGAGCAATAAGATTACTTTT 36933	TGGG AGG
		AAAAGTGATT ATTGCTT	
		TTTTCATTAG TAACGAG	
		AA__ GTT	
GAM1924 C20orf36	3'	TTTAAGTAACTGAGTCATTTTT 20224	TG GA
		AAAAGTGATT G TTGCTTAGG	
		TTTTTACTGA C AATGAATTT	
		GT__	
GAM1924 C20orf55	5'	TAGTCTCGAGTTTTTTTT 25407	T
		AAAAG GATTTGGGATTG	
		TTTTT TTGAGCTCTGAT	
		T	
GAM1924 CBARA1	3'	AGTTCTCAAATCGTTTTT 12722	TT
		AAAAGTGATTTGGGA GCT	
		TTTTTGCTAAACTCT TGA	
		—	
GAM1924 CCR6	5'	TTTGGGCAAATAGGCGTTACTT 25378	TTGGGA
	TT	AAAAGTGAT TTGCTTAGG	

TTTTCATTG AACGGGTTT
 CGGATA
 GAM1924 CECR1 3' CCTGGGTGGTCTCATCCATTCC 18882 T TT___ TG
 TTT AAG GA TGGGAT CTTAGG
 ||| || ||||| |||||
 TTC CT ACTCTG GGGTCC
 _ TACCT GT
 GAM1924 CGI-127 3' TGGTCCTGTGTTGCTTTT 18137 TG T
 AAAAG AT TGGGATTG
 ||||| || |||||
 TTTTC TG GTCCTGGT
 GT T
 GAM1924 CIP29 3' CTAGGAAGTGAATCTTTT 26149 T TG GATTG
 AAAAG GATT G CTTAG
 ||||| ||| | |||||
 TTTT CTAA C GGATC
 _ GT AA___
 GAM1924 CNM4 3' CTTGCTCCCAAGTCCTTTT 21426 T TT TT
 AAAAG GATTGGA GC AG
 ||||| ||||| || ||
 TTTTC CTGAACCCT CG TC
 _ _ T_
 GAM1924 CNOT8 3' TTTGGGTCTTGAGTTGTTTT 11182 TG TG TT
 AAAG ATT GGA GCTTAGG
 |||| ||| || |||||
 TTTT TGA TCT TGGGTTT
 GT GT _
 GAM1924 COLEC12 3' TGGTCGGTGAGGCCCGGGTTAT 25072 A_ TG TAGG
 TTTT AAAGTGATTGGA T CT
 ||||| ||||| | ||
 TTTTATTGGGCCC A GG
 GG GT CTGGTT
 GAM1924 COPS7B 3' CTTGAACAGTTTCAGGTTAT 22934 GG C
 GTGATTG ATTG TTAGG
 ||||| ||||| |||||
 TATTGGAC TGAC AGTTC
 TT A
 GAM1924 CTCF 3' TGATTTCAAACACTTTT 13335 A GG
 AAAAGTG TTTG ATTG
 ||||| ||||| |||||
 TTTTCAC AAAC TAGT
 _ TT
 GAM1924 CYorf15B 5' ATTATGCTTCTAGGTTACTTTT 26304 TT T G
 AAAAGTGATTGGA GC TAG
 ||||| ||||| || |||||
 TTTTCATTGGATCTT CG ATT
 _ T AT
 GAM1924 DDM36 3' TGGAGCTTCCTAAGTTGCTTT 21956 TG TT AGG
 AAAG ATTTGGA GCTT
 |||| ||||| |||||

			TTTC TGAATCCT CGAG		
			GT T_ GTT		
GAM1924	DDX18	3'	GAAAAGAGTCTCAGGTTATTTT 13646	G	AGG
	T		AAAAGTGATTTGGGATT CTT		
			TTTTTATTGGACTCTGA GAA		
			_ AAGA		
GAM1924	DGCR8	5'	GTAAACTAGTCTTAAGCGCTTT 22920	A	CTTAGG
	T		AAAAGTG TTTGGGATTG		
			TTTTCGC GAATTCTGAT		
			_ CAAATGT		
GAM1924	dJ309H15.1	3'	GGGGGCTTCCAAGTTGTTT 28888	TG	TT AGG
			AAG ATTTGGGA GCTT		
			TTT TGAACCTT CGGG		
			GT _ GGT		
GAM1924	DKFZp434D177	5'	TCTGAGCGAGCGCGGTGCTTTT 38779		ATTTGGGA
			AAAAGTG TTGCTTAGG		
			TTTTCGT AGCGAGTCT		
			GGCGCG_		
GAM1924	DKFZP564B1023	3'	TAATCCCTGAGTTCTTTT 25344	T	_
			AAAAG GATTT GGGATTG		
			TTTTC TTGAG CCCTAAT		
			_ T		
GAM1924	DKFZP564I0422	3'	TCTAGTGTGGTTTCAAATAACT 25437	G	GG TG _
	TTT		AAAAGT ATTTG AT C TTAGG		
			TTTTCA TAAAC TG G GATCT		
			A TT GT T		
GAM1924	DKFZp566H0824	5'	TCTGAGTGATTTTAATTTGT 18980	TG T	TG
			G A TTGGGAT CTTAGG		
			T T AATTTTA GAGTCT		
			GT T GT		
GAM1924	DKFZp761D081	3'	CTTATAAAGGTCCCAGGATCAC 19104	_	GCT_
	TTTT		AAAGTGATT TGGGATT TAGG		
			TTTCACTAG ACCCTGG ATTC		
			G AAAT		
GAM1924	DKFZp761G0313	3'	GCTTAGGCAGCATTGATTTAGG 32741	A	_____
	TCACTTT		GATTTGGG TTGCTTAGG C		
			CTGGATTT GACGGATTC G		
			AGTTAC		
GAM1924	DKFZp761G2113	3'	CTTAGCGCTTTTAAGTTATTT 34643	T	T G
			AAGTGATTTGGGA TGCT AG		

TTTATTGAATTTT GCGA TC
 C T
 GAM1924 DKFZp761H079 3' TTTAGGTGATTCTAATTC 29601 T TG
 GA TTGGGAT CTTAGG
 || ||||| |||||
 CT AATCTTA GGATTT
 T GT
 GAM1924 DKFZp762A227 3' CCTGGTCTGGTCTCAGAATCAC 19106 _ _ T
 TTTT AAGTGAT TTGGGATT GCT AGG
 ||||| ||||| || |||
 TTCACTA GACTCTGG TGG TCC
 A TC _
 GAM1924 DKFZp762A227 3' CCTGGTCTGGTCTCAGAATCAC 15318 _ _ T
 TTTT AAGTGAT TTGGGATT GCT AGG
 ||||| ||||| || |||
 TTCACTA GACTCTGG TGG TCC
 A TC _
 GAM1924 DNAJB5 3' TTGAGCACGAGACACTTTT 14589 A GGAT
 AAAAGTG TTTG TGCTTAG
 ||||| ||| |||||
 TTTTCAC GAGC ACGAGTT
 A _
 GAM1924 ELL2 3' GTATTAGTAAACTTGAGTTACT 14368 TG A TAGG
 TTT AAAAGTGATT GG TTGCT
 ||||| || |||||
 TTTTCATTGA TC AATGA
 GT A TTATGA
 GAM1924 ELOVL2 3' TTTGAGTTCATAAATCATTT 19390 G TT
 AAGTGATTTG GA GCTTAGG
 ||||| || |||||
 TTTACTAAAT CT TGAGTTT
 A _
 GAM1924 FGF19 3' TTTATGCCCCCAAATTAT 11596 ATT T
 GTGATTTGGG GC TAGG
 ||||| || |||||
 TATTAAACCC CG ATTT
 C_ T
 GAM1924 FHX 3' GGCCCTAAATTGTTTTT 20461 TG ATT
 AAAAG ATTTGGG GCT
 |||| ||||| |||
 TTTTT TAAATCC CGG
 GT _
 GAM1924 FLJ10246 3' TCTGCTTGCTTCAAATTACTTT 19786 _ ATT TTAGG
 T AAAAGTGATTTGG G GC
 ||||| ||| ||
 TTTTCATTAAACT C CG
 T GTT TCT
 GAM1924 FLJ10298 3' CCTGGGTGATTTTTGTATTTTT 19808 ATTT TG
 AAAAGTG GGGAT CTTAGG
 ||||| |||| |||||

		TTTTTAT TTTTA GGGTCC			
		GT__ GT			
GAM1924	FLJ10535	3' CCTGGCCAATCAGATTGTTTT 19918	TG	GATT	T
		AAAG ATTTGG GCT AGG			
		TTTT TAGACT CGG TCC			
		GT AAC_ _			
GAM1924	FLJ10535	3' TAATTCCATAATTATTTTT 19921	_		
		AAAAGTGATT TGGGATTG			
		TTTTTATTAA ACCTTAAT			
		T			
GAM1924	FLJ10539	3' CTTAGGTGGTTTTATTCATT 19924	TT	TG	
		AGTGA TGGGAT CTTAGG			
		TTACT ATTTTG GGATTC			
		T_ GT			
GAM1924	FLJ10724	3' GAAAGTGGAATCCTGAATCTC 20052	T	TG	TAGG
		TTTT AAAAG GATT GGATTGCT			
		TTTTC CTAA CCTAATGG			
		T GT TGAAAGT			
GAM1924	FLJ10898	3' TTTAGGTAATAATGTATTACTT 29896	TTGGG		
		T AAAGTGAT ATTGCTTAGG			
		TTTCATTA TAATGGATTT			
		TGTAA			
GAM1924	FLJ10961	3' CTTACAGCAATTACAGATTATT 31776	GG	_	
		TTT AAAAGTGATTTG ATTGCT TAGG			
		TTTTTATTAGAC TAACGA ATTC			
		AT C			
GAM1924	FLJ11040	3' CTTATGTTAGTCTCTAAATTAT 20296	_	_	T
		TTTT AAAGTGATTTGG GATTG C TAGG			
		TTTTATTAAATC CTGAT G ATTC			
		T TT			
GAM1924	FLJ11267	3' TTTGAGTAATTTTGGGCAAGCT 21226	GA_	TG	
		AGT TT GGATTGCTTAGG			
		TCG GG TTTAATGAGTTT			
		AAC GT			
GAM1924	FLJ11275	3' CCTGACAGTATTTTTGAATTAT 20403	TG	T	_
		TT AAGTGATT GGA TGCT TAGG			
		TTTATTAA TTT ATGA GTCC			
		GT T CA			
GAM1924	FLJ11320	3' CCTGATGCCCTGAGTTGTTT 20426	TG	TG	ATT _
		AAG ATT GG GC TTAGG			

TTT TGA CC CG AGTCC
 GT GT ____ T
 GAM1924 FLJ11506 3' CCTGGGTGATTGGGTTTTCT 23968 T_ TG G TG
 AG GATT G AT CTTAGG
 || ||| | || ||||
 TC TTGG T TA GGGTCC
 TT GT_ GT
 GAM1924 FLJ12619 3' CCTGGATTTTTTTAAATCATTT 25209 TTGC
 TT AAAAGTGATTGGGA TTAGG
 ||||| ||||
 TTTTACTAAATTTT GGTCC
 TTTA
 GAM1924 FLJ12960 3' CCTGGGCAATTCACCTTAACCTT 23914 GATTTG
 AAGT GGATTGCTTAGG
 ||| |||||
 TTCA CTTAACGGGTCC
 ATTCA_
 GAM1924 FLJ13188 3' CTTGGTATAAAATCACTTTT 22606 GGGAT T
 AAAAGTGATT TGCT AG
 ||||| ||| ||
 TTTTCACTAAA ATGG TC
 AT____ T
 GAM1924 FLJ13213 3' TTTAGGTAATCTGCACT 24101 ATTTG
 AGTG GGATTGCTTAGG
 ||| |||||
 TCAC TCTAATGGATT
 G____
 GAM1924 FLJ13614 3' TTTGAGCTCTCTTAATTGCTTT 29152 TG T TT
 T AAAAG ATT GGGA GCTTAGG
 |||| ||| ||| |||||
 TTTTC TAA TTCT CGAGTTT
 GT _ CT
 GAM1924 FLJ13646 3' GCCTAAATGCTTTAGTTTTAGG 23812 ____
 TCATTT GATTGGGATT GC TTAGG C
 ||||| || |||| |
 CTGGATTTTGA CG AATCC G
 TTT TA
 GAM1924 FLJ14054 5' CTTAAGTAATTCTATAGGATTT 23784 GATT
 T AAAGT TGGGATTGCTTAGG
 |||| |||||
 TTTTA ATCTTAATGAATTC
 GGAT
 GAM1924 FLJ14100 5' TCTGAGGGCTCCTGGGTCCT 24615 TG TTG
 AGTGATT GGA CTTAGG
 ||||| ||| |||||
 TCACTGG CCT GAGTCT
 GT CGG
 GAM1924 FLJ14641 3' TCTGGGCAATCATTTATTTT 26588 TTTGG
 AAAGTGA GATTGCTTAGG
 ||||| |||||

TTTTATT CTAACGGGTCT
 TA____
 GAM1924 FLJ14803 3' TAATTTTATATCGCTTTT 26629 T
 AAAAGTGAT TGGGATTG
 ||||| |||||
 TTTTCGCTA ATTTTAAT
 T
 GAM1924 FLJ20038 3' CCTAAGACTCTTTTCAGGTTCA 19140 _ GG TTG_
 TTTT AGTGA TTTG A CTTAGG
 |||| ||| | ||||
 TTACT GGAC T GAATCC
 T TT TCTCA
 GAM1924 FLJ20051 3' TCTGCAGCATTCTTGAATATTT 21165 A TG T _
 TT AAAAGTG TT GGA TGCT TAGG
 ||||| || ||| ||| ||||
 TTTTAT AA TCT ACGA GTCT
 _ GT T C
 GAM1924 FLJ20079 3' CTTGAGCAGTTTTCCAGTTTTT 19173 T T _
 T AG GA TTGG GATTGCTTAGG
 || ||| |||||
 TC TT GACC TTGACGAGTTC
 T T TT
 GAM1924 FLJ20136 3' CCTGGGTAATTTTTTTTTTTTTT 19230 T TTT
 T AAAAG GA GGGATTGCTTAGG
 |||| || |||||
 TTTT TT TTTTAATGGGTCC
 T TT_
 GAM1924 FLJ20152 5' TCTGAGTAAGGGAGGAGCACTT 21072 A GGGA
 TT AAAAGTG TTT TTGCTTAGG
 ||||| ||| |||||
 TTTTCAC AGG AATGAGTCT
 G AGGG
 GAM1924 FLJ20277 3' CCTGGAGGGCCTGGATTTCCTT 19330 T TG ATTG T
 T AAAAG GATT GG CT AGG
 |||| ||| || |||
 TTTTC TTAG CC GG TCC
 T GT GGGA _
 GAM1924 FLJ20373 3' TTATGGTATATTTTAAGTGA CT 19428 G _ TAGG
 TTT AAAAGT ATTTGGGAT TGCT
 |||| ||||| ||||
 TTTTCA TGAATTTTA ATGG
 G T TATTT
 GAM1924 FLJ20396 3' GTTTAGGTGGTCCTGAATC 19446 TG TG
 GATT GGAT CTTAGG T
 ||| ||| |||| |
 CTAA CCTG GGATTT G
 GT GT
 GAM1924 FLJ20445 3' CAGGGCTTCCAGATCACTTTT 19478 TT AGG
 AAAAGTGATTTGGGA GCTT
 ||||| ||||| ||||

TTTTCACTAGACCTT CGGG
 — ACA
 GAM1924 FLJ20449 3' TCTAGGTGGTCTTTTCCTTATT 19487 TTT_ TG
 T AAGTGA GGGAT CTTAGG
 ||||| ||||| |||||
 TTTATT TTCTG GGATCT
 CCTT GT
 GAM1924 FLJ21415 3' TCTAGGCAGTTATTTTTGTTT 24078 TG TTTGG
 AAG A GATTGCTTAGG
 ||| | |||||
 TTT T TTGACGGATCT
 GT TTTA_
 GAM1924 FLJ22029 3' TCTGAGCCTAGAACTTTAATTA 24507 TG A ____
 CTTTT AGTGATT GG TT GCTTAGG
 ||||| || |||||
 TCATTAA TC AG CGAGTCT
 TT A ATC
 GAM1924 FLJ23151 3' TTTGAGCAGTCCCTGCTGACAT 24137 ATTT_
 TT AAGTG GGGATTGCTTAGG
 ||||| |||||
 TTTAC CCCTGACGAGTTT
 AGTCGT
 GAM1924 FLJ23511 3' TGATCTCAGATTTCTTTT 25968 T
 AAAAG GATTTGGGATTG
 ||||| |||||
 TTTTC TTAGACTCTAGT
 T
 GAM1924 FLJ23563 3' TTAAAGTGATCTTTTGTGATTT 33565 G TT TG
 T AAAGT AT GGGAT CTTAGG
 ||||| || ||||| |||||
 TTTTA TG TTCTA GAATTT
 G TT GT
 GAM1924 FUBP3 3' TCTAAGACCTCCAAGCTTGTTT 31876 TG_ ATTG
 TT AAAAG A TTTGGG CTTAGG
 ||||| | ||||| |||||
 TTTTT T GAACCT GAATCT
 GT C CCA_
 GAM1924 GOLGA1 3' TCTAAGTGATTTAATGCACTTT 7864 ATTTG TG
 AAAGTG GGAT CTTAGG
 ||||| ||| |||||
 TTTCAC TTTA GAATCT
 GTAA_ GT
 GAM1924 GOLPH3 3' CAGTACCAATCTTGAGTTTCTT 22686 T TG CTTAGG
 TT AAAAG GATT GGATTG
 ||||| ||||| |||||
 TTTTC TTGA TCTAAC
 T GT CATGACC
 GAM1924 GREB1 3' TCTAAAGAATCTTGGGTTATTT 16125 TG GC
 T AAAGTGATT GGATT TTAGG
 ||||| ||||| |||||

		TTTTATTGG TCTAA AATCT	
		GT GA	
GAM1924 GRID1	3'	CCTAGGCAATCCATTGACATTT 33979	ATTTG
		AAGTG GGATTGCTTAGG	
		TTTAC CCTAACGGATCC	
		AGTTA	
GAM1924 H2AV	3'	TTAAAGTAATTTTCAGAGCACTT 28913	A GG AGG
TT		AAAAGTG TTTG ATTGCTT	
		TTTTCAC AGAC TAATGAA	
		G TT ATTT	
GAM1924 HH114	3'	CCTGGCATGTTCTAAACTGTTT 26250	GT A _ T
TT		AAAA G TTTGGGAT TGCT AGG	
		TTTT T AAATCTTG ACGG TCC	
		TG C T _	
GAM1924 HRH4	3'	CCTGGGTGTCAATAATTATTTT 22260	TGG T
T		AAAAGTGATT GAT GCTTAGG	
		TTTTTATTAA CTG TGGGTCC	
		TAA _	
GAM1924 HSNV1	3'	CCTAGGAACCTTCCCACAATTG 18965	TG _ TTG__
TTTTT		AG ATT TGGGA CTTAGG	
		TT TAA ACCCT GGATCC	
		GT C TCCAA	
GAM1924 HSPC019	3'	TCTAGTTTCCCTAGAGTCATTT 15252	_ TT T
TT		AAAAGTGATTT GGGG GCT AGG	
		TTTTTACTGAG CCCT TGA TCT	
		AT T_ _	
GAM1924 IBTK	3'	TTGGAGTCATTGTGGGTTATTT 33519	TT G T AGG
TT		AAAAGTGAT G GAT GCTT	
		TTTTTATTG T TTA TGAG	
		GG G C GTTT	
GAM1924 IL14	5'	TTTGGGTGATCTCTTGTC A 45707	TT TG
		TGAT GGGAT CTTAGG	
		ACTG CTCTA GGGTTT	
		TT GT	
GAM1924 KCND1	5'	TCTAGGCAGTCCCAAGACAC 11428	A
		GTG TTTGGGATTGCTTAGG	
		CAC GAACCCTGACGGATCT	
		A	
GAM1924 KIAA0133	3'	TTTAAGAAATAATCCTAATTGT 16611	TG T _
TTTT		AAG ATT GGGATTG CTTAGG	

		TTT TAA TCCTAAT GAATTT	
		GT _ AAA	
GAM1924 KIAA0210	3'	CAATTTAGAATCACTTTT 16420	GG
		AAAAGTGATTT GATTG	
		TTTTCACTAAG TTAAC	
		AT	
GAM1924 KIAA0218	5'	TTTAGTCAATTTTGGATCGCTT 16520	TG _ TAGG
	T	AAAGTGATT GGATTG CT	
		TTTCGCTAG TTAAAC GA	
		GT T TTT	
GAM1924 KIAA0232	3'	CTGGGCTGAGATTGTTTTT 36035	TG G GATT
		AAAAG ATTT G GCTTAG	
		TTTTT TAGA T CGGGTC	
		GT G ____	
GAM1924 KIAA0252	3'	TCTATAGCTGTTTCAGATTTTTT 31450	T GG T _
	TT	AAAG GATTTG AT GCT TAGG	
		TTTT TTAGAC TG CGA ATCT	
		T TT T T	
GAM1924 KIAA0322	3'	TCTGAGCAGAGCCACCATTTTT 44562	ATT GA
		AAAAGTG TGG TTGCTTAGG	
		TTTTTAC ACC GACGAGTCT	
		C__ GA	
GAM1924 KIAA0332	3'	TCTGAGCAACTACTTACTTTTT 31421	TTTG A
		AAAAGTGA GG TTGCTTAGG	
		TTTTCATT TC AACGAGTCT	
		CA__ _	
GAM1924 KIAA0408	3'	CTTCACAATTTTAAGCCACTTT 16233	AT CTT G
	T	AAAAGTG TTGGGATTG AG	
		TTTTCAC AATTTTAAC TC	
		CG ACT	
GAM1924 KIAA0417	3'	CTTGGGTAATCCACTAGGGCTT 35289	GATTTG
	TT	AAAAGT GGATTGCTTAGG	
		TTTTCG CCTAATGGGTTC	
		GGATCA	
GAM1924 KIAA0438	3'	TTTGATCATATCTTGGATCCTT 16786	T TG _ C
	TT	AAAAG GATT GGAT TG TTAGG	
		TTTTC CTAG TCTA AC AGTTT	
		_ GT T T	
GAM1924 KIAA0478	3'	TCCATGGGGTCCCGGTGTTGTT 16986	TG _ TG _
	TTT	AAG AT TTGGGAT CTTA GG	

TTT TG GGCCCTG GGGT CC
 GT T A TT
 GAM1924 KIAA0493 5' CCTGGGCAGTCCTCTGGTT 32139 T_
 GATT GGGATTGCTTAGG
 |||| |||||
 TTGG TCCTGACGGGTCC
 TC
 GAM1924 KIAA0565 3' TTTAGTGTGCCTGGGGTCACTT 33224 _TG ATT TAGG
 TT AAAAGTGAT T GG GCT
 ||||| | || |||
 TTTTCACTG G CC TGA
 G GT GTG TTT
 GAM1924 KIAA0648 3' TCTGATGGTCTGGGCTCATTTT 40221 T G C
 T AAAAGTGA TT GGATTG TTAGG
 ||||| || ||||| |||||
 TTTTACT GG TCTGGT AGTCT
 C G _
 GAM1924 KIAA0663 3' CTTACAGATTCCAGGTCCCTTT 16812 T GCTT G
 T AAAAG GATTTGGGATT AG
 ||||| ||||| ||
 TTTTC CTGGACCTTAG TC
 C ACAT
 GAM1924 KIAA0779 3' TTTGGGCGAAAATCTTGATCA 41503 TG ____
 TTTT AGTGATT GGA TTGCTTAGG
 ||||| || |||||
 TTACTAG TCT AGCGGGTTT
 GT AAA
 GAM1924 KIAA0830 3' TTTAGGTAATGATAAGCATTTT 34546 A GG
 T AAAAGTG TTTG ATTGCTTAGG
 ||||| ||||| |||||
 TTTTAC GAAT TAATGGATTT
 _ AG
 GAM1924 KIAA0854 3' TTTAGATACCTGAGTGCACCTTT 17255 _ TG _ GCTTAGG
 T AAAAGTG ATT GG ATT
 ||||| ||||| || |||
 TTTTCAC TGA CC TAG
 G GT A ATTT
 GAM1924 KIAA0865 3' AAAAAATCATTTCTAGATTATT 30710 T C AGG
 TTT AAAAGTGATTTGGGA TG TT
 ||||| ||||| || ||
 TTTTATTAGATCTT AC AA
 T T AAAAT
 GAM1924 KIAA0884 3' CCTAAGTAACTGCCAAGTTTTT 34776 T GA_
 TTT AAAAG GATTTGG TTGCTTAGG
 ||||| ||||| |||||
 TTTT TTGAACC AATGAATCC
 T GTC
 GAM1924 KIAA0894 3' GTTTTCTTAAATCACTTTT 17058 TT
 AAAAGTGATTTGGGA GC
 ||||| ||||| ||

TTTTCACTAAATTCT TG
 TT
 GAM1924 KIAA0907 3' CCTGTTTTGTTTTGGATTATTT 17276 TG TGCT
 AAGTGATT GGAT TAGG
 ||||| ||| |||
 TTTATTAG TTTG GTCC
 GT TTTT
 GAM1924 KIAA0979 3' CCTGAAGTTCTTGGATTACTTT 17386 TG TT _
 AAAGTGATT GGA GCT TAGG
 ||||| ||| ||| |||
 TTTCAATTAG TCT TGA GTCC
 GT _ A
 GAM1924 KIAA0981 3' CCTAGGTGCAATTAGGTTGTTT 30797 TG GAT
 AAG ATTTGG TGCTTAGG
 ||| ||||| |||||
 TTT TGGATT GTGGATCC
 GT AAC
 GAM1924 KIAA1025 3' TCTGGGAAGTTCTGAATTTCTT 31997 T TG G
 TT AAAAG GATT GGATT CTTAGG
 ||||| ||| ||||| |||||
 TTTTC TTAA CTTGA GGGTCT
 T GT A
 GAM1924 KIAA1026 3' CCTGGGGGTGCGCCCAAGTCAC 35274 ATTG_
 TTT AAAGTGATTTGGG CTTAGG
 ||||| |||||
 TTTCACTGAACCC GGGTCC
 GCGTGG
 GAM1924 KIAA1055 3' CCTCAGCCTCCGAGTTGCTTTT 32850 TG ATT T
 AAAAG ATTTGGG GCT AGG
 ||||| ||||| ||| |||
 TTTTC TGAGCCT CGA TCC
 GT C_ C
 GAM1924 KIAA1145 3' CTTAGGCAGCTCAAGCTTGCTT 32680 TG_ A
 TT AAAAG A TTTGGG TTGCTTAGG
 ||||| | ||||| |||||
 TTTTC T GAACTC GACGGATTC
 GT C _
 GAM1924 KIAA1210 3' TCTGGGCAGTAAACCTAGCTCA 46088 T _
 TTTT AGTGA TTGGG ATTGCTTAGG
 ||||| ||||| |||||
 TTACT GATCC TGACGGGTCT
 C AAA
 GAM1924 KIAA1233 3' TCTGAGCACACGGTCTCTTTT 31593 T T GGAT
 AAAAG GA TTG TGCTTAGG
 ||||| ||| |||||
 TTTTC CT GGC ACGAGTCT
 T _ AC_
 GAM1924 KIAA1277 3' CCTGAGTAGTCCCTGGCTTTT 32205 GATTT
 AAAAGT GGGATTGCTTAGG
 ||||| ||||| |||||

TTTTCG CCCTGATGAGTCC
 GT____
 GAM1924 KIAA1323 3' GAGCATTTAATCATTTTT 31564 TGGGAT
 AAAAGTGATT TGCTT
 ||||| ||||
 TTTTACTAA ACGAG
 TTT____
 GAM1924 KIAA1336 3' CCGTTGAGTAATGCCAAGTTGT 35801 TG G G
 TTTT AAAAG ATTTGG ATTGCTTAG
 |||| |||| |||||
 TTTTT TGAACC TAATGAGTT
 GT G GCCC
 GAM1924 KIAA1357 3' CTAGGCGGTAATTGCTTT 35628 TG TGGG
 AAAG ATT ATTGCTTAG
 ||| || |||||
 TTTC TAA TGGCGGATC
 GT ____
 GAM1924 KIAA1364 3' CTTAGGCAGTTCCAGAGCT 31813 GA
 AGT TTTGGGATTGCTTAGG
 || |||||
 TCG AGACCTTGACGGATTC

 GAM1924 KIAA1432 3' TCTGCATTATGTCCAGATTGCT 33153 TG AT__ TTAGG
 TTT AAG ATTTGGG TGC
 || ||||| ||
 TTC TAGACCT ACG
 GT GTATT TCT
 GAM1924 KIAA1463 3' TTTGCCAGTTCCAGATCTCTTT 35775 T _ TTAGG
 T AAAAG GATTTGGGATTG C
 |||| ||||| |
 TTTTC CTAGACCTTGAC G
 T C TTT
 GAM1924 KIAA1495 3' CTTACATAGTCTTAAGCATTTT 36225 A CT
 T AAAAGTG TTTGGGATTG TAGG
 |||| ||||| ||||
 TTTTAC GAATTCTGAT ATTC
 AC
 GAM1924 KIAA1505 5' TTTGGGCCCTGTCTAGGTTGTT 45194 TG ATT_
 T AAG ATTTGGG GCTTAGG
 || ||||| |||||
 TTT TGGATCT CGGGTTT
 GT GTCC
 GAM1924 KIAA1509 3' CCTAGATTTCCCTGGCTCACTT 30876 _ TT TTG T
 TT AAAAGTGA T GGGA CT AGG
 ||||| | ||| ||||
 TTTTCACT G CCCT GA TCC
 C GT TTA _
 GAM1924 KIAA1594 3' CTTAGGTAATCCCAAAAAC 35674 GA
 AGT TTTGGGATTGCTTAGG
 || |||||

TCA AAACCCTAATGGATTG
 A_
 GAM1924 KIAA1610 3' GTTTTCTAAATCATTTTT 33342 TT
 AAAAGTGATTTGGGA GC
 ||||| ||
 TTTTACTAAATCTT TG
 T_
 GAM1924 KIAA1613 3' CCTGAGCAAGCATCATTTT 32359 TTGGGA
 AAAGTGAT TTGCTTAGG
 ||||| |||||
 TTTTACTA AACGAGTCC
 CG____
 GAM1924 KIAA1727 3' CTTATGGGAATCCTGAGCTGCT 32030 GA TG G _
 TTT AAAAGT TT GGATT CT TAGG
 ||||| || ||||| |||||
 TTTTCG GA CCTAA GG ATTC
 TC GT G T
 GAM1924 KIAA1765 3' CTGAGCCTGAGTCATTT 34956 TG GATT
 AAGTGATT G GCTTAG
 ||||| | |||||
 TTTACTGA C CGAGTC
 GT____
 GAM1924 KIAA1822 3' CTGGGCAGTTCGGGCTTT 33551 GATT G
 AAAGT T GGATTGCTTAG
 |||| | |||||
 TTTCG G CTTGACGGGTC
 ____ G
 GAM1924 KIAA1918 3' TCAGTAAAATCTTAAATGATTT 36217 G ____ TAGG
 TT AAAAGT ATTTGGGAT TGCT
 ||||| ||||| |||||
 TTTTTA TAAATTCTA ATGA
 G AA CT
 GAM1924 KRTHB2 3' TTTGGGCAGTAGATTTACTTT 26925 TTTGGG
 AAAGTGA ATTGCTTAGG
 ||||| |||||
 TTTTATT TGACGGGTTT
 TAGA____
 GAM1924 LALP1 3' GCCTGGATTGTCTGATTTTAGG 21623 ____
 TCACT GATTTGGGATT GC TTAGG C
 ||||| || ||||| |
 CTGGATTTTAG TG GGTCC G
 TC TTA
 GAM1924 LIN-28 3' AGGTTTCCCATTTTCTAATCAT 23979 ____ TTGCTTAGG
 TTTT GTGATT TGGGA
 ||||| |||||
 TACTAA ACCCT
 TCTTTT TT GGAT
 GAM1924 LRRFIP1 3' TTTGAGCAGGGACAGTCATTTT 11121 T GGA
 T AAAAGTGATT G TTGCTTAGG
 ||||| | |||||

TTTTACTGA C GACGAGTTT
 _ AGG
 GAM1924 MAP2K6 3' CCTGGGTGATCACCACATC 8643 T _ TG
 GAT TGG GAT CTTAGG
 ||| ||| ||| |||||
 CTA ACC CTA GGGTCC
 C A GT
 GAM1924 MAP2K6 3' CCTGGGTGATCACCACATC 25702 T _ TG
 GAT TGG GAT CTTAGG
 ||| ||| ||| |||||
 CTA ACC CTA GGGTCC
 C A GT
 GAM1924 MAP4K3 3' CTTAGTTTTGGTTTAAGTCATT 9682 ATT__ T G
 TTT AAAGTGATTTGGG GCT AG
 ||||| ||| ||
 TTTTACTGAATTT TGA TC
 GGTTT T
 GAM1924 MAP4K3 3' TTTAAGTCATTTTTGATTGCTT 9683 TG TG T
 TT AAAAG ATT GGAT GCTTAGG
 |||| ||| ||||| |||||
 TTTTC TAG TTTA TGAATTT
 GT TT C
 GAM1924 MCM10 3' TCTGAGCAATCCCTTTC 20595 TTT
 GA GGGATTGCTTAGG
 || ||||| |||||
 CT CCCTAACGAGTCT
 TT_
 GAM1924 MESDC2 3' CCTAAGTAGTTTTGAATTTCTT 35892 T TG
 T AAAG GATT GGATTGCTTAGG
 |||| ||| ||||| |||||
 TTTTC TTAA TTTGATGAATCC
 T GT
 GAM1924 MGC11034 3' TCTGAGCAGTTTTGTGCTTT 25472 ATT GG
 AAAGTG T GATTGCTTAGG
 |||| | ||||| |||||
 TTTCGT G TTGACGAGTCT
 __ TT
 GAM1924 MGC12335 3' CCTAGCTACTGGTCCTGGGCCA 26476 AT TG ____ T
 TTTT GTG T GGATT GCT AGG
 || | |||| ||| |||
 TAC G CCTGG CGA TCC
 CG GT TCAT _
 GAM1924 MGC12518 3' CAGTTCTAAAATACTTTT 32046 A
 AAAAGTG TTTGGGATTG
 ||||| ||||| |||||
 TTTTCAT AAATCTTGAC
 A
 GAM1924 MGC13090 3' TCTGGGATCTTGTGAGTTACTT 26429 G TTG
 TT AAAAGTGATTTG GA CTTAGG
 ||||| ||| |||||

		TTTTCATTGAGT TT GGGTCT	
		G CTA	
GAM1924	MGC13159	3' CCTAATGTGAAGTTTTAATCAC 26752	TG A_ TG _
		TTTT AAAGTGATT GG T C TTAGG	
		TTTCACTAA TT A G AATCC	
		TT GA GT T	
GAM1924	MGC13183	3' CCTGAGCAGAGCCTGAATTAC 26145	TG A_
		GTGATT GG TTGCTTAGG	
		CATTAA CC GACGAGTCC	
		GT GA	
GAM1924	MGC14258	3' CATTCTGAGGTCATTTTT 26723	G T
		AAAAGTGATTT GGA TG	
		TTTTTACTGGA TCT AC	
		G T	
GAM1924	MGC14433	3' CTAATAACATCTTGAGTTATTT 26726	TG TGC_ G
		TT AAAAGTGATT GGAT TTAG	
		TTTTTATTGA TCTA AATC	
		GT CAAT	
GAM1924	MGC15437	3' GCTCTCCAAAGCACTTTT 26690	A ATT
		AAAAGTG TTTGGG GC	
		TTTTCAC AAACCT CG	
		G CT_	
GAM1924	MGC2508	3' TAGTCCTGAAATATTTTT 23620	A TG
		AAAAGTG TT GGATTG	
		TTTTTAT AA CCTGAT	
		A GT	
GAM1924	MGC2747	3' CTTGGGTTTCTGAGTCTGCTTT 23549	_ TG TT
		T AAAAGT GATT GGA GCTTAGG	
		TTTTCG CTGA CTT TGGGTTC	
		T GT _	
GAM1924	MGC4643	3' CTTGAGTAAGAACAATCCTTTT 26439	T T GGA
		AAAAG GATT G TTGCTTAGG	
		TTTTC CTAA C AATGAGTTC	
		_ _ AAG	
GAM1924	MGC4796	3' CCTGCTGCCCAAGTCAC 30829	ATT TT
		GTGATTTGGG GC AGG	
		CACTGAACCC CG TCC	
		GT_ _	
GAM1924	MGC8721	3' TGAGTTCTGATCACTTTT 30267	TG TT
		AAAAGTGATT GGA GCTTA	

TTTTCAC TAG TCT TGAGT

GAM1924 MGEA6 3' TTAAGTGATTACACTTTT 12562 ATTTGG TG
AAAAGTG GAT CTTAG
||||| ||| |||||
TTTTCAC TTA GAATT
A_____ GT

GAM1924 MIDORI 3' CCTGTATACCCAGATTACTTT 36528 AT TT
AAAGTGATTTGGG TGC AGG
||||||| ||| |||
TTTCATTAGACCC ATG TCC
AT _____

GAM1924 MTHFD2 3' CTTGGGTAAGTACGCAACTTAC 13431 T GGA____
TTTT AAAGTGA TTG TTGCTTAGG
||||| ||| |||||
TTTCATT AAC AATGGGTTC
C GCATG

GAM1924 MYT1 3' TTTGATGCAACCAAGTTATTTT 10878 GA _
T AAAAGTGATTTGG TTGC TTAGG
||||||| ||| |||||
TTTTTATTGAACC AACG AGTTT
_____ T

GAM1924 NAP1L1 3' TCTGGGCAGTCAGCACT 29225 ATTTGG
AGTG GATTGCTTAGG
||| |||||
TCAC CTGACGGGTCT
GA_____

GAM1924 NINJ2 3' CCTGAGTTAAAAAGTGATTTT 18603 G GGGATT
AAAAGT ATTT GCTTAGG
||||| ||| |||||
TTTTTA TGAA TGAGTCC
G AAAT_____

GAM1924 NIP30 3' CCTGTGGCCCGAATCGTGTTT 24498 AG A TG TT
AAA TGATTTGGG T C AGG
||| ||||| | |||
TTT GCTAAGCCC G G TCC
GT _ GT _____

GAM1924 NUDT13 3' TTTAAGTCATTACTGAGTTACT 31665 TG _ T
T AAGTGATT G GAT GCTTAGG
||||| | ||| |||||
TTCATTGA C TTA TGAATTT
GT A C

GAM1924 NY-REN-25 3' TGATTCCACGTTGCTTTT 30419 TG T
AAAAG AT TGGGATTG
||||| |||||
TTTTC TG ACCTTAGT
GT C

GAM1924 OAZ2 3' CCTGGGCAGTGTCTTGAGTTG 8376 TG TG ____
TTTTT AG ATT GG ATTGCTTAGG
|| ||| || |||||

		TT TGA TC TGACGGGTCC	
		GT GT CTG	
GAM1924	OSBPL11	3' CTTGAAAAATTTCAACATTT 23047	A GG GC
	TT	AAAAGTG TTTG ATT TTAGG	
		TTTTTAC AGAC TAA AGTTC	
		A TT AA	
GAM1924	OSBPL1A	3' CTTAGTGCTCTGAATTTACTTT 19770	T G TT T G
	T	AAAAGTGA TT GGA GCT AG	
		TTTTCATT AA TCT TGA TC	
		T G CG T	
GAM1924	OSBPL1A	3' CTTAGTGCTCTGAATTTACTTT 28422	T G TT T G
	T	AAAAGTGA TT GGA GCT AG	
		TTTTCATT AA TCT TGA TC	
		T G CG T	
GAM1924	OSBPL1A	3' CTTAGTGCTCTGAATTTACTTT 27905	T G TT T G
	T	AAAAGTGA TT GGA GCT AG	
		TTTTCATT AA TCT TGA TC	
		T G CG T	
GAM1924	OSBPL3	5' TTTGGGCCACCCAAAATGTTTT 17822	GT A ATT
	T	AAAA G TTTGGG GCTTAGG	
		TTTT T AAACCC CGGGTTT	
		TG A AC_	
GAM1924	PBEF	3' TTTAGGTGATCTCAAATTA 12308	TG
		TGATTTGGGAT CTTAGG	
		ATTAAACTCTA GGATTT	
		GT	
GAM1924	PCDH20	3' TCTGTGTA CTGCAATTGCTTT 23139	TG AT T
		AAAG ATTTGGG TGC TAGG	
		TTTC TAAGCTC ATG GTCT	
		GT _ T	
GAM1924	PDZD2	3' TCTAAGTATTGGATCTCTTTT 39397	T TG GAT
		AAAAG GATT G TGCTTAGG	
		TTTTC CTAG T ATGAATCT	
		T GT _	
GAM1924	PELI2	3' CTGGGGCCTTTTCTGATTTATT 22229	T TG TT_ AGG
	TTT	AAAAGTGA T GGA GCTT	
		TTTTTATT A CTT CGGG	
		T GT TTT GTCT	
GAM1924	PEX11B	3' TAATCAGCAGAATTACTTTT 9944	GG_
		AAAAGTGATTT GATTG	

		TTTTCATTAAG CTAAT		
		ACGA		
GAM1924 PHCA	3'	GTAAAATCCAGATTGTTTT 20377	TG	A_
		AAAAG ATTTGGG TTGC		
		TTTTT TAGACCT AATG		
		GT AA		
GAM1924 PKNOX2	3'	TCTGGGTGATCCAATCATTTTT 43695	TG	TG
		AAAAGTGATT GGAT CTTAGG		
		TTTTTACTAA CCTA GGGTCT		
		— GT		
GAM1924 PLAC3	5'	TTTGTGCCCCTAGATTATTTTT 34370	AT	TTAGG
		AAAAGTGATTTGGG TGC		
		TTTTTATTAGATCC GTG		
		CC TTT		
GAM1924 PPP1R1B	3'	TGAGGTACCCTTAGATCCTTTT 25908	T	AT AGG
		AAAAG GATTTGGG TGCTT		
		TTTTC CTAGATTC ATGA		
		— CC GTT		
GAM1924 PPP2R2A	3'	TTTAGGTAAGGGTAGGGCACTT 8583	A	GGA
TT		AAAAGTG TTTG TTGCTTAGG		
		TTTTCAC GGAT AATGGATTT		
		G GGG		
GAM1924 PRAX-1	3'	CCTGAGAGGCCCCCAGATCACT 11147	ATTG_	
		AGTGATTTGGG CTTAGG		
		TCACTAGACCC GAGTCC		
		CCGGA		
GAM1924 PRO1048	3'	TCTGTAGGAGTCTTAGGTTTTT 20564	T	G _
TT		AAAG GATTTGGGATT CT TAGG		
		TTTT TTGGATTCTGA GA GTCT		
		T G T		
GAM1924 PRO1617	5'	TCTGGTTTTCTGAACCTATTT 20666	_ TG TT T	
TT		AAAAGTGA TT GGA GCT AGG		
		TTTTTATT AA CCT TGG TCT		
		C GT TT _		
GAM1924 PSMF1	3'	TTTGGTGTTCTCCGGATCCTTT 13691	T _ TT TAGG	
T		AAAAG GATTTGG GA GCT		
		TTTTC CTAGGCC CT TGG		
		_ T TG TTT		
GAM1924 RAB10	3'	TTGAGTAGTCTGCATTTT 41283	ATTG	
		AAAGTG GGATTGCTTAG		

TTTTAC TCTGATGAGTT
 G____
 GAM1924 Rab11-FIP2 3' TGATCTCAAGTCCTTTT 17102 T
 AAAAG GATTTGGGATTG
 ||||| |||||
 TTTTC CTGAACTCTAGT
 -
 GAM1924 RBAK 3' TTTAGGCATTAGAGTCATTTT 22143 GGGAT
 AAAGTGATTT TGCTTAGG
 ||||| |||||
 TTTTACTGAG ACGGATTT
 ATT__
 GAM1924 RI58 3' AGTGAGTCTCAAATTGTTTTT 14793 TG _
 AAAAG ATTTGGGATT GCT
 ||||| ||||| |||
 TTTTT TAAACTCTGA TGA
 GT G
 GAM1924 RMP 3' AGCATTTTGAATTACTTTT 9877 TG T
 AAAAGTGATT GGAT GCT
 ||||| ||||| |||
 TTTTCATTAA TTTA CGA
 GT _
 GAM1924 RMP 3' AGCATTTTGAATTACTTTT 28680 TG T
 AAAAGTGATT GGAT GCT
 ||||| ||||| |||
 TTTTCATTAA TTTA CGA
 GT _
 GAM1924 RNPC2 3' CTTGAGAATTCATCTTGAGTTA 11335 _ TG TG____
 TCTTT GTGATT GGAT CTTAGG
 | |||| |||| |||||
 C ATTGA TCTA GAGTTC
 T GT CTTAA
 GAM1924 Rpo1-2 3' CCTAGGCAGGAGCAATCACTT 21099 TGGGA
 AAGTGATT TTGCTTAGG
 ||||| |||||
 TTCACTAA GACGGATCC
 CGAG_
 GAM1924 SCOP 3' TTTAAGTAATCACCCTTTC 44104 TT_ _
 GA TGG GATTGCTTAGG
 || ||||| |||||
 CT ACC CTAATGAATTT
 TTC A
 GAM1924 SCYB11 3' TAAAGAATCAAAGTCATTTT 42259 GG G AGG
 AAAAGTGATTT GATT CTT
 ||||| ||||| |||
 TTTTACTGAA CTAA GAA
 A_ _ ATT
 GAM1924 SDF1 3' CTTGTAATCCGAATCTCTTTT 43689 T G TT
 AAAAG GATTTGG ATTGC AG
 ||||| ||||| ||||| ||

TTTTC CTAAGCC TAATG TC
 T _ T_
 GAM1924 SERHL 3' CTAAGCGTTCCAGTTTGT 45757 TG T
 G A TTGGGATTGCTTAG
 | | |||||
 T T GACCTTGGCGAATC
 GT T
 GAM1924 SLC26A7 3' CTGAGCAGTTATATTTTA 27413 TT G
 TGA TG GATTGCTTAG
 ||| || |||||
 ATT AT TTGACGAGTC
 TT A
 GAM1924 SNX11 3' TCTGAGTTTCTGCAGGTCATTT 14970 _ TT
 AAGTGATTTG GGA GCTTAGG
 ||||| ||| |||||
 TTTACTGGAC TCT TGAGTCT
 G T_
 GAM1924 Spir-1 3' CTGAGCACCGGTTTCCTTTT 32306 T T GAT
 AAAAG GA TTGG TGCTTAG
 |||| || ||| |||||
 TTTTC CT GGCC ACGAGTC
 _ T _
 GAM1924 SYNPO2 3' TCTGAGTGATCTCACAGATTTT 35594 GATT TG
 T AAAAGT TGGGAT CTTAGG
 |||| |||| |||||
 TTTTAA ACTCTA GAGTCT
 GAC_ GT
 GAM1924 SYTL4 3' TTTAAGCAGTTTCCACCTTGCT 28025 TG TT _
 TT AAAG A TGGGA TTGCTTAGG
 |||| | |||| |||||
 TTTC T ACCTT GACGAATTT
 GT CC T
 GAM1924 TA-KRP 3' TCTAGGTACTAAAGCATTTT 26253 A GAT
 AAAAGTG TTTGG TGCTTAGG
 ||||| |||| |||||
 TTTTAC AAATC ATGGATCT
 G _
 GAM1924 TEB4 3' CCTAAGTGGAAGCAATTACTT 30427 TG GG TG
 T AAAGTGATT AT CTTAGG
 ||||| || |||||
 TTTCATTAA TG GAATCC
 CGAA GT
 GAM1924 TGIF2 3' CCTGCAGCCTCAGTTTGAATT 22366 T TG _ _
 CTTTT G GATT GGATT GCT TAGG
 | ||| |||| ||| ||||
 C TTAA TTTGA CGA GTCC
 _ GT CTC C
 GAM1924 TIAM2 3' TTAAAGCATATTTAAGTTATTT 14825 AT AGG
 T AAAGTGATTTGGG TGCTT
 ||||| |||||

			TTTTATTGAATTT ACGAA			
			AT ATTT			
GAM1924	TLR10	5'	TTTGGCAGTAATCCAGATTGCT 25230	TG	___	TAGG
		TTT	AAAG ATTTGGG ATTGCT			
			TTTC TAGACCT TGACGG			
			GT AA TTT			
GAM1924	TNKS2	3'	CTATGAGTGAATCTGGAATTGC 24912	TG	G _	GG
		TTTT	AAAG ATTT GGATT GCTTA			
			TTTC TAAG TCTAA TGAGT			
			GT G G ATCC			
GAM1924	TOPBP1	5'	CTTCAGACAATTCCAAAT 13887	_	T	
			ATTTGGGATTG CT AGG			
			TAAACCTTAAC GA TTC			
			A C			
GAM1924	TRAD	3'	TTAAAGGCCTGGTTCTAAGTCC 13930	T	___	AGG
		TTTT	AAG GATTTGGGATT GCTT			
			TTC CTGAATCTTGG CGGA			
			_ TC AATTT			
GAM1924	TRIM4	3'	CCGCAGTATAGGCTTAAGTCAC 26902	AT	___	TA
		TTTT	AAAGTGATTTGGG TGCT GG			
			TTTCACTGAATTC ATGA CC			
			GGAT CG			
GAM1924	VDU1	3'	TTAGAGTTAGTTTTAGGGCACT 17383	A	_	AGG
		TTT	AAAAGTG TTTGGGATTG CTT			
			TTTTCAC GGATTTTGAT GAG			
			G T ATTC			
GAM1924	VEZATIN	3'	CTAGGTCCTTAGTTATTTTT 19069	T	ATT	
			AAAAGTGATT GGG GCTTAG			
			TTTTTATTGA TCC TGGATC			
			T _			
GAM1924	VPS4B	3'	TTTGGGTTTTCTGTACAGATTG 11296	TG	___	TT
		TTTTT	AG ATTTG GGA GCTTAGG			
			TT TAGAC TCT TGGGTTT			
			GT ATG TT			
GAM1924	YAP1	3'	AACTGGGTATTCTTGAATTGCT 12748	TG	TG T	G
		TTT	AAAAG ATT GGA TGCTTAG			
			TTTTC TAA TCT ATGGGTC			
			GT GT T AAT			
GAM1924	ZDHHC2	3'	TTAGAGCACGTTTTGGTCATTT 18493	T TG	_	AGG
		TT	AAAAGTGA T GGAT TGCTT			

TTTTACT G TTTG ACGAG
 _GT C ATTT
 GAM1924 LOC113763 3' CCTGCTTGTCTGACCACTTT 28803 A TG T_ TT
 T AAAAGTG TT GGAT GC AGG
 ||||| || ||| || |||
 TTTTCAC AG CCTG CG TCC
 C GT TT _
 GAM1924 LOC115123 3' CCTGAGTGGTCTTTTTCAT 36246 TTT TG
 GTGA GGGAT CTTAGG
 ||| |||| |||||
 TACT TTCTG GAGTCC
 TT_ GT
 GAM1924 LOC116437 3' TCTGAGCAGTTTTCTGAATT 36580 TG _
 GATT G GATTGCTTAGG
 ||| | |||||
 TTAA C TTGACGAGTCT
 GT TT
 GAM1924 LOC119392 3' TTTGGGCAGTTCTGGAACT 29759 GA TG
 AGT TT GGATTGCTTAGG
 ||| || |||||
 TCA AG CTTGACGGGTTT
 A_ GT
 GAM1924 LOC123283 3' TCTAGTATGTCTCAGGTATTTT 37425 G _ T
 T AAAAGT ATTTGGGAT TGCT AGG
 ||||| ||||| ||| |||
 TTTTTA TGGACTCTG ATGA TCT
 _ T _
 GAM1924 LOC125144 3' CCTAAGCAATCCTCCAC 36788 ATTT
 GTG GGGATTGCTTAGG
 ||| |||||
 CAC TCCTAACGAATCC
 CC_
 GAM1924 LOC125144 3' CTTGAGTTTTTTTGGGTTTTTTT 36789 T TG TT
 TT AAAAG GATT GGA GCTTAGG
 ||||| ||| ||| |||||
 TTTT TTGG TTT TGAGTTC
 T GT TT
 GAM1924 LOC128708 5' CTTGGGCTGCGTCAAGTCACTT 37318 GATT
 AAGTGATTTGG GCTTAGG
 ||||| |||||
 TTCACTGAACT CGGGTTC
 GCGT
 GAM1924 LOC130589 3' TTAAAGCTATTCTCACATTGCT 29024 TG T TT_ AGG
 TTT AAAAG AT TGGGA GCTT
 |||| | |||| |||
 TTTTC TA ACTCT CGAA
 GT C TAT ATTT
 GAM1924 LOC131873 3' AAGCTCTGAGTTACTTTT 37360 TG ATT
 AAAAGTGATT GG GCTT
 ||||| || |||

	TTTTCATTGA CT CGAA	
	GT ____	
GAM1924 LOC143465 3'	TCTAGGTGGTTTTGTTTACTT 40364	TT GG TG
	AAGTGA T GAT CTTAGG	
	I	
	TTCATT G TTG GGATCT	
	T_ TT GT	
GAM1924 LOC143666 3'	CTTGCCTTCTAGGTCACTT 40369	TT TT
	AAGTGATTTGGGA GC AG	
	TTCACTGGATCTT CG TC	
	C_ T_	
GAM1924 LOC145134 5'	AATCATTGAGTCATTTTT 40500	TG _
	AAAAGTGATT G GATT	
	I	
	TTTTTACTGA T CTAA	
	GT A	
GAM1924 LOC145134 5'	CTTCAGCGTTTTAAATTGTTTT 40501	TG T T
T	AAAAG ATTTGGGAT GCT AGG	
	TTTTT TAAATTTTG CGA TTC	
	GT _ C	
GAM1924 LOC145854 3'	CTTGAACATTCTAAATTACTT 38008	T C
	AAGTGATTTGGGAT G TTAGG	
	I	
	TTCATTAAATCTTA C AGTTC	
	_ A	
GAM1924 LOC145945 5'	TCTAAGACAATGAATCATTTT 40637	GGG _
	AAAGTGATTT ATTG CTTAGG	
	TTTTACTAAG TAAC GAATCT	
	__ A	
GAM1924 LOC146268 3'	TTGGGCCTGGGTGGCTTTT 38126	G TG GATT
	AAAAGT ATT G GCTTAG	
	I	
	TTTTCG TGG C CGGGTT	
	G GT ____	
GAM1924 LOC146268 5'	CCTGGGCAATCTTAACATC 38123	_
	GAT TTGGGATTGCTTAGG	
	CTA AATTCTAACGGGTCC	
	C	
GAM1924 LOC146839 5'	TTTAAGTAGTCTTACTTTTTAT 40758	TT__
TT	AAGTGA TGGGATTGCTTAGG	
	TTTATT ATTCTGATGAATT	
	TTTC	
GAM1924 LOC146952 5'	CTTGAGCTACTTAGTCACTTTT 40768	T GATT
	AAAAGTGATT GG GCTTAGG	

	TTTTCACTGA TC CGAGTTC	
	T AT__	
GAM1924 LOC147219 3'	AGGCAATGAATTACTT 40820	GGG
	AAGTGATTT ATTGCTT	
	TTCATTAAG TAACGGA	

GAM1924 LOC147622 5'	TTAGTGTGGTCTTTAAGTTGCT 40852	TG _ TG TTAGG
	TTT AAAAG ATTTGG GAT C	
	TTTTC TGAATT CTG G	
	GT T GT TGATT	
GAM1924 LOC147694 3'	CCTCCCAGTCCATAGGTTGCTT 38370	TG _ CTT
	TT AAAAG ATTTG GGATTG AGG	
	TTTTC TGGAT CCTGAC TCC	
	GT A CC_	
GAM1924 LOC148530 5'	CCTGGGCATTTCAAGTGCTTTT 40886	G GG T
	AAAAGT ATTTG AT GCTTAGG	
	TTTTCG TGAAC TA CGGGTCC	
	_ TT _	
GAM1924 LOC149302 5'	CTGACCCAAGTTTCTTTT 38705	T ATTGC
	AAAAG GATTTGGG TTAG	
	TTTTC TTGAACCC AGTC	
	T _____	
GAM1924 LOC149332 3'	TTTGGGTGATCCTGATTTTAT 40983	T_ TG TG
	GTGA T GGAT CTTAGG	
	TATT A CCTA GGGTTT	
	TT GT GT	
GAM1924 LOC150170 5'	TCTAAGATCTAAATCATTTT 38863	ATTG
	AAAGTGATTTGGG CTTAGG	
	TTTTACTAAATCT GAATCT	
	A__	
GAM1924 LOC150175 5'	TCTAAGATCTAAATCATTTT 38885	ATTG
	AAAGTGATTTGGG CTTAGG	
	TTTTACTAAATCT GAATCT	
	A__	
GAM1924 LOC150215 5'	TCTAAGATCTAAATCATTTT 38889	ATTG
	AAAGTGATTTGGG CTTAGG	
	TTTTACTAAATCT GAATCT	
	A__	
GAM1924 LOC150218 5'	TCTAAGATCTAAATCATTTT 38916	ATTG
	AAAGTGATTTGGG CTTAGG	

	TTTTACTAAATCT GAATCT	
	A__	
GAM1924 LOC150225 5'	TCTGAGCAATCCTTTTGCTT 41191	TG TTT
	AAG A GGGATTGCTTAGG	
	TTC T TCCTAACGAGTCT	
	GT T__	
GAM1924 LOC150311 5'	CCTAAGGGATATGAATTGTTTT 38926	TG GG G
T	AAAAG ATTTG ATT CTTAGG	
	TTTTT TAAGT TAG GAATCC	
	GT A_ G	
GAM1924 LOC150397 3'	TCTGAGTGGTAGGGAGTCACT 38963	GGG TG
	AGTGATTT AT CTTAGG	
	TCACTGAG TG GAGTCT	
	GGA GT	
GAM1924 LOC150418 5'	TTTGAGCAATTTTCTCGACTT 32637	_ TTT
	AAGT GA GGGATTGCTTAGG	
	TTCA CT TTTAACGAGTTT	
	G C__	
GAM1924 LOC150630 5'	GCCTCAGTTTCAGATTCTTTT 41240	T GG CTT
	AAAAG GATTTG ATTG AGG	
	TTTTT TTAGAC TGAC TCC	
	_ TT __ GT	
GAM1924 LOC150819 5'	TCTGTGGCAAATTTTCAGACTA 41248	A GG _ _
TTTTT	AGTG TTTG AT TGCT TAGG	
	TTAT AGAC TA ACGG GTCT	
	C TT AA T	
GAM1924 LOC151283 3'	AGGCCCCAAGTTATTTTT 39092	ATT
	AAAAGTGATTTGGG GCTT	
	TTTTTATTGAACCC CGGA	

GAM1924 LOC151429 3'	CTTGCTCCAGGTCCTT 41343	ATT TT
	AAGTGATTTGGG GC AG	
	TTCACTGGACCT CG TC	
	__ T__	
GAM1924 LOC152024 5'	CCTAAGGAGTCCAGATTGTTTT 39199	TG G G
T	AAAAG ATTTGG ATT CTTAGG	
	TTTTT TAGACC TGA GAATCC	
	GT _ G	
GAM1924 LOC152220 3'	CTTGCTCCTTTTGAGTTGCTTT 41445	TG TG TT_ TT G
T	AAAAG ATT GGA GC AG	

	TTTTC TGA TTT CG TC	
	GT GT CCT T_	
GAM1924 LOC152220 3'	TTTGAGATGTTGAGTTACTTT 41447	TG G TG
	AAAGTGATT G AT CTTAGG	
	TTTCATTGA T TA GAGTTT	
	GT G _	
GAM1924 LOC152313 5'	TCTAAGCGGTCTCCCTGCTT 41480	ATTT
	AAGTG GGGATTGCTTAGG	
	TTCGT CTCTGGCGAATCT	
	CC_	
GAM1924 LOC152926 3'	CTTAGGCAGCTATGGGTTTCTT 39341	T TT GGA
TT	AAAAG GAT G TTGCTTAGG	
	TTTTC TTG T GACGGATTC	
	T GG ATC	
GAM1924 LOC154739 5'	TTGGGCAGTTGCATTATTT 41723	TT G
	AAGTGA TG GATTGCTTAG	
	TTTATT AC TTGACGGGT	
	_ G	
GAM1924 LOC157858 5'	CCTGGGTAATTTTGTATTTT 41866	ATTT
	AAAAGTG GGGATTGCTTAGG	
	TTTTTAT TTTAATGGGTCC	
	GT_	
GAM1924 LOC157918 3'	CTTAGCATCCTTTGATCATTTT 41897	T_ T T G
T	AAAAGTGATT GGGAT GCT AG	
	TTTTTACTAG TCCTA CGA TC	
	TT _ T	
GAM1924 LOC158014 5'	TTTAATGCTTTCTTGAATAATT 39698	G TG TT _
TTT	AAAAGT ATT GGA GC TTAGG	
	TTTTTA TAA TCT CG AATTT	
	A GT TT T	
GAM1924 LOC158954 3'	TTAGTTATCCCTGCATTATTT 30314	TT_ T TAGG
TT	AAAAGTGAT GGGAT GCT	
	TTTTTATTA CCCTA TGA	
	CGT T TTT	
GAM1924 LOC161003 3'	CTAATGTTTCAGAATTACTTTT 29803	GG TT _
	AAAAGTGATTT GA GC TTAG	
	TTTTCATTAAG CT TG AATC	
	A_ T_ T	
GAM1924 LOC164971 5'	CCTCTGATTTTAGATCAC 40115	CTT
	GTGATTTGGGATTG AGG	

	CACTAGATTTTAGT TCC	
	C__	
GAM1924 LOC168667 3'	CCTGAGGTAGTCAGGTCATT 44565	GG _
	AGTGATTT GATTGC TTAGG	
	TTACTGGA CTGATG AGTCC	
	_ G	
GAM1924 LOC196264 3'	CCTGAGCAAAAAGATACTTTT 42335	A GGGA
	AAAAGTG TTT TTGCTTAGG	
	TTTTCAT AGA AACGAGTCC	
	_ AA_	
GAM1924 LOC196812 3'	TCTGAGCAATACGGAGATCCTT 43138	T GGG_
TT	AAAAG GATTT ATTGCTTAGG	
	TTTTC CTAGA TAACGAGTCT	
	_ GGCA	
GAM1924 LOC197319 3'	CCTGGGCAGTTTTATTC 42476 TT	
	GA TGGGATTGCTTAGG	
	CT ATTTTGACGGGTCC	
	T_	
GAM1924 LOC199678 3'	TTTAAGCTTTTTAAATTATTTT 43229	TT
	AAAGTGATTTGGGA GCTTAGG	
	TTTTATTAAATTT CGAATT	
	T_	
GAM1924 LOC200470 5'	TTTGTGCGTTCTGAGTCATTTT 43311	TG _ TTAGG
T	AAAAGTGATT GGATTG C	
	TTTTTACTGA CTTGGC G	
	GT T TTT	
GAM1924 LOC201895 3'	GATAGGTTTTTAAATTGCTTTT 42927	TG TT GG
	AAAAG ATTTGGGA GCTTA	
	TTTTC TAAATTTT TGGAT	
	GT _ AGT	
GAM1924 LOC202934 5'	TTAGCTACTCCTGATTATTTT 43468	T TG TT_ TAGG
T	AAAAGTGA T GGA GCT	
	TTTTTATT A CCT CGA	
	_ GT CAT TTT	
GAM1924 LOC203536 3'	TCTGGGGGAAATCTTGGGATGC 43058	A TG G_
TTTT	AAAGTG TT GGATT CTTAGG	
	TTTCGT GG TCTAA GGGTCT	
	A GT AGG	
GAM1924 LOC219790 3'	CTTGGGTAGCCATAGAAATCAT 43905	G_ A
TTTT	AAGTGATTT GG TTGCTTAGG	

	TTTACTAAA CC GATGGGTTTC	
	GATA _	
GAM1924 LOC221061 3'	TTTGCATCGCTTGAGTCATTTT 44771	TG AT_ TTAGG
T	AAAAGTGATT GG TGC	
	TTTTTACTGA TC ACG	
	GT GCT TTT	
GAM1924 LOC221288 3'	CCTGAGTAGTTCCTTCCCTT 44968	T TTT
	AAG GA GGGATTGCTTAGG	
	TTC CT CCTTGATGAGTCC	
	C T_	
GAM1924 LOC221474 5'	TTGGGGCAAGTCACTTT 44384	GGATTG
	AAAGTGATTTG CTTAG	
	TTTCACTGAAC GGGTT	
	G_	
GAM1924 LOC221830 3'	AGTGGGAAATTTTCAGATTACTT 44436	GG G GG
TT	AAAAGTGATTTG ATT CTTA	
	TTTTCATAGAC TAA GGGT	
	TT A GAT	
GAM1924 LOC221830 3'	TTTAGCCTTTCTCAGTTTATTT 44439	T TT_ TAGG
TT	AAAAGTGA TTGGGA GCT	
	TTTTTATT GACTCT CGA	
	T TTC TTT	
GAM1924 LOC221964 3'	CTTGAGCAATTTTAATCTCT 45113	T T
	AG GATT GGGATTGCTTAGG	
	TC CTAA TTTTAACGAGTTC	
	T _	
GAM1924 LOC222008 3'	TGCTGTCAGATTCAAAATTGCT 45127	TG G GCT G
TTT	AAAAG ATTT GGATT TAG	
	TTTTC TAAA CTTAG GTC	
	GT A ACT GTT	
GAM1924 LOC222128 5'	TCTGTCTTTCCAATGTTGCTTT 44542	TG _ TT TTAGG
T	AAAAG AT TTGGGA GC	
	TTTTC TG AACCTT TG	
	GT T TC TCT	
GAM1924 LOC253019 3'	CTTACAGATTCCAGGTCCTTT 45667	T GCTT G
T	AAAAG GATTTGGGATT AG	
	TTTTC CTGGACCTTAG TC	
	C ACAT	
GAM1924 LOC253223 5'	TGGGCAGGCCACTTTT 45346	GATTTG A
	AAAAGT GG TTGCTTA	

	TTTTCA CC GACGGGT	
	_____ G	
GAM1924 LOC253258 3'	CTTGCCTTCTAGGTCACCTT 46147	TT TT
	AAGTGATTTGGGA GC AG	
	TTCACTGGATCTT CG TC	
	C_ T_	
GAM1924 LOC253260 3'	CCTAATTTGTTTTTCCAAATCA 45909	TT ____
	TTTTT AGTGATTTGGGA GC TTAGG	
	TTACTAAACCTT TG AATCC	
	TT TTT	
GAM1924 LOC253975 3'	CTTACAGATTCCAGGTCCCTTT 45934	T GCTT G
	T AAAAG GATTTGGGATT AG	
	TTTTC CTGGACCTTAG TC	
	C ACAT	
GAM1924 LOC255045 3'	GCCTAAATGCTTTAGTTTTAGG 46031	____ _
	TCATTT GATTTGGGATT GC TTAGG C	
	CTGGATTTTGA CG AATCC G	
	TTT TA	
GAM1924 LOC255326 3'	CTTGATTTTTGCTCGAATTGCT 46106	TG ATTGC_
	TTT AAAAG ATTTGGG TTAGG	
	TTTTC TAAGCTC AGTTC	
	GT GTTTTT	
GAM1924 LOC255465 5'	TTTAGCTACTCCTGATTATTTT 46460	T TG TT_ TAGG
	T AAAAGTGA T GGA GCT	
	TTTTTATT A CCT CGA	
	_GT CAT TTT	
GAM1924 LOC255465 5'	AGGGAAGTGATGTTGGGTCACCT 46445	TG G TG AGG
	TTT AAAAGTGATT G AT CTT	
	TTTTCACTGG T TA GAA	
	GT G GT GGGAA	
GAM1924 LOC256207 3'	TTTAGTGTGCCTGGGGTCACTT 45624	_TG ATT TAGG
	TT AAAAGTGAT T GG GCT	
	TTTTCACTG G CC TGA	
	G GT GTG TTT	
GAM1924 LOC256273 5'	CTTGTTAACCAAGTTACTTTT 46125	GATT TT
	AAAAGTGATTTGG GC AG	
	TTTTCATTGAACC TG TC	
	AAT_ T_	
GAM1924 LOC256277 5'	CTTAAGTGACTTAAGTTATTTT 45426	A TG
	AAAGTGATTTGGG T CTTAGG	

	TTTTATTGAATTC A GAATTC	
	_GT	
GAM1924 LOC256733 5'	CCTAGGGGCCTGATCATTTTT 46368	T TG ATTG
	AAAAGTGA T GG CTTAGG	
	TTTTTACT A CC GGATCC	
	_GT GG__	
GAM1924 LOC257441 5'	TCTGAGCGAGCGCGGTGCTTTT 45744	ATTG GGA
	AAAAGTG TTGCTTAGG	
	TTTTCGT AGCGAGTCT	
	GGCGCG__	
GAM1924 LOC257486 3'	TCTGGGCAGTAAACCTAGCTCA 34326	T ____
	TTTTT AGTGA TTGGG ATTGCTTAGG	
	TTACT GATCC TGACGGGTCT	
	C AAA	
GAM1924 LOC257513 5'	TGGGCAGGCCACTTTT 46640	GATTTG A
	AAAAGT GG TTGCTTA	
	TTTTCA CC GACGGGT	
	_____ G	
GAM1924 LOC257567 5'	TGGGCAGGCCACTTTT 46699	GATTTG A
	AAAAGT GG TTGCTTA	
	TTTTCA CC GACGGGT	
	_____ G	
GAM1924 LOC51580 3'	CCTAACATCTTTAAATCGC 18014	AT C
	GTGATTTGGG TG TTAGG	
	CGCTAAATTT AC AATCC	
	CT _	
GAM1924 LOC51634 3'	TCTGTCTAGTTCCAAAACATTT 18103	A CT
	TT AAAAGTG TTTGGGATTG TAGG	
	TTTTTAC AAACCTTGAT GTCT	
	A CT	
GAM1924 LOC54499 3'	TGGTCCTAGATGATTTTT 34967	G
	AAAAGT ATTTGGGATTG	
	TTTTTA TAGATCCTGGT	
	G	
GAM1924 LOC55885 3'	TTTGAGTAGTGAGGTTACTTTT 20713	GGG
	AAAAGTGATTT ATTGCTTAGG	
	TTTTCATTGGA TGATGAGTTT	
	G__	
GAM1924 LOC56267 3'	CTTGGGTATTATAGATCACTTT 21227	GGAT
	T AAAAGTGATTTG TGCTTAGG	

	TTTTCACTAGAT ATGGGTTC	
	ATT_	
GAM1924 LOC89932 3'	CCTGGGTAATTTTGTATTTT 30489	ATTT
	AAAAGTG GGGATTGCTTAGG	
	TTTTTAT TTTTAATGGGTCC	
	GT_	
GAM1924 LOC90333 3'	CCTGGGTAATTTTGTGTTT 31223	TG TT
T	AAAG AT GGGATTGCTTAGG	
	TTTT TG TTTTAATGGGTCC	
	TG TT	
GAM1924 LOC91149 3'	TCTGGCTCAGGGTCTCAGGTTG 32458	TG ____ T
C	G ATTTGGGATT GCT AGG	
	C TGGACTCTGG CGG TCT	
	GT GACT _	
GAM1924 LOC91286 3'	TTTAAGAGTGTTAAGTCATT 32624	G G
	AGTGATTTGG ATT CTTAGG	
	TTACTGAATT TGA GAATTT	
	G _	
GAM1924 LOC91496 5'	CCTAAGTGGATAAAATGTACTT 32915	_ GGGA TG
TT	AAAAGTG ATTT T CTTAGG	
	TTTTCAT TAAA G GAATCC	
	G ATA_ GT	
GAM1924 LOC91549 3'	CTTAAGTAACAAAGTAATCACT 33012	TGGGA_
TT	AAAGTGATT TTGCTTAGG	
	TTTCACTAA AATGAATTC	
	TGAAAC	
GAM1924 LOC92231 3'	CCTGATTCCTGAATCATT 34009	TG TTGC
	AGTGATT GGA TTAGG	
	TTACTAA CCT AGTCC	
	GT T__	
GAM1924 LOC92609 3'	CTTAAGCAATCTTCCTGCTTT 36061	ATTT
	AAAGTG GGGATTGCTTAGG	
	TTTCGT TTCTAACGAATTC	
	CC_	
GAM1924 LOC92973 5'	TTTAGGCTTCACAAATTATTTT 35189	G TT
	AAAGTGATTTG GA GCTTAGG	
	TTTTATTAAAC CT CGGATTT	
	A T_	
GAM1924 LOC93356 5'	TCTGAGTAAACAGTAATTACT 35672	TGGGA
	AGTGATT TTGCTTAGG	

		TCATTAA AATGAGTCT		
		TGACA		
GAM1924	LOC93380	3' CTTGAGCAGTCACCTCTCATTT 35725	TTT _	
		T AAAGTGA GG GATTGCTTAGG		
		TTTTACT CC CTGACGAGTTC		
		CT_ A		
GAM1925	ADAM8	3' GAGCTGTGTGCTTGCGGGTG 6765	_ _	
		CACCTGCAAGTAC CA CTC		
		GTGGGCGTTCGTG GT GAG		
		T C		
GAM1925	APC	3' TGTATATTCTGGTATTTGAGGT 5483	G CTCC_	
	G	CACCT CAAGTACCA TGCA		
		GTGGA GTTTATGGT ATGT		
		_ CTTAT		
GAM1925	ARF3	3' TGTGGGTGTGTTTGTGTGTG 7382	C TAC T TG	
		CAC TGCAAG CAC CC CA		
		GTG GTGTTT GTG GG GT		
		T _ T GT		
GAM1925	ATP7A	3' TGCATCCTTGTCCTTGCAAGTG 5498	T CACTCC	
		CACCTGCAAG AC TGCA		
		GTGGACGTTT TG ACGT		
		C TTCCT_		
GAM1925	CDK10	3' GCATCGTGCTGCAGGTG 27555	A CACTCC	
		CACCTGCA GTAC TGC		
		GTGGACGT CGTG ACG		
		_ CT_		
GAM1925	CHGA	5' TGCAGGGGAGCTTGCGGG 6940	ACCA	
		CCTGCAAGT CTCCTGCA		
		GGGCGTTCG GGGGACGT		
		A_		
GAM1925	CKTSF1B1	3' TGTGGATGGGTGCCTGTGGGTG 15027	TG A AC T	
		CACC CA GTACC TCC GCA		
		GTGG GT CGTGG AGG TGT		
		GT C GT _		
GAM1925	DNMT3B	3' TGCAGGGGTAGCCTGAGGTG 13765	G A ACC	
		CACCT CA GT ACTCCTGCA		
		GTGGA GT CG TGGGGACGT		
		_ C A_		
GAM1925	EGFL4	3' TGTGGGGGTGGTGGGGGTG 30969	G AAGT TG	
		CACCT C ACCACTCC CA		

GTGGG G TGGTGGGG GT
 G ____ GT
 GAM1925 EIF4G2 3' TGCCCTTGAAGTGGTTTTGTG 7117 TG T _CT_
 GGTG CC CAAG ACCACT C GCA
 || ||| ||||| | |||
 GG GTTT TGGTGA G CGT
 GT T A TTCC
 GAM1925 HOXD3 3' GGCTGGTGTGTTGTAGTTG 13774 C CT
 CA CTGCAAGTACCA CC
 || ||||| ||
 GT GATGTTTGTGGT GG
 T C_
 GAM1925 HPCA 3' TGCAGGTCTCAGCTTGCGGG 7920 ACCACT
 CCTGCAAGT CCTGCA
 ||||| |||||
 GGGCGTTCG GGACGT
 ACTCT_
 GAM1925 IL13RA1 3' TGTAGGGGAACCTATTTGGGGT 7286 G ACCA_
 G CACCT CAAGT CTCCTGCA
 |||| |||| |||||
 GTGGG GTTTA GGGGATGT
 _ CTCAA
 GAM1925 IRAK1 3' TGCAGGGGTGTGGAGTAGG 7301 AAGTAC
 CCTGC CACTCCTGCA
 |||| |||||
 GGATG GTGGGGACGT
 AGGT_
 GAM1925 PYCR1 3' TGTGGGAGGGTGGTTACTGTGG 34732 TG A _ _ TG
 GTG ACC CA GTA CCAC TCC CA
 || ||| |||| ||| ||
 TGG GT CAT GGTG AGG GT
 GT _ T GG GT
 GAM1925 RAB36 3' GCGGGGGTGGGTGTGGTG 11350 T AGTA
 CACC GCA CCACTCCTGC
 |||| || |||||
 GTGG TGT GGTGGGGGCG
 _ G_
 GAM1925 TFAP2C 3' TGCAGTACAGTGTGTGTGGGTG 9223 TG AGTAC C_
 CACC CA CACT CTGCA
 |||| || |||| |||||
 GTGG GT GTGA GACGT
 GT GT__ CAT
 GAM1925 TNFSF6 3' TGTAGGGGTGTGTGTGTGTGTG 6276 CT AG _
 CAC GCA TAC CACTCCTGCA
 || ||| || |||||
 GTG TGT GTG GTGGGGATGT
 _ GT T
 GAM1925 WRN 5' TGCAGGCCCTGCTTGTGGTG 6168 T CCACT
 CACC GCAAGTA CCTGCA
 |||| ||||| |||||

			GTGG TGTTCTG	GGACGT		
			— CCC—			
GAM1925	ZIC3	5'	TGCAGGAGACTCTTGCAG	9452	TACCA	
			CTGCAAG CTCCTGCA			
			GACGTTG GAGGACGT			
			TCA—			
GAM1925	APCL	3'	TGTGGGAGTGCGGGTGGGGGTG	12504	G AGTAC	TG
			CACCT CA CACTCC CA			
			GTGGG GT GTGAGG GT			
			G GGGC— GT			
GAM1925	ARHU	3'	TGCAGGGTTCGGGCTTGCGGTG	22185	T A _ T	
			CACC GCAAGT CC AC CCTGCA			
			GTGG CGTTCTG GG TG GGACGT			
			— _ C _			
GAM1925	C1orf34	3'	GCTGGAGTGCTGCAGGTG	30437	AGTAC	T A
			CACCTGCA CACTCC GC			
			GTGGACGT GTGAGG CG			
			C— T G			
GAM1925	C20orf55	3'	TGTGGGGCTGCATTTGCGGTG	25408	T AC CT TG	
			CACC GCAAGT CA CC CA			
			GTGG CGTTTA GT GG GT			
			— C_ CG GT			
GAM1925	DKFZP434L1435	5'	TGCAGGAGGCCCTGTGCAGGT	44270	AGTACCA	
	G		CACCTGCA CTCCTGCA			
			GTGGACGT GAGGACGT			
			GTCCCCG			
GAM1925	DKFZP434L1435	5'	TGCAGGAGGCCCTGTGCAGGT	46666	AGTACCA	
	G		CACCTGCA CTCCTGCA			
			GTGGACGT GAGGACGT			
			GTCCCCG			
GAM1925	DKFZP434L1435	5'	TGCAGGAGGCCCTGTGCAGGT	46704	AGTACCA	
	G		CACCTGCA CTCCTGCA			
			GTGGACGT GAGGACGT			
			GTCCCCG			
GAM1925	DKFZP564O0423	3'	TGCAGTCTTGTATTTGTGGTG	44070	T CACTC	
			CACC GCAAGTAC CTGCA			
			GTGG TGTTTATG GACGT			
			— TTCT—			
GAM1925	ETAA16	5'	TGCGGGGTGCGGTTTGTAG	21074	TAC T	
			CTGCAAG CAC CCTGCA			

		GATGTTT GTG GGGCGT		
		GGC _		
GAM1925 FASTK	5'	TGTAGGGGTGGCGCCTGCGGG	24731	A TA
		CCTGCA G CCACTCCTGCA		
		GGGCGT C GGTGGGGATGT		
		C GC		
GAM1925 FLJ13491	3'	TGTGGGGGTGGCAGGCAGGTG	23890	AAGTA TG
		CACCTGC CCACTCC CA		
		GTGGACG GGTGGGG GT		
		GAC__ GT		
GAM1925 FLJ14154	3'	GCAGGGGTGGGGTGGGGG	24273	G AGTA
		CCT CA CCACTCCTGC		
		GGG GT GGTGGGGACG		
		G GG__		
GAM1925 FLJ20343	3'	TGTGGGGGTGGGATGTGAGTG	19401	CT AGTA TG
		CAC GCA CCACTCC CA		
		GTG TGT GGTGGGG GT		
		AG AG__ GT		
GAM1925 FLJ22479	3'	TGTAGAAAATGCTTGTGGTG	24388	T CCACTC
		CACC GCAAGTA CTGCA		
		GTGG TGTTCTG GATGT		
		_ AAAA__		
GAM1925 FLJ23091	3'	TGTGGGGGTGGGGTGGGGGTG	24419	G AGTA TG
		CACCT CA CCACTCC CA		
		GTGGG GT GGTGGGG GT		
		G GG__ GT		
GAM1925 GNG4	3'	TGCAGGAGTGAGGCATGGTG	10814	_ AAGTAC
		CACC TGC CACTCCTGCA		
		GTGG ACG GTGAGGACGT		
		T GA__		
GAM1925 HSPF2	5'	GCAGGGGGCTGGCAGGTG	12049	A ACCA
		CACCTGC AGT CTCCTGC		
		GTGGACG TCG GGGGACG		
		G ____		
GAM1925 IL1RAPL1	3'	TGCAGGGGTGGGGGCGGGT	15556	AAGTA
		ACCTGC CCACTCCTGCA		
		TGGGCG GGTGGGGACGT		
		GG__		
GAM1925 KIAA0408	3'	TGCATGGCCATGTGTTTGTAGG	16236	CACT _
TG		CACCTGCAAGTAC CC TGCA		

		GTGGATGTTTGTG GG ACGT	
		TACC T	
GAM1925 KIAA0855	3'	TGTAGGGAGATATGTAGGTG 17378	A ACCAC
		CACCTGCA GT TCCTGCA	
		GTGGATGT TA GGGATGT	
		A GA__	
GAM1925 KIAA1026	3'	TGTGGGAGTAAATTGAAGGTG 35278	G GTACC TG
		CACCT CAA ACTCC CA	
		GTGGA GTT TGAGG GT	
		A AAA__ GT	
GAM1925 KIAA1203	3'	TGTGGGAGTATTTGTGGTG 35474	T ACC TG
		CACC GCAAGT ACTCC CA	
		GTGG TGT TTA TGAGG GT	
		- ____ GT	
GAM1925 KIAA1340	3'	TGTGGGGGTGTGTGTGTGTGTG 34301	CT AG _ TG
		CAC GCA TAC CACTCC CA	
		GTG TGT GTG GTGGGG GT	
		_ GT T GT	
GAM1925 MGC10715	3'	TGTGGGCAGGGCTTGTGGGTG 23617	TG A ACT TG
		CACC CAAGT CC CC CA	
		GTGG GTTCG GG GG GT	
		GT _ AC_ GT	
GAM1925 MGC2603	3'	TGTAGGAAAATATAGTTGTGGG 23472	TG G CCAC_
TG		CACC CAA TA TCCTGCA	
		GTGG GTT AT AGGATGT	
		GT G ATAAA	
GAM1925 N4BP3	3'	TGTAAAGATGTGCTTGTGGGTG 32941	TG CA CC
		CACC CAAGTAC CT TGCA	
		GTGG GTTCGTG GA ATGT	
		GT TA A_	
GAM1925 PANK	5'	TGTGGGATGTAAATTTGTAGGT 28716	ACC _ TG
		ACCTGCAAGT AC TCC CA	
		TGGATGTTTA TG AGG GT	
		AA_ T GT	
GAM1925 PPFA4	3'	TGTATGGGTGTGTGTGGGTG 34824	TG AGTAC C
		CACC CA CACTC TGCA	
		GTGG GT GTGGG ATGT	
		GT GT__ T	
GAM1925 RHO6	3'	TGTGGGGGTGGTGGTGCTGCAG 15821	A __ TG
G		CCTGCA GTACCACT CC CA	

			GGACGT CGTGGTGG GG GT		
			— TGG GT		
GAM1925	RNF24	5'	GCAGGGGTGAGGCGGTG 14087	T	AAGTAC
			CACC GC CACTCCTGC		
			GTGG CG GTGGGGACG		
			— GA—		
GAM1925	RoXaN	3'	TGCAGGGGTCCCTGTAGGT 24605		AGTACC
			ACCTGCA ACTCCTGCA		
			TGGATGT TGGGGACGT		
			CCC—		
GAM1925	STAT5A	3'	GCATGTGCTTGTGTGTG 9129	C	CACTCC
			CAC TGCAAGTAC TGC		
			GTG GTGTTCTGTG ACG		
			T T—		
GAM1925	SYTL2	3'	GCAGGACCTTTGTAGGT 26175		TACCAC
			ACCTGCAAG TCCTGC		
			TGGATGTTT AGGACG		
			CC—		
GAM1925	SYTL2	3'	GCAGGACCTTTGTAGGT 26759		TACCAC
			ACCTGCAAG TCCTGC		
			TGGATGTTT AGGACG		
			CC—		
GAM1925	TTY2	5'	GGGGAGTGTTGCGAGTG 42072	C	GTAC TG
			CAC TGCAA CACTCC C		
			GTG GCGTT GTGAGG G		
			A — GT		
GAM1925	TUBGCP3	3'	TGCAGGAAGTGCATGCTGCAGG 13014		A C_ C_
	TG		CACCTGCA GTA CA TCCTGCA		
			GTGGACGT CGT GT AGGACGT		
			— AC CA		
GAM1925	UPLC1	3'	TGCAGGGGTGGTCCTTTGGTG 19285	TGC	T
			CACC AAG ACCACTCCTGCA		
			GTGG TTC TGGTGGGGACGT		
			T_ C		
GAM1925	LOC121344	3'	TGTGGGGGTGGTGGGGTACAGG 36658	CAAG_	TG
			CCTG TACCACTCC CA		
			GGAC GTGGTGGGG GT		
			ATGGG GT		
GAM1925	LOC124976	3'	TGCGGGGTGGGGTGGGGG 36785	G	AGTA
			CCT CA CCACTCCTGCA		

GGG GT GGTGGGGGCGT
G GG__
GAM1925 LOC127845 5' GCGGGGGTGGAGCGGG 36912 AAGTA
CCTGC CCACTCCTGC
||||| |||||
GGGCG GGTGGGGGCG
A__
GAM1925 LOC137964 3' TGTGGGGATTAAAGTGCTGCGG 37113 A CAC__ TG
GTG ACCTGCA GTAC TCC CA
||||| ||| ||
TGGGCGT CGTG GGG GT
_ AAATTA GT
GAM1925 LOC139231 3' GGGGGGTGGGCAAGGTG 37143 _ AAGTA TG
CACCT GC CCACTCC C
||||| || ||||| |
GTGGA CG GGTGGGG G
A _____ GT
GAM1925 LOC144266 5' TGTAGGGGTGGTGCCAAGGGTG 37712 GCAA
CACCT GTACCACTCCTGCA
||||| |||||
GTGGG CGTGGTGGGGATGT
AAC_
GAM1925 LOC145826 5' TGTGGGGGATTTTGTGTTGGTG 40610 T TACCA TG
CACC GCAAG CTCC CA
||||| ||| ||
GTGG TGTTT GGGG GT
T TA__ GT
GAM1925 LOC148113 3' TGGGGAGCTGGTTGTGGGTG 38472 TG AGT _ GCA
CACC CA ACCA CTCCT
||||| || |||||
GTGG GT TGGT GAGGG
GT _ C GTG
GAM1925 LOC149566 3' TGTAGCTTGTGCCTGTGGGTG 41019 TG A CACTC
CACC CA GTAC CTGCA
||||| || |||||
GTGG GT CGTG GATGT
GT C TTC__
GAM1925 LOC152633 5' TCGTATGAGTACTTGTGTGTG 41535 C _ CTCC
CAC TGCAAGTAC CA TGCA
||| ||||| || |||||
GTG GTGTTTCATG GT GCGT
T A AT__
GAM1925 LOC153711 5' TGCGGGGGTGGGGACGGCGGTG 41670 T AAGTA
CACC GC CCACTCCTGCA
||||| || |||||
GTGG CG GGTGGGGGCGT
_ GCAGG
GAM1925 LOC159148 5' GGGGAGTGTTGCGAGTG 42079 C GTAC TG
CAC TGCAA CACTCC C
||| ||||| ||||| |

		GTG GCGTT GTGAGG G		
		A _____ GT		
GAM1925	LOC196283 3'	TGCCATGGTATATGTGGGTG 42341	TG A	CTCCT
		CACC CA GTACCA GCA		
		GTGG GT TATGGT CGT		
		GT A AC____		
GAM1925	LOC197358 3'	TGCAGGAGTGGTCCAGGCAGG 42511	AAGT	
		CCTGC ACCACTCCTGCA		
		GGACG TGGTGAGGACGT		
		GACC		
GAM1925	LOC201799 3'	TGTAGGTAGGAAGTATGTGCAG 42918	A CA_ _	
	GTG	CACCTGCA GTAC CT CCTGCA		
		GTGGACGT TATG GA GGATGT		
		G AAG T		
GAM1925	LOC201965 3'	TGTGGGTAGTATTTGTGGT 42936	T	CACT TG
		ACC GCAAGTAC CC CA		
		TGG TGTTTATG GG GT		
		_ AT__ GT		
GAM1925	LOC253891 5'	TGCGGCCTCCTTGTTCAGG 45324		CCACTC
		CCTGCAAGTA CTGCA		
		GGACGTTTGT GGC GT		
		TCCTCC		
GAM1925	LOC253897 3'	TGTGGGGATTAAAGTGCTGCGG 45969	A CAC____ TG	
	GTG	ACCTGCA GTAC TCC CA		
		TGGGCGT CGTG GGG GT		
		_ AAATTA GT		
GAM1925	LOC256806 5'	GCAGAGTATCTGCAGGTG 46142	AG	CACTC
		CACCTGCA TAC CTGC		
		GTGGACGT ATG GACG		
		CT A____		
GAM1925	LOC51608 3'	TGCCTACGGGTACTTGCACTG 31841	C	ACTCCT
		CA CTGCAAGTACC GCA		
		GT GACGTTTATGG CGT		
		C GCATC_		
GAM1925	LOC91694 3'	TGCGTGTGTGCTTGTGGG 33251	TG	_ TCCT
		CC CAAGTAC CAC GCA		
		GG GTTCGTG GTG CGT		
		GT T _____		
GAM1926	GARP 3'	TGTTGACCTGTCAGATCAACA 12035	AAG	_
		TGTT TTGA AGGTCAACA		

	ACAA GACT TCCAGTTGT	
	CTA G	
GAM1926 ARPP-21	5' TGTGGACCCTCAAAGGGCATA 18421	AAG A
	TATGTT TTGA GGTCAACA	
	ATACGG AACT CCAGTTGT	
	GA_ C	
GAM1926 KIAA1577	5' AGTGAATTACCCAACTTAAC 32209	AA CAA_
	GTTAAGTTG GGT CACT	
	CAATTCAAC CCA GTGA	
	_ TTAA	
GAM1926 MGC4400	3' AGTGTTCACCAAACCTAACA 26399	A GAA _
	TGTTA GTT GGT CAACACT	
	ACAAT CAA CCA GTTGTGA	
	_ A_ C	
GAM1926 LOC145622	3' AGGGTTCCTTCAGCCCAACATA 37905	AA TC A
	TATGTT GTTGAAGG AAC CT	
	ATACAA CGACTTCC TTG GA	
	CC _ G	
GAM1926 LOC145622	5' AGGGTTCCTTCAGCCCAACATA 37906	AA TC A
	TATGTT GTTGAAGG AAC CT	
	ATACAA CGACTTCC TTG GA	
	CC _ G	
GAM1927 NINJ1	3' ACCTTGATATACCCTGCACC 10350	_ ATAA C
	GGT CA TA ATACAAGGT	
	CCA GT AT TATGTTCCA	
	C CCC_ A	
GAM1927 WSB1	3' ACCTCAAGCTTTACTGACTTCA 28620	A TACATACA
	TGAGGTCA TAA AGGT	
	ACTTCAGT ATT TCCA	
	C TCGAAC_	
GAM1927 WSB1	3' ACCTCAAGCTTTACTGACTTCA 28614	A TACATACA
	TGAGGTCA TAA AGGT	
	ACTTCAGT ATT TCCA	
	C TCGAAC_	
GAM1927 LOC120856	3' TATGTATTCTGACCTCA 36643	AT
	TGAGGTCA AATACATA	
	ACTCCAGT TTATGTAT	
	C_	
GAM1927 LOC144997	3' ACCTTGATACATGTGAAACCT 40482	CAATA CA
	AGGT ATA TACAAGGT	

			TCCA TGT ATGTTCCA		
			AAG__ AC		
GAM1928	ADAR	3'	CGGTCTTGATTAGGTTTCAGTC 6772	_	T TTG
	A		TGACTGGG CCTAGTCA GATC		
			ACTGACTT GGATTAGT CTGG		
			T T C		
GAM1928	ADAR	3'	CGGTCTTGATTAGGTTTCAGTC 17958	_	T TTG
	A		TGACTGGG CCTAGTCA GATC		
			ACTGACTT GGATTAGT CTGG		
			T T C		
GAM1928	ADAR	3'	CGGTCTTGATTAGGTTTCAGTC 17965	_	T TTG
	A		TGACTGGG CCTAGTCA GATC		
			ACTGACTT GGATTAGT CTGG		
			T T C		
GAM1928	AKAP13	3'	CAGGGAGTTTGGGCTTGGTT 43177	TG	TCATGA
			GAC GGCCTAG TCTTG		
			TTG TCGGGTT GGGAC		
			GT TGA__		
GAM1928	AKAP2	3'	GGATCGTGTCTGCTTA 14061	CT T	
			TGGGC AG CATGATCT		
			ATTCG TC GTGCTAGG		
			_ T		
GAM1928	ALDH3B2	3'	CAGGGTTGGCCAGGCCAGTCA 6357	A	TG
			TGACTGGGCCT GTCA ATCTTG		
			ACTGACCCGGA CGGT TGGGAC		
			C _		
GAM1928	AP2B1	3'	TAAGATCATCCCAGAGGTTTCAG 6954	AGTC_	
			CTGGGCCT ATGATCTTG		
			GACTTGGA TACTAGAAT		
			GACCC		
GAM1928	APTX	3'	CAGGATTAGGAATTTGGGTTTG 19248	T _	A
	TCA		GAC GGCCTAG TC TGATCTTG		
			CTG TTTGGGTT AG ATTAGGAC		
			_ TA G		
GAM1928	APXL	3'	TGTGGTTGGGTTCACTCA 7357	C	GT
			TGA TGGGCCTA CATG		
			ACTACTTGGGT GTGT		
			C TG		
GAM1928	B3GAT1	3'	GGGCAGATGCTAGGTCAGTT 20719	G	CA_ A
			GACTGG CCTAGT TG TCT		

TTGACT GGATCG AC GGG
 _ TAG _
 GAM1928 B3GAT1 3' GGGCAGATGCTAGGTCAGTT 27631 G CA_ A
 GACTGG CCTAGT TG TCT
 ||||| ||||| || |||
 TTGACT GGATCG AC GGG
 _ TAG _
 GAM1928 B4GALT1 3' CAGGGCACAGTTAGGCCTGG 7245 TG CA A
 C GGCCTAGT TG TCTTG
 | ||||| || |||||
 G CCGGATTG AC GGGAC
 GT AC _
 GAM1928 BAALC 3' GGGATTTGGGGTCTGGTTA 24196 TG AGTCAT
 TGAC GGCCT GATCTT
 ||| |||| |||||
 ATTG CTGGG TTAGGG
 GT GT____
 GAM1928 BCL2 3' CAGGATTACATGCATGTTTGGT 6251 TG CTA T _
 TA TGAC GGC G CATG ATCTTG
 ||| || | ||| |||||
 ATTG TTG C GTAC TAGGAC
 GT TA__ AT
 GAM1928 BCL2 3' GAGGGGTGTGGCTGGGCCTGTC 6258 T AT G
 A TGAC GGGCCTAGTCATG CTT
 ||| ||||| ||||| |||
 ACTG TCCGGGTCGGTGT GGA
 _ GG GA
 GAM1928 BCL7A 3' GGGGTCATGGGTTTTGTT 21995 TG TAGT
 GAC GGCC CATGATCTT
 || |||| |||||
 TTG TTGG GTACTGGGG
 TT ____
 GAM1928 CBFA2T2 3' GAGAGAATGAGGCTCAGTT 11549 TAG GA G
 GACTGGGCC TCAT TCTT
 ||||| ||| |||||
 TTGACTCGG AGTA AGAG
 _ AG A
 GAM1928 CD28 3' TGAGATCAGGACCAGCCTGGTC 12784 TG CTA A
 A TGAC GGC GTC TGATCTTG
 ||| || ||| |||||
 ACTG CCG CAG ACTAGAGT
 GT AC_ G
 GAM1928 CD44 3' CAGGGTTAATAGGGCCTGGTC 6211 TG A CA
 GAC GGCCT GT TGATCTTG
 || |||| || |||||
 CTG CCGG TA ATTGGGAC
 GT A _
 GAM1928 CDKN2A 5' CGAGATCTTGAGGTCCGG 27756 AG T
 CTGGGCCT TCA GATCTTG
 ||||| || |||||

GGCCTGGA GGT CTAGAGC
— T
GAM1928 CELSR1 3' TGAGGTCACTGTGGGGCACGGT 15518 G AGT _
T GACTG GCCT CA TGATCTTG
||||| ||| || |||||
TTGGC CGGG GT ACTGGAGT
A GT_ C
GAM1928 CHN1 5' CGGGGCTCCCTGGGCCCGGT 7561 TCAT _
ACTGGGCCTAG GA TCTTG
||||||| || |||||
TGGCCCGGGTC CT GGGGC
C_ C
GAM1928 CKAP1 5' AAGGCGCTTGGCTTGGTT 36400 TG T CAT A
GAC GGCC AGT G TCTT
||| ||| ||| | |||
TTG TCGG TCG C GGAA
GT T _ _
GAM1928 CLCN5 3' TAAGATTGCTATGGTTTAATTA 5536 C _ CAT
TGA TGGGCC TAGT GATCTTG
||| ||||| ||| |||||
ATT ATTTGG ATCG TTAGAAT
A T _
GAM1928 COL4A4 5' CAAGGTCCGGGGGCCAG 5551 AGTCAT
CTGGGCCT GATCTTG
||||||| |||||
GACCCGGG CTGGAAC
GGC_
GAM1928 COL4A5 5' CAAGATTATGTCAATTGGTTA 6109 TG GCCTAGT
TGAC G CATGATCTTG
|||| | |||||
ATTG T GTATTAGAAC
GT AACT_
GAM1928 COL4A5 5' CAAGATTATGTCAATTGGTTA 27215 TG GCCTAGT
TGAC G CATGATCTTG
|||| | |||||
ATTG T GTATTAGAAC
GT AACT_
GAM1928 COL4A5 5' CAAGATTATGTCAATTGGTTA 27212 TG GCCTAGT
TGAC G CATGATCTTG
|||| | |||||
ATTG T GTATTAGAAC
GT AACT_
GAM1928 CX3CR1 3' TCAGACTAGTTTAGTTA 34980 C A
TGA CTGGGC TAGTC TGA
||||||| ||||| |||
ATTGATTTG ATCAG ACT
— —
GAM1928 CYP51 5' CGAGGGGTGGGGCTGGGTTTAG 6437 ATGA_
T ACTGGGCCTAGTC TCTTG
||||||| |||||

			TGATTTGGGTCGG	GGAGC		
			GGTGG			
GAM1928	DAAM2	3'	TAAGAAGGGGCTGGTGCCCAGT	44332	_	ATGA
	C		GA CTGGGC CTAGTC	TCTTG		
			CTGACCCG GGTCGG	AGAAT		
			T	GGA_		
GAM1928	DGKG	3'	TGAGGTTGTGGCTGGCTTAG	7028	T	TG
			CTGGGCC AGTCA	ATCTTG		
			GATTCGG TCGGT	TGGAGT		
			_	GT		
GAM1928	DVL3	3'	TGGGTCTCAGGCTGGGCTCAGC	10700	A	AT_ TG
	A		TG CTGGGCCTAGTC	GATCT		
			AC GACTCGGGTCGG	CTGGG		
			_	ACT T		
GAM1928	EGFL5	3'	TAAGGTCCTGTGGGCCTAGT	41884	GT	T
			ACTGGGCCTA CA	GATCTTG		
			TGATCCGGGT	GT CTGGAAT		
			_	C		
GAM1928	EMP1	3'	CAGGGCTCCTAGGCTCAGT	7132	TCAT	_
			ACTGGGCCTAG	GA TCTTG		
			TGACTCGGATC	CT GGGAC		
			_	C		
GAM1928	ENC1	3'	TGGGATTTTCATGGGGTTTGGTT	9700	TG	AGT _
			GAC GGCCT	CATGA TCTTG		
			TTG TTGGG	GTA CT AGGGT		
			GT	_ TT		
GAM1928	EPS8	3'	CAGGATTTGCTTCTAGGCCCA	10742	TCAT_	
			TGGGCCTAG	GATCTTG		
			ACCCGGATC	TTAGGAC		
			TTCGT			
GAM1928	EXT2	3'	TGCTTCCTGATTAGATCCAGTC	5975	GC	T TCTTG
	A		TGACTGG	CTAGTCA GA		
			ACTGACC	GATTAGT CT		
			TA	C TCGT		
GAM1928	EXTL1	5'	TAGGGTTTGGGGGGCTTGGCA	10758	A TG	AG T
			TG C GGCCT	TCA GATCTTG		
			AC G TCGGG	GGT TTGGGAT		
			_ GT	G_ _		
GAM1928	FBLN1	3'	GAGGGCAGGGATTGTGTCTGGT	13211	TG C	A_ A G
	TA		TGAC GGC	TAGTC TG TCTT		

		ATTG CTG GTTAG AC GGGA	
		GT T GG _ GT	
GAM1928 FCMD	3'	TAAGATTGTGGAGTCTGAGTTA 13575	G C AG TG
		TGACT GG CT TCA ATCTTG	
		ATTGA TC GA GGT TAGAAT	
		G T _ GT	
GAM1928 FLG	3'	GGACGGGCTGGGCCCAGT 35108	A A
		ACTGGGCCTAGTC TG TCT	
		TGACCCGGGTCGG GC AGG	
		— —	
GAM1928 FLNB	3'	GTGAAGTTGGGCTCAGCCG 31146	A _
		TG CTGGGCCTAG TCAT	
		GC GACTCGGGTT AGTG	
		C GA	
GAM1928 FSTL1	3'	CAGGATTAACTAGGTTTGGTT 13949	TG CA
		GAC GGCCTAGT TGATCTTG	
		TTG TTGGATCA ATTAGGAC	
		GT A_	
GAM1928 GALR1	3'	TAGGAAATTCCTAGGTCTAGT 7217	TC GA
		ACTGGGCCTAG AT TCTTG	
		TGATCTGGATC TA AGGAT	
		CT A_	
GAM1928 GJB3	3'	TGGGGCTTGAGCTGGAGCTCGG 23443	_ _ TGA TG
TTA		GACTGGGC CTAG TCA TCT	
		TTGGCTCG GGTC AGT GGG	
		A G TCG T	
GAM1928 GNAI1	5'	CGAGCTCGGCTGGGCTTGGCG 7840	A TG AT T
		TG C GGCCTAGTC GA CTTG	
		GC G TCGGGTCGG CT GAGC	
		_ GT _ C	
GAM1928 GORASP1	3'	CAGGAGGCAGCAGGGTCTGGTC 25645	TG A CA A_
A		TGAC GGCCT GT TG TCTTG	
		ACTG CTGGG CG AC AGGAC	
		GT A _ GG	
GAM1928 GRLF1	3'	CGAGGTTATGCTCACCTGGTCA 38412	TG CCT T
		TGAC GG AG CATGATCTTG	
		ACTG CC TC GTATTGGAGC	
		GT AC_ _	
GAM1928 H3F3B	3'	TAAGATGGTGTGGGTTAGGTT 11796	GG T G
A		TGACT GCCTAG CAT ATCTTG	

ATTGG TGGGTT GTG TAGAAT
 AT _ G
 GAM1928 HD 3' CGACTGTCATGTGGCTTGGTTT 7893 TG T _ CTTG
 GGTCA AC GGCC AGT CATGAT
 || ||| ||| |||||
 TG TTGG TCG GTACTG
 GT T GT TCAGC
 GAM1928 HS3ST3A1 5' GGGTCCAGGCCTAGCA 12678 A AGTCAT
 TG CTGGGCCT GATCT
 || ||||| |||
 AC GATCCGGA CTGGG
 _ C _
 GAM1928 ICAM1 3' CAAGGTCACCAGGTACAGTT 35441 GG A CAT
 GACTG CCT GT GATCTTG
 |||| ||| || |||||
 TTGAC GGA CA CTGGAAC
 AT C _
 GAM1928 ID4 5' GGCCGCGATCGGGCTTAGTC 7273 TA A AT
 GACTGGGCC GTC TG C
 ||||| ||| || |
 CTGATTCCG TAG GC G
 GC C CG
 GAM1928 IDH1 5' TGGGATTGCCAGGCTGTGGTT 30801 _ A CAT
 GACTG GGCCT GT GATCTTG
 |||| |||| || |||||
 TTGGT TCGGA CG TTAGGGT
 G C _
 GAM1928 IL11 3' CAAGGTCAAGATGGTTCA 6279 TA A
 TGGGCC GTC TGATCTTG
 |||| ||| |||||
 ACTTGG TAG ACTGGAAC
 _ A
 GAM1928 IL13RA1 3' GTCTGGGCTGGGTCCGGT 7285 AT
 ACTGGGCCTAGTC GAT
 ||||| ||||| |||
 TGGCCTGGGTCGG CTG
 GT
 GAM1928 ITGB3 3' TAGGAACTGCTGGGCTTGGCA 5709 A TG T TGA
 TG C GGCCTAG CA TCTTG
 || | ||||| || |||||
 AC G TCGGGTC GT AGGAT
 _ GT _ CA _
 GAM1928 ITS1 3' GGGTCACTGGGTCTCGGT 8956 _ CAT
 GACTG GGCCTAGT GATCT
 |||| ||||| |||||
 TTGGC CTGGGTCA CTGGG
 T _
 GAM1928 JRK 3' TGAGGTTATGGGTGTTGGT 41839 _ G
 GCC TA TCATGATCTTG
 ||| || ||||| |||||

			TGG GT GGTATTGGAGT		
			TT G		
GAM1928	JRK	3'	TGGGAGGTGACTAGGCTTAG 41840	GA	
			CTGGGCCTAGTCAT TCTTG		
			GATTCGGATCAGTG AGGGT		
			G_		
GAM1928	JUN	3'	CAAGTTGGACTGGGTTCCGGTC 8010	ATGAT	
			GACTGGGCCTAGTC CTTG		
			CTGGCTTGGGTCAG GAAC		
			GTT_		
GAM1928	KCNA7	3'	AAGAGCTAGGTTAAGTCA 25627	GG	CATGA
			TGACT GCCTAGT TCTT		
			ACTGA TGGATCG AGAA		
			AT		
GAM1928	KCNA7	3'	TAGGGCCATGTTGGGTCAAGTT 25629	G	T AT
	A		TGACT GGCCTAG CATG CTTG		
			ATTGA CTGGGT GTAC GGAT		
			A _ CG		
GAM1928	KCNA7	3'	TAGGTCAGTGTTGGGTTTGGTT 25630	TG	T _ TG
			GAC GGCCTAG CA TGATCT		
			TTG TTGGGT GT ACTGGA		
			GT _ G T		
GAM1928	KCNA7	3'	AGGAAGTTGGGTTGAGTT 25628	G	TCATGA
			GACT GGCCTAG TCTT		
			TTGA TTGGGT AGGA		
			G GA_		
GAM1928	LAMP2	3'	TGGGATTATGTGCCTCCCATTC 15186	C	CCTAGT
	A		TGA TGGG CATGATCTTG		
			ACT ACCC GTATTAGGGT		
			T TCCGT_		
GAM1928	MAFF	3'	CAGGATTCAAAGCTAGGTTTGG 14700	TG	CA _
			C GGCCTAGT TGA TCTTG		
			G TTGGATCG ACT AGGAC		
			GT AA T		
GAM1928	MAPRE2	3'	AGGATTTCAAGGCCAGCA 15544	A	AGTCAT
			TG CTGGGCCT GATCTT		
			AC GACCCGGG TTAGGA		
			_ ACT_		
GAM1928	MAPRE3	3'	GGGTGGTGCTGGCCCAGTT 14716	T T	G
			GACTGGGCC AG CAT ATCT		

TTGACCCGG TC GTG TGGG
 _ _ G
 GAM1928 MAT1A 3' CAGGGGGAGCTGGGCCTGGTC 43665 TG CATGA
 GAC GGCCTAGT TCTTG
 ||| ||||| ||||
 CTG CCGGGTCG GGGAC
 GT AGG__

GAM1928 MGAT1 3' GGGGGCACTGGGCTTGTT 8228 T CATGA
 GAC GGCCTAGT TCTT
 ||| ||||| ||||
 TTG TTCGGGTCA GGGG
 _ CG__

GAM1928 MGEA5 3' TAATCATGTTGGCTGGTCTGGT 14518 TG T ____ CTTG
 CA GAC GGCC AGT CATGAT
 ||| ||||| ||||
 CTG CTGG TCG GTACTA
 GT _ GTT AT

GAM1928 MTMR8 3' GAGGGAGTTTGTATTAGGTCTG 17745 TG _ TGA G
 GTCA GAC GGCCTAGT CA TCTT
 ||| ||||| || ||||
 CTG CTGGATTA GT AGGG
 GT T TTG AGT

GAM1928 NFIB 5' TAAGGAGGACTGGGTTTGTT 12122 T ATGA
 GAC GGCCTAGTC TCTTG
 ||| ||||| ||||
 TTG TTTGGGTCAG GGAAT
 _ GA__

GAM1928 NT5C3 3' GAAATTGTGTTAGGTTTGTTA 18582 TG T TG CTTG
 TGAC GGCCTAG CA AT
 |||| ||||| || ||
 ATTG TTGGATT GT TA
 GT _ GT AAGT

GAM1928 OSR1 5' AGAGGGGCTGGGCCAG 11588 ATGA
 CTGGGCCTAGTC TCT
 ||||| ||||| ||||
 GACCCGGGTCGG AGA
 GG__

GAM1928 PAX5 3' AGGAGTCTCACTGGGCTGGTT 18789 TG G CAT _ G
 GAC G CCTAGT GA TCTT
 ||| | ||||| || ||||
 TTG C GGGTCA CT AGGA
 GT _ CT _ G G

GAM1928 PCDH11X 3' CAAGGGGTATTAGCCCAGTTA 26789 C C GA
 TGA CTGGGC TAGT AT TCTTG
 ||||| ||||| || ||||
 ATTGACCCG ATTA TG GGAAC
 _ _ G_

GAM1928 PCDH11X 3' CAAGGGGTATTAGCCCAGTTA 26804 C C GA
 TGA CTGGGC TAGT AT TCTTG
 ||||| ||||| || ||||

ATTGACCCG ATTA TG GGAAC
 _ _ G_
 GAM1928 PCDH11Y 3' CAAGGGGTATTAGCCCAGTTA 26823 C C GA
 TGACTGGGC TAGT AT TCTTG
 ||||||| ||||| || |||||
 ATTGACCCG ATTA TG GGAAC
 _ _ G_
 GAM1928 PGD 3' AGGATTATGCTTCACTCA 38522 CCT T
 TGGG AG CATGATCTT
 |||| || |||||
 ACTC TC GTATTAGGA
 ACT _
 GAM1928 PIK3CG 3' TAGGATTATTTGCAGGTTTGGT 8512 TG A C_
 T GAC GGCCT GT ATGATCTTG
 ||| ||||| || |||||
 TTG TTGGA CG TATTAGGAT
 GT _ TT
 GAM1928 PIK3R3 3' CAAGATCAGAGGGGTTCA 30601 AG A
 TGGGCCT TC TGATCTTG
 ||||||| || |||||
 ACTTGGG AG ACTAGAAC
 G_ _
 GAM1928 PLAGL1 3' CAGGGTTGGATGTAGTTTAGTT 8528 CTA A
 A TGACTGGGC GTC TGATCTTG
 ||||||| ||| |||||
 ATTGATTG TAG GTTGGGAC
 ATG _
 GAM1928 PLXNA1 3' AGGGTCCCGGGGCGCGTT 35790 AGTCAT
 GACTGGGCCT GATCTT
 ||||||| |||||
 TTGGCCCGGG CTGGGA
 GCC__
 GAM1928 PNUTL1 3' GGGTCGTGACCGCTTA 8547 CTA
 TGGGC GTCATGATCT
 |||| |||||
 ATTCG CAGTGCTGGG
 C_
 GAM1928 PPIL1 3' CAAGATTTTATATGTTTCAGTT 18133 C GTCAT
 GACTGGGC TA GATCTTG
 ||||||| || |||||
 TTGACTTG AT TTAGAAC
 T ATTT_
 GAM1928 PPP2R5E 5' GAGGTTCGGGTCCGGCCG 12922 A AGTCAT
 TG CTGGGCCT GATCTT
 || ||||| |||||
 GC GGCCTGGG TTGGAG
 C C__
 GAM1928 PRDM4 3' AGGGTCCCAGCTTAGTTA 14784 CTAGTCAT
 TGACTGGGC GATCTT
 ||||||| |||||

			ATTGATTCTG	CTGGGA		
			ACC_____			
GAM1928	PSA	3'	TGGGGTCTCCTGGGTTTCAGCG	22132	A	TCAT
			TG CTGGGCCTAG GATCTTG			
			GC GACTTGGGTC CTGGGGT			
			CT__			
GAM1928	PSA	3'	TGGGGTCTCCTGGGTTTCAGCG	27741	A	TCAT
			TG CTGGGCCTAG GATCTTG			
			GC GACTTGGGTC CTGGGGT			
			CT__			
GAM1928	PSAP	3'	TGGGGTTCTGTGGGTTTGG	34375	TG	GT T
			C GGCCTA CA GATCTTG			
			G TTGGGT GT TTGGGGT			
			GT __ C			
GAM1928	PTEN	5'	AGGAGAAGCAGGCCAGTC	5850	A	CATGA
			GACTGGGCCT GT TCTT			
			CTGACCCGGA CG AGGA			
			__ AAG__			
GAM1928	PTGS1	3'	GGGATCCTTGGGCCCATCA	6675	C	TCAT
			TGA TGGGCCTAG GATCTT			
			ACT ACCCGGGT CTAGGG			
			C__			
GAM1928	PTGS1	3'	GGGATCCTTGGGCCCATCA	27896	C	TCAT
			TGA TGGGCCTAG GATCTT			
			ACT ACCCGGGT CTAGGG			
			C__			
GAM1928	PTP4A2	3'	CAGATTCTTGGCTGGGTTTAGT	9551	T_	TG
			ACTGGGCCTAGTCA GATCT			
			TGATTGGGTCGGT TTAGA			
			TC C			
GAM1928	RAD17	5'	AAGATTATAGTACCAGTCA	8782	GC	GTCA
			TGACTGG CTA TGATCTT			
			ACTGACC GAT ATTAGAA			
			AT ____			
GAM1928	RAD17	5'	AAGATTATAGTACCAGTCA	28487	GC	GTCA
			TGACTGG CTA TGATCTT			
			ACTGACC GAT ATTAGAA			
			AT ____			
GAM1928	RAD17	5'	AAGATTATAGTACCAGTCA	28483	GC	GTCA
			TGACTGG CTA TGATCTT			

			ACTGACC GAT ATTAGAA		
			AT ____		
GAM1928	RAD17	5'	AAGATTATAGTACCAGTCA 28485	GC	GTCA
			TGACTGG CTA TGATCTT		
			ACTGACC GAT ATTAGAA		
			AT ____		
GAM1928	RAD17	5'	AAGATTATAGTACCAGTCA 28479	GC	GTCA
			TGACTGG CTA TGATCTT		
			ACTGACC GAT ATTAGAA		
			AT ____		
GAM1928	RAD17	5'	AAGATTATAGTACCAGTCA 28489	GC	GTCA
			TGACTGG CTA TGATCTT		
			ACTGACC GAT ATTAGAA		
			AT ____		
GAM1928	RAD21	3'	GAGCAAAGCTAGGCCTGATTA 12945	CT	CA A
			TGA GGGCCTAGT TG TC		
			ATT TCCGGATCG AC AG		
			AG AA G		
GAM1928	RFXAP	5'	CGGGGTCTGTTGACCCCGGCC 6135	TAG__	
			GGCC TCATGATCTTG		
			CCGG GGTGCTGGGGC		
			CCCCA		
GAM1928	RGS2	3'	TGGGATTATGTGGCCTTAGGT 8827	__	TAGT
			ACT GGGCC CATGATCTTG		
			TGG TCCGG GTATTAGGGT		
			AT T__		
GAM1928	RNF14	5'	CAGGGCGTTTCTAGGCCTGGTC 10503	TG	TC A
			GAC GGCCTAG ATG TCTTG		
			CTG CCGGATC TGC GGGAC		
			GT TT _		
GAM1928	RNMT TA	3'	CAAGATTGTGATTAGACACATT 9879	C GGC	TG
			TGA TG CTAGTCA ATCTTG		
			ATT AC GATTAGT TAGAAC		
			T ACA GT		
GAM1928	RNPEPL1	3'	GGGGTTGGCAGCCTCAGTT 20163	C A	TGA
			GACTGGG CT GTCA TCT		
			TTGACTC GA CGGT GGG		
			C _ TG_		
GAM1928	RP2	5'	GGGGGTGCTGGGCCTGGCG 13794	A TG	T GA
			TG C GGCCTAG CAT TC		

			GC G CCGGGTC GTG GG		
			_GT _ GG		
GAM1928	RUNX1	3'	GGCAGTTATTGGGTTTGGTCA 7501	TG	C GA
			TGAC GGCCTAGT AT TC		
			ACTG TTGGGTTA TG GG		
			GT T AC		
GAM1928	SFRP1	3'	AGACTGATTGGCCTGGTCA 8926	TG T	TGA
			TGAC GGCC AGTCA TCT		
			ACTG CCGG TTAGT AGA		
			GT _ C__		
GAM1928	SFRS7	3'	AAGGTCACGGTCTAGATCA 29897	_	TAGTCA
			TGA CTGGGCC TGATCTT		
			ACT GATCTGG ACTGGAA		
			A C_____		
GAM1928	SFTPA2	3'	TGAGGTCTCTGTGGCAGGCCTG 13810	TG A	_____
			GTCA AC GGCCT GTCAT GATCTTG		
			TG CCGGA CGGTG CTGGAGT		
			GT _ TCT		
GAM1928	SLC11A3	5'	CAGGGCGTCCGCTAGGCTCGG 15942	C_ A	
			CTGGGCCTAGT ATG TCTTG		
			GGCTCGGATCG TGC GGGAC		
			CC _		
GAM1928	SLC12A7	3'	TGGGAGCCTCTGGGCTCGGCA 13377	A	TCATGA
			TG CTGGGCCTAG TCTTG		
			AC GGCTCGGGTC AGGGT		
			_ TCCG__		
GAM1928	SLC19A1	3'	GGAGGGGACTGGTCCCGGTCA 9023	C	ATGA
			TGACTGGG CTAGTC TCT		
			ACTGGCCC GGTCAG AGG		
			T GGG_		
GAM1928	SLC6A6	3'	TGGGGTCATAGCAGGTTCTGGT 9006	TG _ A	TC
			CA TGAC GG CCT G ATGATCTTG		
			ACTG CT GGA C TACTGGGGT		
			GT T _ GA		
GAM1928	SLC6A6	3'	TGGGGTCTCAGGGCTCAG 9007	AGTCAT	
			CTGGGCCT GATCTTG		
			GA CTCGGG CTGGGGT		
			ACT__		
GAM1928	SLC9A3R1	3'	AGGATCATGGGACCAG 34863	G	TAGT
			CTGG CC CATGATCTT		

GACC GG GTACTAGGA
 A ____
 GAM1928 SRP46 3' TAAGATTACGTTATTGGGTTTG 25792 TG CA__
 G C GGCCTAGT TGATCTTG
 | ||||| |||||
 G TTGGGTTA ATTAGAAT
 GT TTGC
 GAM1928 ST7 3' AGGATCAAGTCCTAGTT 22427 C AGTCA
 GACTGGG CT TGATCTT
 ||||| || |||||
 TTGATCC GA ACTAGGA
 T ____
 GAM1928 TCF19 3' TAAGGTAAGTGGGATTTGGTTA 46661 TG _ CATG
 TGAC GG CCTAGT ATCTTG
 ||| || ||||| |||||
 ATTG TT GGGTCA TGGAAT
 GT A A__
 GAM1928 TCF19 3' TAAGGTAAGTGGGATTTGGTTA 46710 TG _ CATG
 TGAC GG CCTAGT ATCTTG
 ||| || ||||| |||||
 ATTG TT GGGTCA TGGAAT
 GT A A__
 GAM1928 TCF2 3' CAGGGTTGGTGGGGGTGAGTCA 13200 G AG TG
 TGAAGTGG CCT TCA ATCTTG
 ||||| ||| || |||||
 ACTGACT GGG GGT TGGGAC
 G GT ____
 GAM1928 TH1L 3' CGAGGTTATGTACTTCCTGTT 18536 T CCT _
 GAC GGG AGT CATGATCTTG
 ||| ||| ||| |||||
 TTG CCT TCA GTATTGGAGC
 T ____ T
 GAM1928 TIMP3 5' CGGGGTCCCCGGGGGCCAGCG 5927 A AGTCAT
 TG CTGGGCCT GATCTTG
 || ||||| |||||
 GC GACCCGGG CTGGGGC
 _ GGGC__
 GAM1928 TMEFF2 5' CGAGATCATGCGCGGGTTTGG 18285 TG A_ T
 C GGCCT G CATGATCTTG
 | |||| | |||||
 G TTGGG C GTACTAGAGC
 GT CG__
 GAM1928 TMEM1 5' CGGGCTCCGGCTGGGCCCCGGCG 9291 A AT T
 TG CTGGGCCTAGTC GA CTTG
 || ||||| || |||||
 GC GGGCCGGGTCGG CT GGGC
 _ C_ C
 GAM1928 TMOD2 3' TGAGGTTGTGATTGGTGACATT 15861 C G_ T TG
 C GA TG GCC AGTCA ATCTTG
 || || || ||||| |||||

			CT AC TGG TTAGT TGGAGT		
			T AG _ GT		
GAM1928	TPI1	5'	AAGTTATTGGGCTCAGT 5936	CATGAT	
			ACTGGGCCTAGT CTT		
			TGACTCGGGTTA GAA		
			TT____		
GAM1928	TRIM37	3'	TGTCTTTGGCTAGAGCTTAGTT 17619	_ T_ CTTG	
			GA CTGGGC CTAGTCA GAT		
			TTGATT CG GATCGGT CTG		
			A TT T		
GAM1928	TRPC6	3'	AGGAAAATTATGCCAGTT 10971	C CATGA	
			GA CTGGGC TAGT TCTT		
			TTGACCCG ATTA AGGA		
			T AA____		
GAM1928	TRPM2	5'	AGGGCAGCAGGCCTGGTT 9310	TG A CA A	
			GAC GGCCT GT TG TCTT		
			TTG CCGGA CG AC GGG A		
			GT _ _ _		
GAM1928	TRPS1	3'	CGAGCTGTGGTTAGGCTTGGTT 15350	TG GT GAT	
	A		TGAC GGCCTA CAT CTTG		
			ATTG TCGGAT GTG GAGC		
			GT TG TC_		
GAM1928	WISP1	3'	CAAGACTCTTTGGGTCCATTCA 9961	C TCATGA	
			TGA TGGGCCTAG TCTTG		
			ACT ACCTGGGTT AGAAC		
			T TCTC_		
GAM1928	WNT5B	3'	CAAGGTCATCTCTGGCCCAGT 26359	T TC	
			ACTGGGCC AG ATGATCTTG		
			TGACCCGG TC TACTGGAAC		
			_ TC		
GAM1928	WNT5B	3'	CAAGGTCATCTCTGGCCCAGT 25057	T TC	
			ACTGGGCC AG ATGATCTTG		
			TGACCCGG TC TACTGGAAC		
			_ TC		
GAM1928	XT3	3'	CAGGGCCACCTGGGATCAGTCA 21442	GG TCA AT	
			TGACTG CCTAG TG CTTG		
			ACTGAC GGGTC AC GGAC		
			TA C_ CG		
GAM1928	ZIC1	3'	TGGGATTGTGGCGTTGTGGTCT 9449	TA_ TG	
			GGGCC GTCA ATCTTG		

TCTGG CGGT TAGGGT
 TGTG GT
 GAM1928 ABTB1 5' CGAGGTCGTTCCGGCTCGG 26273 TAGTC
 CTGGGCC ATGATCTTG
 ||||| |||||
 GGCTCGG TGCTGGAGC
 CT__
 GAM1928 AHCYL1 3' TAAGATCAGGAGGCCCA 13404 AGTCA
 TGGGCCT TGATCTTG
 ||||| |||||
 ACCCGGA ACTAGAAT
 GG__
 GAM1928 ARHF 3' GAGGGGGCTGGGCCTATCA 21120 C ATGA
 TGA TGGGCCTAGTC TC
 || ||||| ||
 ACTATCCGGGTCGG AG
 _ GGG_
 GAM1928 ARL8 5' CGGGTCGGCGTTGGGCTCAGT 44761 TCA TG
 ACTGGGCCTAG TGATCT
 ||||| |||||
 TGA CTGGGTT GCTGGG
 GCG C
 GAM1928 ARNTL2 3' TGGGATATTTATGCTCAGTT 21419 C TCATG
 GACTGGGC TAG ATCTTG
 ||||| || |||||
 TTGACTCG ATT TAGGGT
 T TA__
 GAM1928 ATF3 3' AGGGTTGTGCTTTCTAGCA 10242 A CCT T TG
 TG CTGGG AG CA ATCTT
 || |||| || || |||||
 AC GATCT TC GT TGGGA
 _ T__ _ GT
 GAM1928 BTN1A1 3' AGGGATCGAGATTGGGTCAGGT 7467 G A G
 TA TGA CTGGCCTAGTC TGATCTT
 |||| ||||| |||||
 ATTGG CTGGGTTAG GCTAGGG
 A A AT
 GAM1928 BTN2A2 3' TGAGGTTTGAGGTCCTGGTC 13861 TG _ AGTCAT
 GAC GG CCT GATCTTG
 || || || |||||
 CTG CC GGA TTGGAGT
 GT T GT__
 GAM1928 C11orf11 5' CGGGATCGTGTTGTTCCGGCG 44785 A CCTA
 TG CTGGG GTCATGATCTTG
 || |||| |||||
 GC GGCCT TGGTGCTAGGGC
 _ TG__
 GAM1928 C20orf178 3' GTGGGGTCCAGCGCTGGCTGGG 36936 T____
 CCCAG GGCCTAGTCA GATCTTG T
 ||||| ||||| |

CCGGGTCGGT CTGGGGT G
 CGCGAC
 GAM1928 C20orf42 3' TAAGATTGCTCTAAGGCCCAGC 19215 A _ TCA
 A TG CTGGGCCT AG TGATCTTG
 || ||||| || |||||
 AC GACCCGGA TC GTTAGAAT
 _ A TC_
 GAM1928 C20orf98 3' CAGGCAATTACTAGCCCTAGTT 35412 C C GAT
 GACTGGG CTAGT AT CTTG
 ||||| |||| || ||||
 TTGATCC GATCA TA GGAC
 C T AC_
 GAM1928 C21orf4 5' CAGGGTTGTGGCGCAGCAGTC 12775 G_ CTA TG
 GACTG GC GTCA ATCTTG
 |||| || |||| |||||
 CTGAC CG CGGT TGGGAC
 GA _ GT
 GAM1928 CHL1 3' CAAGGTTGTGACGTTCTGAGCTT 13391 CTA_ TG
 AGTT CTGGGC GTCA ATCTTG
 |||| |||| |||||
 GATTCG CAGT TGGAAC
 AGCTTG GT
 GAM1928 CHODL 5' GGGCAGCTGGGCTCGG 24491 CA A
 CTGGGCCTAGT TG TCT
 ||||| || ||||
 GGCTCGGGTCG AC GGG
 _ _
 GAM1928 CNOT7 3' TGAGATCGTGGACCATCAGTT 15004 GCCTAG
 GACTGG TCATGATCTTG
 |||| |||||
 TTGACT GGTGCTAGAGT
 ACCA_
 GAM1928 CXYorf1 5' TGGGGTGGCAGCTGATTAGGCC 39915 _ AT_ G
 CAGCA CTGGGCCTAGTCA TG CTT
 ||||| || ||||
 GACCCGATTAGT AC GGG
 CG GGT GT
 GAM1928 D4ST-1 3' CAGGATTATGCAGTCCA 28226 CTA T
 TGGGC G CATGATCTTG
 |||| | |||||
 ACCTG C GTATTAGGAC
 A _ _
 GAM1928 D4ST-1 3' TGAGGTTGTGACTGTGGCTGGT 28229 TG G _ TG
 AC G CC TAGTCA ATCTTG
 || || ||||| |||||
 TG C GG GTCAGT TGGAGT
 GT_ T GT
 GAM1928 DAPK2 3' GAGGTCTGGGCCCAGCG 15634 A GTCAT
 TG CTGGGCCTA GATCTT
 || ||||| |||||

GC GACCCGGGT CTGGAG

GAM1928 DDX34 3' TGAGGTTGCATGGGCTTGGTT 16167 TG _ CAT
GAC GGCCTA GT GATCTTG
||| ||||| || |||||
TTG TCGGGT CG TTGGAGT
GT A _

GAM1928 DDX37 3' GACGTTGGCTGTGCTTGGTCA 26390 TG C _ A
TGAC GGC TAGTCA TG TC
|||| | ||||| || ||
ACTG TCG GTCGGT GC AG
GT T T _

GAM1928 DKFZP434C171 5' CAGGATTATGGGAGCCCCAGCC 17882 A C AG
A TG CTGGG CT TCATGATCTTG
|| ||||| || |||||
AC GACCC GA GGTATTAGGAC
C C G _

GAM1928 DKFZP434H0820 3' TGAGTCACTTTATTGGGTTTCAG 31933 CA_ CTTG
TCA GACTGGGCCTAGT TGAT
||||||| |||||
CTGACTTGGGTTA ACTG
TTTC AGT

GAM1928 DKFZp547G183 3' TAAGGTGATCACTGGCTCAGTC 20790 T C G
GACTGGGCC AGT AT ATCTTG
||||||| ||| || |||||
CTGACTCGG TCA TA TGAAT
_ C G

GAM1928 DKFZp547O146 3' TAAGGTCGTGATAAAGTGTT 21485 _ A_
GGC CT GTCATGATCTTG
||| || |||||
TTG GA TAGTGCTGGAAT
T AA

GAM1928 DKFZP564C1940 5' CAAGGTCATTACAGCTGCAGTC 15272 _ CTA C
A TGA CTG GGC GT ATGATCTTG
||||| ||| || |||||
ACTGAC TCG CA TACTGGAAC
G A_ T

GAM1928 DKFZp564K142 3' TAAGAGAAAAATAGGCTCAGTT 25808 GTCATGA
A TGA CTGGGCCTA TCTTG
||||||| |||||
ATTGACTCGGAT AGAAT
AAAAAG_

GAM1928 DKFZP566K023 3' CAGGAAAGGCTAGGTTTCAGT 17757 ATGA
ACTGGGCCTAGTC TCTTG
||||||| |||||
TGACTTGGATCGG AGGAC
AA_

GAM1928 DKFZp761D221 3' TGAGATTGTGACTGGCAATTGT 26060 TGG_ T TG
T GAC GCC AGTCA ATCTTG
||| ||| ||||| |||||

TTG CGG TCAGT TAGAGT
 TTAA _ GT
 GAM1928 DKFZP761G1913 3' TGGGGTGCCTGCTTGGGCTGGG 25546 G T TG_
 TC GACT GGCCTAG CA ATCTTG
 |||| ||||| || |||||
 CTGG TCGGGTT GT TGGGGT
 G C CCG
 GAM1928 DKFZp761N0624 3' GGGGTTATGTCCCAGT 26075 CCTAGT
 ACTGGG CATGATCTT
 ||||| |||||
 TGACCC GTATTGGGG
 T____
 GAM1928 DKFZp762A227 3' CAGGGTTCCCTGGGCCCAGTC 19105 TCAT
 GACTGGGCCTAG GATCTTG
 ||||| |||||
 CTGACCCGGGTC TTGGGAC
 CC_
 GAM1928 DKFZp762A227 3' CAGGGTTCCCTGGGCCCAGTC 15316 TCAT
 GACTGGGCCTAG GATCTTG
 ||||| |||||
 CTGACCCGGGTC TTGGGAC
 CC_
 GAM1928 ECE2 3' CAAGCTGGGCTGGGTCTAGTC 16196 ATGAT
 GACTGGGCCTAGTC CTTG
 ||||| |||||
 CTGATCTGGGTCGG GAAC
 GTC_
 GAM1928 FBXO27 3' GAGAATTCCTGGGTCCAATCA 36837 C TC GA
 TGA TGGGCCTAG AT TC
 || ||||| || ||
 ACT ACCTGGGTC TA AG
 A CT AG
 GAM1928 FLJ10458 3' CAGGGTCATGGTCTGAACTACT 19865 C GCC _
 CA TGA TGG TAG TCATGATCTTG
 ||| ||| || |||||
 ACT ATC GTC GGTACTGGGAC
 C AA_ T
 GAM1928 FLJ10460 3' TGAGGTCATGGTTGCAATGAGT 19869 GG_ CT GT
 CA GACT GC A CATGATCTTG
 ||| || | |||||
 CTGA CG T GTACTGGAGT
 GTAA _ TG
 GAM1928 FLJ10468 3' CGGGAGGTTTAGGCTCAG 19874 TCATGA
 CTGGGCCTAG TCTTG
 ||||| |||||
 GACTCGGATT AGGGC
 TGG_
 GAM1928 FLJ10830 5' CGAGATCTGCGGTCTGGGGTCT 20182 TG _ _ AT_
 GGTT C GGCCT AG TC GATCTTG
 | |||| || || |||||

			G CTGGG TC GG CTAGAGC			
			GT G T CGT			
GAM1928	FLJ10956	3'	AAGAATAAGGTCTGGTTA	20273	TG	A CATGA
			TGAC GGCCT GT TCTT			
			ATTG CTGGA TA AGAA			
			GT A _____			
GAM1928	FLJ11126	3'	AAGGGGCTGGGCCTGGTC	20334	TG	ATGA
			GAC GGCCTAGTC TCTT			
			CTG CCGGGTCGG GGAA			
			GT _____			
GAM1928	FLJ11136	3'	GAGGAACCTGGGCCCATCA	20339	C	TCATGA
			TGA TGGGCCTAG TCTT			
			ACT ACCCGGGTC GGAG			
			— CAA_____			
GAM1928	FLJ11186	3'	CAAGACATTAAGTAGAGCTCAG	20367	— C_ A	
	TT		GACTGGGC CTAGT ATG TCTTG			
			TTGACTCG GATCA TAC AGAAC			
			A AT _			
GAM1928	FLJ11301	3'	CAAGGGACTTGGGTTCAGTTA	20417	_ ATGA	
			TGACTGGGCCTA GTC TCTTG			
			ATTGACTTGGGT CAG GGAAC			
			T _____			
GAM1928	FLJ11726	3'	TGGGACTTTGTAGGTTTAGCC	24528	A	T TGA
	G		TG CTGGGCCTAG CA TCTTG			
			GC GATTGATT GT AGGGT			
			C _ TTC			
GAM1928	FLJ12122	3'	GGGTGTGTTTGGTCTGGTCA	24540	TG	TAGT G
			TGAC GGCC CAT ATCT			
			ACTG CTGG GTG TGGG			
			GT TTT_ _			
GAM1928	FLJ12484	3'	TGGGGTCATAGATTGTCCAGTC	34521	CT _	
	A		TGACTGGGC AGTC ATGATCTTG			
			ACTGACCTG TTAG TACTGGGGT			
			_ A			
GAM1928	FLJ12484	3'	TGGGGTCATAGATTGTCCAGTC	23023	CT _	
	A		TGACTGGGC AGTC ATGATCTTG			
			ACTGACCTG TTAG TACTGGGGT			
			_ A			
GAM1928	FLJ12899	3'	AAGATTGGAGGCTTAATTA	23830	C	AGTCAT
			TGA TGGGCCT GATCTT			

		ATT ATTCGGA	TTAGAA		
		A	GG__		
GAM1928	FLJ13241	3'	GGAGGGTCTGGGTCCAGTTA	24709	TCATGA
			TGACTGGGCCTAG	TCT	
			ATTGACCTGGGTC	AGG	
			TGGG__		
GAM1928	FLJ13912	3'	CAGGGTTCCCTGGGCCCA	23028	TCAT
			TGGGCCTAG	GATCTTG	
			ACCCGGGTC	TTGGGAC	
			CC__		
GAM1928	FLJ14327	3'	CAAGGTCCCTCAGGCTGGTT	24421	TG G _ TCAT
			GAC G CCT AG	GATCTTG	
			TTG C GGA TC	CTGGAAC	
			GT _ C C__		
GAM1928	FLJ14490	3'	TGGGAGCCTGGGCTGGGCTCAG	26546	ATGA_
			CTGGGCCTAGTC	TCTTG	
			GACTCGGGTCGG	AGGGT	
			GTCCG		
GAM1928	FLJ20069	3'	AGGTACAGCTGGGCCAGCCA	19156	A CATG
			TG CTGGGCCTAGT	ATCT	
			AC GACCCGGGTCG	TGGA	
			C	ACA_	
GAM1928	FLJ20085	3'	CAGGATTTCCGTTTGGGTCTAG	19184	TCAT_
	TT		GACTGGGCCTAG	GATCTTG	
			TTGATCTGGGTT	TTAGGAC	
			TGCCT		
GAM1928	FLJ20584	5'	CGGGGTCTGCAGGGCTCAG	19561	A T T
			CTGGGCCT G CA	GATCTTG	
			GACTCGGG C GT	CTGGGGC	
			A _ _		
GAM1928	FLJ20666	3'	TAGGATTGGCAATGGTTCGTTT	19585	C TA_ TG
	A		TGA TGGGCC	GTCA ATCTTG	
			ATT GCTTGG	CGGT TAGGAT	
			T	TAA _	
GAM1928	FLJ21324	5'	GGGCAGAGCTGGGCCTGTC	43830	T CA A
			GAC GGGCCTAGT	TG TCT	
			CTG TCCGGGTCG	AC GGG	
			_	AG _	
GAM1928	FLJ21977	3'	TAGGAAGCTCCTGGGCTTAG	25940	TCATGA
			CTGGGCCTAG	TCTTG	

		GATTCGGGTC	AGGAT		
		CTCGA_			
GAM1928	FLJ22202	3'	CAGGAACGACTGGCCTTGGTCA	24335	_ T ATGA
			TGACTG GGCC AGTC TCTTG		
			ACTGGT CCGG TCAG AGGAC		
			T _ CA__		
GAM1928	FLJ22215	5'	CAGGACACCAGCTGGGTCCAG	46279	CA_ A
			CTGGGCCTAGT TG TCTTG		
			GACCTGGGTCG AC AGGAC		
			ACC _		
GAM1928	FLJ22215	3'	CAGGACACCAGCTGGGTCCAG	23116	CA_ A
			CTGGGCCTAGT TG TCTTG		
			GACCTGGGTCG AC AGGAC		
			ACC _		
GAM1928	FLJ22477	5'	TGGGATTGTGGCAGCCAG	24077	GC A TG
			CTGG CT GTCA ATCTTG		
			GACC GA CGGT TAGGGT		
			_ _ GT		
GAM1928	FLJ22494	5'	TAGCCCGCGGCTCGGCTCAGTC	24202	T A AT TG
			GA CTGGGCC AGTC TG CT		
			CTGACTCGG TCGG GC GA		
			C C CC T		
GAM1928	FLJ22529	5'	CAGGGTGCTCAGGCCTGGTT	24169	TG _ CATG
			GAC GGCCT AGT ATCTTG		
			TTG CCGGA TCG TGGGAC		
			GT C _ _		
GAM1928	FLJ22746	5'	CAGGAGCACGTGTTAGTCTGGT	24163	TG C T A_
	TA		TGAC GGC TAG CATG TCTTG		
			ATTG CTG ATT GTGC AGGAC		
			GT _ _ ACG		
GAM1928	FUSIP1	3'	CAAGATGTCTAGGCCCGG	27623	T TGA
			CTGGGCCTAG CA TCTTG		
			GGCCCGGATC GT AGAAC		
			T _ _		
GAM1928	GBL	3'	GGGCCAGGCTGGGCCAGGTC	22760	G A AT
			GA CTGGGCCTAGTC TG CT		
			CTGG CCGGGTTCGG AC GG		
			A _ CG		
GAM1928	GEMIN7	3'	TGAGACCTCCTGGGTCTAGTCA	24024	TCATGA
			TGACTGGGCCTAG TCTTG		

			ACTGATCTGGGTC	AGAGT	
			CTCC__		
GAM1928	GFPT1	3'	TAGGATTTATATCTAAGTTTGG	7818	TG C TCAT_
	TTA		TGAC GGC TAG GATCTTG		
			ATTG TTG ATC TTAGGAT		
			GT A TATAT		
GAM1928	GPS2	5'	CGGGGTCCAACGGGGGTCTGG	42147	TG A_ CAT
			C GGCCT GT GATCTTG		
			G CTGGG CA CTGGGGC		
			GT GG AC_		
GAM1928	GPT2	3'	CAGGGTCGTGAGGTTTCTGGT	28522	TG__ TAG
			AC G GCC TCATGATCTTG		
			TG C TGG AGTGCTGGGAC		
			GT TT ____		
GAM1928	GRIN3A	3'	CAAGGTTGTGGCCTTAGGTT	28530	__ TG
			GGCCTA GTCA ATCTTG		
			TTGGAT CGGT TGGAAC		
			TC GT		
GAM1928	GRO2	3'	TAAGGTTATGATTGAATCTA	29937	CC
			TGGG TAGTCATGATCTTG		
			ATCT GTTAGTATTGGAAT		
			AA		
GAM1928	HIC2	3'	AAGACCCTGGGTCCAGT	32523	TCATGA
			ACTGGGCCTAG TCTT		
			TGACCTGGGTC AGAA		
			CC__		
GAM1928	HSC3	3'	CAGGATTGTGGACATTTGGTTA	29734	TG CCTAG TG
			TGAC GG TCA ATCTTG		
			ATTG TT GGT TAGGAC		
			GT ACA__ GT		
GAM1928	HSPC067	5'	AGGACACATTAGGATTGGTCA	15458	TG G CA A G
			TGAC G CCTAGT TG TCTT		
			ACTG T GGATTA AC AGGA		
			GT A C_ _ A		
GAM1928	HSPC073	5'	GAGGTCTAGGCTTGGTC	15461	TG GTCAT
			GAC GGCCTA GATCTT		
			CTG TCGGAT CTGGAG		
			GT ____		
GAM1928	HSPC156	3'	CAAGCAGTGATTAGTTTCAGTC	15464	GC GAT
	A		TGACTGG CTAGTCAT CTTG		

ACTGACT GATTAGTG GAAC
 TT AC_
 GAM1928 HUMZD58C02 5' GAGATTGGGGGCCTGTC 38930 T AGTCAT
 GAC GGCCT GATCTT
 ||| ||||| |||||
 CTG TCCGGG TTAGAG
 _ GG____
 GAM1928 IMAGE:4907098 3' AAGATTGTGGGGCCGGGCG 44058 A G AGT TG
 TG CT GGCCT CA ATCTT
 || || ||||| || |||||
 GC GG CCGGG GT TAGAA
 _ G ____ GT
 GAM1928 JDD1 3' AGAGATTCTGCTTGGTCTAGTC 31669 T T T G
 A TGACTGGGCC AG CA GATCTT
 ||||| || || |||||
 ACTGATCTGG TC GT TTAGAG
 T _ C AG
 GAM1928 KCNE4 3' TGGGGTGGGGGACTAGGCTCAG 27969 A ATG_
 CCG TG CTGGGCCTAGTC ATCTTG
 || ||||| |||||
 GC GACTCGGATCAG TGGGGT
 C GGGG
 GAM1928 KIAA0205 3' GGCCACAGGCAGGTCCAGTCA 17008 A A_ AT
 TGACTGGGCCT GTC TG C
 ||||| ||| || |
 ACTGACCTGGA CGG AC G
 _ AC CG
 GAM1928 KIAA0323 3' GGGAAGTGTGTCTGGTCA 31696 TG C CATGA
 TGAC GGC TAGT TCTT
 ||| ||| ||| |||
 ACTG CTG GTCA AGGG
 GT T ____
 GAM1928 KIAA0332 3' CAAGAGACTTGGGTTTAGTTA 31418 _ ATGA
 TGACTGGGCCTA GTC TCTTG
 ||||| ||| |||||
 ATTGATTTGGGT CAG AGAAC
 T ____
 GAM1928 KIAA0335 3' AGGATACTTGGGCTGGTCA 16729 TG G T CATG
 TGAC G CC AGT ATCTT
 ||| | ||| |||||
 ACTG C GG TCA TAGGA
 GT G T ____
 GAM1928 KIAA0376 3' TAGGGTTGATGAAGGCTCGGCC 32675 A AG _
 G TG CTGGGCCT TCAT GATCTTG
 || ||||| ||| |||||
 GC GGCTCGGA AGTA TTGGGAT
 C _ G
 GAM1928 KIAA0450 3' CGGGGTGGGAGCTGGGCCTGGC 16030 A TG _ ATG
 G TG C GGCCTAG TC ATCTTG
 || | ||||| || |||||

GC G CCGGGTC AG TGGGGC
 _GT _ G GG_
 GAM1928 KIAA0478 3' GGGAATACTGGGGTCAGTTA 16982 G C GA
 TGA CTGG CCTAGT AT TC
 ||||| ||||| || ||
 ATTGACT GGGTCA TA GG
 G _ AG
 GAM1928 KIAA0495 5' CGGGGCCGCTGACTGGCCTCGG 31355 _ T _ AT
 TCA GACTG GGCC AGTCA TG CTTG
 |||| |||| |||| || ||||
 CTGGC CCGG TCAGT GC GGGC
 T _ C CG
 GAM1928 KIAA0514 3' AGGCCGGGCTGGGCTCAGCCA 16203 A A AT
 TG CTGGGCCTAGTC TG CT
 || ||||| || ||
 AC GACTCGGGTCGG GC GA
 C _ CG
 GAM1928 KIAA0523 3' TGGGGTCATGAGAGCTAGTTA 33648 GC AG
 TGA CTGG CT TCATGATCTTG
 ||||| || ||||| |||||
 ATTGATC GA AGTACTGGGGT
 _ G_
 GAM1928 KIAA0685 3' CAAGGCCCTCTAGGCCTGGCA 16148 A TG TCATGA
 TG C GGCCTAG TCTTG
 || ||||| ||||
 AC G CCGGATC GGAAC
 GT TCCC
 GAM1928 KIAA0720 3' GGA CTGGTTGGGCTCGG 31235 GT AT _
 CTGGGCCTA C GA TCT
 ||||| || ||||
 GGCTCGGGT G CT AGG
 TG _ C
 GAM1928 KIAA0961 3' CAAGATTCTGAAGACTTAGTTA 17072 C AG T
 TGA CTGGG CT TCA GATCTTG
 ||||| || || |||||
 ATTGATTC GA AGT TTAGAAC
 A _ C
 GAM1928 KIAA1001 3' CAGGGTCGTGGGAAGCTTGGT 17324 TG CTAG
 AC GGC TCATGATCTTG
 || || ||||| |||||
 TG TCG GGTGCTGGGAC
 GT AAG_
 GAM1928 KIAA1018 5' AGGGAGAGTGGCTCGGGCTCAG 17355 _ GA G
 TC GACTGGGCCT AGTCAT TCTT
 ||||| ||||| ||||
 CTGACTCGGG TCGGTG AGGG
 C AG AC
 GAM1928 KIAA1023 3' TGAGCTGTGGGCGGGGCCTAGT 19097 A ATGAT
 CA TGA CTGGGCCT GTC CTTG
 ||||| ||||| ||||

		ACTGATCCGGG CGG GAGT		
		G GTGTC		
GAM1928 KIAA1023	3'	TGAGCTGTGGGCGGGGCCTAGT 19095	A	ATGAT
	CA	TGACTGGGCCT GTC CTTG		
		ACTGATCCGGG CGG GAGT		
		G GTGTC		
GAM1928 KIAA1023	3'	TGAGCTGTGGGCGGGGCCTAGT 19096	A	ATGAT
	CA	TGACTGGGCCT GTC CTTG		
		ACTGATCCGGG CGG GAGT		
		G GTGTC		
GAM1928 KIAA1026	3'	GTCTTGGCTGGGTTTGTCA 35277	T	T
		TGAC GGGCCTAGTCA GAT		
		ACTG TTTGGGTCGGT CTG		
		— T		
GAM1928 KIAA1036	3'	GTTGCAATGATGGCTGGGCCAG 17130	G	G CTTG
	TCA	TGACTGG CCTAGTCAT AT		
		ACTGACC GGGTCGGTA TA		
		— G ACGTTGG		
GAM1928 KIAA1161	5'	AGGAGGACTGGGCTTAGCA 39747	A	ATGA
		TG CTGGGCCTAGTC TCTT		
		AC GATTTCGGGTCAG AGGA		
		— G—		
GAM1928 KIAA1170	3'	TGGGGTCAGTTGGGTGCCCAGT 34614	—	AGTCA
	T	GACTGGGC CT TGATCTTG		
		TTGACCCG GG ACTGGGGT		
		T GTTG—		
GAM1928 KIAA1183	3'	CAGGATTGGGGGCCCGG 31336	AGTCAT	
		CTGGGCCT GATCTTG		
		GGCCCGGG TTAGGAC		
		GG—		
GAM1928 KIAA1233	3'	TAGGGTTAGGACCAGGTTAGGT 31592	GG A A	
	CA	TGACT GCCT GTC TGATCTTG		
		ACTGG TGGA CAG ATTGGGAT		
		AT C G		
GAM1928 KIAA1466	5'	TAGGATCATGGTATTGACCAGT 35603	GCCTAG	
		ACTGG TCATGATCTTG		
		TGACC GGTACTAGGAT		
		AGTTAT		
GAM1928 KIAA1656	3'	CAGGGCTAGGCCAGCCA 32726	A	A
		TG CTGGGCCTAGTC TG		

	AC GACCCGGATCGG AC	
	C G	
GAM1928 KIAA1691	3' CAAGGTTGGTAGTGAATGGGCC 44463	TG G ____
	TGGTT GGCCTA TCAT GATCTTG	
	CCGGGT AGTG TTGGAAC	
	GT A ATGG	
GAM1928 KIAA1913	3' TAGGATTGTGTTTCTTAGTCA 36578	CCTAGT TG
	TGACTGGG CA ATCTTG	
	ACTGATTC GT TAGGAT	
	TTT____ GT	
GAM1928 LGALS8	3' GGGGTCCTCTGGGATTAGTTA 13246	G TCAT G
	TGACTGG CCTAG GATCTT	
	ATTGATT GGGTC CTGGGG	
	A TC____ A	
GAM1928 LIN-28	3' TAGGAGAGGCTGGGCCCGGT 23982	ATGA
	ACTGGGCCTAGTC TCTTG	
	TGGCCCGGGTCGG AGGAT	
	AG____	
GAM1928 MBD2	5' CGGGATTCCAAGGGCTCGGTTA 17945	AGTCAT
	TGACTGGGCCT GATCTTG	
	ATTGGCTCGGG TTAGGGC	
	AACC____	
GAM1928 MGC10960	3' GGGTGTCTGCTGGGCCCACTTA 26382	C T T _ G
	TGA TGGGCCTAG CA GAT CTT	
	ATT ACCCGGGTC GT CTG GGG	
	C _ _ T G	
GAM1928 MGC20496	3' CAAGATTTGGAAGTTTAGTCA 27424	CTAG T
	TGACTGGGC TCA GATCTTG	
	ACTGATTTG GGT TTAGAAC	
	AA____ _	
GAM1928 MGC2474	3' GGGCAACACTATGCCTGGTTA 23419	TG C CA A
	TGAC GGC TAGT TG TCT	
	ATTG CCG ATCA AC GGG	
	GT T CA _	
GAM1928 MGC2628	3' GGGGTCACTGGGCCTGGCCA 23510	A TG CAT G
	TG C GGCCTAGT GATCTT	
	AC G CCGGGTCA CTGGGG	
	C GT ____ A	
GAM1928 MGC26641	3' GGATGGGCTGGGTTTAGT 29585	ATG
	ACTGGGCCTAGTC ATCT	

TGATTTGGGTCGG TAGG
 G__
 GAM1928 MGC2752 5' CGAGATGGACCCTGGGCTCGGC 38368 A TCATG
 G TG CTGGGCCTAG ATCTTG
 || ||||| |||||
 GC GGCTCGGGTC TAGAGC
 _ CCAGG
 GAM1928 MGC35521 3' TGGGTGGCAGGCTGGGCCTAGC 29704 A A _ TG
 A TG CTGGGCCTAGTC TG ATCT
 || ||||| || |||||
 AC GATCCGGGTCGG AC TGGG
 _ _ GG T
 GAM1928 MGC4677 5' CGAGGCTGCTAGGCCAG 27450 CAT AT
 CTGGGCCTAGT G CTTG
 ||||| | |||||
 GACCCGGATCG T GAGC
 _ CG
 GAM1928 MGC7036 5' CGAGGTCGGCGGGGGTCTGG 29693 TG A_ AT
 C GGCCT GTC GATCTTG
 | |||| || |||||
 G CTGGG CGG CTGGAGC
 GT GG _
 GAM1928 MGC9753 3' TTATGGCTGGGTCTGGTT 27246 TG
 GAC GGCCTAGTCATGA
 ||| |||||
 TTG CTGGGTCGGTATT
 GT
 GAM1928 MIG 3' TGGAAGCATGATTGGTGCCCAG 8250 _ A_ TG
 TTA GACTGGGC CTAGTCATG TCT
 ||||| ||||| |||
 TTGACCCG GGTTAGTAC AGG
 T GA T
 GAM1928 MRPL35 3' CCTTTTATACTAGGTCTGGTT 18736 TG C TCTTG
 GAC GGCCTAGT ATGA
 ||| ||||| |||||
 TTG CTGGATCA TATT
 GT _ TTTCCA
 GAM1928 MRPS27 3' CAAGATTGTGCTCTTCTATCA 17474 C CCT T TG
 TGA TGGG AG CA ATCTTG
 ||| |||| || || |||||
 ACT ATCT TC GT TAGAAC
 _ TC_ _ GT
 GAM1928 NBL1 3' GAGGTCCCGGGGCTTAGT 29840 AGTCAT
 ACTGGGCCT GATCTT
 ||||| |||||
 TGATTCGGG CTGGAG
 CC____
 GAM1928 NCK1 3' TGAGAAAATGTTGGGTCCAGTC 12811 T GA
 GACTGGGCCTAG CAT TCTTG
 ||||| || |||||

		CTGACCTGGGTT GTA AGAGT		
		_ AA		
GAM1928 NKX2C	3'	GAGGAGGATGACTGGGTCCGGT 29802	GA	G
C		GACTGGGCCTAGTCAT TCTT		
		CTGGCCTGGGTCAGTA AGGA		
		GG GC		
GAM1928 OBSCN	3'	CAGGAGGCCTGGGCCAG 34988	TCATGA	
		CTGGGCCTAG TCTTG		
		GACCCGGGTC AGGAC		
		CGG__		
GAM1928 ORMDL2	3'	GGGCTCCTGGGCCAGTC 15468	TCAT T	
		GA CTG		
		CTGACCCGGGTC CT GGG		
		__ C		
GAM1928 OSBPL8	3'	CAAGGTGTTTATAGGCTTGTCA 21904	T	GTCATG
		TGAC GGGCCTA ATCTTG		
		ACTG TTCGGAT TGGAAC		
		_ ATTTG_		
GAM1928 OSBPL8	3'	CAGTGCTTGTA TAGGCTTAGT 21905	_ TGAT TG	
TA		TGACTGGGCCTAGT CA CT		
		ATTGATTCGGATCA GT GA		
		T TCGT C		
GAM1928 PDCD10	5'	TGAGGCACTTGGGCTTGGT 14082	TG	TCA A
		GAC GGCCTAG TG TCTTG		
		TTG TCGGGT AC GGAGT		
		GT C__		
GAM1928 PDE4DIP	3'	TGAGGTCATGGTGA CTAGT 16053	CC G	
		ACTGGG TA TCATGATCTTG		
		TGACTC GT GGTACTGGAGT		
		A_ _		
GAM1928 PEPP3	3'	TGGGGTTGTGGTGA CTCCAGT 17237	CC G TG	
		ACTGGG TA TCA ATCTTG		
		TGACCT GT GGT TGGGGT		
		CA _ GT		
GAM1928 PIP3-E	3'	TGAGATTGGAATGATTGAGTTC 33183	C	__
AGTT		CTGGGC TAGTCAT GATCTTG		
		GACTTG GTTAGTA TTAGAGT		
		A AGG		
GAM1928 POMT1	3'	CGAGGTTGAAGGGTCTTGGTCA 14017	TG _ AG TG	
		TGAC GG CCT TCA ATCTTG		

			ACTG TC GGG AGT TGGAGC		
			GT T A_ _		
GAM1928	PPFIA4	3'	CAGGATAGCTGGGTCCATTCA 34818	C	CATG
			TGA TGGGCCTAGT ATCTTG		
			ACT ACCTGGGTCG TAGGAC		
			T A_		
GAM1928	PPP1R14A	5'	CGGGGCCAGGCTGGGTCCAGCA 27088	A	A AT
			TG CTGGGCCTAGTC TG CTTG		
			AC GACCTGGGTCGG AC GGGC		
			_ _ CG		
GAM1928	PPP1R3B	3'	AGAGTTTTGTGGTTGGGTTAGG 23854	GG	GT TG T_ G
	TT		GA CT GCCTA CA A CTT		
			TTGG TGGGT GT T GAG		
			AT TG GT TT AT		
GAM1928	PRO0659	3'	TGAGAAGCAGCACTAGGCCTGT 15408	T	CA A_
	T		GAC GGGCCTAGT TG TCTTG		
			TTG TCCGGATCA AC AGAGT		
			_ CG GA		
GAM1928	PRO1855	3'	CAGCTCAGTGGCTGAGCCCACT 20576	C	_ T TG
	CA		TGACTGGGC TAGTCA TGA CT		
			ACTGACCCG GTCGGT ACT GA		
			A G C C		
GAM1928	PRO2730	3'	AGGGTTATGACTTGCTCA 24898	CT	
			TGGGC AGTCATGATCTT		
			ACTCG TCAGTATTGGGA		
			T_		
GAM1928	RABL4	5'	AGAAGGGCCGGGCTCGGTCA 13728	TA	ATGA
			TGACTGGGCC GTC TCT		
			ACTGGCTCGG CGG AGA		
			GC GA_		
GAM1928	ROBO4	3'	CAAGGCTGGGTCTAGCG 21132	A	A
			TG CTGGGCCTAGTC TG		
			GC GATCTGGGTCGG AC		
			_ A		
GAM1928	RPP14	3'	CAAGAAGTAGGCTGGGCCCGGT 29925	_	GA
			ACTGGGCCTAGTC AT TCTTG		
			TGGCCCGGGTCGG TG AGAAC		
			A A_		
GAM1928	SBB103	3'	TAGGGTCCCTGGTTCCAGTTA 12366	GC	TCAT
			TGACTGG CTAG GATCTTG		

ATTGACC GGTC CTGGGAT
 TT C___
 GAM1928 SDC3 5' AGGTCAGCTGGGTCTAGCA 16076 A CA
 TG CTGGGCCTAGT TGATCT
 || ||||| |||||
 AC GATCTGGGTCG ACTGGA

 — —
 GAM1928 SDCBP 3' TAAGATTATGTAACCTAG 12136 CCTAGT
 CTGGG CATGATCTTG
 |||| | |||||
 GATCC GTATTAGAAT
 AAT___
 GAM1928 SDCCAG1 5' TAGGAAATCACCTGGCTTGGTT 11072 TG TA C GA
 GAC GGCC GT AT TCTTG
 || ||| || || |||||
 TTG TCGG CA TA AGGAT
 GT TC C A_
 GAM1928 SES2 3' CAGGACCTGGGCCCGGTT 25481 _ A
 GACTGGGCCTAG TC TG
 ||||| || ||
 TTGGCCCGGGTC AG AC
 C G
 GAM1928 SIPL 3' TAGGATTATGCCTAGTTTGTCA 20242 TGGGC T
 TGAC CTAG CATGATCTTG
 ||| ||| |||||
 ACTG GATC GTATTAGGAT
 TTT___ C
 GAM1928 SLC11A2 3' GGGTCTGGGTGGGTCCAGTCA 6225 G T
 TGACTGGGCCTA TCA GATCT
 ||||| || |||||
 ACTGACCTGGGT GGT CTGGG
 G _
 GAM1928 SMC4L1 3' CAAGGTTGTGCTATCAAGGCTC 12001 ___ T TG
 AGCA CTGGGCCT AG CA ATCTTG
 ||||| || || |||||
 GACTCGGA TC GT TGGAAC
 ACTA _ GT
 GAM1928 SPTLC2 3' TGAGTATGAGTTATGTTTAGTC 11286 C _ A TTG
 A TGACTGGGC TAG TCATG TC
 ||||| || ||||| ||
 ACTGATTTG ATT AGTAT AG
 T G G T
 GAM1928 SPTLC2 3' TAGGGTTATGGGCAGTTGTT 11285 TGG_ TAGT
 GAC GCC CATGATCTTG
 || || |||||
 TTG CGG GTATTGGGAT
 TTGA ___
 GAM1928 STK17A 3' TAGGATTGAACAGTTCAGTT 11152 CTAG TG
 GACTGGGC TCA ATCTTG
 ||||| || |||||

			TTGACTTG AGT TAGGAT		
			ACA_ _		
GAM1928	SYT13	3'	CAGGATTCCTGGGTTCTGTT 44888	T	TCAT
			GAC GGCCTAG GATCTTG		
			TTG CTTGGGTC TTAGGAC		
			T C_		
GAM1928	TAF5L	3'	GACTGGGGCTAGGTTTGGTTA 15751	TG	ATGA
			TGAC GGCCTAGTC TC		
			ATTG TTGGATCGG AG		
			GT GGTC		
GAM1928	TGIF2	3'	CAGACTCTGCTTGGGTTTGGTT 22364	TG	T T _ TG
			GAC GGCCTAG CA GA TCT		
			TTG TTGGGTT GT CT AGA		
			GT C _ C C		
GAM1928	THEA	3'	CAGGATTGGACCCAGTTA 32949	C	A
			TGACTGGG CTAGTC TG		
			ATTGACCC GGTTAG AC		
			A G		
GAM1928	TLOC1	5'	TAGGGTTTCAGTAGGTCTCAGTC 9274	_	GTCAT
			GACTG GGCCTA GATCTTG		
			CTGAC CTGGAT TTGGGAT		
			T GAC_		
GAM1928	TNRC5	5'	AGGGTCCGGGCCCGGCCG 13345	A	AGTCAT
			TG CTGGGCCT GATCTT		
			GC GGCCCGGG CTGGGA		
			C C_		
GAM1928	TRAF3	3'	CAGGGTTGGGTGGCTCAGT 30041	T G	TG
			ACTGGGCC A TCA ATCTTG		
			TGACTCGG T GGT TGGGAC		
			_ G _		
GAM1928	TUB	3'	CAGGGCTGCTGTGGCCAGTC 9320	_	CAT AT
			GACTGGGCC TAGT G CTTG		
			CTGACCCGG GTCG T GGAC		
			T _ CG		
GAM1928	YAP1	3'	CAGGGTCGGTGGGGGGGTTGGT 12751	TG G	AG _
	T		GAC G CCT TCAT GATCTTG		
			TTG T GGG GGTG CTGGGAC		
			GT G G_ G		
GAM1928	ZFP91	3'	TAAGATTATTATAGTCTGGTT 27577	TG	C GTC
			GAC GGC TA ATGATCTTG		

			TTG CTG AT TATTAGAAT		
			GT _ AT_		
GAM1928	ZNF304	3'	TGAGAAAAGAATTGGGTTCTGT 21831	T	CATGA
	CA		TGAC GGCCTAGT TCTTG		
			ACTG CTTGGGTTA AGAGT		
			T AGAA		
GAM1928	ZNF333	3'	TGAGATTTGCTATTAGGTCTGG 26203	TG	CAT_
	T		AC GGCCTAGT GATCTTG		
			TG CTGGATTA TTAGAGT		
			GT TCGT		
GAM1928	ZNF33A	3'	TAAGATTATACAGTCTAGT 43900	CTA C	
			ACTGGGC GT ATGATCTTG		
			TGATCTG CA TATTAGAAT		
			A_ _		
GAM1928	ZNF340	3'	TGGGATTTCCGAGGCCAG 41035	AGTCAT	
			CTGGGCCT GATCTTG		
			GACCCGGA TTAGGGT		
			GCCT_		
GAM1928	LOC115574	3'	TGGGGTCCCTCAGGCCTGG 36368	TG _ TCAT	
			C GGCCT AG GATCTTG		
			G CCGGA TC CTGGGGT		
			GT C C_		
GAM1928	LOC116228	5'	GGGGCTGTCTGGCTCGGTTA 36535	T T TGA	
			TGACTGGGCC AG CA TCT		
			ATTGGCTCGG TC GT GGG		
			_ T CG_		
GAM1928	LOC124044	3'	CGGGGTCTTGTTGGGTCCAGT 37430	G T	
			ACTGGGCCTA TCA GATCTTG		
			TGACCTGGGT GGT CTGGGGC		
			_ T		
GAM1928	LOC126006	5'	TGAGAGTCCCTGGGGTCCAGTC 36802	_ TC GA TTG	
	A		TGACTGGGCCT AG AT TC		
			ACTGACCTGGG TC TG AG		
			G CC AG T		
GAM1928	LOC130497	3'	AAGGACCCTAGGCCAGCG 36991	A TCATGA	
			TG CTGGGCCTAG TCTT		
			GC GACCCGGATC GGAA		
			_ CCA_		
GAM1928	LOC130589	3'	CAGGGCTAGGCTCAGCCA 29022	A A	
			TG CTGGGCCTAGTC TG		

		AC GACTCGGATCGG AC		
		C G		
GAM1928	LOC130612 3'	GGAGAGGGCTGGCCTGGTCA 37000	TG T	ATGA
		TGAC GGCC AGTC TCT		
		ACTG CCGG TCGG AGG		
		GT _ GAG_		
GAM1928	LOC132299 5'	CGAGGCCTGCTGGGCTTGGCA 37024	A TG	T TGA
		TG C GGCCTAG CA TCTTG		
		AC G TCGGGTC GT GGAGC		
		_GT _ CC_		
GAM1928	LOC133362 5'	CAAGGTGATGTCATTGGGCCTA 37378	_ G	
		TGGGCCTAGT CAT ATCTTG		
		ATCCGGGTTA GTA TGGAAC		
		CT G		
GAM1928	LOC137075 3'	AGTTCAGGTTGGGTTTGGTT 37102	TG	GT A T
		GAC GGCCTA C TGA CT		
		TTG TTGGGT G ACT GA		
		GT TG_ T		
GAM1928	LOC143286 5'	CAAGAGAACTCTGGCCTAGTCA 40354	T	TCATGA
		TGACTGGGCC AG TCTTG		
		ACTGATCCGG TC AGAAC		
		_ TCAAG_		
GAM1928	LOC143677 5'	AAGGTGCTGTGTCTAGTCA 40372	C	CATG
		TGACTGGGC TAGT ATCTT		
		ACTGATCTG GTCG TGGAA		
		T _		
GAM1928	LOC143916 5'	TAGGAAACAGGATTGGGCCTGT 37653	T	A A_
	T	GAC GGCCTAGTC TG TCTTG		
		TTG TCCGGGTTAG AC AGGAT		
		_ G AA		
GAM1928	LOC144058 5'	CAAGAAGTCTGGGCTGGGTCCA 37675	AT	_
	GTC	GACTGGGCCTAGTC GA TCTTG		
		CTGACCTGGGTCGG CT AGAAC		
		GT GA		
GAM1928	LOC144308 5'	GACAGCATTGGGTCTGGTT 40406	TG	CA A
		GAC GGCCTAGT TG TC		
		TTG CTGGGTTA AC AG		
		GT CG _		
GAM1928	LOC144453 3'	CGGGATTCTGGGGTCCAGCCA 37747	A	AGTCAT
		TG CTGGGCCT GATCTTG		

	AC GACCTGGG	TTAGGGC		
	C	GTCC__		
GAM1928	LOC144486	3' CAAGATTATGATTTTCAGGCT	40417	___
		GGCCT AGTCATGATCTTG		
		TCGGA TTAGTATTAGAAC		
		CTT		
GAM1928	LOC144587	5' CAGGGCTGGGTCAGTTA	33269	G A
		TGACTGG CCTAGTC TG		
		ATTGACT GGGTCGG AC		
		— G		
GAM1928	LOC144920	3' GAGGTAAC TGGGCTTAG	40466	CATG G
		CTGGGCCTAGT ATCTT		
		GATTCGGGTCA TGGAG		
		A__ G		
GAM1928	LOC145333	5' CAGGGTTGGGAGGCCTAG	40532	AGTCA
		CTGGGCCT TGATCTTG		
		GATCCGGA GTTGGGAC		
		GG__		
GAM1928	LOC145566	5' GTCTTGATTAGATCCAGTT	37899	GC T
		GA CTGG CTAGTCA GAT		
		TTGACC GATTAGT CTG		
		TA T		
GAM1928	LOC145858	5' TGATTCCAGGCTGGGCTCGGTT	38003	AT_ TTG
		GA CTGGGCCTAGTC GATC		
		TTGGCTCGGGTCGG TTAG		
		ACC T		
GAM1928	LOC145899	5' GGGTTGACTGGGTCCAG	40624	TG
		CTGGGCCTAGTCA ATCT		
		GACCTGGGTCAGT TGGG		
		—		
GAM1928	LOC145942	5' CAAGATTGGCTCAGTCA	38015	T A
		TGACTGGGCC AGTC TG		
		ACTGACTCGG TTAG AC		
		— A		
GAM1928	LOC145945	5' GGGGAATAAGAGTAGGCTCAGT	40633	G A A G
	T	GA CTGGGCCTA TC TG TCTT		
		TTGACTCGGAT AG AT AGGG		
		G A A GG		
GAM1928	LOC146224	5' TCTGGCTAGGCTCGGCG	38078	A T
		TG CTGGGCCTAGTCA GA		

GC GGCTCGGATCGGT CT

GAM1928 LOC146603 5' CAGGATCATGCACCCTTGTTA 38216 T_ CCTA T
TGAC GGG G CATGATCTTG
||||| ||| | |||||
ATTG CCC C GTACTAGGAC
TT A____

GAM1928 LOC146669 5' CGAGTGTGAGGTTAGGTCCAGC 38222 A GT ATGAT
A TG CTGGGCCTA C CTTG
|| ||||| | |||
AC GACCTGGAT G GAGC
TG AGTGT

GAM1928 LOC147077 3' TAAGATCATGGTTTAGGGT 38293 __ GT
GCCT A CATGATCTTG
|||| | |||||
TGGG T GTACTAGAAT
AT TG

GAM1928 LOC147180 5' GACAGACCATGATTAGGTCTGT 40816 T A TG
CA TGAC GGGCCTAGTCATG TCT
|||| ||||| |||
ACTG TCTGGATTAGTAC AGA
C CAGG

GAM1928 LOC148113 3' TGGGGTCCAGGCTGGGCCAGT 38473 AT
ACTGGGCCTAGTC GATCTTG
||||||| |||||
TGACCCGGGTCGG CTGGGGT
AC

GAM1928 LOC148936 5' TGGGTGGAATGATAGGGTTTGG 40934 TG A G__ TG
TT GAC GGCCT GTCAT ATCT
|| |||| |||| |||
TTG TTGGG TAGTA TGGG
GT A AGG T

GAM1928 LOC148938 5' TGGGTGGAATGATAGGGTTTGG 40927 TG A G__ TG
TT GAC GGCCT GTCAT ATCT
|| |||| |||| |||
TTG TTGGG TAGTA TGGG
GT A AGG T

GAM1928 LOC149692 3' CAAGAGTCTTGAGGTTCA GTCA 41038 TAG T _
TGACTGGGCC TCA GA TCTTG
||||||| ||| || |||||
ACTGACTTGG AGT CT AGAAC
__ T G

GAM1928 LOC149692 3' CAAGAGTTGGGCCAGGTT 41039 G _ A
GACT GGCCTAG TC TG
|||| ||||| || |||
TTGG CCGGGTT AG AC
A G A

GAM1928 LOC149711 3' AAGGTTCTAAGGTTTCAGT 41067 _ TCAT
ACTGGGCCT AG GATCTT
||||||| || |||||

		TGACTTGGA TC TTGGAA		
		A ____		
GAM1928	LOC150095 5'	AGGACCGTTGGTCCAGTT 41129	GC GTC A	
		GA CTGG CTA ATG TCTT		
		TTGACC GGT TGC AGGA		
		TT ____ C		
GAM1928	LOC150271 3'	GAGATTGTGTGCCTAGCA 41171	A CTAGT TG	
		TG CTGGGC CA ATCTT		
		AC GATCCG GT TAGAG		
		_ T ____ GT		
GAM1928	LOC150407 5'	AAGGTCATGGCAACAGTT 38948	GGCCTA	
		GA CTG GTCATGATCTT		
		TTGAC CGGTACTGGAA		
		AA ____		
GAM1928	LOC151176 3'	CAGGGCCTGGCTGGGTCCAGCG 41313	A TGA	
		TG CTGGGCCTAGTCA TCTTG		
		GC GACCTGGGTCGGT GGGAC		
		_ CC _		
GAM1928	LOC151571 5'	CAGGGGGCTTGGGTCTCGTT 41371	T _ ATGA	
		GAC GGGCCTA GTC TCTTG		
		TTG TCTGGGT CGG GGGAC		
		C T ____		
GAM1928	LOC151959 5'	GAGACACCTGGGTTCAGTC 41407	TCA A G	
		GA CTGGGCCTAG TG TCTT		
		CTGACTTGGGTC AC AGAG		
		C _ _ A		
GAM1928	LOC152185 5'	TGGGATCCAGGCGCCCGGTT 29539	CTA AT	
		GA CTGGGC GTC GATCTTG		
		TTGGCCCG CGG CTAGGGT		
		_ AC		
GAM1928	LOC154282 5'	GTTCATCTGATTGGGACTGGTT 41700	TG G T CTTG	
	A	TGAC G CCTAGTCA GAT		
		ATTG C GGGTTAGT CTA		
		GT A _ CTTGG		
GAM1928	LOC154881 3'	TGGAGCATGGCAGGGCTTGGTT 39501	TG A A TG	
	A	TGAC GGCCT GTCATG TCT		
		ATTG TCGGG CGGTAC AGG		
		GT A G T		
GAM1928	LOC158177 5'	CAGGTGTGGGGCTGGGCATGGT 39761	GG ATGAT	
	CA	TGACT GCCTAGTC CTTG		

	ACTGG CGGGTCGG GGAC		
	TA GGTGT		
GAM1928 LOC158969 3'	TGGGAAGTGCTTGGGTTCCGG 39924	T GA TG	
	CTGGGCCTAG CAT TCT		
	GGCTTGGGTT GTG GGG		
	C AA T		
GAM1928 LOC163682 5'	AGGGTCAGCAGCTCAGTCA 42084	CTA CA	
	TGACTGGGC GT TGATCTT		
	ACTGACTCG CG ACTGGGA		
	A _ _		
GAM1928 LOC197408 5'	GTCCTGGCTGGGCTGAGTCA 43208	G T	
	TGACT GGCCTAGTCA GAT		
	ACTGA TCGGGTCGGT CTG		
	G C		
GAM1928 LOC199796 5'	CAGGATCGTGAGGACCAGTC 36807	G TAG	
	GA CTGG CC TCATGATCTTG		
	CTGACC GG AGTGCTAGGAC		
	A _ _		
GAM1928 LOC200609 5'	TGTGATTGGCTTAGTTA 43338	T	
	TGACTGGGCC AGTCATG		
	ATTGATTCCGG TTAGTGT		
	-		
GAM1928 LOC201164 3'	GGCACGACTGGGGTTGGTT 42531	TG G A A	
	GAC G CCTAGTC TG TC		
	TTG T GGGTCAG AC GG		
	GT G C _		
GAM1928 LOC201181 5'	TGGGGTCCTTGGGCTTTGTCA 42535	TG TCAT	
	TGAC GGCCTAG GATCTTG		
	ACTG TCGGGTT CTGGGGT		
	TT C _		
GAM1928 LOC201191 3'	CGAGATTGGAAGGTTTCATCA 43215	C AG A	
	TGA TGGGCCT TC TGATCTTG		
	ACT ACTTGGA AG GTTAGAGC		
	- A _ -		
GAM1928 LOC201799 3'	CATGGCCAGGTCTGGTCA 42913	TG A	
	TGAC GGCCT GTCATG		
	ACTG CTGGA CGGTAC		
	GT C		
GAM1928 LOC203292 5'	CAGGTGTGGGGCTGGGTATGGT 43501	G ATGAT	
CA	TGACTG GCCTAGTC CTTG		

		ACTGGT TGGGTCGG GGAC		
		A GGTGT		
GAM1928	LOC204970 3'	GGGGAGGAGATCTGGGCCAGT 43072		_ ATGA G
	CA	TGACTGGGCCTAG TC TCTT		
		ACTGACCCGGGTC AG AGGG		
		T AGG_ GC		
GAM1928	LOC219649 3'	TAAGAGGAACGGCTGGGATCAG 44668	GG	ATGA_
	TTA	TGACTG CCTAGTC TCTTG		
		ATTGAC GGGTCGG AGAAT		
		TA CAAGG		
GAM1928	LOC219654 3'	AAGATAGCTGGGCCAGT 43870	CATG	
		ACTGGGCCTAGT ATCTT		
		TGACCCGGGTCG TAGAA		
		A_		
GAM1928	LOC219690 3'	TGAGATCATGGCTAGGAAACGG 44706	GG_	
		CTG CCTAGTCATGATCTTG		
		GGC GGATCGGTACTAGAGT		
		AAA		
GAM1928	LOC219790 3'	TGAGATTTTAGAGGCCTAGTT 43906	AGTCAT	
		GACTGGGCCT GATCTTG		
		TTGATCCGGA TTAGAGT		
		GATT_		
GAM1928	LOC219920 5'	GGGATCCTGGGCCTGTTA 44810	T	TCAT
		TGAC GGGCCTAG GATCTT		
		ATTG TCCGGGTC CTAGGG		
		_ _		
GAM1928	LOC220038 5'	GTGGCTGGGCCTCAGTTA 44081	_	
		TGACTG GGCCTAGTCAT		
		ATTGAC CCGGGTCGGTG		
		T		
GAM1928	LOC220763 5'	CAAGATCAAAGATGTGGGTTCA 36300	_	A_
	G	CTGGGCCTA GTC TGATCTTG		
		GACTTGGGT TAG ACTAGAAC		
		G AA		
GAM1928	LOC220766 5'	CAGGATTATAATAGGCCTGTTA 43649	T	GTC
		TGAC GGGCCTA ATGATCTTG		
		ATTG TCCGGAT TATTAGGAC		
		_ AA_		
GAM1928	LOC220776 3'	TGAGATCTCGAGTTTGGGTTTG 33938	T	_ AT
	TT	GAC GGGCCTAG TC GATCTTG		

		TTG TTTGGGTT AG CTAGAGT		
		— TG CT		
GAM1928	LOC221431 3'	AAGGTTATCCAGTTCAGT 44219	CTAGTC	
		ACTGGGC ATGATCTT		
		TGACTTG TATTGGAA		
		ACC__		
GAM1928	LOC221810 3'	CAAGATGTCCTTAGGTCTGGTT 45083	TG TC G	
		GAC GGCCTAG AT ATCTTG		
		TTG CTGGATT TG TAGAAC		
		GT CC _		
GAM1928	LOC222183 3'	TGAGGTTAAAAGGGGTTTCAGGT 45187	_ AGTCA	
	CA	TGAC TGGGCCT TGATCTTG		
		ACTG ACTTGGG ATTGGAGT		
		G GAAA_		
GAM1928	LOC222256 3'	CAAGATCAGCCTGGCCTAG 45248	T TCA	
		CTGGGCC AG TGATCTTG		
		GATCCGG TC ACTAGAAC		
		_ CG_		
GAM1928	LOC253296 5'	CAGGGTGCGCTGGTCCCGGTC 45345	C CATG	
		GA CTGGG CTAGT ATCTTG		
		CTGGCCC GGTCG TGGGAC		
		T CG_		
GAM1928	LOC253649 5'	CAGGTGTGGGGCTGGGCATGGT 45999	GG ATGAT	
	CA	TGACT GCCTAGTC CTTG		
		ACTGG CGGGTCGG GGAC		
		TA GGTGT		
GAM1928	LOC253650 5'	CAGGTGTGGGGCTGGGCATGGT 45997	GG ATGAT	
	CA	TGACT GCCTAGTC CTTG		
		ACTGG CGGGTCGG GGAC		
		TA GGTGT		
GAM1928	LOC255042 3'	TAAGAGACAACTGGGTCTGTT 45650	T CATGA	
		GAC GGGCCTAGT TCTTG		
		TTG TCTGGGTCA AGAAT		
		_ ACAG_		
GAM1928	LOC256306 3'	TAGGGTTATGTTTTTCAGTT 46237	CCTAGT	
		GA CTGGG CATGATCTTG		
		TTGACTT GTATTGGGAT		
		TT__		
GAM1928	LOC256905 3'	GAGATTTCAAGGCTCAGCA 46297	A AGTCAT	
		TG CTGGGCCT GATCTT		

	AC GACTCGGA	TTAGAG		
	— ACT—			
GAM1928 LOC256925	5' CAGGATCTTCCAGGCTTGGCA	46610	A TG	AGTCAT
	TG C GGCCT GATCTTG			
	AC G TCGGA CTAGGAC			
	GT CCTT			
GAM1928 LOC256942	3' TAGGGTCCCTGGTTCCAGTTA	45365	GC	TCAT
	TGACTGG CTAG GATCTTG			
	ATTGACC GGTC CTGGGAT			
	TT C—			
GAM1928 LOC257408	5' GGGCTAGGCTGGGCCGGGT	45956	G	A AT
	GA CT GGCCTAGTC TG CT			
	TTGG CCGGGTCGG AT GG			
	G _ CG			
GAM1928 LOC257570	5' CAGGGTGCGCTGGTCCCGGTC	46698	C	CATG
	GA CT GGG CTAGT ATCTTG			
	CTGGCCC GGTCG TGGGAC			
	T CG—			
GAM1928 LOC51157	5' CGGGGTTTTGCAGAGCTCAGTT	18298	_ A T T	
	GA CT GGGC CT G CA GATCTTG			
	TTGACTCG GA C GT TTGGGGC			
	A _ _ T			
GAM1928 LOC51285	3' CAGGAAGCCTAGGCTCGGT	18636	TCATGA	
	ACTGGGCCTAG TCTTG			
	TGGCTCGGATC AGGAC			
	CGA—			
GAM1928 LOC89890	3' CAGGATCAACAGGGTTTGTT	30381	T A CA	
	GA C GGCCT GT TGATCTTG			
	TTG TTTGGG CA ACTAGGAC			
	_ A _			
GAM1928 LOC90139	3' TGAGGTTTGGTCTGGGCTCAGT	28274	_ T	
	ACTGGGCCTAG TCA GATCTTG			
	TGACTCGGGTC GGT TTGGAGT			
	T _			
GAM1928 LOC90499	5' CAGGTGTGGGGCTGGGCATGGT	31582	GG	ATGAT
CA	TGACT GCCTAGTC CTTG			
	ACTGG CCGGTCGG GGAC			
	TA GGTGT			
GAM1928 LOC91040	5' TGGGGTGGCAGCTGATTAGGCC	32325	_ AT_ G	
CAGCA	CTGGGCCTAGTCA TG CTT			

GACCCGGATTAGT AC GGG
 CG GGT GT
 GAM1928 LOC91291 5' TGGGATTATAGGTGCCCATCA 32631 C _ AGTC
 TGA TGGGC CT ATGATCTTG
 ||| ||||| || |||||
 ACT ACCCG GG TATTAGGGT
 _ T A__
 GAM1928 LOC91516 5' CGAGGTTGTGGTGGCCCTGCTC 32955 CT_ TAG TG
 A TGA GGGCC TCA ATCTTG
 ||| ||||| ||| |||||
 ACT CCCGG GGT TGGAGC
 CGT T__ GT
 GAM1928 LOC92078 3' AGGCTAGGATTGGGCTAGTTA 33742 G A AT
 TGA CTGG CCTAGTC TG CT
 ||||| ||||| || ||
 ATTGATC GGGTTAG AT GA
 _ G CG
 GAM1928 LOC92360 5' AGGAACCTGGACCCAGTT 34239 _ TA CATGA
 GACTGGG CC GT TCTT
 ||||| || || |||||
 TTGACCC GG CA AGGA
 A TC ____
 GAM1928 LOC93550 5' GGGTCGTTGGGCCCTGTC 35933 T GTC
 GAC GGGCCTA ATGATCT
 ||| ||||| |||||
 CTG CCCGGGT TGCTGGG
 T ____
 GAM1928 LOC93622 3' TGAGATTAAGAAGGCCAGT 28950 AG A
 ACTGGGCCT TC TGATCTTG
 ||||| || |||||
 TGACCCGGA AG ATTAGAGT
 _ A
 GAM1929 ADCY7 3' TCTCTTCTTTCTTTAGTCTT 6786 GT CAGCTAT
 AAG TAAGG GAAGAGG
 ||| ||||| |||||
 TTC ATTTC CTTCTCT
 TG CTTT__
 GAM1929 ADM 3' CTTCGCTTCCTTAGCCTT 6794 C TAT
 AAGGTTAAGG AGC GAAG
 ||||| || |||||
 TTCCGATTCC TCG CTTC
 T ____
 GAM1929 AKT1 3' CTTTTCGACGCTTAACCTT 11651 G AGCTA
 AAGGTTAAG C TGAAGAG
 ||||| || |||||
 TTCCAATTC G GCTTTTC
 _ CA__
 GAM1929 ALS2 3' CTTTAAACTGCAGTTTAACT 21929 A TATG_ G
 TT AAGGTTAAGGC GC AAGAG
 ||||| || |||||

TTTCAATTTTG CG TTTTC
 A TCAAA
 GAM1929 AP2B1 3' TTTCTTCATGATACTTAGTCT 6957 GT GCAGC
 AG TAAG TATGAAGAGG
 || ||| |||||
 TC ATTC GTACTTCTTT
 TG ATA__
 GAM1929 APBA1 3' CCTCTTCGTGGTTGTGTTTCTC 34646 TT G
 GG AA GCAGCTATGAAGAGG
 || || |||||
 CT TT TGTTGGTGCTTCTCC
 CT G
 GAM1929 ARHGEF12 3' TTTTATGAGCTTTTTGGCTTT 17631 C _
 AAGGTTAAGG AGCT ATGAAG
 ||||| ||| ||||
 TTTCGGTTTT TCGA TATTTT
 _ G
 GAM1929 ATM 5' CCTTTTGAGCTGTCTTGACGTT 28707 G ATG
 AA GTTAAGGCAGCT AAGAGG
 || ||||| ||||
 TT CAGTTCTGTCTGA TTTTCC
 G G__
 GAM1929 ATM 5' CCTTTTGAGCTGTCTTGACGTT 28705 G ATG
 AA GTTAAGGCAGCT AAGAGG
 || ||||| ||||
 TT CAGTTCTGTCTGA TTTTCC
 G G__
 GAM1929 ATP11B 3' TCTTTTGCATGCTTTAATCT 39148 _ TAT
 AGGTTAAGGCA GC GAAGA
 ||||| || ||||
 TCTAATTCGT CG TTTCT
 A T__
 GAM1929 ATP1B2 3' TCTCTTCAGACCCCTTTGCCTT 7394 T CAGCTA
 AAGGT AAGG TGAAGAGG
 |||| ||| |||||
 TTCCG TTCC ACTTCTCT
 T CCAG__
 GAM1929 ATP6V1A1 3' CTTCTATACAACTTGTTTAAAC 7409 C__ _ AGG
 CTT GTTAAGGCAG TAT GAAG
 ||||| || ||||
 CAATTTTGTT ATA CTTC
 CAAC T G
 GAM1929 ATP7A 3' TCTTTTTGGCAATCTTGAACCTT 5496 _ CA T GG
 T AAGGT TAAGG GCTA GAAGA
 |||| |||| ||| ||||
 TTTCA GTTCT CGGT TTTCT
 A AA T
 GAM1929 B4GALT5 3' CTTTGTCCCTGCCTTGGCTTT 11169 CT TG
 AAGGTTAAGGCAG A AAG
 ||||| ||| |||

			TTTCGGTTCCGTC T TTC		
			CC GT		
GAM1929 BCRP2	3'	TCTTTTCATGTTAAAAGCCTTA 31277	_____ T		
ATCT		TTAAGGC AGC ATGAAGAGG			
		AATTCCG TTG TACTTTTCT			
		AAAA _			
GAM1929 BPGM	3'	TCTCATTTTGGTTTGTTTTAAT 7456	_ T A		
TTT		AAGGTTAAGGCAG CTA GA GAGG			
		TTTTAATTTTGTT GGT TT CTCT			
		T T A			
GAM1929 BTG2	3'	CTTCTTTATGATGTTCACTTT 13627	TAA GC		
		AAGGT GGCA TATGAAGAGG			
		TTTCA TTGT GTATTTCTTC			
		C_ A_			
GAM1929 CAPZA1	3'	CTCTGACTGCTTTGATC 35949	CTATGA		
		GGTTAAGGCAG AGAG			
		CTAGTTTCGTC TCTC			
		AG_____			
GAM1929 CD83	3'	TTTTTACCTCTGTCTTGGCTTT 10427	CTA		
		AAGGTTAAGGCAG TGAAGA			
		TTTCGGTTCTGTC ATTTTT			
		TCC			
GAM1929 CDH1	3'	CTTTTTGGAATTGTCTTGATTT 10564	CTA G		
T		AAGGTTAAGGCAG TGAAGAG			
		TTTTAGTTCTGTT GTTTTTC			
		AAG			
GAM1929 CDH6	3'	TTTTTTCATTGTTTTTAACTTT 11379	GC T		
		AAGGTTAAG AGC ATGAAGAGG			
		TTTCAATTT TTG TACTTTTTT			
		_ T			
GAM1929 CERD4	3'	CCTCAGCCTAGTTGCTTTAATC 14346	TGAA		
T		AGGTTAAGGCAGCTA GAGG			
		TCTAATTTCGTTGAT CTCC			
		CCGA			
GAM1929 CHD2	3'	TAACCTCATAGCAGCTTTGGTT 6935	GG A AGAGG		
TT		AA TTAAGGC GCTATGA			
		TT GGTTTCG CGATACT			
		TT A CCAATT			
GAM1929 CIS4	3'	TTTCTGTTGCCTTCGTTTT 10424	TT TAT		
		AAGG AAGGCAGC GAAG			

		TTTT TTCCGTTG CTTT		
		GC T__		
GAM1929	CLCN4	5' TTTCGGTAGCGTTTAACTTT 7575	A	_
		AAGGTTAAGGC GCTAT GAAG		
		TTTCAATTTTG CGATG CTTT		
		_ G		
GAM1929	CLCN6	3' CTTTTTCATTTTCCTTAAGTTT 6961	G	CAGCT
		AAG TTAAGG ATGAAGAGG		
		TTT AATTCC TACTTTTTC		
		G TT__		
GAM1929	CLCN6	3' CTTTTTCATTTTCCTTAAGTTT 22338	G	CAGCT
		AAG TTAAGG ATGAAGAGG		
		TTT AATTCC TACTTTTTC		
		G TT__		
GAM1929	CLCN6	3' CTTTTTCATTTTCCTTAAGTTT 22343	G	CAGCT
		AAG TTAAGG ATGAAGAGG		
		TTT AATTCC TACTTTTTC		
		G TT__		
GAM1929	CLN2	3' CTTCTTCATGGAATGCTGACCT 5967	AA	G_
	T	AAGGTT GGCA CTATGAAGAGG		
		TTCCAG TCGT GGTACTTCTTC		
		_ AA		
GAM1929	CLN5	3' CTTTTTCACTTAAGTGCTTTAG 13227	GG	G A__
	TTT	TTAAGGCA CT TGAAGAGG		
		GATTTCGT GA ACTTTTTC		
		TT _ ATTC		
GAM1929	CLOCK	3' CATAGTGCCTTGATTTT 11332	G	
		AAGGTTAAGGCA CTATG		
		TTTTAGTTCCGT GATAC		
		-		
GAM1929	CNN2	3' TTTTTTCCCCTTTGCCTTGATC 10585		CTAT
		GGTTAAGGCAG GAAGAGG		
		CTAGTTCCGT CTTTTT		
		TCCC		
GAM1929	COX15	3' TTTCTTTATGATCTTAAGTT 27795		CAGC
		AGGTTAAGG TATGAAGAGG		
		TTCAATTCT GTATTCTTT		
		A__		
GAM1929	CYB561	3' CTTCTTTAAAACCCTTTAGCC 7631		CAGCTA
		GGTTAAGG TGAAGAGG		

CCGATTTC ATTTCTTC
 CCAA_

GAM1929 CYP4A11 3' TCTTTTCTCACTGCTTTGACT 6419 CTAT
 GGTTAAGGCAG GAAGAGG
 ||||| |||||
 TCAGTTTCGTC CTTTCT
 ACT_

GAM1929 CYP8B1 3' TCTCCCAGCTTGCTTTAGTTTT 10626 GG _ ATGAA
 AA TTAAGGCA GCT GAGG
 || ||||| || ||||
 TT GATTTCGT CGA CTCT
 TT T CC_

GAM1929 DACH 5' CCTTTTCACCTTCATCCTTAAC 28036 CAGCTA_
 TTT AAGGTAAAGG TGAAGAGG
 ||||| |||||
 TTTCAATTCC ACTTTTCC
 TACTTCC

GAM1929 DDX20 3' TTTTTCAGATTGTTTTGATTT 14068 CTA
 AGGTAAAGGCAG TGAAGAG
 ||||| |||||
 TTTAGTTTTGTT ACTTTTT
 AG_

GAM1929 DDX6 3' TCTCTTTGTGGGTTTTTCATCT 10649 T_ AG TG
 T AAGGT AAGGC CTA AAGAGG
 |||| |||| || |||||
 TTCTA TTTTG GGT TTCTCT
 CT _ GT

GAM1929 DLX4 3' TTTCTTTGTATGCCTTTGGCCT 28695 _ GC TG
 T AAGGTAA GGCA TA AAGAGG
 ||||| |||| || |||||
 TTCCGGTT CCGT AT TTCTTT
 T _ GT

GAM1929 DLX4 3' TTTCTTTGTATGCCTTTGGCCT 7647 _ GC TG
 T AAGGTAA GGCA TA AAGAGG
 ||||| |||| || |||||
 TTCCGGTT CCGT AT TTCTTT
 T _ GT

GAM1929 DMRT2 3' TTTTTTGCCCACCTGCCTTGAT 13324 CTAT_ G
 TT AGGTTAAGGCAG GAAGAG
 ||||| |||||
 TTTAGTTCCGTC TTTTT
 CACCCG

GAM1929 DNASE1 5' TTCTTCATAGACTACTTT 11717 C _
 AAGG AG CTATGAAGAG
 ||| || |||||
 TTTC TC GATACTTCTT
 A A

GAM1929 DSP 3' TCTCTTCTGTGTTTCGATTTT 10677 TA GCTAT
 AAGGT AGGCA GAAGAGG
 |||| |||| |||||

			TTTTA TTTGT CTTCTCT		
			GC GT___		
GAM1929	DUSP6	3'	TCTCTTTATGTAGTTTGA	32811	G A T
			GGTTAAG C GC ATGAAGAGG		
			I		
			TCAGTTT G TG TATTTCTCT		
			_ A _		
GAM1929	DVL3	3'	CCTCTTTAGCTCTCTTTATCTT	10695	T C TG
			AAGGT AAGG AGCTA AAGAGG		
			TTCTA TTCT TCGAT TTCTCC		
			T C _		
GAM1929	DYRK2	3'	CTTTTCAGCACTTAATTTT	9632	_ AGCTA
			AAGGTTAAG GC TGAAGAG		
			TTTTAATTC CG ACTTTTC		
			A _		
GAM1929	DYRK2	3'	CTTTTCAGCACTTAATTTT	13208	_ AGCTA
			AAGGTTAAG GC TGAAGAG		
			TTTTAATTC CG ACTTTTC		
			A _		
GAM1929	EFNA3	3'	CCTCTTTAACCCCTGACCTT	11395	A CAGCTA
			AAGGTTA GG TGAAGAGG		
			TTCCAGT CC ATTTCTCC		
			C CCA___		
GAM1929	EFNB1	3'	TAGTTTTGTAGTTTCTTGCTT	10713	C TG AGG
	T		AAGGTTAAGG AGCTA AAG		
			TTTCGGTTCT TTGAT TTT		
			_ GT GATT		
GAM1929	EHD3	3'	CTTCTTCGGCAAACCTTGCTTT	15958	T CA_ AT
			AAGGT AAGG GCT GAAGAGG		
			TTTCG TTCC CGG CTTCTTC		
			_ AAA _		
GAM1929	EHD4	3'	TCTCCAGGCTGCCTGGGCTTT	29257	TA A A
			AAGGT AGGCAGCT TG AGA		
			TTTCG TCCGTCGG AC TCT		
			GG _ C		
GAM1929	EIF2C1	3'	TCTCTTTACCTGGGGCCTGGCT	14505	A AG _
	TT		AAGGTTA GGC CTA TGAAGAGG		
			TTTCGGT CCG GGT ATTTCTCT		
			_ G_ CC		
GAM1929	EIF2S3	3'	TCTTTTTAGGCCTTCATTTT	7112	T AG T
			AAGGT AAGGC CTA GAAGA		

TTTTA TTCCG GAT TTTCT
 C _ T
 GAM1929 EIF4G2 3' TTTTTTTGTAGTGTAAATGTCTT 7118 _ TG
 AATC TTAAGGCA GCTA AAGAGG
 ||||| ||| |||||
 AATTCTGT TGAT TTTTTT
 AATG GT
 GAM1929 EIF5A2 3' TTTCTCAGTTGTTTTTGCTTT 21662 T AT
 AAGGT AAGGCAGCT GAAG
 |||| ||||| |||
 TTTCTG TTTTGTTGA CTTT
 T CT
 GAM1929 ELMO1 3' CTCTCCCTGCTTTTGCCTT 28202 T CTAT A
 AAGGT AAGGCAG GA GAG
 |||| ||||| || |||
 TTCCG TTTCGTC CT CTC
 T C _ _
 GAM1929 ENAM 3' TTTTTTGCTTGTGTTGATCTT 25635 G _ TAT
 AAGGTAA GCA GC GAAG
 ||||| ||| || |||||
 TTCTAGTT TGT CG TTTT
 G T TT_
 GAM1929 EPHA3 3' GTCTCTTTGTACAGGAACTGCA 11742 G C _ TG
 TTGACTTT AA GCAG TA AAGAGG T
 || |||| || ||||| |
 TT CGTC AT TTCTCT G
 A AAGGAC GT
 GAM1929 ERBB2IP 3' ATAGTTAGCCTTGATTTT 20770 _
 AAGGTAAAGGC AGCTAT
 ||||| ||||| |||||
 TTTTAGTTCCG TTGATA
 A
 GAM1929 ERBB2IP 3' CCTCTTTGATTTTTGTTTGGCC 20773 G CT _
 TT AAGGTAAAG CAG AT GAAGAGG
 ||||| ||| || |||||
 TTCCGGTTT GTT TA TTTCTCC
 _ TT G
 GAM1929 EXT2 3' TCTTTGGTTTGGCTTT 5974 G GCTATG
 AAGGTAAAG CA AAGA
 ||||| || |||||
 TTTCGGTTT GT TTCT
 G _ _
 GAM1929 FACL4 3' CCTTTCATTTTGCTTTAAGTTT 10763 G CT A
 AAG TTAAGGCAG ATGA GAGG
 || ||||| ||| |||||
 TTT AATTTCGTT TACT TTCC
 G T _ _
 GAM1929 FACL4 3' CCTTTCATTTTGCTTTAAGTTT 23253 G CT A
 AAG TTAAGGCAG ATGA GAGG
 || ||||| ||| |||||

			TTT AATTTCGTT TACT TTCC		
			G T_ _		
GAM1929	FBN2	3'	TTTCTTTCTCCCTGTCTTAGA 7727	G	CTAT_
	CTT		AAG TTAAGGCAG GAAGAGG		
			TTC GATTCTGTC TTTCTTT		
			A CCTCC		
GAM1929	FEN1	3'	TTTCATGCGCTGTTTTGTTTT 10322	TT	_
			AAGG AAGGCAGC TATGAAG		
			TTTT TTTTGTCTG GTACTTT		
			GT C		
GAM1929	FLRT2	3'	TTTCTTTATAGTAAGAGCTTTA 14889	A__	
			TAAGGC GCTATGAAGAGG		
			ATTTCTG TGATATTTCTTT		
			AGAA		
GAM1929	FOXF1	3'	CCTCTTCTGTTATGTTTTGTCT 7184	T	GCTAT
	T		AGG TAAGGCA GAAGAGG		
			TTC GTTTTGT CTTCTCC		
			T ATTGT		
GAM1929	FREB	3'	TCTGTCGTTGCCTTGATCTT 26468		TATGA
			AAGGTTAAGGCAGC AGA		
			TTCTAGTTCCGTTG TCT		
			CTG__		
GAM1929	FXVD6	3'	CCTGAGGCGGCTGCTTGAACCT 22549	A	ATGAAG
	T		AAGGTT AGGCAGCT AGG		
			TTCCAA TTCGTCGG TCC		
			G CGGAG_		
GAM1929	GCH1	3'	CCTTTTCATATCCATGATCTT 5666	A	CAGC
			AAGGTTA GG TATGAAGAGG		
			TTCTAGT CC ATACTTTTCC		
			A T__		
GAM1929	GCH1	3'	CTTTGATGCTTGCTTTAACTTT 5667	_	TAT
			AAGGTTAAGGCA GC GAAG		
			TTTCAATTTCTG CG TTTC		
			T TAG		
GAM1929	GLRX	3'	TTTCTTCTGGATGAGCTCTTG 7832	C	AT__
	GTTTT		TTAAGG AGCT GAAGAGG		
			GGTTTC TCGA CTTCTTT		
			_ GTAGGT		
GAM1929	GRM1	3'	TCTTGGCTGTCATAACTTT 6500	A	T
			AAGGTTA GGCAGCTA GA		

TTTCAAT CTGTCGGT CT
A T

GAM1929 GRM1 3' TTTTCTTGCTGTTTGTATTT 6501 TAT
AGGTTAAGGCAGC GAAGAGG
||||||| |||||
TTTAGTTTTGTCG CTTTTT
TT_

GAM1929 GRPR 5' CCTTTTGTGGCTAAGTTTTG 11791 _ TG
TAAGGC AGCTA AAGAGG
||||| ||||| |||||
GTTTTG TCGGT TTTTCC
AA GT

GAM1929 HDAC4 3' CCTTTTCCGCACAGCTGTGTTG 12662 G AT_
ACTTT GTTAA GCAGCT GAAGAGG
||||| ||||| |||||
CAGTT TGTCGA CTTTTCC
G CACGC

GAM1929 HDGF 3' TCTTTTGTAGCTGGGGCTTTG 10833 _ TG
ATGTT GTTAAGGC AGCTA AAGAGG
||||||| ||||| |||||
TAGTTTCG TCGAT TTTTCT
GGG GT

GAM1929 HGF 3' CCTTTGTATACTTCTTTAATT 45222 C C _
TT AAGGTTAAGG AG TATG AAGAGG
||||||| || ||||| |||||
TTTTAATTTC TC ATAT TTTTCC
T _ G

GAM1929 HIC1 5' CCTCTTGTGGCCTGGACCT 42210 A AGC TG
AGGTT AGGC TA AAGAGG
||||| ||||| || |||||
TCCAG TCCG GT TTCTCC
G _ GT

GAM1929 HOXB5 3' CTTTGGTATTTGTTTGTAGCT 7925 _ C G G
TT AAGGTTA AGGCAG TAT AAGAG
||||||| ||||| || |||||
TTTCGAT TTTGTT ATG TTTTC
G T G

GAM1929 HOXC4 5' CTTCTTGCAACTCTCCTTAATT 15974 C CTA _
TT AAGGTTAAGG AG TG AAGAGG
||||||| || || |||||
TTTTAATTCC TC AC TTCTTC
_ TCA G

GAM1929 HSPA4 3' TTCTTCATATTTACCTT 42976 T GCAGC
AAGGT AAG TATGAAGAG
||||| || |||||
TTCCA TTT ATACTTCTT
C _

GAM1929 ICMT 3' TCTTTTAGTTCCATGATCTT 14782 A C T
AAGGTTA GG AGCTA GAAGA
||||||| || ||||| |||||

			TTCTAGT CC TTGAT TTTCT		
			A _ T		
GAM1929	IL2RB	3'	TTTCTTGAGGTTGTCTGAGTCT 6576	GT A	ATG
	T		AAG T AGGCAGCT AAGAGG		
			TTC A TCTGTTGG TTCTTT		
			TG G AG_		
GAM1929	ITGA6	3'	TTTCTGGGTTGCCTTTGTTTT 5706	TT	AT
			AAGG AAGGCAGCT GAAG		
			TTTT TTCCGTTGG CTTT		
			GT GT		
GAM1929	JAG2	3'	TTTCTACGTTTCTTTAACCTT 8007	C	TAT
			AAGGTTAAGG AGC GAAG		
			TTCCAATTTTCTTG CTTT		
			T CAT		
GAM1929	KIF1B	3'	CCTGGGACAGTGGCTGCTCTTG 17448	_	GAAG_
	ACTTT		GTTAAG GCAGCTAT AGG		
			CAGTTC CGTCGGTG TCC		
			T ACAGGG		
GAM1929	LAMC1	3'	CCTTTTATATGTGCCTTCACTT 8075	T	GC A
	T		AAGGT AAGGCA TATGA GAGG		
			TTTCA TTCCGT ATATT TTCC		
			C GT _		
GAM1929	LDB3	3'	CTTTGGGTTGTCTTTGGCCTT 37562	_	A
			AAGGTTAAGG CAGCT TGAAG		
			TTCCGGTTTC GTTGG GTTTC		
			T _		
GAM1929	LENG4	3'	TCTCTGGCACAGTTTGCCTTGG 23587	_	A A_
	CCTT		AGGTTAAGGCAG CT TG AGAGG		
			TCCGGTTCCGTT GA AC TCTCT		
			T C GG		
GAM1929	LIFR	3'	CCTTTTCATTATTTTGTAGCTT 8101	C	CT
	T		AAGGTTAAGG AG ATGAAGAGG		
			TTTCGATTTT TT TACTTTTCC		
			_ AT		
GAM1929	LRP8	3'	CCTACCAGGGCTTTCTTGGCTT 27129	C	A AAG
	T		AAGGTTAAGG AGCT TG AGG		
			TTTCGGTTCT TCGG AC TCC		
			T G CA_		
GAM1929	LRP8	3'	CCTACCAGGGCTTTCTTGGCTT 11005	C	A AAG
	T		AAGGTTAAGG AGCT TG AGG		

TTTTCGGTTCT TCGG AC TCC
 T G CA_
 GAM1929 LUZP1 3' CCTTTTCCAATTTGTTGTCTTC 27353 T TAT____
 ATTTT GT AAGGCAGC GAAGAGG
 || ||||| |||||
 TA TTCTGTTG CTTTCC
 C TTTAAC
 GAM1929 LZTS1 3' TCTCTTTGTGGTTTCTTG 22010 C TG
 TAAGG AGCTA AAGAGG
 ||||| ||||| |||||
 GTTCT TTGGT TTCTCT
 _ GT
 GAM1929 MADD 5' TGTAGCATGCCTTGTTTT 28238 GG _
 AA TTAAGGCA GCTATG
 || ||||| |||||
 TT GGTCCGT CGATGT
 TT A
 GAM1929 MADH4 3' CTTTGTCTGCTTTATCTTT 11833 T CTAT
 AAGG TAAGGCAG GAAG
 ||||| ||||| |||||
 TTTC ATTCGTC TTTC
 T TTGT
 GAM1929 MAOB 3' TCTCCAGCTGATTTTAACTTT 30149 _ ATGAA
 AAGGTTAAGG CAGCT GAGG
 ||||| ||||| |||||
 TTTCAATTTT GTCGA CTCT
 A C____
 GAM1929 MBL2 3' CTTCTTCCCAATTGCTTTACCT 5762 T CTAT
 T AAGGT AAGGCAG GAAGAGG
 ||||| ||||| |||||
 TTCCA TTTCGTT CTTCTTC
 _ AACC
 GAM1929 MBNL 3' CTTCAAACATGTTGCTTTGCTT 22027 T TA____ AGG
 T AGGT AAGGCAGC TGAAG
 ||||| ||||| |||||
 TTCG TTTCGTTG ACTTC
 _ TACAA
 GAM1929 MEF2C 3' TCTCTTTGTAGAAGTTTTGTTT 8213 T AG TG
 TT AAGG TAAGGC CTA AAGAGG
 ||||| ||||| ||||| |||||
 TTTT GTTTTG GAT TTCTCT
 T AA GT
 GAM1929 MEIS1 3' TTTTTCATAGTCCCACCTT 8220 TAA CA
 AAGGT GG GCTATGAAGAG
 ||||| ||||| ||||| |||||
 TTCCA CC TGATACTTTT
 _ C_
 GAM1929 MGEA5 3' TTTTGCATCAGCTGTTTAACTT 14521 G _ _ GG
 T AAGGTTAAG CAGCT ATG AAGA
 ||||| ||||| ||||| |||||

TTTCAATTT GTCGA TAC TTTT
 _ C G
 GAM1929 MID1 5' TTTCGCCGGGTTGCTTTTGTCT 5957 TT ATGAA
 T AAGG AAGGCAGCT GAGG
 |||| ||||| ||||
 TTCT TTTCGTTGG CTTT
 GT GCCG_
 GAM1929 MLF2 3' CTTCTCTGCCTTTATTTT 11925 T CTAT
 AAGGT AAGGCAG GAAG
 |||| ||||| ||||
 TTTTA TTCCGTC CTTC
 T T____
 GAM1929 MMP19 5' CCTCTTTGTCTGCCTTTAATTT 23075 _ CT TG
 T AAGGTAA GGCAG A AAGAGG
 ||||| |||| | |||||
 TTTTAATT CCGTC T TTCTCC
 T _ GT
 GAM1929 MNT 3' CCTCTGGGCAGCCTGCTTTGGC 21562 _ ATGA
 CTT AAGGTAAAGGCAG CT AGAGG
 ||||| |||| || |||||
 TTCCGTTTCGTC GA TCTCC
 C CGGG
 GAM1929 MOX2 3' CTTTTTCCATGCGTTAACTTT 33237 G GCTAT
 AAGGTAA GCA GAAGAGG
 ||||| || |||||
 TTTCAATT CGT CTTTTTC
 G AC____
 GAM1929 MS4A1 3' CCTTTTCATCCAGCCTTAATTT 5632 AGCT
 AGGTAAAGGC ATGAAGAGG
 ||||| |||||
 TTTAATTCCG TACTTTTCC
 ACC_
 GAM1929 MTMR3 3' CCTTG GTTGTCTTAATTTT 22071 ATGAA
 AAGGTAAAGGCAGCT GAGG
 ||||| |||||
 TTTTAATTCTGTTGG TTCC

 GAM1929 MXI1 3' CCTTACCCCTGGCTGTTTGGAC 28194 A TGAA_
 TTT AAGGTT AGGCAGCTA GAGG
 |||| ||||| ||||
 TTTCAG TTTGTCTGGT TTCC
 G CCCCCA
 GAM1929 MXI1 3' CCTTACCCCTGGCTGTTTGGAC 12584 A TGAA_
 TTT AAGGTT AGGCAGCTA GAGG
 |||| ||||| ||||
 TTTCAG TTTGTCTGGT TTCC
 G CCCCCA
 GAM1929 MYB 3' TTTTTTGCTGCTATGGTCTT 29945 GT A TAT
 AAG TA GGCAGC GAAG
 || || ||||| ||||

TTC GT TCGTCG TTTT
 TG A TT_
 GAM1929 NCKAP1 3' CTTTTTATATATGTTTAA 15096 GC G
 TTAAGGCA TATGAAGAG
 ||||| |||||
 AATTTTGT ATATTTTC
 AT
 GAM1929 NCOA3 3' TCTTTTCAATCTCTTAATCT 13288 CAGCTA
 AGGTAAAGG TGAAGAGG
 ||||| |||||
 TCTAATTCT ACTTTTCT
 CTA__
 GAM1929 NEB 5' TCTTTTCATAGTCTTCTTTGTA 10892 _ C _
 TTTT AGGT TAAGG AG CTATGAAGAGG
 ||| |||| || |||||
 TTTA GTTTC TC GATACTTTTCT
 T T T
 GAM1929 NEK4 3' CTTTTTATATCTCTTTGGC 9138 C C
 GTTAAGG AG TATGAAGAGG
 ||||| || |||||
 CGGTTTC TC ATATTTTTC
 _ T
 GAM1929 NFE2L1 3' TTTCTTGCGCTTTGATTTT 9199 A TAT
 AAGGTTAAGGC GC GAAG
 ||||| || |||
 TTTTAGTTTCG CG CTTT
 _ TT_
 GAM1929 NGFRAP1 5' CTCTCCTTGCCCTTTGTCTT 15715 TT CTAT A
 AAGG AAGGCAG GA GAG
 ||| ||||| || |||
 TTCT TTCCGTT CT CTC
 GT C__ _
 GAM1929 NIPSNAP1 3' CCTGGTCCTGCTGTCTTGTTT 9701 GG TAT AG
 T AA TTAAGGCAGC GA AGG
 || ||||| || |||
 TT GGTCTGTCTG CT TCC
 TT TC_ GG
 GAM1929 NRCAM 3' CTATGTATAGCTGTCGTTAGTC 11450 GT _ AAG G
 TT AAG TAA GGCAGCTATG AG
 ||| || ||||| ||
 TTC ATT CTGTGATAT TC
 TG G GTA
 GAM1929 OAS2 3' CTTTTTCCTTGGCTTTAGCCTT 18806 AGCTAT
 AAGGTTAAGGC GAAGAGG
 ||||| |||||
 TTCCGATTTCTG CTTTTTC
 GTTC__
 GAM1929 OPA1 3' CCTTTTCACTAAGCCTTTACTT 28322 T AGCTA
 T AAGGT AAGGC TGAAGAGG
 ||||| |||||

			TTTCA TTCCG	ACTTTTCC		
			T	AATC_		
GAM1929	OPA1	3'	CCTTTTCACTAAGCCTTTACTT	28330	T	AGCTA
	T		AAGGT AAGGC	TGAAGAGG		
			TTTCA TTCCG	ACTTTTCC		
			T	AATC_		
GAM1929	OPA1	3'	CCTTTTCACTAAGCCTTTACTT	28338	T	AGCTA
	T		AAGGT AAGGC	TGAAGAGG		
			TTTCA TTCCG	ACTTTTCC		
			T	AATC_		
GAM1929	OPA1	3'	CCTTTTCACTAAGCCTTTACTT	28346	T	AGCTA
	T		AAGGT AAGGC	TGAAGAGG		
			TTTCA TTCCG	ACTTTTCC		
			T	AATC_		
GAM1929	OPA1	3'	CCTTTTCACTAAGCCTTTACTT	28354	T	AGCTA
	T		AAGGT AAGGC	TGAAGAGG		
			TTTCA TTCCG	ACTTTTCC		
			T	AATC_		
GAM1929	OXCT	3'	TTTCTTCAGCCTCCTCTGACTT	6021	_	CA AT
	T		AAGGTTA AGG	GCT GAAGAGG		
			TTTCAGT TCC	CGA CTTCTTT		
			C	TC _		
GAM1929	P2RY1	3'	CTTTTCCCCTCTTTAACTTT	8411	C	CTAT
			AAGGTTAAGG AG	GAAGAG		
			TTTCAATTC TC	CTTTTC		
			_	CC_		
GAM1929	PAICS	5'	TCTCTTTCAGAGCATTAGCCT	13165	GCA	A _
	T		AAGGTTAAG	GCT TGAA GAGG		
			TTCCGATTT	CGA ACTT CTCT		
			A_	G T		
GAM1929	PDE7A	3'	CTTTTTCAAAGCATCTAATCTT	32642	A	CA A
			AAGGTTA GG	GCT TGAAGAGG		
			TTCTAAT CT	CGA ACTTTTTC		
			_	A_ A		
GAM1929	PEA15	3'	CTTTTTTGTGGTGTCTAGC	9849	A	G TG
			GTTA GGCA CTA	AAGAGG		
			CGAT CTGT GGT	TTTTTC		
			_	_ GT		
GAM1929	PER2	3'	TCTTTTTATGACCTGTTTGCCT	23094	TA	C_
	T		AAGGT AGGCAG	TATGAAGAGG		

		TTCCG TTTGTC GTATTTTCT	
		— CA	
GAM1929 PKHD1	3'	CCTCTTTGTAGATGATGATTT 28939	TAAGG G TG
T		AAGGT CA CTA AAGAGG	
		TTTTA GT GAT TTCTCC	
		TGTA_ A GT	
GAM1929 PLAG1	5'	CCTCTTGGTGCTGCCTTGGCC 8519	T G
		GGTTAAGGCAGC AT AAGAGG	
		CCGTTCCGTCG TG TTCTCC	
		_ G	
GAM1929 PLEK	3'	CTTCTACTTGCTCTTGGCCTT 8532	_ C T
		AAGGTTAAG GCAG TA GAAG	
		TTCCGGTTC CGTT AT CTTC	
		T C _	
GAM1929 POU3F1	3'	TCTTTTGTTCGGTTGCTTTGG 29833	_ TG
		TTAAGGCAGCT A AAGAGG	
		GGTTTCGTTGG T TTTTCT	
		CT GT	
GAM1929 PPARGC1	3'	TCTTTTAAATGCTGTTTTG 14933	TA_
		TAAGGCAGC TGAAGAGG	
		GTTTTGTCG ATTTTCT	
		TAAA	
GAM1929 PRDM2	5'	CTTAGGCGTTTTGACCTT 14535	A ATGAA
		AAGGTTAAGGC GCT GAG	
		TTCCAGTTTTG CGG TTC	
		_ A _	
GAM1929 PRDM2	5'	CTTAGGCGTTTTGACCTT 18003	A ATGAA
		AAGGTTAAGGC GCT GAG	
		TTCCAGTTTTG CGG TTC	
		_ A _	
GAM1929 PREP	3'	CCTTTTGTAGCAAGGCCTTGGTG 8589	G TT AGCTA
TT		AA G AAGGC TGAAGAGG	
		TT T TTCCG ATTTTCC	
		G GG GAACG	
GAM1929 PRKAR1A	3'	TCTCTTTGTGCAGTGTTAG 8608	G A T TG
		TTAA GC GC A AAGAGG	
		GATT TG CG T TTCTCT	
		G A _ GT	
GAM1929 PSMB9	3'	CTTTTTCAGTAGCATTTAGACC 8676	A CA _
TT		AAGGTT AGG GCTA TGAAGAGG	

TTCCAG TTT CGAT ACTTTTTC
 A A_ G
 GAM1929 PTTG1IP 3' CTTGGAGTGCCTTAATTTT 10534 G ATGAA
 AAGGTTAAGGCA CT GAG
 ||||| || ||
 TTTTAATTCCGT GA TTC
 _ GG_
 GAM1929 RAD51L1 3' TCTTTTATGGCTGAATAAT 8788 AGG
 GTTA CAGCTATGAAGAGG
 ||| |||||
 TAAT GTCGGTATTTTCT
 AA_
 GAM1929 RAD51L1 3' TCTTTTATGGCTGAATAAT 28577 AGG
 GTTA CAGCTATGAAGAGG
 ||| |||||
 TAAT GTCGGTATTTTCT
 AA_
 GAM1929 RAD51L3 3' CTTCTTCATCTCTGTTTTGCTC 28578 GT CT
 TT AAG TAAGGCAG ATGAAGAGG
 || ||||| |||||
 TTC GTTTTGTC TACTTCTC
 TC TC
 GAM1929 RAD51L3 3' CTTCTTCATCTCTGTTTTGCTC 28580 GT CT
 TT AAG TAAGGCAG ATGAAGAGG
 || ||||| |||||
 TTC GTTTTGTC TACTTCTC
 TC TC
 GAM1929 RAD51L3 3' CTTCTTCATCTCTGTTTTGCTC 8789 GT CT
 TT AAG TAAGGCAG ATGAAGAGG
 || ||||| |||||
 TTC GTTTTGTC TACTTCTC
 TC TC
 GAM1929 RDX 3' TCTCTTGCTTTTTTGATTTT 8809 C TATG
 AAGGTTAAGG AGC AAGAGG
 ||||| || |||||
 TTTTAGTTTT TCG TTCTCT
 T TG_
 GAM1929 RELN 3' TTCTTCGTGGATTGTTTT 45285 _
 AAGGCAG CTATGAAGAG
 ||||| |||||
 TTTTGTT GGTGCTTCTT
 A
 GAM1929 RFX5 3' CCTTTTCCTGTTTCTTAATTTT 6047 C TAT
 AAGGTTAAGG AGC GAAGAGG
 ||||| || |||||
 TTTTAATTCT TTG CTTTTC
 _ TC_
 GAM1929 RGR 3' CTTTTTATGGCAGTGTAGTA 8825 AG _
 TA GCA GCTATGAAGAGG
 || ||| |||||

			AT TGT CGGTATTTTTTC		
			GA GA		
GAM1929	RNASE6	5'	TTTCTTTAAGTTGGTTTAGCCT 12133	G A	
	T		AAGGTTAAG CAGCT TGAAGAGG		
			TTCCGATTT GTTGA ATTTCTTT		
			G _		
GAM1929	RNF4	3'	CCTGGCCACCTGTCTTGGCTT 8842	CTATGAAG	
	T		AAGGTTAAGGCAG AGG		
			TTTCGGTTCTGTC TCC		
			CACCCGG_		
GAM1929	RPL15	3'	CTTTTTTGTCTTTGCTTTATCT 8861	T CT TG	
	T		AAGGT AAGGCAG A AAGAGG		
			TTCTA TTTCGTT T TTTTC		
			_ TC GT		
GAM1929	RRM2B	3'	TTTCTTTATGGTTTTAAACTC 33691	_ AAGGC	
	TT		AAG GTT AGCTATGAAGAGG		
			TTC CAA TTGGTATTTCTTT		
			T AATT_		
GAM1929	RUNX1	3'	CTTCTTTCTTGCTTTGACC 7499	CTAT	
			GGTTAAGGCAG GAAGAGG		
			CCAGTTTCGTT TTTCTTC		
			C__		
GAM1929	RUNX1	3'	TTTCTGCTGCCTTGGGTTT 7504	G TAT	
			AAG TTAAGGCAGC GAAG		
			TTT GGTTCGTCG CTTT		
			G T__		
GAM1929	SAR1	3'	CTTCAGTGTTAGTTTCTTAAT 21352	C ____ AGG	
	TTT		GTTAAGG AGCTA TGAAG		
			TAATTCT TTGAT ACTTC		
			T TGTG G		
GAM1929	SCN3A	3'	TTTCTAGATGGCTTTAATTTT 13799	AG_ T	
			AAGGTTAAGGC CTA GAAG		
			TTTTAATTTCG GAT CTTT		
			GTA _		
GAM1929	SIRT1	3'	TCTTTTTATATTGTACATAGTC 14544	GT AG_ C	
	TT		AAG TA GCAG TATGAAGAGG		
			TTC AT TGTT ATATTTTCT		
			TG ACA _		
GAM1929	SLC20A2	3'	CTTTTTCTGTGCTTTGAC 13601	GCTAT	
			GTTAAGGCA GAAGAGG		

			CAGTTTCGT	CTTTTC		
			GT__			
GAM1929	SLC21A9	3'	TTCTTTGAGCCTTAGCC	14128	AGCTA	
			GGTTAAGGC	TGAAGAG		
			CCGATTCCG	GTTTCTT		
			A__			
GAM1929	SLC2A2	3'	CTTCTTTGTCTTAGCT	5892	CTAT	
			GGTTAAGGCAG	GAAG		
			TCGATTCTGTT	CTTC		
			T__			
GAM1929	SLC4A7	3'	TTTCTTTAGATGCCTTGATTT	9676	GCTA	
			AGGTAAAGGCA	TGAAGAGG		
			TTTAGTTCCGT	ATTTCTTT		
			AG__			
GAM1929	SLC4A8	3'	CTTCTGTCTGTTCTTAATTTT	11267	_ C T	
			AAGGTAAAGG	CAG TA GAAG		
			TTTTAATTCT	GTC GT CTTC		
			T T _			
GAM1929	SMARCD1	3'	CCTCATAGTATCTGCCTTGGTC	29143	GT	C GAA
	TT		AAG TAAGGCAG TAT	GAGG		
			TTC GTTCCGTC ATG	CTCC		
			TG	T ATA		
GAM1929	SMARCD1	3'	CCTCATAGTATCTGCCTTGGTC	9045	GT	C GAA
	TT		AAG TAAGGCAG TAT	GAGG		
			TTC GTTCCGTC ATG	CTCC		
			TG	T ATA		
GAM1929	SMP1	3'	TTTCTTTGTAGTTGTTCTGAT	15613	AG	TG
			GTTA GCAGCTA	AAGAGG		
			TAGT TGTTGAT	TTCTTT		
			CT	GT		
GAM1929	SNL	3'	TCTCACTCTGGGTGTCTTGGTC	9067	GT	G T A_
	TT		AAG TAAGGCA CTA	GA GAGG		
			TTC GTTCTGT GGT	CT CTCT		
			TG	G _ CA		
GAM1929	SNX9	3'	CTCCCGCTGCTTTCATTTT	18330	T	TATGAA
			AAGGT AAGGCAGC	GAG		
			TTTTA TTTCGTCG	CTC		
			C	CC__		
GAM1929	SORBS1	3'	TCTTTTCCCATATCCTTGGCTT	17689		CAGCTAT
	T		AAGGTAAAGG	GAAGAGG		

		TTTCGGTTCC	CTTTTCT	
		TATACC_		
GAM1929	SPTBN4	3' CTTCCAATGCTGCCTTGATCT	24884	TAT_
		AGGTAAAGGCAGC	GAAG	
		TCTAGTTCGTCG	CTTC	
		TAAC		
GAM1929	SSPN	3' TCTCTTCAGCTCCCTTAGCTT	11537	C AT
		AGGTAAAGG	AGCT GAAGAGG	
		TTCGATTCC	TCGA CTTCTCT	
		C		
GAM1929	STAU2	3' TCTTTTTATGATGATTTTACCT	15724	T G GC
	T	AAGGT	AAG CA TATGAAGAGG	
		TTCCA	TTT GT GTATTTTCT	
		T A A_		
GAM1929	TACC1	3' TCTCTTTGTGGTCATGTGATT	12969	AGGCA TG
		GGTTA	GCTA AAGAGG	
		TTAGT	TGGT TTCTCT	
		GTAC_	GT	
GAM1929	TBR1	3' TCTCTTCTCTCTCTTTTAATTT	13358	C CTAT
	T	AAGGTAAAGG	AG GAAGAGG	
		TTTTAATTT	TC CTTCTCT	
		C TCT_		
GAM1929	TGFBR2	3' CTTTTTCATTACACTTGACTT	9242	GCAGCT
		AGGTAAAG	ATGAAGAGG	
		TTCAGTTC	TACTTTTC	
		ACAT_		
GAM1929	THBD	3' TTTCTTTGTGTAGCTTTGCTCT	5923	GT A T TG
	T	AAG	TAAGGC GC A AAGAGG	
		TTC	GTTTCG TG T TTCTTT	
		TC	A _GT	
GAM1929	THBD	3' TTTTGTTGCTGTTTTGATTT	5924	T TG
		AGGTAAAGGCAGC	A AAG	
		TTTAGTTTTGTCG	T TTT	
		T GT		
GAM1929	TIA1	3' TTTTTTCACAAATTTGTCTTGC	22560	T CTA_
	CTT	AGGT	AAGGCAG TGAAGAGG	
		TCCG	TTCTGTT ACTTTTTT	
		_	TAAAC	
GAM1929	TIA1	3' TTTTTTCACAAATTTGTCTTGC	22735	T CTA_
	CTT	AGGT	AAGGCAG TGAAGAGG	

TCCG TTCTGTT ACTTTTTT
 _ TAAAC
 GAM1929 TLL1 3' TTTTTCAAACAAGTTTTTGAC 14838 GC A____
 CTT GGTAAAG AGCT TGAAGAGG
 ||||| ||| |||||
 CCAGTTT TTGA ACTTTTTT
 _ ACAA
 GAM1929 TMOD2 3' TTTCTTATTGGGTTGTCTTGCT 15863 T ATG_
 TT AAGGT AAGGCAGCT AAGAGG
 ||||| ||||| |||||
 TTTTCG TTCTGTTGG TTCTTT
 _ GTTA
 GAM1929 TNFAIP1 3' CCTCTTTAGGGCTTTGGTTTT 22112 GG AGCTA
 AA TTAAGGC TGAAGAGG
 || ||||| |||||
 TT GGTTTCG ATTTCTCC
 TT GG____
 GAM1929 TOX 3' TTTCTTTGATGTTTAACTTT 16330 GCTAT
 AAGGTTAAGGCA GAAGAGG
 ||||| |||||
 TTTCAATTTTGT TTTCTTT
 AG____
 GAM1929 TRIM14 3' TCTTTTCACCTGTCTCAGTCTT 16670 GT A CTA
 AAG T AGGCAG TGAAGAGG
 ||| | ||||| |||||
 TTC A TCTGTC ACTTTTCT
 TG C C____
 GAM1929 TRPC1 3' CCTCTGCGTTCTGCCTTGGTT 9306 TT CT A
 GG AAGGCAG ATG AGAGG
 || ||||| ||| |||||
 TT TTCCGTC TGC TCTCC
 GG T_ G
 GAM1929 TRPC1 3' TCTCGACATTTGGTTTGTTTTA 9308 _ _ AA
 ATTTT GTTAAGGCAG CT ATG GAGG
 ||||| || ||| |||||
 TAATTTTGTT GG TAC CTCT
 T TT AG
 GAM1929 TRRAP 3' CTTTCGCTAGCTTTAGTCTT 9588 GT _ TAT
 AAG TAAGGC AGC GAAG
 ||| ||||| ||| |||||
 TTC ATTTTCG TCG CTTC
 TG A ____
 GAM1929 TSN 3' TTTCTGATGTTGCCTTAAT 10990 TATGA
 GTTAAGGCAGC AGAGG
 ||||| |||||
 TAATTCGTTG TCTTT
 TAG____
 GAM1929 TXNRD1 3' TTTTCTGGTAGCTTTAGCTTT 9338 A T
 AAGGTTAAGGC GCTA GAAGAG
 ||||| ||||| |||||


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          TTTTCGATTTTCG TGGT CTTTTT
                A _
GAM1929 TYRP1 3' TCTTTTCAATGGGTTTAAATTT 35796      AG _
                T      AAGGTTAAGGC CTAT GAAGAGG
                ||||| ||| |||||
                TTTTAATTTTG GGTA CTTTCT
                        _ A
GAM1929 UBE3A 3' TCGTTGTTGTTTAAAGTTT 28366      G      T
                AAG TTAAGGCAGC ATGA
                ||| ||||| |||
                TTT AATTTTGTTG TGCT
                        G      T
GAM1929 UBE3A 3' TCGTTGTTGTTTAAAGTTT 28362      G      T
                AAG TTAAGGCAGC ATGA
                ||| ||||| |||
                TTT AATTTTGTTG TGCT
                        G      T
GAM1929 UBE3A 3' TCGTTGTTGTTTAAAGTTT 6081      G      T
                AAG TTAAGGCAGC ATGA
                ||| ||||| |||
                TTT AATTTTGTTG TGCT
                        G      T
GAM1929 UNG 3' TCTCTTTATCTCCCTTGCCTT 28127      T C CT
                AAGGT AAGG AG ATGAAGAGG
                |||| ||| || |||||
                TTCCG TTCC TC TATTTCTCT
                        _ C _
GAM1929 UNG 3' TCTCTTTATCTCCCTTGCCTT 9389      T C CT
                AAGGT AAGG AG ATGAAGAGG
                |||| ||| || |||||
                TTCCG TTCC TC TATTTCTCT
                        _ C _
GAM1929 VSNL1 3' CCTTTTGGGTTTGCCTTAATT 9416      _ ATG
                GGTTAAGGCAG CT AAGAGG
                ||||| || |||||
                TTAATTCCGTT GG TTTTCC
                        T G_
GAM1929 XPR1 3' TCTTTTCTTCTGGTTTAAATTT 11125      G CTAT
                AAGGTTAAG CAG GAAGAGG
                ||||| || |||||
                TTTTAATTT GTC CTTTCT
                        G TT_
GAM1929 XYLB 3' CCTCTTTATCCCTCCTGTTTAA 11584      T CT_
                CTTT      GGT AAGGCAG ATGAAGAGG
                ||| ||||| |||||
                TCA TTTTGTC TATTTCTCC
                        _ CTCCC
GAM1929 YWHAG 3' CCTTTGCTAGTTGTTTGGGCTT 14854      TA      TGA
                T      AAGGT AGGCAGCTA AGAGG
                |||| ||||| |||||

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		TTTCG TTTGTTGAT TTTCC		
		GG CG_		
GAM1929	YWHAH	3' TTTCAGTAGCTCCTTGGTTTT 9441	GG C _	
		AA TTAAGG AGCTA TGAAG		
		TT GGTTC TCGAT ACTTT		
		TT _ G		
GAM1929	ZHX1	3' TTTTTCATACTACTGTAACT 14093	AG C_	
	TT	AAGGTTA GCAG TATGAAGAGG		
		TTTCAAT TGTC ATACTTTTTT		
		_ ATC		
GAM1929	ZNF36	3' TCTTTGGCCTCTCCTTGGCTTT 45104	CA_ AT	
		AAGGTTAAGG GCT GAAGA		
		TTTCGGTTCC CGG TTTCT		
		TCTC _		
GAM1929	ZNF80	3' TTTCTCAGCTTCTTTGGCCTT 13988	C AT	
		AAGGTTAAGG AGCT GAAG		
		TTCCGGTTTC TCGA CTTT		
		T CT		
GAM1929	ACP33	3' CCTCTTTGGTTTTCTTAGCTTT 18744	C AT	
		AAGGTTAAGG AGCT GAAGAGG		
		TTTCGATTCT TTGG TTTCTCC		
		T _		
GAM1929	AF311304	3' TCTTGAGTTGTTTTAATTTT 25260	ATG	
		AAGGTTAAGGCAGCT AAGA		
		TTTTAATTTTGTGA TTCT		
		G_		
GAM1929	AGMAT	3' TTGTACTGCTTTGATTTT 24107	C TG	
		AAGGTTAAGGCAG TA A		
		TTTTAGTTTCGTC AT T		
		_ GT		
GAM1929	AKAP8	3' CTTTTTTATTTTTTTCCTTAAT 12464	CAGCT_	
	TTT	AAGGTTAAGG ATGAAGAGG		
		TTTTAATTCC TATTTTTTC		
		TTTTTT		
GAM1929	AP3M2	3' TTTTTTCCTTAGCCTT 13679	CAGCTAT	
		AAGGTTAAGG GAAGA		
		TTCCGATTCC TTTT		
		T_____		
GAM1929	APOL4	3' TTTCTTATGCCTGTCTTTACTT 24979	T C A	
	T	AAGGT AAGGCAG TATGA GAGG		

TTTCA TTCTGTC GTATT CTTT
 T C _
 GAM1929 ARHE 3' TCTTTTTTGGAAATCCTGACCTT 11669 A CAG T
 AAGGTTA GG CTA GAAGA
 ||||| || |||||
 TTCCAGT CC GGT TTTCT
 _ TAA T
 GAM1929 ARHGEF3 3' CCTCTTTGTCCAGCCTTGATTT 21209 AGCT TG
 AGGTTAAGGC A AAGAGG
 ||||| || |||||
 TTTAGTTCCG T TTCTCC
 ACC_ GT
 GAM1929 ARHGEF9 3' CTTTTCATGGATAGACCTT 17540 AAGGCAG
 AAGGTT CTATGAAGAG
 ||||| |||||
 TTCCAG GGTACTTTTC
 ATA____
 GAM1929 ARL8 3' CTTTGAAAGTAGTTGTTTAAC 44762 G GA____ G
 TTT GGTAAAG CAGCTAT AGAG
 ||||| ||||| |||||
 TCAATTT GTTGATG TTTC
 _ AAAGG
 GAM1929 ARNTL2 3' CTTACATATTGTTTTGGCTTT 21413 C _
 AAGGTTAAGGCAG TATG AAG
 ||||| ||||| |||||
 TTTCGGTTTTGTT ATAC TTC
 _ A
 GAM1929 ATP10B 3' TTTCTTCAACAACCTTGACTT 31737 CAGCTA
 AGGTTAAGG TGAAGAGG
 ||||| |||||
 TTCAGTTCC ACTTCTTT
 AACA____
 GAM1929 ATP9A 3' TCTTTTTATACTTTGTCTTGTT 31087 T C_
 TTT AAGG TAAGGCAG TATGAAGAGG
 ||||| ||||| |||||
 TTTT GTTCTGTT ATATTTTCT
 T TC
 GAM1929 BCMP1 3' CTCAGTTGATTTAATCTT 25456 G ATGAA
 AAGGTTAAG CAGCT GAG
 ||||| ||||| |||||
 TTCTAATTT GTTGA CTC
 A _____
 GAM1929 C12orf22 3' CCTCTTTGTGAGATCTGAGCTT 25126 A CAGC TG
 T AAGGTT AGG TA AAGAGG
 ||||| ||||| |||||
 TTTCGA TCT GT TTCTCC
 G AGA_ GT
 GAM1929 C13orf1 3' CCTCTTCATGACCCTGAGTCTT 21691 GT A CAGC
 AAG T AGG TATGAAGAGG
 ||||| ||||| |||||

TTC A TCC GTACTTCTCC
 TG G CA__
 GAM1929 C1orf22 3' CTTTTTTATAGTAAAGCC 24839 A__
 GGC GCTATGAAGAGG
 ||| |||||
 CCG TGATATTTTTTC
 AAA
 GAM1929 C1orf24 3' CTTTAAGGCTTTTAAATTTT 27532 C A
 AAGGTTAAGG AGCT TGAAG
 ||||| ||| ||||
 TTTTAATTTT TCGG ATTTC
 _ A
 GAM1929 C20orf130 3' TCTCTTTATTCCCTTTGATC 30938 CAGCT
 GGTTAAGG ATGAAGAGG
 ||||| |||||
 CTAGTTTC TATTTCTCT
 CCT__
 GAM1929 C21orf41 3' CTTGCGCCAGCAGCCTTGTTTTT 28730 GG A A_
 AA TTAAGGC GCT TGAAG
 || ||||| ||| ||||
 TT GGTTC CGA GCTTC
 TT A CC
 GAM1929 C5orf6 3' CCTCCACTTTAGCTGTTTTGAC 18702 TGAA_
 T GGTTAAGGCAGCTA GAGG
 ||||| ||||
 TCAGTTTTGTCGAT CTCC
 TTCAC
 GAM1929 CAMKK1 3' CTTTTTGTGTCTTTTACTTT 26070 T_ TAT G
 AAGGT AAGGCAGC GAAGAG
 |||| ||||| |||||
 TTTCA TTCTGTTG TTTTTC
 TT T__
 GAM1929 CCR6 3' TCTCTTCCTGAGCCTTAACT 25373 AGC T
 GGTTAAGGC TA GAAGAGG
 ||||| || |||||
 TCAATTCCG GT CTTCTCT
 A__ C
 GAM1929 CCR6 3' TCTCTTCCTGAGCCTTAACT 10579 AGC T
 GGTTAAGGC TA GAAGAGG
 ||||| || |||||
 TCAATTCCG GT CTTCTCT
 A__ C
 GAM1929 CGI-57 3' CCTTTTCACTCCCATTCCTTAG 36574 CAGCTA__
 CTTT AGGTTAAGG TGAAGAGG
 ||||| |||||
 TTCGATTCC ACTTTTCC
 TTACCCTC
 GAM1929 CHFR 3' TTTCAACTGTTGTCTTGCTCTT 20150 GT TA_
 AAG TAAGGCAGC TGAAG
 || ||||| ||||

TTC GTTCTGTTG ACTTT
 TC TCA
 GAM1929 CHST4 3' TTCTTCTTTTCTTGATCTT 12340 CAGCTAT
 AAGGTTAAGG GAAGAG
 ||||| ||||
 TTCTAGTTCT CTTCTT
 TTT____
 GAM1929 CHSY1 3' CTTTTTCCCCTCCTTAATTTT 17173 C CTAT
 AAGGTTAAGG AG GAAGAGG
 ||||| || |||||
 TTTTAATTCC TC CTTTTTC
 _ CC_
 GAM1929 CKAP4 3' TCTTTAATGGCTGTCTTGCCCT 13705 T _ GG
 T AAGG TAAGGCAGCTAT GAAGA
 ||| ||||| |||||
 TTCC GTTCTGTCTGGTA TTTCT
 C A
 GAM1929 CLDN4 3' CTTCTTTGTGGTTTCTGTTTTG 6988 _ TG
 TAAGGCAG CTA AAGAGG
 ||||| || |||||
 GTTTTGTC GGT TTCTTC
 TTT GT
 GAM1929 CRNKL1 3' TCTCTTTATAGTTAGGCTT 18774 _
 AGGC AGCTATGAAGAGG
 ||| ||||| |||||
 TTCG TTGATATTTCTCT
 GA
 GAM1929 CTPS2 3' CCTTTTTATTTCTGTGGCTTT 21262 AAG CT
 AAGGTT GCAG ATGAAGAGG
 ||||| ||| |||||
 TTTCGG TGTC TATTTTCC
 _ TT
 GAM1929 D2S448 3' TCTGTAAAAATGGTTGTCTTAA 36395 GA_ GG
 CTT TTAAGGCAGCTAT AGA
 ||||| |||
 AATTCTGTTGGTA TCT
 AAAATG G
 GAM1929 DJ971N18.2 3' CCAAATATAGTTGTTGTTGAT 22134 _ AAGAGG
 TTT AAGGTTAA GGCAGCTATG
 ||||| |||||
 TTTTAGTT TTGTTGATAT
 G AAAACC
 GAM1929 DKFZP434C0826 5' CCTCTTCGTCACCTCCCTGGCTT 40844 A C CT
 T AAGGTTA GG AG ATGAAGAGG
 ||||| || |||||
 TTTCGGT CC TC TGCTTCTCC
 C _ AC
 GAM1929 DKFZP434D1335 3' TTTTGATTGTTTTCTTAACCTT 32468 C T G
 AAGGTTAAGG AGC AT AAGA
 ||||| ||| || |||

	TTTCAATTCT TTG TA TTTT		
	T T G		
GAM1929 DKFZp434D177 3'	TCTTTTTGTTGTTGTCATTGAT 26010	_	T TG
TTT	AAGGTAA GGCAGC A AAGAGG		
	TTTTAGTT CTGTTG T TTTTCT		
	A T GT		
GAM1929 DKFZP434J1813 3'	CTTCTGAACCTTTGTTTTGACCT 30949		CTATGA
	AGGTAAAGGCAG AGAGG		
	TCCAGTTTTGTT TCTTC		
	TCAAG_		
GAM1929 DKFZP434O125 3'	TCTTTTAATTGTCTTAATTTT 32407		CTAT
	AAGGTAAAGGCAG GAAGA		
	TTTTAATTCTGTT TTTCT		
	AAT_		
GAM1929 DKFZp547I224 5'	CTTTTTCATTCCCCTTTACCTT 21477	T	CAGCT
	AAGGT AAGG ATGAAGAGG		
	TTCCA TTCC TACTTTTTC		
	T CCT__		
GAM1929 DKFZP564I0422 3'	CCTTTTTATAATCAAATGCTTT 25434	TT	GC_____
TGTCTT	AAGGCA TATGAAGAGG		
	TTTCGT ATATTTTTC		
	GT AAATA		
GAM1929 DKFZP564L2423 3'	TTCTTCCCTGCCTTACCTT 31259	T	CTAT
	AAGGT AAGGCAG GAAGAG		
	TTCCA TTCCGTC CTTCTT		
	_ C__		
GAM1929 DKFZP564O0823 3'	TTGTTGGTATGGTTGTTTTTGT 29938	TT	AA GG
TTT	AAGG AAGGCAGCTATG GA		
	TTTT TTTTGGTGGTAT TT		
	GT GG GTTT		
GAM1929 DKFZp566H0824 5'	TCTCGAGGAGGTTCCCTTAACCT 18979	C	ATGAA
T	AAGGTAAAGG AGCT GAGG		
	TTCCAATTCC TTGG CTCT		
	_ AGGAG		
GAM1929 DKFZP727C091 3'	CTTCTCTGTTTTGACT 32905		CTAT
	GGTTAAGGCAG GAAG		
	TCAGTTTTGTC CTTC		
	T__		
GAM1929 DKFZp761D0614 3'	CCTCTTACTGTGCCTTTAGCCT 42310	_	G TATG
T	AAGGTAA GGCA C AAGAGG		

TTCCGATT CCGT G TTCTCC
 T _ TCA_
 GAM1929 DKFZP761F241 3' TCTTACGTTGCTTGAGTCTT 25478 GT A TATG
 AAG T AGGCAGC AAGA
 ||| | ||||| ||||
 TTC A TTCGTTG TTCT
 TG G CA_
 GAM1929 DNAJA4 3' TCTCTTCACCCTTCCTGGCCTT 20679 A C CTA
 AAGGTTA GG AG TGAAGAGG
 ||||| || || |||||
 TTCCGGT CC TC ACTTCTCT
 _ T CC_
 GAM1929 DNAJC6 3' TTTTTTGTTTTGTTTTAACTT 16663 CT TG G
 T AAGGTTAAGGCAG A AAGAG
 ||||| ||||| | |||||
 TTTCAATTTTGTT T TTTTT
 TT GT
 GAM1929 DUSP9 3' TCTGGTGCGCTGTTTTGTTTTT 7091 T ATGA
 AAGG TAAGGCAGCT AGA
 ||| ||||| |||
 TTTT GTTTTGTCGG TCT
 T GTGG
 GAM1929 EIF5 3' TTTTCGTTCAAGTGTGGCTTTAA 7702 A TA _
 TTTT AGGTTAAGGC GC TGAA GAGG
 ||||| || ||| |||||
 TTTAATTTTCG TG ACTT CTTT
 G TG G TT
 GAM1929 ELAC1 3' TTTTTTTATTTCTTGTTTTAGT 43723 GT CT_
 CT AG TAAGGCAG ATGAAGAGG
 || ||||| |||||
 TC ATTTTGTT TATTTTTTT
 TG CTT
 GAM1929 ELF4 3' TCTCTTCGTGGCTCCCTGCTT 7128 TA C
 AGGT AGG AGCTATGAAGAGG
 ||| || |||||
 TTCG TCC TCGGTGCTTCTCT
 _ C
 GAM1929 ESDN 3' CCTTTTGTGGTATGGTTTTTTG 28152 C ____
 GCCTT TTAAGG AGCTATG AAGAGG
 ||||| ||||| |||||
 GGTTTT TTGGTAT TTTTCC
 _ GGTG
 GAM1929 EVI5 3' CATTATTGCTTTGACCTT 12209 CT
 AAGGTTAAGGCAG ATG
 ||||| ||||| |||
 TTCCAGTTTCGTT TAC
 AT
 GAM1929 FLJ10292 3' TTTTTTTGTAGTGCTATTTAAT 19803 _ G TG
 TTT AGGTTAA GGCA CTA AAGAGG
 ||||| ||| ||| |||||

TTTAATT TCGT GAT TTTTT
 TA _ GT
 GAM1929 FLJ10493 3' TTTCTAGTGGCTACTGTTT TAG 19885 GG ____ GA
 TTTT TTAAGGCA GCTAT AGAGG
 ||||| ||| ||||
 GATTTTGT CGGTG TCTTT
 TT CAT A_
 GAM1929 FLJ10546 3' CTTCTTAGTTGTCTTGTCTTT 29913 T T
 AAGG TAAGGCAGCTA GAAG
 ||| ||||| ||||
 TTTC GTTCTGTTGAT CTTC
 T T
 GAM1929 FLJ10726 3' TTTCTTCTATGCCTTAGGCTT 20061 G GCTAT
 AAG TTAAGGCA GAAGAGG
 || ||||| |||||
 TTC GATTCCGT CTTCTTT
 G AT____
 GAM1929 FLJ10803 3' CTTCACTGTTGTCTTACTTT 20154 T TA
 AAGGT AAGGCAGC TGAAG
 |||| ||||| ||||
 TTTCATTCTGTTG ACTTC
 _ TC
 GAM1929 FLJ10852 3' TTTCTTTTCAGTGTGGCTGCTTT 21119 ____
 GGCTT TTAAGGCAGCTAT GAAGAGG
 ||||| |||||
 GGTTTCGTCGGTG TTTCTTT
 TGAC
 GAM1929 FLJ10996 3' TCAGTGTTGTTTAAATTTT 21128 TA
 AAGGTTAAGGCAGC TGA
 ||||| ||||| |||
 TTTTAATTTTGTTG ACT
 TG
 GAM1929 FLJ11184 3' TCTGCAGAAGTTGTTTAGTCTT 20365 GT G A_ A
 AAG TAAG CAGCT TG AGA
 || |||| |||| || |||
 TTC ATTT GTTGA AC TCT
 TG _ AG G
 GAM1929 FLJ12154 5' CTTCTTCATGGCTTGTTTACTC 22464 GT GC
 TT AAG TAAG AGCTATGAAGAGG
 || |||| ||||| |||||
 TTC ATTT TCGGTACTTCTTC
 TC GT
 GAM1929 FLJ12425 3' TTTTATATATTCTTTAACCTT 41565 CAGC
 AAGGTTAAGG TATGAAGA
 ||||| |||||
 TTCCAATTTC ATATTTT
 TTAT
 GAM1929 FLJ12443 3' TCTGAGGCTGTTTGGGCTTT 24226 TA ATGA
 AAGGT AGGCAGCT AGA
 |||| ||||| |||

TTTTCG TTTGTCGG TCT
 GG AG__
 GAM1929 FLJ12581 5' TCTTAAAGCTGCCTTAACCTT 24302 ATG
 AAGGTTAAGGCAGCT AAGA
 |||||
 TTCCAATTCCGTCGA TTCT
 AA_
 GAM1929 FLJ12770 3' TTCTTTACCTCTTAGCC 25888 CAGCTA
 GGTTAAGG TGAAGAG
 ||||| |||||
 CCGATTCT ATTTCTT
 CC____
 GAM1929 FLJ12895 3' TTTTGTGTCAGCTGTTTAGCCTT 23406 G _TG
 AAGGTTAAG CAGCT A AAG
 ||||| ||||| | |||
 TTCCGATTT GTCGA T TTT
 _ C GT
 GAM1929 FLJ12903 3' GCTTCTGTAGGTACTAGCTGCC 22981 TGA____
 TTGATTTT AAGGCAGCTA AGAGG C
 ||||| ||||| |
 TTCCGTCGAT TCTTC G
 CATGGATG
 GAM1929 FLJ13213 3' TCTTAGCTGTCTAATTTT 24100 A T
 AAGGTTA GGCAGCTA GA
 ||||| ||||| ||
 TTTTAAT CTGTCGAT CT
 _ T
 GAM1929 FLJ13315 3' TTTCTTCTTTGCTTAAATCTT 24578 A CTAT
 AAGGTT AGGCAG GAAGAGG
 ||||| ||||| |||||
 TTCTAA TTCGTT CTTCTTT
 A T____
 GAM1929 FLJ13646 3' TTTCTTTATAGAGAAAGTACCT 23817 TAAGGCAG
 T AAGGT CTATGAAGAGG
 ||||| |||||
 TTCCA GATATTTCTTT
 TGAAAGA_
 GAM1929 FLJ13842 3' TTTTTTTATGATGTTTGGCCT 23931 G GC
 AGGTTAAG CA TATGAAGAGG
 ||||| || |||||
 TCCGGTTT GT GTATTTTTTT
 _ A_
 GAM1929 FLJ14466 3' CTTCCAGTGCTTTGGCCTT 26544 G AT
 AAGGTTAAGGCA CT GAAG
 ||||| || |||||
 TTCCGGTTTCGT GA CTTC
 _ C_
 GAM1929 FLJ14564 3' CTAGGGCTGCCTTTGCTTT 37597 T ATGAAG
 AAGGT AAGGCAGCT AG
 ||||| ||||| ||

TTTTCG TTCCGTCGG TC
 T GA____
 GAM1929 FLJ14621 3' TCTTTAACCTCTTTAACCTT 26583 C CTA
 AAGGTTAAGG AG TGAAGA
 ||||| || |||||
 TTCCAATTTC TC ATTTCT
 _ CA_
 GAM1929 FLJ20232 3' CTTCCGTCAAGTTGTCTTATTT 21084 T A A_
 TT AAGG TAAGGCAGCT TGA GAGG
 ||| ||||| ||| |||||
 TTTT ATTCTGTTGA ACT CTTC
 T _ GC
 GAM1929 FLJ20273 3' TCTCCATGTGCCTTAGCCTT 21116 GC A
 AAGGTTAAGGCA TATG AGA
 ||||| ||| |||
 TTCCGATTCCGT GTAC TCT
 _ C
 GAM1929 FLJ20337 3' CCTCTTTGTAGCAGATATGATT 19393 AGGCA TG
 TT AAGGTTA GCTA AAGAGG
 ||||| ||| |||||
 TTTTAGT CGAT TTCTCC
 ATAGA GT
 GAM1929 FLJ20508 5' TCTCACGCTTTGGCTGTCTGGA 19520 A TGAA_
 CTTT AGGTT AGGCAGCTA GAGG
 ||||| ||||| |||
 TTCAG TCTGTCCGT CTCT
 G TTCGCA
 GAM1929 FLJ20509 3' TCTCACAAAGCTGCCTTGACT 19524 A AA
 GGTTAAGGCAGCT TG GAGG
 ||||| ||| |||
 TCAGTTCCGTCGA AC CTCT
 A A_
 GAM1929 FLJ20542 3' TCTCCAGGCTGTCTTGCCTT 25893 T A A
 AAGGT AAGGCAGCT TG AGA
 ||||| ||||| ||| |||
 TTCCG TTCTGTCCG AC TCT
 _ _ C
 GAM1929 FLJ20666 3' TTTCTTAAACATAGCTGCTTTA 20338 ____
 ATT GTTAAGGCAGCTATG AAGAGG
 ||||| ||||| |||||
 TAATTCGTCGATAC TTCTTT
 AAA
 GAM1929 FLJ20700 5' TCTCTTTGTGGTTCCTGGTCCT 19620 TTA C TG
 AGG AGG AGCTA AAGAGG
 ||| ||| ||||| |||||
 TCC TCC TTGGT TTCTCT
 TGG _ GT
 GAM1929 FLJ20793 3' CTTTTTGTGTGTGTTTGCTTT 44109 T GC TG
 AAGGT AAGGCA TA AAGAG
 ||||| ||||| ||| |||||

TTTTCG TTTTGT GT TTTTC
 _ GT GT
 GAM1929 FLJ20972 3' CTTCTTGCCTTTTTGTCTAAGC 24626 A ____ TAT AGG
 CTT TT AGGCA GC GAAG
 || |||| || ||||
 GA TCTGT CG CTTC
 A TTTTC TT_ G
 GAM1929 FLJ21032 3' CTTCTTTGTCTTTTTTGATCTT 24400 C CT TG
 AAGGTTAAGG AG A AAGAGG
 ||||| || | |||||
 TTCTAGTTTT TC T TTCTTC
 T _ GT
 GAM1929 FLJ21477 3' CTTTTTTATGGCTGCATAAT 24790 AG
 GTTA GCAGCTATGAAGAGG
 ||| |||||
 TAAT CGTCGGTATTTTTTC
 A_
 GAM1929 FLJ21551 3' CCTTTTTGTGTTTGCTTTTGTT 24179 TT C TG
 TT AAGG AAGGCAG TA AAGAGG
 ||| ||||| || |||||
 TTTT TTTCGTT GT TTTTCC
 GT T GT
 GAM1929 FLJ21615 3' CCTTTTTGCGGCCTTATATTTT 25910 _ A TAT
 AAGGT TAAGGC GC GAAGAGG
 |||| ||||| || |||||
 TTTTA ATTCCG CG TTTTCC
 T G _
 GAM1929 FLJ21777 3' TTTCTTCTATACTGCCTTA 25925 C _
 TAAGGCAG TAT GAAGAGG
 ||||| || |||||
 ATTCCGTC ATA CTTCTTT
 _ T
 GAM1929 FLJ22028 3' CTTCTTCTGGAAGTTGCCTGAA 24285 A AT_
 TTTT AGGTT AGGCAGCT GAAGAGG
 |||| ||||| |||||
 TTTAA TCCGTTGA CTTCTTC
 G AGGT
 GAM1929 FLJ22055 3' TCTCTCCCAAGTGCCTTGATCT 24148 G A A_
 T AAGGTTAAGGCA CT TG AGAGG
 ||||| || || |||||
 TTCTAGTTCCGT GA AC TCTCT
 _ _ CC
 GAM1929 FLJ22169 5' CCTCTTTGTGGTTGCCTTCACT 23522 T TG
 GGT AAGGCAGCTA AAGAGG
 || ||||| |||||
 TCA TTCCGTTGGT TTCTCC
 C GT
 GAM1929 FLJ22724 3' TCTTTTCATGGTTTATAAC 23736 AGGC
 GTTA AGCTATGAAGAGG
 ||| |||||

			CAAT TTGGTACTTTTCT		
			AT__		
GAM1929	FLJ30058	3'	TCTCTTTTACCCCTGATCTTGG 29583	_	CTAT_
			CTTT AGGTTAAGG CAG GAAGAGG		
			TTCGGTTCT GTC TTTCTCT		
			A CCCAT		
GAM1929	FREQ	3'	TTTTTTCAGATACTGTGCTTGA 15565	_	CTA_
			TTTT AGGTTAAG GCAG TGAAGAGG		
			TTTAGTTC TGTC ACTTTTTT		
			G ATAG		
GAM1929	FUBP3	3'	TTTCTTGTATCTTGGCTGTCT 31878	T	_____
			AGGCAGCTA GA AGAGG		
			TCTGTCGGT CT TCTTT		
			T ATGT		
GAM1929	FUT10	3'	TTTCTAGGTTGCCTTAAT 26394	AT	
			GTTAAGGCAGCT GAAG		
			TAATTCCGTTGG CTTT		
			AT		
GAM1929	G2	3'	CCTCAACGAGTTTCTTTGGTCT 33111	GT	C A AA
			T AAG TAAGG AGCT TG GAGG		
			TTC GTTTC TTGA GC CTCC		
			TG T _ AA		
GAM1929	GOLPH3	3'	TTTCTGGTCTACTTTGACTTT 22690	C _	T
			AAGGTTAAGG AG CTA GAAG		
			TTTCAGTTTC TC GGT CTTT		
			A T _		
GAM1929	GPR107	3'	CCTTTTGCATCTCCTTGACTTT 21949	C CT	_
			AAGGTTAAGG AG ATG AAGAGG		
			TTTCAGTTCC TC TAC TTTTCC		
			_ _ G		
GAM1929	GS3955	3'	TTTTTCATGTTTTGCTTT 22307	C_	
			AAGGCAG TATGAAGAG		
			TTTCGTT GTACTTTTT		
			TT		
GAM1929	H2AV	3'	CTTACCTGATGCCTTGATTTT 28910	GCTATG	
			AAGGTTAAGGCA AAG		
			TTTLAGTTCCGT TTC		
			AGTCCA		
GAM1929	H326	3'	TCTCTTTGGTTTAGGTTTTTGA 17941	_	AGCTA_
			CCTT AGGTTAAGG C TGAAGAGG		

		TCCAGTTTT G	GTTTCTCT		
		T GATTTG			
GAM1929	HEMK	3'	CCTTTTATCCCCATAGCTTT 18268	A	CAGCT
			AAGGTTA GG ATGAAGAGG		
			TTTCGAT CC TATTTTCC		
			A CC__		
GAM1929	HNRPA3	3'	TCTTTTATCTGTTGTAGCTTT 12326	AG	CTAT
			AAGGTTA GCAG GAAGA		
			TTTCGAT TGTC TTTCT		
			GT TAT_		
GAM1929	HOMER-2B	3'	CCTTTTCTTGTTTAAATTT 11247	AGCTAT	
			AGGTTAAGGC GAAGAGG		
			TTTAATTTTG CTTTCC		
			GTT__		
GAM1929	HPIP	3'	CCTTTGCCCTTGCCCTTGCCCTT 21737	T	CTATGA
			AAGG TAAGGCAG AGAGG		
			TTCC GTTCCGTT TTTCC		
			C CCCG__		
GAM1929	HSA249128	3'	CCTCAATGGCTGCTTTGAACTT 19025	G	GAA
			AAG TTAAGGCAGCTAT GAGG		
			TTC AGTTTCGTCGGTA CTCC		
			A A__		
GAM1929	HSA277841	3'	CTTCTCACTATTGCCTTGGCC 20633	CTA	AG G
			GGTTAAGGCAG TGA AG		
			CCGGTTCCGTT ACT TC		
			ATC CT		
GAM1929	HSPC129	3'	CCTTTTACATTTTGTACCT 18535	CAGCTA	
			AGGTTAAGG TGAAGAGG		
			TCCAGTTTT ATTTTCC		
			TAC__		
GAM1929	INA	3'	CTTTTTCATCCCCTTACCCTT 26453	T	CAGCT
			AAGG TAAGG ATGAAGAGG		
			TTCC ATTCC TACTTTTC		
			C CC__		
GAM1929	ING4	3'	CCTTTTCATTCTCCTTGCTTT 30026	T	C CT
			AAGGT AAGG AG ATGAAGAGG		
			TTTCG TTCC TC TACTTTCC		
			_ _ T_		
GAM1929	K-ALPHA-1	5'	CTTCAGGGCTTCTTGTTTT 37742	GG	C A
			AA TTAAGG AGCT TGAAG		

TT GGTTC TCGG ACTTC
 TT _ G
 GAM1929 KIAA0087 3' TCTTTCACATTGCTTTTGA CTT 16560 _ CTA AGG
 T AAGGTTAAG GCAG TGAAG
 ||||| ||| ||||
 TTTCA GTTT CGTT ACTTT
 T AC_ CT
 GAM1929 KIAA0185 3' CCTCTTCGCTTGCTTTA 31538 _ TAT
 TAAGGCA GC GAAGAGG
 ||||| || |||||
 ATTCGT CG CTTCTCC
 T ____
 GAM1929 KIAA0186 3' TCTTTTTGAGATTTGTTTTGGC 22038 __ AT_ GG
 T GGTAAAGGCAG CT GAAGA
 ||||| || |||||
 TCGGTTTTGTT GA TTTCT
 TA GTT
 GAM1929 KIAA0215 3' CTCTTTTCTTCTTAGCCTT 16383 C CTAT
 AAGGTTAAGG AG GAAGAG
 ||||| || |||||
 TTCCGATTCT TC TTTCTC
 _ T____
 GAM1929 KIAA0215 3' TCTTACCTGCTTTAATTTT 16386 CTATG
 AAGGTTAAGGCAG AAGA
 ||||| |||||
 TTTTAATTTCGTC TTCT
 CA____
 GAM1929 KIAA0255 5' CTGATTGGTTGCCGTGGTCTT 16417 GT A TGA
 AAG TA GGCAGCTA AG
 ||| || ||||| ||
 TTC GT CCGTTGGT TC
 TG G TAG
 GAM1929 KIAA0255 3' TTTTTTGTGGGTTGCTTT 16418 _TG
 AAGGCAGCT A AAGAG
 ||||| | |||||
 TTTCGTTGG T TTTTT
 G GT
 GAM1929 KIAA0265 3' CCTCTAAGACTGTGTTGGTCTT 34626 GT G _ ATGA
 AAG TAA GCAG CT AGAGG
 ||| || |||| || |||||
 TTC GTT TGTC GA TCTCC
 TG G A A____
 GAM1929 KIAA0303 5' TTTTTTTATTTTGGCCTTGTC 34424 T AGCT_
 TT AGG TAAGGC ATGAAGAGG
 ||| ||||| |||||
 TTC GTTCCG TATTTTTTT
 T GTTTT
 GAM1929 KIAA0318 3' TTATTACCTGCCTTAGCTTT 34190 CT_
 AAGGTTAAGGCAG ATGA
 ||||| ||||| |||||

TTTTCGATTCCGTC TATT
 CAT
 GAM1929 KIAA0323 3' CCTTGATTGAGTTGCTTGGGCT 31693 TA ATGAA
 TT AAGGT AGGCAGCT GAGG
 |||| ||||| |||
 TTTTCG TTCGTTGA TTCC
 GG GTTAG
 GAM1929 KIAA0349 3' TTTTTTTATGGCAAGACTTTTG 44343 CA____
 GCTTT GTTAAGG GCTATGAAGAGG
 ||||| |||||
 CGGTTTT CGGTATTTTTTT
 CAGAA
 GAM1929 KIAA0417 3' CTTTTGTACTGTCCTTAATTT 35290 _ CT TG AGG
 T AAGGTTAAGG CAG A AAG
 ||||| ||| | |||
 TTTTAATTCC GTC T TTT
 T AT GT C
 GAM1929 KIAA0431 3' CTTCTTTGTGTTTCTTTGCCTT 17579 T C T TG
 AAGGT AAGG AGC A AAGAGG
 |||| ||| ||| |||||
 TTCCG TTCT TTG T TTCTTC
 T _ _ GT
 GAM1929 KIAA0435 5' CCTAAATACTTGCTTTGATTTT 16719 C GAAG
 AAGGTTAAGGCAG TAT AGG
 ||||| ||| |||
 TTTTAGTTTCGTT ATA TCC
 C AA____
 GAM1929 KIAA0446 3' TTTCTTCATGGCTGCCGCAC 34156 TAA
 GT GGCAGCTATGAAGAGG
 || |||||
 CA CCGTCGGTACTTCTTT
 CG_
 GAM1929 KIAA0494 3' TTTCTTTATGGTTGCTGTTC 16594 TTAA
 GG GGCAGCTATGAAGAGG
 || |||||
 CT TCGTTGGTATTTCTTT
 TG_
 GAM1929 KIAA0515 3' CCTTTTGTATGTTTTGGCCT 31923 GCT G
 T AAGGTTAAGGCA AT AAGAGG
 ||||| |||||
 TTCCGGTTTTGT TG TTTTCC
 ATT _
 GAM1929 KIAA0522 3' CCTCTTTGCTTCCTCGGTTTT 35623 GG TA C TAT
 AA T AGG AGC GAAGAGG
 || | ||| |||||
 TT G TCC TCG TTTCTCC
 TT GC T ____
 GAM1929 KIAA0682 3' CCTTTTCCTGCCGCCTTGGTCT 16902 GT A TAT
 T AAG TAAGGC GC GAAGAGG
 || ||||| || |||||

TTC GTTCCG CG CTTTTC
 TG C TC_
 GAM1929 KIAA0802 3' TTTTTCATAGCTCAGAAACT 31354 AAGGC
 GGTT AGCTATGAAGAGG
 ||| |||||
 TCAA TCGATACTTTTT
 AAGAC
 GAM1929 KIAA0825 3' TTTCTGAATCAGTTTTCTTAAC 30595 C _ GA
 TTT AAGGTTAAGG AGCT AT AGAGG
 ||||| ||| || ||||
 TTTCAATTCT TTGA TA TCTTT
 T C AG
 GAM1929 KIAA0844 3' TCTCTTCGCTGGCTTAAC TTT 17286 G TAT
 AAGGTTAAG CAGC GAAGAGG
 ||||| ||| |||||
 TTTCAATTC GTCG CTTCTCT
 G _
 GAM1929 KIAA0848 3' TTTT TTTATAGTTGTAGTTTTG 17215 _
 ATTT GTTAAG GCAGCTATGAAGAGG
 |||| | |||||
 TAGTTT TGTGATATTTTTTT
 TGA
 GAM1929 KIAA0854 3' CTTTTTCAGTTAGTCCTAACTT 17254 A _ AT
 T AAGGTTA GGC AGCT GAAGAGG
 ||||| ||| ||| |||||
 TTTCAAT CTG TTGA CTTTTTC
 C A _
 GAM1929 KIAA0865 3' TTTCTTTGTAGCTACTTG 30712 GC TG
 TAAG AGCTA AAGAGG
 ||| |||| |||||
 GTTC TCGAT TTCTTT
 A_ GT
 GAM1929 KIAA0882 3' CTTTTTTATTACTGTTATGATT 40217 AG CT
 TT AAGGTTA GCAG ATGAAGAGG
 ||||| ||| |||||
 TTTTAGT TGTC TATTTTTTC
 AT AT
 GAM1929 KIAA0894 3' TCTTTGCCTGTTTAACT 17059 CTA
 GGTTAAGGCAG TGAAGA
 ||||| |||||
 TCAATTTTGTC GTTTCT
 C_
 GAM1929 KIAA0894 5' TCTTTT TAGCAGCTTTCAGCTT 17060 _ A T GG
 T AAGGTT AAGGC GCTA GAAGA
 |||| | ||| |||||
 TTTCGA TTTCG CGAT TTTCT
 C A T
 GAM1929 KIAA0924 5' TTTCTTTATAGTCTGAACT 17070 AAGG _
 GGTT CAG CTATGAAGAGG
 ||| ||| |||||

TCAA GTC GATATTTCTTT
____ T
GAM1929 KIAA0931 3' TTTTTCATGGCTTTGTTTT 33489 ____
AAGGCA GCTATGAAGAG
||||| |||||||
TTTTGT CGGTACTTTTT
TT
GAM1929 KIAA1033 3' CCTCCAACAGCTGCTTTAA 32230 ATGAA
TTAAGGCAGCT GAGG
||||||| |||
AATTCGTCGA CTCC
CAAC_
GAM1929 KIAA1034 3' CTTACAGTGAGTCGCTTTGGC 31309 A____ A AGG
TTT GTTAAGGC GCT TGAAG
||||| ||| |||
CGGTTTCG TGA ACTTC
CTGAG C G
GAM1929 KIAA1034 3' TCTTTTATGTCTGTTTGT 31312 T C
TT AAGG TAAGGCAG TATGAAGAGG
||| ||||||| |||||||
TTTT GTTTTGTC GTATTTTCT
T T
GAM1929 KIAA1040 3' CTTTTCACCTTGCTTTCATTTT 35740 T CTA
AAGGT AAGGCAG TGAAGAG
||||| ||||||| |||||||
TTTTA TTTCGTT ACTTTTC
C C_
GAM1929 KIAA1040 3' TTTTATATTGGCTGTCTGGA 35747 A ____ G
TTTT GGTT AGGCAGCT ATGAAGAG
||| ||||||| |||||||
TTAG TCTGTCGG TATTTTTT
G TTA
GAM1929 KIAA1054 3' CTTACAGCTGCCCTTGGTCTT 33954 GT _ AT
AAG TAAGG CAGCT GAAG
||| ||||| ||||| |||
TTC GTTCC GTCGA CTTC
TG C _
GAM1929 KIAA1084 3' TTTCTTTGTGGCTCATGCTTT 17141 ____ TG
AAGGCA GCTA AAGAGG
||||| ||| |||||||
TTTCGT CGGT TTCTTT
ACT GT
GAM1929 KIAA1164 3' TTTTTCAACTATGTCATTAAC 34443 _ GCTA
TTT AAGGTAA GGCA TGAAGAGG
||||||| ||| |||||||
TTTCAATT CTGT ACTTTTTT
A ATCA
GAM1929 KIAA1190 3' TTTCTTCCTTGCACTCCTTGAT 35227 CA_ TAT
CTT AAGGTAAAGG GC GAAGAGG
||||||| || |||||||

TTCTAGTTCC CG CTTCTTT
 TCA TTC
 GAM1929 KIAA1200 3' CCTCTTTTAAATGTACTTGACT 31263 _ GCTAT
 TT AAGGTTAAG GCA GAAGAGG
 ||||| || |||||
 TTTCAGTTC TGT TTTCTCC
 A AAAT_
 GAM1929 KIAA1223 3' TCTTTTTGTGGCAAAAGAAACT 35248 AAGGCA TG
 T AGGTT GCTA AAGAGG
 |||| ||| |||||
 TTCAA CGGT TTTTCT
 AGAAAA GT
 GAM1929 KIAA1223 3' TTTCTCAATATTGTTTTGGCT 35251 C GA
 GGTTAAGGCAG TAT AGAGG
 ||||| ||| |||||
 TCGGTTTTGTT ATA TCTTT
 _ AC
 GAM1929 KIAA1238 3' TTTTTCATGGTCCCTTGCTTT 35218 T CA
 AAGGT AAGG GCTATGAAGAGG
 |||| ||| |||||
 TTTCG TTCC TGGTACTTTTTT
 _ C_
 GAM1929 KIAA1280 5' CTTGGGGCTGGTTTGGTTTT 34552 GG G ATGAA
 AA TTAAG CAGCT GAG
 || ||||| |||
 TT GGTTC GTCGG TTC
 TT G GG_
 GAM1929 KIAA1297 3' TCTGCGGCGCCTTGCCCTT 35721 A ATGA
 AAGGTTAAGGC GCT AGA
 ||||| ||| |||
 TTCCGGTTCCG CGG TCT
 _ CG_
 GAM1929 KIAA1318 3' CCTCTCACTTGGCTGATTTGAC 33430 G _ A
 CTT AGGTTAAG CAGCTA TGA GAGG
 ||||| ||||| ||| |||||
 TCCAGTTT GTCGGT ACT CTCC
 A TC _
 GAM1929 KIAA1318 3' CCTCTTGATCTGTTGTTTATGG 33431 _ T_ G
 CCTT AGGTTA AGGCAGC AT AAGAGG
 ||||| ||||| ||| |||||
 TCCGGT TTTGTTG TA TTCTCC
 A TC G
 GAM1929 KIAA1432 5' TTCTTTATGGAGTGTTTT 33160 G_
 AAGGCA CTATGAAGAG
 ||||| |||||
 TTTTGT GGTATTTCTT
 GA
 GAM1929 KIAA1434 3' TCTCTTTATAGTGAGAAAATTT 34490 AAGGCA
 AGGTT GCTATGAAGAGG
 |||| |||||

TTTAA TGATATTTCTCT
 AAGAG_
 GAM1929 KIAA1437 3' CTTTCAGTATTTGTGGCAGTTTT 30385 A TG ____
 AGTTTT TTAAGGC GCTA AA GAGG
 ||||| ||| || ||||
 GATTTTG CGGT TT CTTC
 A GT ATGA
 GAM1929 KIAA1492 3' TTTCCAGTTGCATTTAATTTT 32227 _ AT
 AAGGTTAAG GCAGCT GAAG
 ||||| ||||| ||||
 TTTTAATTT CGTTGA CTTT
 A C_
 GAM1929 KIAA1495 3' TTTCTTCAATCTTTGGTCTTAG 36227 GG AGCTA__
 TTTT A TTAAGGC TGAAGAGG
 | ||||| |||||
 T GATTCTG ACTTCTTT
 TT GTTTCTA
 GAM1929 KIAA1509 3' TCTTATCTGCTGCTTTGTGTCT 30878 GT_ TATG GG
 T AAG TAAGGCAGC AAGA
 ||| ||||| ||||
 TTC GTTTCGTCG TTCT
 TGT TCTA
 GAM1929 KIAA1511 3' CTTCTCCATCTGCTTTACTTT 34757 T CT A
 AAGGT AAGGCAG ATG AGAGG
 |||| ||||| ||| |||||
 TTTCA TTTCGTC TAC TCTTC
 _ _ C
 GAM1929 KIAA1530 3' CTTCAAGGCTGTTTTGACT 33732 A
 GGTTAAGGCAGCT TGAAG
 ||||| ||||| |||||
 TCAGTTTTGTTCGG ACTTC
 A
 GAM1929 KIAA1559 3' CCTTTGATCTGTTTTAACCTT 36162 CTATGA
 AAGGTTAAGGCAG AGAGG
 ||||| ||||| |||||
 TTCCAATTTTGTC TTTCC
 TAG_
 GAM1929 KIAA1577 3' CTTCTATCTTGCCTTGTCTT 32211 T CTAT
 AGG TAAGGCAG GAAG
 ||| ||||| |||||
 TTC GTTCCGTT CTTC
 T CTAT
 GAM1929 KIAA1677 3' CCTTTATGCGTGTTGTTTTCAC 33291 T T AA_
 TTT AGGT AAGGCAGC ATG GAGG
 |||| ||||| ||| |||||
 TTCA TTTTGTTG TGC TTCC
 C _ GTAT
 GAM1929 KIAA1677 3' TCTCTTCCGTGTCTTTGACCTT 33294 CA TAT
 AAGGTTAAGG GC GAAGAGG
 ||||| || |||||

TTCCAGTTTC TG CTTCTCT
 _ TGC
 GAM1929 KIAA1798 3' CCTCTTCTTTAGTTGCTTTCGT 30403 TT T_
 TTT AAGG AAGGCAGCTA GAAGAGG
 |||| ||||| |||||
 TTTT TTTCGTTGAT CTTCTCC
 GC TT
 GAM1929 KIAA1826 3' TTTCTTTCAGTCATTGTCTTAG 33379 GG CTA_ _
 TTT A TTAAGGCAG TGAA GAGG
 | ||||| ||| |||
 T GATTCTGTT ACTT CTTT
 TT ACTG T
 GAM1929 KIAA1831 3' CCTCTTCACCCCTTTGACCT 31903 CAGCTA
 AGGTAAAGG TGAAGAGG
 ||||| |||||
 TCCAGTTTC ACTTCTCC
 CCC_
 GAM1929 KIAA1878 3' CTTCTCATCTGCCTTGGTCCT 44076 _ CT AG
 AGG TTAAGGCAG ATGA AG
 || ||||| ||| ||
 TCC GGTCCGTC TACT TC
 T _ CT
 GAM1929 KIAA1987 3' CCTTTTATGGCTGAGCAGTAT 42496 TAAGG_
 CT AGGT CAGCTATGAAGAGG
 ||| |||||
 TCTA GTCGGTATTTTCC
 TGACGA
 GAM1929 KPNB3 3' TTCTTTATGTATTAACCT 8064 G GCTA
 AGGTAA GCA TGAAGAG
 ||||| ||| |||||
 TCCAATT TGT ATTTCTT
 A _
 GAM1929 LEPROTL1 3' CCTCTGAAGTGTGTTTATTTT 17651 CTATGA
 AAGGTAAAGGCAG AGAGG
 ||||| |||||
 TTTTAGTTTTGTC TCTCC
 AAG_
 GAM1929 LIG-1 3' TCTTTTACAGAGGCTATTTTAA 31955 C A_ _
 TCTT AGGTAAAGG AGCT TG AAGAGG
 ||||| ||| || |||||
 TCTAATTTT TCGG AC TTTTCT
 A AG A
 GAM1929 LRP1B 5' CTTTGGGGTTGTTTGGCTTT 20638 T ATG
 AAGGT AAGGCAGCT AAGAG
 |||| ||||| |||||
 TTTCG TTTTGTGG TTTTC
 _ GG_
 GAM1929 LRRFIP2 3' CCTTTTAGTACTGTTTTGAGTT 19313 G C G
 T AAG TTAAGGCAG TAT AAGAGG
 || ||||| ||| |||||

TTT AGTTTTGTC ATG TTTTCC
 G _ A
 GAM1929 MACF1 3' CTTCTTTATAAACTTGACTT 14377 GCAGC
 AGGTTAAG TATGAAGAGG
 ||||| |||||
 TTCAGTTC ATATTTCTTC
 AA__
 GAM1929 MAP4K3 3' CCTTTTCATATTTCTTTTGA CT 9681 C C
 T AGGTTAAGG AG TATGAAGAGG
 ||||| || |||||
 TTCAGTTTT TT ATACTTTTCC
 C T
 GAM1929 MAT2B 3' TCTTTTGTTGCTTTAATTTT 14955 TAT
 AAGGTTAAGGCAGC GAAGA
 ||||| |||||
 TTTTAATTTCGTTG TTTCT
 T__
 GAM1929 MCM10 3' CCTTTTACAAATTTGATTTTAA 20593 _ CTA_
 CTTT AGGTTAAGG CAG TGAAGAGG
 ||||| || |||||
 TTCAATTTT GTT ATTTTCC
 A TAAC
 GAM1929 MGC1203 3' CTCTTCAAACGTGACTTT 23576 AAG CTA
 AAGGTT GCAG TGAAGAG
 ||||| ||||| |||||
 TTTCAG TGTC ACTTCTC
 __ AA_
 GAM1929 MGC13090 3' CTTCTGTGTTGGCTGTCTGGCCT 26426 A TGAA
 T AAGGTTA GGCAGCTA GAGG
 ||||| ||||| |||||
 TTCCGGT CTGTCGGT CTTC
 _ TGTC
 GAM1929 MGC16075 3' CCTTTTCATATATTTTGCCTT 26504 C__
 AAGGCAG TATGAAGAGG
 ||||| |||||
 TTCCGTT ATACTTTTCC
 TTAT
 GAM1929 MGC2474 3' CTTTTTTATTCTTTGACCTT 23418 CAGCT
 AAGGTTAAGG ATGAAGAGG
 ||||| |||||
 TTCCAGTTTC TATTTTTC
 T__
 GAM1929 MGC3329 3' CCTGACACCTGGCTGTTTTGAT 23527 G TGAAG_
 GTT AA GTTAAGGCAGCTA AGG
 || ||||| ||||| |||||
 TT TAGTTTTGTCGGT TCC
 G CCACAG
 GAM1929 MGC3329 3' TTTTTTTGTGGCTTCACTTG 23529 GC_ TG
 TAAG AGCTA AAGAGG
 ||||| ||||| |||||

		GTTC TCGGT TTTTT	
		ACT GT	
GAM1929 MGC4643	3'	TCTTAAGTACTGACTGCTTTGA 26442	C___ G_ GG
		CTTT GTTAAGGCAG TAT AAGA	
		CAGTTTCGTC ATG TTCT	
		AGTC AA	
GAM1929 MGC5508	3'	CCTCTGCTGCTGCCTTGGCTT 23535	TATGA
		AGGTTAAGGCAGC AGAGG	
		TTCGGTTCCGTCG TCTCC	
		TCG__	
GAM1929 MLL3	5'	CCTTAGTTGCTGGCTTTGACCT 22202	_ TATG AGG
		T AAGGTTAAGGC AGC AAG	
		TTCCAGTTTCG TCG TTC	
		G TTGA C	
GAM1929 NAALAD2	3'	TCTTTTCATGTCATGTTTGTAT 11964	GC_
		T GGTTAAGGCA TATGAAGAGG	
		TTAGTTTTGT GTACTTTTCT	
		ACT	
GAM1929 NFASC	3'	CTTCTCATTGTCTTAATTT 34830	GCT AG
		AGGTTAAGGCA ATGA AG	
		TTTAATTCTGT TACT TC	
		___ CT	
GAM1929 NIBAN	3'	CTTTAAGGCTTTTAAATTTT 22629	C A
		AAGGTTAAGG AGCT TGAAG	
		TTTTAATTTT TCGG ATTC	
		_ A	
GAM1929 NICN1	3'	CCTGATCTGCCTGCCTTGGCCT 26117	C T AG
		T AAGGTTAAGGCAG TA GA AGG	
		TTCCGGTTCCGTC GT CT TCC	
		C _ AG	
GAM1929 NKX2B	3'	TTTCTTTGTGGCTTGT TT 8344	_ TG
		AGGCA GCTA AAGAGG	
		TTTGT CGGT TTCTTT	
		T GT	
GAM1929 NRF	5'	TCTTTGACAGTTTCCTTGGTTT 18989	GG C AT_ GG
		T AA TTAAGG AGCT GAAGA	
		TT GGTTC TTGA TTTCT	
		TT T CAG	
GAM1929 NY-REN-25	3'	CATGGATGTTGCCTTAGCCTT 30416	___
		AAGGTTAAGGCAGC TATG	

TTCCGATTCCGTTG GTAC
 TAG
 GAM1929 NY-REN-41 3' CTTCTTTGGCTTGT TTTTGT TTTT 27942 T _ AT
 T AAGG TAAGGCA GCT GAAGAGG
 |||| ||||| || |||||
 TTTT GTTTTGT CGG TTTCTTC
 T T _
 GAM1929 OSBPL3 3' TTTCTTAAATGCTGTTT TAG 17821 TATG
 TTAAGGCAGC AAGAGG
 ||||| |||||
 GATTTTGTCTG TTCTTT
 TAAA
 GAM1929 P450RAI-2 3' TTTTTCATAAATGTTATAATT 21272 AG GC
 TT AAGGTTA GCA TATGAAGAGG
 ||||| || |||||
 TTTTAAT TGT ATACTTTTTT
 AT AA
 GAM1929 PABPC5 5' CCTTTTGCCTGCCTTGGCTTT 28096 CTATG
 AAGGTTAAGGCAG AAGAGG
 ||||| |||||
 TTTCGGTTCCGTC TTTTCC
 CG____
 GAM1929 PC4 3' TCTAGTTGTTTAAATCT 13541 T
 AGGTTAAGGCAGCTA GA
 ||||| |||||
 TCTAATTTTGTTGAT CT
 _
 GAM1929 PCDH19 3' CTTTGTCTGCCTTGGTCTT 31864 GT CT TG
 AAG TAAGGCAG A AAG
 || ||||| | |||
 TTC GTTCCGTC T TTC
 TG T_GT
 GAM1929 PER3 3' TCTTTTGTAGTTGAATTGTCT 18823 T GG TG
 T AGG TAA CAGCTA AAGAGG
 || || ||||| |||||
 TTC GTT GTTGAT TTTTCT
 T AA GT
 GAM1929 PHCA 3' TTTCTTCACCTACTAGCCTTAG 20379 GG _ CTA_
 TTTT A TTAAGGC AG TGAAGAGG
 | ||||| || |||||
 T GATTCCG TC ACTTCTTT
 TT A ATCC
 GAM1929 PHRET1 3' TCTCTTTATAGCTGTGACT 22177 AAG
 GGTT GCAGCTATGAAGAGG
 |||| |||||
 TCAG TGTCGATATTTCTCT
 _
 GAM1929 PI15 5' TTTTTCATAGACCCTAACT 18030 A CAG
 GGTTA GG CTATGAAGAGG
 |||| || |||||

TCAAT CC GATACTTTTT
 _ CA_
 GAM1929 PIP5K2B 3' CCTTTTGGTACCTTGTAACCT 9610 _ CA AT
 T AAGGTTA AGG GCT GAAGAGG
 ||||| ||| ||| |||||
 TTCCAAT TCC TGG TTTTCC
 GT A_ _
 GAM1929 PLPL 3' CCTTTTGTGCCTTTCTTGACC 21399 C C TG
 T AGGTTAAGG AG TA AAGAGG
 ||||| || || |||||
 TCCAGTTCT TC GT TTTTCC
 T C GT
 GAM1929 PMX2B 3' TCTTGTTGTTGTTTTATTTT 10016 T T TG
 AAGGT AAGGCAGC A AAGA
 |||| ||||| | |||
 TTTTA TTTTGTTG T TTCT
 T T GT
 GAM1929 POFUT1 3' CATGGTTTTTTGACCTT 34885 C
 AAGGTTAAGG AGCTATG
 ||||| |||||
 TTCCAGTTTT TTGGTAC
 _
 GAM1929 PPP1R1B 3' CCTCTTTGTTGCGTTTTGTGCT 25907 _ A T TG
 TT AAGGT TAAGGC GC A AAGAGG
 |||| ||||| || | |||||
 TTTCG GTTTTG CG T TTCTCC
 T _ T GT
 GAM1929 PPP1R3B 3' TCTTTATTTTCTGTTTGCCT 23861 T CTATG
 T AAGGT AAGGCAG AAGAGG
 |||| ||||| |||||
 TTCCG TTTTGTC TTTTCT
 _ TTTTA
 GAM1929 PPP1R3B 3' TTTCTGTTTTGCCTTATCTT 23862 T CTAT
 AAGGT AAGGCAG GAAG
 |||| ||||| |||
 TTCTA TTCCGTT CTTT
 _ TTGT
 GAM1929 PRDM10 3' TTTTATGGCAGTTGTTTAAAGT 21500 G _ AGG
 TT AG TTAAGGCA GCTATGAAG
 || ||||| |||||
 TT AATTTTGT CGGTATTTT
 G TGA
 GAM1929 PREI3 3' CTTCTCATTTCCTTAACCTT 32964 CAGCT AG
 AAGGTTAAGG ATGA AG
 ||||| ||| ||
 TTCCAATTCC TACT TC
 CTT_ CT
 GAM1929 PRMT3 3' CCTCTTTGTGACTATTCCTTAG 32437 C_ C TG
 CCTT AAGGTTAAGG AG TA AAGAGG
 ||||| || || |||||

		TCCGATTCC TC GT TTCTCC	
		TTA A GT	
GAM1929 PRMT6	3'	CCTTTTCAGTTTTGTTTTG 19934	CTA
		TAAGGCAG TGAAGAGG	
		GTTTTGTT ACTTTTCC	
		TTG	
GAM1929 PRO0246	5'	TCTGCTGGGTGCCTTGACCTT 15381	G TGA
		AAGGTTAAGGCA CTA AGA	
		TTCCAGTTCCGT GGT TCT	
		G CG_	
GAM1929 PRO0767	5'	TTTCTTCCTGCCGTTCTTAGCT 15310	_A TAT
TT		AAGGTTAAGG C GC GAAGAGG	
		TTTCGATTCT G CG CTTCTTT	
		T C TC_	
GAM1929 PTP4A1	3'	CCTCTTCATACCAGTTTAACAC 9533	_ G AGC
TT		AAG GTTAAG C TATGAAGAGG	
		TTC CAATTT G ATACTTCTCC	
		A _ACC	
GAM1929 Rab11-FIP2	3'	TCTTTTTATGGGGAAATTGATT 17101	GGCAG
TT		AAGGTTAA CTATGAAGAGG	
		TTTTAGTT GGTATTTTCT	
		AAAGG	
GAM1929 RAB3GAP	3'	TCTTTTTGTGGTTGCTGGCT 33246	AA TG
		GGTT GGCAGCTA AAGAGG	
		TCGG TCGTTGGT TTTTCT	
		_ GT	
GAM1929 RAI	3'	TTTAGTAATCTGCCTTAGCCTT 13474	CTA__
		AAGGTTAAGGCAG TGAA	
		TTCCGATTCCGTC ATTT	
		TAATG	
GAM1929 RASSF2	3'	TTTCCCAATTGTTTTAGCCTT 16401	CTAT
		AAGGTTAAGGCAG GAAG	
		TTCCGATTTTGTT CTTT	
		AACC	
GAM1929 RERG	3'	TCTTTTCACCAAACCCTGACTT 26740	A CAGCTA
T		AAGGTTA GG TGAAGAGG	
		TTTCAGT CC ACTTTTCT	
		C AAACC_	
GAM1929 RHOBTB3	3'	TTGTGTTGTCTTAGCTTT 17079	T TG
		AAGGTTAAGGCAGC A A	

TTTTCGATTCTGTTG T T
 _ GT
 GAM1929 RI58 3' CTTTTTAGTTACAGATGTTTTG 14796 GCTA____ G
 ACTTT TTAAGGCA TGAAGAG
 ||||| |||||
 AGTTTTGT ATTTTTC
 AGACATTG
 GAM1929 RNAHP 3' TTTCTTGGAAGCTGTTTTGGT 14302 _ ATG_
 CCT AGG TTAAGGCAGCT AAGAGG
 || ||||| |||||
 TCC GGTTTTGTCGA TTCTTT
 T AGGG
 GAM1929 RNF2 3' CTTTTTATAGCCTATTTCTTT 14075 CA____
 AAT TTAAGG GCTATGAAGAGG
 ||||| |||||
 AATTTC CGATATTTTTC
 TTTATC
 GAM1929 RNPS1 3' TCTCTTTTGAGTTTATACCTT 13539 _ AGCTAT
 AAGGT TAAGGC GAAGAGG
 ||||| |||||
 TTCCA ATTTTG TTTCTCT
 T AGT____
 GAM1929 RNPS1 3' TCTCTTTTGAGTTTATACCTT 27904 _ AGCTAT
 AAGGT TAAGGC GAAGAGG
 ||||| |||||
 TTCCA ATTTTG TTTCTCT
 T AGT____
 GAM1929 SB52 3' TTTCTGCACGTGGTTGCCTTAG 28736 GT A____
 TC G TAAGGCAGCTATG AGAGG
 | ||||| |||||
 C ATTCCGTTGGTGC TCTTT
 TG ACG
 GAM1929 SCAND2 3' CCTCTTCATACTATTAAATTTT 22575 A GC C
 AAGGTT AG AG TATGAAGAGG
 ||||| || |||||
 TTTTAA TT TC ATACTTCTCC
 A A_ _
 GAM1929 SEC63L 3' TTTCTTTGTTTCAGCTTTAGTTT 14080 GG AGCT TG
 T AA TTAAGGC A AAGAGG
 || ||||| | |||||
 TT GATTTCG T TTCTTT
 TT ACT_ GT
 GAM1929 SH3BGRL 3' CCTTTTTATTTCAGTTTAGCC 31024 G AGCT
 GGTTAAG C ATGAAGAGG
 ||||| | |||||
 CCGATTT G TATTTTCC
 _ ACTT
 GAM1929 SH3BGRL2 3' CTTCTTTCTGTTGTGTTTGATT 25530 _ TAT
 TT AAGGTTAAG GCAGC GAAGAGG
 ||||| ||||| |||||

			TTTTAGTTT TGTTG TTTCTTC		
			G TC_		
GAM1929	SLC11A2	3'	CCTTTTCAGTTATTTTAATT 6224	C	AT
			GGTTAAGG AGCT GAAGAGG		
			TTAATTTT TTGA CTTTTC		
			A _		
GAM1929	SMARCF1	3'	CCTCTTAGAACTGGTTTAAACC 20519		AGCTATG
		TT	AAGGTTAAGGC AAGAGG		
			TTCCAATTTTG TTCTCC		
			GTCAAGA		
GAM1929	SMARCF1	3'	CCTCTTAGAACTGGTTTAAACC 29162		AGCTATG
		TT	AAGGTTAAGGC AAGAGG		
			TTCCAATTTTG TTCTCC		
			GTCAAGA		
GAM1929	SMARCF1	3'	CCTCTTAGAACTGGTTTAAACC 12624		AGCTATG
		TT	AAGGTTAAGGC AAGAGG		
			TTCCAATTTTG TTCTCC		
			GTCAAGA		
GAM1929	SMC1L1	3'	CTTACTAGTTGTTTGACCTT 35619	G	TG
			AAGGTTAAG CAGCTA AAG		
			TTCCAGTTT GTTGAT TTC		
			_ CA		
GAM1929	SPTLC2	3'	CTTAAGCTAGCTCCTTTGGCTT 11279	C	TGAA G
		T	AAGGTTAAGG AGCTA GAG		
			TTTCGGTTTC TCGAT TTC		
			C CGAA		
GAM1929	SPTLC2	3'	CTTTTCAACTTTTGTCTTGC 11280	T	CTA__
		TTT	AGGT AAGGCAG TGAAGAGG		
			TTCG TTTCGTT ACTTTTTC		
			_ TTTCA		
GAM1929	SRCRB4D	3'	TCTTTTATAGCACCAGACT 28030	AA	CA
			GGTT GG GCTATGAAGAGG		
			TCAG CC CGATATTTTCT		
			A_ A_		
GAM1929	ST13	3'	TCTTTTAAATGCTTTATCTTT 10035	T	GCTA
			AAGG TAAGGCA TGAAGAGG		
			TTTC ATTCGT ATTTTCT		
			T AA__		
GAM1929	ST7L	3'	TTTCTTCATTAGCTTAGCCTT 19338	G	AGCT
			AAGGTTAAG C ATGAAGAGG		

		TTCCGATTC G TACTTCTTT	
		_ ACT _	
GAM1929 ST7L	3'	TTTCTTCATT CAGCTTAGCCTT 29211	G AGCT
		AAGGTTAAG C ATGAAGAGG	
		TTCCGATTC G TACTTCTTT	
		_ ACT _	
GAM1929 ST7L	3'	TTTCTTCATT CAGCTTAGCCTT 28980	G AGCT
		AAGGTTAAG C ATGAAGAGG	
		TTCCGATTC G TACTTCTTT	
		_ ACT _	
GAM1929 STAT2	3'	TCTTTTCATATCTCTTTGCCCT 11891	T C C
T		AAGG TAAGG AG TATGAAGAGG	
		TTCC GTTTC TC ATACTTTTCT	
		C _ T	
GAM1929 STAT5A	3'	CCTTGCTTGGCTGCTTGGCCTT 9128	G TGAA
		AAGGTTAAG CAGCTA GAGG	
		TTCCGGTTC GTCGGT TTCC	
		_ TCG _	
GAM1929 STK36	3'	TTTCTGGAGCTCCTTTAATCTT 35691	C ATGA
		AAGGTTAAGG AGCT AGAGG	
		TTCTAATTTT TCGA TCTTT	
		C GG _	
GAM1929 STRIN	3'	CCTTTTTAAGACTTTTGACC 18395	CAG A
		GGTTAAGG CT TGAAGAGG	
		CCAGTTTT GA ATTTTCC	
		CA _ _	
GAM1929 STRN3	3'	TCTTTTTATATATTTAGCCT 15936	GCAGC
		AGGTTAAG TATGAAGAGG	
		TCCGATTT ATATTTTCT	
		AT _	
GAM1929 SYPL	3'	TCTTGCTGTTGCCTTATTTTT 44646	T TATG
		AAGG TAAGGCAGC AAGA	
		TTTT ATTCCGTTG TTCT	
		T TCG _	
GAM1929 SYTL2	5'	TTTTTGTTGTGTTTAATCTT 26760	GC TG
		AAGGTTAAGGCA TA AAGA	
		TTCTAATTTTGT GT TTTT	
		_ GT	
GAM1929 TA-PP2C	3'	TCTTTTTGTGTTATGCACTTAA 29286	_ GC _ TG
TTTT		AGGTTAAG GCA TA AAGAGG	

			TTTAATTC CGT GT TTTTCT		
			A ATT GT		
GAM1929	TAF5L	3'	CTTCTCTGCTTTTAATCTT 15750	_	CTAT
			AAGGTTAAG GCAG GAAG		
			TTCTAATTT CGTC CTTC		
			T T__		
GAM1929	TAF9L	3'	TTTCTTTGACTTCCTTAACTT 18076	C	CTA
			AGGTTAAGG AG TGAAGAGG		
			TTCAATTCC TC GTTCTTT		
			T A__		
GAM1929	TBDN100	3'	CTTTTCCCTTATGCTTTGGCTT 24695	GCTAT	G
	T		AAGGTTAAGGCA GAAGAG		
			TTTCGGTTTCGT CTTTTC		
			ATTCC		
GAM1929	TCFL5	3'	CTTTGTACTTTCTTTAATCTT 13382	C C	TG
			AAGGTTAAGG AG TA AAG		
			TTCTAATTTT TT AT TTC		
			T C GT		
GAM1929	TCL6	5'	TCTTTTGGACTTTAATCTT 14846	CAG	T
			AAGGTTAAGG CTA GAAGA		
			TTCTAATTTT GGT TTTCT		
			A__ T		
GAM1929	TCL6	5'	TCTTTTGGACTTTAATCTT 15770	CAG	T
			AAGGTTAAGG CTA GAAGA		
			TTCTAATTTT GGT TTTCT		
			A__ T		
GAM1929	TCL6	5'	TCTTTTGGACTTTAATCTT 21772	CAG	T
			AAGGTTAAGG CTA GAAGA		
			TTCTAATTTT GGT TTTCT		
			A__ T		
GAM1929	TCL6	5'	TCTTTTGGACTTTAATCTT 21763	CAG	T
			AAGGTTAAGG CTA GAAGA		
			TTCTAATTTT GGT TTTCT		
			A__ T		
GAM1929	TGIF2	3'	TTTCTTTTGCTGTTTGT TTTT 22368	T	TAT
			AAGG TAAGGCAGC GAAGAGG		
			TTTT GTTTGTCTG TTTCTTT		
			T T__		
GAM1929	TIP-1	3'	CCTCTTGCCTGTGGGTTTAAC 15966	__	CTA
	TTT		GGTTAAG GCAG TGAAGAGG		

			TCAATTT TGTC GTTCTCC		
			GGG C__		
GAM1929	TNRC5	5'	CTTCTTCTCGGGTCTTGGTCCT 13346	_	AGCTAT
			AGG TTAAGGC GAAGAGG		
			TCC GGTTCTG CTTCTTC		
			T GGCT__		
GAM1929	TOB2	3'	CTCCTGTTGTTTGGCCTT 45768	G	TATGAA
			AAGGTTAAG CAGC GAG		
			TTCCGGTTT GTTG CTC		
			_ TC__		
GAM1929	TOLLIP	3'	CTTTTTCACAAGCGCTTTATTT 21093	T	A A_
	TT		AAGG TAAGGC GCT TGAAGAGG		
			TTTT ATTTCTG CGA ACTTTTTC		
			T _ AC		
GAM1929	TOPK	3'	TCTTTGTTTTTGTCTTAATTT 20554	CTA_	GG
			AGGTTAAGGCAG TGAAGA		
			TTTAATTTCTGTT GTTTCT		
			TTTG		
GAM1929	TTY9	3'	CTATTAGTGCCTTGATCTT 25679	G	TGAAG
			AAGGTTAAGGCA CTA AG		
			TTCTAGTTCCGT GAT TC		
			_ TA__		
GAM1929	UBE2G1	3'	TCTAATGAAGTGTTTTAACCTT 9349		CTATGA
			AAGGTTAAGGCAG AGA		
			TTCCAATTTTGTC TCT		
			AAGTAA		
GAM1929	UNC5D	3'	TCTCTTGATATGCTTTTGTTTT 28116	TT	GC G
			AAGG AAGGCA TAT AAGAGG		
			TTTT TTTCGT ATA TTCTCT		
			GT _ G		
GAM1929	USP15	3'	TTTTTCATATACTGGCCTT 13007	_ C_	
			AAGGC AG TATGAAGAG		
			TTCCG TC ATACTTTT		
			G AT		
GAM1929	USP25	3'	TCTTTTGTAGTTCTTAACC 15049	CA	T
			GGTTAAGG GCTA GAAGA		
			CCAATTCT TGAT TTTCT		
			_ T		
GAM1929	USP8	3'	CCTTTTCACTGTTATGGCCTT 11630	AG	CTA
			AAGGTTA GCAG TGAAGAGG		

		TTCCGGT TGTC ACTTTTCC	
		AT ____	
GAM1929 VEZATIN	3'	TTTTTCCATGCTGTTTAACT 19073	TAT
T		AGGTAAAGGCAGC GAAGAGG	
		TTCAATTTTGTCTG CTTTTT	
		TAC	
GAM1929 VMP1	3'	TTTCTTGAGCGTTTTGATTTT 25208	A AT_
		AAGGTAAAGGC GCT GAAG	
		TTTGTAGTTTTG CGA CTTT	
		_ GTT	
GAM1929 X123	3'	CTATTTATAGTTGCCTTTGGCC 34649	_ G G
TT		AAGGTAA GGCAGCTATGAA AG	
		TTCCGGTT CCGTTGATATTT TC	
		T A	
GAM1929 YAP1	3'	CCTGGCACAGTGCTTTGATCTT 12753	G A AAG
		AAGGTAAAGGCA CT TG AGG	
		TTCTAGTTTCGT GA AC TCC	
		_ C GG_	
GAM1929 YWHAQ	3'	CCTTGATTTGTGTTTGTCTTGG 13707	C TG _
CCTT		AGGTAAAGGCAG TA AA GAGG	
		TCCGGTTCTGTT GT TT TTCC	
		T GT AG	
GAM1929 ZFP91	3'	CTTTTTGTTTCTTGCTTTGCTT 27575	T CT_ TG G
T		AAGGT AAGGCAG A AAGAG	
		TTTCG TTTCGTT T TTTTC	
		_ CTT GT	
GAM1929 ZFP91	3'	CCTATATAATAATTGCTTTGGC 27573	C GAAG_
TTT		AAGGTAAAGGCAG TAT AGG	
		TTTCGGTTTCGTT ATA TCC	
		A ATATA	
GAM1929 ZFP91	3'	CTTCCAGGGAGCTCTTTTAATC 27574	C AT__ AGG
TT		AGGTAAAGG AGCT GAAG	
		TCTAATTTT TCGA CTTC	
		C GGGAC	
GAM1929 ZNF262	3'	TTTCTCCCGTTGTTTTACCTT 11560	T TAT_
		AAGGT AAGGCAGC GAAG	
		TTCCA TTTTGTG CTTT	
		_ CCCT	
GAM1929 ZNF323	3'	CTCTTTAATTCATAGCCTT 25169	A CAGCTA
		AAGGTAA GG TGAAGAG	

		TTCCGAT CT ATTTCTC	
		A TA_____	
GAM1929	ZNF361	5' CTCCTGTGCCTTGGCCTT 20636	G TAT
		AAGGTTAAGGCA C GAAG	
		TTCCGGTTCCGT G CTTC	
		TC	
GAM1929	ZNF363	3' TTTCAGTAGTAGTCTTGACTTT 36358	A _
		AAGGTTAAGGC GCTA TGAAG	
		TTTCAGTTCTG TGAT ACTTT	
		A G	
GAM1929	LOC112885	3' CCTTTTCTGTTGGTTTGGTTTT 28786	GG G TAT
		AA TTAAG CAGC GAAGAGG	
		TT GGTTT GTTG CTTTCC	
		TT G T__	
GAM1929	LOC115297	3' CCTCTTTGTGGCAACAGATCT 36070	AAGGCA TG
		AGGTT GCTA AAGAGG	
		TCTAG CGGT TTCTCC	
		ACAA__ GT	
GAM1929	LOC120856	3' CTTCTTTGGCATTCTTGACCT 36638	CA AT
		AGGTTAAGG GCT GAAGAGG	
		TCCAGTTCT CGG TTTCTTC	
		TA _	
GAM1929	LOC121219	5' CTTGGAGCTGTCTTAATCT 36650	ATGAA
		AGGTTAAGGCAGCT GAG	
		TCTAATTCTGTCTGA TTC	
		GG__	
GAM1929	LOC121838	5' TTTCATCAATTGCCTTGACTTT 37420	CT_
		AAGGTTAAGGCAG ATGAAG	
		TTTCAGTTCCGTT TACTTT	
		AAC	
GAM1929	LOC123036	3' CTTCTACTGCTCTGATTTT 36717	AG C T
		AAGGTTA GCAG TA GAAG	
		TTTTAGT CGTC AT CTTC	
		CT _ _	
GAM1929	LOC126526	3' TTTCTTCTCTGGCTGTGGCCTT 36847	AAG T_
		AAGGTT GCAGCTA GAAGAGG	
		TTCCGG TGTCGGT CTTCTTT	
		__ CT	
GAM1929	LOC126528	5' CCTTTTGTACCTCTTGACCT 36844	CAGCTAT
		AGGTTAAGG GAAGAGG	

	TCCAGTTCT	TTTTTCC		
	CCAG__			
GAM1929 LOC131000 5'	TTTTTTTAA	CAGTTGTCTTGTT 37352	T	A_
TTT	AAGG	TAAGGCAGCT TGAAGAGG		
	TTTT	GTTCTGTTGA ATTTTTTT		
	T	CA		
GAM1929 LOC131000 3'	TTTCTTCTTTT	GCTATAATTTT 37351	A	CTAT
	AAGGTTA	GGCAG GAAGAGG		
	TTTTAAT	TCGTT CTTCTTT		
	A	TT__		
GAM1929 LOC132166 3'	CTTCCG	TATGCTGTTTGACTTT 37019	G	_ _
	AAGGTTAAG	CAGC TATG AAG		
	TTTCAG	TTT GTCG ATGC TTC		
	_	T C		
GAM1929 LOC132235 5'	TCTCTTCAGCACCCTCAGCCTT 37482		A	CA AT
	AAGGTT	AGG GCT GAAGAGG		
	TTCCGA	TCC CGA CTTCTCT		
	C	CA _		
GAM1929 LOC135398 3'	TCTTGGCTCTTTGATCTT 37388		C	T
	AAGGTTAAGG	AGCTA GA		
	TTCTAG	TTTC TCGGT CT		
	_	T		
GAM1929 LOC139673 3'	CTCAAGTTGTTT	AGTCT 37404	GT	ATGAA
	AG	TAAGGCAGCT GAG		
	TC	ATTTGTTGA CTC		
	TG	A__		
GAM1929 LOC143310 5'	CTTTTTTGT	CCTTGCTTTTACC 37607	T	CT TG
TT	AAGGT	AAGGCAG A AAGAGG		
	TTCCA	TTTCGTT T TTTTTC		
	T	CC GT		
GAM1929 LOC143888 3'	CCTCTTACAAGCTGCTTTTGGC 37669		_	A _
TTT	AGGT	TAAAG GCAGCT TG AAGAGG		
	TTCGG	TTT CGTCGA AC TTCTCC		
	T	_ A		
GAM1929 LOC145786 5'	TTTGCATCAGTTTGTCTTGGCT 40593		_ _	AAGAGG
TT	AAGGT	TAAAGGCAG CT ATG		
	TTTCGG	TTTCTGTT GA TAC		
	T	C GTTT		
GAM1929 LOC145845 3'	CCTTTTCATTTAGGTTTACTTT 40616		TA	AGCT
	AAGGT	AGGC ATGAAGAGG		

TTTCA TTTG TACTTTTCC
 _ GATT
 GAM1929 LOC146138 3' CCTCTTTGTAGCTCTGTGCTT 40655 TAA C TG
 AGGT GG AGCTA AAGAGG
 ||| || ||| |||||
 TTCG TC TCGAT TTCTCC
 TG_ _ GT
 GAM1929 LOC146515 3' TTTTGTGTTGGTTGGTTTGGC 38196 _ TGA
 TTT AAGGTTAAGGC AGCTA AGAGG
 ||||| ||| |||
 TTTCGGTTTGT TTGGT TTTT
 G TTG
 GAM1929 LOC146713 3' TCTCTTCGCTAGGTCCTGGGTT 40718 GG TA CAG _
 TT AA T AGG CTA TGAAGAGG
 || | ||| || |||||
 TT G TCC GAT GCTTCTCT
 TT GG TG_ C
 GAM1929 LOC147136 3' CTTCTTCATGGCTGCGTTG 38304 G
 TAA GCAGCTATGAAGAGG
 || |||||
 GTT CGTCGGTACTTCTTC
 G
 GAM1929 LOC147353 3' CTTTACTTGGTTGCCATAATTT 40835 A _ AGG
 T AAGGTTA GGCAGCTA TGAAG
 ||||| ||||| |||
 TTTTAAT CCGTTGGT ATTC
 A TC
 GAM1929 LOC147515 3' CCTGGGCCAGTTGATTTGACCT 40843 G ATGAAG
 T AAGGTTAAG CAGCT AGG
 ||||| ||| |||
 TTCCAGTTT GTTGA TCC
 A CCGGG_
 GAM1929 LOC147639 5' CCTTTCATAATTACTTTAGCTT 38345 C C A
 T AAGGTTAAGG AG TATGA GAGG
 ||||| || ||| |||
 TTTCGATTTT TT ATACT TTCC
 A A _
 GAM1929 LOC148809 5' CTTCTTTGATGGGTCTTGGCTT 38595 AG _
 AGGTTAAGGC CTAT GAAGAGG
 ||||| ||| |||||
 TTCGGTTCTG GGTA TTTCTTC
 _ G
 GAM1929 LOC148936 5' TCTCTGCACAAGCTGTCTTTGT 40933 TT A_ A
 CTT AAGG AAGGCAGCT TG AGAGG
 ||| ||||| || |||
 TTCT TTCTGTCTGA AC TCTCT
 GT AC G
 GAM1929 LOC148938 5' TCTCTGCACAAGCTGTCTTTGT 40926 TT A_ A
 CTT AAGG AAGGCAGCT TG AGAGG
 ||| ||||| || |||

		TTCT TTCTGTCGA AC TCTCT		
		GT AC G		
GAM1929	LOC149073 5'	CCTTTTGTGTGGTGCCCTTGG 40944	GG	CA _
	TTT	A TTAAGG GCTAT GAAGAGG		
		T GGTTC TGGTG TTTTCC		
		TT CG TG		
GAM1929	LOC149113 3'	TCTCTGACACCTTGACTTTAAC 38641	_	CTATGA
	CTT	AAGGTTAAGG CAG AGAGG		
		TTCCAATTTC GTT TCTCT		
		A CCACAG		
GAM1929	LOC149267 3'	CTTCCAAGCTGCTTAGCCTT 28832	G	AT
		AAGGTTAAG CAGCT GAAG		
		TTCCGATTTC GTCGA CTTC		
		_ AC		
GAM1929	LOC149322 5'	CCTTAGTTGCTGGCTTTGACCT 29946	_	TATG AGG
	T	AAGGTTAAGGC AGC AAG		
		TTCCAGTTTCG TCG TTC		
		G TTGA C		
GAM1929	LOC149373 3'	TTTTTCTGCTGTTGACCTT 38722	AG	TAT
		AAGGTTA GCAGC GAAGAG		
		TTCCAGT TGTCG CTTTTT		
		_ T _		
GAM1929	LOC149670 3'	TCTCTCACTTGTCTTGGTTTT 38806	GG	CTA A
		AA TTAAGGCAG TGA GAGG		
		TT GGTCTGTT ACT CTCT		
		TT C _ _		
GAM1929	LOC149692 3'	TCATTGCTTCTTGGCCTT 41040	C	T
		AAGGTTAAGG AGC ATGA		
		TTCCGGTTCT TCG TACT		
		_ T		
GAM1929	LOC149995 3'	CCTGGGCCAGTTGATTTGACCT 41128	G	ATGAAG
	T	AAGGTTAAG CAGCT AGG		
		TTCCAGTTT GTTGA TCC		
		A CCGGG _		
GAM1929	LOC150142 5'	CTTCTTCTGTTTTGACT 38852	CTAT	
		GGTTAAGGCAG GAAG		
		TCAGTTTTGTC CTTC		
		TT _		
GAM1929	LOC150271 5'	CCTTGGACAGGGCTCCTTGGCC 41168	C	A AA _
	TT	AAGGTTAAGG AGCT TG GAGG		

TTCCGGTTCC TCGG AC TTCC
 _ G AGG
 GAM1929 LOC150271 3' TTTTTTTGGCTCTCTGGACTTT 41177 A C T
 AAGGTT AGG AGCTA GAAGA
 ||||| ||| ||||| |||||
 TTTCAG TCT TCGGT TTTTT
 G C T
 GAM1929 LOC150577 3' TCATTGTTGTTTTAATTT 41225 T
 AGGTTAAGGCAGC ATGA
 ||||| ||||| |||||
 TTTAATTTTGTTG TACT
 T
 GAM1929 LOC150848 5' TTTCTTTCTGTCTTAAACTT 41263 G CTAT
 AAG TTAAGGCAG GAAGAGG
 ||| ||||| |||||
 TTC AATTCTGTC TTTCTTT
 A C__
 GAM1929 LOC151277 5' TTTTTTATGGCAGTTTTTATT 39095 T A
 TT AAGGT AAGGC GCTATGAAGAGG
 ||||| ||||| ||||| |||||
 TTTTA TTTTG CGGTATTTTTTT
 T A
 GAM1929 LOC151361 3' CCTCTTTTTTGTCTTCAACTTT 41329 _ CTAT
 AAGGTT AAGGCAG GAAGAGG
 ||||| ||||| |||||
 TTTCAA TTTTGTT TTTCTCC
 C T__
 GAM1929 LOC151556 5' CAAAAACATGGTTGTACTTAAT 39132 _ AAGAGG
 TTT AAGGTTAAG GCAGCTATG
 ||||| ||||| |||||
 TTTTAATTC TGTTGGTAC
 A AAAA ACT
 GAM1929 LOC151701 5' TTTCTTCTGTCCCTTGACCTT 41387 CA TAT
 AAGGTTAAGG GC GAAGAGG
 ||||| || |||||
 TTCCAGTTCC TG CTTCTTT
 C_ T__
 GAM1929 LOC151827 5' CTTCTTTGTAGCCCCAGCC 39169 AA CA TG
 GGTT GG GCTA AAGAGG
 |||| || ||||| |||||
 CCGA CC CGAT TTCTTC
 _ C_ GT
 GAM1929 LOC152559 3' CTTTGAAAATGGCTGTTTTACC 39284 T GA__ G
 TT AAGGT AAGGCAGCTAT AGAG
 ||||| ||||| ||||| |||||
 TTCCA TTTTGTCGGTA TTTC
 _ AAAG
 GAM1929 LOC152804 3' CCTTTTGTCTGCTCTTG GCC 41555 _ CT TG
 GGTTAAG GCAG A AAGAGG
 ||||| ||||| ||||| |||||

CCGGTTTC CGTC T TTTTCC
 T __GT
 GAM1929 LOC153027 3' TCTCTTTTGAGTTTTATACCTT 33491 _ AGCTAT
 AAGGT TAAGGC GAAGAGG
 ||||| ||||| |||||
 TTCCA ATTTTG TTTCTCT
 T AGT__
 GAM1929 LOC153196 3' TTTCTATGACTGTGTTAGCTTT 41596 G C _
 AAGGTAA GCAG TAT GAAG
 ||||| ||||| |||||
 TTTCGATT TGTC GTA CTTT
 G A T
 GAM1929 LOC153232 5' TCTCTTTATCTCTTTGTCTTGT 41598 GT_ CT_
 GTCTT TAAGGCAG ATGAAGAGG
 ||||| |||||
 GTTCTGTT TATTTCTCT
 TGT TCTC
 GAM1929 LOC153346 3' TTTCTCTGTCTTACCTT 41619 T CTAT
 AAGGT AAGGCAG GAAG
 ||||| ||||| |||||
 TTCCA TTCTGTC CTTT
 _ T__
 GAM1929 LOC154043 3' TTTAAGTGTAGCAGCTTTGACT 39461 A AAGAGG
 TT AAGGTAAAGGC GCTATG
 ||||| |||||
 TTTCAGTTTCG CGATGT
 A GAATTTT
 GAM1929 LOC154403 3' CTTCTGACACCTTGACTTTAGC 39469 _ CTATGA
 CTT AAGGTAAAGG CAG AGAGG
 ||||| ||||| |||||
 TTCCGATTTC GTT TCTTC
 A CCACAG
 GAM1929 LOC154992 3' CCTCTGACACCTTGACTTTAGC 39519 _ CTATGA
 CTT AAGGTAAAGG CAG AGAGG
 ||||| ||||| |||||
 TTCCGATTTC GTT TCTCC
 A CCACAG
 GAM1929 LOC155081 3' CTTTTCATCCTAAATCTT 39545 A CAGCT
 AAGGTT AGG ATGAAGAG
 ||||| ||||| |||||
 TTCTAA TCC TACTTTTC
 A ____
 GAM1929 LOC157503 3' CCTCAGGAGGTTGTACTTAATT 41813 _ ATGAA
 TT AAGGTAAAG GCAGCT GAGG
 ||||| ||||| |||||
 TTTTAATTC TGTTGG CTCC
 A AGGA_
 GAM1929 LOC157653 5' TCTCTTTCCAGTGTCTTAGACT 39635 G G AT
 T AAG TTAAGGCA CT GAAGAGG
 ||||| ||||| |||||

TTC GATTCTGT GA TTTCTCT
 A _ CC
 GAM1929 LOC158014 5' CTTTTTTGTATGTTGACCTT 39692 _ _ TG
 AAGG CAGC TA AAGAGG
 |||| ||| || |||||
 TTCC GTTG AT TTTTTC
 A T GT
 GAM1929 LOC158055 3' CTTTTTCAACTTCCTTAGTCT 39704 GT C CTA
 AG TAAGG AG TGAAGAGG
 || ||||| || |||||
 TC ATTCC TC ACTTTTTC
 TG T A__
 GAM1929 LOC158382 3' CTTTTCCCCATTGCCTTAACT 41966 CTAT G
 GGTTAAGGCAG GAAGAG
 ||||| |||||
 TCAATTCCGTT CTTTTC
 ACCC
 GAM1929 LOC158549 5' CCTTTTTATGGCTAAATGATGT 42006 G AGGC
 T AA GTTA AGCTATGAAGAGG
 || ||| |||||
 TT TAGT TCGGTATTTTTC
 G AAA_
 GAM1929 LOC196027 3' TTTCTTCATTACACTAACCTT 42308 A GCAGCT
 AAGGTTA G ATGAAGAGG
 ||||| | |||||
 TTCCAAT C TACTTCTTT
 ACAT
 GAM1929 LOC196446 3' TTTTTCAGGCTTTAGCTT 42373 AGCTA
 AGGTTAAGGC TGAAGAG
 ||||| |||||
 TTCGATTTTCG ACTTTTT
 G____
 GAM1929 LOC196761 3' CCTTTTTGTCCCTTAATTT 43128 CAGCT TG
 AGGTTAAGG A AAGAGG
 ||||| | |||||
 TTTAATTCC T TTTTCC
 C____GT
 GAM1929 LOC196761 3' TTTTTCATTGCTTTGTGACTT 43130 AG C T
 T AAGGTTA G AGC ATGAAGAGG
 ||||| | ||| |||||
 TTTCAGT T TCG TACTTTTTT
 GT _ T
 GAM1929 LOC196812 3' TCTTTTTGTTGTCTTTAACTT 43139 _ TAT GG
 T AAGGTT AAGGCAGC GAAGA
 ||||| ||||| |||||
 TTTCAA TTCTGTTG TTTCT
 AT TT_
 GAM1929 LOC197131 3' CCTTTTCATAAACTCTGGTTT 42446 G C____
 AAG CAG TATGAAGAGG
 ||| ||| |||||

	TTT GTC ATACTTTTCC		
	G TCAA		
GAM1929 LOC197319 3'	TTTTTTCCTGGTTTGTGTTGATC 42478	GC	T
TT	AAGGTTAAG AGCTA GAAGAGG		
	TTCTAGTTT TTGGT CTTTTTT		
	GT C		
GAM1929 LOC199699 3'	CCTCGTGATCTGCCTGCCTTGG 42595	_	TATGAA_
CCTT	AGGTAAAGGCAG C GAGG		
	TCCGGTTCGTC G CTCC		
	C TCTAGTG		
GAM1929 LOC199775 3'	TTTTTTCAGTGGCTTTAACCT 42616	AGCTA	
	AGGTAAAGGC TGAAGAGG		
	TCCAATTTCG ACTTTTTT		
	GTG_		
GAM1929 LOC200014 3'	TTTCAGTCTGCTGCTTTGCTCT 42697	GT	TA_ AGG
T	AAG TAAGGCAGC TGAAG		
	TTC GTTTCGTCG ACTTT		
	TC TCTG		
GAM1929 LOC200107 3'	CCTTTTCGTCAGGTTTGA CTT 42707	G	AGCT
	AGGTAAAG C ATGAAGAGG		
	TTCAGTTT G TGCTTTTCC		
	_ GAC_		
GAM1929 LOC200138 3'	TTTTTAAAGCTGCTTTAG 43281	A	GG
	TTAAGGCAGCT TGAAGA		
	GATTTCGTCGA ATTTTT		
	A		
GAM1929 LOC200558 3'	TTTTTTGTTGCCTTGCCTT 42820	T	TAT
	AAGGT AAGGCAGC GAAG		
	TTCCG TTCCGTTG TTTT		
	_ TT_		
GAM1929 LOC200563 5'	TCTTTTAAACAGTTCTGACCT 43319	AG	AGCTA
T	AAGGTTA GC TGAAGAGG		
	TTCCAGT TG ATTTTCT		
	CT ACAA_		
GAM1929 LOC200609 5'	CTTTTCAAGATTGCTTTGGCT 43329	_	A
	GGTTAAGGCAG CT TGAAGAGG		
	TCGGTTTCGTT GA ACTTTTTC		
	A _		
GAM1929 LOC200609 5'	TCTAGTAAGTGTGTTTAACTT 43336	_ _	GA GG
T	AAGGTTAAGGCA GCT AT AGA		

	TTTCAATTTTGT TGA TG TCT	
	G A A_	
GAM1929 LOC200830 3'	TTTCTTTATAGGCAATGGCCT 43350	AG AG
	AGGTTA GC CTATGAAGAGG	
	TCCGGT CG GATATTTCTTT	
	AA _	
GAM1929 LOC201182 5'	TCTTTATCCTGCCTGTGGTTTT 43212	GG _ CT
	AA TTA AGGCAG ATGAAGA	
	TT GGT TCCGTC TATTTCT	
	TT G C_	
GAM1929 LOC201868 3'	CCTCTGACACCTTGACTTTAGC 42922	_ CTATGA
CTT	AAGGTTAAGG CAG AGAGG	
	TTCCGATTTT C GTT TCTCC	
	A CCACAG	
GAM1929 LOC201965 5'	CCTCTGGGCCGCTGCCTTCGCT 42932	T TATGA
TT	AAGGT AAGGCAGC AGAGG	
	TTTCG TTCCGTCG TCTCC	
	C CCGGG	
GAM1929 LOC201965 3'	CTTTTTGTAGTTTCTTTTAATT 42933	_ C TG G
TT	AAGGTTAAG G AGCTA AAGAG	
	TTTTAATTT C TTGAT TTTTC	
	TT GT	
GAM1929 LOC202781 3'	ATGTTTCTGGTTGTTTTAGTC 43443	GT T GG
TT	AAG TAAGGCAGCTA GAAGA	
	TTC ATTTTGTTGGT CTTTT	
	TG _ GTAA	
GAM1929 LOC202802 3'	CTTTTCATCCTAAATCTT 42990	A CAGCT
	AAGGTT AGG ATGAAGAG	
	TTCTAA TCC TACTTTTC	
	A _	
GAM1929 LOC202934 5'	CCTTTTACAGCTTTTGA CT 43457	GC A
	AGGTTAAG AGCT TGAAGAGG	
	TTCAGTTT TCGA ATTTTTC	
	_ C	
GAM1929 LOC203248 3'	TTTCCGGCTTGCTTTGACTTT 43021	_ AT
	AAGGTTAAGGCA GCT GAAG	
	TTTCAGTTTCGT CGG CTTT	
	T C_	
GAM1929 LOC203536 3'	CCTTTTGTAGTATTTT TAGTC 43057	GT CA TG
TT	AAG TAAGG GCTA AAGAGG	

	TTC ATTTT TGAT TTTTCC		
	TG TA GT		
GAM1929 LOC205327 3'	TCTTTTGGTGTTTTAACACTT 43107	_	G T
	AAG GTTAAGGCA CTA GAAGA		
	TTC CAATTTTGT GGT TTTCT		
	A _ T		
GAM1929 LOC219654 3'	TTTTTTACTATGCTTTGGTCT 43880	GT	GCTA
	AG TAAGGCA TGAAGAG		
	TC GTTTCGT ATTTTT		
	TG ATC_		
GAM1929 LOC219942 3'	TCTGCCAGTGCCTTGATCTT 44828		G ATGA
	AAGGTTAAGGCA CT AGA		
	TTCTAGTTCCGT GA TCT		
	_ CCG_		
GAM1929 LOC220469 5'	TTTTTATGCCTTCTTAACCTT 37557	CA	T
	AAGGTTAAGG GC ATGAAGA		
	TTTCAATTCT CG TATTTTT		
	TC _		
GAM1929 LOC220635 5'	CCTTAGTTGCTGGCTTTGACCT 43639	_	TATG AGG
T	AAGGTTAAGGC AGC AAG		
	TTCCAGTTTCG TCG TTC		
	G TTGA C		
GAM1929 LOC220729 5'	CTTTGCGAGCTGCATTTGGCCT 35447	_	ATGA G
T	AAGGTTAAG GCAGCT AGAG		
	TTCCGGTTT CGTCGA TTTC		
	A GCG_		
GAM1929 LOC220963 3'	CCTTATGCAGTTGCATTTAACC 43956	_	ATGAA
TT	AAGGTTAAG GCAGCT GAGG		
	TTCCAATTT CGTTGA TTCC		
	A CGTA_		
GAM1929 LOC220988 3'	TCTTTTATCTGTTGTAGCTTT 43686	AG	CTAT
	AAGGTTA GCAG GAAGA		
	TTTCGAT TGTC TTTCT		
	GT TAT_		
GAM1929 LOC221178 3'	TTCTTTGTCTTTGGCCT 44931	CAGCT	TG
	AGGTTAAGG A AAGAG		
	TCCGGTTTC T TTCTT		
	_____GT		
GAM1929 LOC221312 3'	CCTTTGTAAGTTGGTTTGATCT 44139	G _TG	AGG
T	AAGGTTAAG CAGCT A AAG		

	TTCTAGTTT GTTGA T TTC		
	G AGT C		
GAM1929 LOC221814 5'	CTAGTAGTTCTTTAACTTT 45091	C	GA
	AAGGTTAAGG AGCTAT AG		
	TTTCAATTTT TTGATG TC		
	_ A_		
GAM1929 LOC221815 5'	CTAGTAGTTCTTTAACTTT 45087	C	GA
	AAGGTTAAGG AGCTAT AG		
	TTTCAATTTT TTGATG TC		
	_ A_		
GAM1929 LOC222070 5'	CTTCGTTGCTTCTTTGGTCTT 45182	GT	C T
	AAG TAAGG AGC ATGAAG		
	TTC GTTTC TCG TGCTTC		
	TG T T		
GAM1929 LOC222159 5'	TTATACTTGCCTTGGCTTT 45148	C	
	AAGGTTAAGGCAG TATGA		
	TTTCGGTTCCGTT ATATT		
	C		
GAM1929 LOC222161 5'	TCTTTTTGTAACACCTTAATTT 44582	CAGC	TG
T	AAGGTTAAGG TA AAGAGG		
	TTTTAATTCC AT TTTTCT		
	ACA_ GT		
GAM1929 LOC222178 3'	CCTGGAGTCATCTGTTTTGGTC 45189	GT	CT AG__
TT	AAG TAAGGCAG ATGA AGG		
	TTC GTTTTGTC TACT TCC		
	TG _ GAGG		
GAM1929 LOC222228 3'	CTTTTCATCCTAAATCTT 45276	A	CAGCT
	AAGGTT AGG ATGAAGAG		
	TTCTAA TCC TACTTTTC		
	A _		
GAM1929 LOC222233 3'	CTTTTCATCCTAAATCTT 45245	A	CAGCT
	AAGGTT AGG ATGAAGAG		
	TTCTAA TCC TACTTTTC		
	A _		
GAM1929 LOC222237 3'	TCTCTTTCATCTGCTTGACTTT 45271	G CT	_
	AAGGTTAAG CAG ATGAA GAGG		
	TTTCAGTTC GTC TACTT CTCT		
	_ _ T		
GAM1929 LOC222256 3'	TCTCTTCATGGTTATGTCT 45249	_	
	AGGCA GCTATGAAGAGG		

	TCTGT TGGTACTTCTCT	
	AT	
GAM1929 LOC253776 3'	TTTTATGATGCTTTGACCTT 46527	GC
	AAGGTTAAGGCA TATGAAG	
	TTCCAGTTTCGT GTATTTT	
	A_	
GAM1929 LOC253786 5'	TCTTGTTCTTAACCTT 46364	C TAT
	AAGGTTAAGG AGC GA	
	TTTCAATTCC TTG CT	
	_ TT_	
GAM1929 LOC253890 5'	TCTTTTCGAAGCTGTTAATTTT 45785	AG A
	AAGGTTA GCAGCT TGAAGAGG	
	TTTTAAT TGTCGA GCTTTTCT	
	_ A	
GAM1929 LOC254532 3'	TCTTTTCTGTGTTTTAAC 46215	GCTAT
	GTTAAGGCA GAAGAGG	
	CAATTTTGT CTTTCT	
	GT__	
GAM1929 LOC255045 3'	TTTCTTTATAGAGAAAGTACCT 46036	TAAGGCAG
T	AAGGT CTATGAAGAGG	
	TTCCA GATATTTCTTT	
	TGAAAGA_	
GAM1929 LOC255465 5'	CCTTTTACAGTTTTTGAAGT 46450	GC A
	AGGTTAAG AGCT TGAAGAGG	
	TTCAGTTT TTGA ATTTTCC	
	_ C	
GAM1929 LOC255515 3'	CTTTGACTGTTTTAGCTTT 45962	CTA
	AAGGTTAAGGCAG TGAAG	
	TTTCGATTTTGTC GTTTC	
	A_	
GAM1929 LOC255520 3'	TTTGAAATGGCTGTTTTTAAT 45882	_ GAAGAGG
TTT	AAGGTTAAGG CAGCTAT	
	TTTTAATTTT GTCGGTA	
	T AAGGTTT	
GAM1929 LOC256867 5'	TTTTTTTACCCCTCCTTAGCTT 45478	C CTA
T	AAGGTTAAGG AG TGAAGAGG	
	TTTCGATTCC TC ATTTTTTT	
	_ CCC	
GAM1929 LOC257017 5'	CCTTTCCTTTGTCTTGATCT 46493	CTAT A
	AGGTTAAGGCAG GA GAGG	

TCTAGTTCTGTT CT TTCC
 TC__ _
 GAM1929 LOC257017 5' TCTTTGTGGTAGTTTCCTTAGT 46499 GG C GA_
 TTT AA TTAAGG AGCTAT AGAGG
 || ||||| ||||| |||||
 TT GATTCC TTGATG TTTCT
 TT T GTG
 GAM1929 LOC51313 3' CTTTTTAGAAGCTGGCTTTAAC 18720 _ A_ G
 TTT AGGTTAAGGC AGCT TGAAGAG
 ||||| ||||| |||||
 TTCAATTCG TCGA ATTTTC
 G AG
 GAM1929 LOC51631 3' TTCTTCAGTCCTTAAGCTT 33769 G CAGCTA
 AAG TTAAGG TGAAGAG
 ||| ||||| |||||
 TTC AATTCC ACTTCTT
 G TG____
 GAM1929 LOC57149 3' CTTTTTTGTTGTCTTTTGACC 21682 _ TAT G
 GGTTA AGGCAGC GAAGAG
 ||||| ||||| |||||
 CCAGT TCTGTTG TTTTC
 TT T____
 GAM1929 LOC84549 3' TCTTTTCATGCTACCTTCAATC 26263 _ C T
 TT AAGGTT AAGG AGC ATGAAGAGG
 ||||| ||||| ||||| |||||
 TTCTAA TTCC TCG TACTTTTCT
 C A _
 GAM1929 LOC90309 5' CTTCTTTATGCCACTTAGGCTT 31152 G GCA T
 AAG TTAAG GC ATGAAGAGG
 ||| ||||| || |||||
 TTC GATTC CG TATTTCTTC
 G AC_ _
 GAM1929 LOC90624 3' TCTTTGTACTTTTAACTTT 31817 C C TG
 AAGGTTAAGG AG TA AAGA
 ||||| || || |||||
 TTTCAATTTT TC AT TTCT
 _ _ GT
 GAM1929 LOC91012 3' CTTTTTTGCCCTTGGCTCTT 32282 _ CA TAT
 AAG GTTAAGG GC GAAGAG
 ||| ||||| || |||||
 TTC CGGTTCC CG TTTTC
 T _ T____
 GAM1929 LOC91250 5' CCTTTTCATATACTTAATCT 32546 GCAGC
 AGGTTAAG TATGAAGAGG
 ||||| |||||
 TCTAATTC ATACTTTTC
 AT____
 GAM1929 LOC91300 5' TTCTTCATCGTTGAGCTTT 29007 AAGG T
 AAGGTT CAGC ATGAAGAG
 ||||| ||||| |||||

	TTTCGA GTTG TACTTCTT	
	_____ C	
GAM1929 LOC91300 5'	TTCTTCATCGTTGAGCTTT 45388	AAGG T
	AAGGTT CAGC ATGAAGAG	
	TTTCGA GTTG TACTTCTT	
	_____ C	
GAM1929 LOC91308 5'	TTTTTTCATGAACTTTAATC 32659	CAGC
	GGTTAAGG TATGAAGAGG	
	CTAATTTC GTACTTTTTT	
	AA__	
GAM1929 LOC92231 3'	TCTGGACTGTTTTAATTTT 34011	_ T
	AAGGTTAAGGCAG CTA GA	
	TTTTAATTTTGTC GGT CT	
	A _	
GAM1929 LOC92597 3'	CCTTTTCATATATTTATAACTT 34674	AGGCAGC
T	AAGGTTA TATGAAGAGG	
	TTTCAAT ATACTTTTCC	
	ATTTAT_	
GAM1930 C1orf34 3'	ATGTTCTACTTATGCACTGCC 30435	AT CC
	GGCA TGC GTG TAGAACAT	
	CCGT ACGTAT ATCTTGTA	
	C_ TC	
GAM1930 FLJ14106 3'	GTTCCAGGCACGCATCTA 24666	CAAT A
	TAGG TGC GTGCCT GAAC	
	ATCT ACGCACGGA CTTG	
	_____ C	
GAM1930 GENX-3414 3'	TGTTCTAAGACTGCCTA 10061	ATTGC GCC
	TAGGCA GT TAGAACA	
	ATCCGT CA ATCTTGT	
	_____ GA_	
GAM1930 SMCR5 3'	TGTTCCAGGCACTGTCCTA 29566	_ ATTGC A
	TAGG CA GTGCCT GAACA	
	ATCC GT CACGGA CTTGT	
	T _____ C	
GAM1930 SNPH 3'	ATGCTCCAACAGCCATTGCCTA 16288	T G CCTA A
	TAGGCAAT GC TG GA CAT	
	ATCCGTTA CG AC CT GTA	
	C _ AAC_ C	
GAM1930 LOC145845 3'	TCTAGGCATGCTGCC 40618	ATT
	GGCA GCGTGCCTAGA	

CCGT CGTACGGATCT

GAM1930 LOC146229 3' TCTAGAATCATATTGTCTA 38117 TGC GC
TAGGCAAT GT CTAGA
||||||| || |||||
ATCTGTTA TA GATCT
TAC A_

GAM1930 LOC148534 3' TTCAGACATGCAATCACCTA 38550 CA C A
TAGG ATTGCGTG CT GAA
||| ||||||| || |||
ATCC TAACGTAC GA CTT
AC A _

GAM1930 LOC151201 3' TTCTAAGCTGTCTTAATTGTCT 41326 _ T C
A TAGGCAATT GCG GC TAGAA
||||||| ||| || |||||
ATCTGTAA TGT CG ATCTT
TTC _ A

GAM1930 LOC152991 3' ATGTTCTGCTGTGATAACTGCC 41566 _ TG T CT
GGCA AT CG GC AGAACAT
||| || || || |||||
CCGT TA GT CG TCTTGTA
CAA GT _ _

GAM1930 LOC57406 3' TGTTCTAGACATCTGTCTA 21839 ATTGC C
TAGGCA GTG CTAGAACA
||||| ||| |||||
ATCTGT TAC GATCTTGT
C_ A

GAM1931 COL6A1 3' AGACCCTCGAGATTAACGGTGC 7584 CT_ CACTAT
TA TAGCACCG ATC GTCT
||||||| ||| |||||
ATCGTGGC TAG CAGA
AAT AGCTCC

GAM1931 HIP12 3' GAGACATAGCGGCCCGGGCGCT 32922 A_ CTAT A
G TAGC CCG CC CTATGTCTC
||| ||| || |||||
GTCG GGC GG GATACAGAG
CG CC_ C

GAM1931 SFRS1 3' GACTTAGGTGGGTAGCAATGC 13801 CC AT_
GCA GCTATCCACT GTC
||| ||||||| |||
CGT CGATGGGTGG CAG
AA ATT

GAM1931 FLJ20436 3' AGACACAGTGGATATTTTGGGC 19472 A C_ A
GC CCG TATCCACT TGTCT
|| ||| ||||||| |||||
CG GGT ATAGGTGA ACAGA
_ TTT C

GAM1931 KIAA1622 3' GAGACATAATGACAGCTGATGT 27766 C_ A CAC
TA TAGCA C GCT TC TATGTCTC
||||| ||| || |||||

ATTGT G CGA AG ATACAGAG
 A T C TA_
 GAM1931 ZNF212 3' GAGAGCAGGGGACACGGTGCTA 14557 CTA ACTA _
 TAGCACCG TCC TG TCTC
 ||||| || |||||
 ATCGTGGC AGG AC AGAG
 AC_ GG_ G
 GAM1931 LOC145761 5' GAGACACAGTGAAAAGGGGT 40584 G ATC A
 ACC CT CACT TGTCTC
 ||| || ||| |||||
 TGG GA GTGA ACAGAG
 G AAA C
 GAM1931 LOC146603 5' ACATAGTGGACAGCATTGT 38215 CC A
 GCA GCT TCCACTATGT
 ||| ||| |||||
 TGT CGA AGGTGATACA
 TA C
 GAM1931 LOC202986 3' GAGACATAACGATTTGGATTGC 43470 _ CT CAC
 TA TAGCA CCG ATC TATGTCTC
 |||| ||| ||| |||||
 ATCGT GGT TAG ATACAGAG
 TA T_ CA_
 GAM1931 LOC51312 5' GAAATATGGATAGCAGC 20659 ACC C G
 GC GCTATCCA TAT TC
 || ||||| ||| ||
 CG CGATAGGT ATA AG
 A_ _ A
 GAM1931 LOC57105 3' GAGATATAGCAACTAACGACGC 21639 AC C TCCA
 TA TAGC CG TA CTATGTCTC
 |||| ||| |||||
 ATCG GC AT GATATAGAG
 CA A CAAC
 GAM1932 B4GALT4 5' CCACGCAACACTTCCT 9858 G CATGCG
 AGGAAGTG TTGCG GG
 ||||| |||| ||
 TCCTTCAC AACGC CC
 _ A_
 GAM1932 GFPT2 3' GGCCACATCCCTCCACTTCT 11594 TTGCGC C
 GGAAGTGG ATG GGGCC
 ||||| ||| |||||
 TCTTCACC TAC CCCGG
 TCCC_ A
 GAM1932 SLC1A5 5' GCCCGCATCCCACCCTCC 12142 A_ TTGCGC
 GGA GTGG ATGCGGGC
 ||| |||| |||||
 CCT CACC TACGCCCG
 CC C_
 GAM1932 SLC1A5 5' GCCCGCATCCCACCCTCC 38402 A_ TTGCGC
 GGA GTGG ATGCGGGC
 ||| |||| |||||

			CCT CACC TACGCCCG		
			CC C_____		
GAM1932	HAPIP	3'	CTGGCAACAACCACTTCCT 10068	CGCA	G
			AGGAAGTGGTTG TGC GG		
			TCCTTCACCAAC ACG TC		
			A___ G		
GAM1932	KCNT1	3'	GCCCGACCACCACTTCCT 30974	TGCGCATG	
			AGGAAGTGGT CGGGC		
			TCCTTCACCA GCCCG		
			CCA_____		
GAM1932	KIAA0258	3'	GCCCGCATGCGTGCCTGCT 16648	TG TT	
			AG G GCGCATGCGGGC		
			TC C TGCGTACGCCCG		
			GT CG		
GAM1932	KIAA0514	3'	GCCCACATCCCACTTCCT 16208	TTGCGC	C
			AGGAAGTGG ATG GGGC		
			TCCTTCACC TAC CCCG		
			C_____ A		
GAM1932	KIAA1987	3'	GCACGCCACCACTTCCT 42498	T CA	
			AGGAAGTGGT GCG TGC		
			TCCTTCACCA CGC ACG		
			C _		
GAM1932	MGC15854	5'	GGCCCCACTCCACGACAACCAC 29644	_ CA_	C
			TTCC GGAAGTGGTTG CG TG GGGCC		
			CCTTCACCAAC GC AC CCCGG		
			A ACCTC _		
GAM1932	MGC16279	5'	GGCCCGCAGGTAACCACCTCCT 31487	A	GCA
			AGGA GTGGTTGC TGCGGGCC		
			TCCT CACCAATG ACGCCCGG		
			C G_		
GAM1932	MGC16279	5'	GGCCCGCGGGTAACCACCTCCT 26733	A	GCA
			AGGA GTGGTTGC TGCGGGCC		
			TCCT CACCAATG GCGCCCGG		
			C G_		
GAM1932	MYT1	5'	CCCGCACGCAGGCTTCC 10876	GG	CA
			GGAAGT TTGCG TGCGGG		
			CCTTCG GACGC ACGCCC		
			— —		
GAM1932	NY-REN-25	3'	GCCCGCATGCCCTAGACTCACT 30417	_ GC_	
			AGTG GTT GCATGCGGGC		

			TCAC CAG CGTACGCCCG		
			T ATCC		
GAM1932	PLAGL2	3'	GTACGCAGCCACCTCCT 34878	A	CA
			AGGA GTGGTTGCG TGC		
			TCCT CACCGACGC ATG		
			C _		
GAM1932	PRO0902	5'	CTGCGGGCCAACAGCAACCACT 27609		ATGCGG
		TCC	AAGTGGTTGC GC G		
			TTCACCAACG CG C		
			ACAAIIC GGC GTA		
GAM1932	SFXN2	3'	GCAATGCACAGCCACTTCC 36604	C	_
			GGAAGTGGTTG GCAT GC		
			CCTTCACCGAC CGTA CG		
			A A		
GAM1932	Ubc6p	3'	GCCCGCACGCGCTCATCTTTCT 27715	_ TT	A
			AGGAAG TGG GCGC TGC GGGC		
			TCTTTC ACT CGCG ACGCCCG		
			T _ C		
GAM1932	LOC157450	5'	GGCCCGCGGGTAACCACCTCCT 35148	A	GCA
			AGGA GTGGTTGC TGCGGGCC		
			TCCT CACCAATG GCGCCCGG		
			C G _		
GAM1932	LOC51336	5'	GCCCCTGGCAACCACCATCCT 18758	A _	G TGC
			AGGA GTGGTTGC CA GGGC		
			TCCT CACCAACG GT CCCG		
			AC _ C _		
GAM1932	LOC91409	3'	GCCCCTAAACCACTTCCT 32805		GCGCATGC
			AGGAAGTGGTT GGGC		
			TCCTTCACCAA CCCG		
			ATC _		
GAM1933	CDH8	5'	CACGTGGCAGAGCTGTAA 7550		CACGTG
			TTGCAGC GCCACGTG		
			AATGTCG CGGTGCAC		
			AGA _		
GAM1933	GRM7	3'	CACTGCCAACTTGGCTGCAA 6516	CG _	CAC
			TTGCAGCCA TGGC GTG		
			AACGTCGGT ACCG CAC		
			TCA T _		
GAM1933	MOCS1	3'	CACGTGGCCCTGAGCCACA 44186	CA _	CGT
			TG GC CA GGCCACGTG		

		AC CG GT CCGGTGCAC		
		AC A C__		
GAM1933	NEURL	3' CACATGGACAGGCTGCAG 10410	ACG G C	
		TTGCAGCC TG CCA GTG		
		GACGTCGG AC GGT CAC		
		__ A A		
GAM1933	RUNX1	3' CACTACTGTCCGTGGCTACAA 7495	C T CAC_	
		TTG AGCCACG GGC GTG		
		AAC TCGGTGC CTG CAC		
		A _ TCAT		
GAM1933	TRIM8	3' CACACCCCGTGGCTGGAA 25179	G T CCAC	
		TT CAGCCACG GG GTG		
		AA GTCGGTGC CC CAC		
		G _ CCA_		
GAM1933	ALDH5A1	3' CACGTGCCTGTGGCTGCAG 6740	T C	
		TTGCAGCCACG GGC ACGTG		
		GACGTCGGTGT CCG TGCAC		
		_ _		
GAM1933	C22orf20	3' GTGGCACACGGCTGTAA 24902	AC _	
		TTGCAGCC GTG GCCAC		
		AATGTCGG CAC CGGTG		
		_ A		
GAM1933	FLJ22969	3' CACGTGGCCATTTTCCTTCAA 34064	C CCAC	
		TTG AG GTGGCCACGTG		
		AAC TC TACCGGTGCAC		
		T CTTT		
GAM1933	KIAA0441	3' CATGTGGCTAGTGGCTGC 16707	G	
		GCAGCCAC TGGCCACGTG		
		CGTCGGTG ATCGGTGTAC		
		_		
GAM1933	KIAA1265	3' CATGTCGTGGCTGGCTACAA 35031	C C G C	
		TTG AGCCA GT GC ACGTG		
		AAC TCGGT CG TG TGTAC		
		A _ G C		
GAM1933	KIAA1789	5' CATGTGGCCTGTGGGCTGCAA 33309	_ T	
		TTGCAGCC ACG GGCCACGTG		
		AACGTCGG TGT CCGGTGTAC		
		G _		
GAM1933	NFASC	3' CACGTAGACAGGCTGTAA 34827	ACG GCC	
		TTGCAGCC TG ACGTG		

		AATGTCGG AC TGCAC	
		___ AGA	
GAM1933	PMX2B	3' ACGTAACTGGCTGCAG 10013	C GGCC
		TTGCAGCCA GT ACGT	
		GACGTCGGT CA TGCA	
		_ A__	
GAM1933	PPP1R16B	3' CACGTACCATTGGCTGTAA 30766	C CC
		TTGCAGCCA GTGG ACGTG	
		AATGTCGGT TACC TGCAC	
		_ A_	
GAM1933	LOC146138	3' CACGTGGCCAACCTGCCGCAA 40653	A CACG
		TTGC GC TGGCCACGTG	
		AACG CG ACCGGTGCAC	
		C TCCA	
GAM1933	LOC146332	3' CACAGGTACAGGTGGCTGCAG 38127	G _ AC
		TTGCAGCCAC TG GCC GTG	
		GACGTCGGTG AC TGG CAC	
		G A A_	
GAM1933	LOC150311	5' CGCGTAAGCTAGGGCTGCAA 38927	ACG C_
		TTGCAGCC TGGC ACGTG	
		AACGTCGG ATCG TGCGC	
		G__ AA	
GAM1933	LOC150383	3' CACTGTAGGTGGCTGCAA 38944	G GC C
		TTGCAGCCAC TG CA GTG	
		AACGTCGGTG AT GT CAC	
		G __ _	
GAM1933	LOC154449	5' CACGTGGTGAGGCTGCA 39474	A GTG
		TGCAGCC C GCCACGTG	
		ACGTCGG G TGGTGCAC	
		A __	
GAM1933	LOC158654	5' CACAGCCTTCTGGCTGCAA 39875	CGT CAC
		TTGCAGCCA GGC GTG	
		AACGTCGGT CCG CAC	
		CTT A__	
GAM1933	LOC253443	3' CACGTGGCCAAGGCCCGCAG 45883	A__ ACG
		TTGC GCC TGGCCACGTG	
		GACG CGG ACCGGTGCAC	
		CCC A__	
GAM1933	LOC255388	5' CACAGCTGGCTCGTGGCTG 46418	T C__
		CAGCCACG GGCCA GTG	

		GTCGGTGC TCGGT CAC	
		— CGA	
GAM1933	LOC256310 3'	CACGTAGGCTCAGGTGGCTGCA 46095	G _ _
	G	TTGCAGCCAC TG GCC ACGTG	
		GACGTCGGTG AC CGG TGCAC	
		G T A	
GAM1933	LOC51701 3'	CACGTGAGCTGATCGTGGCTGC 18345	T__ _
	A	TGCAGCCACG GGC CACGTG	
		ACGTCGGTGC TCG GTGCAC	
		TAG A	
GAM1934	ACADSB 3'	GGCATCTGAAGTACAAT 7315	CCCGGA
		GTTGTACT AGATGCC	
		TAACATGA TCTACGG	
		AG__	
GAM1934	PPP1R3A 3'	AGGGCAAAGTCAATGAGTACAA 8563	CCG AGA
	CT	AGTTGTACTC GA TGCCCT	
		TCAACATGAG CT ACGGGA	
		TAA GAA	
GAM1934	DKFZP564C103 3'	AGGGCATCTTCCAGGTGGGGAA 17900	GTA _ _
	AC	GTT CTC CC GGAAGATGCCCT	
		CAA GGG GG CCTTCTACGGGA	
		AG_ T A	
GAM1934	FLJ22479 3'	AGAGCATCTTCCACATCAACT 24384	TACTCCC C
		AGTTG GGAAGATGC CT	
		TCAAC CCTTCTACG GA	
		TACA__ A	
GAM1934	GDAP2 3'	AGAGCATCTTCCAAGACTCCAG 19239	TAC CC C
	C	GTTG TC GGAAGATGC CT	
		CGAC AG CCTTCTACG GA	
		CTC AA A	
GAM1934	KIAA1317 5'	TATTTTCCAAGAGCACACCT 41629	T A CC
		AG TGT CTC GGAAGATG	
		TC ACA GAG CCTTTTAT	
		C C AA	
GAM1934	MAGEB1 5'	ATCATCCAGGAGTACAAC 8174	C A
		AGTTGTACTCC GGA GAT	
		TCAACATGAGG CCT CTA	
		A A	
GAM1934	MISS 3'	AGGGCATTTCATGAAAGAACAAC 29382	A CC GAA
	T	AGTTGT CT CG GATGCCCT	

	TCAACA GA GT TTACGGGA	
	A AA AC_	
GAM1934 LOC126669 3'	AGGGCATCATCAGCGCACAAC 37156	ACTCCCG A
	GTTGT GA GATGCCCT	
	CAACA CT CTACGGGA	
	CGCGA_ A	
GAM1934 LOC149670 3'	GGGCATCCTTGGGCCAACT 38805	TACT AA
	AGTTG CCCGG GATGCCC	
	TCAAC GGGTT CTACGGG	
	C_ C_	
GAM1934 LOC150174 5'	AGGGCATCCTCCAGCTCAGC 38870	TA CCC A
	GTTG CT GGA GATGCCCT	
	CGAC GA CCT CTACGGGA	
	TC _ C	
GAM1934 LOC153894 3'	AGGGCATTTCATGAAAGAACAAC 39426	A CC GAA
T	AGTTGT CT CG GATGCCCT	
	TCAACA GA GT TTACGGGA	
	A AA AC_	
GAM1934 LOC161357 3'	CATCATGGAAGTATAACT 40018	C GAA
	AGTTGTACT CCG GATG	
	TCAATATGA GGT CTAC	
	A A_	
GAM1934 LOC255452 3'	AGGGCATCCCCCAGACTCAACT 46571	TAC CC AA
	AGTTG TC GG GATGCCCT	
	TCAAC AG CC CTACGGGA	
	TC_ A_ CC	
GAM1934 LOC51652 3'	AGGAGCTGACCAGGAGCACACT 18151	T A C AAGAT _
	AGT GT CTCC GG GC CCT	
	TCA CA GAGG CC CG GGA	
	_ C A AGT_ A	
GAM1935 CA12 3'	CGGAGCTCCCGGGCACATC 6880	_____
	GATGTGCCTG GCTCTG	
	CTACACGGGC CGAGGC	
	CCT	
GAM1935 CLTCL1 3'	GCAGAGCAGGCACACCT 31836	A G
	AG TGTGCCTG CTCTGT	
	TC ACACGGAC GAGACG	
	C _	
GAM1935 CSNK1G3 3'	TCTGGACACAGACAGATC 10612	G C GCTC
	GAT TG CTG TGTCCAGA	

CTA AC GAC ACAGGTCT
 G A ____
 GAM1935 EBAF 3' TTCTGGACTTTTGTAAACATAC 32610 A CCTG TCT_
 CT AG TGTG GC GTCCAGAA
 || ||| || |||||
 TC ATAC TG CAGGTCTT
 C AAA_ TTTT
 GAM1935 GLP1R 3' GACAGAGCCGCAAATC 7824 G CT
 GAT TGC GGCTCTGTC
 ||| ||| |||||
 CTA ACG CCGAGACAG
 A ____
 GAM1935 IL10RA 3' TTCTGGACACTCAAACACATC 30000 CC CTC
 GATGTG TGG TGTCCAGAA
 ||||| ||| |||||
 CTACAC ACT ACAGGTCTT
 AA C____
 GAM1935 MPL 3' CTGGACAGAGCTAAACTCT 11850 T GCC
 AGA GT TGGCTCTGTCCAG
 ||| || |||||
 TCT CA ATCGAGACAGGTC
 _ A____
 GAM1935 ARNTL2 3' TCTGATTCCAGGCACTCT 21418 T CTCT C
 AGA GTGCCTGG GTC AGA
 ||| ||||| ||| |||
 TCT CACGGACC TAG TCT
 _ T_____
 GAM1935 BCL2L1 3' CTGCCTGGCCAGGCAGATCT 28894 G CTGTC
 AGAT TGCCTGGCT CAG
 |||| ||||| |||
 TCTA ACGGACCGG GTC
 G TCC____
 GAM1935 CSNK1G1 3' TTCTGGACAAAAGTCACATAT 22570 CC C_
 ATGTG TGGCT TGTCCAGAA
 |||| |||| |||||
 TATAC ACTGA ACAGGTCTT
 _ AA
 GAM1935 DKFZP566G1424 5' TCTGGTCAGGGCCAGGACAC 41117 _ T
 GTG CCTGGCTCTG CCAGA
 ||| ||||| |||||
 CAC GGACCGGGAC GGTCT
 A T
 GAM1935 DKFZp586I021 3' CTGGAGAGGGGGCCAGGCACA 26025 G_
 TGTGCCTGGCTCT TCCAG
 ||||| |||||
 ACACGGACCGGGG AGGTC
 GAG
 GAM1935 FLJ12547 3' CTGTCCAGAACCCCGACAGGCA 24549 GC_____ GTCC
 CATC TGTGCCTG TCT AG
 ||||| ||| ||

ACACGGAC AGA TC
 AGCCCCIIIA CCTG
 GAM1935 FLJ20281 5' TCTGGACATGACACAT 43729 CCTGGC _
 ATGTG TC TGTCCAGA
 |||| | |||||
 TACAC AG ACAGGTCT
 _____ T
 GAM1935 FLJ22341 3' CTGACCCAAGCTCAGGCACA 23848 _ CT_ C
 TGTGCCTG GCT GTC AG
 ||||| || ||||
 ACACGGAC CGA CAG TC
 T ACC _
 GAM1935 HEMK 3' TCAGGGAAAGCCAGGCCACCT 18271 A T CTG A
 AG TG GCCTGGCT TCC GA
 || ||||| ||||
 TC AC CGGACCGA GGG CT
 C C AA_ A
 GAM1935 KCND1 5' TCTAGACGCCCCAGACACCTC 11427 T C CTC C
 T
 AGA GTG CTGG TGTC AGA
 || || || || || || ||
 TCT CAC GACC GCAG TCT
 C A CCC A
 GAM1935 KIAA0939 3' CTGGGCTAGAGCAAGCACATCT 31063 CTG _
 AGATGTGC GCTCT GTCCAG
 ||||| |||| |||||
 TCTACACG CGAGA CGGGTC
 AA_ T
 GAM1935 KIAA1199 3' CAGAGTGCCCAGGCACTCCT 35899 AT _
 AG GTGCCTGG CTCTG
 || ||||| ||||
 TC CACGGACC GAGAC
 CT CGT
 GAM1935 KIAA1280 5' CTAGACAGACTGCGGGCACA 34550 GC_ C
 TGTGCCTG TCTGTC AG
 ||||| |||| ||
 ACACGGGC AGACAG TC
 GTC A
 GAM1935 KLHL6 3' TCTGTGCCAGGCACTTC 28214 T TCTGTC
 GA GTGCCTGGC CAGA
 || ||||| ||||
 CT CACGGACCG GTCT
 T T_____
 GAM1935 KPNA6 3' TCTGGACAGACAGAACCATCT 14690 TGC GC
 AGATG CTG TCTGTCCAGA
 |||| || |||||
 TCTAC GAC AGACAGGTCT
 CAA _
 GAM1935 MBLL39 3' TCTGGACAGACCACAAC 12319 GCC C
 GT TGG TCTGTCCAGA
 || || |||||

			CA ACC AGACAGGTCT			
			AC_ _			
GAM1935	MBLL39	3'	TCTGGACAGACCACAAC	29576	GCC C	
			GT TGG TCTGTCCAGA			
			CA ACC AGACAGGTCT			
			AC_ _			
GAM1935	MED8	5'	TTCTGGACAGCTGAACACTCT	27457	T CC CT	
			AGA GTG TGGCT GTCCAGAA			
			TCT CAC GTCGA CAGGTCTT			
			_ AA _			
GAM1935	P66	3'	CTGGGAGCCAGGCCACCT	21846	A T TGT	
			AG TG GCCTGGCTC CCAG			
			TC AC CGGACCGAG GGTC			
			C _ _			
GAM1935	SIAT4B	5'	CTGGCAGCCAGGCAATC	13813	G CT T	
			GAT TGCCTGGCT G CCAG			
			CTA ACGGACCGA C GGTC			
			_ _ _			
GAM1935	SSB-4	3'	TCTGGATGCCCAGACACCTCT	28105	T C CTC	
			AGA GTG CTGG TGTCCAGA			
			TCT CAC GACC GTAGGTCT			
			C A C_			
GAM1935	UBE3B	3'	GACAGCCAGGCCCATCT	37774	T CT	
			AGATG GCCTGGCT GTC			
			TCTAC CGGACCGA CAG			
			C _			
GAM1935	LOC129198	3'	TTCCAGACAGAACCAGTGTACA	37466	_ C CA	
		TCT	AGATGTGC CTGG TCTGTC GAA			
			TCTACATG GACC AGACAG CTT			
			T A AC			
GAM1935	LOC158972	3'	CTGATACATGGAACAGGCACAT	42044	GC _ C_	
		CT	AGATGTGCCTG TC TGT CAG			
			TCTACACGGAC GG ACA GTC			
			AA T TA			
GAM1935	LOC164395	5'	TCTGCTGGGACCAGGCACAACT	40146	A _ TGTC	
			AG TGTGCCTGG CTC CAGA			
			TC ACACGGACC GGG GTCT			
			A A TC_			
GAM1935	LOC200261	3'	GACCCGCCAGGCACACCT	42750	A TCT	
			AG TGTGCCTGGC GTC			

TC ACACGGACCG CAG
 C CC_
 GAM1935 LOC221683 5' TCAGGGAGAGCCAAGCACATTT 45006 C G A
 AGATGTGC TGGCTCT TCC GA
 ||||| ||||| || ||
 TTTACACG ACCGAGA GGG CT
 A _ A
 GAM1935 LOC254428 3' TCTGGACAGGAGACAC 45720 C GGC
 GTG CT TCTGTCCAGA
 ||| || |||||
 CAC GA GGACAGGTCT
 A ____
 GAM1935 LOC84549 3' TTCCAGACTTGGTCAGGCACAT 26264 CT CA
 ATGTGCCTGGCT GTC GAA
 ||||| || |||
 TACACGGA CTG CAG CTT
 TT AC
 GAM1935 LOC91056 3' TTCCAGACAGAACCCGGCAC 45440 T C CA
 GTGCC GG TCTGTC GAA
 |||| || ||||| |||
 CACGG CC AGACAG CTT
 C A AC
 GAM1936 ADRB3 3' TCTACCTTCCCACTCACCT 5463 G CAC T
 AGGTG AGTGGGA AG TAGA
 |||| ||||| || ||||
 TCCAC TCACCCT TC ATCT
 _ _ C
 GAM1936 HSF4 5' TCTACCCCCACCCACC 30067 A ACACA T
 GGTGG GTGGG GT AGA
 |||| |||| || |||
 CCACC CACCC CA TCT
 C _ _ C
 GAM1936 SLC17A7 3' CTAAAGGTTCCCTCTCCACC 21557 T C AG
 GGTGGAG GGGA AC TTAG
 ||||| |||| || ||||
 CCACCTC CCCT TG AATC
 T _ GA
 GAM1936 SLC7A5 3' CTGTGTGCCCCACTCCAGCCT 9577 _ _
 AGG TGGAGTGGG ACACAG
 || ||||| |||||
 TCC ACCTCACCC TGTGTC
 G CG
 GAM1936 CDCA4 3' CTAGGCCCGTCCCACTCACCT 19662 G ACAG
 AGGTG AGTGGGAC TTAG
 |||| ||||| ||||
 TCCAC TCACCCTG GATC
 _ CCG
 GAM1936 CTPS2 3' CTATCTTCCCCTCCACCT 21263 T CAC T
 AGGTGGAG GGGA AG TAG
 ||||| |||| || |||

TCCACCTC CCCT TC ATC
 _ _ _ T
 GAM1936 dJ309H15.1 3' CTCTAGACACCCCTCTCCACC 28887 T ACACAG
 GGTGGAG GGG TTAGAG
 ||||| ||| |||||
 CCACCTC CCC GATCTC
 T CACA_

GAM1936 DKFZP434C171 3' CTCTAGGTGTTTCCACTCCACC 17884 C G
 GGTGGAGTGGGA ACA TTAGAG
 ||||| ||| |||||
 CCACCTCACCTT TGT GATCTC
 _ G

GAM1936 DKFZP727C091 3' CTATCCCCTCCCCT 32903 T CACAGT
 AGG GGAGTGGGA TAG
 ||| ||||| |||
 TCC CCTCACCT ATC
 _ T_

GAM1936 HSA243666 3' CTCTAACTCTACCCACACCCAC 19020 A_ ACAC
 CT AGGTGG GTGGG AGTTAGAG
 ||||| ||||| |||||
 TCCACC CACCC TCAATCTC
 CA ATC_

GAM1936 KIAA0237 3' CTCTGGGAACCCACCCCACT 16446 A ACACAG
 GGTGG GTGGG TTAGAG
 ||||| ||||| |||||
 TCACC CACCC GGTCTC
 C CAAG_

GAM1936 KIAA0953 3' CTAAGTGTGCCCTCGACCACTT 33167 AGT_ A
 AGGTGG GGG CACAGTTAG
 ||||| ||| |||||
 TTCACC CCC GTGTCAATC
 AGCT _

GAM1936 KIAA1191 3' TTGCATCCCCTCCCCT 21685 T CA
 AGG GGAGTGGGA CAG
 ||| ||||| |||
 TCC CCTCACCT GTT
 _ AC

GAM1936 KIAA1719 3' TCTAACTAATACCCCT 33824 T A GGACAC
 AGG GG GTG AGTTAGA
 ||| ||| |||||
 TCC CC CAT TCAATCT
 _ C AA_

GAM1936 KIAA1853 5' CTCCGATCTCTCCCACCCACC 34388 A CACA TA
 GGTGG GTGGGA GT GAG
 ||||| ||||| ||| |||
 CCACC CACCT TA CTC
 C CTC_ GC

GAM1936 KIAA1922 5' CTGATCCACTCCACCT 36454 ACA
 AGGTGGAGTGGG CAG
 ||||| |||

TCCACCTCACCT GTC
 A__
 GAM1936 RAI17 3' CTGCATCCTACCCACCT 43860 A CA
 AGGTGG GTGGGA CAG
 ||||| ||||| ||
 TCCACC CATCCT GTC
 C AC
 GAM1936 SCYA5 3' CTCACTATCCTACCCACC 8882 A CAC T
 GGTGG GTGGGA AGT AG
 ||||| ||||| ||| ||
 CCACC CATCCT TCA TC
 C A__ C
 GAM1936 STK39 3' CTGTCATGCCCCACCGCCACC 14893 A_ A____
 GGTGG GTGGG C ACAG
 ||||| ||||| | ||||
 CCACC CACCC G TGTC
 GC C TAC
 GAM1936 TIAF1 3' CTCCAGCCCCCACCACCCACC 27799 A ACACA A
 GGTGG GTGGG GTT GAG
 ||||| ||||| ||| ||||
 CCACC CACCC CGA CTC
 C C____ C
 GAM1936 LOC113763 3' AACTACACCCCGCCTCCCCT 28799 T _ ACAC
 AGG GGAG TGGG AGTT
 ||| |||| |||| ||||
 TCC CCTC GCCC TCAA
 _ C CACA
 GAM1936 LOC138389 5' CTACTTCCCTCTCCACCT 37505 T CAC T
 AGGTGGAG GGGA AGT AG
 ||||| |||| ||| ||
 TCCACCTC CCCT TCA TC
 T ____ _
 GAM1936 LOC144465 3' CTCTGCAGTGTCCCATCCACC 37752 G A T
 GGTGGA TGGGACAC GT AGAG
 ||||| ||||| || ||||
 CCACCT ACCCTGTG CG TCTC
 _ A _
 GAM1936 LOC146346 5' TCTAACTGCACCCCTTC 38138 T ACA
 GGAG GGG CAGTTAGA
 |||| ||| ||||| ||
 CTTC CCC GTCAATCT
 _ AC_
 GAM1936 LOC151176 3' CTAACCGTGTCTACCT 41316 A A
 GG GTGGGACAC GTTAG
 || ||||| ||||| ||||
 TC CATCTTGTG CAATC
 _ C
 GAM1936 LOC163782 3' AGCGTGTCCCACTCCAAC 39963 G A
 AG TGGAGTGGGACAC GTT
 || ||||| ||||| ||||

		TC ACCTCACCCCTGTG CGA		
		A _		
GAM1936	LOC200953 5'	TTAGCCCCCTCCACCT 43369	T	ACACA
		AGGTGGAG GGG GTTAG		
		TCCACCTC CCC CGATT		
		_ C _		
GAM1936	LOC220846 3'	TCTACCTTCCCACTCACCT 43664	G	CAC T
		AGGTG AGTGGGA AG TAGA		
		TCCAC TCACCCT TC ATCT		
		_ _ C		
GAM1936	LOC257000 3'	CTCCAAGTGTGCCCCATTTCCA 46274	_	A A
	CC	GGTGGAG TGGG CACAGTT GAG		
		CCACCTT ACCC GTGTCAA CTC		
		T C C		
GAM1936	LOC92080 5'	AACCCTGTCCACCCCACC 33755	A	CA
		GGTGG GTGGGACA GTT		
		CCACC CACCCTGT CAA		
		C CC		
GAM1937	RANBP3 5'	TCCAGCGGCGCGCTGCTAGTGA 14238		ACAACC
		TCACTGGCAGCGTG GGA		
		AGTGATCGTCGCGC CCT		
		GGCGA_		
GAM1937	TIM3 3'	CCAAGTGTGAGTGCCAGTG 26523	G G	ACC
		CACTGGCA C TGACA GG		
		GTGACCGT G ACTGT CC		
		_ _ CAA		
GAM1937	ALK7 5'	CCGGCTGCGGGGCCAGTGG 37295	AG	ACAA
		TCACTGGC CGTG CCGG		
		GGTGACCG GCGT GGCC		
		GG C_		
GAM1937	C3F 3'	TCCAGCTGTGCCTCTGCTGCCA 12332	T	CA_ C_
	G	CTGGCAGCG GA AC GGA		
		GACCGTCGT CT TG CCT		
		_ CCG TCGA		
GAM1937	DKFZP434N014 5'	TCCAGCTGTGCGGCCAGT 30390	AGC	ACC
		ACTGGC GTGACA GGA		
		TGACCG CGCTGT CCT		
		_ CGA		
GAM1937	FLJ11565 3'	TGGCCACACTGTCAGTGA 23961	C	A_
		TCACTGGCAG GTG CA		

		AGTGACTGTC CAC GT		
		A CG		
GAM1937	FLJ14775	3' TCCAATTCAGACTGTCA GTGA	26618	CG CAACC
		TC ACTGGCAG TGA GGA		
		AGTGACTGTC ACT CCT		
		AG TAA__		
GAM1937	FLJ20174	3' TCCAGTTGTCACCCTGCCCAG	19271	_ C C
		CTGG CAG GTGACAAC GGA		
		GACC GTC CACTGTTG CCT		
		C C A		
GAM1937	KIAA0620	3' TCCAGTTGGTCCTGCTGCCA	31124	T _ C
		TGGCAGCG GAC AAC GGA		
		ACCGTCGT CTG TTG CCT		
		C G A		
GAM1937	MAP3K2	3' TCCGGTTGTCACAATTGGAGGG	13388	A GG C_
	A	TC CT CAG GTGACAACCGGA		
		AG GG GTT CACTGTTGGCCT		
		_ AG AA		
GAM1937	NXPH3	3' CTGACCACATGCCAGTGA	32719	GC ACAAC
		TC ACTGGCA GTG CGG		
		AGTGACCGT CAC GTC		
		A_ CA__		
GAM1937	STARD7	5' CCGGCGTCTGCTGCCATGA	21356	C T AA
		TCA TGGCAGCG GAC CCGG		
		AGT ACCGTCGT CTG GGCC		
		_ _ C_		
GAM1937	TREX1	5' CCGCCACTGCTGCCAGCGA	18520	A _ ACAAC
		TC CTGGCAGC GTG CGG		
		AG GACCGTCG CAC GCC		
		C T C__		
GAM1937	TREX1	5' CCGCCACTGCTGCCAGCGA	27345	A _ ACAAC
		TC CTGGCAGC GTG CGG		
		AG GACCGTCG CAC GCC		
		C T C__		
GAM1937	TREX1	5' CCGCCACTGCTGCCAGCGA	27336	A _ ACAAC
		TC CTGGCAGC GTG CGG		
		AG GACCGTCG CAC GCC		
		C T C__		
GAM1937	LOC145566	5' TCCAGTTGAATGCTGGCCAGTG	37900	_ GA C
	A	TC ACTGGC AGCGT CAAC GGA		

			AGTGACCG TCGTA GTTG CCT		
			G A_ A		
GAM1937	LOC149373	3'	TCCTGCTCACACTGCCAG 38720	C _ ACC	
			CTGGCAG GTGA CA GGA		
			GACCGTC CACT GT CCT		
			A C _		
GAM1937	LOC149668	5'	TCCGGCTGTCATGTCCTGTGA 41031	T CA A	
			TCAC GG GCGTGACA CCGGA		
			AGTG CC TGTACTGT GGCCT		
			T _ C		
GAM1938	CDK2	3'	CAAGTAAAACAAAACCACTGG 7553	C_	
			TCAGTGGTTTTGTTT CTTG		
			GGTCACCAAAACAAA GAAC		
			AT		
GAM1938	ZNF83	3'	TTGAGAGAAACAAAACACTGA 20293	G _ TG	
			TCAGTG TTTTGTTTC CT A		
			AGTCAC AAAACAAAG GA T		
			A A GT		
GAM1938	BIRC1	3'	CAAAAAACAAAACCACT 10881	CC	
			AGTGGTTTTGTTT TTG		
			TCACCAAAACAAA AAC		
			A_		
GAM1938	FLJ20651	3'	CAAGGAGAAAAAAACCAC 19574	G_	
			GTGGTTTT TTTCTTG		
			CACCAAAA AGAGGAAC		
			AA		
GAM1938	KIAA0391	3'	GTTTAGAAACAAAACCCT 16140	T CTT	
			AG GGTTTTGTTTC GAT		
			TC CAAAACAAAG TTG		
			_ AT_		
GAM1938	LATS1	3'	TATCAAGGACCACCACCAC 30238	TT TT	
			GTGGT TG TCCTTGATA		
			CACCA AC AGGAACTAT		
			CC C_		
GAM1938	MGC2452	5'	TTAAATAACAAAACCACT 26375	TCC	
			AGTGGTTTTGTT TTGA		
			TCACCAAAACAA AATT		
			TA_		
GAM1938	LOC144473	5'	TACCAAGAACCACCACTGG 40414	TTT TC A	
			TCAGTGGT GTT CTTG TA		

		GGTCACCA CAA GAAC AT		
		C__ _ C		
GAM1939	KCND1	5' CTTATTTAGTCTTCATAGATC 11423		CATA
		GATCTGT ACTAAATAAG		
		CTAGATA TGATTTATTC		
		CTTC		
GAM1939	LOC122553	3' AGTCAGTGACAGACCTCA 36686	A	A_
		TGAG TCTGTCAT ACT		
		ACTC AGACAGTG TGA		
		C AC		
GAM1939	LOC157869	3' CTTATCATGTAATGACAGATTC 39676	A	A TAA
	A	TGAG TCTGTCAT AC ATAAG		
		ACTT AGACAGTA TG TATTC		
		_ A TAC		
GAM1940	CLECSF5	3' TCATATTTTTTTATTACAACACT 14923	-	-
	AA	TTAGTGTT TAATAAAAA TATGG		
		AATCACAA ATTATTTTT ATACT		
		C T		
GAM1940	IL21R	3' CCCAAGAGATATTTATTAAACA 22354	A	A__
	C	GTGTTTAATAAA AT TGGG		
		CACAAATTATTT TA ACCC		
		A GAGA		
GAM1940	KERA	3' TCCATAGCTTATTAACACTAA 13910	T	AAA
		TTAGTGTT AATAA TATGGG		
		AATCACAA TTATT ATACCT		
		_ CG_		
GAM1940	YES1	3' CCCAAGTATTAAACTCTAA 11913	T	AAAATA
		TTAG GTTTAATA TGGG		
		AATC CAAATTAT ACCC		
		T GA__		
GAM1940	LOC200059	3' ATTTTTTTTAAACACTAA 42700	T	
		TTAGTGTTTAA AAAAAT		
		AATCACAAATT TTTTAA		
		-		
GAM1941	ADAT1	3' ACCTAGAGAAAGCCAGCAAA 14381	ATCAG	A
		TTTGTTGG TCTCTA GT		
		AAACGACC AGAGAT CA		
		GAA__ C		
GAM1941	NBS1	3' ACTCTGGTGATCCAAACAAA 34433	_	GTC TA
		TTTGTT GGATCA TC AGT		

AAACAA CCTAGT GG TCA
 A ____ TC
 GAM1941 NCOA3 5' CTCAGAGACCAATAAA 13285 ATCAG A
 TTTGTTGG TCTCT AG
 ||||| |||||
 AAATAACC AGAGA TC
 ____ C
 GAM1941 PPP1R2 3' ACTTAGAGACTGATTAGAC 12906 G
 GTT GATCAGTCTCTAAGT
 ||| |||||
 CAG TTAGTCAGAGATTCA
 A
 GAM1941 SLC10A2 5' ACTTAACTGAAATTATCCAACA 6062 ____ CTC
 AA TTTGTTGGA TCAGT TAAGT
 ||||| |||||
 AAACAACCT AGTCA ATTCA
 ATTAA ____
 GAM1941 SLC10A2 5' ACTTAACTGAAATTATCCAACA 6061 ____ CTC
 AA TTTGTTGGA TCAGT TAAGT
 ||||| |||||
 AAACAACCT AGTCA ATTCA
 ATTAA ____
 GAM1941 SLC38A2 3' ACTTGTTTACATCCAACAAA 21048 CA CTC
 TTTGTTGGAT GT TAAGT
 ||||| || |||||
 AAACAACCTA CA GTTCA
 ____ TTT
 GAM1941 ZNF141 3' TTTGGATGATCCACAAA 9498 T GTC
 TTTGT GGATCA TCTAAG
 ||||| |||||
 AAACA CCTAGT AGGTTT

 GAM1941 CREG 3' ACTTAACTGAGATCCAGCAAA 9946 ____ CTC
 TTTGTTGGA TCAGT TAAGT
 ||||| |||||
 AAACGACCT AGTCA ATTCA
 AG ____
 GAM1941 KIAA0349 3' ACTTAGAGGGCTTTCCAA 44339 TC _
 TTGGA AGTC TCTAAGT
 ||||| |||||
 AACCT TCGG AGATTCA
 T_ G
 GAM1941 LOC153743 3' ACTTAGAGACTAATTAGAC 30348 G C
 GTT GAT AGTCTCTAAGT
 ||| ||| |||||
 CAG TTA TCAGAGATTCA
 A A
 GAM1941 LOC200227 3' GCTTGCTGATCCAACAAA 42747 CTCT
 TTTGTTGGATCAGT AAGT
 ||||| |||||

AAACAACCTAGTCG TTCG

GAM1942 CDKN1A 3' GCGACCTTCCTCATCCAC 27782 AAT TTCC A
GTG TGA GGAAG TCGC
||| ||| ||||| |||||
CAC ACT CCTTC AGCG
CT_ _ _ C

GAM1942 PIP5K1C 3' AGCGACCTTGGCCTCAGTTCAC 35014 TT GA A
GTGAATTGA CCG AG TCGCT
||||||| ||| || |||||
CACTTGACT GGT TC AGCGA
CC _ _ C

GAM1942 LOC253792 5' CGATCTTCCGGAAGACAC 46430 AATTGA
GTG TTCCGGAAGATCG
||| ||||| ||||| |||||
CAC AAGGCCTTCTAGC
AG_ _ _

GAM1943 PRKAR2B 3' ACATAAGATGAATTTAATTATA 8610 _ G _
TTCA TGAATATA TTAAA TTATTT ATGT
||||||| ||||| ||||| |||||
ACTTATAT AATTT AGTAGA TACA
T A A

GAM1944 OGN 3' TCACTTGTACCCCACTA 15276 A AC
TAGTG GG ACAAGTGA
||||| || ||||| |||||
ATCAC CC TGTTCACT
_ CA

GAM1944 OGN 3' TCACTTGTACCCCACTA 23656 A AC
TAGTG GG ACAAGTGA
||||| || ||||| |||||
ATCAC CC TGTTCACT
_ CA

GAM1944 OGN 3' TCACTTGTACCCCACTA 26900 A AC
TAGTG GG ACAAGTGA
||||| || ||||| |||||
ATCAC CC TGTTCACT
_ CA

GAM1944 CNOT7 5' CTTGTGCCCTCACTATGC 27634 A
GCGTAGTGAGG CACAAG
||||||| ||||| |||||
CGTATCACTCC GTGTTC
C

GAM1944 CNOT7 5' CTTGTGCCCTCACTATGC 15001 A
GCGTAGTGAGG CACAAG
||||||| ||||| |||||
CGTATCACTCC GTGTTC
C

GAM1944 DIM1 3' TCACCTGTGTCCTCCCTG 13526 T A
TAG GAGGACACA GTGA
||| ||||| ||||| |||||

GTC CTCCTGTGT CACT
 C C
 GAM1944 DKFZp434F142 3' TTCACAGTGGCCTCACTACGC 25998 A AA
 GCGTAGTGAGG CAC GTGAA
 ||||| ||| ||||
 CGCATCACTCC GTG CACTT
 G A_

GAM1944 FLJ13769 3' TTCACCTGTGTCCTCTGC 24597 TAGT A
 GCG GAGGACACA GTGAA
 || ||||| ||||
 CGT CTCCTGTGT CACTT
 C

GAM1944 KIAA0750 5' TTCACCTGTGTCCTCGCCGC 16000 TA A
 GCG GTGAGGACACA GTGAA
 || ||||| ||||
 CGC CGCTCCTGTGT CACTT
 C

GAM1944 SP2 3' CACCTGTGTCCTCCCTGGGC 9079 G T A
 GC TAG GAGGACACA GTG
 || || ||||| |||
 CG GTC CTCCTGTGT CAC
 G C C

GAM1944 LOC120772 5' CACTTGTGCCCCCAGCTCAGC 36627 GT GA_ A
 GC AGT GG CACAAGTG
 || || || |||||
 CG TCG CC GTGTTCAC
 AC ACC C

GAM1944 LOC147929 5' CACTTGTGCAGAGACACGCGC 38419 A AGGA_
 GCGT GTG CACAAGTG
 ||| || |||||
 CGCG CAC GTGTTCAC
 _ AGAGAC

GAM1944 LOC256867 5' CACTTGTGCCCCCAGCTCAGC 45470 GT GA_ A
 GC AGT GG CACAAGTG
 || || || |||||
 CG TCG CC GTGTTCAC
 AC ACC C

GAM1945 RP2 3' ATATAGAATTTGATAATA 13790
 TATTATCAGATTCTATAT
 ||||| |||||
 ATAATAGTTTAAGATATA

GAM1945 caspr5 3' TCAAATATATGATTGCTGATAG 28267 AT_ T C
 TA TATTATCAG TC ATATATT GA
 ||||| || ||||| ||
 ATGATAGTC AG TATATAA CT
 GTT _ A

GAM1945 FLJ11252 3' CAATATATAGTGATAATG 33566 GATT C
 TATTATCA CTATATATT G
 ||||| ||||| |

			GTAATAGT GATATATAA C	
			_____ A	
GAM1946 AGTR1	3'	TTAGCTACTTTTCAGAATTGA 6343	CG__ CAC	
		TCAA GA AAAGTAGCTAA		
		AGTT CT TTTCATCGATT		
		AAGA ____		
GAM1946 AGTR1	3'	TTAGCTACTTTTCAGAATTGA 11244	CG__ CAC	
		TCAA GA AAAGTAGCTAA		
		AGTT CT TTTCATCGATT		
		AAGA ____		
GAM1946 AGTR1	3'	TTAGCTACTTTTCAGAATTGA 14310	CG__ CAC	
		TCAA GA AAAGTAGCTAA		
		AGTT CT TTTCATCGATT		
		AAGA ____		
GAM1946 AGTR1	3'	TTAGCTACTTTTCAGAATTGA 25595	CG__ CAC	
		TCAA GA AAAGTAGCTAA		
		AGTT CT TTTCATCGATT		
		AAGA ____		
GAM1946 AGTR1	3'	TTAGCTACTTTTCAGAATTGA 25770	CG__ CAC	
		TCAA GA AAAGTAGCTAA		
		AGTT CT TTTCATCGATT		
		AAGA ____		
GAM1946 FPRL1	3'	GCTTTTGTGTCCCTGA 7194 AC GT		
		TCA GGACACAAA AGC		
		AGT CCTGTGTTT TCG		
		C_ ____		
GAM1946 HGF	3'	TTATTTTGTGTCATTGA 45231 CG		
		TCAA GACACAAAGTAG		
		AGTT CTGTGTTTTATT		
		A_ ____		
GAM1946 MADD	3'	CTATTTTGTGTCCTTGA 28241 C		
		TCAA GGACACAAAGTAG		
		AGTT CCTGTGTTTTATC		

GAM1946 MADD	3'	CTATTTTGTGTCCTTGA 28246 C		
		TCAA GGACACAAAGTAG		
		AGTT CCTGTGTTTTATC		

GAM1946 MADD	3'	CTATTTTGTGTCCTTGA 28251 C		
		TCAA GGACACAAAGTAG		

AGTT CCTGTGTTTTATC

GAM1946 MADD 3' CTATTTTGTGTCCTTGA 28256 C
TCAA GGACACAAAGTAG
|||||
AGTT CCTGTGTTTTATC

GAM1946 MADD 3' CTATTTTGTGTCCTTGA 9786 C
TCAA GGACACAAAGTAG
|||||
AGTT CCTGTGTTTTATC

GAM1946 MADD 3' CTATTTTGTGTCCTTGA 28235 C
TCAA GGACACAAAGTAG
|||||
AGTT CCTGTGTTTTATC

GAM1946 PLCB2 5' GCCTGCCTGTGTCTGCTGA 10918 A AA _
TCA CGGACACA GTAG C
|||||
AGT GTCTGTGT CGTC G
C C_ C

GAM1946 RPE 3' TGTCAGCTACTTCATTCCTGT 31158 ACACA A
ACGG AAGTAGCT ACA
|||||
TGTC TTCATCGA TGT
CTTAC C

GAM1946 SLC6A3 3' GTTGTCCGTGTCTGTTGA 6712 AAAG
TCAACGGACAC TAGC
|||||
AGTTGTCTGTG GTTG
CCT_

GAM1946 TEC 3' GTTAGCTGATGCCAGTTGA 9220 _ ACACAAAG
TCAAC GG TAGCTAAC
|||||
AGTTG CC GTCGATTG
A GTA_

GAM1946 XK 3' AGTTACTTGTGTTCAATTGA 22053 C A
TCAA GGACACAA GTAGCT
|||||
AGTT CTTGTGTT CATTGA
A _

GAM1946 CYLD 3' GCTTTTGTGTCCCTGA 17576 AC GT
TCA GGACACAAA AGC
|||||
AGT CCTGTGTTT TCG
C_ _

GAM1946 FLJ10925 3' GCCTGTCTTGTGTCTGCTGA 20261 A AG _
TCA CGGACACAA TAG C
|||||

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AGT GTCTGTGTT GTC G
C    CT C
GAM1946 FLJ11274 3' GCTACTTTATCCATTGA 20400 C CAC
TCAA GGA AAAGTAGC
||||| ||| |||||
AGTT CCT TTTCATCG
A A__
GAM1946 KIAA0161 3' TGTCAGTACATTTTGTGCC 16435 A A_ A
GG CACAAAGT GCT ACA
|| ||||| ||| |||
CC GTGTTTTA TGA TGT
_ CA C
GAM1946 MGC15438 5' GCAGCTTCAAGTCCGTTGA 26694 ACA A
TCAACGGAC AAGT GC
||||| ||| ||
AGTTGCCTG TTCG CG
AAC A
GAM1946 PRO2214 5' GCTATTTTGTATCCTTGA 20588 C C
TCAA GGA ACAAAGTAGC
||||| ||| |||||
AGTT CCT TGTTTTATCG
_ A
GAM1946 SLC21A14 3' TTGCTTTGTGCTCATTGA 18892 C GA
TCAA G CACAAAGTAG
|||| | |||||
AGTT C GTGTTTCGTT
A TC
GAM1946 X123 3' TGTGCTGCTCCCGTGTCTGCTGA 34651 A AAAGT
TCA CGGACAC AGCTAACA
||| ||||| |||||
AGT GTCTGTG TCGGTTGT
C CCC__
GAM1946 LOC120856 3' TGTTAGCTACTTTGAGAACC 36646 ACA_
GG CAAAGTAGCTAACA
|| |||||
CC GTTTCATCGATTGT
AAGA
GAM1946 LOC153339 5' TGTTCCCTTTCTTTGTGTCCTTG 41616 C TAGCT
A TCAA GGACACAAAG AACA
||||| ||| |||
AGTT CCTGTGTTTC TTGT
_ TTTCC
GAM1946 LOC159091 5' GCCTAACTTTGTGTTCACTGA 29038 AC A__
TCA GGACACAAAGT GC
||| ||||| ||
AGT CTTGTGTTTCA CG
CA ATC
GAM1946 LOC255520 3' TTGCTCGTGTCTGTTGA 45881 AA
TCAACGGACAC AGTAG
||||| |||

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AGTTGTCTGTG TCGTT
 C_
 GAM1947 SLC19A2 3' CAGCATCTGCCTCTAT 34194 TTTT
 ATAGAGGCG ATGCTG
 ||||| ||||
 TATCTCCGT TACGAC
 C__
 GAM1948 ABCG1 3' AGACGTGGACACCATCTCCACT 11351 C_ CT G
 GA TCAGTGGAGATGG TCC TG CT
 ||||| || ||
 AGTCACCTCTACC AGG GC GA
 AC T_ A
 GAM1948 CLECSF5 3' AGCCAAGGGAGCCAAACACACT 14917 _ GAGA
 AGA TC AGTG TGGCTCCCTTGGCT
 || ||| |||||
 AG TCAC ACCGAGGGAACCGA
 A ACAA
 GAM1948 OAS3 3' CCAAGGGAAGCTCCTCTGA 12858 T ATGGC
 TCAG GGAG TCCCTTGG
 ||| ||| |||||
 AGTC CCTC AGGGAACC
 T GA__
 GAM1948 POLH 3' CATGGCAAACCATCTCTACT 13249 CTC_ T
 AGTGGAGATGG CC TG
 ||||| ||
 TCATCTCTACC GG AC
 AAAAC T
 GAM1948 HSA249128 3' CCAAAGGAGCCTGCACTGG 19024 G GAT C
 TCAGTG A GGCTCC TTGG
 |||| | |||| ||||
 GGTCAC T CCGAGG AACC
 G_ A
 GAM1948 MGC4655 3' AGCCAAGGAATGTCTTCCCCTG 27145 T A T TC_
 A TCAG GG GA GGC CCTTGGCT
 ||| || || || |||||
 AGTC CC CT CTG GGAACCGA
 _ _ T TAA
 GAM1948 TOB2 3' AGCCAAGGGAGCAGGGTCATT 45763 AGATG
 AGTGG GCTCCCTTGGCT
 |||| |||||
 TTACT CGAGGGAACCGA
 GGGA_
 GAM1948 LOC90917 3' GCCAAGGAAGCCCAGCTGA 32168 GGAGAT C
 TCAGT GGCT CCTTGGC
 |||| ||| |||||
 AGTCG CCGA GGAACCG
 AC__ A
 GAM1949 KERA 3' AAATACTTCATCACTAA 13905 CGG
 TTAGTGATGAA ATTT
 ||||| |||

			AATCACTACTT TAAA		
			CA_		
GAM1950	CYP4F3	3'	TTATGTTTATACTGCCA 6594	T	TTGGT
			TG GCAGTATA CATAA		
			AC CGTCATAT GTATT		
			_ TT__		
GAM1950	F2RL3	3'	TATGATTGTACCACTGCAC 10085		ATAT
			GTGCAGT TGGTCATA		
			CACGTCA GTTAGTAT		
			CCAT		
GAM1950	MTCP1	5'	GGGTCATGAAGAATACTGCA 15488		A GG A
			TGCAGTAT TT TCAT ACCC		
			ACGTCATA AG AGTA TGGG		
			_ A_ C		
GAM1950	AP4S1	3'	ATGATTGTGCTACTGCAC 13941		TAT
			GTGCAGTA TGGTCAT		
			CACGTCAT GTTAGTA		
			CGT		
GAM1950	CARD14	3'	GCCACTTGTAAGTGCACA 23556		_ T_
			TGTGCAGT ATA TGGT		
			ACACGTCA TGT ACCG		
			A TC		
GAM1950	KIAA0844	3'	TTATGATTGTTACTGCA 17287		TATT
			TGCAGTA GGTCATAA		
			ACGTCAT TTAGTATT		
			TG__		
GAM1950	KIAA1952	5'	GGGTTATGGGTGACCTACACA 36220		C TATA G
			TGTG AG TTG TCATAACCC		
			ACAC TC AGT GGTATTGGG		
			A C__ G		
GAM1950	LIPG	3'	GTTATGACATATGTAATACACA 12655		CAG TG
			TGTG TATAT GTCATAAC		
			ACAC ATGTA CAGTATTG		
			ATA TA		
GAM1950	MRPS10	3'	GACTGAATATACTTCACA 19940		C _
			TGTG AGTATATT GGTC		
			ACAC TCATATAA TCAG		
			T G		
GAM1950	ZNF297B	5'	TATGATTGTGCCACTGCAC 15222		ATAT
			GTGCAGT TGGTCATA		

		CACGTCA GTTAGTAT		
		CCGT		
GAM1950	LOC113523 3'	GACTTGTATAAACTGCACA 36153	_____	T
		TGTGCAGT ATAT GGTC		
		ACACGTCA TATG TCAG		
		CAAA T		
GAM1950	LOC145387 3'	TATGATTGTGCCACTGCAC 40539		ATAT
		GTGCAGT TGGTCATA		
		CACGTCA GTTAGTAT		
		CCGT		
GAM1950	LOC153577 5'	GATACAACATACTGCACA 41645		A _
		TGTGCAGTAT TTG GTC		
		ACACGTCATA AAC TAG		
		C A		
GAM1950	LOC199733 3'	GGGCTATGATTGCACCACTGCA 43246		ATATT A
	C	GTGCAGT GGTCATA CCC		
		CACGTCA TTAGTAT GGG		
		CCACG C		
GAM1950	LOC221822 5'	GTTATGACTTGGACTGGACA 44624	G	ATATT
		TGT CAGT GGTCATAAC		
		ACA GTCA TCAGTATTG		
		G GGT__		
GAM1950	LOC92973 5'	TATGATTGTGCCACTGCAC 35187		ATAT
		GTGCAGT TGGTCATA		
		CACGTCA GTTAGTAT		
		CCGT		
GAM1951	ABCB9 3'	CAGCTCTGTGAGTCTGGCCA 21241	C	ACAAA
		TGGCCAGATTCA CTG		
		ACCGGTCTGAG TGT GAC		
		_ CTC__		
GAM1951	ADAM17 3'	CAGTTGAATTTATGGAATCTAC 22408	CC	CAACA__
	CA	TGG AGATTCCA AACTG		
		ACC TCTAAGGT TTGAC		
		A_ ATTTAAG		
GAM1951	ADAM17 3'	CAGTTGAATTTATGGAATCTAC 9155	CC	CAACA__
	CA	TGG AGATTCCA AACTG		
		ACC TCTAAGGT TTGAC		
		A_ ATTTAAG		
GAM1951	EPHB2 3'	CAGTCTAGGGATCTGGCCA 10733		ACAACAA
		TGGCCAGATTCC ACTG		

ACCGGTCTAGGG TGAC
 ATC____
 GAM1951 FUT9 3' CAATTTGTTGTGATTTTCAGC 33698 CA TTC C
 GC GA CACAACAAA TG
 || || ||||| ||
 CG TT GTGTTGTTT AC
 AC TTA A
 GAM1951 C20orf126 3' CAGCCGTCAGGAATCTGGCCA 25135 ACA AAA
 TGGCCAGATTCC AC CTG
 ||||| || ||
 ACCGGTCTAAGG TG GAC
 AC_ CC_
 GAM1951 CLIC5 3' CAGTTTGTTCAGTGCCA 18846 CAG CCA
 TGGC ATT CAACAACTG
 ||| || |||||
 ACCG TGA GTTGTGTTGAC
 ____ C____
 GAM1951 FLJ31890 3' TCAGCGTGCATGTGGAATCCAT 43894 CCA A_ AA
 CCA TGG GATTCCACA CA CTGA
 ||| ||||| || |||
 ACC CTAAGGTGT GT GACT
 TAC AC GC
 GAM1951 KIAA0365 3' CAGCTTGTTGGCCCTGGTCA 38470 ATTCCA A
 TGGCCAG CAACAA CTG
 ||||| ||||| |||
 ACTGGTC GTTGTT GAC
 CCG____ C
 GAM1951 PRDM13 3' TCAGAGGTGGCGTAAATCTGGC 22256 ____ AACAAA
 CA GGCCAGATT CCAC CTGA
 ||||| ||| |||
 CCGGTCTAA GGTG GACT
 ATGC GA____
 GAM1951 LOC143308 5' CAGTTTGCTGAGCCTGCCA 40347 C AT CACAA
 TGGC AG TC CAACTG
 ||| || |||||
 ACCG TC AG GTTTGAC
 _ CG TC____
 GAM1952 CYP7A1 3' CTGACAATTATGAAAAATGTT 6422 CCC G T
 GACAT TTT AT GTTGTCAG
 |||| ||| |||||
 TTGTA AAA TA TAACAGTC
 AA_ G T
 GAM1952 FBXW1B 3' CAAAGATCAAGGAATGTCA 14661 C T G
 TGACAT CCTT GATT TTG
 ||||| ||| ||| |||
 ACTGTA GGAA CTAG AAC
 A _ A
 GAM1952 FBXW1B 3' CAAAGATCAAGGAATGTCA 27363 C T G
 TGACAT CCTT GATT TTG
 ||||| ||| ||| |||

		ACTGTA GGAA CTAG AAC		
		A _ A		
GAM1952	FBXW1B	3' CAAAGATCAAGGAATGTCA 27373	C T G	
		TGACAT CCTT GATT TTG		
		ACTGTA GGAA CTAG AAC		
		A _ A		
GAM1952	HAL	5' ACAAAAACCAAAGGGACAGCA 7888	ACA A G	
		TG TCCCTTTG TT TTGT		
		AC AGGGAAAC AA AACA		
		GAC C A		
GAM1952	ITPR2	3' CTGACAACATAACAGGATGT 7991	CT AT	
		ACATCC TTG TGTGTCAG		
		TGTAGG AAT ACAACAGTC		
		AC _		
GAM1952	FLJ10508	3' CAACAAAAGCAACAGGATGTCA 19890	CT A__	
		TGACATCC TTG TTGTTG		
		ACTGTAGG AAC AACAAC		
		AC GAA		
GAM1952	FLJ13110	3' CTGTGCATCAAAGGGATGT 23221	T TGT	
		ACATCCCTTTGAT GT CAG		
		TGTAGGGAACTA CG GTC		
		_ T__		
GAM1952	IL17D	3' GGTGGACCAAAGGGATGCA 28701	A ATTG TG	
		TG CATCCCTTTG T TC		
		AC GTAGGGAAAC G GG		
		_ CA__GT		
GAM1952	KIAA1600	3' GATACAATCAAAGGAACTTCA 35393	CATC T	
		TGA CCTTTGATTGT GTC		
		ACT GAAACTAACA TAG		
		TCAA _		
GAM1952	TOM1L1	3' CTGACAACAGCGTGAGATTTCA 11983	C CCTT A	
		TGA ATC TG TTGTTGTCAG		
		ACT TAG GC GACAACAGTC		
		T AGT_ _		
GAM1952	LOC221143	3' CTGACAACCTGGCAAAGATGTCA 44941	CC ATT	
		TGACATC TTTG GTTGTGTCAG		
		ACTGTAG AAAC CAACAGTC		
		_ GGT		
GAM1953	G6PD	3' CATTGACCTCAGCTGCA 5978	A_ TAAGA	
		TGCG TG AGGTCAATG		

ACGT AC TCCAGTTAC
 CG _____
 GAM1953 PRDM2 3' CATTGGCCGACATCACA 14531 C AAGAA
 TG GATGT GGTCAATG
 || |||| |||||
 AC CTACA CCGGTTAC
 A G____
 GAM1953 FLJ20257 5' CATCTTCCTCCTCCCGACATCG 21221 AA_ _ TCA
 CA TGCGATGT GA AGG ATG
 ||||| || ||| ||
 ACGCTACA CT TCC TAC
 GCC CC TTC
 GAM1953 KIAA1030 3' CATTGACCCTCTCCTTTCCCA 44818 C TGTA A
 TG GA AGA GGTCAATG
 || || || |||||
 AC CT TCT CCAGTTAC
 C TTCC C
 GAM1953 PDE8A 3' TCATTGATTACTTCATCACA 31379 C T AA
 TG GATG AAG GGTCAATGA
 || |||| || |||||
 AC CTAC TTC TTAGTTACT
 A _ A_
 GAM1953 PEG10 3' CATTGACCCTGCTGCA 17428 AT AGAA
 TGCG GTA GGTCAATG
 ||| || |||||
 ACGT CGT CCAGTTAC
 _ C____
 GAM1953 LOC204084 5' TCATCAACTCCTTTACATC 43088 AA CA
 GATGTAAG GGT ATGA
 ||||| || |||
 CTACATTT TCA TACT
 CC AC
 GAM1953 LOC204084 5' TCACTGACCTTCACTTCG 43087 T AA A
 CGA GT GAAGGTCA TGA
 ||| || ||||| |||
 GCT CA CTTCCAGT ACT
 T _ C
 GAM1953 LOC57826 3' CATTGACCTCAGCAGCA 22161 GA AAGA
 TGC TGT AGGTCAATG
 ||| || |||||
 ACG ACG TCCAGTTAC
 _ AC____
 GAM1954 COX15 3' AAGCAAGATATTGATGGCCACT 10599 _ T
 AA TTAGTG CCATTAGTGT CTTGCTT
 ||||| ||||| |||||
 AATCAC GGTAGTTATA GAACGAA
 C _
 GAM1954 TNFRSF9 3' AAGCAAGAACACCATCCTAC 7287 CCATTA
 GTG GTGTTCTTGCTT
 ||| |||||

			CAT CACAAGAACGAA		
			CCTAC_		
GAM1954	C20orf121	3'	AAGCAAGAACAATCAGGAC 23627	G	ATTAG
			GT CC TGTTCTTGCTT		
			CA GG ACAAGAACGAA		
			_ ACTA_		
GAM1954	LNX	3'	AAGCAAGAGTGTACAGCAGTA 26337	G	CATTA TG
	A		TTA TGC G TTCTTGCTT		
			AAT ACG T GAGAACGAA		
			G ACAC_ GT		
GAM1954	LOC202181	5'	AAGCAAGAACACCAACTTGAAC 42967	GC	TTA__
			GT CA GTGTTCTTGCTT		
			CA GT CACAAGAACGAA		
			A_ TCAAC		
GAM1954	LOC93206	3'	AAGAGGCACTAATGACAT 35515	C	_
			GTG CATTAGTGT TCTT		
			TAC GTAATCACG AGAA		
			A G		
GAM1955	ATRX	3'	TTCTTTGGGTGTAAAGCGTTT 6098	T	GTG_
			AAAC GC TACCCAAAGAG		
			TTTG CG GTGGGTTTCTT		
			_ AAAT		
GAM1955	ATRX	3'	TTCTTTGGGTGTAAAGCGTTT 28687	T	GTG_
			AAAC GC TACCCAAAGAG		
			TTTG CG GTGGGTTTCTT		
			_ AAAT		
GAM1955	C7	3'	CTCTTTGGGGTTTTAGTATGTG 6189	A	CGTGTA
			TATA ACTG CCCAAAGAG		
			GTGT TGAT GGGTTTCTC		
			A TTTG__		
GAM1955	CLN5	3'	TTGCCTAATGTAGTTTATG 13231		GTACC
			TATAAACTGCGT CAA		
			GTATTTGATGTA GTT		
			ATCC_		
GAM1955	CNN2	3'	CTTTTGTGAGCTGAGCAGTTTG 10583	GT_ ACC	AG
	TG		TATAAACTGC GT CAAAG		
			GTGTTTGACG CG GTTTT		
			AGT ACT C		
GAM1955	CSPG3	3'	TTTTTTGGGGGTCTTGTTTA 10616	GCGTGTA	
	TG		TATAAACT CCCAAAGAG		

		GTATTTGG GGGTTTTT	
		TTCTGGG	
GAM1955 DMC1	3'	TTTGTGTGTGTGTGTGTTTGTG 13934	_ TG C
		TATAAAC TGCG TAC CAAA	
		GTGTTTG GTGT GTG GTTT	
		T GT T	
GAM1955 DNAJB9	3'	TTTGTGTGTGTGTAGTTTAT 14719	TG C
		ATAAACTGCG TAC CAAA	
		TATTTGATGT GTG GTTT	
		GT T	
GAM1955 DUSP6	3'	CTCTTTATGTAGTTTG 32809	TACCCA
		TAAACTGCGTG AAGAG	
		GTTTGATGTAT TTCTC	
GAM1955 DXS1283E	3'	CTCTAGCAAACATGTAGTTTA 35063	ACCCAA
		TAAACTGCGTGT AGAG	
		ATTTGATGTACA TCTC	
		AACGA_	
GAM1955 FBXW1B	3'	GTCATTGCGTGTGTGTGGTTTG 14665	TG TG C A G
TG		TATAAAC CG TAC CAA GA	
		GTGTTTG GT GTG GTT CT	
		GT GT C A GT	
GAM1955 FBXW1B	3'	TTGCGTGTGTGTGGTTTGTG 27381	TG TG C
		TATAAAC CG TAC CAA	
		GTGTTTG GT GTG GTT	
		GT GT C	
GAM1955 FBXW1B	3'	GTCATTGCGTGTGTGTGGTTTG 27377	TG TG C A G
TG		TATAAAC CG TAC CAA GA	
		GTGTTTG GT GTG GTT CT	
		GT GT C A GT	
GAM1955 FBXW1B	3'	TTGCGTGTGTGTGGTTTGTG 14669	TG TG C
		TATAAAC CG TAC CAA	
		GTGTTTG GT GTG GTT	
		GT GT C	
GAM1955 FBXW1B	3'	GTCATTGCGTGTGTGTGGTTTG 27367	TG TG C A G
TG		TATAAAC CG TAC CAA GA	
		GTGTTTG GT GTG GTT CT	
		GT GT C A GT	
GAM1955 FBXW1B	3'	TTGCGTGTGTGTGGTTTGTG 27371	TG TG C
		TATAAAC CG TAC CAA	

			GTGTTTG GT GTG GTT		
			GT GT C		
GAM1955	FSTL1	3'	TCTGTGTGTGTAGTTTTG 13954 T TG CCAA		
			A AAAGTGCCTAC AGA		
			G TTTGATGT GTG TCT		
			T GT ____		
GAM1955	GLO1	3'	CTTTTTGGGTGAAATGGATTTA 13529 _ GCGTG		
	TG		TATAAA CT TACCCAAAGAG		
			GTATTT GG GTGGGTTTTTC		
			A TAAA_		
GAM1955	IRS2	3'	CTTTTTGGGTACGTATTGTTT 30032 TGCG		
			AAAC TGTACCCAAAGAG		
			TTTG GCATGGGTTTTTC		
			TTAT		
GAM1955	JAM3	3'	CTTTTTGGATCAGCATTTTGTA 26554 C G TAC		
			TATAAA TGC TG CCAAAGAG		
			ATGTTT ACG AC GGTTTTTC		
			T _ TA_		
GAM1955	LRP8	3'	CTCTGTGTGTGTATGTGTGTGT 11007 _ TG C_ A		
	TTATA		AAAC TGCG TAC CA AGAG		
			TTTG GTGT ATG GT TCTC		
			T GT TGT G		
GAM1955	LRP8	3'	CTCTGTGTGTGTATGTGTGTGT 27131 _ TG C_ A		
	TTATA		AAAC TGCG TAC CA AGAG		
			TTTG GTGT ATG GT TCTC		
			T GT TGT G		
GAM1955	MTMR8	3'	TTCTTATTGCACTGGTTTATA 17749 C CCCA		
			TATAAACTG GTGTA AAGAG		
			ATATTTGGT CACGT TTCTT		
			_ TA_		
GAM1955	NEDD4	3'	TTTTGTTAATATGCAGTTTTA 34694 T ACC		
			A AAAGTGCCTGT CAAAG		
			A TTTGACGTATA GTTTT		
			T ATT		
GAM1955	PCDHA9	3'	TTTTTGTTATGTGGTTTATA 15217 TG TACC		
			TATAAAC CGTG CAAAGA		
			ATATTTG GTAT GTTTTT		
			GT T_		
GAM1955	PKDREJ	3'	TTCTTTGGTGCCTGCAGTTTA 12716 T C		
			TAAAGTGCCTGTACC AAAGAG		

ATTTGACGT CGTGG TTTCTT
 C _
 GAM1955 PRNP 3' CTTTGAAATATGCATGTACTTT 5848 C CC__ AG
 ATA TAAA TGC GTGTA CAAAG
 |||| ||||| ||||
 ATTT ATGTACGT GTTTC
 C ATAAA
 GAM1955 RAB1A 3' CTTTGTGTGCTGGTTTATA 34788 CGT C
 TATAAACTG GTAC CAAAG
 ||||| ||| ||||
 ATATTTGGT CGTG GTTTC
 _ T
 GAM1955 RNMT 3' TTTTGTGTCATGTATTTGTA 9894 C CC
 TATAAA TGC GTGTA CAAAGA
 |||| ||||| ||||
 ATGTTT ATGTACGT GTTTTT
 _ T_
 GAM1955 RNTRE 3' TTTTAAGGCTATATGTAGTGTA 16191 A C AAAGAG
 TG TATA ACTGCGTGTA CC
 ||| ||||| ||
 GTAT TGATGTATAT GG
 G C AATTTT
 GAM1955 SLC4A7 3' TTCTAAAGTGTGTGTATGTTTG 9675 _ TG CCAA
 TG TATAAAC TGCG TAC AGAG
 ||||| ||| ||| ||||
 GTGTTTG ATGT GTG TCTT
 T GT AAA_
 GAM1955 SOST 3' TTCTGTCCTCTGCGCGTGTTT 24919 TG CCCAA_
 G TAAAC CGTGTA AGAG
 |||| |||| |||
 GTTTG GCGCGT TCTT
 GT CTCCTG
 GAM1955 TAPBP 3' TTTTGGGTATGTGGGTT 9185 G TG
 AACT CG TACCCAAAG
 ||| || ||||| ||||
 TTGG GT ATGGGTTTT
 _ GT
 GAM1955 TOX 3' CTTTGACAGGCGGTTTGTG 16326 G ACC
 TATAAACTGC TGT CAAAG
 ||||| ||| ||||
 GTGTTTGCG ACA GTTTC
 G _
 GAM1955 5T4 3' TTTTGTGATTGCAGTTTATA 13486 TGTACC
 TATAAACTGCG CAAAGA
 ||||| ||| ||||
 ATATTTGACGT GTTTTT
 TA_
 GAM1955 ABHD3 3' TTCTTTGGGTGCATTTTGT 28741 TGC
 AC GTGTACCCAAAGAG
 || ||||| |||||

		TG TACGTGGGTTTCTT		
		TTT		
GAM1955 ACAS2L	3'	TTTTTAACATGTAGTT	33767	ACCC
		AACTGCGTGT	AAAGA	
		TTGATGTACA	TTTTT	
		A__		
GAM1955 ARHGAP5	3'	CTTTGGAGTGTTTATA	37819	TGCGTGT _
		TATAAAC	AC CCAAAG	
		ATATTTG	TG GGTTTC	
		_____A		
GAM1955 BM046	3'	CTTTGAGCAGTTTGTG	20532	GTGTACC
		TATAAACTGC	CAAAG	
		GTGTTTGACG	GTTTC	
		A_____		
GAM1955 BPES	3'	CTCTTTGTCCCTCAGTTTATG	23324	CGTGTACC
		TATAAACTG	CAAAGAG	
		GTATTTGAC	GTTTCTC	
		TCCCT__		
GAM1955 DJ473B4	3'	CTCTAACACATATGCAGTTTTA	21212	T ACCCAA
		A AAACTGCGTGT	AGAG	
		A TTTGACGTATA	TCTC	
		T CACAA_		
GAM1955 DJ971N18.2	3'	CTTTGGCCTGCAGTTTGTA	22136	T TAC
		TATAAACTGCG G	CCAAAG	
		ATGTTTGACGT C	GGTTTC	
		C__		
GAM1955 DKFZP434E2318	3'	TTCTAAGTTAAATGTAGTTTGT	25818	GT_ CCAA
A		TATAAACTGCGT	AC AGAG	
		ATGTTTGATGTA	TG TCTT	
		AAT AA__		
GAM1955 DKFZP434I1735	3'	TTTTTGTGTGTGTGCGTGGGGT	42423	____ TG C G
TTGTG		AACT GCG TAC	CAAAGA	
		TTGG CGT	GTG GTTTTT	
		GGTG GT	T	
GAM1955 DKFZP434P0721	3'	CTTTAAGTATGTGCAGTTTGT	31870	TG CC
		ATAAACTGCG	TAC AAAG	
		TGTTTGACGT	ATG TTTC	
		GT AA		
GAM1955 DKFZP586M0622	5'	CTCTCCTCTCATGCAGTTTATG	17848	TACCCAA
		TATAAACTGCGTG	AGAG	

			GTATTTGACGTAC	TCTC	
			TCTCC__		
GAM1955	EFA6R	3'	TTTTTTGGTGCAGTGGTCTTGT	17629	_ TG G C G
	G		TATAA AC C TGTACC AAAGA		
			GTGTT TG G ACGTGG TTTTT		
			C GT_ T		
GAM1955	ERp44	3'	TTTTTTGGTGCTGTAGTATATG	39727	A T C
			TATA ACTGCG GTACC AAAGA		
			GTAT TGATGT CGTGG TTTTT		
			A _ T		
GAM1955	FHOD2	3'	TTCCTTGATGTGTAGTT	36555	TG AC A
			AACTGCG T CCAA GAG		
			TTGATGT A GGTT CTT		
			GT__ C		
GAM1955	FLJ10008	3'	TTCTGGCCTGCACGCAGTGTGT	19693	A C_ AAGAG
	G		TATA ACTGCGTGTA CCA		
			GTGT TGACGCACGT GGT		
			G CC CTT		
GAM1955	FLJ12587	3'	CTCTTCAGCTTTGCAGTGGTTT	22850	TG G CCCA__
	GTG		ATAAAC C TGTA AAGAG		
			TGTTTG G ACGT TTCTC		
			GT_ TTCGAC		
GAM1955	FLJ13340	3'	CTTTTTGTGGAACATGTAGTTT	27705	A _
	ATA		TATAAACTGCGTGT CC CAAAGAG		
			ATATTTGATGTACA GG GTTTTTC		
			A T		
GAM1955	FLJ20276	3'	CTCTCATTGATGTGCTGGTTTA	19328	_ TG ACCCAA
	TG		TATAAACT GCG T AGAG		
			GTATTTGG CGT A TCTC		
			T GT GTTAC_		
GAM1955	FLJ20294	3'	CTCTTAACTGTACGTGTAGTTT	19346	CCA_
			AAACTGCGTGTAC AAGAG		
			TTTGATGTGCATG TTCTC		
			TCAA		
GAM1955	GT650	3'	TTTTTTGCATTATATGCATTTA	27435	C CC_
	TG		TATAAA TGCGTGTA CAAAGAG		
			GTATTT ACGTATAT GTTTTTT		
			_ TAC		
GAM1955	KIAA0447	3'	TGGGGCGCGTGGTGTGTG	35496	A TG A
			TATA AC CGTGT CCCA		

	GTGT TG GCGCG GGGT	
	G GT _	
GAM1955 KIAA0753	3' TTTGTGTGGCAGTTTGTA 16738	GTG C
	TATAAACTGC TAC CAAA	
	ATGTTTGACG GTG GTTT	
	_ T	
GAM1955 KIAA0820	3' TTCTGTAAGTATGTGTATTTTA 34223	C TG CCAA
TG	TATAAA TGCG TAC AGAG	
	GTATTT ATGT ATG TCTT	
	T GT AATG	
GAM1955 KIAA0836	3' CTCTTCCATTGTACATGTGGGT 32246	A TG CCA_
TATA	ATAA C CGTGAC AAGAG	
	TATT G GTACATG TTCTC	
	G GT TTACC	
GAM1955 KIAA1005	3' TTCTTTGATGCATGCAGTTT 35780	CC
	AAACTGCGTGTA CAAAGAG	
	TTTGACGTACGT GTTTCTT	
	A_	
GAM1955 KIAA1041	3' TTTTGCTGCAAGCAGTTTATA 17268	G CC
	TATAAACTGC TGTA CAAAG	
	ATATTTGACG ACGT GTTTT	
	A C_	
GAM1955 KIAA1468	3' CTTTTGGACATCAGTTTGTG 44101	C A C
	TATAAACTG GTGT CC AAAG	
	GTGTTTGAC TACA GG TTTC	
	_ _ T	
GAM1955 KIAA1546	3' CTTTTTGAATGCAGTTT 33714	GTACC
	AAACTGCGT CAAAGAG	
	TTTGACGTA GTTTTTC	
	AA_	
GAM1955 KIAA1727	3' TTCTTTTATGTAACATGTAGTT 32039	_ CC_
TA	TAAACTGCGTGT AC AAAGAG	
	ATTTGATGTACA TG TTTCTT	
	A TAT	
GAM1955 KIAA1764	5' TGTGTATGCTGTAGTTTGTG 34355	_ C
	TATAAACTGC GTGTAC CA	
	GTGTTTGATG CGTATG GT	
	T T	
GAM1955 KIAA1765	3' TTTTGTTATGTGCAGTTTAT 34958	TG CC
	ATAAACTGCG TA CAAAG	

		TATTTGACGT AT GTTTT	
		GT T_	
GAM1955 KLHL8	3'	CTTTTTGTAGACTGTAGTTTAT 31477	T ACC
		ATAAACTGCG GT CAAAGAG	
		TATTTGATGT CA GTTTTTC	
		_ GAT	
GAM1955 LIN-28	3'	GGGTGTGTGTGTGTTTGTA 23981	_ TG
		TATAAAC TGCG TACCC	
		ATGTTTG GTGT GTGGG	
		T GT	
GAM1955 MGC12466	3'	TTTGCATGTATGTGAAGTTTAT 38611	G TG C_ GAG
A		TATAAACT CG TAC CAAA	
		ATATTTGA GT ATG GTTT	
		A GT TAC	
GAM1955 MGC14859	3'	TTCTTTGGCCTGGGTGGTTTAT 31007	TG G TAC
A		TATAAAC C TG CCAAAGAG	
		ATATTTG G GT GGTTTCTT	
		GT G CC_	
GAM1955 MGC23937	3'	TTCTTTGTCCCACTGTAGTTTG 29683	_ TACC
		TAAACTGC GTG CAAAGAG	
		GTTTGATG CAC GTTTCTT	
		T CCT_	
GAM1955 MGC29898	3'	TTTTTTGGCAATCAGTTTGTA 29680	CG TAC
		TATAAACTG TG CCAAAGAG	
		ATGTTTGAC AC GGTTTTTT	
		TA _	
GAM1955 NUDT13	3'	CTCTGTACATGCTCAGTTTGT 31663	_ ACCCAA
G		TATAAACT GCGTGT AGAG	
		GTGTTTGA CGTACA TCTC	
		CT CTG_	
GAM1955 OCT11	3'	TTTTTTGTGGGCCAGTTTGTA 15681	C GTA _
		TATAAACTG GT CC CAAAGAG	
		ATGTTTGAC CG GG GTTTTTT	
		_ _ T	
GAM1955 PELI2	3'	CTTTGTACATATACGTAATTTA 22230	C CC_ AG
TA		TATAAA TGCGTGTA CAAAG	
		ATATTT ATGCATAT GTTTC	
		A ACAT	
GAM1955 RDC1	3'	CTTTGTAATGCAGTTTGTG 35848	GTACC
		TATAAACTGCGT CAAAG	

GTGTTTGACGTA GTTTC
 AT____
 GAM1955 RES4-22 3' CTCGTGTGCGTGTAGTCTGTG 9804 A CCAAA
 TATA ACTGCGTGTAC GAG
 ||| ||||| ||
 GTGT TGATGTGCGTG CTC
 C TG____
 GAM1955 SE57-1 3' TTCTTTGTAGGTGGAGTTTGTG 24894 G TG CC
 TATAAACT CG TAC AAAGAG
 ||||| || || |||||
 GTGTTTGA GT ATG TTTCTT
 G GG ____
 GAM1955 SP192 3' TTTTGGGTACAGCTGT 22300 T G
 AC GC TGTACCCAAAGA
 || || |||||
 TG CG ACATGGGTTTTT
 T _
 GAM1955 TBDN100 3' CTTTTTGTGGAACATGTAGTTT 24696 A _
 ATA TATAAACTGCGTGT CC CAAAGAG
 ||||| || |||||
 ATATTTGATGTACA GG GTTTTTC
 A T
 GAM1955 TNFRSF21 3' TTTGGGGTGTGTGTGTGTGTTT 15804 ____ TG AAAGAG
 GTG TAAAC TGCG TACCC
 |||| ||| ||||
 GTTTG GTGT GTGGG
 TGT GT GTT
 GAM1955 UBF-fl 3' TTTTGAGTCAGTGGTTTATG 26603 TG G T C
 TATAAAC C TG AC CAAAG
 ||||| | || |||||
 GTATTTG G AC TG GTTTT
 GT _ _ A
 GAM1955 UBP1 3' CTTTTTGGGTCTCAAGATTTTAT 15849 _ GCGTGT
 G TATAAA CT ACCCAAAGAG
 ||||| || |||||
 GTATTT GA TGGGTTTTTC
 A ACTC____
 GAM1955 UBP1 3' CTTTTTACACTGTATGCGGTTT 15848 CCC_
 G TAAACTGCGTGTA AAAGAG
 ||||| |||||
 GTTTGGCGTATGT TTTTTC
 CACA
 GAM1955 UNC5D 3' CTCTAACTAACATGTGGTATGT 28112 A TG ACCCAA
 A TATA AC CGTGT AGAG
 ||| || |||| |||
 ATGT TG GTACA TCTC
 A GT ATCAA_
 GAM1955 ZFP106 3' TTCTTAACAATTATGTGCAGTG 22838 A TG CCCA____
 TGTG ATA ACTGCG TA AAGAG
 || ||||| || |||||

	TGT TGACGT AT TTCTT G GT TAACAA	
GAM1955 LOC120856 3'	ATCTGTGTGTGCGTGTTTGTG 36631 TATAAAC GCG TAC AGA GTGTTTG TGC GTG TCT _ GT TG__ AA	T TG CCAA G
GAM1955 LOC122792 3'	TTCTTTGGGGAAGGTGATTTGT 29765 G TATAAA GC CCCAAAGAG GTGTTT TG GGGTTTCTT AG GAAG_	CT GTGTA
GAM1955 LOC130074 3'	CTTCTTGGTGTGGTTTGTGTA 37473 TATAAAC CG CCAA AG ATGTTTG GT GGTT TC GT _____ CT	TG TGTAC AG
GAM1955 LOC135154 3'	CTTTATGTCGTGTAGTTTGTGTA 37091 TATAAACTGCGTG AC AAAG ATGTTTGATGTGC TG TTTC _ TA	T CC
GAM1955 LOC146880 3'	CTCTTTCTTAAATGTGGTTTGT 38260 ATAAAC CGT AAAGAG TGTTTG GTA TTTCTC GT AATTC_	TG GTACCC
GAM1955 LOC151963 3'	CTCTGATAATGTGTCGTGTGGT 39175 TTGTG AAAC CGTG TAC AGAG TTTG GTGC GTG TCTC GT T TAATAG	TG _ CCAA__
GAM1955 LOC152580 3'	TTCTTCCTGACGTGGCAGTTTA 41525 TG TATAAACTGC GTGT AAGAG GTATTTGACG TGCA TTCTT G GTCC_	_ ACCCA
GAM1955 LOC158402 5'	TTCTTTGGGTCCGTGGGCTTGT 41979 G TATAA C CG ACCCAAAGAG GTGTT G GC TGGGTTTCTT CG GT C__	A_ TG TGT
GAM1955 LOC168667 3'	CTTTGGGATCTAAGTGTGGTTT 44567 GTG TAAAC CG TA CCCAAAG GTTTG GT AT GGGTTTC GT GA CTA	TG TG ____ AG
GAM1955 LOC253263 3'	CTCTTTGGGTAGTGTGGTATG 46360 TA TATA AC CG ACCCAAAGAG 	A TG TGT

		ATGT TG GT TGGGTTTCTC	
		A GT GAT	
GAM1955	LOC90161	3' TTTTTCGAGAGGTATCAGTTT 30904	CGT ____
		ATG AACTG GTACC CAAAGAG	
		TTTGAC TATGG GTTTTTT	
		____ AGAC	
GAM1955	LOC90317	3' TTTTGTAGCAATGCAGTT 31209	GTACC
		AACTGCGT CAAAGAG	
		TTGACGTA GTTTTTT	
		ACGAT	
GAM1955	LOC91351	3' GGTATTGTTGTAGTTTATG 32697	T__
		TATAAACTGCG GTACC	
		GTATTTGATGT TATGG	
		TGT	
GAM1956	ABCA1	5' CGTCCCTGCTGTGAGCTCT 12013	C TG CCGA
		AGAGTTCGC GG G GGCG	
		TCTCGAGTG TC C CTGC	
		_ GT C__	
GAM1956	ASPH	3' TGCAACATCGGTGGATTTT 26225	GCCGAG
		AGAGTTCGCCGGTG GCG	
		TTTTAGGTGGCTAC CGT	
		AA____	
GAM1956	BACH1	3' GCAATGTTACGGTGAATTCT 6859	G CGAG
		AGAGTTCGCCG TGGC GC	
		TCTTAAGTGGC ATTG CG	
		_ TAA_	
GAM1956	BRCA1	5' GTAAAGCTGCTTGTGAATTTT 14183	C TG CGAG
		AGAGTTCGC GG GC GC	
		TTTTAAGTG TC CG TG	
		T GT AAA_	
GAM1956	CEP2	5' GCCAGAAGCCCGTTGGCGAGCT 13651	GG _ CGA_ GC
	CT	AGAGTTCGCC TGG C GGC	
		TCTCGAGCGG GCC G CCG	
		TT C AAGA	
GAM1956	CPS1	3' TGCTCTAATTGTGAACTTT 7603	CGG CCGA
		AGAGTTCGC TGG GGCG	
		TTTCAAGTG ATC TCGT	
		TTA ____	
GAM1956	DGCR2	3' GCACGTCACTGGCGGGCTC 11613	CGAG
		GAGTTCGCCGGTGGC GC	

CTCGGGCGGTCACTG CG
CA__

GAM1956 DPYD 3' GTGAAACAGTTGCTGTGAACTT 30318 C TG CGAGG
T AGAGTTCGC GG GC CGC
||||||| || || ||
TTTCAAGTG TC TG GTG
_ GT ACAA

GAM1956 DYRK1A 5' TAGTTTTGCCGCTGGACTCT 28164 TCG C GC
AGAGT CCGGTGGC GAGGC
|||| ||||||| ||||
TCTCA GGTGCGCCG TTTTG
_ _ ATA

GAM1956 DYRK1A 5' TAGTTTTGCCGCTGGACTCT 28187 TCG C GC
AGAGT CCGGTGGC GAGGC
|||| ||||||| ||||
TCTCA GGTGCGCCG TTTTG
_ _ ATA

GAM1956 DYSF 5' GCGCCTCGGCCCTCCCGACCTT 9586 T CC T
T AGAG TCG GG GGCCGAGGCGC
|||| || |||||||||
TTTC AGC TC CCGGCTCCGCG
C CC _

GAM1956 EHD2 5' CGCCCCGTCGGCAGCTCT 15963 C GT CCGA
AGAGTT GCCG GG GGCG
||||| ||| || ||||
TCTCGA CGGC CC CCGC
_ TG _

GAM1956 ELK4 3' GTGTCTTGTTACCCATTATTC 22351 TCGCC
GAGT GGTGGCCGAGGCGC
|||| |||||||||
CTTA CCATTGGTTCTGTG
TTAC_

GAM1956 EP300 5' GCGCCTCTAGAGCCGCGAGTTC 7151 GT C GGCC
T AGA TCGC GGT GAGGCGC
||| ||||| ||| ||||||
TCT AGCG CCG CTCCGCG
TG _ AGAT

GAM1956 EPHA2 3' GTGCCATGCTGGGCCACTGGGG 10715 G G ____
ACTTT TTC CCGGTGGCC A GGCGC
||| ||||||| | ||||
AGG GGTCACCGG T CCGTG
_ G CGTA

GAM1956 EVC 3' GCGCATGTAGGCTGCCGGTGGC 15894 T TG GAG__
TTT GAGT CGCCGG GCC GCGC
|||| ||||| ||| ||||
TTCG GTGGCC CGG CGCG
_ GT ATGTA

GAM1956 EXTL3 3' GCGCCTGACCCTGGTGGGCT 7170 T C G
AGTTCGCCGG GG C AGGCGC
||||||| || | |||||

			TCGGGTGGTC CC G TCCGCG		
			— A —		
GAM1956	FGFR1	5'	GCACAAGCCACGGCGGACTCT 23362	G	CGAG
			AGAGTTCGCCG TGGC GC		
			TCTCAGGCGGC ACCG CG		
			— AAC A		
GAM1956	FGFR1	5'	GCACAAGCCACGGCGGACTCT 23366	G	CGAG
			AGAGTTCGCCG TGGC GC		
			TCTCAGGCGGC ACCG CG		
			— AAC A		
GAM1956	FGFR1	5'	GCACAAGCCACGGCGGACTCT 23373	G	CGAG
			AGAGTTCGCCG TGGC GC		
			TCTCAGGCGGC ACCG CG		
			— AAC A		
GAM1956	FGFR1	5'	GCACAAGCCACGGCGGACTCT 17979	G	CGAG
			AGAGTTCGCCG TGGC GC		
			TCTCAGGCGGC ACCG CG		
			— AAC A		
GAM1956	FGFR1	5'	GCACAAGCCACGGCGGACTCT 6208	G	CGAG
			AGAGTTCGCCG TGGC GC		
			TCTCAGGCGGC ACCG CG		
			— AAC A		
GAM1956	FGFR1	5'	GCACAAGCCACGGCGGACTCT 23377	G	CGAG
			AGAGTTCGCCG TGGC GC		
			TCTCAGGCGGC ACCG CG		
			— AAC A		
GAM1956	FLRT3	5'	GCAGCTGCCGTGGGCTTT 14949	C	TG CGAG
			AGAGTTCGC GG GC GC		
			TTTCGGGTG CC CG CG		
			— GT A —		
GAM1956	FSTL3	3'	GTGCCCCTAGGTTGGTGGGTCT 12470	G	GTG GA__
			AGA TTCGCCG GCC GGCGC		
			TCTGGGTGGT TGG CCGTG		
			— ____ ATCC		
GAM1956	FUT5	3'	TCTCGGCTGTTGGGGACTTT 7790	G	TG
			AGAGTTC CCGG GCCGAGG		
			TTTCAGG GGTT CGGCTCT		
			— GT		
GAM1956	FUT6	3'	CCTCGGCTGTTGGGGACTTT 5650	G	TG
			AGAGTTC CCGG GCCGAGG		


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TTTCAGG GGTT CGGCTCC
  _ GT
GAM1956 G6PT1 5' GCGTCTTGGCTGGTAGGGCCT 7200 A _ GGT
                AG GTTC GCC GGCCGAGGCGC
                || ||| ||| |||||
                TC CGGG TGG TCGGTTCTGCG
                _ A _
GAM1956 GNA11 3' GTGTTTTTACCTTGGTGAATCT 37455 G T CC
                AGA TTCGCCGG GG GAGGCGC
                ||| ||||| || |||||
                TCT AAGTGGTT CC TTTTGTG
                _ _ AT
GAM1956 GNA15 3' GCGCCTTCGGGCGTGGACTCT 30105 CGGT G _
                AGAGTTCGC G CCGA GGCGC
                ||||| | ||| ||||
                TCTCAGGTG C GGCT CCGCG
                _ _ G T
GAM1956 GPC6 5' GCGCCGCTGCCTCTGGCGGGCT 12260 T CGA
TT                AGAGTTCGCCGG GGC GGCGC
                ||||| ||| ||||
                TTTCGGGCGGTC CCG CCGCG
                T TCG
GAM1956 GRM1 3' GTGTCTTGGCTGTCATAACTTT 6497 CGCC TG
                AGAGTT GG GCCGAGGCGC
                |||| | |||||
                TTTCAA CT CGGTTCTGTG
                TA_ GT
GAM1956 HRH1 3' GTGCATTTTTATCTGTGAGTTC 6526 GT C CCGAG
T                AGA TCGC GGTGG GCGC
                || ||| |||| |||
                TCT AGTG CTATT CGTG
                TG T TTTA_
GAM1956 HS2ST1 5' GCGCTGTTTGCTGCGCGGGCTT 14575 _ TG CCGA
T                AGAGTTCGC CGG G GGCGC
                ||||| ||| | ||||
                TTTCGGGCG GTC T TCGCG
                C GT TG_
GAM1956 HTRA3 3' GTGTCTCAAGGGGCATTTGTGA 42943 CG G _
GCTTT                GTTCGC GTG CC GAGGCGC
                |||| ||| || |||||
                CGAGTG TAC GG CTCTGTG
                TT G GAA
GAM1956 IRS2 3' GTGTTTGGAAACATCTGTGGAC 30035 C G_ G
TCT                GAGTTCGC GGTG CCGAG CGC
                ||||| ||| |||| |||
                CTCAGGTG CTAC GGTTT GTG
                T AAA _
GAM1956 ITGAM 3' GCGTGGGTAAGCCGCTGCTGGG 6249 TT C CGAG_
TTTT                GAG CG CGGTGGC GCGC
                || || ||||| |||

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TTT GT GTCGCCG TGCG
 GG C AATGGG
 GAM1956 LDHC 5' GCGCCTCAACTGTCGTTGGTGT 8092 T GG C____
 ATTTT GT CGCC TGGC GAGGCGC
 || ||| ||| |||||
 TA GTGG GCTG CTCCGCG
 T TT TCAA
 GAM1956 LOXL2 3' GTGTTTTCTGATTTGGTGAGCT 8134 TGGCC
 C GAGTTCGCCGG GAGGCGC
 ||||| |||||
 CTCGAGTGGTT TTTTGTG
 TAGTC
 GAM1956 MYEOV 5' GTGCCTCACCACTGCTGAGCT 29002 _ C CC
 CT AGAGTTC GC GGTGG GAGGCGC
 ||||| || ||||| |||||
 TCTCGAG CG CCACC CTCCGTG
 T T A_
 GAM1956 PCM1 5' GCGCTCCCGCCGGCGAGTTCT 12870 GT CCGA
 AGA TCGCCGGTGG GGCGC
 || ||||| |||||
 TCT AGCGGCCGCC TCGCG
 TG C____
 GAM1956 PDGFRA 3' GTCAGCTGCTGTTGAACTTT 12885 C TG CGA
 AGAGTTCG CGG GC GGC
 ||||| || || |||
 TTTCAAGT GTC CG CTG
 T GT A_
 GAM1956 PIM1 3' GTGTCCAGCATTGCTGGACTCT 43757 C G CGA
 AGAGTTCG CGGTG C GGCGC
 ||||| ||||| |||||
 TCTCAGGT GTTAC G CTGTG
 C _AC_
 GAM1956 PLIN 3' GCGCCCCGGGCGCGGGTTT 8536 TT GG A
 GAG CGCCGGT CCG GGCGC
 || ||||| || |||||
 TTT GCGGCCG GGC CCGCG
 GG _ C
 GAM1956 POMZP3 5' GCGCGACATCGGCGAAC 14529 GC AG
 GTTCGCCGGTG CG GC
 ||||| || ||
 CAAGCGGCTAC GC CG
 A_ G_
 GAM1956 PON1 3' TGGTAGTGCTGGTGGGTTTT 6033 TT ____
 AGAG CGCCGGTG GCCG
 ||| ||||| |||||
 TTTT GTGGTCGT TGGT
 GG GA
 GAM1956 PROX1 5' TGCCCAGCTGACGAGCTTT 8651 C GGCCGA
 AGAGTTCG CGGT GGCG
 ||||| ||| |||||

		TTTCGAGC GTCG CCGT		
		A AC_____		
GAM1956 PSAP	3'	GTGCTTGGGCACTGGTGGGCCT 34374	A	G G
		AG GTTCGCCGGTG CC AGGCGC		
		TC CGGGTGGTCAC GG TTCGTG		
		— — G		
GAM1956 PTGS2	3'	GTGTCAAGCACTGTGGGTTTT 6684	TT C	G CGA
		AGAG CGC GGTG C GGCGC		
		TTTT GTG TCAC G CTGTG		
		GG — — AA_		
GAM1956 RALBP1	3'	GTGAACCTACTGGTGGACTC 13665		CCGAGG
		GAGTTCGCCGGTGG CGC		
		CTCAGGTGGTCATC GTG		
		CAA_____		
GAM1956 RARA	3'	GTGCACCTGTTACTGTTGGGCT 6689	C	CGAG
TT		AGAGTTCG CGGTGGC GCGC		
		TTTCGGGT GTCATTG CGTG		
		T TCCA		
GAM1956 RP42	3'	GTGTTTTGTTTGGGGGAATT 21802	G	GGT
TT		AGAGTTC CC GGCCGAGGCGC		
		TTTTAAG GG TTGGTTTTGTG		
		G GGT		
GAM1956 RPN2	5'	GCGTCCCCTGTGGCGGGCTCT 8863	GT	CCGA
		AGAGTTCGCCG GG GGCGC		
		TCTCGGGCGGT CC CTGCG		
		GT C_____		
GAM1956 SCA1	5'	GCTGCTGTTGGCGGATT 5880	TG	CGA
		AGTTCGCCG GC GGC		
		TTAGGCGGTT CG TCG		
		GT _____		
GAM1956 SDC1	3'	GTGTCTTGGGCAGAGCTGGCTC 8888	TC	CGG G
T		AGAGT GC TG CCGAGGCGC		
		TCTCG CG AC GGTCTGTG		
		GT AG_ G		
GAM1956 SOCS5	3'	GTGCTCTGTACCACTGGTGAGT 15229	AG	C_ AG
GCT		AG TTCGCCGGTGG CG GCGC		
		TC GAGTGGTCACC GT CGTG		
		GT AT CT		
GAM1956 SOX13	3'	GTGCCTCGGCCTCCAAGGGGCT 12244	GCC	T
TT		AGAGTTC GG GGCCGAGGCGC		

		TTTCGGG CC CCGGCTCCGTG	
		GAA T	
GAM1956	SWAP70	3' GTGCTTTGGCTAAGATAGATAC 35349	_ GCCGG
	T	AGT TC TGGCCGAGGCGC	
		TCA AG ATCGGTTTCGTG	
		T ATAGA	
GAM1956	TAF6	5' GCGTCTCGGCTGCCGCTAGAGT 12174	GT GC_ TG
	TT	GA TC CGG GCCGAGGCGC	
		TT AG GCC CGGCTCTGCG	
		TG ATC GT	
GAM1956	TRAF5	3' GTGTCACTGCTGGTGAAC 10967	TG CC G
		AGTTCGCCGG G GA GC	
		TCAAGTGGTC C CT TG	
		GT A_ G	
GAM1956	UVRAG	5' GTGCCTCTCGGGTGGCGGGT 9394	G G ____
		GCC GT GCC GAGGCGC	
		TGG CG TGG CTCCGTG	
		G G GCT	
GAM1956	VDR	3' GTGCCCTGGCTGCTGGGCTCT 5948	TCG TG A
		AGAGT CCGG GCCG GGCGC	
		TCTCG GGTC CGGT CCGTG	
		____ GT C	
GAM1956	WHSC1	3' TGTCCCGCGGGCGAGTTCT 28454	GT G CCGA
		AGA TCGCC GTGG GGCG	
		TCT AGCGG CGCC CTGT	
		TG G ____	
GAM1956	WHSC1	3' TGTCCCGCGGGCGAGTTCT 28471	GT G CCGA
		AGA TCGCC GTGG GGCG	
		TCT AGCGG CGCC CTGT	
		TG G ____	
GAM1956	WHSC1	3' TGTCCCGCGGGCGAGTTCT 17190	GT G CCGA
		AGA TCGCC GTGG GGCG	
		TCT AGCGG CGCC CTGT	
		TG G ____	
GAM1956	ZNF74	5' GTGCCACGACAGGTGGGCTTT 9475	GG GC A
		AGAGTTCCGC TG CG GGCGC	
		TTTCGGGTGG AC GC CCGTG	
		____ A_ A	
GAM1956	ACF	5' GTGCCAAAAACCTGTGGATTTT 29059	C GGCCGA
		AGAGTTCCGC GGT GGCGC	

		TTTTAGGTG CCA CCGTG	
		T AAAA__	
GAM1956 ACF	5'	GTGCCAAAAACCTGTGGATTTT 15938	C GGCCGA
		AGAGTTCGC GGT GGCGC	
		TTTTAGGTG CCA CCGTG	
		T AAAA__	
GAM1956 AGTRL2	5'	GTGCCTCTGTTGGCTGAGCTCT 11647	_ GTG C
		AGAGTTC GCCG GC GAGGCGC	
		TCTCGAG CCGT TG CTCCGTG	
		T ____ T	
GAM1956 BOLL	5'	GCCACTGCTGCTGGCGGATTT 26922	TG CGA
		GAGTTCGCCGG GC GGC	
		TTTAGGCGGTC CG CCG	
		GT TCA	
GAM1956 C22orf2	3'	GCCTGGGGCTGCTGATGAGCTT 45335	C TG _ G GC
T		AGAGTTCG CGG GC C AGGC	
		TTTCGAGT GTC CG G TCCG	
		A GT G G	
GAM1956 CBX3	3'	GCGTTGGAAGAGTTGTTGGGGG 14142	TT G TG CGA__
TTTT		AG C CCGG GC GGCGC	
		TT G GGTT TG TTGCG	
		GG _ GT AGAAGG	
GAM1956 CBX3	3'	GCGTTGGAAGAGTTGTTGGGGG 18662	TT G TG CGA__
TTTT		AG C CCGG GC GGCGC	
		TT G GGTT TG TTGCG	
		GG _ GT AGAAGG	
GAM1956 CENTB5	3'	GCGTCTTTTCTCTGTGGA CTCT 45725	C T CC
		AGAGTTCGC GG GG GAGGCGC	
		TCTCAGGTG TC CT TTCTGCG	
		_ T T_	
GAM1956 CHRAC1	3'	TGTCTAGTCTGTGAATTTT 18909	CGGT CG
		AGAGTTCGC GGC AGGCG	
		TTTAAAGTG CTG TCTGT	
		T__ A_	
GAM1956 CHST3	5'	GTCGGGGCCGCCGGTGGAGTCT 10484	G GA
		AGA TTCGCCGGTGGCC GGC	
		TCTAGGTGGCCGCCGG CTG	
		G GG	
GAM1956 CRMP5	3'	TGCCTTGGCCTCGGCGGGCTTT 21334	T C
		AGAGTTCGCCGG GGCCGAGGCG	

				TTTCGGGCGGCT CCGGTTCCGT			
				- C			
GAM1956	DDX17	5'	GTTATGTTGTTGGTAGATTTT	25156	CG	TG	CGA
			AGAGTT CCGG GC GGC				
			TTTTAG GGTT TG TTG				
			AT GT TA_				
GAM1956	DKFZP434B044	3'	TGCTCTGCTGCTGGACTTT	25554	TCG	TG	C G
			AGAGT CCGG GC GAG CG				
			TTTCA GGTC CG CTC GT				
			_ GT T _				
GAM1956	DKFZP762D096	5'	GCGCTTGAGCTGCTGAGCTTT	32666	C	GG	G
			AGAGTTCG CCGT CCGAG CGC				
			TTTCGAGT GTCG GGTTT GCG				
			C A_ _				
GAM1956	ESM1	3'	GTGCTGTGACTTCGGTGAATTT	13913	T	C	A
	T		AGAGTTCGCCGG GG CG GGCGC				
			TTTTAAGTGGCT TC GT TCGTG				
			_ A G				
GAM1956	FENS-1	3'	GTATGCCACAGGTGAATTT	21892	G	CGAG	
			AGAGTTCGCC GTGGC GC				
			TTTCAAGTGG CACCG TG				
			A TA__				
GAM1956	FLB6421	3'	GTGCCTGGCTTTGCTGTGGATT	21302	C	_	G
	CT		AGAGTTCGC GGT GGCC AGGCGC				
			TCTTAGGTG TCG TCGG TCCGTG				
			_ TT _				
GAM1956	FLJ10521	3'	TGTTTTGGGGAGGAGTTT	19912	G	G	GGTGG
			AGA TTC CC CCGAGGCG				
			TTT AGG GG GGTTTTGT				
			G A _____				
GAM1956	FLJ10713	3'	GTGCTGCTGACAGGTGAATCT	20042	G	_	CGA
			AGAGTTCGCC GT GGC GGCGC				
			TCTCAAGTGG CA TCG TCGTG				
			A G _				
GAM1956	FLJ11164	3'	GTGCCTCTCATTAAGTGGACTTT	20358	CG	CC	
			AGAGTTCGC GTGG GAGGCGC				
			TTTCAGGTG TACT CTCCGTG				
			AT _				
GAM1956	FLJ11362	5'	GCGTCTTGGCTATAAGGAT	22471	GCCG		
			GTTC GTGGCCGAGGCGC				

TAGG TATCGGTTCTGCG
 AA__
 GAM1956 FLJ13197 3' GTGTCCGGAATTGGTGGGTTCT 23872 TT GG A
 AGAG CGCCGGT CCG GGCGC
 ||| ||||| || |||||
 TCTT GTGGTTA GGC CTGTG
 GG A_ _
 GAM1956 FLJ13441 3' GCGCTCTGCTGTTGCCGGTGAG 23394 G TG _ AG
 TCT GA TTCGCCGG GC CG GGCG
 || ||||| || || |||
 CT GAGTGGCC TG GT CGCG
 _ GT TC CT
 GAM1956 FLJ13993 3' GCGGCTGCCACTGTGGGCTCT 30327 C CG G
 AGAGTTCGC GGTGGC AG CGC
 ||||| ||||| || |||
 TCTCGGGTG TCACCG TC GCG
 _ _ G
 GAM1956 FLJ14075 3' GTGCCTTGTGGGTTGGACTTT 24376 _ G TGGC
 AGAGTTCG CC G CGAGGCGC
 ||||| || | |||||
 TTTCAGGT GG T GTTCCGTG
 T G ____
 GAM1956 FLJ22548 5' GCGCCGGCAGCGGCCGCGGTGG 22794 TT G A ____
 GTTCT CGCCG TGGCCG GGCGC
 |||| ||||| |||||
 GTGGC GCCGGC CCGCG
 GG _ GACGG
 GAM1956 FLJ23042 3' GCATGGCCATTGGCGGGTCT 24797 G AG
 AGA TTCGCCGGTGGCCG GC
 || ||||| ||||| ||
 TCT GGGCGGTTACCGGT CG
 _ A_
 GAM1956 FLJ23360 5' GTCCAGGTGCTGGCCGGCTC 23336 TC GA_ GC
 T AGAGT GCCGGTGGCC GGC
 |||| ||||| |||||
 TCTCG CGGTCGCTGG CTG
 GC ACC
 GAM1956 FLJ30681 3' TGCTTTGGTGGAGAATTTT 44106 G GGTG
 AGAGTTC CC GCCGAGGCG
 ||||| || |||||
 TTTTAAG GG TGGTTTCGT
 A ____
 GAM1956 GMPPB 5' GTGCCAGGTGCTGGGGGCTCT 45817 G G GA
 AGAGTTC CCGGTG CC GGCGC
 ||||| ||||| || |||||
 TCTCGGG GGTCTG GG CCGTG
 _ _ A_
 GAM1956 GTPBP2 3' GCCCTGCCATTGGCGGCTCT 21173 T CGA
 AGAGT CGCCGGTGGC GGC
 |||| ||||| ||||| |||

TCTCG GCGGTTACCG CCG
 _ TC_
 GAM1956 HIC2 3' GTGCCTGCAGCTCACCTGTGGG 32531 TT C _ CG_
 TTTT GAG CGC GGTG GC AGGCGC
 ||| ||| ||| || ||| |||
 TTT GTG CCAC CG TCCGTG
 GG T T ACG
 GAM1956 HIG2 5' GCGCTTTTGTCTCCGGTGAGTT 14978 GT T C
 TT AGA TCGCCGG GGC GAGGCGC
 ||| ||| ||| ||| ||| |||
 TTT AGTGGCC CTG TTTCGCG
 TG T T
 GAM1956 HSC3 3' GTGTTTTGGTTAATCACAAATT 29735 CGCCGG
 TT AGAGTT TGGCCGAGGCGC
 ||| ||| ||| ||| ||| ||| |||
 TTTTAA ATTGGTTTTGTG
 AACTA
 GAM1956 HYPH 3' GTGTAGGGCTAATGGTGAATTT 45483 G GAG
 T AGAGTTCGCCG TGGCC GCGC
 ||| ||| ||| ||| ||| ||| ||| |||
 TTTTAAGTGGT ATCGG TGTG
 A GA_
 GAM1956 IL1F10 5' TGGAAGCCTTGGTGGATTCT 26284 _ GG
 AGAGTTCGCC GGT CCG
 ||| ||| ||| ||| ||| ||| ||| |||
 TCTTAGGTGG CCG GGT
 TT AA
 GAM1956 KIAA0057 3' GTGTCTTTTTGCTTTTGGTGAA 14624 T C_
 CTTT GAGTTCGCCGG GGC GAGGCGC
 ||| ||| ||| ||| ||| ||| ||| |||
 TTCAAGTGGTT TCG TTCTGTG
 T TTT
 GAM1956 KIAA0317 3' GTGTTTCTTATTTTGGCCAGTT 16796 GT C TGGCC
 CT AGA T GCCGG GAGGCGC
 ||| ||| ||| ||| ||| ||| ||| |||
 TCT A CGGT CTTTGTG
 TG C TTATT
 GAM1956 KIAA0453 3' GTGTCTTGCTGCTTGGTGGGTG 34230 A TT _TG C
 CT AG G CGCCG G GC GAGGCGC
 || ||| ||| ||| ||| ||| ||| |||
 TC T GTGGT C CG TTCTGTG
 G GG T GT _
 GAM1956 KIAA0618 3' GTGTCTCGGTTACACAGC 16837 CG_
 GC GTGGCCGAGGCGC
 || ||| ||| ||| ||| ||| ||| |||
 CG CATTGGCTCTGTG
 ACA
 GAM1956 KIAA0931 3' GTGCAATACATTGGTGAGTTC 33487 GT GCCGAG
 GA TCGCCGGTG GCGC
 || ||| ||| ||| ||| ||| ||| |||

			CT AGTGGTTAC	CGTG	
			TG	ATAA__	
GAM1956	KIAA1013	3'	GTGCCTTAAATGGTGAAC	42859	GTGGCC
			GTTCGCCG	GAGGCGC	
			CAAGTGGT	TTCCGTG	
			AAAA__		
GAM1956	KIAA1017	5'	GTGTCTCGGAAATGGTTGGCTT	14081	TC GTGG
	T		AGAGT GCCG	CCGAGGCGC	
			TTTCG TGGT	GGCTCTGTG	
			GT	AAA_	
GAM1956	KIAA1193	3'	GTGCTTTGGTGTATTGAGT	33591	- -
			GC CGGTG GCCGAGGCGC		
			TG GTTAT TGGTTTCGTG		
			A	G	
GAM1956	KIAA1193	3'	GTGCTTTGGTGTATTGAGT	33606	- -
			GC CGGTG GCCGAGGCGC		
			TG GTTAT TGGTTTCGTG		
			A	G	
GAM1956	KIAA1193	3'	GTGCTTTGGTGTATTGAGT	33604	- -
			GC CGGTG GCCGAGGCGC		
			TG GTTAT TGGTTTCGTG		
			A	G	
GAM1956	KIAA1193	3'	GTGCTTTGGTGTATTGAGT	33605	- -
			GC CGGTG GCCGAGGCGC		
			TG GTTAT TGGTTTCGTG		
			A	G	
GAM1956	KIAA1193	3'	GTGCTTTGGTGTATTGAGT	33600	- -
			GC CGGTG GCCGAGGCGC		
			TG GTTAT TGGTTTCGTG		
			A	G	
GAM1956	KIAA1193	3'	GTGCTTTGGTGTATTGAGT	33603	- -
			GC CGGTG GCCGAGGCGC		
			TG GTTAT TGGTTTCGTG		
			A	G	
GAM1956	KIAA1193	3'	GTGCTTTGGTGTATTGAGT	33590	- -
			GC CGGTG GCCGAGGCGC		
			TG GTTAT TGGTTTCGTG		
			A	G	
GAM1956	KIAA1193	3'	GTGCTTTGGTGTATTGAGT	33592	- -
			GC CGGTG GCCGAGGCGC		

			TG GTTAT TGGTTTCGTG		
			A G		
GAM1956	KIAA1193	3'	GTGCTTTGGTGTATTGAGT	33594	— —
			GC CGGTG GCCGAGGCGC		
			TG GTTAT TGGTTTCGTG		
			A G		
GAM1956	KIAA1193	3'	GTGCTTTGGTGTATTGAGT	33597	— —
			GC CGGTG GCCGAGGCGC		
			TG GTTAT TGGTTTCGTG		
			A G		
GAM1956	KIAA1193	3'	GTGCTTTGGTGTATTGAGT	33586	— —
			GC CGGTG GCCGAGGCGC		
			TG GTTAT TGGTTTCGTG		
			A G		
GAM1956	KIAA1193	3'	GTGCTTTGGTGTATTGAGT	33587	— —
			GC CGGTG GCCGAGGCGC		
			TG GTTAT TGGTTTCGTG		
			A G		
GAM1956	KIAA1193	3'	GTGCTTTGGTGTATTGAGT	33588	— —
			GC CGGTG GCCGAGGCGC		
			TG GTTAT TGGTTTCGTG		
			A G		
GAM1956	KIAA1193	3'	GTGCTTTGGTGTATTGAGT	33589	— —
			GC CGGTG GCCGAGGCGC		
			TG GTTAT TGGTTTCGTG		
			A G		
GAM1956	KIAA1193	3'	GTGCTTTGGTGTATTGAGT	33595	— —
			GC CGGTG GCCGAGGCGC		
			TG GTTAT TGGTTTCGTG		
			A G		
GAM1956	KIAA1193	3'	GTGCTTTGGTGTATTGAGT	33596	— —
			GC CGGTG GCCGAGGCGC		
			TG GTTAT TGGTTTCGTG		
			A G		
GAM1956	KIAA1193	3'	GTGCTTTGGTGTATTGAGT	33593	— —
			GC CGGTG GCCGAGGCGC		
			TG GTTAT TGGTTTCGTG		
			A G		
GAM1956	KIAA1193	3'	GTGCTTTGGTGTATTGAGT	33601	— —
			GC CGGTG GCCGAGGCGC		

		TG GTTAT TGGTTTCGTG		
		A G		
GAM1956 KIAA1193	3'	GTGCTTTGGTGTATTGAGT 33602	_	_
		GC CGGTG GCCGAGGCGC		
		TG GTTAT TGGTTTCGTG		
		A G		
GAM1956 KIAA1193	3'	GTGCTTTGGTGTATTGAGT 33598	_	_
		GC CGGTG GCCGAGGCGC		
		TG GTTAT TGGTTTCGTG		
		A G		
GAM1956 KIAA1193	3'	GTGCTTTGGTGTATTGAGT 33599	_	_
		GC CGGTG GCCGAGGCGC		
		TG GTTAT TGGTTTCGTG		
		A G		
GAM1956 KIAA1254	3'	TGTAGGTGTTGTGAGCTTT 34699		CGGTG GAG
		AGAGTTCGC GCC GCG		
		TTTCGAGTG TGG TGT		
		TTG__ A__		
GAM1956 KIAA1323	3'	GTGCTAGTACTTGTGGGTTTT 31568	TT C	G CGA
		AGAG CGC GGTG C GGCGC		
		TTTT GTG TCAT G TCGTG		
		GG T _A__		
GAM1956 KIAA1332	3'	GTGTCTCGGCCAAGGCGAGC 35260		GG
		GTTCGCC TGGCCGAGGCGC		
		CGAGCGG ACCGGCTCTGTG		
		A_		
GAM1956 KIAA1450	3'	GTGTTTCGGTTGGTAAGTTCT 32749	GT CG	GTG
		AGA T CCG GCCGAGGCGC		
		TCT A GGT TGGCTTTGTG		
		TG AT ____		
GAM1956 KIAA1627	5'	GTAAGCTCCCGGTGAATTTT 39344		TG CGAG
		AGAGTTCGCCGG GC GC		
		TTTTAAGTGGCC CG TG		
		CT AA__		
GAM1956 KIAA1878	3'	TTAGCTTCCTATCAGTGGGCTT 44078	C CC	GC
T		AGAGTTCGC GGTGG GAGGC		
		TTTCGGGTG CTATC CTTCG		
		A __ ATTT		
GAM1956 KIAA1900	5'	CGAAGCTACTGCGGGTTCT 36259	TT C	CGAGG
		AGAG CGC GGTGGC CG		

TCTT GCG TCATCG GC
 GG _ AA____
 GAM1956 KIAA1932 5' GTCAGGAGCTGCCGGCGGCTCT 36350 T TG CGA_
 AGAGT CGCCGG GC GGC
 ||||| ||||| || |||
 TCTCG GCGGCC CG CTG
 _ GT AGGA
 GAM1956 KR18 3' CGTTTCAATGTGAACTTT 27117 CG GGCC
 AGAGTTCGC GT GAGGCG
 ||||| || |||||
 TTTCAAGTG TA CTTTGC
 _ A____
 GAM1956 LIG-1 3' GTGTTGGTACCTGTGGATTTT 31953 C G G
 AGAGTTCGC GGTG CCGA GC
 ||||| ||||| ||||| ||
 TTTTAGGTG CCAT GGTT TG
 T _ G
 GAM1956 LIMK2 3' GTGAACCTGCCTGTGAACTCT 12096 C TG CCGAGG
 AGAGTTCGC GG G CGC
 ||||| || | |||
 TCTCAAGTG CC C GTG
 T GT CAA____
 GAM1956 LIMK2 3' GTGAACCTGCCTGTGAACTCT 18787 C TG CCGAGG
 AGAGTTCGC GG G CGC
 ||||| || | |||
 TCTCAAGTG CC C GTG
 T GT CAA____
 GAM1956 MAC30 5' GCGGTGCTGCCGCGCGAGCTCT 31406 _ TG CGAG
 AGAGTTCGC CGG GC GC
 ||||| ||||| || ||
 TCTCGAGCG GCC CG CG
 C GT TGG_
 GAM1956 MAPKAPK2 3' GTGCCTTGGCCACAATGCG 11151 CG_
 CGC GTGGCCGAGGCGC
 ||| ||||| |||||
 GCG CACCGGTTCCGTG
 TAA
 GAM1956 MGC13040 5' GTGGGATCGGTTATCGGTGCGC 26755 T GG_
 TCT AGAGT CGCCGGTGGCCGA CGC
 ||||| ||||| ||||| |||||
 TCTCG GTGGCTATTGGCT GTG
 C AGG
 GAM1956 MGC14386 5' TGTCCCACTAGCGGGCTCT 27307 CG CCGA
 AGAGTTCGC GTGG GGCG
 ||||| ||||| |||||
 TCTCGGGCG CACC CTGT
 AT ____
 GAM1956 MGC20481 3' GTGTCTCACAGCTTGGCTGAGC 31425 _ GT C_
 TCT AGTTC GCCG GGC GAGGCGC
 ||||| ||||| ||||| |||||

TCGAG CGGT TCG CTCTGTG
T _ ACA
GAM1956 MGC2477 5' GTGTCTTCATGGTTGCCGTGGG 23544 TT C TG _
TTTT AG CGC GG GCC GAGGCGC
|| ||| || ||| |||||
TT GTG CC TGG TTCTGTG
GG _ GT TAC
GAM1956 MGC2477 5' GCAGTCACCCGCGAGTTTT 23543 GT C CGAG
AGA TCGC GGTGGC GC
||| |||| ||||| ||
TTT AGCG CCACTG CG
TG C A _
GAM1956 MGC34923 5' GTGTCCGGAATTGGTGGGTTCT 29537 TT GG A
AGAG CGCCGGT CCG GGCGC
|||| ||||| ||| |||||
TCTT GTGGTTA GGC CTGTG
GG A _ _
GAM1956 MGC4342 3' GCCCAGGCCACCGGCCGGGTTC 23625 TT _ GA GC
T AGAG CG CCGGTGGCC GGC
|||| || ||||| |||
TCTT GC GGCCACCGG CCG
GG C AC
GAM1956 MGC4701 5' CGTCGCGGTGGTGGACTCT 32242 GGTG A
AGAGTTCGCC GCCG GGCG
||||||| ||| |||||
TCTCAGGTGG TGGC CTGC
_ G
GAM1956 MGC9753 5' GTGTATGTGGGTACCGTTGGG 27243 C GAG_
CTCT GAGTTCG CGGTGGCC GCGC
|||||| ||||| |||
CTCGGGT GCCACTGG TGTG
T GTGTA
GAM1956 MIC2L1 3' TTCTGTCCCGGTGAGCTCT 25494 T C
AGAGTTCCGCCG GGC GAG
||||||| ||| |||
TCTCGAGTGGCC CTG CTT
_ T
GAM1956 NEDD5 3' GTGTTTTGTGAGGTGAATGTCT 10658 _ GGTGGC
AGA GTTCGCC CGAGGCGC
||| ||||| |||||
TCT TAAGTGG GTTTTGTG
G AGT_
GAM1956 PPP1R3B 3' GTGCCTTGCTCCTAGAGTTTT 23860 GT GCC T
AGA TC GG GGCCGAGGCGC
||| || || |||||
TTT AG CC TCGGTTCCGTG
TG AT_ _
GAM1956 PRO0971 5' GTGCCCTCACGCCCGGGGCTC 20652 TCG C_ _
T AGAGT CCGGTGGC GAGG CGC
|||| ||||| ||| |||

TCTCG GGCCGCCG CTCC GTG
 _____ CA C
 GAM1956 RHOBTB2 3' TGTCTTGTTGCTGCTCT 30562 TCGCC TG
 AGAGT GG GCCGAGGCG
 ||||| || |||||
 TCTCG TC TGGTTCTGT
 _____ GT
 GAM1956 RNPC1 3' TGTCTTGAGGGAGGACTTT 18959 G GGTGGC
 AGAGTTC CC CGAGGCG
 ||||| || |||||
 TTTCAGG GG GTTCTGT
 A GA____
 GAM1956 Rpo1-2 3' GCTTTTTGTTGCTGTTGAGTT 21105 GT C TG C
 TT AGA TCG CGG GCCGAGG GC
 ||| ||| ||| ||||| ||
 TTT AGT GTC TGGTTTT CG
 TG T GT T
 GAM1956 Rpo1-2 3' GCTTTTTGTTGCTGTTGAGTT 25935 GT C TG C
 TT AGA TCG CGG GCCGAGG GC
 ||| ||| ||| ||||| ||
 TTT AGT GTC TGGTTTT CG
 TG T GT T
 GAM1956 SAE1 3' GTGTTTCACATATGTTGTGAAT 12006 CG_ GCC
 TTT AGAGTTCGC GTG GAGGCGC
 ||||| || |||||
 TTTTAAGTG TAT CTTTGTG
 TTG ACA
 GAM1956 SDCCAG3 3' GTGCCTCTTTGGCTGGGGGTTT 13435 TT G GGCC
 T AGAG C CCGGT GAGGCGC
 |||| | |||| |||||
 TCTT G GGTCG CTCCGTG
 GG_ GTTT
 GAM1956 SEC61A1 3' GCGCCTCGGAAGGGGAGCTCT 14985 G GGTGG
 AGAGTTC CC CCGAGGCGC
 ||||| || |||||
 TCTCGAG GG GGCTCCGCG
 G AA____
 GAM1956 SEMA3C 5' GCGTCTGGCCAGCCGCGAGCTC 13074 C _ G
 T AGAGTTCGC GG TGGCC AGGCGC
 ||||| || |||| |||||
 TCTCGAGCG CC ACCGG TCTGCG
 _ G _
 GAM1956 SERP1 3' GTGTCTTGTTAACTAATTCT 15797 CGCC _
 AGAGTT GGT GGCCGAGGCGC
 ||||| || |||||
 TCTTAA TCA TTGGTTCTGTG
 _____ A
 GAM1956 SHARP 3' GCGCTTCGGTACAGCACGGGT 17368 G ____
 GCC GTG GCCGAGGCGC
 ||| ||| |||||

TGG CAC TGGCTTCGCG
 G GACA
 GAM1956 SMARCF1 5' GCGCCTCGGCCGCCGCCGCCGC 20520 A T_ C
 CT AG GT CG CGGTGGCCGAGGCGC
 || || || |||||
 TC CG GC GCCGCCGGCTCCGCG
 _ CC C
 GAM1956 SMARCF1 5' GCGCCTCGGCCGCCGCCGCCGC 12625 A T_ C
 CT AG GT CG CGGTGGCCGAGGCGC
 || || || |||||
 TC CG GC GCCGCCGGCTCCGCG
 _ CC C
 GAM1956 SMARCF1 5' GCGCCTCGGCCGCCGCCGCCGC 29163 A T_ C
 CT AG GT CG CGGTGGCCGAGGCGC
 || || || |||||
 TC CG GC GCCGCCGGCTCCGCG
 _ CC C
 GAM1956 STK29 5' TGTCAGGTGGTGAGCTCT 42318 GGTG GA
 AGAGTTCGCC GCC GGCG
 ||||| ||| |||
 TCTCGAGTGG TGG CTGT
 _ A_
 GAM1956 SYT13 3' TGAGTCATTGGCTGGGTTCT 44892 TT _ _
 AGAG C GCCGGTGGC CG
 ||| | ||||| ||
 TCTT G CGGTTACTG GT
 GG T A
 GAM1956 SZF1 3' GTGTCTGGAATTGGTGGGTTCT 18174 TT GG G
 AGAG CGCCGGT CC AGGCGC
 ||| ||||| || |||||
 TCTT GTGGTTA GG TCTGTG
 GG A_ _
 GAM1956 TEX27 3' GTGCCTTGGCCACGGGAGGCTG 22461 _ CG G
 CT AG AGTT CC GTGGCCGAGGCGC
 || ||| || |||||
 TC TCGG GG CACCGGTTCCGTG
 G A_ G
 GAM1956 TRIM11 3' GTGTTTTGGCCACTTGGAGGAC 36055 A G _
 CT AG GTTC CCG GTGGCCGAGGCGC
 || ||| || |||||
 TC CAGG GGT CACCGGTTTTGTG
 _ A T
 GAM1956 TRIM38 3' GCTGAAATGGCTGTTGGCAGTT 13051 GT C TG A_ GC
 CT GA T GCCGG GCCG GGC
 || | |||| ||| |||
 CT A CGGTT CGGT TCG
 TG_ GT AAAG
 GAM1956 UBE2G1 3' TTGGCCGTTGTGAGCTCT 9350 C GG
 AGAGTTCG C TGGCCGA
 ||||| | |||||

		TCTCGAGT G GCCGGTT		
		_ TT		
GAM1956	ZFD25	5' GCCCAGGGTCACTGGGAACTCT 18322	G	GA_
		AGAGTTC CCGGTGGCC GGC		
		TCTCAAG GGTCAGTGG CCG		
		_ GAC		
GAM1956	ZNF238	3' TACTATTGGTGTGTTGGTGAAT 13045	GT_	GGCGC
	TTT	AGAGTTCGCCG G GCCGA		
		TTTTAAGTGGT T TGGTT		
		TG G ATCATG		
GAM1956	LOC124460	3' GCCTGAGGCCGCTGGTAGACTT 37446	CG	G_ GC
	T	AGAGTT CCGGTGGCC AGGC		
		TTTCAG GGTCGCCGG TCCG		
		AT AG		
GAM1956	LOC130412	5' GCAATGCTGCCGGGAGCTCT 37292	G	TG CGAG
		AGAGTTC CCGG GC GC		
		TCTCGAG GGCC CG CG		
		_ GT TAA_		
GAM1956	LOC144486	3' GTGCCTTGTTGGGCTTTGATT 40418	C__	GGT
	CT	AGAGTT GCC GGCCGAGGCGC		
		TCTTAG CGG TTGGTTCCGTG		
		TTT G__		
GAM1956	LOC145082	5' TGTCCTGTCGGTGTGCTCT 40496	T	TG CCGA
		AGAGT CGCCGG G GGCG		
		TCTCG GTGGCT C CTGT		
		T GT ____		
GAM1956	LOC145622	3' GTGTCCGGAATTGGTGGGTTCT 37914	TT	GG A
		AGAG CGCCGGT CCG GGCGC		
		TCTT GTGGTTA GGC CTGTG		
		GG A_ _		
GAM1956	LOC145955	3' GTGACTGTTGTGGACTCT 40645	_	G
		AGAGTTCGC CCGT GC		
		TCTCAGGTG GTCA TG		
		TT G		
GAM1956	LOC146146	5' GTGCCTTGTTTCCTGGCCTCT 38072	TTC _	TG
		AGAG GCC GG GCCGAGGCGC		
		TCTC CGG CC TGGTTCCGTG		
		_ T TT		
GAM1956	LOC146774	3' GTGCCAGCCACCGTGTGAACTC 38236	_	CGA
	T	AGAGTTCGC CCGTGGC GGCGC		

TCTCAAGTG GCCACCG CCGTG
 T A__
 GAM1956 LOC148254 3' GTAAGTCATCGCTGAGCTTT 38504 C CGAG
 AGAGTTCG CCGTGGC GC
 ||||| ||||| ||
 TTTCGAGT GCTACTG TG
 C AA__
 GAM1956 LOC148938 3' TGTCTCTTTGGCGAACCCCT 40928 A TGGCC
 AG GTTCGCCGG GAGGCG
 || ||||| |||||
 TC CAAGCGGT CTCTGT
 C T____
 GAM1956 LOC149276 5' GCTGATGCTGGTGGGCTTT 40976 GCCGA
 AGAGTTCGCCGGTG GGC
 ||||| ||||| |||||
 TTTCGGGTGGTCGT TCG
 AG____
 GAM1956 LOC149705 3' GCTGCTGCTGTGGATTCT 41053 C TG CGA
 AGAGTTCGC GG GC GGC
 ||||| || || |||||
 TCTTAGGTG TC CG TCG
 _ GT ____
 GAM1956 LOC152137 5' CGCGAGCCCTGCCGGCCGGA CT 39222 _ _ _ AGGCGC
 TT AGTTCG CCGGT GGC CG
 ||||| ||||| |||||
 TCAGGC GGCCG CCG GC
 C TC A G CG
 GAM1956 LOC153811 3' GTCTCACGGGGGCTCT 39418 G GTGGCC
 AGAGTTC CCG GAGGC
 ||||| ||||| |||||
 TCTCGGG GGC CTCTG
 _ A____
 GAM1956 LOC157867 5' TGCCTTGGAGTGGACTT 41857 CGGTGG
 GAGTTCGC CCGAGGCG
 ||||| ||||| |||||
 TTCAGGTG GGTTCGT
 A____
 GAM1956 LOC158308 3' GCCCTGGTTATTGCTGAGCTCT 41941 C A
 AGAGTTCG CCGTGGCCG GGC
 ||||| ||||| |||||
 TCTCGAGT GTTATTGGT CCG
 C C
 GAM1956 LOC159121 3' GTCAAAGGTTGCCAGCGGGCTC 42063 C TG GA_ GC
 T AGAGTTCGC GG GCC GGC
 ||||| ||||| |||||
 TCTCGGGCG CC TGG CTG
 A GT AAA
 GAM1956 LOC162022 5' CGCGGTGGTGGTGGGCTTT 40043 GGTG AG
 AGAGTTCGCC GCCG GCG
 ||||| ||||| |||||

	TTTCGGGTGG TGGT CGC	
	____ GG	
GAM1956 LOC169966 3'	GTGCCTCTTCGTGTGAATTTT 40166	_ TGGCC
	AGAGTTTCG CGG GAGGCGC	
	TTTTAAGTG GCT CTCCGTG	
	T T ____	
GAM1956 LOC196500 3'	GTTCAAGGCCATCGGGAGCTCT 42391	G GA_
	AGAGTTC CCGGTGGCC GGC	
	TCTCGAG GGCTACCGG TTG	
	____ AAC	
GAM1956 LOC199688 5'	GCGTCTCCTCCGAGCTGTTGGG 43230	C ____ CC
CTTT	GAGTTCG CGGT GG GAGGCGC	
	TTCGGGT GTCG CC CTCTGCG	
	T AG TC	
GAM1956 LOC199699 3'	GTGCTTTGGTCATTGCTCCTCT 42596	TTCGC
CT	AGAG CGGTGGCCGAGGCGC	
	TCTC GTTACTGGTTTCGTG	
	TCCTC	
GAM1956 LOC199796 5'	GCGCCTCTTCCGCTGGCTGGTT 36812	TC CC
CT	AGAGT GCCGGTGG GAGGCGC	
	TCTTG CGGTCGCC CTCCGCG	
	GT TT	
GAM1956 LOC200035 5'	GCGTCCGGAGTCGGTGAGCTT 36263	TGG A
	GAGTTCGCCGG CCG GGCGC	
	TTCGAGTGGCT GGC CTGCG	
	GA_ _	
GAM1956 LOC201707 5'	GCGCCTCCTTCTGCGGACTCT 42902	C T CC
	AGAGTTTCG CG GG GAGGCGC	
	TCTCAGGCG TC TC CTCCGCG	
	_ T _	
GAM1956 LOC202020 5'	GCTGGCGCGCCGGCGGACTTT 42953	_ GA
	AGAGTTCGCCGGTG GCC GGC	
	TTTCAGGCGGCCGC CGG TCG	
	G _	
GAM1956 LOC202934 3'	GTGTCTGAACTACCACTGAGTT 43464	GT C CCG
TT	AGA TCGC GGTGG AGGCGC	
	TTT AGTG CCATC TCTGTG	
	TG A AAG	
GAM1956 LOC205085 5'	AAAACTGGCTGCGGTGAGCTCT 43599	G TG AGGCGC
	AGAGTTCGCC G GCCG	

TCTCGAGTGG C CGGT
 _GT CAAAAG
 GAM1956 LOC219649 5' GTGCTTTGGTCACAAAGC 44667 CG_
 GC GTGGCCGAGGCGC
 || |||||
 CG CACTGGTTTCGTG
 AAA
 GAM1956 LOC220020 5' GCGTCAGATGGCACTGGCGGGT 44866 TT G A_
 TT GAG CGCCGGTG CCG GGCGC
 ||| ||||| ||| |||||
 TTT GCGGTCAC GGT CTGCG
 GG _ AGA
 GAM1956 LOC220906 3' GTGTTTTGTTGTTTTGGGAATT 43927 G TGGC_
 TT AGAGTTC CCGG CGAGGCGC
 ||||| ||| |||||
 TTTTAAG GGTT GTTTTGTG
 _ TTGTT
 GAM1956 LOC253758 5' CGCCGAGTCCGCGAGCTCT 46319 C TG CGA
 AGAGTTCGC GG GC GGCG
 ||||| || || |||||
 TCTCGAGCG CC TG CCGC
 _ _ AG_
 GAM1956 LOC253782 3' TGGTTATTGGAGAACTTT 45801 G
 AGAGTTC CCGGTGGCCG
 ||||| |||||
 TTTCAAG GGTTATTGGT
 A
 GAM1956 LOC254170 3' GTCTGAGGTTGCTGGCTAACTT 45504 C TG G_ GC
 T AGAGTT GCCGG GCC AGGC
 ||||| ||||| ||| |||||
 TTTCAA CGGTC TGG TCTG
 T GT AG
 GAM1956 LOC255465 3' GTGTCTGAACTACCACTGAGTT 46456 GT C CCG
 TT AGA TCGC GGTGG AGGCGC
 ||| ||| ||||| |||||
 TTT AGTG CCATC TCTGTG
 TG A AAG
 GAM1956 LOC255520 5' GCGCCTGGGCCGCGGGTCTT 45879 _ GGT G
 GAG TTCGCC GGCC AGGCGC
 ||| ||||| ||| |||||
 TTC GGGCGG CCGG TCCGCG
 T _ G
 GAM1956 LOC54103 5' CGCTTTGGGGCAGATTTT 45207 TC GGTGG
 AGAGT GCC CCGAGGCG
 ||||| ||| |||||
 TTTTA CGG GGTTTCGC
 GA _
 GAM1956 LOC58525 5' GCGAGTTCTGTGGTGAGTTCT 38459 GT GGTG C G_
 AGA TCGCC GC GAG CGC
 ||| ||||| || ||| |||

TCT AGTGG TG CTT GCG
 TG ____ T GA
 GAM1956 LOC84570 5' GCGCCTCGGCCGTTGCCCTC 26267 TTC C GG
 GAG G C TGGCCGAGGCGC
 ||| || |||||
 CTC C G GCCGGCTCCGCG
 C__ TT
 GAM1956 LOC89985 3' GCTGCTGCTGGTGAGCTT 30584 TG CGA
 GAGTTCGCCGG GC GGC
 ||||| || |||
 TTCGAGTGGTC CG TCG
 GT ____
 GAM1956 LOC90170 5' GCGTTGGCCACTGGTGCAATTT 30911 T G
 AGAGT CGCCGGTGGCCGA GC
 |||| ||||| ||
 TTTTA GTGGTCACCGGTT CG
 C G
 GAM1956 LOC90408 5' GGTTACTGGCTGAGTTCT 31398 GT _
 AGA TC GCCGGTGGCC
 ||| || |||||
 TCT AG CGGTCATTGG
 TG T
 GAM1956 LOC90509 5' TGTCTTGGTATGAATTT 31612 GCCGGTG
 GAGTTC GCCGAGGCG
 |||| |||||
 TTTAAG TGTTCTGT
 TA____
 GAM1956 LOC90624 3' GTGCTTTTACAAATTGGTGAGT 31816 GT GGCC_
 TTT AGA TCGCCGGT GAGGCGC
 ||| ||||| |||||
 TTT AGTGGTTA TTTCGTG
 TG AACAT
 GAM1956 LOC90625 5' GTGTTGTCTGTTGGCGCGCTCT 31819 T TG C G
 AGAGT CGCCGG G CGA GC
 |||| |||| | |||
 TCTCG GCGGTT C GTT TG
 C GT T G
 GAM1956 LOC90785 3' GTGTCCAGAATTGGTGGGTTCT 32008 TT GGCC G GC
 AGAG CGCCGGT GA GC
 |||| |||| |||
 TCTT GTGGTTA CT TG
 GG AGAC G
 GAM1956 LOC91818 5' GTGCAGCTGTTGTTGGATTTT 33405 C TG CGAG
 AGAGTTCG CGG GC GCGC
 ||||| ||| || |||
 TTTTAGGT GTT CG CGTG
 T GT A____
 GAM1956 LOC91948 3' GTGTCCAGAATTGGTGGGTTCT 33575 TT GGCC G GC
 AGAG CGCCGGT GA GC
 |||| |||| |||

TCTT GTGGTTA CT TG
 GG AGAC G
 GAM1956 LOC92661 3' TCTGGTCTTGGCGAGCTCT 34727 T G
 AGAGTTCCCGG GGCC AGG
 ||||| ||| |||
 TCTCGAGCGGTT CTGG TCT

— —
 GAM1956 LOC93626 3' GTGTTTTTACCTTGGTGAATCT 36044 G T CC
 AGA TTCGCCGG GG GAGGCGC
 || ||||| || |||||
 TCT AAGTGGTT CC TTTTGTG

— — AT
 GAM1957 ABCB4 5' GGTAAGTGGAAAAATATCATG 6031 CC__
 CATG TTTTCCATTTACT
 ||| |||||
 GTAC AAAAGGTGAATGG
 TATA

GAM1957 ABCB4 5' GGTAAGTGGAAAAATATCATG 20836 CC__
 CATG TTTTCCATTTACT
 ||| |||||
 GTAC AAAAGGTGAATGG
 TATA

GAM1957 ADAMTS4 3' GTGGATGGAAGGGGCTG 11567 T
 CA GCCTTTTCCATTTAC
 || |||||
 GT CGGGGAAGGTAGGTG

—
 GAM1957 AK1 3' GGTGGGTGGGGAGTCAGTC 6088 A C T T T
 GAC TG C T CCATTTACT
 ||| || |||||
 CTG AC G A GGTGGGTGG
 — T _ GG

GAM1957 BACE 3' AGTGAATGGGAAAGGGTG 14417 G
 CAT CCTTTTCCATTTACT
 ||| |||||
 GTG GGAAAGGGTAAGTGA

—
 GAM1957 BACE 3' AGTGAATGGGAAAGGGTG 29085 G
 CAT CCTTTTCCATTTACT
 ||| |||||
 GTG GGAAAGGGTAAGTGA

—
 GAM1957 BAZ2A 3' GGTGGATGGGGGAGTGAAATTG 15120 CATGC TT
 TG CACGA CTT CCATTTACT
 |||| || |||||
 GTGTT GAG GGTAGGTGG
 AAAGT GG

GAM1957 BCLG 3' GGTGGATGGGAAAAAATACTTG 25051 CATGCC
 CGA TTTTCCATTTACT
 ||| |||||

			GTT AAAGGGTAGGTGG		
			CATAAA		
GAM1957	BN51T	3'	GGTAGATGGGGAGGGTCTGTGT 42285	G T TT	
	G		CAC ACA GCCTT CCATTTACT		
			GTG TGT TGGGA GGTAGATGG		
			_ C GG		
GAM1957	CDKN1B	5'	AGTGCGAGAGAGGCGGTCGTG 10273	A _ _	
			CACGAC TGCCTTT TC CATT		
			GTGCTG GCGGAGA AG GTGA		
			_ G C		
GAM1957	CSNK1E	5'	AGTGGGTGGGGAGGTGGTG 45773	GC TT	
			CAT CTT CCATTTACT		
			GTG GGA GGTGGGTGA		
			GT GG		
GAM1957	DAAM2	3'	GGTGAATGGGGAAGGGTC 44331	ATG TT	
			GAC CCTT CCATTTACT		
			CTG GGAA GGTAAGTGG		
			_ GG		
GAM1957	DCK	3'	AGTAAATGGTAGTGTGTC 6441	CTTTT	
			GACATGC CCATTTACT		
			CTGTGTG GGTAATGA		
			AT_		
GAM1957	DEDD	3'	GGTGGATGGAGAAGAGGTTG 26881	ATGC	
			CGAC CTTTTCCATTTACT		
			GTTG GAAGAGGTAGGTGG		
			GA_		
GAM1957	DNMT2	3'	GGTGGATGGGGAGGATGGTTG 10671	ATG T TT	
			CGAC CC T CCATTTACT		
			GTTG GG A GGTAGGTGG		
			GTA _ GG		
GAM1957	DSCR4	3'	GGTTTTTGGGAAGGGTGTGCGT 12488	A TTT	
	G		CACG CATGCCTTTTCCA ACT		
			GTGC GTGTGGGAAGGGT TGG		
			_ TTT		
GAM1957	GPR81	3'	AGTAAATGGGTATATGTGTTTG 26279	C GCCTTT	
			A GACAT TCCATTTACT		
			G TTGTG GGGTAAATGA		
			T TATAT_		
GAM1957	GSTM5	3'	AGTGGATGGGTGTGTGTGTG 6519	_ TT TACT	
			CACG ACATGCCT TCCATT		

GTGT TGTGTGGG AGGTGA
 G T_ T
 GAM1957 HD 3' GGTAAGTGGAGGAAATGTTG 7896 GCC
 CGACAT TTTTCCATTTACT
 ||||| |||||
 GTTGTA AGGAGGTGAATGG
 A_
 GAM1957 HOXB9 3' GTGAATGGGGAAGGGAGTC 23447 ATG TT
 GAC CCTT CCATTTAC
 ||| ||| |||||
 CTG GGAA GGTAAGTG
 AG_ GG
 GAM1957 HTRA3 3' AGTGTGTCTCAAGGGGCATTTG 42938 C CCATT_
 TG CACGA ATGCCTTTT TACT
 ||||| ||||| |||
 GTGTT TACGGGGAA GTGA
 _ CTCTGT
 GAM1957 IL1F5 3' GGTGAGTGGAGGAGACCCATG 14604 C_
 CATG CTTTTCCATTTACT
 ||||| |||||
 GTAC GAGGAGGTGAGTGG
 CCA
 GAM1957 KCNQ3 5' GGTGGGTGGGGAGGGGCGCGCG 10847 ACA _TT
 CG TGCCT T CCATTTACT
 || ||||| |||||
 GC GCGGG A GGTGGGTGG
 GC_ G GG
 GAM1957 KCNS2 3' AGTGAGGAAGGGCATGTTGT 33898 _
 ACGACATGCCTTTTC CATT
 ||||| |||||
 TGTGTACGGGAAGG GTGA
 A
 GAM1957 LOH11CR2A 5' GGTGGATGGGAAGAAAATTGT 15989 TGCC_
 ACA TTTTCCATTTACT
 ||| |||||
 TGT GAAGGGTAGGTGG
 TAAAA
 GAM1957 MAFF 3' GTGGGTGGGAAGACTAGTG 14702 GCC_
 CAT TTTTCCATTTAC
 ||| |||||
 GTG GAAGGGTGGGTG
 ATCA
 GAM1957 MAPK14 3' GGTGGAAGGGGTGTGCGTG 29108 _ G
 CACG ACAT CCTTTTCCATT
 ||||| ||||| |||||
 GTGC TGTG GGGGAAGGTGG
 G _
 GAM1957 MAPK14 3' GGTGGAAGGGGTGTGCGTG 7004 _ G
 CACG ACAT CCTTTTCCATT
 ||||| ||||| |||||

			GTGC TGTG GGGGAAGGTGG		
			G _		
GAM1957	MAPK14	3'	GGTGGAAGGGGTGTGCGTG	29115	_ G
			CACG ACAT CCTTTTCCATT		
			GTGC TGTG GGGGAAGGTGG		
			G _		
GAM1957	MAX	5'	GTGAGTGAGTGTGTGTGTG	8200	G _ TTTC
			CAC ACATGC CT CATTAC		
			GTG TGTGTG GA GTGAGTG		
			_ T _		
GAM1957	MAX	5'	GTGAGTGAGTGTGTGTGTG	29717	G _ TTTC
			CAC ACATGC CT CATTAC		
			GTG TGTGTG GA GTGAGTG		
			_ T _		
GAM1957	MAX	5'	GTGAGTGAGTGTGTGTGTG	29719	G _ TTTC
			CAC ACATGC CT CATTAC		
			GTG TGTGTG GA GTGAGTG		
			_ T _		
GAM1957	MAX	5'	GTGAGTGAGTGTGTGTGTG	29722	G _ TTTC
			CAC ACATGC CT CATTAC		
			GTG TGTGTG GA GTGAGTG		
			_ T _		
GAM1957	MCL1	3'	GTGGATGGAGAGACATTTG	22487	C CC
			CGA ATG TTTTCCATTTAC		
			GTT TAC GAGAGGTAGGTG		
			_ A _		
GAM1957	NUP153	3'	AGTGAGTGAGTTGGGTGTATTG	11607	C TTTC
	TG		CACGA ATGCCT CATTACT		
			GTGTT TGTGGG GTGAGTGA		
			A TTGA		
GAM1957	PCOLCE2	5'	GGTGGGTGCGGAGGGGCGTGTG	15009	G _
	TG		CAC ACATGCCTTTTC CATTACT		
			GTG TGTGCGGGGAGG GTGGGTGG		
			_ C		
GAM1957	PPEF2	3'	GGTGGGTGGGGTGTGTGTG	12904	G TTT
			CACGACAT CC TCCATT		
			GTGTTGTG GG GGGTGG		
			G TT_		
GAM1957	RAB3A	3'	GGTGGGGGGGTGTGCTGTG	8770	A T TT
			CACG CATGCC T CCATT		

			GTGT GTGTGG G GGTGG		
			C _ GG		
GAM1957	RXRA	3'	GGTGGATGGGGGGGATACCG 8871	AC G TT	
			CG AT CCT TCCATTTACT		
			GC TA GGG GGGTAGGTGG		
			CA G _		
GAM1957	TEM6	3'	AGTGGGTGTTGTGTGTGTG 22960	G CTTT	
			CAC ACATGC TCCATT		
			GTG TGTGTG GGGTGA		
			_ TTGT		
GAM1957	TPD52L2	3'	GGTGTGGTGAGAAGGCAGGTTG 9298	A CATT	
	TG		CACGAC TGCCTTTTC TACT		
			GTGTTG ACGGAAGAG GTGG		
			G TGGT		
GAM1957	TRIM34	3'	GGTTCTTGAGGGTATGTCAGT 22251	_ TT TTT	
	G		CAC GACATGCCT TCCA ACT		
			GTG CTGTATGGG AGGT TGG		
			A _ TCT		
GAM1957	TRIM34	3'	GGTTCTTGAGGGTATGTCAGT 28175	_ TT TTT	
	G		CAC GACATGCCT TCCA ACT		
			GTG CTGTATGGG AGGT TGG		
			A _ TCT		
GAM1957	WHSC1	3'	AGTGAATGGGGACACTCGTG 28441	CA CCT TT	
			CACGA TG T CCATTTACT		
			GTGCT AC A GGTAAGTGA		
			C_ _ GG		
GAM1957	WHSC1	3'	AGTGAATGGGGACACTCGTG 17177	CA CCT TT	
			CACGA TG T CCATTTACT		
			GTGCT AC A GGTAAGTGA		
			C_ _ GG		
GAM1957	WHSC1	3'	AGTGAATGGGGACACTCGTG 28458	CA CCT TT	
			CACGA TG T CCATTTACT		
			GTGCT AC A GGTAAGTGA		
			C_ _ GG		
GAM1957	ZIC1	3'	GGTGGGTGGGATTGTGGCGTTG 9448	AT TT_	
	TG		CACGAC GCC TTCCATTTACT		
			GTGTTG CGG AGGGTGGGTGG		
			_ TGTT		
GAM1957	AKL3L	3'	AGTAAGTGGTTCTTATGTGTTT 18409	C GCCTTTT	
	TG		CA GACAT CCATTTACT		

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GT TTGTG  GGTGAATGA
T  TATTCTT
GAM1957 ATP9A  3' AGTGTGTGGGGGGTGTGTGTG 31076  G  TT  T
CAC ACATGCCT TCCAT TACT
||| ||||| |||| |||
GTG TGTGTGGG GGGTG GTGA
_  _  T
GAM1957 BLCAP  3' AGTGAGTGGGAGAGTACCTGTG 13519  G  TGC_
TG  CAC ACA  CTTTTCCATTTACT
||| ||| ||||| |||||
GTG TGT  GAGAGGGTGAGTGA
_  CCAT
GAM1957 BRD4  3' AGTGCCGTGGAGGTGTGTGTG 27774  G  TTT  T_
CAC ACATGCC TCCAT TACT
||| ||||| |||| |||
GTG TGTGTGG AGGTG GTGA
_  _  CC
GAM1957 CTNNBIP1 3' GTAGGTGGTTCGTGCTGTG 21544  A  CCTTTT
CACG CATG  CCATTTAC
||| ||| |||||
GTGT GTGC  GGTGGATG
C  TT___
GAM1957 DKFZP566K1924 3' AGTGAATGGGACTCAAATGTTG 36517  GCCTT
TG  CACGACAT TTCCATTTACT
||||| |||||
GTGTTGTA AGGGTAAGTGA
AACTC
GAM1957 DKFZP667O116 3' GGTGGGTGGAGGGGGATGCTG 45265  A  G
CG CAT CCTTTTCCATTTACT
|| ||| ||||| |||||
GT GTA GGGGGAGGTGGGTGG
C  _
GAM1957 FBX30  3' GGTAGATGGGGAGCAGGATTG 27041  CA_  CT TT
CGA  TGC T CCATTTACT
||| ||| | |||||
GTT  ACG A GGTAGATGG
AGG  _  GG
GAM1957 FLJ10079 3' GGTGGCAGGAGGTATGTC 30216  _
GACATGCCTTTT CCATT
||||||| ||||
CTGTATGGAGGA GGTGG
C
GAM1957 FLJ11164 3' GGTAGATGGGAGGACATTTC 20357  C  _  TT
GA ATG CCTT CCATTTACT
|| ||| ||| |||||
CT TAC GGAG GGTAGATGG
T  A  _
GAM1957 FLJ11506 3' GGTGGGTGGGGGAAGTGAAATGT 23969  GC__ TT
T  GACAT  CTT CCATTTACT
||||| ||| |||||

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TTGTA GAA GGTGGGTGG
 AAGT GG
 GAM1957 FLJ11715 3' AGTAAGTGTTAGTGTGTTAGTG 23788 _ CTT TC
 CAC GACATGC T CATTACT
 ||| ||||| | |||||
 GTG TTGTGTG A GTGAATGA
 A _ TT
 GAM1957 FLJ12783 3' GGTGGATGAAGTATGTGTG 25419 G C T
 CAC ACATGC TT TCCATT
 ||| ||||| || |||||
 GTG TGTATG AG AGGTGG
 _ A T
 GAM1957 FLJ14146 3' AGTGAGTGGGAAGGAGAGTG 24030 GC_
 CAT CTTTTCCATTTACT
 ||| |||||
 GTG GGAAGGGTGAGTGA
 AGA
 GAM1957 FLJ20034 3' GGTAGGTGGGGAGGGGCCACGC 19135 ACAT _ TT
 G CG GCCT T CCATTTACT
 || |||| | |||||
 GC CGGG A GGTGGATGG
 GCAC G GG
 GAM1957 FLJ20034 3' GTAGATGGAGAAGTTGTT 19136 TGC
 GACA CTTTTCCATTTAC
 |||| |||||
 TTGT GAAGAGGTAGATG
 T_
 GAM1957 FLJ20174 5' GGTAAGTGGGGGGATTCTCG 19270 CATG TT
 CGA CCT TCCATTTACT
 ||| ||| |||||
 GCT GGG GGGTGAATGG
 CTTA _
 GAM1957 FLJ20312 3' AGTGGGTGGAAAGGGCATTG 19374 C
 CGA ATGCCTTTTCCATTTACT
 ||| |||||
 GTT TACGGGAAAGGTGGGTGA
 _
 GAM1957 FLJ20378 3' GGTGGAAGGGGCATGTGTG 19437 G _
 CAC ACATGCCT TTTCCATT
 ||| ||||| |||||
 GTG TGTACGGG AAAGGTGG
 _ G
 GAM1957 FLJ20400 3' GGTAAGGGGTAGTTGTG 33046 A _
 CACGAC TGCCTTTT CC
 ||||| ||||| ||
 GTGTTG ATGGGAAA GG
 _ AT
 GAM1957 FLJ20574 3' GAAGGGGAAGAGCGTGTGTTGTG 19555 _ TT A
 CACGACATGC CTT CC TTT
 ||||| ||| || |||

GTGTTGTGCG GAA GG AAG
 A GG _
 GAM1957 FLJ22833 3' GTGAGTGTGCATGTTGT 23122 CTTTTC
 ACGACATGC CATTAC
 ||||| |||||
 TGTTGTACG GTGAGTG
 T_____
 GAM1957 FLJ23277 3' GGTGGGTGGGAGGGGGCAAGT 25955 A _
 AC TGCCTTTTCC ATTTACT
 || ||||| |||||
 TG ACGGGGGAGG TGGGTGG
 A G
 GAM1957 GMEB2 3' AGTGGGTGGGGAAGGTTGTTGT 14739 T TT
 ACGACA GCCTT CCATTACT
 |||| |||| |||||
 TGTTGT TGGAA GGTGGGTGA
 _ GG
 GAM1957 GPS2 5' GGTGGATGGAGAGGATATG 10827 C
 CATG CTTTTCATTACT
 ||| |||||
 GTAT GGAGAGGTAGGTGG
 A
 GAM1957 HSGP25L2G 3' GGTGGGTGGAGGGGTTTGCAGT 31135 GA T T
 G CAC CA GCCTTT CCATTACT
 ||| || ||||| |||||
 GTG GT TGGGGA GGTGGGTGG
 AC T _
 GAM1957 KIAA0082 3' AGTGGGTGGAGACCTGCTGTC 44262 T CT_
 GACA GC TTTCCATTACT
 |||| || |||||
 CTGT CG AGAGGTGGGTGA
 _ TCC
 GAM1957 KIAA0092 3' GGAGAAGGGATATGTTGTG 16155 _
 CACGACATG CCTTTTCC
 ||||| |||||
 GTGTTGTAT GGAAGAGG
 AG
 GAM1957 KIAA0232 3' GGTGGGTGGGTGTGTGTGTGTG 36037 _ CTTT
 TG CACG ACATGC TCCATTACT
 |||| |||| |||||
 GTGT TGTGTG GGGTGGGTGG
 G TGT_
 GAM1957 KIAA0275 3' GTGAGTGCAGCGTGTGTG 16554 G CTTTTC
 CAC ACATGC CATTAC
 || |||| |||||
 GTG TGTGCG GTGAGTG
 _ AC____
 GAM1957 KIAA0321 3' TGAGTGAGTATGTGTG 31270 G CTTTTC
 CAC ACATGC CATTTA
 || |||| |||||

		GTG TGTATG GTGAGT		
		— A —		
GAM1957	KIAA0418	3' AGTGGATGGGGTTTCTGTTGT 15995	T__	TT
		ACGACA GCCT TCCATT		
		TGTTGT TGGG AGGTGA		
		CTT GT		
GAM1957	KIAA0427	3' GTGGAGGGGGCTGTGTTGTG 16580	—	
		CACGACAT GCCTTTTCCAT		
		GTGTTGTG CGGGGGAGGTG		
		T		
GAM1957	KIAA0478	3' GGTACCCCAGGAGGCATGATGT 16983	A	CCATT
	G	CACG CATGCCTTTT TACT		
		GTGT GTACGGAGGA ATGG		
		A CCCC_		
GAM1957	KIAA0522	3' GGTGGGTGGGACCCTGCTTGT 35625	T CTT_	
		ACA GC TTCCATTTACT		
		TGT CG AGGGTGGGTGG		
		T TCCC		
GAM1957	KIAA0537	3' AGTGGGTGGAGAGGAAGCAT 16862	—	
		ATGC CTTTTCCATTTACT		
		TACG GGAGAGGTGGGTGA		
		AA		
GAM1957	KIAA0652	3' AGTGGTTAGGGGATGTTGTG 16406	G TT	
		CACGACAT CCTT CCATT		
		GTGTTGTA GGGA GGTGA		
		G TT		
GAM1957	KIAA1274	3' GGTGGGTGGAGGGGACAGTGTT 43913	GC_	
		GACAT CTTTTCCATTTACT		
		TTGTG GGGGAGGTGGGTGG		
		ACA		
GAM1957	KIAA1297	3' AGTGGATGGGGAGTCTGTGTG 35707	G T CT TT	
		CAC ACA GC T CCATTTACT		
		GTG TGT TG A GGTAGGTGA		
		— C — GG		
GAM1957	KIAA1522	3' GGTGGATGGAAGGGAGCAT 32419	—	
		ATGC CTTTTCCATTTACT		
		TACG GGGAAGGTAGGTGG		
		A		
GAM1957	KIAA1560	3' GGTAATGGAGAAAATATTTT 32104	C CC	
		GA ATG TTTTCCATTTACT		

CT TAT AAGAGGTAAATGG
 T AA
 GAM1957 KIAA1580 5' AGTGGATGGAAGGGGACTG 34408 TG
 CA CCTTTTCCATTTACT
 || |||||
 GT GGGGAAGGTAGGTGA
 CA
 GAM1957 KIAA1649 3' GGAGGGGGCTGTGTTGTG 33258 _
 CACGACAT GCCTTTTCC
 ||||| |||||
 GTGTTGTG CGGGGGAGG
 T
 GAM1957 KIAA1691 3' AGTAGGTGGAGGGGAGCG 44462 _
 TGC CTTTCCATTTACT
 || |||||
 GCG GGGGAGGTGGATGA
 A
 GAM1957 KIAA1826 3' GTAGGTGGGGAAGATGT 33377 GC TT
 ACAT CTT CCATTTAC
 ||| || |||||
 TGTA GAA GGTGGATG
 _ GG
 GAM1957 KIAA1831 3' GGTGGGTGGAGAGCCCTGTTTG 31906 C T_ CT
 A GACA GC TTTCCATTTACT
 | ||| || |||||
 G TTGT CG AGAGGTGGGTGG
 T CC _
 GAM1957 MGC3248 3' TGGGAAAGGTGTTTGTG 26240 C
 CACGA ATGCCTTTTCCA
 |||| |||||
 GTGTT TGTGGAAAGGGT
 _
 GAM1957 MGC4549 3' GTGAGTGTGGGTGTGTGTG 26172 G TTTC
 CAC ACATGCCT CATTTAC
 || ||||| |||||
 GTG TGTGTGGG GTGAGTG
 _ T_
 GAM1957 MGC4655 3' AGTAGCACAGAGGTGTGTTCTG 27146 C TCCAT
 CA GACATGCCTT TTTACT
 || ||||| |||||
 GT TTGTGTGGAGA GATGA
 C CAC_
 GAM1957 N4BP3 3' GGTGGGTGTGTCTGAGGGGGTG 32937 _
 TGT TTG CATGCCTTTT CATTACT
 ||||| |||||
 GTGTGGGGGAG GTGGGTGG
 TCTGT
 GAM1957 PAPOLG 5' AGTAAGTGGGAAAGTGAGCG 23154 _
 TGC CTTTCCATTTACT
 || |||||

GCG GAAAGGGTGAATGA
 AGT
 GAM1957 PRDM10 3' GGAGAAGGGGCATTTTGTG 21497 C ____
 CACGA ATGCCT TTTCC
 |||| |||| ||||
 GTGTT TACGGG AGAGG
 T GA
 GAM1957 PRTD-NY3 5' GGTAGAAGGCCTGTTGTG 25194 T _
 CACGACA GCCTTTT CC
 ||||| ||||| ||
 GTGTTGT CGGAAGA GG
 C T
 GAM1957 RAB10 3' GTGTTTGGAGGGTGTGTTGTG 41281 G TTT TT
 CACGACAT CC TCCA TAC
 ||||| || ||| |||
 GTGTTGTG GG AGGT GTG
 _ _ TT
 GAM1957 RASAL2 3' GTAAAGTAGGAATGTTGTG 11250 G TTTCCA
 CACGACAT CCT TTTAC
 ||||| || ||||
 GTGTTGTA GGA AAATG
 A TG____
 GAM1957 RASGRP4 5' GGTGGGTGGGGAGGGGCAGTT 27505 A _TT
 GAC TGCCT T CCATTTACT
 || |||| | |||||
 TTG ACGGG A GGTGGGTGG
 _ G GG
 GAM1957 RNPS1 3' AGTGAGTGGAGAGCCAGC 27902 C__
 GC TTTTCCATTTACT
 || |||||
 CG GAGAGGTGAGTGA
 ACC
 GAM1957 RNPS1 3' AGTGAGTGGAGAGCCAGC 13537 C__
 GC TTTTCCATTTACT
 || |||||
 CG GAGAGGTGAGTGA
 ACC
 GAM1957 RRN3 3' GTAAGTGGGGTCTTTGTG 20488 CAT TTTT
 CACGA GCC CCATTTAC
 |||| || |||||
 GTGTT TGG GGTGAATG
 TC_ ____
 GAM1957 SEMA3E 3' AGTGTTAAGTAGCAGGTGTGTT 14808 TTTCCATT_
 GTG CACGACATGCCT TACT
 ||||| ||||
 GTGTTGTGTGGA GTGA
 CGATGAATT
 GAM1957 SIAT8A 5' AGTAAGAGAACCAAAGGTGTGT 8983 G ____ CA
 GTG C ACATGCCTTT TC TTTACT
 | ||||| || |||||

G TGTGTGGAAA AG GAATGA
 _ CCA A_
 GAM1957 SRF 3' GGTGGCTCTGGGGTATGTGTG 9103 G TT__ TACT
 CAC ACATGCCTT CCATT
 ||| ||||| ||||
 GTG TGTATGGGG GGTGG
 _ TCTC T
 GAM1957 STK38L 3' AGTGAATGGAAAATAAGTGT 34286 GCC
 ACAT TTTTCCATTTACT
 ||| |||||
 TGTG AAAAGGTAAGTGA
 AAT
 GAM1957 SULT1C2 3' GGTGGGTGGAGGGGTTTGCAGT 13354 GA T T
 G CAC CA GCCTTT CCATTTACT
 ||| || ||||| |||||
 GTG GT TGGGGA GGTGGGTGG
 AC T _
 GAM1957 SYTL4 5' AGTGAAAGAGGCGTGTGT 28023 C
 ACGACATGCCTTTT CATT
 ||||| ||||| ||||
 TGTGTGCGGAGAA GTGA
 A
 GAM1957 TBX21 3' AGTGGGTGGGAGGGGTCAGGTG 14995 ACA _
 TG CACG TG CCTTTTCCATTTACT
 ||| || |||||
 GTGT AC GGGGAGGGTGGGTGA
 GG_ T
 GAM1957 TPRA40 5' AGTGGGTGGGGAGGGTGGTTTA 18502 C A TT
 A GAC TGCCTT CCATTTACT
 ||| ||||| |||||
 A TTG GTGGGA GGTGGGTGA
 T _ GG
 GAM1957 UXS1 5' AGTGAGGAAGGCATGTGTG 24676 G TC
 CAC ACATGCCTTT CATT
 ||| ||||| ||||
 GTG TGTACGGAAG GTGA
 _ GA
 GAM1957 XYLT1 3' GGTAAGTGGGAAAGCCTTTTG 38139 CAT C
 CGA GC TTTTCCATTTACT
 ||| || |||||
 GTT CG AAAGGGTGAATGG
 TTC _
 GAM1957 YF13H12 5' AGTGGGTGGAAGTCCGGT 15594 T__
 GCC TTTCCATTTACT
 ||| |||||
 TGG GAAGGTGGGTGA
 CCT
 GAM1957 LOC120114 3' GTGGGTGGGGGAGGAAGTT 37211 ATG TT
 GAC CCTT CCATTTAC
 ||| ||| |||||

	TTG GGAG GGTGGGTG		
	AA_ GG		
GAM1957 LOC130644 3'	AGTGGAGGAAGGTGTGCTGTG 37303	A	_
	CACG CATGCCTTT TCCATT		
	GTGT GTGTGGAAG AGGTGA		
	C G		
GAM1957 LOC142955 5'	AGTGAGTGGGGGAGAAATG 37571	GC	TT
	CAT CTT CCATTTACT		
	GTA GAG GGTGAGTGA		
	AA GG		
GAM1957 LOC143916 5'	GGTAGTGGGGAGGCAAGTTGTG 37652	A	T TT T
	CACGAC TGCC T CCATT ACT		
	GTGTTG ACGG A GGTGA TGG		
	A _ GG _		
GAM1957 LOC145371 3'	GGTGGCCTGGGGCATGTC 37849	TT_	
	GACATGCCTT CCATT		
	CTGTACGGGG GGTGG		
	TCC		
GAM1957 LOC148764 5'	AGTGAATGGGATGGATGTTTG 38590	C	G TT
	A GACAT CC TTCCATTTACT		
	G TTGTA GG AGGGTAAGTGA		
	T _ T_		
GAM1957 LOC150577 3'	GGTGCGTTAAGAAGGCATGTC 41222	CC	T
	GACATGCCTTTT AT TACT		
	CTGTACGGAAGA TG GTGG		
	AT C		
GAM1957 LOC150967 5'	AGATGGGAGGAGGTGTGCGTG 39034	A	_
	CACG CATGCCTTTTCC ATTT		
	GTGC GTGTGGAGGAGG TAGA		
	_ G		
GAM1957 LOC151475 3'	GGTGAATGTGTGGGTGTGTGTG 41358	G	TTTC
	CAC ACATGCCT CATTACT		
	GTG TGTGTGGG GTAAGTGG		
	_ TGT_		
GAM1957 LOC157869 3'	GGTGGATGGTGTGTGTCG 39677	TTT	
	CGACATGCC TCCATT		
	GCTGTGTGG AGGTGG		
	T_		
GAM1957 LOC202025 5'	GTGAATGTGTGTGTGTGTG 43404	G	CTTTTC
	CAC ACATGC CATTAC		

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GTG TGTGTG  GTAAGTG
_  TGT___
GAM1957 LOC255327 5' GTGGATGGAAAAGTTGTG 46022 GC
CAT CTTTTCCATTTAC
||| |||||
GTG GAAAAGGTAGGTG
TT
GAM1957 LOC51336 3' AGTAGGTGGGACTACAGATGTG 18754 G GCCTT_
TG CAC ACAT TTCCATTTACT
||| ||| |||||
GTG TGTA AGGGTGGATGA
_ GACATC
GAM1957 LOC55971 5' AGTTGGGGAGGGGTCTGTTGTG 20827 T ATTT
CACGACA GCCTTTTCC ACT
||||| ||||| |||
GTGTTGT TGGGGAGGG TGA
C GT___
GAM1958 ABP1 3' ACTGTGATCGTGTGGCCT 31613 G
GGGCCA GCGGTCGCGGT
||||| |||||
TCCGGT TGCTAGTGTCA
G
GAM1958 ACK1 3' ACTTGAATGGGACTTGCTGGC 12358 G _ G G
CT GGGCCAG CG GTC CG TTCAGGT
||||| || ||| || |||||
TCCGGTC GT CAG GT AAGTTCA
G T G _
GAM1958 ADAR 3' CTGAACTGTGGCTACTGTGC 6773 _ GC
GC CAG GGTCGCGGTTTCAG
|| ||| |||||
CG GTC TCGGTGTCAAGTC
T A_
GAM1958 ADAR 3' CTGAACTGTGGCTACTGTGC 17959 _ GC
GC CAG GGTCGCGGTTTCAG
|| ||| |||||
CG GTC TCGGTGTCAAGTC
T A_
GAM1958 ADAR 3' CTGAACTGTGGCTACTGTGC 17966 _ GC
GC CAG GGTCGCGGTTTCAG
|| ||| |||||
CG GTC TCGGTGTCAAGTC
T A_
GAM1958 ADCY6 3' GCTTGGATCATGCTCGTCTGCC 21976 C GT C
C GGGC AGGCG CG GGTTCAGGT
|||| |||| || |||||
CCCG TCTGC GT CTAGGTTTCG
_ TC A
GAM1958 ADCY6 3' GCTTGGATCATGCTCGTCTGCC 17588 C GT C
C GGGC AGGCG CG GGTTCAGGT
|||| |||| || |||||

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CCGG TCTGC GT CTAGGTTTCG
 _ TC A
 GAM1958 ADORA2A 3' GCTTGGGCACAGCAGACTGGCC 6331 _ _ G__
 TGGCCC CAGGC GGTC GC GTTCAGGT
 ||||| ||| || |||||
 GTCCG TCAG CG CGGGTTTCG
 G A ACA
 GAM1958 ADORA2A 5' TCTGGGCCCCCTCCGCCTGGGCC 6332 G TCGC GT
 GG CCAGGCGG GGTTCAG
 || ||||| |||||
 CC GGTCCGCC CCGGGTC
 G TCC_ TG
 GAM1958 ANXA5 5' ACTTGGGTCCCACAGTCTGGTC 6823 G CGC TT
 C GGGCCAGGC GT GG CAGGT
 ||||| || || |||||
 CCTGGTCTG CA CT GTTCA
 A CC_ GG
 GAM1958 AOC3 3' CCTTTGTTGCTGTCTGGCTT 9824 C TTC T
 GGGCCAGGCGGT GCGG AGG
 ||||| ||| |||
 TTCGGTCTGTCG TGTT TCC
 T _ C
 GAM1958 AP2B1 5' ACCTGGGCTGTGCTCTCCGGCT 6948 A C GT
 C GGGCC GG G CGCGGTTTCAGGT
 |||| || | |||||
 CTCGG CC C GTGTCGGGTCCA
 _ TTC
 GAM1958 ARHA 3' ACCTGGACTTAAGCATCTGGCT 35002 CG CGC
 C GGGCCAGG GT GGTTCAGGT
 ||||| || |||||
 CTCGGTCT CG TCAGGTCCA
 A_ AAT
 GAM1958 ARHGEF7 3' CCTGGTGGATGCCTGGTTC 9981 GT GGTT
 GGGCCAGGCG CGC CAGG
 ||||| ||| |||
 CTTGGTCCGT GTG GTCC
 AG _
 GAM1958 ARSB 3' CCTGGGTTCACTTGGCCC 5488 C TCGCG TT
 GGGCCAGG GG G CAGG
 ||||| || | |||
 CCGGTTTC CT T GTCC
 A _ GG
 GAM1958 ARVCF 3' GCTTGGATCGTGGAAGAAGGGC 7383 AGGCGG
 C GGCC TCGCGGTTTCAGGT
 ||| |||||
 CCGG GGTGCTAGGTTCG
 GAAGAA
 GAM1958 ATP11A 3' CTTGTGTGGCCGCCCTGGCTT 37807 _ GTT T
 GGGCCAGG CGGTCGCG CAGG
 ||||| ||||| |||

			TTCGGTCC GCCGGTGT GTTC	
			C _ _ C	
GAM1958	ATP7B	3'	GCTTGAACCTGCTTCCTGGCTC 5506	C T C
			GGGCCAGG GG CG GGTTCAGGT	
			CTCGGTCC TC GT CCAAGTTCG	
			T _ _	
GAM1958	ATP8B2	5'	GCCTGGGCTGCGGGTGGGGC 32516	AGG G
			GCC CG TCGCGGTTCAGGT	
			CGG GT GGCGTCGGGTCCG	
			G _ G	
GAM1958	ATRX	3'	ACTGAAGTTGTGGTTGTTAGGT 6093	AG GT _ GT
	TC		GGGCC GCG CGCGG TTCAG	
			CTTGG TGT GTGTT AAGTC	
			AT TG G A	
GAM1958	ATRX	3'	ACTGAAGTTGTGGTTGTTAGGT 28681	AG GT _ GT
	TC		GGGCC GCG CGCGG TTCAG	
			CTTGG TGT GTGTT AAGTC	
			AT TG G A	
GAM1958	AXUD1	3'	ATCTATGTCTGCTGCCTGGCTC 26918	GTC TTC_
			GGGCCAGGCG GCGG AGGT	
			CTCGGTCCGT CGTC TCTA	
			_ TGTA	
GAM1958	B3GAT1	3'	ACCTCGGCTGCTAGGCC 27628	A C
			GGGCC GGCGGTCTG GGT	
			CCCGG TCGTCGGC CCA	
			A T	
GAM1958	B3GAT1	3'	ACCTCGGCTGCTAGGCC 20716	A C
			GGGCC GGCGGTCTG GGT	
			CCCGG TCGTCGGC CCA	
			A T	
GAM1958	B4GALT2	3'	GCTTGGATCAGTAAGTCTGGTT 24956	GGTC _
	C		GGGCCAGGC GC GGTTCAGGT	
			CTTGGTCTG TG CTAGGTTCG	
			AA _ A	
GAM1958	B4GALT2	3'	GCTTGGATCAGTAAGTCTGGTT 9865	GGTC _
	C		GGGCCAGGC GC GGTTCAGGT	
			CTTGGTCTG TG CTAGGTTCG	
			AA _ A	
GAM1958	BAPX1	3'	ACCGCAGTGCCGCTGCCTGGCC 6860	C GTTCA
	C		GGGCCAGGCGGT GCG GGT	

CCCGGTCCGTCG CGT CCA
 C GACG_
 GAM1958 BDKRB2 3' CCTGAGCCAGCCTGCTC 6238 C GGTCGC
 GGGC AGGC GGTTCAGG
 |||| ||| |||||
 CTCG TCCG CCGAGTCC
 _ A____
 GAM1958 BSN 3' TCTGGCAAACCCTTGGCCC 9520 C CGCG T
 GGGCCAGG GGT GT CAGG
 ||||| ||| || ||||
 CCCGGTTC CCA CG GTCT
 _ AA__ _
 GAM1958 CACNA2D2 3' CCTGAGCTGGCCAGGCC 12651 A GGTCG
 GGGCC GGC CGGTTTCAGG
 |||| ||| |||||
 CCCGG CCG GTCGAGTCC
 A ____
 GAM1958 CACNA2D2 3' ATCTGAGCTGCAGCCTGGCT 12648 GGTC
 GGCCAGGC GCGGTTTCAGGT
 ||||| |||||
 TCGGTCCG CGTCGAGTCTA
 A____
 GAM1958 CALCR 3' ACTTGTGGTTGACCGCTTGTTT 7477 GC CGGTT
 C GG CAGGCGGTTCG CAGGT
 || ||||| ||||
 CT GTTCGCCAGT GTTCA
 TT TGGT_
 GAM1958 CARPX 5' ACTTGCCGCGGACTGCCTGGGC 21395 G _ TT
 T GG CCAGGCGGTC GCGG CAGGT
 || ||||| ||| ||||
 TC GGTCCGTCAG CGCC GTTCA
 G G ____
 GAM1958 CASP8 5' GCCTTGCCGCGCCTGAGCCC 6897 _ C
 GGGC CAGGCGGTTCG GGT
 ||| ||||| |||
 CCCG GTCCGCCGGT CCG
 A T
 GAM1958 CASP8 5' GCCTTGCCGCGCCTGAGCCC 27210 _ C
 GGGC CAGGCGGTTCG GGT
 ||| ||||| |||
 CCCG GTCCGCCGGT CCG
 A T
 GAM1958 CBFA2T3 3' GCCTGGCCTCCGATGCCTGGCC 11691 G C TT
 T GGGCCAGGCG TCG GG CAGGT
 ||||| ||| || ||||
 TCCGGTCCGT AGC TC GTCCG
 _ C CG
 GAM1958 CD80 5' ACTTGGGTCCAAATTGTTGGCT 11695 G CGC TT
 T GGGCCAG CCGT GG CAGGT
 ||||| ||| || ||||

TTCGGTT GTTA CT GTTCA
 _ AAC GG
 GAM1958 CD83 3' ACTTGGGCCCTTCCCTTCTTGG 10426 C_ TCGC
 TTT GGGCCAGG GG GGTTCAGGT
 ||||| || |||||
 TTTGGTTC CC CCGGGTTCA
 TT CTTC
 GAM1958 CDH23 3' CTGGGGACCAGCTTGGCTC 22669 _ GCGG
 GGGCCAGGC GGTC TTCAG
 ||||| ||| ||||
 CTCGGTTCG CCAG GGGTC
 A ____
 GAM1958 CDKN1A 3' GCCTGGACTGTTTTCTCTCGGC 27781 AG C TC
 TC GGGCC G GG GCGGTTTCAGGT
 |||| | || |||||
 CTCGG C CT TGTCAGGTCCG
 CT T TT
 GAM1958 CENPB 3' ACTTTGGCCCTTGTTT 34463 C C
 GGGCCAGG GGTCG GGT
 ||||| ||||| |||
 TTTGGTTC CCGGT TCA
 _ T
 GAM1958 CENPB 5' TTGCTCATCGCCTGGTTC 34466 C_
 GGGCCAGGCGGT GCGG
 ||||| ||||| ||||
 CTTGGTCCGCTA CGTT
 CT
 GAM1958 CENTD2 5' ATCTGGGTCTCTGTGTGGTCT 17575 G TCGC TT
 GGGCCA GCGG GG CAGGT
 ||||| |||| || |||||
 TCTGGT TGTC CT GTCTA
 G T__ GG
 GAM1958 CEP2 5' ACAGGTGGCTGTTGGTCT 14042 G G_
 GGGCCAG CGGTCGC GT
 ||||| ||||| ||
 TCTGGTT GTCGGTG CA
 _ GA
 GAM1958 CHRN1 3' GCCTGAACTGTCTGCCCTGAT 30360 GC C C_
 CT GG CAGG GGT GCGGTTTCAGGT
 || |||| || |||||
 TC GTCC CCG TGTCAAGTCCG
 TA _ TC
 GAM1958 CHST5 3' GCCCCGAACTGTGGTCGCCAGG 14439 A GT A_
 CCC GGGCC GGCG CGCGGTTTC GGT
 ||||| |||| ||||| |||
 CCCGG CCGC GTGTCAAG CCG
 A TG CC
 GAM1958 CLCN7 3' CTTGGGAGCTGCTTGGCCT 6964 CGCGG
 GGGCCAGGCGGT TTCAGG
 ||||| ||||| |||||

			TCCGGTTCGTCG	GGGTTC		
			A			
GAM1958	CLECSF5	3'	CTGAACTAAGGCTTGGCCT	14919	GGT GC	
			GGGCCAGGC C GGTTCAG			
			TCCGGTTCG G TCAAGTC			
			AA			
GAM1958	CLTCL1	3'	TCTGGAGCTTTTCTGGTCC	31838	CG TC GG	
			GGGCCAGG G GC TTCAGG			
			CCTGGTCT T CG AGGTCT			
			TT			
GAM1958	COL11A2	3'	AGGTGTTGGCTGCCTGGCCC	27979	_ G	
			GGGCCAGGCGGTTCG CG TT			
			CCCGGTCCGTCGGT GT GA			
			T G			
GAM1958	COL11A2	3'	AGGTGTTGGCTGCCTGGCCC	27974	_ G	
			GGGCCAGGCGGTTCG CG TT			
			CCCGGTCCGTCGGT GT GA			
			T G			
GAM1958	COL4A4	5'	GCCTCCAACTTGCGGCCGCGG	5553	A _ C_	
	GCTT		GGCC GGCGGTCGCG GTT AGGT			
			TCGG CCGCCGGCGT CAA TCCG			
			G T CC			
GAM1958	COLQ	3'	ATCTTGACCTCTTGGCTC	27855	C C	
			GGGCCAGG GGTCG GGT			
			CTCGGTTC CCAGT CTA			
			T T			
GAM1958	COLQ	3'	ATCTTGACCTCTTGGCTC	27858	C C	
			GGGCCAGG GGTCG GGT			
			CTCGGTTC CCAGT CTA			
			T T			
GAM1958	COLQ	3'	ATCTTGACCTCTTGGCTC	27864	C C	
			GGGCCAGG GGTCG GGT			
			CTCGGTTC CCAGT CTA			
			T T			
GAM1958	COLQ	3'	ATCTTGACCTCTTGGCTC	27852	C C	
			GGGCCAGG GGTCG GGT			
			CTCGGTTC CCAGT CTA			
			T T			
GAM1958	COLQ	3'	ATCTTGACCTCTTGGCTC	27861	C C	
			GGGCCAGG GGTCG GGT			

			CTCGGTTC CCAGT CTA		
			T T		
GAM1958	COLQ	3'	ATCTTGACCTCTTGGCTC 12232	C C	
			GGGCCAGG GGTCG GGT		
			CTCGGTTC CCAGT CTA		
			T T		
GAM1958	CPNE3	3'	GCTTGCTGTGGTGGTTGCCTAG 9994	C GT G TT_	
	CCC		GGGC AGGCG CGC G CAGGT		
			CCCG TCCGT GTG T GTTCG		
			A TG G GTC		
GAM1958	CPNE7	3'	CTGCGGGGTCTGCCTGGCCT 15787	___	
			GGGCCAGGCGG TCGCGG		
			TCCGGTCCGTC GGCCTC		
			TGG		
GAM1958	CRSP6	5'	CTGAGCGTTGCGTTCGGTTT 10471	AG G C G	
			GGGCC GCG T GCG TTCAG		
			TTTGG TGC G TGC GAGTC		
			CT _ T _		
GAM1958	CSRP1	3'	ACTTGAACCTGGGCATCTGGCT 10277	CG GC	
	C		GGGCCAGG GTC GGTTTCAGGT		
			CTCGGTCT CGG TCAAGTTCA		
			A_ GT		
GAM1958	CTSD	3'	CTTGGGCCAGCTGGGCTC 7627	A GGTCGC	
			GGGCC GGC GGTTTCAGG		
			CTCGG TCG CCGGGTTC		
			G AC___		
GAM1958	CUL4B	3'	ACTGTTGATTGTTTGCTT 9639	C _	
			GGGC AGGCGGTCTG CGGT		
			TTCG TTTGTTAGT GTCA		
			_ T		
GAM1958	CXCL16	3'	GCCCTTACTGTGATTCCTGGCT 22600	C TCA	
	T		GGGCCAGG GGTCGCGGT GGT		
			TTCGGTCC TTAGTGTCA CCG		
			_ TTC		
GAM1958	CYP1A1	3'	ATCTGGGCTGTGGGCAAGCCT 6112	CAG GG	
			GGGC GC TCGCGGTTCAGGT		
			TCCG CG GGTGTCGGGTCTA		
			AA_ _		
GAM1958	CYP1B1	3'	CTTGAGATTTACCTGGCTT 5564	CG TC GG	
			GGGCCAGG G GC TTCAGG		

			TTCGGTCC T TG AGG TTC		
			AT _ _		
GAM1958	CYP27B1	3'	CTCTCTGCTTGCTTGGCCC 6432	TC	TTC
			GGGCCAGGCGG GCGG AG		
			CCCGGTTGTT CGTC TC		
			_ TC _		
GAM1958	DAG1	3'	ACTTGACCTTGCCGCTTTGTC 10630	C	C T
	C		GGGC AGGCGGTCG GGT CAGGT		
			CCTG TTCGCCGGT CCA GTTCA		
			T T _		
GAM1958	DAG1	3'	GCCGGGCGGCCCCCTGGCTC 10634	C	_
			GGGCCAGG GGTCGC GGT		
			CTCGGTCC CCGGCG CCG		
			C GG		
GAM1958	DBN1	5'	GAGGGACCCCGCTTGGGCT 28124	G	TCGC AGGT
			GG CCAGGCGG GTTC		
			TC GGTTGCGC CCAGG		
			G _ GAGT		
GAM1958	DDX11	3'	GCCTGGATTTGTATCCTTGGCT 10653	C	C _
	T		GGGCCAGG GGT GCGG TTCAGGT		
			TTCGGTTC CTA TGTT AGGTCCG		
			_ _ T		
GAM1958	DDX11	3'	GCCTGGATTTGTATCCTTGGCT 24986	C	C _
	T		GGGCCAGG GGT GCGG TTCAGGT		
			TTCGGTTC CTA TGTT AGGTCCG		
			_ _ T		
GAM1958	DHCR24	3'	ACCTGGGCTCATTCTTCTTGGC 16522	C	TCGC
	TC		GGGCCAGG GG GTTTCAGGT		
			CTCGGTTC TC TCGGGTCCA		
			T TTAC		
GAM1958	DHFR	3'	TGATGTGACTGCTTAGCCC 6450	C	GT
			GGGC AGGCGGTCGCG TCA		
			CCCG TTCGTCAGTGT AGT		
			A _		
GAM1958	DMPK	5'	GCCTGGACAGGGGCTGCCAGGC 10666	A	GCG
	CC		GGGCC GGCGGTC GTTCAGGT		
			CCCGG CCGTCGG CAGGTCCG		
			A GGA		
GAM1958	DNAJB1	3'	CCTTCCTGACCTCTGGCTC 12787	C	C TTC
			GGGCCAGG GGTCG GG AGG		

		CTCGGTCT CCAGT CC TCC	
		— — T—	
GAM1958 DPH2L1	5'	CTTGAATTAGCCTGCGCTC 7054	— GGTCGCG
		GGGC CAGGC GTTCAGG	
		CTCG GTCCG TAAGTTC	
		C AT—	
GAM1958 DTNA	3'	CTGAACCTGTGGTCAGGCTC 7082	AGGC GT —
		GGGCC G CGC GGTTTCAG	
		CTCGG C GTG CCAAGTC	
		A— TG T	
GAM1958 DTNA	3'	CTGAACCTGTGGTCAGGCTC 26844	AGGC GT —
		GGGCC G CGC GGTTTCAG	
		CTCGG C GTG CCAAGTC	
		A— TG T	
GAM1958 DTNA	3'	CTGAACCTGTGGTCAGGCTC 26839	AGGC GT —
		GGGCC G CGC GGTTTCAG	
		CTCGG C GTG CCAAGTC	
		A— TG T	
GAM1958 DTNA	3'	CTGAACCTGTGGTCAGGCTC 26849	AGGC GT —
		GGGCC G CGC GGTTTCAG	
		CTCGG C GTG CCAAGTC	
		A— TG T	
GAM1958 DTR	5'	GCCTGGGTCCCGGCCAGGCTT 7662	AGGC C TT
		GGGCC GGTCG GG CAGGT	
		TTCGG CCGGC CT GTCCG	
		A— C GG	
GAM1958 ED1	3'	GCCTGGGCTCAGCCTGGTTT 7098	GGTCGCG
		GGGCCAGGC GTTTCAGGT	
		TTTGGTCCG TCGGGTCCG	
		AC—	
GAM1958 EFNA3	3'	ACCTGGGGGACCCCTGGCCC 11394	C GCGG
		GGGCCAGG GGTC TTCAGGT	
		CCCGGTCC CCAG GGGTCCA	
		C G—	
GAM1958 EGFL6	5'	GCCCCTGCCGCGGTGCCTGGCC 17765	G TCA
T		GGGCCAGGCG TCGCGGT GGT	
		TCCGGTCCGT GGCGCCG CCG	
		— TCC	
GAM1958 EGLN1	5'	ACTTGATTTTTAGTTTCGGTTT 22579	AG GGTCGCG
		GGGCC GC GTTTCAGGT	

			TTTGG TG TTAGGTTCA		
			CT ATTT__		
GAM1958	EGLN2	3'	GCCTGGGTCTACCTGTCTGG 18991	TCGC _	
	TC		GGCCAGGCGG GG TTCAGGT		
			CTGGTCTGTC CC GGGTCCG		
			CCAT T		
GAM1958	EGLN3	3'	ATTGAGTTCTCGTCTGTCCC 22618	C TC GGT	
			GGG CAGGCGG GC TCAGGT		
			CCC GTCTGCT TG AGTTTA		
			T CT ____		
GAM1958	EHD4	3'	ACCTGGGCCTCAGGCCTGCTC 29254	C GGTCGC	
			GGGC AGGC GGTTCAGGT		
			CTCG TCCG CCGGGTCCA		
			_ GACT__		
GAM1958	EIF4A2	3'	ATTGAATGCATTTTGTGGT 7696	TC_ G	
			GCCAGGCGG GCG TTCAGGT		
			TGGTTTGTT CGT AAGTTTA		
			TTA _		
GAM1958	ELL	3'	ATCTGAGCCAGCACCGCCGGCT 13280	A C _	
	T		GGGCC GGCAGT GC GGTTCAGGT		
			TTCGG CCGCCA CG CCGAGTCTA		
			_ _ A		
GAM1958	ENTPD6	3'	ATCTGGCCAGAGGGCTGTCTGG 6918	_ GC__ T	
	ACCT		G CCAGGCGGTC GGT CAGGT		
			C GGTCTGTCGG CCG GTCTA		
			A GAGA _		
GAM1958	EP300	5'	CTTGGGCCAGGCCGCCCC 7149	AGGC GC	
			GGGCC GGTC GGTTCAGG		
			CCCGG CCGG CCGGGTTC		
			_____ A_		
GAM1958	EPB49	5'	GCTTGATGACTTGCCTCGTTT 7709	C _ GCG	
			GGGC AGGCG GTC GTTCAGGT		
			TTTG TCCGT CAG TAGGTTTG		
			C T ____		
GAM1958	EPM2A	5'	CTGGACGATCGCCTGGCTT 12226	GCG	
			GGGCCAGGCGGTC GTTCAG		
			TTCGGTCCGCTAG CAGGTC		

GAM1958	ETS2	3'	ATCTGGGCTTATATCTGGCCT 11748	CGGTCGC	
			GGGCCAGG GGTTCAGGT		

			TCCGGTCT	TCGGGTCTA		
			ATAT__			
GAM1958	EXTL1	3'	GCCTCGGCCGTCTGCC	10756	C	C
			GGGC AGGCGGTCTG GGT			
			CCCG TCTGCCGGC CCG			
			__ T			
GAM1958	EXTL2	3'	CCTGAAAAGCTGCTTGGC	7162		CGCGG
			GCCAGGCGGT TTCAGG			
			CGGTTCGTCA AAGTCC			
			A__			
GAM1958	FANCF	3'	TGAAAAGCTGTTGGCCT	22925	G	CGCGG
			GGGCCAG CGGT TTCA			
			TCCGGTT GTCG AAGT			
			__ AA__			
GAM1958	FGF1	3'	CTGGGTCTGGGTTTGATCT	6470	_	GG C TT
			GGG CCAGGC TCG GG CAG			
			TCT GGTTTG GGT CT GTC			
			A __ _ GG			
GAM1958	FGF1	3'	CTGGGTCTGGGTTTGATCT	26987	_	GG C TT
			GGG CCAGGC TCG GG CAG			
			TCT GGTTTG GGT CT GTC			
			A __ _ GG			
GAM1958	FGF1	3'	CTGGGTCTGGGTTTGATCT	26989	_	GG C TT
			GGG CCAGGC TCG GG CAG			
			TCT GGTTTG GGT CT GTC			
			A __ _ GG			
GAM1958	FLRT2	3'	CTTGATGCTGCCTGGCC	14881		CGCGGT
			GGCCAGGCGGT TCAGG			
			CCGGTCCGTCG AGTTC			
			T__			
GAM1958	FMR1	3'	CTGTAAGCTGTTTGTTT	7777	C_	
			GGGCCAGGCGGT GCGG			
			TTTGTTTGTCG TGTC			
			AA			
GAM1958	FOSB	5'	ACTTGAAAGCTGATTGTTGTG	13581	_	CGG_
	GTTC		GGCCA GCGGTCTG TTCAGGT			
			TTGGT TTGTTAGT AGGTTCA			
			G TCAA			
GAM1958	FOXI1	3'	ACCTGGGAAGTGTGTTTG	14474	T	GG
			CAGGCGG CGC TTCAGGT			

GTTTGTG GTG GGGTCCA
 _ AA
 GAM1958 G22P1 5' GTTGAGGCCCGCCTGCGCTT 7203 _ TC GG GG
 GGGC CAGGCGG GC TTCA T
 |||| ||||| || |||| |
 TTCG GTCCGCC CG GAGT G
 C _ _ TT
 GAM1958 G6PC 3' TTGGAGGGTCGCCTGGCTT 5660 GT GCGG
 GGGCCAGGCG C TTCAG
 ||||| || ||||
 TTCGGTCCGC G AGGTT
 TG G _
 GAM1958 GALNT2 3' ATCTGAGCCCTGCACGCTGGGC 10797 A GT C
 CT GGGCC GGCG CG GGTTCAGGT
 |||| ||| || |||||
 TCCGG TCGC GT CCGAGTCTA
 G AC C
 GAM1958 GARP 3' GCTTGGCCCACAGTCTGGCTC 12033 G CGC TT
 GGGCCAGGC GT GG CAGGT
 ||||| || || ||||
 CTCGGTCTG CA CC GTTCG
 A _ CG
 GAM1958 GCN1L1 3' GCCCAGTGTGGTGTGTCTGGCT 34568 GG_ GTTCA
 T GGGCCAGGC TCGCG GGT
 ||||| |||| ||
 TTCGGTCTG GGTGT CCG
 TGT GAC _
 GAM1958 GLP1R 3' TTTGAGTTGTTTGGTGTC 7828 G CGGTC GG
 G GCCAGG GC TTCAGG
 | |||| || |||||
 C TGGTTT TG GAGTTT
 G _ _ TT
 GAM1958 GLS 3' ATTTGATGCTGTTGTCTGTCT 17104 C GTC _
 GGG CAGGCG GCGGT TCAGGT
 || ||||| |||| |||||
 TCT GTCTGT TGTCG AGTTTA
 _ _ T
 GAM1958 GLUL 3' GCTTGTGGGACTAGCCTGGCTT 7836 _ G GTT
 GGGCCAGGC GGTC CG CAGGT
 ||||| |||| || ||||
 TTCGGTCCG TCAG GT GTTCG
 A G _
 GAM1958 GPC1 3' ACCTCCGGCTGCCTAGCCC 7868 C C_
 GGGC AGGCGGTCTG GGT
 ||| ||||| ||
 CCCG TCCGTCGGC CCA
 A CT
 GAM1958 GPR61 3' ATTTGAACAAATTCCTGGCTC 38563 C CGCG
 GGGCCAGG GGT GTTCAGGT
 ||||| || |||||

			CTCGGTCC TTA CAAGTTTA		
			AA		
GAM1958	GRB10	3'	GCTTGAGTTGTCACTTGGTCC 11786	C	GTC GG
			GGGCCAGG G GC TTCAGGT		
			CCTGGTTC C TG GAGTTCG		
			A TT		
GAM1958	GRF2	3'	ACCGGTGGTTTTCTGGTTT 11789	C	GT _
			GGGCCAGG G CGC GGT		
			TTTGGTCT T GTG CCA		
			T TG G		
GAM1958	GRM7	3'	ACCTGGCATAGGACTCTTTGGT 6514	C	GCG_ T
	CC		GGGCCAGG GGTC GT CAGGT		
			CCTGGTTT TCAG CG GTCCA		
			C GATA _		
GAM1958	GUCY1B2	3'	ACTTTGCCGTCTGGTTT 10334	T	C
			GGGCCAGGCGG CG GGT		
			TTTGGTCTGCC GT TCA		
			_ T		
GAM1958	GYS1	3'	GCTGTGTCTGCACCGCTTGGTT 42624	C	TT_ GT
	T		GGGCCAGGCGGT GCGG CAG		
			TTTGGTTCGCCA CGTC GTC		
			_ TGT G		
GAM1958	HADHSC	3'	ATCTGAATGATTACTGTCTGTC 11798	C	CGCG
	T		GGGC AGGCGGT GTTCAGGT		
			TCTG TCTGTCA TAAGTCTA		
			_ TTAG		
GAM1958	HAP1	3'	GCAAAAGCTGTGGCTGCCAGGC 10075	A	CAG
	CT		GGGCC GGCGGTCGCGGT GT		
			TCCGG CCGTCGGTGTCTGA CG		
			A AAA		
GAM1958	HCCS	5'	GCTGGCCGCGGCGGTTTGGTC 11806	_	T GT
	T		GGGCCAGGC GGTCGCGGT CAG		
			TCTGGTTTG CCGGCGCCG GTC		
			G _ G		
GAM1958	HDAC5	3'	TCTCTCCCTGTGGCTGGTCTGG 29223	_	TTC T
	TTC		GGCCAGGC GGTCGCGG AGG		
			TTGGTCTG TCGGTGTC TCT		
			G CC_ CTC		
GAM1958	HDGF	3'	ACCTGGATGGGGCAGGCCACCT 10830	C	_ G_
	GGCTC		CCAGG GGTC GC GTTCAGGT		

GGTCC CCGG CG TAGGTCCA
A A GGG
GAM1958 HOXB7 3' GTCTGGACTAACCTGTGGTTG 10837 GT _____ GT
CCTGCCC GGCG CGC GGTTCAG
||||| ||| |||||
CCGT GTG TCAGGTC
TG TCCCAA TG
GAM1958 HOXC5 3' GCCTGGGCCGTATCTCCGGCTC 21021 A C C
GGGCC GG GGT GCGGTTTCAGGT
||||| || ||| |||||
CTCGG CC CTA TGCCGGGTCCG
_ T _
GAM1958 HTR2C 3' ATCTGAATTTCTAAAACCCTTG 6531 C CGC____
GTCT GCCAGG GGT GGTTCAGGT
||||| ||| |||||
TGGTTC CCA TTAAGTCTA
_ AAATCT
GAM1958 ICA1 3' GCCTCAGACCTGACTGCCTGGT 22738 C C_
TC GGGCCAGGCGGTCG GGTT AGGT
||||| ||||| ||| |||
CTTGGTCCGTCACT CCAG TCCG
_ AC
GAM1958 ICOS 3' ACTTGACAACCTGACTGGCTT 14385 G TCGCG
GGGCCAG CGG GTTCAGGT
||||| ||| |||||
TTCGGTC GTC CAGGTTCA
A CAA_
GAM1958 IDH3A 3' GCTTGGGCTTAGGCTTGGGCTC 12052 AGGC GC
GGGCC GGTC GGTTTCAGGT
||||| ||| |||||
CTCGG TCGG TCGGGTTCG
GT_ AT
GAM1958 IFNAR1 3' GTCTGAACACGTTATCACTTGG 6246 C C _ GT
TTT GGGCCAGG GGT GCG GTTCAG
||||| ||| ||| |||||
TTTGGTTC CTA TGC CAAGTC
A T A TG
GAM1958 IL1R1 3' ACTTGAGCCTCCATTTCTGGCT 6562 C_ TCGC
T GGGCCAGG GG GTTCAGGT
||||| || |||||
TTCGGTCT CC CCGAGTTCA
TTA T_
GAM1958 INHBC 3' ACCTGAGCTCCCCTGCCCTCTG 12063 C CGC_
GCTT GGCCAGG GGT GGTTCAGGT
||||| ||| |||||
TCGGTCT CCG TCGAGTCCA
C TCCCC
GAM1958 IRAK4 3' GCCTGGGCTGACACCTGG 30694 CG GC
CCAGG GTC GGTTCAGGT
||||| ||| |||||

GGTCC CAG TCGGGTCCG
A_ _
GAM1958 ITGA2 3' ACCTTCTGTGGCTGTCTTGTTT 7961 C TTC
GGGC AGGCGGTGCGCG AGGT
||||| |||||
TTTG TCTGTCGGTGTC TCCA
T T_

GAM1958 ITGA6 3' ATTTGGATTAAAAGCCTGCTC 5701 C GGTCGC
GGGC AGGC GGTTCAGGT
||||| |||||
CTCG TCCG TTAGGTTTA
_ AAAAT_

GAM1958 JJA21 3' ACTTGAACATTTTGCTTG 17655 TCGCG
CAGGCGG GTTCAGGT
||||| |||||
GTTTCGTT CAAGTTCA
TTA_

GAM1958 JMJ 3' TCCAATGTGGTTGTCCGTTT 11419 A GT GTTCA T
GGGCC GGCG CGCG GG
||||| ||||| ||
TTTGG CTGT GTGT CC
C TG AA_ TT

GAM1958 JRK 3' GCTTGAGCTGGGACTTGGCACC 41837 _ GGC G
GG GCCA GGTC CGGTTTCAGGT
|| ||||| |||||
CC CGGT TCAG GTCGAGTTCTG
A _ G

GAM1958 KCNAB1 3' ACTGTTGCTTGCCCC 30545 GTC
GGGCCAGGCG GCGGT
||||| |||||
CCCGGTTCGT TGTCA

GAM1958 KCNJ16 5' ACTTGAGCTGGGAAATCCTTTG 20726 C _ G
GCCT GCCAGG GG TC CGGTTTCAGGT
||||| || |||||
CGGTTT CC AG GTCGAGTTCA
_ TAA G

GAM1958 KCNS3 5' ATTTTCCAGTGATTGCTTTGGC 8049 _ _ TTCAGGT
CT GGGCCAG GCGGTGCG GG
||||| ||||| ||
TCCGGTT CGTTAGTG CC
T A TTTA

GAM1958 KHK 3' CTGAACTGCTCTGGCT 13214 CGGTC
GGCCAGG GCGGTTTCAG
||||| |||||
TCGGTCT CGTCAAGTC

GAM1958 KHK 3' CTGAACTGCTCTGGCT 5729 CGGTC
GGCCAGG GCGGTTTCAG
||||| |||||

TCGGTCT CGTCAAGTC

GAM1958 KIF3B 3' ACTTGAATAGGTGCCTGTTCT 11214 GC GTCGCG
GG CAGGCG GTTCAGGT
|| ||||| |||||
TC GTCCGT TAAGTTCA
TT GGA__

GAM1958 KIF5C 3' CTGCCTCAACTGTCTGGTTT 10853 C__
GGGCCAGGCGGT GCGG
||||||| |||
TTTGGTCTGTCA CGTC
ACTC

GAM1958 KNSL3 5' GCCTGGGTCTGGAGCCGTCCTG 11824 _ CG _
GCCT GGCCAGG CGGT CGG TTCAGGT
||||| ||| || |||||
CCGGTCC GCCG GTC GGGTCCG
T AG T

GAM1958 KNSL3 5' GCCTGGGTCTGGAGCCGTCCTG 24962 _ CG _
GCCT GGCCAGG CGGT CGG TTCAGGT
||||| ||| || |||||
CCGGTCC GCCG GTC GGGTCCG
T AG T

GAM1958 KRT16 5' ACCTCGGTGACCGCCTGGCCT 45628 GGTTC
GGGCCAGGCGGTTCGC AGGT
||||||| |||
TCCGGTCCGCCAGTG TCCA
GC__

GAM1958 LANGERIN 3' GCCTGAACCCGTTCTTCTCTGG 17931 _ C T_ C
TTC GGCCAG G GG CG GGTTTCAGGT
||||| || || |||||
TTGGTC C TC GC CCAAGTCCG
T T TT _

GAM1958 LDLR 3' GCTTGGGTTGGGATTTTGGTTT 6128 CG G TT
GGGCCAGG GTC CGG CAGGT
||||| ||| || |||||
TTTGGTTT TAG GTT GTTCG
_ G GG

GAM1958 LENG4 3' CTGGGCCGGGGCTGGGCTT 23584 AGG G
GGGCC CGGTC CGGTTCAG
|||| |||| |||||
TTCGG GTCGG GCCGGGTC
_ G

GAM1958 LNK 3' CTGAGCCAGCATGCTGGCTT 11974 G GTC _
GGGCCAG CG GC GGTTTCAG
||||| || || |||||
TTCGGTC GT CG CCGAGTC
_ A_ A

GAM1958 LPL 3' ATTTGGGTTGTGACCCAGGGTG 5749 G AGGC TT
C G GCC GGTCGCGG CAGGT
||| ||||| |||||

			CTGG CCAGTGTT GTTTA		
			G GAC_ GG		
GAM1958 LRAT	3'	ACTTGAACAATTTGATTTGGCT 30180	_ TCGCG		
T		GGGCCAGG CGG GTTCAGGT			
		TTCGGTTT GTT CAAGTTCA			
		A TAA_			
GAM1958 LRP4	3'	GCTTGAGTGAATGTTAGGCCT 32202	AG G GGT		
		GGGCC GCG TCGC TCAGGT			
		TCCGG TGT AGTG AGTTCG			
		AT A _			
GAM1958 LZTR1	3'	CCTGGGCTGCTCCTGTCCC 13637	C CGGTC		
		GGG CAGG GCGGTTTCAGG			
		CCC GTCC CGTCGGGTCC			
		T T_			
GAM1958 MAFF	3'	CCTGGGGGTGCCTGGCCT 14701	G GCGGT		
		GGGCCAGGCG TC TCAGG			
		TCCGGTCCGT GG GGTCC			
		G _			
GAM1958 MAN2A2	3'	CCTGAATTCTCTTTGGCTT 12766	C TCGC		
		GGGCCAGG GG GGTTCAGG			
		TTCGGTTT TC TTAAGTCC			
		C _			
GAM1958 MAP2	3'	ATTTGAGCTGTGGTTGAGG 25581	AGG GT		
		CC CG CGCGGTTTCAGGT			
		GG GT GTGTCGAGTTTA			
		A_ TG			
GAM1958 MAP2K2	5'	GCCTGGGCCGCGGCCGAGCCC 24995	CAG		
		GGGC GCGGTCGCGGTTTCAGGT			
		CCCG CGCCGGCGCCGGGTCCG			
		A_			
GAM1958 MAPK1	5'	CCGAGTGGCTGTCTGGCTC 29063	A GGTTC		
		GGGCC GGCGGTCGC GG			
		CTCGG CTGTCTGGTG CC			
		_ AG_			
GAM1958 MAPK1	5'	CCGAGTGGCTGTCTGGCTC 8616	A GGTTC		
		GGGCC GGCGGTCGC GG			
		CTCGG CTGTCTGGTG CC			
		_ AG_			
GAM1958 MAPK4	3'	GTTGAACTGGACCCTGGCTT 8622	CG G GG		
		GGGCCAGG GTC CGGTTCA T			

				TTCGGTCC CAG GTCAAGT G		
				— — TT		
GAM1958	MAPK9	3'	ACCTGATAGGATTGCCTGCTT	29135	C	GCGGT
			GGGC AGGCGGTC TCAGGT			
			TTCG TCCGTTAG AGTCCA			
			— GAT—			
GAM1958	MAPK9	3'	ACCTGATAGGATTGCCTGCTT	29137	C	GCGGT
			GGGC AGGCGGTC TCAGGT			
			TTCG TCCGTTAG AGTCCA			
			— GAT—			
GAM1958	MAPK9	3'	ACCTGATAGGATTGCCTGCTT	29139	C	GCGGT
			GGGC AGGCGGTC TCAGGT			
			TTCG TCCGTTAG AGTCCA			
			— GAT—			
GAM1958	MAPK9	3'	ACCTGATAGGATTGCCTGCTT	8630	C	GCGGT
			GGGC AGGCGGTC TCAGGT			
			TTCG TCCGTTAG AGTCCA			
			— GAT—			
GAM1958	MAPRE3	3'	GCCTGGACCCCATTTGTCTGTCT	14715	C	CGC
			GGGC AGGCGGT GGTTCAGGT			
			TCTG TCTGTTA CCAGGTCCG			
			— CC—			
GAM1958	MAPT	3'	CTGAGCGGCCCGCCTGTCCT	12541	C	GGT
			GGG CAGGCGGTCGC TCAG			
			TCC GTCCGCCGGCG AGTC			
			T —			
GAM1958	MAPT	3'	CTGAGCGGCCCGCCTGTCCT	18829	C	GGT
			GGG CAGGCGGTCGC TCAG			
			TCC GTCCGCCGGCG AGTC			
			T —			
GAM1958	MAPT	3'	CTGAGCGGCCCGCCTGTCCT	18835	C	GGT
			GGG CAGGCGGTCGC TCAG			
			TCC GTCCGCCGGCG AGTC			
			T —			
GAM1958	MAPT	3'	CTGAGCGGCCCGCCTGTCCT	18841	C	GGT
			GGG CAGGCGGTCGC TCAG			
			TCC GTCCGCCGGCG AGTC			
			T —			
GAM1958	MAT1A	3'	CCTGAGCAGTCCTTGGCCT	43667	C	GTC G
			GGGCCAGG G GC GTTCAGG			

TCCGGTTC C TG CGAGTCC
 — A

GAM1958 MAX 3' GCCCAGGTGGCCTCCTGGCCC 29716 C —
 GGGCCAGG GGTCGC GGT
 ||||| ||||| ||
 CCCGGTCC CCCGTG CCG
 T GAC

GAM1958 MAX 3' GCCCAGGTGGCCTCCTGGCCC 8199 C —
 GGGCCAGG GGTCGC GGT
 ||||| ||||| ||
 CCCGGTCC CCCGTG CCG
 T GAC

GAM1958 MAZ 5' ACCTCGACGGTCGCCGTGGCCC 36323 _ GT _ GTTC
 GGGCCA GGCG CG CG AGGT
 ||||| ||||| || || |||||
 CCCGGT CCGC GC GC TCCA
 G TG A —

GAM1958 MCM2 3' ACCTGGCATGACTGTTTGTTC 33721 GC CG T
 GG CAGGCGGTCTG GT CAGGT
 || ||||| || |||||
 CT GTTTGTCACT CG GTCCA
 TT A _ _

GAM1958 MEN1 5' ATCTGAAAACCCTGCTTGGTTC 44840 TCGC —
 GGGCCAGGCGG GGT TCAGGT
 ||||| || |||||
 CTTGGTTCGTC CCA AGTCTA
 — AA

GAM1958 MEOX1 3' CTGGACACCACCTGGCCT 10864 C CGCG
 GGGCCAGG GGT GTTCAG
 ||||| || |||||
 TCCGGTCC CCA CAGGTC
 A —

GAM1958 MEOX1 3' CTGGACACCACCTGGCCT 15188 C CGCG
 GGGCCAGG GGT GTTCAG
 ||||| || |||||
 TCCGGTCC CCA CAGGTC
 A —

GAM1958 MFI2 3' TCTGGTGCGGGTGTTCGTTT 27154 G GT T
 GGGCCAGGCG TCGCG TCAGG
 ||||| ||||| |||||
 TTTGGTTTGT GGCGT GGTCT
 G _ C

GAM1958 MGAT5 5' CTGGAATCAGGCTGCCTGGTC 8238 GC A T
 GGCCAGGCGGTC GGTTTC GG
 ||||| ||||| ||
 CTGGTCCGTCGG CTAAG TC
 A _ G T

GAM1958 MKI67 3' CTGGGCCAAGGTTTGCCC 8255 C GGT GC
 GGGC AGGC C GGTTTCAG
 ||||| ||||| | |||||

		CCCG TTTG G CCGGGTC	
		— — AA	
GAM1958	MMP15	3' TTGGAGACTGTCTGGCCC 8265	GCGG
		GGGCCAGGCGGTC TTCAG	
		CCCGGTCTGTCAG AGGTT	
GAM1958	MNT	3' ACCTGTGGGAGCGCCTGGCCC 21558	G G GTT
		GGGCCAGGCG TC CG CAGGT	
		CCCGGTCCGC AG GT GTCCA	
		G G —	
GAM1958	MPO	3' GCCTGGGTTCCAATCCTGGCTC 5786	C__ TCGC TT
		GGGCCAGG GG GG CAGGT	
		CTCGGTCC CC TT GTCCG	
		TAA — GG	
GAM1958	MTL5	3' GCCTGAGCATTGTTTGTCTGGC 11359	T CG
	CC	GGGCCAGGCGG CG GTTCAGGT	
		CCCGGTCTGTT GT CGAGTCCG	
		T TA	
GAM1958	MTL5	3' ACTTGAATTGTGAAAAGCTC 11358	CAGGCGG
		GGGC TCGCGGTTTCAGGT	
		CTCG GGTGTTAAGTTCA	
		AAAA—	
GAM1958	MTM1	3' ACTTGAAGTACCAGGCCGTTTG 5788	C GC —
	CTT	GC AGGCGGTC GGT TCAGGT	
		CG TTTGCCGG CCA AGTTCA	
		— A_ TGA	
GAM1958	MTMR8	3' TCGTGTAGTTGTCTGGTTT 17748	T__
		GGGCCAGGCGG CGCGG	
		TTTGGTCTGTT GTGCT	
		GAT	
GAM1958	MYO10	3' ACCTGAACGCACCACCCTCTGG 14729	C C__ G
	CCT	GGCCAGG GGT GCG TTCAGGT	
		CCGGTCT CCA CGC AAGTCCA	
		C CCA _	
GAM1958	NAGLU	5' CCCGGAAGCCGCGACTCCTGGC 5804	C _ A T
	CC	GGGCCAGG GGTCGCGGTT C GG	
		CCCGGTCC TCAGCGCCGA G CC	
		— A G CA	
GAM1958	NAPB	3' TTGAGTCCTCTGTTTT 34769	CGGTCGC _
		GGGCCAGG GG TTCAG	

TTTGGTCT CC GAGTT
 _____ T
 GAM1958 NAV2 3' TCTGGACGAGCCTTGCCCTGACC 30206 C TC G_ GT
 T
 GGG CAGGCGG GC GTTCAG
 ||| ||||| || |||||
 TCC GTCCGTT CG CAGGTC
 A C_ AG TG
 GAM1958 NCALD 3' CTGAGTTGCTGTTTGGTCT 25744 GTC GG
 GGGCCAGGCG GC TTCAG
 ||||||| || |||||
 TCTGGTTTGT CG GAGTC
 _____ TT
 GAM1958 NCAM1 5' CCTGGCAATTGTCTGCCC 6216 C C GGTT
 GGGC AGGCGGT GC CAGG
 ||| ||||| || |||||
 CCCG TCTGTTA CG GTCC
 _____ A _____
 GAM1958 NCOA3 3' ATCTGGGTTAATTCATTTGGTT 13282 C TCGC TT
 C
 GGGCCAGG GG GG CAGGT
 ||||||| || || |||||
 CTTGGTTT CT TT GTCTA
 A TAA_ GG
 GAM1958 NDRG1 3' GCCAGTGCGGCTGCCAGGTTC 29968 A GTTCA
 GGGCC GGCGGTCGCG GGT
 ||||| ||||| ||||| |||
 CTTGG CCGTCGGCGT CCG
 A GA____
 GAM1958 NFATC3 5' TTGCCGTGGAGTCGCGACCTCT 10897 C _ _
 TGGCCC GCCAGG GGTCGCGG TTCA GGT
 ||||| ||||| ||||| ||||| |||
 CGGTTC CCAGCGCT AGGT CCG
 T G G TTT
 GAM1958 NFE2 5' ACCTGGACCAGACTCTGGCCC 12818 GC GC
 GGGCCAG GGTC GGTTCAGGT
 ||||||| ||||| ||||| |||||
 CCCGGTC TCAG CCAGGTCCA
 _____ A_ _____
 GAM1958 NFE2L1 5' CTGGAGTGTGTCCTTGGCCT 9197 C T G
 GGGCCAGG GG CGCG TTCAG
 ||||||| || ||||| |||||
 TCCGGTTC CT GTGT AGGTC
 _____ _ G
 GAM1958 NKX3A 3' GCCTGAATTGCTTTCTGCT 12828 TC_
 GGCGG GCGGTTTCAGGT
 ||||| ||||| ||||| |||||
 TCGTC CGTTAAGTCCG
 TTT
 GAM1958 NPTX1 3' TCTACTGCACTGCCTGGCTC 8357 C TC
 GGGCCAGGCGGT GCGGT AGG
 ||||||| ||||| ||||| |||

CTCGGTCCGTCA CGTCA TCT

GAM1958 NR4A2 5' GCCTGTCCAGCCGGCCGCCTGT 12857 C __ TT
CCC GG CAGGCGGTCTG C GG CAGGT
|| ||||| | || ||||
CC GTCCGCCGGC G CC GTCCG
T C A T_

GAM1958 Nrap 3' ATCTGCCCTGGCTGTTTGCCC 29236 C C TT
GGGC AGGCGGTCTG GG CAGGT
||| ||||| || ||||
CCCG TTTGTCTGGT CC GTCTA
_ _ C_

GAM1958 NTRK2 5' GCCTCGCTGGCTGCTTCGCTC 12846 C _ GTTC
GGGC AGGCGGTCT GCG AGGT
||| ||||| || ||||
CTCG TTCGTCTGG CGC TCCG
C T _

GAM1958 NUCB1 3' GCCTGGGTTGTGGCCGCCCTAG 12852 CA_ TT
C GC GGCGGTCTGCGG CAGGT
|| ||||| ||||
CG CCGCCGGTGTT GTCCG
ATC GG

GAM1958 NUMA1 5' TTGGAGTGACTGTCTGGC 44883 GG
GCCAGGCGGTCTGC TTCAG
||| ||||| ||||
CGGTCTGTCAGTG AGGTT

GAM1958 NUP98 3' GTTGGTTTGGTCCCTGGTTT 18444 C GT CGGT GG
GGGCCAGG G CG TCA T
||| || | || |
TTTGGTCC C GT GGT G
_ TG TT_ TT

GAM1958 OAS2 3' GCCTTTGGCTTTTGGCTC 8374 C C_
GGGCCAGG GGTCG GGT
||| |||| |
CTCGGTTT TCGGT CCG
_ TT

GAM1958 OGT 5' GTTTGGATTGCAGCATTCTGCT 9662 C CG C GG
C GGC AGG GT GCGTTCA T
||| || || ||||| |
CTCG TCT CG CGTTAGGT G
_ TA A TT

GAM1958 OLIG2 3' ACCTGATCGAGCGCTGTCTGGC 12381 T GGT_
TT GGGCCAGGCGG CGC TCAGGT
||| |||| |
TTCGGTCTGTC GCG AGTCCA
_ AGCT

GAM1958 OPHN1 3' CCTGGGCCGTAGCTTGTCT 8401 _ CG
AGGCG GT CGGTTCAAG
||| || |||||

TCTGT CG GCCGGGTCC
 T AT
 GAM1958 OTOF 3' GCTTGCGGGGGCCGCCTGTCCT 11225 C _G GTT
 GGG CAGGCGGT C CG CAGGT
 ||| ||||| | || ||||
 TCC GTCCGCCG G GC GTTCG
 T G G _
 GAM1958 PACSIN1 3' CCTGCAAGGCTCTTGGCCT 44315 C GCGGTT
 GGGCCAGG GGTC CAGG
 ||||| ||| |||
 TCCGGTTC TCGG GTCC
 _ AAC_
 GAM1958 PAICS 5' CTTGAGTTCTGCCTCGCTT 13163 C TC GGT
 GGGC AGGCGG GC TCAGG
 ||| ||||| || ||||
 TTCG TCCGTC TG AGTTC
 C T _
 GAM1958 PART1 3' ATCTGGGCCAAGAATGATTGCT 18666 A C_
 AGGTCC C GGCGGTCTG GTTTCAGGT
 | ||||| |||||
 G TCGTTAGT CCGGGTCTA
 A AAGAA
 GAM1958 PBP 3' ACTTTTCCTGCTGCCTGGCCT 8415 T C TTC
 GGGCCAGGCGG CG GG AGGT
 ||||| ||| |||
 TCCGGTCCGTC GT CC TTCA
 _ _ TT_
 GAM1958 PCDHB16 5' ACCGTTGGGCTGCTTGGTTC 21943 _
 GGGCCAGGCGGTC GCGGT
 ||||| ||||
 CTTGGTTTCGTCGG TGCCA
 GT
 GAM1958 PFKFB3 3' ACCTCCACGTGACTGTTTGGTG 40318 G GTTC
 C G GCCAGGCGGTCTGCG AGGT
 | ||||| ||||
 C TGGTTTGTCAGTGC TCCA
 G ACC_
 GAM1958 PIK3R3 3' GCCTGGATAGACTGCCTGCGTC 30605 _ GCG
 C GGGC CAGGCGGTC GTTCAGGT
 ||| ||||| |||||
 CCTG GTCCGTCAG TAGGTCCG
 C A_
 GAM1958 PKD1 5' GCCTGAGCTGCGGTCTCCGC 5841 CA C GT
 GC GG G CGCGGTTTCAGGT
 || || | |||||
 CG CC C GCGTCGAGTCCG
 _ T TG
 GAM1958 PLA2G2D 3' GCTTGGTCTGACCCCTTGGCCT 14772 C GC TT
 GGGCCAGG GGTC GG CAGGT
 ||||| ||| || ||||

		TCCGGTTC CCAG TC GTTCG	
		C _ TG	
GAM1958	PLA2G2D	3' CCTGAACCAGCCTGGCTT 14769	GGTCGC
		GGGCCAGGC GGTTCAGG	
		TTCGGTCCG CCAAGTCC	
		A_____	
GAM1958	PLA2G7	5' CTTGGGTCGCGTTGGTGC 11534 G	GCGGT TT
		G GCCAG CGCGG CAGG	
		C TGGTT GCGCT GTTC	
		G _____ GG	
GAM1958	PLCB2	5' ATTTGAGCCCAGCTTGGCTC 10916	GGTCGC
		GGGCCAGGC GGTTCAGGT	
		CTCGGTTCG CCGAGTTTA	
		AC_____	
GAM1958	PPP1CB	3' ATCTGTATCCATTGTCTGGCT 8556	CGC TT_
	T	GGGCCAGGCGGT GG CAGGT	
		TTCGGTCTGTTA CC GTCTA	
		C_ TAT	
GAM1958	PPP2R5A	3' CTAGTTGTCACTGCCTGGCTT 12909	C GG C
		GGGCCAGGCGGT GC TT AG	
		TTCGGTCCGTCA TG GA TC	
		C TT _	
GAM1958	PPT1	3' GCTTGGA AAAAATCTTGCTTGGC 30956	TCGCGG
	T	GGCCAGGCGG TTCAGGT	
		TCGGTTCGTT AGGTTCG	
		CTAAAA	
GAM1958	PRKCABP	5' ATCTGAGCCTATCGCCCTGGCC 14787	_ CGC
	T	GGGCCAGG CGGT GGTTCAGGT	
		TCCGGTCC GCTA CCGAGTCTA	
		C T_	
GAM1958	PTGFR	3' GTCTGGCAGACAGGTTGCCTGA 6664	C GT GCG_ T GT
	CCC	GG CAGGCG C GT CAG	
		CC GTCCGT G CG GTC	
		A TG ACAGA _ TG	
GAM1958	PTGS1	3' GCCTGATCTTGCCTGTCTGGCT 6674	TC T_
	C	GGGCCAGGCGG GCGG TCAGGT	
		CTCGGTCTGTC CGTT AGTCCG	
		_ CT	
GAM1958	PTGS1	3' GCCTGATCTTGCCTGTCTGGCT 27895	TC T_
	C	GGGCCAGGCGG GCGG TCAGGT	

CTCGGTCTGTC CGTT AGTCCG
 — CT

GAM1958 PTPN11 5' TCTGTGCGCGGCCGGCTGGCTC 27911 G GTT GT
 GGGCCAG CGGTCGCG CAG
 ||||| ||||| ||
 CTCGGTC GCCGGCGC GTC
 G GT_ TG

GAM1958 PTPN11 5' TCTGTGCGCGGCCGGCTGGCTC 8712 G GTT GT
 GGGCCAG CGGTCGCG CAG
 ||||| ||||| ||
 CTCGGTC GCCGGCGC GTC
 G GT_ TG

GAM1958 PTTG1IP 3' TGCTTGAATTATAAATGTGGTG 10539 G _____
 TTTGGCCT GCG TCGCG GTTCAGGT G
 ||| |||| ||||| |
 TGT GGTGT TAAGTTCG T
 — AAATAT

GAM1958 PXN 3' GTCTGGTGTGTAGATTGCTTTG 8757 C _ GT GT
 TCT GGC AGGCGGTC GCG TCAG
 ||| ||||| ||| ||||
 TCTG TTCGTTAG TGT GGTC
 T A GT TG

GAM1958 PYGB 3' ATCTGGGCTGCGGGGAGGCTC 8764 AGGCGG
 GGGCC TCGCGGTTTCAGGT
 |||| ||||| |||||
 CTCGG GGCCTCGGGTCTA
 AGG_

GAM1958 PYGO2 3' GCCTGGATTGCTCACTGTTT 32000 C_
 AGGCGGT GCGGTTTCAGGT
 ||||| ||||| |||||
 TTTGTCA CGTTAGGTCCG
 CT

GAM1958 RABL2A 3' ACCTCTGACTCCCTGGTTC 15077 C C_
 GGGCCAGG GGTCG GGT
 ||||| |||| |||
 CTTGGTCC TCAGT CCA
 C CT

GAM1958 RABL2B 3' ACCTCTGACTCCCTGGTTC 13944 C C_
 GGGCCAGG GGTCG GGT
 ||||| |||| |||
 CTTGGTCC TCAGT CCA
 C CT

GAM1958 RAD1 5' ACCTGGGCTCAAGTGGCTTGGC 28499 G TCGC
 CT GGGCCAGGC G GTTTCAGGT
 ||||| | |||||
 TCCGGTTCG T TCGGGTCCA
 G GAAC

GAM1958 RAD54L 5' GCCTGCTTTTGACCTTTGGCTC 9629 C C TT
 GGGCCAGG GGTCG GG CAGGT
 ||||| |||| || ||||

		CTCGGTTT CCAGT TT GTCCG	
		— — TC	
GAM1958	RAI3	3' TCTGAGCTCACGCTGGCTC 10115	G GTCGC
		GGGCCAG CG GTTCAGG	
		CTCGGTC GC TCGAGTCT	
		— AC—	
GAM1958	RALBP1	3' CTGAGCAGCTCCTGGCTC 13660	CGGTC G
		GGGCCAGG GC GTTCAG	
		CTCGGTCC CG CGAGTC	
		T— A	
GAM1958	RALBP1	3' GCCTGGTGGGTGTTCCCTGGCC 13662	C GT GGT
	C	GGGCCAGG G CGC TCAGGT	
		CCCGGTCC C GTG GGTCCG	
		— TT GGT	
GAM1958	RBM8A	3' ATTTGAGTTGCGAATAAATGTT 11578	GC GGCGG GG
	CC	GG CA TCGC TTCAGGT	
		CC GT AGCG GAGTTTA	
		TT AAATA TT	
GAM1958	RECQL5	3' CTGAGGGCTGCTTGGT 10449	GCGG
		GCCAGGCGGTC TTCAG	
		TGGTTCGTCCG GAGTC	
		—	
GAM1958	RECQL5	3' CCTGGATTGAATTGGGCC 10448	AGG CG
		GGGCC CGGT CGGTTTCAGG	
		CCCGG GTTA GTTAGGTCC	
		— A—	
GAM1958	RERE	3' CCTTCTCGGCTTCTGGTTT 14405	C C TTC
		GGGCCAGG GGTCG GG AGG	
		TTTGGTCT TCGGC CT TCC	
		— T—	
GAM1958	RERE	3' GCTTGGACCGAGGCCTGGTC 14408	GGTCG
		GGCCAGGC CGGTTTCAGGT	
		CTGGTCCG GCCAGGTTTCG	
		GA—	
GAM1958	RFP	5' GCTTTGCCCGCCTGGCCC 13261	T C
		GGGCCAGGCGG CG GGT	
		CCCGGTCCGCC GT TCG	
		C T	
GAM1958	RIG	3' TCTGGGTCAGCTTGGCACC 13108	GGTCGC TT
		GG GCCAGGC GG CAGG	

CC CGGTTCG CT GTCT
 A A_____ GG
 GAM1958 RPE 3' GCCTGGACAACCTGGGTTTGTGTC 31156 _____ CG____
 TGGCTT CAGGCGG TCG GTTCAGGT
 ||||| || |||||
 GTCTGTT GGT CAGGTCCG
 TG TCAA
 GAM1958 RPE 3' CTTGGGTTTGTCTGGCTT 31154 TCGCG TT
 GGGCCAGGCGG G CAGG
 ||||| || ||||
 TTCGGTCTGTT T GTTC
 _____ GG
 GAM1958 RXRA 3' TTGGGGCCTCCCTGGGCTC 8875 C_ G
 GGGCCAGG GGTC CGG
 ||||| |||||
 CTCGGTCC CCGG GTT
 CT G
 GAM1958 SALL2 3' ACCAGTGCTGTTTGGCCT 31935 T _
 GGGCCAGGCGG CGC GGT
 ||||| |||||
 TCCGGTTTGTG GTG CCA
 _ A
 GAM1958 SALL2 3' GCTTGTGTCTTTGTGATTGTCT 31936 C TT____
 GGTTCC CCAGGCGGT GCGG CAGGT
 ||||| |||||
 GGTCTGTTA TGTT GTTCG
 C TCTGT
 GAM1958 SCN4A 3' ATCTGGGACTGTGCCTGGGCTC 5888 GGTC _
 GGGCCAGGC GCGGTTT AGGT
 ||||| |||||
 CTCGGTCCG TGTCAGG TCTA
 _____ G
 GAM1958 SDHC 3' CCTGTGGGTTGCTGGGCTT 34381 G GT G GTT
 GGGCCAG CG C CG CAGG
 ||||| || |||||
 TTCGGTC GT G GT GTCC
 _ TG _ _
 GAM1958 SERPINB13 3' ATTTGGGTTGTCTGTCTTGTCT 14761 C TC TT
 GGGC AGGCGG GCGG CAGGT
 ||||| |||||
 TCTG TCTGTC TGTT GTTTA
 T _ GG
 GAM1958 SHOC2 3' ATTTGGACTGTTGTTCTGCTT 14303 TC____
 AGGCGG GCGGTTT CAGGT
 ||||| |||||
 TTCGTC TGTCAGGTTTA
 TTGT
 GAM1958 SHOX 3' CCTGAGCTGTTTCTGGTT 6055 CGGTC
 GGCCAGG GCGGTTT CAGG
 ||||| |||||

TTGGTCT TGTCGAGTCC
 T____
 GAM1958 SIM1 3' GCCTGGGCTCTAGTTTCCTGGT 11511 CGGTCGC
 TT GGGCCAGG GGTTTCAGGT
 ||||| |||||
 TTTGGTCC TCGGGTCCG
 TTTGATC
 GAM1958 SLC16A2 3' GCTTGGAACCAACCCTGGCCT 13270 C CGC _
 GGGCCAGG GGT GGTTTC AGGT
 ||||| || |||| ||||
 TCCGGTCC CCA CCAAG TTCG
 _ _ GG
 GAM1958 SLC18A1 3' ACTTGAGCTGTGACGGGTTC 9015 AGGCG
 GGGCC GTCGCGGTTTCAGGT
 |||| |||||
 CTTGG CAGTGTCGAGTTCA
 G____
 GAM1958 SLC1A4 3' CTGTGGTGGTCTCTGGTCC 8995 C GT G TT
 GGGCCAGG G CGC G CAG
 ||||| | || | ||
 CCTGGTCT C GTG T GTC
 _ TG G _
 GAM1958 SLC1A5 3' TCCCCACCGTGACCTGCCTGGC 12143 _ TCA T
 CT GGGCCAGGC GGTCGCGGT GG
 ||||| ||||| ||
 TCCGGTCCG CCAGTGCCA CC
 T CC_ TG
 GAM1958 SLC1A5 3' TCCCCACCGTGACCTGCCTGGC 38403 _ TCA T
 CT GGGCCAGGC GGTCGCGGT GG
 ||||| ||||| ||
 TCCGGTCCG CCAGTGCCA CC
 T CC_ TG
 GAM1958 SLC21A9 3' GCCTGGGCTGGTGTGAGGCC 14126 A GTCG
 GGGCC GGCG CGGTTTCAGGT
 |||| |||| |||||
 CCCGG CTGT GTCGGGTCCG
 A G____
 GAM1958 SLC25A14 5' CTTAACGGTCCTCTGGTCT 23086 C TC G C
 GGGCCAGG GG GC GTT AGG
 ||||| || || ||||
 TCTGGTCT CC TG CAA TTC
 _ _ G _
 GAM1958 SLC25A14 5' CTTAACGGTCCTCTGGTCT 10087 C TC G C
 GGGCCAGG GG GC GTT AGG
 ||||| || || ||||
 TCTGGTCT CC TG CAA TTC
 _ _ G _
 GAM1958 SLC29A1 3' CTGTCAGACTGTCTGCCT 11399 C _
 GGGC AGGCGGTC GCGG
 |||| ||||| ||||

TCCG TCTGTCAG TGTC
 _ AC
 GAM1958 SLC29A1 3' GCTTGAGTTTCTCCACTCTTGG 11400 C__ TCGCGG
 CTC GGCCAGG GG TTCAGGT
 ||||| || |||||
 TCGGTTC CC GAGTTCG
 TCA TCTTT_
 GAM1958 SLC4A1AP 5' CTGGGCGGCTGTCTGGACCT 19976 _ GGT
 GGG CCAGGCGGTCCG TCAG
 || ||||| ||||
 TCC GGTCTGTCGGCG GGTC
 A _
 GAM1958 SLC6A8 3' TCTGGGCTGCTAACCTGGCCT 12152 CGGTC GT
 GGGCCAGG GCGGTTCA
 ||||| |||||
 TCCGGTCC CGTCGGGTC
 AAT__ TG
 GAM1958 SLC7A6 5' ACCTCCGACTCCCTGGTTC 10123 C C_
 GGGCCAGG GGTCG GGT
 ||||| |||| ||
 CTTGGTCC TCAGC CCA
 C CT
 GAM1958 SMARCA5 5' ACCTCAGTGACCCGTCTGGCCC 9655 _ GGTTTC
 GGGCCAGGCGG TCGC AGGT
 ||||| |||| ||||
 CCCGGTCTGCC AGTG TCCA
 C AC__
 GAM1958 SMARCD1 3' ATTTGGGCCCTGTGCTGCCTGC 9043 C T _
 CT GGC AGGCGG CGC GGTTTCAGGT
 || ||||| || |||||
 CCG TCCGTC GTG CCGGGTTTA
 _ _ TC
 GAM1958 SMARCD1 3' ATTTGGGCCCTGTGCTGCCTGC 29141 C T _
 CT GGC AGGCGG CGC GGTTTCAGGT
 || ||||| || |||||
 CCG TCCGTC GTG CCGGGTTTA
 _ _ TC
 GAM1958 SMURF1 5' GCCTGGGCCGCGGAGTTTGTGT 44414 _ GG
 CC GGGC CAGGC TCGCGGTTTCAGGT
 ||| |||| |||||
 CCTG GTTTG GGCGCCGGGTCCG
 T A_
 GAM1958 SNL 3' GCCTGGGCTGCCGACACCTGGG 9065 G CG _
 CC GG CCAGG GTCG CGGTTTCAGGT
 || |||| |||| |||||
 CC GGTCC CAGC GTCGGGTCCG
 G A_ C
 GAM1958 SPOCK 3' GTTTGGAAGACAACTGCTTGTT 31458 GC CGCGG GG
 CC GG CAGGCGGT TTCA T
 || ||||| |||| |

CC GTTCGTCA AGGT G
 TT ACAGA TT
 GAM1958 SQSTM1 3' GCCTGGGCCTTGGCTGGGCCT 9990 AGG C
 GGGCC CGGTTCG GGTTCAGGT
 |||| |||| ||||
 TCCGG GTCGGT CCGGGTCCG
 ____ T
 GAM1958 SRC 3' CCTGGGGGACCCCTGGCTC 11888 C GCGG
 GGGCCAGG GGTC TTCAGG
 ||||| ||| ||||
 CTCGGTCC CCAG GGGTCC
 _ G_
 GAM1958 STAT6 3' GCCTGGGCCAGATGAGCCTGCC 9131 C G_ GC
 C GGC AGGC GTC GGTTCAGGT
 ||| ||| || |||||
 CCCG TCCG TAG CCGGGTCCG
 _ AG A_
 GAM1958 STK10 3' ACTTGGTCTGCTGGCCTGGCCT 12613 GGTC TT
 GGGCCAGGC GCGG CAGGT
 ||||| ||| ||||
 TCCGGTCCG CGTC GTTCA
 GT__ TG
 GAM1958 STK11 3' ATTTGAGCTGTGGCTGTGAGGG 6069 AG__
 GT GCC GCGGTCGCGTTCAGGT
 || |||||
 TGG TGTCGGTGTGAGTTTA
 GGAG
 GAM1958 STK11 3' TACCTGGAAGCCGCGCGGCCGC 6070 _ _ _
 TTTGGTTT G GCGGT CGCGGT TCAGGT A
 | |||| |||| |||| |
 T CGCCG GCGCCG GGTCCA T
 T GC AA
 GAM1958 STK24 3' ACTTGAGTCTATTGCCTTGCCT 9627 C CGC GT
 GGGC AGGCGGT G TCAGGT
 ||| ||||| | ||||
 TCCG TCCGTTA C AGTTCA
 T T__ TG
 GAM1958 SURF4 3' CTGGGTGCTGCTGGCCT 27012 G T GGT
 GGGCCAG CGG CGC TCAG
 ||||| ||| ||| ||||
 TCCGGTC GTC GTG GGTC
 _ _ _
 GAM1958 SWAP70 3' CCTCACACTGCCTGGCCC 35347 CGCG TC
 GGGCCAGGCGGT GT AGG
 ||||| || |||
 CCCGGTCCGTCA CA TCC
 ____ C_
 GAM1958 SYNGR1 3' GCCACAGTGACCGCCTGCC 11066 C G TCA
 GGGC AGGCGGTGCG GT GGT
 ||| ||||| || |||

			CCCG TCCGCCAGTG CA CCG		
			— A —		
GAM1958	SYNGR3	3'	ACCTTGGCTTCCTGGCCC 10405	C	C
			GGGCCAGG GGTCG GGT		
			CCCGGTCC TCGGT CCA		
			T T		
GAM1958	TAF1C	5'	GCCAGTGTGGTGCTTGGTCC 12236	GT_	_
			GGGCCAGGCG CGC GGT		
			CCTGGTTCGT GTG CCG		
			GGT A		
GAM1958	TAL1	3'	TTGCTGATGGTCTGGTCT 9175	G	_
			GGGCCAGGC GTC GCGG		
			TCTGGTCTG TAG CGTT		
			G T		
GAM1958	TAZ	3'	GCCTGAGGTCTGGCTGCTTGCC 5586	C	CGG
	C		GGGC AGGCGGTCTG TTCAGGT		
			CCCG TTCGTCTGGT GAGTCCG		
			— CTG		
GAM1958	TBL1X	3'	GCCTGAGGGAGCCCTGGCTT 12187	C	CGCGG
			GGGCCAGG GGT TTCAGGT		
			TTCGGTCC CCG GAGTCCG		
			— AGG—		
GAM1958	TBL2	3'	GCCGCGCCGTGCCGCTGGCCC 26868	T	TCA
			GGGCCAGGCGG CGCGGT GGT		
			CCCGGTCCGCC GTGCCG CCG		
			— CG_		
GAM1958	TBP	5'	CCTGGGCCGCCGGCTGTTT 32330	_	
			AGGCGGTCTG CGGTTCAAG		
			TTTGTCGGC GCCGGGTCC		
			C		
GAM1958	TEC	3'	GCCTGAGCTGTGGCGGAGGATC 9217	_	AGGCG
	C		GGG CC GTCGCGGTTCAAGT		
			CCT GG CGGTGTCGAGTCCG		
			A AGG—		
GAM1958	TES	3'	ACTTGTATAGATGATTTTGGC 35630	C	CG_ T
	TT		GGGCCAGG GGTCG GT CAGGT		
			TTCGGTTT TTAGT TA GTTCA		
			— AGA T		
GAM1958	TESK1	5'	ACCGCCACCGCCTGGTCC 12971	C	
			GGGCCAGGCGGT GCGGT		

CCTGGTCCGCCA CGCCA
 C
 GAM1958 TFEB 3' GTTGGACTTAGTGCCTGTCT 44240 C GTCGC GG
 GGG CAGGCG GGTTCA T
 ||| ||||| ||||| |
 TCT GTCCGT TCAGGT G
 _ GAT_ TT
 GAM1958 TGFB3 5' ATCTGGGGAGGCCGCTGGTTT 9232 GCGG
 GGGCCAGGCGGTC TTCAGGT
 ||||| |||||
 TTTGGTCCGCCG GGGTCTA
 AG_
 GAM1958 TIMM23 3' TCTGTGTGCTGCTGTCTGGCTC 30200 C GTT T
 GGGCCAGGCGGT GCG CAGG
 ||||| ||| |||
 CTCGGTCTGTCTG CGT GTCT
 T GT_ T
 GAM1958 TIRAP 3' ACCTGGATTTTTTGTGGT 27472 TCGC
 CCAGGCGG GGTTTCAGGT
 ||||| |||||
 GGTTTGTT TTAGGTCCA
 TT_
 GAM1958 TJP1 5' TCCCAGGTCGTGGCCGTCTTGC 9266 C GT CA T
 TC GGGC AGGCGGTCGCG T GG
 ||| ||||| ||| | ||
 CTCG TCTGCCGGTGC G CC
 T TG AC TC
 GAM1958 TJP1 5' CTTGGCGGCCGCCGGTTC 9264 A GGTT
 GGGCC GGCGGTCGC CAGG
 ||||| ||||| |||
 CTTGG CCGCCGGCG GTTC
 _ _
 GAM1958 TLX1 5' ATCTGTCCTCGGCTTCTGGCCT 12044 C C TT
 GGGCCAGG GGTCG GG CAGGT
 ||||| ||||| || |||||
 TCCGGTCT TCGGC CC GTCTA
 _ T T_
 GAM1958 TLX1 5' GCCTGAACTACCGTCCTGCCTA 12045 _ _ T C_
 GGCCT CC AGGC GG CG GGTTTCAGGT
 || |||| || || |||||
 GG TCCG CC GC TCAAGTCCG
 A T T CA
 GAM1958 TM7SF3 3' ACTTGAGAAATTACCTTTTGGT 30009 C CGCGG
 TT GGGCCAGG GGT TTCAGGT
 ||||| ||| |||||
 TTTGGTTT CCA GAGTTCA
 T TTAAA
 GAM1958 TMEPAI 3' ACATGTGATGTCTGGTCT 21401 G _
 GGGCCAGGCG TCGCG GT
 ||||| ||||| ||

TCTGGTCTGT AGTGT CA
 — A
 GAM1958 TNFSF15 5' ATTTGAAGGGTCTGGTGCCTGG 11599 GTC_ GG
 CCT GGGCCAGGCG GC TTCAGGT
 ||||||| || |||||
 TCCGGTCCGT TG AAGTTTA
 GGTC GG
 GAM1958 TOP3A 5' ATTTGAGCCTCATCTCTGGCTT 10961 C CGC
 GGGCCAGG GGT GGTTCAGGT
 ||||||| ||| |||||
 TTCGGTCT CTA CCGAGTTTA
 — CT_
 GAM1958 TPR 5' CTGGGTCCTGCTGGTCT 9302 G TCGC TT
 GGGCCAG CGG GG CAG
 ||||||| ||| || |||
 TCTGGTC GTC CT GTC
 — ——— GG
 GAM1958 TRIM14 3' ATCTGACCTGTCCCCTGGCCC 16666 C T C T
 GGGCCAGG GG CG GGT CAGGT
 ||||||| || || ||| |||||
 CCCGGTCC CC GT CCA GTCTA
 — T — —
 GAM1958 TRPC6 3' CAAACACTGTGGTTGTTTGGTT 10972 GT TCAGGT
 C GGGCCAGGCG CGCGGT
 ||||||| |||||
 CTTGTTTGT GTGTCA
 TG CAAACA
 GAM1958 TUFT1 3' GCTTGAGCTACTGTGCCCGGCC 21317 A GTCGC
 C GGGCC GGCG GGTTCAGGT
 |||| |||| |||||
 CCCGG CCGT TCGAGTTCG
 C GTCA_
 GAM1958 TWIST 3' CTGAACAGTTGTTTGTGTTT 6083 _ GTC G
 GGGC CAGGCG GC GTTCAG
 ||| ||||| || |||||
 TTTG GTTTGT TG CAAGTC
 T ——— A
 GAM1958 UNC119 3' CTGGGCCCTAGGCCTAGCCC 27648 C GGTCGC
 GGGC AGGC GGTTCAG
 ||| |||| |||||
 CCCG TCCG CCGGGTC
 A GATC_
 GAM1958 UNC119 3' CTGGGCCCTAGGCCTAGCCC 11621 C GGTCGC
 GGGC AGGC GGTTCAG
 ||| |||| |||||
 CCCG TCCG CCGGGTC
 A GATC_
 GAM1958 WBSCR1 3' GTTGGGCTGCGGTGCTGC 22723 _ GG
 GCGGT CGCGTTCA T
 |||| ||||| |

			CGTCG GCGTCGGGT G		
			TG TT		
GAM1958	WBSCR1	3'	GTTGGGCTGCGGTGCTGC 25706	—	GG
			GCGGT CGCGTTCA T		
			CGTCG GCGTCGGGT G		
			TG TT		
GAM1958	WHN	3'	CCAGCGTTTGCCTGGTCT 9649	T _	
			GGGCCAGGCGG CGC GG		
			TCTGGTCCGTT GCG CC		
			T A		
GAM1958	WHSC1	3'	CCTGTTGACTGCTGGGCCC 14249	A	CGGTT
			GGGCC GCGGTCG CAGG		
			CCCGG TCGTCAGT GTCC		
			G T_____		
GAM1958	WHSC1	3'	GCCAGGCGGCCGCTTGGCC 17182	—	
			GGCCAGGCGGTCGC GGT		
			CCGGTTCGCCGGCG CCG		
			GA		
GAM1958	WHSC1	3'	GCCAGGCGGCCGCTTGGCC 28463	—	
			GGCCAGGCGGTCGC GGT		
			CCGGTTCGCCGGCG CCG		
			GA		
GAM1958	WHSC1	3'	GCCAGGCGGCCGCTTGGCC 28474	—	
			GGCCAGGCGGTCGC GGT		
			CCGGTTCGCCGGCG CCG		
			GA		
GAM1958	WHSC1	3'	GCCAGGCGGCCGCTTGGCC 28446	—	
			GGCCAGGCGGTCGC GGT		
			CCGGTTCGCCGGCG CCG		
			GA		
GAM1958	WNT11	3'	CTGAGCCTGCTGGGCCC 10996	A	GTCGC
			GGGCC GGCG GGTTTCAG		
			CCCGG TCGT CCGAGTC		
			G _____		
GAM1958	WRN	5'	GCCTGGGTTGCAGGCCCTGCTT 6167	CA C _	TT
			GGGC GG GGTC GCGG CAGGT		
			TTCG TC CCGG CGTT GTCCG		
			— _ A GG		
GAM1958	XRCC3	3'	GCCTGGGCCGTGGCACAGCT 11908	CAGGCG	
			GGC GTCGCGGTTTCAGGT		

		TCG CGGTGCCGGGTCCG	
		ACA__	
GAM1958 ZFP103	5'	ATCTGAGTTATTTTTTGGTCT 12218	CG C GGT
		GGGCCAGG GT GC TCAGGT	
		TCTGGTTT TA TG AGTCTA	
		TT T __	
GAM1958 ZNF136	3'	ATTTGAACAGATGTTTTGGCTC 30098	CG GCG
		GGGCCAGG GTC GTTCAGGT	
		CTCGGTTT TAG CAAGTTTA	
		TG A__	
GAM1958 ZNF215	3'	GTTGAAGGAATTTCTGGTTT 14914	CG CGCGG GG
		GGGCCAGG GT TTCA T	
		TTTGGTCC TA AAGT G	
		TT AGG__ TT	
GAM1958 ZNF261	3'	ACTTGGGTTGAGGCTGGGTTC 11562	AGG G TT
		GGGCC CGGTC CGG CAGGT	
		CTTGG GTCGG GTT GTTCA	
		__ A GG	
GAM1958 ZNF278	3'	ACCTGGGCCCTGCCCTTGGCTC 25779	C T C
		GGGCCAGG GG CG GGTTCAAGT	
		CTCGGTTT CC GT CCGGGTCCA	
		__ _ C	
GAM1958 A2BP1	5'	CCAGTGGCCGCCAGGTCC 20806	A _
		GGGCC GGCGGTCGC GG	
		CCTGG CCGCCGGTG CC	
		A A	
GAM1958 ABIN-2	3'	GCCCTTGCGGCCTCCTGGCCC 23603	C TTCA
		GGGCCAGG GGTCGCGG GGT	
		CCCGGTCC CCGGCGTT CCG	
		T C__	
GAM1958 AKAP12	3'	ACTTGTTATGGTTGTTTGGACC 11571	G GT CG TT
		GG CCAGGCG CG G CAGGT	
		CC GGTGTTGT GT T GTTCA	
		A TG AT__	
GAM1958 AKAP12	3'	ACTTGTTATGGTTGTTTGGACC 29311	G GT CG TT
		GG CCAGGCG CG G CAGGT	
		CC GGTGTTGT GT T GTTCA	
		A TG AT__	
GAM1958 AMOTL2	3'	ACTTTGACTTCTGGTCT 18292	C C
		GGGCCAGG GGTCG GGT	

			TCTGGTCT TCAGT TCA		
			— T		
GAM1958	AMSH	3'	ATTTGACCAGATTGTTTGGCT 13180	GC	T
			GGCCAGGCGGTC GGT CAGGT		
			TCGGTTTGTTAG CCA GTTTA		
			A_ _		
GAM1958	AND-1	3'	GTTGAAGCAACTGTTTGTCTT 13955	C	C GG GG
			GGG CAGGCGGT GC TTCA T		
			TTC GTTTGTCA CG AAGT G		
			T A _ TT		
GAM1958	ANKRD5	5'	GCCTGGGCGCCTCCGCCGGGCT 22635	A	TC G
	C		GGGCC GGCGG GCG TTCAGGT		
			CTCGG CCGCC CGC GGGTCCG		
			G TC _		
GAM1958	AP3M2	3'	ATTTGTTTAGCTTGCTTGGCTT 13674	TC	GGTT
			GGGCCAGGCGG GC CAGGT		
			TTCGGTTCGTT CG GTTTA		
			_ ATTT		
GAM1958	AP3M2	3'	TCTCCATCGAGCTGTTTGGTTC 13677	CG	TCAGGT
			GGGCCAGGCGGT CGGT		
			CTTGGTTTGTCTG GCTA		
			A_ CCTCTG		
GAM1958	AP3S2	3'	TCTGGGGAAGACTGTTTGGC 12440	GCGG	GT
			GCCAGGCGGTC TTCAG		
			CGGTTTGTCTAG GGGTC		
			AAG_ TG		
GAM1958	APCL	3'	CTTGGGTCTGGCTGGCTC 12500	G	TCGCG TT
			GGGCCAG CGG G CAGG		
			CTCGGTC GTC T GTTC		
			G _ _ _ GG		
GAM1958	APH2	5'	TGGATTGAGCCGGGCC 26135	AGG	CG
			GGGCC CGGT CGGTTCA		
			CCCGG GCCG GTTAGGT		
			_ A_		
GAM1958	ARHGAP11A	5'	GCCTGAGCAGCCGGCTGGTCC 16637	G	CGCG
			GGGCCAG CGGT GTTCAGGT		
			CCTGGTC GCCG CGAGTCCG		
			G A_ _		
GAM1958	ARHGEF4	5'	GCTTGGGCACAGTGCCCTGGCT 26874	CG T	G_ _
	C		GGGCCAGG G CGC GTTCAGGT		

CTCGGTCC C GTG CGGGTTCG
 — ACA
 GAM1958 ARL8 3' GCCTGAATTTCTGCTTGGTT 44765 TCGC
 GGCCAGGCGG GGTTTCAGGT
 ||||| |||||
 TTGGTTCGTC TTAAGTCCG
 T—
 GAM1958 ATP6V0A1 3' CCTGCAGCCTGCCTGGCTC 11676 TC GGTT
 GGGCCAGGCGG GC CAGG
 ||||| || |||
 CTCGGTCCGTC CG GTCC
 — AC—
 GAM1958 ATP9A 3' ATAAAGCTGTGGCTGCTTGTTC 31077 GC CAGGT
 C GG CAGGCGGTCGCGGT
 || |||||
 CT GTTCGTCGGTGTCGA
 TT AATA
 GAM1958 BANK 3' GCCTGAATTTGGATTGCCTGCT 19627 C GC
 C GGGC AGGCGGTC GGTTTCAGGT
 ||| ||||| |||||
 CTCG TCCGTTAG TTAAGTCCG
 — GT
 GAM1958 BCMP1 3' TCTGGTTATCACCTGGTCC 25459 C C GGTT
 GGGCCAGG GGT GC CAGG
 ||||| || |||
 CCTGGTCC CTA TG GTCT
 A T —
 GAM1958 BIRC1 5' CCTCTTCGACTGCCTGTTC 10885 GC C TTC
 G CAGGCGGTCG GG AGG
 | ||||| || |||
 C GTCCGTCAGC TC TCC
 TT T —
 GAM1958 BM045 3' CTGAACTGACTGGCCC 20531 GCGGTTCG
 GGGCCAG CGGTTCAG
 ||||| |||||
 CCCGGTC GTCAAGTC
 A—
 GAM1958 BNIP2 3' ATTTGAACTCGGTAGTTGTTTG 33162 C TC —
 ACCT GG CAGGCGG GC GGTTTCAGGT
 || ||||| || |||||
 CC GTTTGTT TG TCAAGTTTA
 A GA GC
 GAM1958 BPESC1 3' ACCTCCGGCCCTTTGGTTT 22374 C C—
 GGGCCAGG GGTGC GGT
 ||||| ||||| |||
 TTTGGTTT CCGGC CCA
 C CT
 GAM1958 C11orf11 5' ATCGTGGGCATCGTCTGGCTC 44781 —
 GGGCCAGGCGGT CGCGGT
 ||||| |||||

CTCGGTCTGCTA GTGCTA
CGG

GAM1958 C16orf5 3' TCTGGGCGACCTCTGGCCC 15057 C GGT
GGGCCAGG GGTCGC TCAGG
||||| ||||| ||||
CCCGGTCT CCAGCG GGTCT

GAM1958 C1orf24 3' ATCTGTGGGACTGTCTGGGCC 27529 G G GTT
GG CCAGGCGGTC CG CAGGT
|| ||||| || ||||
CC GGTCTGTCAG GT GTCTA
G G ____

GAM1958 C20orf103 3' GCCTGGGTATCTGAGGCTTGCT 14571 _ G ____
TGGCTT CAGGCG GTC CGG TTCAGGT
||||| ||| ||| |||||
GTTTCGT CGG GTC GGGTCCG
T A TAT

GAM1958 C20orf160 3' ATCTGGGTCCCATTCTGGTCT 27932 C_ TCGC TT
GGGCCAGG GG GG CAGGT
||||| || || |||||
TCTGGTCT CC CT GTCTA
TA ____ GG

GAM1958 C20orf162 5' ATCTGGGAATGATTGTCTAGCC 27912 C CGG
T GGGC AGGCGGTCG TTCAGGT
||| ||||| |||||
TCCG TCTGTTAGT GGGTCTA
A AA_

GAM1958 C20orf162 5' GCCTGGGCGAGCTTGCTGTGGT 27917 _ TC G_
CC GGGCCA GGCGG GC GTTCAGGT
||||| |||| || |||||
CCTGGT TCGTT CG CGGGTCCG
G _ AG

GAM1958 C20orf42 3' ACTTGGCAAGGGACCCCTGGT 19212 C GCG_ T
TC GGGCCAGG GGTC GT CAGGT
||||| |||| || |||||
CTTGGTCC CCAG CG GTTCA
C GGAA _

GAM1958 C20orf54 5' ATCTGAGAAAGCCTCTGGCCC 27227 C CGCGG
GGGCCAGG GGT TTCAGGT
||||| ||| |||||
CCCGGTCT CCG GAGTCTA
_ AAA_

GAM1958 C21orf18 3' ACCATGGTGGTGGTTTGGCTT 18897 G G TCA
GGGCCAGGC GTCGC GT GGT
||||| |||| || |||
TTCGGTTTG TGGTG TA CCA
G G ____

GAM1958 C3IP1 5' CTGGGCGGCGCTTCGGCTC 22274 _ G GGT
GGGCC AGGCG TCGC TCAG
||||| |||| |||| ||||

CTCGG TTCGC GGCG GGTC
C _ _ _
GAM1958 C5orf4 3' ACTGGAGGCTGCCTGGCTC 26178 G_
GGGCCAGGCGGTC CGGT
||||| |||
CTCGGTCCGTCGG GTCA
AG
GAM1958 C5orf4 3' ACTGGAGGCTGCCTGGCTC 18473 G_
GGGCCAGGCGGTC CGGT
||||| |||
CTCGGTCCGTCGG GTCA
AG
GAM1958 C7orf13 3' ATTTGAGTCCTGAGGCTGGCCC 26340 G GG C GT
GGGCCA GC TCG G TCAGGT
||||| || ||| |||
CCCGGT CG AGT C AGTTTA
_ G_ C TG
GAM1958 C7orf13 5' GCCTGGCGTCGTCCGTGACTCC 26342 C T____
TGGCCC AGG GGTCGCGG TCAGGT
||| ||| |||
TCC TCAGTGCC GGTCCG
_ TGCTGC
GAM1958 C8orf13 3' TCTGAGCTATTTTGCTCGGTTT 39656 AG TCGC GT
GGGCC GCGG GGTTTCAG
||||| ||| |||
TTTGG CGTT TCGAGTC
CT TTA_ TG
GAM1958 C8orf4 3' TTTTGGTCTGTGATGCTTGGTC 21326 G TT T
T GGGCCAGGCG TCGCGG CAGG
||||| ||| |||
TCTGGTTCGT AGTGTC GTTT
_ TG TC
GAM1958 C9orf12 5' ACCTAAGATGGCCGCCGCCCC 22991 A CGGTTC
GGGCC GCGGTCG AGGT
||||| ||| |||
CCCGG CCGCCGGT TCCA
_ AGAA_
GAM1958 C9orf7 3' CTGGGCTGTGTGTGGCGCC 19033 _ G GGTC
GG GCCA GC GCGGTTTCAG
|| ||| || |||
CC CGGT TG TGTCGGGTC
G G _
GAM1958 C9orf9 3' ATTTGGATTTTACTGGTTGGTC 21024 G CGC
C GGGCCAG CGGT GGTTTCAGGT
||||| ||| |||
CCTGGTT GTCA TTAGGTTTA
G TT_
GAM1958 CACNG4 3' CCTGAGGCTGCCTGGCCT 15744 GCGGT T
GGGCCAGGCGGTC TCAGG
||||| ||| |||

TCCGGTCCGTCGG AGTCC
 _____ T
 GAM1958 CALN1 3' TGGGCTGGCCTGGCC 25521 GGTCG
 GGCCAGGC CGGTTCA
 ||||| |||||
 CCGGTCCG GTCGGGT

 GAM1958 CAMKK2 3' GCCTGGATCGCTCGACCTGGC 13312 _ TC
 GCCAGG CGG GCGGTTTCAGGT
 ||||| ||| |||||
 CCGTCC GCT CGCTAGGTCCG
 A _
 GAM1958 CBX1 5' CTGGAACAATGTTGCTTGGCT 13680 T CG A T
 GGCCAGGCGG CG GTTC GG
 ||||| || ||| ||
 TCGGTTTCGTT GT CAAG TC
 _ AA G T
 GAM1958 CBX6 3' CCTGGACTGCCTCTCGCCT 15575 _ TC
 AGGCG G GCGGTTTCAGG
 ||||| |||||
 TCCGC C CGTCAGGTCC
 T TC
 GAM1958 CD109 3' ACATGTGATTGTTTTGTTT 28569 C _
 GGGC AGGCGGTCGCG GT
 ||| ||||| ||
 TTTG TTTGTTAGTGT CA
 T A
 GAM1958 CDH24 3' GCCTGGGTTTCCTGCCCTGGCC 45506 _ TCGC TT
 C GGGCCAGG CGG GG CAGGT
 ||||| ||| || |||||
 CCCGGTCC GTC TT GTCCG
 C CT_ GG
 GAM1958 CDKL2 5' CCTGGGCGGTATCTGTCT 10071 TC
 AGGCGG GCGGTTTCAGG
 ||||| |||||
 TCTGTC TGCCGGGTCC
 TA
 GAM1958 CENTA1 3' GCCTGGGCGCGGTGAGGCC 13740 AG GGT
 GGCC GC CGCGGTTTCAGGT
 ||| || |||||
 CCGG TG GCGCCGGGTCCG
 AG _
 GAM1958 CENTG1 3' GCTTGGACATGCCCGCTTGTGC 16567 _ TC _
 CC GGGC CAGGCGG GCG GTTCAGGT
 ||| ||||| || |||||
 CCCG GTTCGCC CGT CAGGTTCG
 T _ A
 GAM1958 CG012 5' ATTTGAGTAGCACTGTTTGGT 40485 C GG
 GCCAGGCGGT GC TTCAGGT
 ||||| || |||||

		TGGTTTGTCA CG GAGTTTA	
		_ AT	
GAM1958 CLIC4	3'	GTTGAGTACCCGCTTGGTTT 15132	TC GGT GG
		GGGCCAGGCGG GC TCA T	
		TTTGGTTCGCC TG AGT G	
		CA ____ TT	
GAM1958 CNNM4	3'	TCTGGGTTCTTCCTTTTGGTTC 21427	C TCGC TT GT
		GGGCCAGG GG GG CAG	
		CTTGGTTT CC TT GTC	
		T TTC_ GG TG	
GAM1958 COP9	3'	GCTTATATTTATCGCTTGGCTC 13535	CGC TC
		GGGCCAGGCGGT GGT AGGT	
		CTCGGTTTCGCTA TTA TTCG	
		T__ TA	
GAM1958 CPR2 CT	3'	ACCTGGGTTGTTACCTGCCTGT 25172	C _ C TT
		GGGC AGGC GGT GCGG CAGGT	
		TCTG TCCG CCA TGTT GTCCA	
		_ T T GG	
GAM1958 CRELD1 C	5'	TCTGGATCCTTCCCTGCCGGCT 17775	A TCGC_ GT
		GGGCC GGCGG GGTTCAG	
		CTCGG CCGTC CTAGGTC	
		_ CCTTC TG	
GAM1958 CSMD1 C	5'	GCCCTCGGGTGATTATTTGGCT 36193	CG GGTTC A
		GGGCCAGG GTCGC GGT	
		CTCGGTTT TAGTG CCG	
		AT GGCTC_	
GAM1958 CSMD1 C	5'	GCCCTCGGGTGATTATTTGGCT 27070	CG GGTTC A
		GGGCCAGG GTCGC GGT	
		CTCGGTTT TAGTG CCG	
		AT GGCTC_	
GAM1958 CYYR1 TC	3'	ATCTGGAGTATTAATGTTTGGT 27512	GTCGCGG
		GGGCCAGGCG TTCAGGT	
		CTTGGTTTGT AGGTCTA	
		AATTATG	
GAM1958 DDM36	3'	TCTGGGAAGTGCCTGGTTT 21955	GGTC GG
		GGGCCAGGC GC TTCAGG	
		TTTGGTCCG TG GGGTCT	
		____ AA	
GAM1958 DDX12 T	3'	GCCTGGATTTGTATCCTTGGCT 30024	C C _
		GGGCCAGG GGT GCGG TTCAGGT	

TTCGGTTC CTA TGTT AGGTCCG
 _ _ T
 GAM1958 DDX34 3' GCCTGAACCCCCAGCCTGGGCT 16164 G _ TCGC
 GG CCAGGC GG GGTTCAGGT
 || ||||| || |||||
 TC GGTCCG CC CCAAGTCCG
 G A C__
 GAM1958 DGKD 3' CCCCTCTCGTGGTCGTTCTGGC 29879 _ GT TTC T
 CC GGCCAGG CG CGCGG AGG
 ||||| || ||||| ||
 CCGGTCT GC GTGCT TCC
 T TG C__ CCT
 GAM1958 DGKD 3' GCCACGGCAGTCGCTTGTTTT 29884 TC G TCA
 GGGCCAGGCGG GC GT GGT
 ||||| || || |||||
 TTTGGTTCGCT CG CA CCG
 GA G __
 GAM1958 DIO2 3' ACTTGATCTTCCCTTGGTCC 15162 C TCGC
 GGGCCAGG GG GGTTCAGGT
 ||||| || |||||
 CCTGGTTC CC CTAGGTTCA
 _ TT__
 GAM1958 DIO2 3' ACTTGATCTTCCCTTGGTCC 6452 C TCGC
 GGGCCAGG GG GGTTCAGGT
 ||||| || |||||
 CCTGGTTC CC CTAGGTTCA
 _ TT__
 GAM1958 DIS3 3' CTTGAGTAGTCTTTGGTCC 17300 C TC GGT
 GGGCCAGG GG GC TCAGG
 ||||| || || |||||
 CCTGGTTT CT TG AGTTC
 _ GA __
 GAM1958 DKFZP434B044 3' ACCTGTTTTCTGCCGTGACCTT 25551 C T____
 TGGTCC AGG GGTCGCGGT CAGGT
 || ||||| |||||
 TTT CCAGTGCCG GTCCA
 _ TCTTT
 GAM1958 DKFZp434C0328 3' CTTGAACTAAGATTGGCTT 19012 GGCG GC
 GGGCCA GTC GGTTCAGG
 ||||| || |||||
 TTCGGT TAG TCAAGTTC
 _ AA
 GAM1958 DKFZP434C0826 5' GCTTTGGCTGTTTTGTCT 40846 C C
 GGGC AGGCGGTCTG GGT
 ||||| ||||| |||||
 TCTG TTTGTCGGT TCG
 T T
 GAM1958 DKFZP434C1715 3' GCCTTGCTGTCTGGCTT 41674 T C
 GGGCCAGGCGG CG GGT
 ||||| || |||||

	TTCGGTCTGTC GT CCG		
	_ T		
GAM1958 DKFZP434E2135 3'	TCTGGATTGCGGAGGGTGGTTC 25119	GGCGG	GT
	GGGCCA TCGCGGTTCA		
	CTTGGT GCGGTTAGGTC		
	GGGA_ TG		
GAM1958 DKFZp434F1719 3'	ACTTTGACCGTGGGCTGTCTGG 25986	_ C	
CCC	GGGCCAGGCGGTC GCGGTT AGGT		
	CCCGGTCTGTCGG TGCCAG TTCA		
	G T		
GAM1958 DKFZP434H204 5'	ACCTGGGCTGTGGGGAAGTGGT 33015	GCGG	
CT	GGGCCAG TCGCGGTTCAAGT		
	TCTGGTC GGTGTCGGGTCCA		
	AAGG		
GAM1958 DKFZP434I216 3'	ATCTTACTGGTTGTTAGGCCT 38099	AG GT GC TC	
	GGGCC GCG C GGT AGGT		
	TCCGG TGT G TCA TCTA		
	AT TG _ T_		
GAM1958 DKFZP434I216 3'	GCCTGAATAGGCTCCTGGCCC 38101	C GCG	
	GGGCCAGG GGTC GTTCAGGT		
	CCCGGTCC TCGG TAAGTCCG		
	_ A_		
GAM1958 DKFZP434I216 5'	GCCTGAATTGCAGTTCCTGTGC 38102	_ C TC	
CC	GGGC CAGG GG GCGGTTCAAGT		
	CCCG GTCC TT CGTTAAGTCCG		
	T _ GA		
GAM1958 DKFZP434J154 3'	ACTTGAAAGGTTGCCTGGACTC 17880	_ GT GCGG	
	GGG CCAGGCG C TTCAGGT		
	CTC GGTCCGT G AAGTTCA		
	A TG A_		
GAM1958 DKFZP434K2235 3'	ATCTGGGACCTGCAGTTTGGCT 40595	G T C _	
T	GGGCCAGGC G CG GGTTC AGGT		
	TTCGGTTTG C GT CCAGG TCTA		
	A _ _ G		
GAM1958 DKFZp434O0320 3'	GCTTGGAGAGCCATCTGGTCC 40706	GC CGCGG	
	GGGCCAG GGT TTCAGGT		
	CCTGGTC CCG AGGTTCG		
	TA AG_		
GAM1958 DKFZP434P0111 3'	GCCTGGGCCCCCAGCTTGGCC 33457	_ TCGC	
	GGCCAGGC GG GGTTCAGGT		

	CCGGTTCG CC CCGGGTCCG		
	A C__		
GAM1958 DKFZP434P0111 3'	ACCTGGGTCCAGTGTAGCCTGG 33450	GGT	_ _
CTC	GGCCAGGC CGC GG TTCAGGT		
	TCGGTCCG GTG CC GGGTCCA		
	AT_ A T		
GAM1958 DKFZP564I1171 5'	GCCTGAGCTGTCGCACCTGGC 35446	CG	C
	GCCAGG GT GCGGTTTCAGGT		
	CGGTCC CG TGTCGAGTCCG		
	A_ C		
GAM1958 DKFZP564O0463 3'	TCTGAATTGTGATTCCCAGTTC 15445	CA	CG GT
	GGGC GG GTCGCGGTTTCAG		
	CTTG CC TAGTGTTAAGTC		
	A_ CT TG		
GAM1958 DKFZP566M1046 5'	GCCTGGTATAACCTCTGGCTC 25812	C	CGCGGT
	GGGCCAGG GGT TCAGGT		
	CTCGGTCT CCA GGTCCG		
	_ ATAT__		
GAM1958 DKFZP586F1524 3'	GCCTGGAGGAGTTTCCTGGCCT 17853	CGGTC	GG_
	GGGCCAGG GC TTCAGGT		
	TCCGGTCC TG AGGTCCG		
	TT__ AGG		
GAM1958 DKFZP727C091 3'	GCCTGTGGAACATTGTCTGGTC 32906	CGCGGTT	
C	GGGCCAGGCGGT CAGGT		
	CCTGGTCTGTTA GTCCG		
	CAAGGT_		
GAM1958 DKFZp761G2113 3'	GCCTGGGCTTCTCTATTCTTGG 34644	C__	TCGC
CCC	GGCCAGG GG GGTTCAGGT		
	CCGGTTC TC TCGGGTCCG		
	TTA TCT_		
GAM1958 DKFZp761J139 5'	GCCTGTGGGTGGGCCGCTTGGC 26037	G G	_
TC	GGGCCAGGCGGTC CG TT CAGGT		
	CTCGGTTCCGCCG GT GG GTCCG		
	_ G T		
GAM1958 DKFZp761K1423 5'	ATCTGAGCTCTAGTGTCTGACT 20469	C	GTCGC
T	GGG CAGGCG GGTTCAGGT		
	TTC GTCTGT TCGAGTCTA		
	A GATC_		
GAM1958 DKFZp762K222 5'	GTTTGGGTCTTTTGCCGTGG 35236	_	GTCGC TT GG
CTC	GGGCCA GGCG GG CA T		

CTCGGT CCGT CT GT G
 G GTTTT GG TT
 GAM1958 DKFZp762P2111 3' CCTGTGGGTCTTTTGGTTT 41755 C GT G GTT
 GGGCCAGG G C CG CAGG
 ||||| | | || |||
 TTTGGTTT C G GT GTCC
 T TG _ _
 GAM1958 DMWD 5' GCCTGAGTCGGAGAGCCTGTTC 30532 GC GG G GT
 C GG CAGGC TC CG TCAGGT
 || |||| || || |||||
 CC GTCCG AG GC AGTCCG
 TT AG _ TG
 GAM1958 DRIL2 3' GTTGGACGTGTCCGTCTGTCC 13189 C T G GG
 GGGC AGGCGG CGCG TTCA T
 ||| |||| ||| ||| |
 CCTG TCTGCC GTGC AGGT G
 _ T _ TT
 GAM1958 EAT2 3' GCCTGGGCTACTCTCCTCCTGG 38708 C TCGC_
 TTC GGGCCAGG GG GGTTCAGGT
 ||||| || |||||
 CTTGGTCC CC TCGGGTCCG
 T TCTCA
 GAM1958 EMILIN-2 3' GTTTGGGCTGTTCCACGCTTGG 25767 GTC_ GG
 CTC GGGCCAGGCG GCGGTTCA T
 ||||| ||||| |
 CTCGGTTCGC TGTCGGGT G
 ACCT TT
 GAM1958 ENDOGLYX1 3' GCCTGAACCTTGGCTTGGC 24103 GGT C
 GCCAGGC CG GGTTCAGGT
 ||||| || |||||
 CGGTTCG GT CCAAGTCCG
 _ T
 GAM1958 ERF 3' ATTTGAATTGAGGCTTTGGCCT 13234 GC G
 GGGCCAG GGTC CGGTTCAGGT
 ||||| ||| |||||
 TCCGGTT TCGG GTTAAGTTTA
 _ A
 GAM1958 FEM-2 3' ACCAAGTATTGCTTGGCTT 16006 C _
 GGGCCAGGCGGT GC GGT
 ||||| || |||
 TTCGGTTCGTTA TG CCA
 _ AA
 GAM1958 FIGNL1 5' ATTTGAAAGCAGGCAGCCTGGC 22661 G _ GG
 TC GGGCCAGGC GTC GC TTCAGGT
 ||||| ||| || |||||
 CTCGGTCCG CGG CG AAGTTTA
 A A A_
 GAM1958 FKSG14 5' ATCTGGGTGCCATCATTTTCTG 33670 C_ C G TT
 GTTC GCCAGG GGT GC G CAGGT
 ||||| ||| || |||||

		TGGTCT CTA CG T GTCTA		
		TTTA C _ GG		
GAM1958	FLJ00024	5' CTGAGCTGCCTGCAGGTTTC 31891	AG	TC
		GGGCC GCGG GCGGTTTCAG		
		CTTGG CGTC CGTCGAGTC		
		A_ _		
GAM1958	FLJ00024	3' GCCCCTGTGGCTGGCTGGCCC 31894	G	TTCA
		GGGCCAG CGGTCGCGG GGT		
		CCCGGTC GTCGGTGTC CCG		
		G C_		
GAM1958	FLJ00058	5' CTCAGCTGCGACCTCTGGCCT 38509	C	C
		GGGCCAGG GGTCGCGGTT AG		
		TCCGGTCT CCAGCGTCGA TC		
		_ C		
GAM1958	FLJ10101	3' ACCTGAACCTCCTTGCCTGGGC 24044	G	TCGC
	T	GG CCAGGCGG GGTTCAGGT		
		TC GGTCCGTT CCAAGTCCA		
		G CCT_		
GAM1958	FLJ10101	3' GCCTGGGCTGCCCGCCTGGGT 24047	G	TC
	C	GG CCAGGCGG GCGGTTTCAGGT		
		CT GGTCCGCC CGTCGGGTCCG		
		G C_		
GAM1958	FLJ10297	3' GCCTGGATCTGTTTTGTTTTGG 19805	_ TC _	
	TTT	GGCCAGG CGG GCGG TTCAGGT		
		TTGGTTT GTT TGTC AGGTCCG		
		T T_ T		
GAM1958	FLJ10342	5' CCGCGACCCGCTTGGCTC 19834	_	
		GGGCCAGGCGG TCGCGG		
		CTCGGTTCCGCC AGCGCC		
		C		
GAM1958	FLJ10388	3' ATTTGATTTGGTCAGCCTGGCT 19842	_ GT CGGT	
	T	GGGCCAGGC G CG TCAGGT		
		TTCGGTCCG C GT AGTTTA		
		A TG TT_		
GAM1958	FLJ10420	3' TCTGGCCAGTTGTCTGGTTT 19858	GTC _ T T	
		GGGCCAGGCG GC GGT CAGG		
		TTTGGTCTGT TG CCG GTCT		
		_ A _ C		
GAM1958	FLJ10713	3' ATTTGAAATGTCCTTGGCTT 20040	C T CGG	
		GGGCCAGG GG CG TTCAGGT		

TTCGGTTC CT GT AGGTTTA
 _ _ AA_
 GAM1958 FLJ10751 3' GCTTGAAGAACCTTGACTGCTT 20095 C ____
 GGTCC CCAGGCGGTCTG GGT TCAGGT
 ||||| ||| |||||
 GGTTCGTCAGT CCA AGTTCG
 T AGA
 GAM1958 FLJ10751 3' GCTTGAAGAACCTTGACTGCTT 20194 C ____
 GGTCC CCAGGCGGTCTG GGT TCAGGT
 ||||| ||| |||||
 GGTTCGTCAGT CCA AGTTCG
 T AGA
 GAM1958 FLJ10769 3' ATCTGGCTGCTGGTGTGGCT 20112 GTC T
 T GGGCCAGGCG GCGGT CAGGT
 ||||| ||| |||||
 TTCGGTTTGT CGTCG GTCTA
 GGT _
 GAM1958 FLJ10803 3' CCTGGATGGCGTTGGGTCT 20152 AGG T G
 GGGCC CGG CGC GTTCAGG
 |||| ||| ||| |||||
 TCTGG GTT GCG TAGGTCC
 _ _ G
 GAM1958 FLJ10811 3' ATTTGAGTGGGTTGGTTGGCCC 20165 G GT G G T
 GGGCCAG CG C CG T CAGGT
 ||||| || ||| |||||
 CCCGGTT GT G GT A GTTTA
 G TG _ G _
 GAM1958 FLJ10829 3' GCCTGGAGTCTGTGCCTGGTCC 20180 GGTC ____
 GGGCCAGGC GCGG TTCAGGT
 ||||| ||| |||||
 CCTGGTCCG TGTC AGGTCCG
 _ TG
 GAM1958 FLJ10849 3' GCCTGAGCTTGTGGGTCTGTTC 20205 GC GG _
 G CAGGC TCGCG GTTCAGGT
 | |||| |||| |||||
 C GTCTG GGTGT CGAGTCCG
 TT _ T
 GAM1958 FLJ10895 3' ATCTGGGCCTAATGTTGGCTT 21158 G GTCGC
 GGGCCAG CG GTTCAGGT
 ||||| || |||||
 TTCGGTT GT CCGGTCTA
 _ AAT_
 GAM1958 FLJ10925 3' GCCTGGCAGAGCTGCCTGTCTT 20260 C CGCG T
 GGG CAGGCGGT GT CAGGT
 || ||||| || |||||
 TTC GTCCGTCG CG GTCCG
 T AGA _ _
 GAM1958 FLJ11362 5' CCTGGAGACCATCTGGCTC 22470 GC GCGG
 GGGCCAG GGTC TTCAGG
 ||||| ||| |||||

		CTCGGTC CCAG AGGTCC	
		TA ____	
GAM1958	FLJ11362	3' GCTTGGGTTGCTTCCCTGTCCC 22472	C C TC TT
		GGG CAGG GG GCGG CAGGT	
		CCC GTCC CT CGTT GTTCG	
		T _ T_ GG	
GAM1958	FLJ11457	3' ATTTGAACCTTAGGTGTTGGTTT 24095	G GTCGC
		GGGCCA GCG GGTTCAGGT	
		TTTGGT TGT TCAAGTTTA	
		_ GGAT_	
GAM1958	FLJ11726	3' GCCTGGGACTTTGTAGGTTT 24527	AG TCGC _
		GGGCC GCGG GTTC AGGT	
		TTTGG TGTT TCAGG TCCG	
		AT ____ G	
GAM1958	FLJ12057	3' CTTGAGTCTCTGCTGGCTC 24127	G TCGC GT
		GGGCCAG CGG G TCAGG	
		CTCGGTC GTC C AGTTC	
		_ T__ TG	
GAM1958	FLJ12484	3' ACTGTGGCTGTTGGGTTT 23016	AG
		GGGCC GCGGTCGCGGT	
		TTTGG TGTCGGTGTCA	
		GT	
GAM1958	FLJ12484	3' GCTTTGATCCCTTGGTCT 23020	C C
		GGGCCAGG GGTCG GGT	
		TCTGGTTC CTAGT TCG	
		C T	
GAM1958	FLJ12484	3' ACTGTGGCTGTTGGGTTT 34514	AG
		GGGCC GCGGTCGCGGT	
		TTTGG TGTCGGTGTCA	
		GT	
GAM1958	FLJ12484	3' GCTTTGATCCCTTGGTCT 34518	C C
		GGGCCAGG GGTCG GGT	
		TCTGGTTC CTAGT TCG	
		C T	
GAM1958	FLJ12526	3' CCTCATGGATGTCTGGTCC 24167	G G GTTC
		GGGCCAGGCG TC CG AGG	
		CCTGGTCTGT AG GT TCC	
		_ _ AC_	
GAM1958	FLJ12700	3' ATTTGAACCAGAGACCGCTTGG 24413	GC_
	CCT	GGGCCAGGCGGTC GGTTCAGGT	

TCCGGTTCGCCAG CCAAGTTTA
 AGA
 GAM1958 FLJ12783 3' TTCAGGTTGTGGCTCTTGGTTC 25422 C GG CAGGT
 GGGCCAGG GGTCGC TT
 ||||| ||| ||
 CTTGGTTC TCGGTG GG
 _ TT ACTTT
 GAM1958 FLJ12960 3' ACTTGACAGAGCCCTGCCTGG 23912 TC G_
 CCT GGCCAGGCGG GC GTTCAGGT
 ||||| || |||||
 CCGGTCCGTC CG CAGGTTCA
 C_ AGA
 GAM1958 FLJ12960 3' CTGGCGTCTGCTTGGTTT 23916 T GGTT
 GGGCCAGGCGG CGC CAG
 ||||| ||| |||
 TTTGGTTCGTC GCG GTC
 T ____
 GAM1958 FLJ13052 3' GCTTCCCGCAGCCGCTGGCCC 23286 C TTC
 GGGCCAGGCGGT GCGG AGGT
 ||||| ||| |||
 CCCGGTCCGCCG CGCC TTCG
 A C_
 GAM1958 FLJ13055 3' CTGAGCCGACGCCCTTGCCC 22944 C C T _
 GGGC AGG GG CG CGGTTCA
 ||| || || |||||
 CCCG TTC CC GC GCCGAGTC
 _ _ _ A
 GAM1958 FLJ13114 3' GCCTGGGGCTGTGCTTGGCTT 23750 GGTC _
 GGGCCAGGC GCGGTTT AGGT
 ||||| ||||| |||
 TTCGGTTCG TGTCGGG TCCG
 _ G
 GAM1958 FLJ13154 3' ACTGTGACCTCTGGCTT 23836 C
 GGGCCAGG GGTCGCGGT
 ||||| |||||
 TTCGGTCT CCAGTGTCA
 _
 GAM1958 FLJ13189 3' ATTTGGACAATTATGTCCTGGT 24327 _ GTCGCG
 CT GGGCCAGG CG GTTCAGGT
 ||||| || |||||
 TCTGGTCC GT CAGGTTTA
 T ATTA_
 GAM1958 FLJ13213 3' GCCTTAGCTCTGTGGTGTCTGG 24099 GT_ C C
 CTC GGGCCAGGCG CG GGTT AGGT
 ||||| || ||| |||
 CTCGGTCTGT GT TCGA TCCG
 GGT C T
 GAM1958 FLJ13224 3' CCTTTCGGCCGCCGGGCTC 24177 A CGGTTC
 GGGCC GGCGGTCTG AGG
 |||| ||||| |||

CTCGG CCGCCGGC TCC
G TT____
GAM1958 FLJ13241 3' GCCTGGGCTCAAGCCTGGCCC 24708 GGTCGC
GGGCCAGGC GGTTTCAGGT
||||||| |||||||
CCCGGTCCG TCGGGTCCG
AAC____
GAM1958 FLJ13262 3' CCTGGATTGATCTGGTC 24432 GCGGTTCG
GGCCAG CGGTTTCAGG
||||| |||||||
CTGGTC GTTAGGTCC
TA____
GAM1958 FLJ13615 5' GCCTCCGCTGGTTGCCAGGCTT 24763 A GT_ TTC
GGGCC GGCG C GCGG AGGT
||||| ||| ||| |||
TTCGG CCGT G CGCC TCCG
A TG T ____
GAM1958 FLJ13659 5' GCCTGAGCTCCAGGTCTCGTCT 24832 C ____ TCGC
GGGC AGGC GG GGTTTCAGGT
||| ||| || |||||||
TCTG TCTG CC TCGAGTCCG
C GA ____
GAM1958 FLJ13693 3' ACCTGGGCTCCAAGTCTGAGTT 24185 _ GGTCGC
C GGGC CAGGC GGTTTCAGGT
||||| |||||||
CTTG GTCTG TCGGGTCCA
A AACC____
GAM1958 FLJ13910 3' GCTTGAGAGTGTGTGTGGTCC 23057 G TC G
GGGCCA GCGG GCG TTCAGGT
||||| ||| |||||||
CCTGGT TGTT CGT AGGTTTCG
G _ G
GAM1958 FLJ14106 3' CTGGATCTCTGTTGGGTTT 24665 AG TCGC
GGGCC GCGG GGTTTCAG
||||| ||| |||||||
TTTGG TGTC CTAGGTC
GT T____
GAM1958 FLJ14146 3' CTTCTTCTGTGCTGCCTGGTTT 24033 T TTC T
GGGCCAGGCGG CGCGG AGG
||||||||| ||| |||
TTTGGTCCGTC GTGTC TTC
_ TTC T
GAM1958 FLJ14327 3' ACCACTGTTTGGTCC 24420 CGC
GGGCCAGGCGGT GGT
||||||||| |||
CCTGGTTTGTCA CCA

GAM1958 FLJ14451 3' ATTTGGGTCTAGTTGCTTGG 26539 TCGC TT
CCAGGCGG GG CAGGT
||||||| || |||||

GGTTCGTT CT GTTTA
GATC GG
GAM1958 FLJ14564 3' GTTTGAATTGCCAAAGTTGCC 37598 CA GGTC_ GG
C GGGC GGC GCGGTTCA T
||||| ||| ||||||| |
CCCG TTG CGTTAAGT G
_ AAACC TT
GAM1958 FLJ14810 3' ACCTGGACCCAGGCCAGGCC 26630 AGGC GC
GGGCC GGTC GGTTCAAGT
||||| ||| |||||||
CCCGG CCGG CCAGGTCCA
A_ AC
GAM1958 FLJ20034 5' ATCTGGCATTCTGGCTC 19129 CG_ C
GGGCCAGG GTCG GGT
||||| ||| |||
CTCGGTCT CCGT CTA
TTA _
GAM1958 FLJ20040 3' TCCAGCACGTCGTGGCCTCTGG 21068 C TTCA_ T
TCC GGCCAGG GGTGCGCG GG
||||| ||||||| ||
CTGGTCT CCGGTGCT CC
_ GCACGA TG
GAM1958 FLJ20294 3' GCCTGAGCCAGGGCTTGGCTTG 19349 _ GC
GCCT GGCCAGGC GGTC GGTTCAAGT
||||| ||| |||||||
CCGGTTTCG TCGG CCGAGTCCG
GT GA
GAM1958 FLJ20298 3' TTATGACTGTTTTGGTTC 19364 _ CG
GGGCCAGG CGGTCT G
||||| ||||||| |
CTTGTTTT GTCAGT T
T AT
GAM1958 FLJ20320 3' ACCTGGGTCTGGGACCTGGCTC 19381 GGC G _
GGGCCA GGTC CGG TTCAGGT
||||| ||| ||| |||||||
CTCGGT CCAG GTC GGGTCCA
_ G T
GAM1958 FLJ20375 3' ACTTGATTCTTTATTTGGC 19432 CG TCGC
TT GGGCCAGG G GGTTCAAGT
||||| | |||||||
TTCGGTTT T TTAGGTTCA
AT TCTT
GAM1958 FLJ20401 5' GCTGGGCCGCCTGGCCC 19447 G
GGGCCAGGCGGTC CCGT
||||||||| |||
CCCGGTCCGCCGG GTCG
_ -
GAM1958 FLJ20413 3' GTCTGAGCAGAGACATTGATT 19452 _ _ GCG GT
GGTTT CCAGG CG GTC GTTCAG
||||| || ||| |||||||

GGTTT GT CAG CGAGTC
A TA AGA TG
GAM1958 FLJ20421 5' CCCGCGCGGCGCCTGGCCC 19461 G GTTCA
GGGCCAGGCG TCGCG GG
||||||| |||| ||
CCCGGTCCGC GGCGC CC
_ GC_

GAM1958 FLJ20435 3' CTTGGGCTGACCTGACCC 19470 C CGGTCG
GGG CAGG CGGTTCAGG
||| ||| |||||
CCC GTCC GTCGGGTTC
A A_

GAM1958 FLJ20508 5' GCTTTGGCTGTCTGGA CT 19519 _ C
GGG CCAGGCGGTTCG GGT
||| ||||| |||
TTC GGTCTGTCCGT TCG
A T

GAM1958 FLJ20539 5' ACCTGAGCCGCCCGCCTCGTCC 19542 C TC
GGGC AGGCGG GCGGTTCAGGT
||||| |||||
CCTG TCCGCC CGCCGAGTCCA
C _

GAM1958 FLJ20584 3' ATCTGAGGGGTGGCCTGGCCT 19557 GGT GG
GGGCCAGGC CGC TTCAGGT
||||||| ||| |||||
TCCGGTCCG GTG GAGTCTA
_ GG

GAM1958 FLJ20668 3' ACTTGAATTGCGATGTGT 19588 _
GCG GTCGCGGTTCAGGT
||| |||||
TGT TAGCGTTAAGTTCA
G

GAM1958 FLJ20671 3' ACCTGGATTCCATTGGCTGGTT 19591 G CGC
T GGGCCAG CGGT GGTTCAGGT
||||| ||| |||||
TTTGGTC GTTA TTAGGTCCA
G CC_

GAM1958 FLJ20695 3' GCCTGGTGAAGTGACCCTTGGC 19614 C GGT_
CT GGGCCAGG GGTCGC TCAGGT
||||| ||||| |||||
TCCGGTTC CCAGTG GGTCCG
_ AAGT

GAM1958 FLJ20783 3' GTTTGAACTGTGCTATTTTGTT 19671 C CG T GG
C GGGC AGG G CGCGGTTC A T
||| ||| | ||||| |
CTTG TTT C GTGTCAAGT G
T AT_ TT

GAM1958 FLJ21032 3' CTGTTAGGTCCGCTTGGTCC 24399 _ _
GGGCCAGGCGG TC GCGG
||||||| || |||

CCTGGTTCGCC GG TGTC
 T AT
 GAM1958 FLJ21324 5' CCTGAGCCTGTATGGCCC 43827 G GTCGC
 GGGCCA GCG GGTTTCAGG
 ||||| ||| |||||
 CCCGGT TGT CCGAGTCC
 A _____
 GAM1958 FLJ21324 5' GCTTTGATTCTTGGTTC 43829 C C
 GGGCCAGG GGTCG GGT
 ||||| ||||| |||
 CTTGGTTC TTAGT TCG
 _ T
 GAM1958 FLJ21438 3' ACCTGAGCTGCCCATCCTGCCT 30843 C C_ TC
 GGGC AGG GG GCGGTTTCAGGT
 ||| ||| || |||||
 TCCG TCC CC CGTCGAGTCCA
 _ TA _
 GAM1958 FLJ21841 3' GCCCTCCTGGGCCGTCTGGCCT 23863 G TTCA
 GGGCCAGGCGGTC CGG GGT
 ||||| ||| |||
 TCCGGTCTGCCGG GTC CCG
 _ CTC_
 GAM1958 FLJ22167 3' GCCCCGAAGTGTGGTCGCCAGG 23741 A GT A_
 CCC GGGCC GGCG CGCGGTTC GGT
 ||||| ||| ||||| |||
 CCCGG CCGC GTGTCAAG CCG
 A TG CC
 GAM1958 FLJ22283 5' ACCTCCCCCGCCGCCTGGCCT 25945 TC TTC
 GGGCCAGGCGG GCGG AGGT
 ||||| ||| |||
 TCCGGTCCGCC CGCC TCCA
 _ CCC
 GAM1958 FLJ22405 5' CTGGAGCTGTTTGGCC 22865 CGCGG
 GGCCAGGCGGT TTCAG
 ||||| |||
 CCGGTTTGTCTG AGGTC

 GAM1958 FLJ22593 5' CTGAACTCACCTGGCCT 24018 C GTCGC
 GGGCCAGG G GGTTTCAG
 ||||| | |||||
 TCCGGTCC C TCAAGTC
 A _____
 GAM1958 FLJ22593 5' GCCTGGGAAGCACCGTCTGCCC 24019 C C GG
 GGGC AGGCGGT GC TTCAGGT
 ||| ||||| || |||||
 CCCG TCTGCCA CG GGGTCCG
 _ _ AA
 GAM1958 FLJ22635 3' GTCTGAGCCTGCATCACCTCTG 24719 C C_ _ GT
 GCCT GCCAGG GGT GC GGTTTCAG
 ||||| ||| || |||||

CCGTCT CCA CG CCGAGTC
 _ CTA T TG
 GAM1958 FLJ22969 3' GCCTGGGTTGTGACTTCTACTG 34065 GC__ TT
 CAG GGTTCGCG CAGGT
 ||| ||||| ||||
 GTC TCAGTGTT GTCCG
 ATCT GG
 GAM1958 FLJ23027 3' TCTGGGCAAAATGTTTGGTTT 25954 GTCGCG GT
 GGGCCAGGCG GTTCAG
 ||||| ||||
 TTTGGTTTGT CGGGTC
 AAAA__ TG
 GAM1958 FLJ23058 3' ACCTGAGCCCAAATCCTGGCCC 24004 CGGTTCG
 GGGCCAGG GTTCAGGT
 ||||| |||||
 CCCGGTCC CCGAGTCCA
 TAAAC__
 GAM1958 FLJ23129 3' TTACGACGTTGCCTGGTCT 24121 __ CG
 GGGCCAGGCG GTCG G
 ||||| ||| |
 TCTGGTCCGT CAGC T
 TG AT
 GAM1958 FLJ23309 3' ACCTCTCATGGCTTTTTGGTTC 24377 C C TTC
 GGGCCAGG GGTTCG GG AGGT
 ||||| |||| || ||||
 CTTGGTTT TCGGT CT TCCA
 T A C__
 GAM1958 FLJ25416 5' GCCTGGGCCCGTTCCTGGTCT 29626 CGGT C
 GGGCCAGG CG GTTCAGGT
 ||||| || |||||
 TCTGGTCC GC CCGGGTCCG
 TT__ _
 GAM1958 FLJ31101 3' ATTTGGATTTTGGTATCTTTGG 19683 C __ CG
 TTT GGCCAGG GGT CG GTTCAGGT
 ||||| ||| || |||||
 TTGGTTT CTA GT TAGGTTTA
 _ TG TT
 GAM1958 FLJ32334 3' ACCTGGACTTCCAGTCTGGCTC 29364 _ TCGC
 GGGCCAGGC GG GTTCAGGT
 ||||| || |||||
 CTCGGTCTG CC TCAGGTCCA
 A T__
 GAM1958 FREQ 3' AGGTGTGGCTTCTGGCCT 15561 C G
 GGGCCAGG GGTTCGCG TT
 ||||| ||||| ||
 TCCGGTCT TCGGTGT GA
 _ G
 GAM1958 FUBP3 3' TTCTTGATCTTGGCTGTCTGG 31877 C T T
 TTT GGGCCAGGCGGTTCG GGT CAGG
 ||||| ||||| ||| ||||

TTTGGTCTGTCGGT CTA GTTC
 T T TTT
 GAM1958 GAPCENA 3' TCTGAAGCCACCTGGTTC 14495 C CGCGG
 GGGCCAGG GGT TTCAGG
 ||||| || |||||
 CTTGGTCC CCG AAGTCT
 A ____
 GAM1958 GBTS1 3' GCCTGTCCTGGCTGCTGGCCC 29730 G C TT
 GGGCCAG CGGTCG GG CAGGT
 ||||| ||||| || |||||
 CCCGGTC GTCGGT CC GTCCG
 _ _ T_
 GAM1958 GIT1 3' ACCTGAGCCTGGGGCTGGCTC 15255 GGCG G_
 GGGCCA GTC C GGTTCAAGT
 ||||| ||| |||||
 CTCGGT CGG G CCGAGTCCA
 ____ GT
 GAM1958 GNG4 5' CCTCGCCGGCCCTGGTCC 10809 C _ GTTC
 GGGCCAGG GGTCG CG AGG
 ||||| ||||| || |||||
 CCTGGTCC CCGGC GC TCC
 _ C ____
 GAM1958 GP5 3' TTGTAACTGTGGTTGCCTGCC 10823 C GT CAGGT
 T GGGC AGGCG CGCGGTT
 ||| |||| |||||
 TCCG TCCGT GTGTCAA
 _ TG ATGTTT
 GAM1958 GPA33 3' GCTTGGGCCCTGCATTGGCCTG 12405 _ _ C
 GCCT GGCCAGGC GGT CG GGTTCAAGT
 ||||| ||| || |||||
 CCGGTCCG TTA GT CCGGGTTTCG
 G C C
 GAM1958 GR6 3' GTCTGAGGGTTCCGGTTGTCTT 14286 _ GT C ____ GT
 GGCCT CAGG CG CG GG TTCAG
 ||| || || || |||||
 GTTC GT GC CT GAGTC
 T TG _ TGG TG
 GAM1958 GS3955 3' GCTTGTAAGGCCCTCTGGTTT 22304 C GCGGTT
 GGGCCAGG GGTC CAGGT
 ||||| |||| |||||
 TTTGGTCT CCGG GTTCG
 C AAT____
 GAM1958 GTF3C2 3' GCCTGGACCTTTAGGCCTGCCT 7262 _ GC____
 AGGC GGTC GGTTCAAGT
 ||| |||| |||||
 TCCG CCGG CCAGGTCCG
 T ATTT
 GAM1958 H-L(3)MBT 3' ATTTGAGCTGTTTACTGTCT 17754 C_
 AGGCGGT GCGGTTCAAGT
 ||||| |||||

		TCTGTCA TGTCGAGTTTA	
		TT	
GAM1958 H-plk	5'	ATCTCTCCGGCCTCCTGGTTC 17982	C C TTC
		GGGCCAGG GGTCG GG AGGT	
		CTTGGTCC CCGGC TC TCTA	
		T C ____	
GAM1958 HCA4	3'	TCTGGGTTGAGATCCTGGCCC 38028	CG G TT GT
		GGGCCAGG GTC CGG CAG	
		CCCGGTCC TAG GTT GTC	
		__ A GG TG	
GAM1958 HERC3	3'	ACTTGAAATGCCTCTGGCTT 15971	C CGCGG
		GGGCCAGG GGT TTCAGGT	
		TTCGGTCT CCG AGGTTCA	
		_ TAA__	
GAM1958 HEYL	3'	ACCAGACGTCTGTGCTGCCTGG 15927	T T__ A
TTT		GGCCAGGCGG CGCGG TC GGT	
		TTGGTCCGTC GTGTC AG CCA	
		_ TGC A	
GAM1958 HEYL	3'	TCTGGTTACTGCCTGGCC 15933	C GGTT
		GGCCAGGCGGT GC CAGG	
		CCGGTCCGTCA TG GTCT	
		T ____	
GAM1958 HRH4	3'	CCTGGAACCTCCTTGGCTC 22259	C CGCGG
		GGGCCAGG GGT TTCAGG	
		CTCGGTTT TCA AGGTCC	
		C ____	
GAM1958 HRIHFB2436	5'	ACCGCGGCCCGCCGGGCCT 15664	A
		GGGCC GGCGGTCGCGGT	
		TCCGG CCGCCGGCGCCA	
		G	
GAM1958 HSA404617	5'	CTGGGCGGCTCCTGGTTC 36002	C GGT
		GGGCCAGG GGTCGC TCAG	
		CTTGGTCC TCGGCG GGTC	
		- ____	
GAM1958 HSNV1	3'	GCTTGAGCCACCGTGCCAGGCC 18966	A __ CGC
T		GGGCC GGC GGT GGTTCAGGT	
		TCCGG CCG CCA CCGAGTTCG	
		A TG ____	
GAM1958 HSPB7	3'	GCCCCAGTGACTCTTGGTTT 15781	C _ TTCA
		GGGCCAGG GGTCGC GG GGT	

TTTGGTTC TCAGTG CC CCG
 _ A C _
 GAM1958 HSPC055 5' ACCTGGCACAGTGCCTGGCCT 15435 GGTC G _
 GGGCCAGGC GC GT TCAGGT
 ||||| || |||||
 TCCGGTCCG TG CA GGTCCA
 _ A C
 GAM1958 HSU79303 3' GCTTGGGCTGCCCAGCCCTGTC 14961 CA _ TC
 C GGGC GGC GG GCGGTTTCAGGT
 ||| ||| || |||||
 CCTG CCG CC CGTCGGGTTTCG
 TC A _
 GAM1958 ITGB8 5' GTTTGGGTTTGATTGTGTTTGG 7979 _ C TT GG
 CTC GGCCAGGCG GTCG GG CA T
 ||||| ||| || || |
 TCGGTTTGT TAGT TT GT G
 GT _ GG TT
 GAM1958 JAM1 3' ACTTGGGGGATCTCCTTGGCCT 18858 _ C GCGG
 GGGCCA GG GGTC TTCAGGT
 ||||| || ||| |||||
 TCCGGT CC CTAG GGGTTCA
 T T G _
 GAM1958 JAM1 3' ACTTGGGGGATCTCCTTGGCCT 29325 _ C GCGG
 GGGCCA GG GGTC TTCAGGT
 ||||| || ||| |||||
 TCCGGT CC CTAG GGGTTCA
 T T G _
 GAM1958 JAM1 3' ACTTGGGGGATCTCCTTGGCCT 29334 _ C GCGG
 GGGCCA GG GGTC TTCAGGT
 ||||| || ||| |||||
 TCCGGT CC CTAG GGGTTCA
 T T G _
 GAM1958 JAM1 3' ACTTGGGGGATCTCCTTGGCCT 29345 _ C GCGG
 GGGCCA GG GGTC TTCAGGT
 ||||| || ||| |||||
 TCCGGT CC CTAG GGGTTCA
 T T G _
 GAM1958 KATII 5' ACTTGACGAGGCTCTTTGGTTT 18342 C G GT
 GGGCCAGG GGTC CG TCAGGT
 ||||| ||| || |||||
 TTTGGTTT TCGG GC AGTTCA
 C A _
 GAM1958 KCNS1 3' GCTTGAACCTCTGGGCTTGGTGC 8044 G GG C
 G GCCAGGC TCG GGTTCAGGT
 | ||||| || |||||
 C TGGTTCG GGT TCAAGTTTCG
 G _ C
 GAM1958 KCNS1 3' TCTGAAGGGCCCTGGCCT 8047 C GCGG
 GGGCCAGG GGTC TTCAGG
 ||||| ||| |||||

TCCGGTCC CCGG AAGTCT
 _ G_
 GAM1958 KCNT1 3' GCCTGGACACCACGCCGGGCTC 30975 A GTCGCG
 GGGCC GGCG GTTCAGGT
 ||||| ||| |||||
 CTCGG CCGC CAGGTCCG
 G ACCA_
 GAM1958 KHDRBS3 5' GCCTTCCGGCCGACCGCCCGGC 13326 A _ TTC
 TT GGGCC GGCGGTCTG CGG AGGT
 ||||| ||||| ||| |||
 TTCGG CCGCCAGC GCC TCCG
 C CG T_
 GAM1958 KIAA0014 3' GCCTGGGCTCGCGGCCGGCCC 16115 AGGC _
 GGGCC GGTCGCG GTTCAGGT
 ||||| ||||| |||||
 CCCGG CCGGCGC CGGGTCCG
 _ T
 GAM1958 KIAA0053 5' GCCTGGGTTTTATTCTTGGCCT 17031 _ TCGC_ TT
 GGCCC CCAGGC GG GG CAGGT
 ||||| || || |||||
 GGTCCG TC TT GTCCG
 GT TTATT GG
 GAM1958 KIAA0121 3' GCTTCCACGGCGTGTTTGTTTC 35970 _ C TTC
 GGGCCAGGCG GTCG GG AGGT
 ||||| ||||| ||| |||
 CTTGGTTTGT CGGC CC TTCG
 G A _
 GAM1958 KIAA0141 3' ACCTGGGCCTCCTGACTCCTGG 16583 C C_
 CCC GGCCAGG GGTCG GGTTCAGGT
 ||||| ||||| |||||
 CCGGTCC TCAGT CCGGGTCCA
 _ CCT
 GAM1958 KIAA0141 3' GCCTGGATGTGTCTGCTTGACT 16585 C T G
 T GGG CAGGCGG CGCG TTCAGGT
 ||| ||||| ||||| |||||
 TTC GTTCGTC GTGT AGGTCCG
 A T _
 GAM1958 KIAA0143 3' ATTTGAACTGTGACTTGT 32349 _
 GCG GTCGCGGTTTCAGGT
 ||| ||||| |||||
 TGT CAGTGTCAAGTTTA
 T
 GAM1958 KIAA0146 5' ATCTGGATTGTGCAGAGCCTGC 39583 C GGT_
 CT GGGC AGGC CGCGGTTTCAGGT
 ||||| ||||| |||||
 TCCG TCCG GTGTTAGGTCTA
 _ AGAC
 GAM1958 KIAA0152 3' CCTGGGAACTGTTTGGTCC 16334 CGCGG
 GGGCCAGGCGGT TTCAGG
 ||||| ||||| |||||

CCTGGTTTGTCA GGGTCC
 A____
 GAM1958 KIAA0152 3' GTTTGAGCTTTGTCATTGCTTG 16339 C C __ GG
 TCTC GG CAGGCGGT GC GGTTC A T
 || ||||| || ||||| |
 TC GTTCGTTA TG TCGAGT G
 T C TT TT
 GAM1958 KIAA0161 3' ACCTGGGCTGTGGCTCTCTGTC 16428 C C
 GGC AGG GGTCGCGGTTTCAGGT
 ||| ||| |||||
 CTG TCT TCGGTGTCGGGTCCA
 _ C
 GAM1958 KIAA0161 3' GAATTGCTGCCGTCTGGCCT 16431 C
 GGGCCAGGCGGT GCGGTTC
 ||||| |||||
 TCCGGTCTGCCG CGTTAAG
 T
 GAM1958 KIAA0194 3' CTGATGAATTGCTTAGCCT 32824 C _ CGGT
 GGGC AGGCGGT CG TCAG
 ||| ||||| || |||
 TCCG TTCGTTA GT AGTC
 A A ____
 GAM1958 KIAA0227 3' ATTTGAACCAGGCCTGCCTGAC 30449 C _ GC
 TC GGG CAGGC GGTC GGTTTCAGGT
 ||| ||||| ||| |||||
 CTC GTCCG CCGG CCAAGTTTA
 A T A_
 GAM1958 KIAA0247 3' CTTGGCATATGTTTGGTCT 16375 GTC GGTT
 GGGCCAGGCG GC CAGG
 ||||| || |||
 TCTGGTTTGT CG GTTC
 ATA ____
 GAM1958 KIAA0265 3' ATTTGAACACATTTCTTTGGCT 34623 C TCGCG
 C GGGCCAGG GG GTTCAGGT
 ||||| || |||||
 CTCGGTTT CT CAAGTTTA
 _ TTACA
 GAM1958 KIAA0266 3' ACCTGGATATTCTGACTCCTGG 22308 C CG__
 CCC GGCCAGG GGTCG GTTCAGGT
 ||||| ||||| |||||
 CCGGTCC TCAGT TAGGTCCA
 _ CTTA
 GAM1958 KIAA0298 3' GGACTGTGATCCCTGGCCC 37626 C
 GGGCCAGG GGTCGCGGTTC
 ||||| |||||
 CCCGGTCC CTAGTGTCAAG
 _
 GAM1958 KIAA0318 3' CTTGAAGCCCCTTGGCTT 34186 C CGCGG
 GGGCCAGG GGT TTCAGG
 ||||| || |||||

TTCGGTTC CCG AAGTTC
 C ____
 GAM1958 KIAA0321 3' ATTTGGGCTAAAGTTTGGCTT 31266 GGTCGC
 GGGCCAGGC GGTTCAGGT
 ||||| |||||
 TTCGGTTTG TCGGGTTTA
 AAA__
 GAM1958 KIAA0335 3' GTTTGGATCAAATTTTGTGCTGGT 16733 G TCGC_ GG
 TC GGGCCAG CGG GGTTC A T
 ||||| || ||||| I
 CTTGGTC GTT CTAGGT G
 _ TTAAA TT
 GAM1958 KIAA0349 3' GTTGGGCTGTGGTTGGC 44341 GCGG GG
 GCCAG TCGCGGTTCA T
 |||| ||||| I
 CGGT GGTGTCGGGT G
 ____ TT
 GAM1958 KIAA0390 3' ATCTGGACTTGCCCTTGTCTGT 16270 GC TC _
 TC G CAGGCGG GCG GTTCAGGT
 I ||||| || |||||
 C GTCTGTT CGT CAGGTCTA
 TT CC T
 GAM1958 KIAA0420 3' ACTTGAAGCCTGATCTGGCCT 31722 GCG C _
 GGGCCAG GTCG GGTT CAGGT
 ||||| ||||| |||||
 TCCGGTC TAGT CCGA GTTCA
 ____ _ A
 GAM1958 KIAA0430 3' GTTTGAACACTTTTGTGTGGT 21151 _ TCGCG GG
 TC GGGCCA GGCGG GTTCA T
 ||||| ||||| ||||| I
 CTTGGT TTGTT CAAGT G
 G TTCA_ TT
 GAM1958 KIAA0444 3' ATCTGAGAATGTCCTTCTTGGT 31239 C_ T CGG
 TT GGGCCAGG GG CG TTCAGGT
 ||||| || |||||
 TTTGGTTC CC GT GAGTCTA
 TT T AA_
 GAM1958 KIAA0444 3' CTGGAGCGATTGCCTGGCCC 31241 GG
 GGGCCAGGCGGTTCG TTCAG
 ||||| |||||
 CCGGTCCGTTAGCG AGGTC

 GAM1958 KIAA0444 3' GCCTGGGCCCCCTGCACTGCCT 31243 C ____
 GGTCC CAGGCGGT GC GGTTCAGGT
 ||||| || |||||
 GTCCGTCA CG CCGGTCCG
 _ TCCC
 GAM1958 KIAA0444 3' TCCCCTGTGAGCCGTGGCTTGT 31245 _ _ T
 CTGGTCT CCAGGCG GTCGCGGTTCA GG
 ||||| ||||| ||||| ||

		GGTCTGT CGGTGCCGAGT CC	
		T GT CCTC	
GAM1958 KIAA0478	5'	CCTCTGGTGTGCTTGGCTT 16977	GT _ TTC
		GGGCCAGGCG CGC GG AGG	
		TTCGGTTCGT GTG TC TCC	
		_ G _	
GAM1958 KIAA0493	3'	ACCTGATTTGGCTTCTGGCTC 32136	C CGGT
		GGGCCAGG GGTCG TCAGGT	
		CTCGGTCT TCGGT AGTCCA	
		_ TT _	
GAM1958 KIAA0493	5'	ACCTGGGCAGTCCTCTGGTTT 32137	C TC G
		GGGCCAGG GG GC GTTCAGGT	
		TTTGGTCT CC TG CGGGTCCA	
		_ _ A	
GAM1958 KIAA0514	3'	TTGATGTGTTTGTGGCTT 16212	T GT
		GGGCCAGGCGG CGCG TCAG	
		TTCGGTTTGTT GTGT AGTT	
		T _	
GAM1958 KIAA0515	3'	ACCTGAGCTTCTTGTCTGCTT 31916	C TCGC
		GGGC AGGCGG GGTTTCAGGT	
		TTCG TCTGTT TCGAGTCCA	
		_ CT _	
GAM1958 KIAA0515	3'	ATTTGGGGGTTTTGTTTGGTTC 31919	TC GG
		GGGCCAGGCGG GC TTCAGGT	
		CTTGGTTTGTT TG GGGTTTA	
		T_ G_	
GAM1958 KIAA0543	3'	TTGCTTGCTGCCTGGCTC 34181	C_
		GGGCCAGGCGGT GCGG	
		CTCGGTCCGTCG CGTT	
		TT	
GAM1958 KIAA0552	3'	TCTGAGCCGGAGGCCCTTG 16349	C G_ GT
		CAGG GGTC CGGTTTCAG	
		GTTC CCGG GCCGAGTC	
		_ AG TG	
GAM1958 KIAA0557	3'	CTGGCTGCTGCTTGGCCC 38205	GTC T
		GGGCCAGGCG GCGGT CAG	
		CCCGGTTCGT CGTCG GTC	
		_ _	
GAM1958 KIAA0560	5'	GCTTGGGCTGTTGTACGGGTTC 30837	AG_ GTC
		GGGCC GCG GCGGTTCAGGT	

CTTGG TGT TGTCGGGTTCG
 GCA ____
 GAM1958 KIAA0562 3' ATTTGAACAATGTACTCCCTGG 16240 C _ CG
 CCT GGGCCAGG GGT CG GTTCAGGT
 ||||| ||| || |||||
 TCCGGTCC TCA GT CAAGTTTA
 C T AA
 GAM1958 KIAA0596 3' GCTTGAGCTGCTCCAAACCTGG 31463 C__ TC
 CCC GGCCAGG GG GCGGTTTCAGGT
 ||||| || |||||
 CCGGTCC CC CGTCGAGTTCG
 AAA T_
 GAM1958 KIAA0632 3' GCCTGGGCGCCCGCCGCGGGTT 17808 A TC
 C GGGCC GGCGG GCGGTTTCAGGT
 ||||| ||| |||||
 CTTGG CCGCC CGCCGGGTCCG
 G C_
 GAM1958 KIAA0638 3' CCTCCAGCTGTCTGGCCT 35845 CGC TTC
 GGGCCAGGCGGT GG AGG
 ||||| || |||
 TCCGGTCTGTCTG CC TCC
 A__ ____
 GAM1958 KIAA0668 5' GCCCGGCGCGCGGCCTGGCCT 33051 G _ TTCA
 GGGCCAGGC GTCGC GG GGT
 ||||| ||| || |||
 TCCGGTCCG CGGCG CC CCG
 G G ____
 GAM1958 KIAA0676 3' GCCTGGGCTGTAGCAAGCTGTC 17394 C C____
 TGCCC AGGCGGT GCGGTTTCAGGT
 ||||| |||||
 TCTGTCTG TGTCGGGTCCG
 _ AACGA
 GAM1958 KIAA0682 3' ATCTGGGCTCACCTCCCTGGTT 16899 C_ CGC
 C GGGCCAGG GGT GTTCAGGT
 ||||| ||| |||||
 CTTGGTCC CCA TCGGGTCTA
 CT C_
 GAM1958 KIAA0720 3' GCCTGAGCTACTGCGCTTGGCC 31234 GTCGC
 C GGGCCAGGCG GTTCAGGT
 ||||| |||||
 CCCGGTTCGC TCGAGTCCG
 GTCA_
 GAM1958 KIAA0729 3' GCCTCCGATCGCTGTGGTTC 45805 _ C_
 GGGCCA GGCGGTCTG GGT
 ||||| ||||| |||
 CTTGGT TCGCTAGC CCG
 G CT
 GAM1958 KIAA0759 3' CTGAGCCCCAGGTCTGTCT 33440 _ GC_
 AGGCGG TC GGTTCAG
 ||||| || |||||

TCTGTC GG CCGAGTC
 T ACC
 GAM1958 KIAA0767 3' CCCCAGGCTGCGGTTGCCTGG 30408 GT CA T
 CCAGGCG CGCGGTT GG
 ||||| ||||| ||
 GGTCCGT GCGTCGG CC
 TG AC CC
 GAM1958 KIAA0773 3' ACCTGGGCTGTGGGCTTCTGGG 16192 G C _
 TC GG CCAGG GGTC GCGGTTCAAGT
 || |||| ||| |||||
 CT GGTCT TCGG TGTCGGGTCCA
 G _ G
 GAM1958 KIAA0806 3' GCCATGCGTTGTTTGGTCT 16780 T _
 GGGCCAGGCGG CGC GGT
 ||||| ||| |||
 TCTGGTTTGTG GCG CCG
 _ TA
 GAM1958 KIAA0819 3' GCCTGGGCCGCTTGCTGGCTGT 31809 _ G C_
 GGCCT CCA G CGGT GCGGTTCAAGT
 ||| |||| |||||
 GGT C GTCG CGCCGGGTCCG
 GT G TT
 GAM1958 KIAA0831 3' GCCTGAGCCACCGCGCCCGGCC 17208 A GT C_
 C GGGCC GGCG CG GGTTCAGGT
 |||| ||| || |||||
 CCCGG CCGC GC CCGAGTCCG
 C _ CA
 GAM1958 KIAA0870 5' ACCTGGACCGCTCCATTTGGT 39608 C TC
 GCCAGG GG GCGGTTCAAGT
 |||| || |||||
 TGGTTT CC CGCCAGGTCCA
 A T_
 GAM1958 KIAA0923 3' TCTGAGTTGTTTGTGTTGACTT 15245 _ TC GG GT
 GGG CCAGGCGG GC TTCAG
 || ||||| || |||||
 TTC GGTGTTGTT TG GAGTC
 A _ TT TG
 GAM1958 KIAA0924 3' GCCTGAATCAGAACGCTGGCTT 17065 G G GC
 GGGCCAG CG TC GGTTCAGGT
 ||||| || || |||||
 TTCGGTC GC AG CTAAGTCCG
 _ A A_
 GAM1958 KIAA0953 3' ATCTGAATCCTGGTGCCTGGC 33165 G C
 GCCAGGCG TCG GGTTCAGGT
 ||||| || |||||
 CCGTCCGT GGT CTAAGTCTA
 _ C
 GAM1958 KIAA0978 3' TTGACACTGATCTGGTCC 34891 _ CG
 GGGCCAGG CGGT CGG
 ||||| ||| |||

		CCTGGTCT GTCA GTT	
		A CA	
GAM1958 KIAA1014	3'	CTGAAGCTTTTCTGGCCT 32569	CG TC GG
		GGGCCAGG G GC TTCAG	
		TCCGGTCT T CG AAGTC	
		TT T_ _	
GAM1958 KIAA1036	3'	GCCTGGAATGTTTTCTGGCTC 17129	CGGTC G
		GGGCCAGG GCG TTCAGGT	
		CTCGGTCT TGT AGGTCCG	
		TT_ _ A	
GAM1958 KIAA1041	3'	TTGGGCATTGCTTGGCTC 17267	CGCG
		GGGCCAGGCGGT GTTCAG	
		CTCGGTTCGTTA CGGGTT	

GAM1958 KIAA1045	3'	ATCTGGGCTCAGGTGTATGGCC 35192	G GTCGC
	C	GGGCCA GCG GGTTCAGGT	
		CCCGGT TGT TCGGGTCTA	
		A GGAC_	
GAM1958 KIAA1052	3'	GCCTGAGGAGCTGCCTGCCT 17313	C CGCGG
		GGGC AGGCGGT TTCAGGT	
		TCCG TCCGTCG GAGTCCG	
		_ AG_	
GAM1958 KIAA1077	3'	TTTGGGTTGGCTTGGTTT 36098	GGTCG TT
		GGGCCAGGC CGG CAGG	
		TTTGGTTTCG GTT GTTT	
		_____ GG	
GAM1958 KIAA1118	5'	TGGGCGCGACTGGTTC 34486	GGCG G
		GGGCCA GTCGCG TTCA	
		CTTGGT CAGCGC GGGT	
		_____ -	
GAM1958 KIAA1128	3'	TCTGGGGATTGTTTGGCCT 33973	GCGG
		GGGCCAGGCGGTC TTCAGG	
		TCCGGTTTGTTAG GGGTCT	

GAM1958 KIAA1130	3'	GCCTGGGTCTCTGATTTGGCCT 31284	_ TCGC TT
		GGGCCAGG CGG GG CAGGT	
		TCCGGTTT GTC CT GTCCG	
		A T_ _ GG	
GAM1958 KIAA1143	3'	GCTTGGATTGCTGACCTCTGAC 34075	C C _
	TT	GGG CAGG GGTC GCGGTTCAGGT	

TTC GTCT CCAG CGTTAGGTTCTG
 A _ T
 GAM1958 KIAA1161 5' ACCTGAACTGTGGCTGATTTGG 39746 _
 TCC GGGCCAGG CGGTCGCGGTTCAAGT
 ||||| |||||
 CCTGGTTT GTCGGTGTCAAGTCCA
 A
 GAM1958 KIAA1181 5' GCCGCGGCCCGCCTGGCCT 33923 _
 GGGCCAGGCGG TCGCGGT
 ||||| |||||
 TCCGGTCCGCC GGCGCCG
 C
 GAM1958 KIAA1185 3' TCTGGGCTCTCGTCGTTGGCCT 31370 G T C _ GT
 GGGCCAG CGG CG G GTTCAG
 ||||| ||| || |||||
 TCCGGTT GCT GC C CGGGTC
 _ _ T T TG
 GAM1958 KIAA1196 3' CCTGTGTGACCGTTGGCCC 30818 G GTT T
 GGGCCAG CGGTCGCG CAGG
 ||||| ||||| |||
 CCCGGTT GCCAGTGT GTCC
 _ _ _ T
 GAM1958 KIAA1211 3' GTTGAAAATTCCTTTGGTCT 34165 C TCGCGG GG
 GGGCCAGG GG TTCA T
 ||||| || ||| |
 TCTGGTTT CC AAGT G
 C TTAA _ TT
 GAM1958 KIAA1228 3' CCTGGAGGTGCTTGGCCT 32439 GGTC GG
 GGGCCAGGC GC TTCAGG
 ||||| || |||||
 TCCGGTTCG TG AGGTCC
 _ _ G _
 GAM1958 KIAA1277 3' CCTGAGTAGTCCCTGGCTT 32204 C TC GGT
 GGGCCAGG GG GC TCAGG
 ||||| || || |||||
 TTCGGTCC CT TG AGTCC
 _ GA _
 GAM1958 KIAA1280 5' TTGGGGCTGGTTTGGTTT 34558 _ G
 GGGCCAGGC GGTC CGG
 ||||| ||||| |||
 TTTGGTTTG TCGG GTT
 G G
 GAM1958 KIAA1322 3' TTGAGGGCTGTTTGGCTC 36032 GCGG
 GGGCCAGGCGGTC TTCAG
 ||||| ||||| |||||
 CTCGGTTTGTCCG GAGTT
 _ _
 GAM1958 KIAA1332 3' GCCTGGAACCAGACTGTTTGCT 35257 C GC _
 T GGGC AGGCGGTC GGTTC AGGT
 ||| ||||| ||||| |||||

TTCG TTTGTCAG CCAAG TCCG
 _ A_ G
 GAM1958 KIAA1348 3' GCTTGAATGACTTGT TTTTGGT 34029 _ _ GCGG
 TT GGGCCAGG CG GTC TTCAGGT
 ||||| || ||| |||||
 TTTGGTTT GT CAG AGGTTTCG
 T T TA__
 GAM1958 KIAA1432 5' ACTTGAAGTGTGGAGAGGCTT 33145 AGGCGG
 GGGCC TCGCGGTTTCAGGT
 |||| |||||
 TTCGG GGTGTCAAGTTCA
 AGA__
 GAM1958 KIAA1432 3' ATTTTATTGTGGTGT TTTGGTT 33148 G TC
 C GGGCCAGGCG TCGCGGT AGGT
 ||||| ||||| |||
 CTTGGTTTGT GGTGTTA TTTA
 _ TT
 GAM1958 KIAA1437 5' CTGGGCACTGGCTGGTCT 30384 G CGCG
 GGGCCAG CGGT GTTCAG
 ||||| ||| |||||
 TCTGGTC GTCA CGGGTC
 G ____
 GAM1958 KIAA1493 3' AGCTGTGGTTGTCTCGTTT 32086 C GT
 GGGC AGGCG CGCGGTT
 ||| |||| |||||
 TTTG TCTGT GTGTCGA
 C TG
 GAM1958 KIAA1560 3' ACCTGAGACTTGCCGTCTGGC 32099 CGCGG
 GCCAGGCGGT TTCAGGT
 ||||| |||||
 CGGTCTGCCG GAGTCCA
 TTCA_
 GAM1958 KIAA1571 3' ACTTGAAGTGAATATTGGCT 30563 GC CG
 T GGGCCAG GGT CGGTTTCAGGT
 ||||| ||| |||||
 TTCGGTT TTA GTCAAGTTCA
 A_ AA
 GAM1958 KIAA1576 3' ATCTGGGTTTGGTTTGGTTT 32771 GGTCGC TT
 GGGCCAGGC GG CAGGT
 ||||| || |||||
 TTTGGTTTGT TT GTCTA
 GT__ GG
 GAM1958 KIAA1610 3' ACTTTTTCAGTGGTTCTTGGTC 33337 C GT GGTTTC
 C GGGCCAGG G CGC AGGT
 ||||| | ||| |||
 CCTGGTTC T GTG TTCA
 _ TG ACTTT
 GAM1958 KIAA1656 3' GCTGCGCTGCTGGCCGCCTGGC 32733 _ T GT
 TT GGGCCAGGCGGTC GCGGT CAG
 ||||| ||||| |||

		TTCGGTCCGCCGG CGTCG GTC		
		T C G		
GAM1958 KIAA1719	3'	GCCTGGGATGATGCTTGGTCT 33820	G	GCGG
		GGGCCAGGCG TC TTCAGGT		
		TCTGGTTCGT AG GGGTCCG		
		_ TA_		
GAM1958 KIAA1750	3'	GCCTGGACCTTGTCTTGGCTC 33877	CGGT	C
		GGGCCAGG CG GGTTCAGGT		
		CTCGGTTC GT CCAGGTCCG		
		TT_ T		
GAM1958 KIAA1754	3'	CTGGCTTGCAGTCTGGCCC 31680	GGTC	TT
		GGGCCAGGC GCGG CAG		
		CCCGGTCTG CGTT GTC		
		A_ CG		
GAM1958 KIAA1814	3'	GCCTGGGTGAGTGTTGGGCTC 34837	AG	G GGT
		GGGCC GCG TCGC TCAGGT		
		CTCGG TGT AGTG GGTCCG		
		GT G _		
GAM1958 KIAA1821	3'	ACCTGGCTTGTGCTTGGCTT 35550	GTC	TT
		GGGCCAGGCG GCGG CAGGT		
		TTCGGTTCGT TGTT GTCCA		
		_ CG		
GAM1958 KIAA1854	3'	CTGAGCGGCGTTTGGTTC 35530	G	GGT
		GGGCCAGGCG TCGC TCAG		
		CTTGGTTTGC GGCG AGTC		
		- _		
GAM1958 KIAA1887	5'	ACTTTGACCCTTTGGCCC 37713	C	C
		GGGCCAGG GGTCG GGT		
		CCCGGTTT CCAGT TCA		
		C T		
GAM1958 KIAA1894	3'	ACCTGGGAGCGCTGCTTGGCTC 36559	T	GG
		GGGCCAGGCGG CGC TTCAGGT		
		CTCGGTTCGTC GCG GGGTCCA		
		_ A_		
GAM1958 KIAA1904	3'	GCAGTGGCTGCCTGTCCC 36378	C	G
		GGG CAGGCGGTTCGC GT		
		CCC GTCCGTCGGTG CG		
		T A		
GAM1958 KIAA1904	3'	GCCCAGAGTGACCGTTGGGCTC 36379	AG	GGTTCA
		GGGCC GCGGTCGC GGT		

CTCGG TGCCAGTG CCG
GT AGAC__

GAM1958 KIAA1922 5' GCTTGAGCCACTGCGCCTGGCC 36457 GTCGC
T GGGCCAGGCG GGTTCAGGT
||||||| |||||
TCCGGTCCGC CCGAGTTCG
GTCA_

GAM1958 KIAA1924 3' CCTGGGTCCCGCCTAGCCT 36474 C TCGC TT
GGGC AGGCGG GG CAGG
||| ||||| || |||
TCCG TCCGCC CT GTCC
A ____ GG

GAM1958 KIAA1940 3' ACCTGAGCTGGAGCCACTTGGC 39003 C CG
TT GGGCCAGG GGT CGGTTCAGGT
||||||| ||| |||||
TTCGGTTC CCG GTCGAGTCCA
A AG

GAM1958 KIAA1940 5' GCTCGACGCCGCCGCTGGCCC 39007 C GT AG
GGGCCAGGCGGT GCG TC GT
||||||| ||| || ||
CCCGGTCCGCCG CGC AG CG
C ____ CT

GAM1958 KIAA1948 3' CCTCTGTGACTGCTTCGCC 40081 C TTC T
GGGC AGGCGGTCGCGG AGG
||| ||||| ||| |||
CCCG TTCGTCAGTGTC TCC
C ____ C

GAM1958 KOC1 5' GTTGGGTTGTAGCTAGGCTT 43780 A GGTC TT GG
GGGCC GGC GCGG CA T
||||| ||| ||| || |
TTCGG TCG TGTT GT G
A A__ GG TT

GAM1958 KRTAP1-5 3' ATCTGATCCATCCCTTGGTTT 25697 C TCGC T
GGGCCAGG GG GG TCAGGT
||||||| || || |||||
TTTGGTTC CC CC AGTCTA
_ TA_ T

GAM1958 L3MBTL 3' GCCTGAACTGTGGCCGTGTCT 34456 CAG
GGGC GCGGTCGCGGTTTCAGGT
||| |||||
TCTG TGCCGGTGTCAAGTCCG

GAM1958 L3MBTL2 3' GCCTGAGTGTGCACTTTGGCTC 42790 GC _ G T
GGGCCAG GGT CGCG T CAGGT
||||| ||| ||| | |||||
CTCGGTT TCA GTGT A GTCCG
_ C G_

GAM1958 LAMP3 3' CTTGAATTCATGTTGGTCT 29919 G GTCGC
GGGCCAG CG GGTTCAGG
||||| || |||||

			TCTGGTT GT	TTAAGTTC		
			— AC —			
GAM1958	LASP1	3'	CTTGATTCATCTCTGGTTT	12797	C	CGC GT
			GGGCCAGG GGT G TCAGG			
			TTTGGTCT CTA C AGTTC			
			— — TT			
GAM1958	LGI3	5'	GCGGGGGCCGCGCGCCGCGGCC	29278	A	AG
	C		GGGCC GCGGTCGCGGTTC GT			
			CCCGG CCGCCGGCGCCGGG CG			
			— GG			
GAM1958	MAP2K3	5'	GCCTGGCCTGGGCGGTCTGCCC	29715	C	G TT
			GGGC AGGCGGTC CGG CAGGT			
			CCCG TCTGCCGG GTC GTCCG			
			— — CG			
GAM1958	MAP3K3	3'	GCCTGAGTCGTGACCTGCTAGG	8222	A	— GT
	CC		GGCC GGC GGTGCG TCAGGT			
			CCGG TCG CCAGTGC AGTCCG			
			A T TG			
GAM1958	MAWBP	5'	ACCTCAATGATCGTCTGTTTC	22680	GC	GCG C
			GG CAGGCGGTC GTT AGGT			
			CT GTCTGCTAG TAA TCCA			
			TT — C			
GAM1958	MBLL39	3'	AAGTGTGGTGTGTTGGTTT	29568	G	G
			GGGCCAGGCG TCGCG TT			
			TTTGGTTTGT GGTGT AA			
			— G			
GAM1958	MBLL39	5'	GCCTCGGCCACTTGGTTC	29571	C	C
			GGGCCAGG GGTCG GGT			
			CTTGGTTC CCGGC CCG			
			A T			
GAM1958	MBLL39	3'	GGATCATCGCCTGTTCT	29572	GC	CGC
			GG CAGGCGGT GTTC			
			TC GTCCGCTA CTAGG			
			TT —			
GAM1958	MBLL39	5'	TTGATGAGTGATTGCCTGTCC	29578	C	GGT
			GGGC AGGCGGTGCG TCAG			
			CCTG TCCGTTAGTG AGTT			
			— AGT			
GAM1958	MBLL39	3'	AAGTGTGGTGTGTTGGTTT	12317	G	G
			GGGCCAGGCG TCGCG TT			

		TTTGGTTTGT GGTGT AA		
		— G		
GAM1958	MBLL39	5' GCCTCGGCCACTTGGTTC 12318	C	C
		GGGCCAGG GGTCTG GGT		
		CTTGGTTC CCGGC CCG		
		A T		
GAM1958	MBLL39	5' TTGATGAGTGATTGCCTGTCC 12321	C	GGT
		GGGC AGGCGGTCTGC TCAG		
		CCTG TCCGTTAGTG AGTT		
		— AGT		
GAM1958	MDS030	5' GTTTGCGTACCGGTCTGCCTGGT 20538		GT CG TT GG
	CC	GGGCCAGGCG CG G CA T		
		CCTGGTCCGC GC T GT G		
		TG CA GC TT		
GAM1958	MGC:5244	5' GCTTGGACCGCGATGGGGCTGG 25258	A	G__
	GCCC	GGCC GGC GTCGCGGTTTCAGGT		
		CCGG TCG TAGCGCCAGGTTTCG		
		G GGG		
GAM1958	MGC10765	3' GTTGGGTCAAGATCCTGGTTC 23646		CG GC TT GG
		GGGCCAGG GTC GG CA T		
		CTTGGTCC TAG CT GT G		
		— AA GG TT		
GAM1958	MGC11034	3' ATCTGGGTGGATGCCTTGCCT 25470	C	GT GGT
		GGGC AGGCG CGC TCAGGT		
		TCCG TCCGT GTG GGTCTA		
		T AG —		
GAM1958	MGC12335	3' CTTGAGAACTCTTGGTTT 26477	C	CGCGG
		GGGCCAGG GGT TTCAGG		
		TTTGGTTC TCA GAGTTC		
		— A —		
GAM1958	MGC12679	3' CGGCTGGGGCTGCGGCCGCGTG 26457	G	A
	GCTC	GGGCCA GCGGTCGCGGTTC GGT		
		CTCGGT CGCCGGCGTCTGGG TCG		
		G G GCT		
GAM1958	MGC12679	3' TCTGGGCTTCCAGCGCTGGCCT 26459	—	— TCGC GT
		GGGCCAG GC GG GGTTCAG		
		TCCGGTC CG CC TCGGGTC		
		G A T — TG		
GAM1958	MGC12760	3' ATCTGAATCATCAGTATTGTCT 26446	C	C —
	GCTT	AGGCGGT GC GGTTCAGGT		

TCTGTTA TG CTAAGTCTA
 _ _ ACTA
 GAM1958 MGC13090 3' GCCTTCCTGTTGGCTGTCTGGC 26427 _ TTC
 CT GGGCCAGGCGGTCTG CGG AGGT
 ||||| ||| |||
 TCCGGTCTGTCGGT GTC TCCG
 T CT_
 GAM1958 MGC13170 5' CCTGGGCCAGAGCTGGTTC 26432 G GG GC
 GGGCCAG C TC GGTCAGG
 ||||| | || |||||
 CTTGGTC G AG CCGGGTCC
 _ _ A_
 GAM1958 MGC14161 3' ATCTGGACAATGGGACTGTTT 26716 C GCG_
 AGTTT C AGGCGGTC GTTCAGGT
 | ||||| |||||
 G TTTGTCAG CAGGTCTA
 A GGGTAA
 GAM1958 MGC14407 5' GCTTGAAGCAAAGACCTCTGGT 26729 C GCG _
 TT GGGCCAGG GGTC GTT CAGGT
 ||||| ||| || |||||
 TTTGGTCT CCAG CGA GTTCG
 _ AAA A
 GAM1958 MGC15476 3' TTGGGGATTGCTTGGGCT 29691 G _ G
 GG CCAGGCGG TC CGG
 || ||||| || |||
 TC GGTCGTT GG GTT
 G TA G
 GAM1958 MGC16169 5' ACCTTGGCTGACTTGGCTC 26963 _ C
 GGGCCAGG CGGTCTG GGT
 ||||| ||||| |||
 CTCGGTTC GTCGGT CCA
 A T
 GAM1958 MGC16491 5' CTGAGGTGTTCCCTGGCTT 27501 C TC G
 GGGCCAGG GG GCG TTCAG
 ||||| || || |||||
 TTCGGTCC CT TGT GAGTC
 _ _ G
 GAM1958 MGC1842 5' ATCTGGACCATCGACCTGGCCT 32685 _ CGC
 GGGCCAGG CGGT GTTCAGGT
 ||||| ||| |||||
 TCCGGTCC GCTA CCAGGTCTA
 A _
 GAM1958 MGC20253 3' TCTGAAGCCTCTGTTGTGGCTC 29399 _ TC GG GT
 GGGCCA GGCGG GC TTCAG
 ||||| |||| || |||||
 CTCGGT TTGTC CG AAGTC
 G TC _ TG
 GAM1958 MGC20470 3' GCCTGGGTTGGCTTCCTGCCC 29687 C C CG TT
 GGGC AGG GGTCG G CAGGT
 ||| || |||| | |||||

CCGG TCC TCGGT T GTCCG
 _ T _ GG
 GAM1958 MGC21854 3' CCTGAATAATGCTGGCTC 27447 G GTCGCG
 GGGCCAG CG GTTCAGG
 ||||| || |||||
 CTCGGTC GT TAAGTCC
 _ AA_
 GAM1958 MGC21945 5' GCCTGGGCTCCTGCCATGGCCC 29692 _ TCGC
 GGGCCA GGCGG GTTCAGGT
 ||||| ||||| |||||
 CCCGGT CCGTC TCGGGTCCG
 A C_
 GAM1958 MGC22014 3' GCTTGGCAGGTGCTTTTTGGTT 32220 C T G_ T
 C GGGCCAGG GG CGC GT CAGGT
 ||||| || ||| || |||||
 CTTGGTTT TC GTG CG GTTCG
 T _ GA _
 GAM1958 MGC2306 3' GCTTTACTGTGGCTGTCTGGAT 26354 _ TC
 CC GGG CCAGGCGGTGCGCGT AGGT
 ||| ||||| ||||| |||||
 CCT GGTCTGTGCGGTGTCA TTCG
 A T_
 GAM1958 MGC2452 5' ACCTGGGCTCTCTGTGTTTGG 26363 GTCGC_
 TTC GGGCCAGGCG GTTCAGGT
 ||||| ||||| |||||
 CTTGGTTTGT CCGGGTCCA
 GTCTCT
 GAM1958 MGC3113 5' ACCTGGACTCGGCGCGCCTAGC 23468 C _ C
 TC GGGC AGGCG GTCG GGTTCAGGT
 ||| ||||| ||||| |||||
 CTCG TCCGC CGGC TCAGGTCCA
 A G _
 GAM1958 MGC33182 3' TGAAACGTGGTGTCTGGTTT 37235 G G
 GGGCCAGGCG TCGCG TTCA
 ||||| ||||| |||||
 TTTGGTCTGT GGTGC AAGT
 _ A
 GAM1958 MGC35558 3' ATTTGAGTCCAGCCATCTTGGT 29613 C_ CGC _
 TC GGGCCAGG GGT GG TTCAGGT
 ||||| ||| || |||||
 CTTGGTTC CCG CC GAGTTTA
 TA A_ T
 GAM1958 MGC4342 3' GCCTGAATCCTTGCCGTGTGTCT 23626 _ TCGC
 GGGC CAGGCGG GTTCAGGT
 ||| ||||| |||||
 TCTG GTCCGTT CTAAGTCCG
 T C_
 GAM1958 MGC4504 3' TTGCGACCGCTTGAGCCC 23561 _
 GGGC CAGGCGGTGCGCG
 ||| ||||| |||||

CCGG GTTCGCCAGCGTT
 A
 GAM1958 MGC4549 3' GCCTGAACTGATCTCACTTGGC 26170 C TCG
 TC GGGCCAGG GG CGGTTCAAGT
 ||||| || |||||
 CTCGGTTC CT GTCAAGTCCG
 A CTA
 GAM1958 MGC4604 5' CCTGGGCCGTGGTCTCCTG 25577 C GT
 CAGG G CGCGGTTCAAG
 ||| | |||||
 GTCC C GTGCCGGGTCC
 T TG
 GAM1958 MGC4643 3' TGATGATGGCTGCCTGGTTT 26444 CGGT
 GGGCCAGGCGGTTCG TCA
 ||||| |||
 TTTGGTCCGTCCGT AGT
 AGT_
 GAM1958 MGC4796 3' GCTCGATTGTTTGGTTT 30833 C
 GGGCCAGGCGGTTCG GGT
 ||||| |||
 TTTGGTTTGTAGC TCG
 —
 GAM1958 MGC5601 5' CCTACAGCTGCCTGGCTC 24926 CGCG TC
 GGGCCAGGCGGT GT AGG
 ||||| || |||
 CTCGGTCCGTTCG CA TCC
 A___
 GAM1958 MIC2L1 3' ACCTGGCGTGAGCTGCCTGGT 25488 ___ GT
 TT GGGCCAGGCGGT CGCG TCAGGT
 ||||| ||| |||||
 TTTGGTCCGTTCG GTGC GTCCA
 AG___
 GAM1958 MIG-6 3' TGAAGATTCTGGCTT 21020 C GCGG
 GGGCCAGG GGTC TTCA
 ||||| ||| |||
 TTCGGTCT TTAG AAGT
 — —
 GAM1958 MOST2 5' CCTAGGTGCTGCCTGGCCC 21549 T GGTTT
 GGGCCAGGCGG CGC AGG
 ||||| || |||
 CCGGTCCGTC GTG TCC
 — GA___
 GAM1958 MST4 3' GTTTGGATCTGCACAGTTTGGT 18609 G C _ GG
 TT GGGCCAGG GT GCGG TTCA T
 ||||| || ||| ||| |
 TTTGGTTTGA CA CGTC AGGT G
 A _ T TT
 GAM1958 MY014 3' ATCTGGGTTTTCTCCTGGCTT 25188 C TCGC TT
 GGGCCAGG GG GG CAGGT
 ||||| || || ||||

			TTCGGTCC TC TT GTCTA		
			_ TT_ GG		
GAM1958	N4BP3	3'	CCTGAGCTCCTGTCTGCCT 32934 C TCGC		
			GGGC AGGCGG GGTTCAGG		
			TCCG TCTGTC TCGAGTCC		
			_ C_		
GAM1958	NBL1	3'	CCTGGGGTGGCCTGGCCC 29838 GGTCG G		
			GGGCCAGGC CG TTCAGG		
			CCCGGTCCG GT GGGTCC		
			_____ G		
GAM1958	NCKX3	3'	TTGGGATTTTGTGGTTT 21840 _ G		
			GGGCCAGGCG GTC CGG		
			TTTGGTTTGT TAG GTT		
			TT G		
GAM1958	NECL1	3'	CCTGAACTGCCTCTGCTT 22165 TC		
			AGGCGG GCGGTTTCAGG		
			TTCGTC CGTCAAGTCC		
			TC		
GAM1958	NIBAN	3'	ATCTGTGGGACTGTCTGGGCC 22627 G G GTT		
			GG CCAGGCGGTC CG CAGGT		
			CC GGTCTGTCAG GT GTCTA		
			G G _		
GAM1958	NIN283	3'	ATTTGGACCCAGGTTGCCTGCT 26012 C GT GC		
	C		GGGC AGGCG C GGTTCAGGT		
			CTCG TCCGT G CCAGGTTTA		
			_ TG AC		
GAM1958	NINJ2	3'	GCCTGGTAAAGTTGTTTGTGTC 18604 _ GTC GGT_		
	T		GGGC CAGGCG GC TCAGGT		
			TCTG GTTTGT TG GGTCCG		
			T _ AAAT		
GAM1958	NIP30	3'	TGAATGTGTTGTTTGGTTC 24499 T G		
			GGGCCAGGCGG CGCG TTCA		
			CTTGTTTGT GTGT AAGT		
			- -		
GAM1958	NKIR	3'	GCCTCATCGACCGTCTGCCC 29117 C CGGTTC		
			GGGC AGGCGGTCG AGGT		
			CCCG TCTGCCAGC TCCG		
			_ TAC_		
GAM1958	NPD009	5'	ACTTGAGGTCTGACTTTTGGCT 45560 C CGG		
	C		GGGCCAGG GGTCG TTCAGGT		

			CTCGGTTT TCAGT GAGTTCA		
			— CTG		
GAM1958	NPTXR	3'	ACTTGGACCGCTTCAGCCTGGG 15583	G	GGTC
	CT		GG CCAGGC GCGGTTTCAGGT		
			TC GGTCCG CGCCAGGTTCA		
			G ACTT		
GAM1958	NPTXR	3'	ACTTGGACCGCTTCAGCCTGGG 27731	G	GGTC
	CT		GG CCAGGC GCGGTTTCAGGT		
			TC GGTCCG CGCCAGGTTCA		
			G ACTT		
GAM1958	NRF	3'	GCTTGAACGTGTTTGTCTTGGT 18987	G	CGGTC
	GC		G GCCAGG GCGGTTTCAGGT		
			C TGGTTC TGTCAAGTTCG		
			G TTGTT		
GAM1958	NXN	3'	CTTGGGCTGACCTGACCC 22810	C	CGGTCCG
			GGG CAGG CGGTTCAGG		
			CCC GTCC GTCGGGTTC		
			A A_____		
GAM1958	NXPH3	3'	ACTTCTGTGCCCGCTTGGTCC 32713	T	TTC
			GGGCCAGGCGG CGCGG AGGT		
			CCTGGTTCGCC GTGTC TTCA		
			C _____		
GAM1958	NY-REN-25	5'	TGGGCGCGGCCGACCTGGTCC 30421	—	G
			GGGCCAGG CGGTCGCG TTCA		
			CCTGGTCC GCCGGCGC GGGT		
			A _____		
GAM1958	OCIA	5'	TTCTGCCCCTGATCGCTTGGTT 19492	C	TT T
	T		GGGCCAGGCGGTCTG GG CAGG		
			TTTGGTTCGCTAGT CC GTCT		
			— CC TC		
GAM1958	OPRL1	3'	GCTTCATGTGACTCTTGGCCT 6617	C	GTTC
			GGGCCAGG GGTCGCG AGGT		
			TCCGGTTC TCAGTGT TTCG		
			— AC__		
GAM1958	P2RX1	5'	GCCTCCAGCTGACCTCTGGCTC 33356	C	— — TTC
			GGGCCAGG GGTC GC GG AGGT		
			CTCGGTCT CCAG CG CC TCCG		
			— T A _____		
GAM1958	P2RX1	3'	GCTTGAGCCCTGTTTCTTCCTG 33357	C	TC —
	GCCT		GGCCAGG GG GC GGTTCAGGT		

CCGGTCC TC TG CCGAGTTCCG
T TT TC

GAM1958 PALMD 5' ACATGTGTCTGTCTGGCCT 19319 T _
GGGCCAGGCGG CGCG GT
||||||| ||| ||
TCCGGTCTGTC GTGT CA
T A

GAM1958 PER3 5' TGAGCGTGACCCCTGGCTC 18824 C G
GGGCCAGG GGTCGCG TTCA
||||| ||||| |||
CTCGGTCC CCAGTGC GAGT
C _

GAM1958 PI15 5' GCTTGAGTTCAACATTTGTTTG 18029 TCGCGG__
G CCAGGCGG TTCAGGT
||||| |||||
GGTTTGTT GAGTTCG
TACAACCT

GAM1958 PILR(ALPHA) 5' GCCTGGACGGCTCTGCTGGTCT 15101 G TC G
GGGCCAG CGG GC GTTCAGGT
||||| ||| || |||||
TCTGGTC GTC CG CAGGTCCG
_ T_ G

GAM1958 PILR(ALPHA) 5' GTTGGGGAAGGCTCCTGGCCC 15102 C GCGG GG
GGGCCAGG GGTC TTCA T
||||| ||| ||| |
CCCGGTCC TCGG GGGT G
_ AAG_ TT

GAM1958 PILR(BETA) 5' GCCTGGACAGCTCTGCTGGTCT 15104 G TC G
GGGCCAG CGG GC GTTCAGGT
||||| ||| || |||||
TCTGGTC GTC CG CAGGTCCG
_ T_ A

GAM1958 PIP3-E 3' CCTGGTGGCTGTTTGGCT 33177 GGTT
GGCCAGGCGGTCGC CAGG
||||||| |||
TCGGTTTGTCGGTG GTCC

GAM1958 PISD 3' ACCTGAGCTGTTTTCTGTTGGC 15653 G TC_
CC GGGCCAG CGG GCGGTTCAAGT
||||| ||| |||||
CCCGGTT GTC TGTCGAGTCCA
_ TTT

GAM1958 PM5 5' GCCTGGGCTGTCAGCCGGCCT 30496 A GGTC
GGGCC GGC GCGGTTCAAGT
||||| ||| |||||
TCCGG CCG TGTCGGGTCCG
_ AC_

GAM1958 PNMA5 3' GCCAGTGGCTGCTTGTCT 36442 GC _
GG CAGGCGGTCGC GGT
|| ||||| |||

TC GTTCGTCGGTG CCG
 TT A
 GAM1958 POLA2 5' CTGAGGTCTTGCTTGGGCC 8548 G TC GG
 GG CCAGGCGG GC TTCAG
 || ||||| || ||||
 CC GGTTCGTT TG GAGTC
 G C_ _
 GAM1958 PP2447 3' TCTGGGCCCCGGCCTCGCCTGCC 24869 C _ C GT
 C GGGC AGGC GGTCG GGTTCAG
 ||| ||| |||| |||||
 CCCG TCCG CCGGC CCGGGTC
 _ CT _ TG
 GAM1958 PPM1A 5' TCTGAGCCGCGAGGGCGCC 21998 G_ _
 GGCG TCGCGGTTTCAGG
 ||| |||||
 CCGC AGCGCCGAGTCT
 GGG
 GAM1958 PPP1R10 3' ACTTGGGCCCCGGCGTGCTGGGC 8573 A _ C
 CT GGGCC GGCG GTCG GGTTCAGGT
 |||| ||| ||| |||||
 TCCGG TCGT CGGC CCGGGTTCA
 G G _
 GAM1958 PPP4R1L 5' ATTTGGA CTCTGGTTTTGCCT 38815 C GGT C
 GGGC AGGC CG GGTTCAGGT
 ||| ||| || |||||
 TCCG TTTG GT TCAGGTTTA
 T _ C
 GAM1958 PRDM7 3' CTTGGAGTCCATCTGGTTT 27568 GC TC GG
 GGGCCAG GG GC TTCAGG
 ||||| || || |||||
 TTTGGTC CC TG AGGTTC
 TA _ _
 GAM1958 PRIC285 3' GCCTGGGCCAGCCTGCCTCCTG 30805 C C_ _
 GCCT GGCCAGG GGT GC GGTTCAGGT
 ||||| ||| || |||||
 CCGGTCC CCG CG CCGGGTCCG
 T TC A
 GAM1958 PRKWNK2 3' CCATCCGTGACCGCGTGGCCT 43518 G TTCA T
 GGGCCA GCGGTCGCGG GG
 ||||| ||||| || ||
 TCCGGT CGCCAGTGCC CC
 G TA_ _ T
 GAM1958 PRKWNK2 3' GAGCGTGATGCTTGCTC 43522 G G
 GGGCCAGGCG TCGCG TTC
 ||||| ||||| |||
 CTCGGTTCGT AGTGC GAG
 _ _
 GAM1958 PRO1386 3' ACCTGAACCAACATCTGGTTC 25287 CG CGC
 GGGCCAGG GT GGTTCAGGT
 ||||| || |||||

CTTGGTCT CA CCAAGTCCA
 A_ A_
 GAM1958 PRO1598 3' ATTTGGGTTTCTGGCTATGGCT 20568 GGC C_ TT
 T GGGCCA GGTCTG GG CAGGT
 ||||| |||| | ||||
 TTCGGT TCGGT TT GTTTA
 A_ CT GG
 GAM1958 PRO2214 5' CTTGGTGTCTGGCTT 20587 GTCGCGGT
 GGGCCAGGCG TCAGG
 ||||| ||||
 TTCGGTCTGT GTTTC

 GAM1958 PRO2900 5' ACTTGGGCTAAGCCGTCTGGGT 20707 G CGC
 C GG CCAGGCGGT GTTTCAGGT
 || ||||| |||||
 CT GGTCTGCCG TCGGGTTCA
 G AA_
 GAM1958 PRPF8 3' ATCTGGGCCGCTCACCCGGCT 30674 A C TC
 C GGGCC GG GG GCGGTTTCAGGT
 |||| | || |||||
 CTCGG CC CT CGCCGGGTCTA
 C A C_
 GAM1958 PRPF8 3' CTTGGCAACCTCCTGGCCC 30682 C C GGTT
 GGGCCAGG GGT GC CAGG
 ||||| || | ||||
 CCCGGTCC CCA CG GTTC
 T A _
 GAM1958 PSKH1 3' ACTTGGGCCTTCATGCCATGGC 33865 _ GTCGC
 CT GGGCCA GGCG GTTTCAGGT
 ||||| || |||||
 TCCGGT CCGT CCGGGTTCA
 A ACTT_
 GAM1958 PSR 3' ACTTGGAAGCACTGCCTGGGCT 32496 G C GG
 GG CCAGGCGGT GC TTCAGGT
 || ||||| || |||||
 TC GGTCCGTCA CG AGGTTCA
 G _ A_
 GAM1958 PSR 3' ATTTGGATATTCCTTCCCTGGT 32499 C_ TCGCG
 CC GGGCCAGG GG GTTTCAGGT
 ||||| || |||||
 CCTGGTCC CC TAGGTTTA
 CTT TTA_
 GAM1958 PTDSS2 3' GCCTGGTCAGCCCCGTGGCCTC 25078 C T____
 TGGCCC AGG GGTCTGCGG TCAGGT
 || ||||| |||||
 TCT CCGGTGCC GGTCCG
 _ CCGACT
 GAM1958 PTK6 3' ACCTGAAAGTTTTTTTGGTTT 12595 CG TC GG
 GGGCCAGG G GC TTCAGGT
 ||||| | || |||||

TTTGGTTT T TG AAGTCCA
 TT __ A_
 GAM1958 RA-GEF-2 3' ATTTGAATTGTTGTGGTTTTGT 18461 C G TC
 TT GGGC AGGC G GCGGTT CAGGT
 |||| |||| | |||||
 TTTG TTTG T TGTTAAGTTTA
 T G GT
 GAM1958 RAB34 5' GCCGCGGGTGATCGTCGGGTCT 25682 A ____
 GGGCC GGCGGTC GCGGT
 |||| ||||| ||||
 TCTGG CTGCTAG CGCCG
 G TGGG
 GAM1958 RAB3D 3' GCCGTGGCTGCCAGGTTC 10496 A
 GGGCC GGCGGTCGCGGT
 |||| |||||
 CTTGG CCGTCGGTGCCG
 A
 GAM1958 RALGPS1A 3' CCTAGAGGCTGCTTGCCCC 16018 GCGGT _
 GGGCCAGGCGGTC TC AGG
 ||||| ||||
 CCCGGTTCGTCGG AG TCC
 ____ A
 GAM1958 RASSF2 3' ACTTGATTCAACGTTTGGTTC 16387 GTCGC GT
 GGGCCAGGCG G TCAGGT
 ||||| | ||||
 CTTGGTTTGC C AGTTCA
 AA__ TT
 GAM1958 RASSF2 3' GCTTGGACCTGGGTGCCTGGCT 16395 G C
 GGCCAGGCG TCG GGTT CAGGT
 ||||| || |||||
 TCGGTCCGT GGT CCAGGTT CG
 G _
 GAM1958 RCD-8 3' ACCTTGACTGCCAGGCC 15640 A C
 GGGCC GGCGGTCG GGT
 |||| ||||| |||
 CCCGG CCGTCAGT CCA
 A T
 GAM1958 RLUCL 3' GCCTGGGAGACCCATCTGGTCC 27755 C_ GCGGT
 GGGCCAGG GGTC TCAGGT
 ||||| ||| |||||
 CCTGGTCT CCAG GGTCCG
 AC AG__
 GAM1958 ROBO4 3' TACCTGGGCTGTGGTGTGTGGG 21135 _GG____
 TCTTGGCCT G C TCGCGGTT CAGGT A
 || ||||| |||
 C G GGTGTCGGGTCCA T
 T GGTGTGT
 GAM1958 SAD1 5' CTGAGTCGCGGGGCAGCTC 32009 CAG GG GT
 GGGC GC TCGCG TCAG
 ||| || |||| |||

		CTCG CG GGCGC AGTC	
		A__ G_ TG	
GAM1958	SAST	5' GCCGGTGGTCTCTGGCCT 31541	C GT _
		GGGCCAGG G CGC GGT	
		TCCGGTCT C GTG CCG	
		_TG G	
GAM1958	SCAMP-4	3' CCTGGGGAGTTCCTGGTCC 27821	CGGTC GG
		GGGCCAGG GC TTCAGG	
		CCTGGTCC TG GGGTCC	
		T____ AG	
GAM1958	SCAMP5	3' GCCTGAGCCAATGTGTCTGTCT 29076	T ____
		AGGCGG CGC GGTTCAGGT	
		TCTGTC GTG CCGAGTCCG	
		T TAA	
GAM1958	SCAMP5	3' GCTTGGGCCTGAGAGTTTGATC 29077	GC GG C
	T	GG CAGGC TCG GGTTCAGGT	
		TC GTTTG AGT CCGGGTTTCG	
		TA AG _	
GAM1958	SCYD1	3' ACCTGATTGTGTCTCTTGGTCC 43708	C T T
		GGGCCAGG GG CGCGGT CAGGT	
		CCTGGTTC TC GTGTTA GTCCA	
		_ T _	
GAM1958	SDC3	3' GCTTGGGCTCCAGGCACTGGCT 16087	GCG GC_
	T	GGGCCAG GTC GGTTCAGGT	
		TTCGGTC CGG TCGGGTTTCG	
		A__ ACC	
GAM1958	SEF	3' TTTGGTTGGCCTTCTGGTCT 34427	C CGGT
		GGGCCAGG GGTCG TCAGG	
		TCTGGTCT CCGGT GGTTT	
		T T__	
GAM1958	SEMA4B	3' GCTTGGGCTGCGTGCGTTCTGC 34226	CA GT
	CT	GGGC GGCG CGCGGTTTCAGGT	
		TCCG TTGC GCGTCGGGTTTCG	
		TC GT	
GAM1958	SEMA4F	3' CTGGAAGACTGTTGTGGCCT 10457	_ GCGG
		GGGCCA GGCGGTC TTCAG	
		TCCGGT TTGTCAG AGGTC	
		G A__	
GAM1958	SEMA4G	5' GCCTGAGCCCCGGCCTGGCTC 45412	GGT C
		GGGCCAGGC CG GGTTCAGGT	

CTCGGTCCG GC CCGAGTCCG
 ____ C
 GAM1958 SEMA5A 3' GCCTGGAAGTCCACCTGTCTGG 10104 _ C_ GG
 TCC GGCCAGGC GGT GC TTCAGGT
 ||||| || || |||||
 CTGGTCTG CCA TG AGGTCCG
 T CC A_

GAM1958 SEMA5A 5' GGCCAGCCGCGGCCCTTGGCCC 10106 C CA
 GGGCCAGG GGTCGCGGTT GGT
 ||||| ||||| |||||
 CCCGGTTC CCGGCGCCGA CCG
 _ _ GA

GAM1958 SEMA7A 3' GCCGCAGGCGGCTGCTGGGCC 9665 A G_ TCA
 GGGCC GGCGGTCGC GT GGT
 |||| ||||| || |||||
 CCCGG TCGTCGGCG CG CCG
 G GA _

GAM1958 SEP15 3' ATCTGAATTTGGAATTCTTCTG 10452 C _ GC
 GTTT GGCCAGG GG TC GGTTCAAGT
 ||||| || || |||||
 TTGGTCT CT AG TTAAGTCTA
 T TA GT

GAM1958 SERF1B 3' TCTGAAATGAGGTCTCCTGGCC 23260 C GT G G GT
 C GGGCCAGG G C CG TTCAG
 ||||| | || |||||
 CCCGGTCC C G GT AAGTC
 T TG A A TG

GAM1958 SFRS12 5' CTTGATATCGTTTGGTTC 29177 CGCGGT
 GGGCCAGGCGGT TCAGG
 ||||| |||||
 CTTGGTTTGCTA AGTTC
 T_

GAM1958 SHANK3 5' GCCTGGATTCTGTGCCTGCTC 32634 C GTCGC
 GGGC AGGCG GGTTCAAGT
 |||| ||||| |||||
 CTCG TCCGT TTAGGTCCG
 _ GTCC_

GAM1958 ShrmL 3' ATCTGGGTTATTGGTGTGTTTGT 21911 GC GTCGC TT
 CC GG CAGGCG GG CAGGT
 || ||||| || |||||
 CC GTTTGT TT GTCTA
 TT GGTTA GG

GAM1958 SLC12A5 3' ATCTGGGCCAGATTGTCTGGT 21852 GC
 T GGCCAGGCGGTC GGTTCAAGT
 ||||| ||||| |||||
 TTGGTCTGTAG CCGGGTCTA
 AC

GAM1958 SLC26A10 5' TGAACCCCTTTGGCCT 28562 C TCGC
 GGGCCAGG GG GGTTC
 ||||| || |||||

TCCGGTTT CC CCAAGT

GAM1958 SLC38A5 5' CTGAGTTGCGGCCACTTCA 27297 C C GG
C AGG GGTCGC TTCAG

I III IIIII IIIII

A TTC CCGGCG GAGTC

C A TT

GAM1958 SLC38A5 5' TTGGGGAGCTGTCTGGCTC 27299 ___ G

GGGCCAGGCGGT C CGG

IIIIIIIIII I III

CTCGGTCTGTCTG G GTT

AG G

GAM1958 SLIT1 5' TCAGCGGCTGCTGCCGTCTGGC 9031 C CAGGT

TC

GGGCCAGGCGGT GCGGTT

IIIIIIIIII IIIII

CTCGGTCTGCCG CGTCGG

T CGACTG

GAM1958 SNAP29 3' TCTGAGCACAGTAGCCTGGCCC 11188 GGTCGCG GT

GGGCCAGGC GTTCAG

IIIIIIII IIIII

CCCGGTCCG CGAGTC

ATGACA_ TG

GAM1958 SNAP91 3' CTGTGCTGATGGCTTGGCTT 16870 G GC T

GGGCCAGGC GTC GGT CAG

IIIIIIII III III III

TTCGGTTCTG TAG TCG GTC

G _ T

GAM1958 SNPH 3' ATCTGCCAAGGTTGCTTGCCC 16287 C GT GC TT

GGGC AGGCG C GG CAGGT

III IIIII I II IIIII

CCCG TTCGT G CC GTCTA

_ TG AA _

GAM1958 SNPH 3' GCTTGAGTTGCCCATAGGCC 16299 AGGC TC GG

GGGCC GG GC TTCAGGT

IIII II II IIIIIII

CCCGG CC CG GAGTTCG

ATA_ _ TT

GAM1958 SOX7 3' GTCTGAACTGCGGCCCCAGAGC 25452 CA_ C GT

CT

GGGC GG GGTCGCGGTTTCAG

III II IIIIIIIIIII

TCCG CC CCGGCGTCAAGTC

AGA _ TG

GAM1958 SPTLC2 3' GCCTGGATACTTACCTGGCCC 11282 CG TCGCG

GGGCCAGG G GTTCAGGT

IIIIII I IIIIIII

CCCGGTCC T TAGGTCCG

AT CA_

GAM1958 SSH2 3' CTTGAGCTGAACCTGGTC 31183 CGGTCTG

GGCCAGG CGGTTCAGG

IIIIII IIIIIIIII

CTGGTCC GTCGAGTTC
AA____

GAM1958 STAM2 5' GCCGTAGCGGCCGCTGACCC 12459 C GGTTCAGGTCAGGTCGC GGT
||| ||||| |||
CCC GTCCGCCGGCG CCG
A ATG____

GAM1958 STARD7 5' GCCTGAGCTGTCTGTCTCGTTT 21359 C TC
GGGC AGGCGG GCGGTTTCAGGT
||| ||||| |||||
TTTG TCTGTC TGTCGAGTCCG
C ____

GAM1958 STARD7 5' GCCTGAGCTGTCTGTCTCGTTT 29261 C TC
GGGC AGGCGG GCGGTTTCAGGT
||| ||||| |||||
TTTG TCTGTC TGTCGAGTCCG
C ____

GAM1958 STAT5A 3' CCTTGCTTGGCTGCTTGGCCT 9127 C TC T
GGGCCAGGCGGTTCG GGT AGG
||||||| ||| |||
TCCGGTTCGTCCGT TCG TCC
_ T_ T

GAM1958 STIM2 5' GCCTCGACTCCTGGCCC 21914 C C
GGGCCAGG GGTTCG GGT
||||| ||||| |||
CCCGGTCC TCAGC CCG
_ T

GAM1958 STOML1 3' GCCTGACAGCAGCTGGTTTGGT 11232 _ C GGT
CC GGGCCAGGCG GGT GC TCAGGT
||||||| ||| ||| |||||
CCTGGTTTG TCG CG AGTCCG
G A AC_

GAM1958 SYT13 3' GCCTGAGCCACCGCGCCCGGCC 44891 A GT C_
T GGGCC GGCG CG GGTTCAGGT
||||| ||| ||| |||||
TCCGG CCGC GC CCGAGTCCG
C _ CA

GAM1958 TA-PP2C 3' ATTTGAGTAAGTGTGAGGCTT 29282 A CG GGT
GGGCC GGCGGT C TCAGGT
||||| ||||| | |||||
TTCGG CTGTCA G AGTTTA
A AT ____

GAM1958 TBC1D2 5' TGCTTGAACCTTCCCAGCGCTT 20468 T _____
GTCTGGCTT GCGG CGC GGTTCAGGT G
||| ||| ||||| |
TGTT GCG CCAAGTTCG T
C ACCCTT

GAM1958 TCL6 5' ATTTGAACCCAGGTCTCGTCT 14842 C GGTCGC
GGGC AGGC GGTTCAGGT
||||| |||||

			TCTG TCTG CCAAGTTTA		
			C GAC__		
GAM1958	TCL6	3'	GGCTGCTGGCTGTCTGGCTT 14844		—
			GGGCCAGGCGGTC GCGGTT		
			TTCGGTCTGTCGG CGTCGG		
			T		
GAM1958	TCL6	5'	ATTGAACCCAGGTCTCGTCT 21759	C	GGTCGC
			GGGC AGGC GGTTCAGGT		
			TCTG TCTG CCAAGTTTA		
			C GAC__		
GAM1958	TCL6	5'	ATTGAACCCAGGTCTCGTCT 21768	C	GGTCGC
			GGGC AGGC GGTTCAGGT		
			TCTG TCTG CCAAGTTTA		
			C GAC__		
GAM1958	TCL6	5'	ATTGAACCCAGGTCTCGTCT 15765	C	GGTCGC
			GGGC AGGC GGTTCAGGT		
			TCTG TCTG CCAAGTTTA		
			C GAC__		
GAM1958	TCL6	3'	GGCTGCTGGCTGTCTGGCTT 15768		—
			GGGCCAGGCGGTC GCGGTT		
			TTCGGTCTGTCGG CGTCGG		
			T		
GAM1958	TIAF1	5'	CCTGCTGGTTCTTGGCCC 27798	CGGT	CG TT
			GGGCCAGG CGG CAGG		
			CCCGGTTC GTC GTCC		
			TTG__		
GAM1958	TIP-1	3'	GCTTCTGCTGACCGCTGGGCCC 15969	A	— TTC
			GGGCC GCGGTC GCGG AGGT		
			CCCGG TCGCCAG CGTC TTCG		
			G T		
GAM1958	TOR2A	3'	ATCTGAGTCTCAGCCTGGGTCC 28217		— GGTCGC GT
			GGGCC AGGC G TCAGGT		
			CCTGG TCCG C AGTCTA		
			G ACT__ TG		
GAM1958	TRAF3	3'	GCCTGGAAGCCTGACCCTCTGG 30046	C	C —
	TTC		GGCCAGG GGTCG GGT TCAGGT		
			TTGGTCT CCAGT CCG GGTCCG		
			C — AA		
GAM1958	TRAF3	3'	GCTTGGGGTGCTGCTTG 30047	T	GG
			CAGGCGG CGC TTCAGGT		

GTTCGTC GTG GGGTTTCG
 _ G_
 GAM1958 TRAF3 5' TTTGAACCGGTCTGTCT 30049 TCG
 AGGCCG CGGTTTCAGG
 ||||| |||||
 TCTGTC GCCAAGTTT
 TG_
 GAM1958 TRAF3 5' CCGCGGCGGCCCGCGGCTC 9303 A G TCA
 GGGCC GGCGGTCGC GT GG
 ||||| ||||| || ||
 CTCGG CCGCCGGCG CG CC
 _ G _
 GAM1958 TREX1 5' TCTGGCACCACTGCCCTGGTCC 18522 _ CGC _ GT
 GGGCCAGG CGGT GGT TCAG
 ||||| |||| || ||||
 CCTGGTCC GTCA CCA GGTC
 C _ C TG
 GAM1958 TREX1 5' TCTGGCACCACTGCCCTGGTCC 27342 _ CGC _ GT
 GGGCCAGG CGGT GGT TCAG
 ||||| |||| || ||||
 CCTGGTCC GTCA CCA GGTC
 C _ C TG
 GAM1958 TREX1 5' TCTGGCACCACTGCCCTGGTCC 27349 _ CGC _ GT
 GGGCCAGG CGGT GGT TCAG
 ||||| |||| || ||||
 CCTGGTCC GTCA CCA GGTC
 C _ C TG
 GAM1958 TRIM16 5' ACTTGGGCTGCACAGATCCTGG 13195 G CG_ C
 GCC G CCAGG GT GCGGTTTCAGGT
 | |||| || |||||
 C GGTCC CA CGTCGGGTTC
 G TAGA _
 GAM1958 TSPEAR 3' GCCCCAGTGACGGTCTGGTCT 29598 G _ TTCA
 GGGCCAGGC GTCGC GG GGT
 ||||| |||| || ||
 TCTGGTCTG CAGTG CC CCG
 G A _
 GAM1958 TTC4 3' ACCTGAGCGGCACCTGGTCT 32958 CG GGT
 GGGCCAGG GTCGC TCAGGT
 ||||| |||| |||||
 TCTGGTCC CGGCG AGTCCA
 CA _
 GAM1958 TTTY2 5' ATTTGGA CTTGCCTTTGTCTTG 42069 _ TC _
 GTTC GGCCAGG CGG GCG GTTCAGGT
 ||||| || || |||||
 TTGGTTC GTT CGT CAGGTTTA
 T TC T
 GAM1958 TTTY2 5' TCTGGAAACTCCTGGTTT 42073 C CGCGG
 GGGCCAGG GGT TTCAGG
 ||||| || |||||

TTTGGTCC TCA AGGTCT
 _ AA_
 GAM1958 TTYH2 3' CCTGAGCTGGCTGCCTGGCCC 26377 GC T
 GGGCCAGGCGGTC GGTTCAGG
 |||||
 CCCGGTCCGTCGG TCGAGTCC
 _ C
 GAM1958 U5-116KD 3' CTTGGGAGTTGTTGGGTTC 10439 AG GTC GG
 GGGCC GCG GC TTCAGG
 |||| ||| || |||||
 CTTGG TGT TG GGGTTC
 GT _ A_
 GAM1958 UBAP 5' ACGGTGACGGCCTGGCCC 37535 G G
 GGGCCAGGC GTCGC GT
 ||||| ||||| ||
 CCCGGTCCG CAGTG CA
 G G
 GAM1958 UHRF1 3' GCTTGGGAACCGTTTGAGCCT 14952 _ CGCGG
 GGGC CAGGCGGT TTCAGGT
 ||| ||||| |||||
 TCCG GTTTGCCA GGGTTCG
 A A_
 GAM1958 VI 3' ACCTGGGTTCTGTCCCCTGGCT 15105 C T CG TT
 C
 GGGCCAGG GG CG G CAGGT
 ||||| || || | |||||
 CTCGGTCC CC GT T GTCCA
 _ T CT GG
 GAM1958 VMP1 3' CCTGGGGATTCTTGTGTTT 25205 CG GCGG
 GGGCCAGG GTC TTCAGG
 ||||| ||| |||||
 TTTGGTTC TAG GGGTCC
 TT _
 GAM1958 VPS39 3' TCTGGGCCAGCTTGGA CT 31473 _ GGTCGC
 GGG CCAGGC GGTTCAGG
 ||| ||||| |||||
 CTC GGTTCC CCGGGTCT
 A A_
 GAM1958 WDR5B 5' GCCAAAGTACTGGACTGCCTGG 21148 G TCA_
 TTC
 GGCCAGGCGGTC CGGT GGT
 ||||| ||||| |||
 TTGGTCCGTCAG GTCA CCG
 _ TGAAA
 GAM1958 ZDHC1 5' CTGGGTCTGGCCTGGCC 38079 GGT C TT
 GGCCAGGC CG GG CAG
 ||||| || || |||
 CCGGTCCG GT CT GTC
 _ _ GG
 GAM1958 ZDHC3 3' CTTCTCTGGCCTCTGGTTT 18686 C C TTC
 GGGCCAGG GGTCG GG AGG
 ||||| ||||| || |||

TTTGGTCT CCGGT TC TTC
 — C —
 GAM1958 ZF 3' ACCTGAATTGGTCTTTGGTTT 22188 C GT CG
 GGGCCAGG G CG GTTCAGGT
 ||||||| I II |||||||
 TTTGGTTT C GT TAAGTCCA
 — TG —
 GAM1958 ZFD25 5' GCCTGAGTCTCTCCTGCCTGCC 18323 C TCGC GT
 T GGGC AGGCGG G TCAGGT
 ||| ||||| I |||||
 TCCG TCCGTC C AGTCCG
 — CTCT TG
 GAM1958 ZFP95 3' GTTTCTGCTGACTTGCCTGGCT 15922 — — TTCAGGT
 T GGGCCAGGCG GTC GCGG
 ||||||| ||| |||
 TTCGGTCCGT CAG CGTC
 T T TTTG
 GAM1958 ZFP95 3' GTTTCTGCTGACTTGCCTGGCT 29712 — — TTCAGGT
 T GGGCCAGGCG GTC GCGG
 ||||||| ||| |||
 TTCGGTCCGT CAG CGTC
 T T TTTG
 GAM1958 ZNF-U69274 3' TCTGTGTGACTGTCTGCTT 15762 C GTT
 GGGC AGGCGGTCGCG CAGG
 ||| ||||||||| |||
 TTCG TCTGTCAGTGT GTCT
 — —
 GAM1958 ZNF197 3' ACCTTTGATTCCTGGCTT 13854 C C_
 GGGCCAGG GGTCG GGT
 ||||||| ||||| |||
 TTCGGTCC TTAGT CCA
 — TT
 GAM1958 ZNF213 3' ATTTGACTGTGTGGCTCTTTGG 32462 C GT_
 CCC GGGCCAGG GGTCGCG TCAGGT
 ||||||| ||||||| |||||
 CCCGGTTT TCGGTGT AGTTTA
 C GTC
 GAM1958 ZNF213 5' GCCTCTGGCCGCCTGGCTC 32464 C_
 GGGCCAGGCGGTCTG GGT
 ||||||| ||||| |||
 CTCGGTCCGCCGGT CCG
 CT
 GAM1958 ZNF294 3' ATCTTGGCTTCTGGCCC 35055 C C
 GGGCCAGG GGTCG GGT
 ||||||| ||||| |||
 CCCGGTCT TCGGT CTA
 — T
 GAM1958 ZNF340 5' CTGTGGTGCACCGCCTGGCTT 41034 C GTT
 GGGCCAGGCGGT GCG CAG
 ||||||| ||||| |||

TTCGGTCCGCCA CGT GTC
_ GGT
GAM1958 LOC114987 3' TCTGGGTCTGCCTGACTC 29755 C TCGCG TT
GGG CAGGCCG G CAGG
||| ||||| | |||
CTC GTCCGTC T GTCT
A _ GG
GAM1958 LOC115123 5' GCCGCGGCGGCCGCCAGGCTT 36247 A G TCA
GGGCC GGCGGTTCGC GT GGT
||||| ||||| || |||
TTCGG CCGCCGGCG CG CCG
A G _
GAM1958 LOC121642 5' ACTTGAGCAATTTCTGTCTTGG 36674 _ TCGCG
CCT GGGCCAGG CGG GTTCAGGT
||||| ||| |||||
TCCGGTTC GTC CGAGTTCA
T TTAA
GAM1958 LOC122416 5' ACCTGAGTTCTAGGCCTGGCTC 36682 GGTCGCGG
GGGCCAGGC TTCAGGT
||||| |||||
CTCGGTCCG GAGTCCA
GATCTT_
GAM1958 LOC122525 5' GCCTGGGCGCTGGAGCTGCTGT 37422 _ C_ G
GGCTC CA GGCGGT GCG TTCAGGT
|| ||||| || |||||
GT TCGTCG CGC GGGTCCG
G AGGT _
GAM1958 LOC124044 3' GTCTGGGCCTCTGGTTGCCTTG 37433 C GT C_ GT
TCC GGGC AGGCG CG GGTTCA
||||| ||| |||||
CCTG TCCGT GT CCGGGTC
T TG CT TG
GAM1958 LOC124460 5' CAGGGTGGACTGTGACCCCTTG 37444 C GGT
GCCT GGGCCAGG GGTCGCGGTTCA
||||| |||||
TCCGGTTC CCAGTGTCAAGGT
C GGGACT
GAM1958 LOC126917 3' ACTTGGGTCCCTCTGCCTTGCC 36866 C TCGC TT
T GGGC AGGCGG GG CAGGT
||||| ||| |||||
TCCG TCCGTC CT GTTCA
T TCC_ GG
GAM1958 LOC126917 3' GCCTCCCTGACCGCTTGCTT 36872 C C TTC
GGGC AGGCGGTTCG GG AGGT
||||| ||||| |||
TTCG TTCGCCAGT CC TCCG
_ C _
GAM1958 LOC127703 5' GCCTGGACCGCGGAGACGCC 36909 G_
GGCG TCGCGGTTCAAGT
||||| |||||

		CCGC GGCGCCAGGTCCG		
		AGA		
GAM1958	LOC132332 3'	CTTGGTATCCCCTGGTCT 37487	C TC	GGTT
		GGGCCAGG GG GC CAGG		
		TCTGGTCC CC TG GTTC		
		_ TA _		
GAM1958	LOC133634 3'	GCCTGAGCTCACTTGTGTGGC 37049	_ TCGC	
	CT	GGGCCA GGCGG GGTTCAGGT		
		TCCGGT TTGTT TCGAGTCCG		
		G CAC_		
GAM1958	LOC135398 3'	CCTGAAACTCCTTGGCTT 37386	C CGCGG	
		GGGCCAGG GGT TTCAGG		
		TTCGGTTC TCA AAGTCC		
		C _		
GAM1958	LOC135763 3'	GCCTGAAGCCTTCCTCTGGCTT 28883	C TCGC	_
		GGGCCAGG GG GGTT CAGGT		
		TTCGGTCT CC CCGA GTCCG		
		_ TT_ A		
GAM1958	LOC138617 5'	GCTTCGGCTTTTGGCCT 37396	C C	
		GGGCCAGG GGTCG GGT		
		TCCGGTTT TCGGC TCG		
		_ T		
GAM1958	LOC142927 3'	ATCTTGATCTTTGGCTT 37565	C C	
		GGGCCAGG GGTCG GGT		
		TTCGGTTT CTAGT CTA		
		_ T		
GAM1958	LOC143381 3'	ACTTCGGCTGTCTGCCT 37611	C C	
		GGGC AGGCGGTCG GGT		
		TCCG TCTGTCGGC TCA		
		_ T		
GAM1958	LOC143914 5'	GCCTGCACAGATCTCTGGTTC 37636	C GCG T	
		GGGCCAGG GGTC GT CAGGT		
		CTTGGTCT CTAG CA GTCCG		
		_ A_ C		
GAM1958	LOC144305 3'	CTTGAGCCCAGGCTGGTCT 40400	GGCG GC	
		GGGCCA GTC GGTTCAGG		
		TCTGGT CGG CCGAGTTC		
		_ AC		
GAM1958	LOC144373 3'	GCCTGGATTTGTATCCTTGGCT 37729	C C _	
	T	GGGCCAGG GGT GCGG TTCAGGT		

TTCGGTTC CTA TGTT AGGTCCG
 _ _ T
 GAM1958 LOC144577 3' ACTTGGGTTTCATGCCTGCCC 37768 C GTCGC TT
 GGGC AGGCG GG CAGGT
 |||| |||| || ||||
 CCCG TCCGT TT GTTCA
 _ ACT_ GG
 GAM1958 LOC144893 3' ATTTGAGTTGTGAAAAAGGTCT 40457 AGGCGG GG
 GGGCC TCGC TTCAGGT
 |||| |||| ||||
 TCTGG AGTG GAGTTTA
 AAAA_ TT
 GAM1958 LOC145195 3' GCCTGAACCATGCTCACTTCTG 40515 C C_ _
 GTCC GCCAGG GGT GC GGTTCAGGT
 |||| || || ||||
 TGGTCT TCA CG CCAAGTCCG
 _ CT TA
 GAM1958 LOC145438 5' GCCGGGGGCGGCTGTTTGGCCT 40536 GG A
 GGGCCAGGCGGTTCG TTC GGT
 |||| |||| || ||||
 TCCGGTTTGTCCGCG GGG CCG
 _ G
 GAM1958 LOC145608 5' ACCTGGAAATCAGCCTGGCTT 40541 GGTCGCGG
 GGGCCAGGC TTCAGGT
 |||| ||||
 TTCGGTCCG AGGTCCA
 ACTAA_
 GAM1958 LOC145678 3' ACTTGAAAGGTGTGCTTGGTTT 40552 GT GG
 GGGCCAGGCG CGC TTCAGGT
 |||| || || ||||
 TTTGGTTCGT GTG AAGTTCA
 _ GA
 GAM1958 LOC145815 5' ACCGTGTTCTGTGGCCGACCTGG 40600 _ TTCA
 CCT GGGCCAGG CGGTCGCGG GGT
 |||| |||| || ||||
 TCCGGTCC GCCGGTGCT CCA
 A TGTG
 GAM1958 LOC145820 3' ATTTGGGTTGTTTCCAGGTTT 37990 AGGC TC TT
 GGGCC GG GCGG CAGGT
 |||| || || || ||||
 TTTGG CC TGTT GTTTA
 A_ TT GG
 GAM1958 LOC145826 5' ATCTGAATTCTTGTCTGGT 40609 TCGC
 GCCAGGCGG GGTTCAGGT
 |||| |||| || ||||
 TGGTCTGTT TTAAGTCTA
 C_
 GAM1958 LOC145989 3' GCCTGGGCTGCGGATGCCTGGG 29953 G GT
 CC GG CCAGGCG CGCGGTTTCAGGT
 || |||| |||| |||| ||||

CC GGTCCGT GCGTCGGGTCCG
 G AG
 GAM1958 LOC146050 3' TCTGAATTTCTGTCTGTCT 38057 T CG
 AGGCCG CG GTTCAGG
 ||||| || |||||
 TCTGTC GC TAAGTCT
 T TT
 GAM1958 LOC146108 5' ACCTGGGCCGTGATTGGGCGC 38059 G AGG
 G GCC CGGTCGCGGTTCAGGT
 | || |||||
 C CGG GTTAGTGCCGGGTCCA
 G _
 GAM1958 LOC146108 5' ACTTGGAGAGCAAGCTGTTTGA 38060 _ C_ GG
 GTCT GGC CAGGCGGT GC TTCAGGT
 || ||||| || |||||
 CTG GTTTGTCTG CG AGGTTCA
 A AA AG
 GAM1958 LOC146435 5' ACCTGAGCACGTCTTGCCCTGAG 38153 _ TC _
 TCC GGC CAGGCGG GCG GTTCAGGT
 || ||||| || |||||
 CTG GTCCGTT TGC CGAGTCCA
 A C_ A
 GAM1958 LOC146445 3' TGGATCTGGCCTGGC 40698 GGT C
 GCCAGGC CG GGTTCA
 ||||| || |||||
 CGGTCCG GT CTAGGT
 _ _
 GAM1958 LOC146455 5' GCTTTGACTATTTGGCCT 38158 CG C
 GGGCCAGG GTCG GGT
 ||||| |||||
 TCCGGTTT CAGT TCG
 AT T
 GAM1958 LOC146488 5' GCTGTTGCTGCTTGGTCT 35047 C
 GGGCCAGGCGGT GCGGT
 |||||
 TCTGGTTCTGTCG TGTCG
 T
 GAM1958 LOC146488 5' GCTTGGAGTGCTGCTGCCTGGC 35048 C G
 GCCAGGCGGT GCG TTCAGGT
 ||||| || |||||
 CGGTCCGTCG CGT AGGTTCTG
 T G
 GAM1958 LOC146488 3' TCTGGGCTGCTAACCTGGCCT 35049 CGGTC GT
 GGGCCAGG GCGGTTCAG
 ||||| |||||
 TCCGGTCC CGTCGGGTC
 AAT_ TG
 GAM1958 LOC146540 3' ACCTGGATTCTAGCTTGGCTC 38197 GGTCGC
 GGGCCAGGC GTTCAGGT
 ||||| |||||

	CTCGGTTTCG	TTAGGTCCA		
	ATCC__			
GAM1958	LOC146669	3' GCTTGGGCCCCAGGTCTGTCT 38225	_ GC	
		AGGCCG TC GGTTCAGGT		
		TCTGTC GG CCGGGTTCG		
		T AC		
GAM1958	LOC146756	3' CTGAGTCTGGGTCTGGGTC 40735	G GG C GT	
		GG CCAGGC TCG G TCAG		
		CT GGTCTG GGT C AGTC		
		G _ _ TG		
GAM1958	LOC146756	3' GCTTGGGTCTGAGTCTGGGTC 40738	G GG C TT	
		GG CCAGGC TCG GG CAGGT		
		CT GGTCTG AGT CT GTTCG		
		G _ _ GG		
GAM1958	LOC146823	3' CCTGACAGTCCCTTGTTTC 40746	C TC GGT	
		GGGCCAGG GG GC TCAGG		
		CTTGTTTC CC TG AGTCC		
		_ _ AC_		
GAM1958	LOC146839	5' GCCTGATGGTGACTGTTGTTT 40756	G G T	
		GGGCCAG CGGTCGC GT CAGGT		
		TTTGTT GTCAGTG TA GTCCG		
		_ G _		
GAM1958	LOC146990	5' GCCTGGACCGTTGGAGTGGGTC 40776	AG GGTC	
	C	GGGCC GC GCGGTTTCAGGT		
		CCTGG TG TGCCAGGTCCG		
		G_ AGGT		
GAM1958	LOC147054	5' GCCCCAGCTGTTGCCTGGCTT 40794	GTC CA	
		GGGCCAGGCG GCGGTT GGT		
		TTCGGTCCGT TGTCGA CCG		
		_ CC		
GAM1958	LOC147057	3' GCTTGAGTCGTGAGGGCCTGG 40784	GG GT	
		CCAGGC TCGCG TCAGGT		
		GGTCCG AGTGC AGTTCG		
		GG TG		
GAM1958	LOC147077	3' TTGTGGCTGGTCTGGCTT 38297	_	
		GGGCCAGGC GGTCGCGG		
		TTCGGTCTG TCGGTGTT		
		G		
GAM1958	LOC147136	3' GTTTGAACTGCTCCTCCCTGGC 38305	C TC GG	
	CT	GGGCCAGG GG GCGGTTCA T		

TCCGGTCC TC CGTCAAGT G
 C CT TT
 GAM1958 LOC147160 5' GCTTGAGCCGCCGGCCTTGTC 40810 C GGTC
 C GGGC AGGC GCGGTTCAAGT
 |||| ||| |||||
 CCTG TCCG CGCCGAGTTCG
 T GGC_

GAM1958 LOC147353 3' ACCGTGGCCTCTGGTTT 40833 C
 GGGCCAGG GGTCGCGGT
 ||||| |||||
 TTTGGTCT CCGGTGCCA

GAM1958 LOC148114 5' GCCAGCGGCTGTTTGTTC 38467 GC _
 GG CAGGCGGTCGC GGT
 || ||||| |||
 CC GTTGTGCGGCG CCG
 TT A

GAM1958 LOC148479 3' GCTTGAACCGTAATTTGGCT 38542 GCG CG
 GGCCAG GT CCGTTCAGGT
 |||| || |||||
 TCGGT TA GCCAAGTTCG
 _ AT

GAM1958 LOC148603 5' ACCTTGCTGTGATTGGCTTGG 38568 _ TC
 TTC GGGCCAGGC GGTCGCGGT AGGT
 ||||| ||||| |||
 CTTGGTTCG TTAGTGTCG TCCA
 G GT

GAM1958 LOC148697 3' AATGATGGTTGTCTGGTTT 38570 GT CG
 GGGCCAGGCG CG GTT
 ||||| || |||
 TTTGGTCTGT GT TAA
 TG AG

GAM1958 LOC148809 5' ATCTGAGTTTCTTTGGCTTCTG 38592 C C _
 GCTC GCCAGG GGTCG GG TTCAGGT
 |||| |||| || |||||
 CCGTCT TCGGT TC GAGTCTA
 _ T TTT

GAM1958 LOC148894 3' ACTGAGGTGTGACTGTTTGGAC 40915 _ G GT
 CC GGG CCAGGCGGTGCGG TTCAG
 || ||||| |||||
 CCC GGTTTGTCAAGTGT GAGTC
 A G A

GAM1958 LOC148894 5' GACCTGGCTCCTGGCTT 40918 C C
 GGGCCAGG GGTCG GGTT
 ||||| |||| |||
 TTCGGTCC TCGGT CCAG

GAM1958 LOC149182 5' ACTTGGGCCTGGAGTCTG 40969 GG C
 CAGGC TCG GGTTCAAGT
 |||| || |||||

	GTCTG GGT CCGGGTTCA	
	A_ _	
GAM1958 LOC149271 3'	CCAAGTGATTGCTGGTCC 38680	G _
	GGGCCAG CGGTCGC GG	
	CCTGGTC GTTAGTG CC	
	_ AA	
GAM1958 LOC149332 3'	ACCTGAATTTTATTCTGGCTT 40980	C CGC
	GGGCCAGG GGT GGTTCAGGT	
	TTCGGTCT TTA TTAAGTCCA	
	_ TT_	
GAM1958 LOC149332 5'	GCCTGACATGGTCCCTGGCTC 40981	C GT CG T
	GGGCCAGG G CG GT CAGGT	
	CTCGGTCC C GT CA GTCCG	
	_ TG A_ _	
GAM1958 LOC149372 3'	ATTTGGTGGCAGCTCTTGGTCC 38724	C C GGT
	GGGCCAGG GGT GC TCAGGT	
	CCTGGTTC TCG CG GGTTA	
	_ A GT_	
GAM1958 LOC149421 5'	ATCTGCATTGATTACCTGGTCT 38745	CG CG T
	GGGCCAGG GTCG GT CAGGT	
	TCTGGTCC TAGT TA GTCTA	
	AT _ C	
GAM1958 LOC149501 3'	GCCTGGGCTCCAGCTTTGGCTC 37108	_ _ TCGC
	GGGCCAG GC GG GGTTCAGGT	
	CTCGGTT CG CC TCGGGTCCG	
	T A _	
GAM1958 LOC149684 5'	ATCTGAGTTGGCCAAGCCAGGC 41047	A _ CGG
TC	GGGCC GGC GGTGC TTCAGGT	
	CTCGG CCG CCGGT GAGTCTA	
	A AA T_	
GAM1958 LOC149773 5'	GCTTGGAGTCTACCGACTGTCT 38800	C C_ _
GTCTC	CAGGCGGTGC GG TTCAGGT	
	GTCTGTCAGC CT AGGTTGC	
	T CAT G	
GAM1958 LOC149950 5'	GCCTGAGCTGTGACGGGTGCCC 38840	CAG G_
	GGGC GC GTCGCGGTTTCAGGT	
	CCCG TG CAGTGTGAGTCCG	
	_ GG	
GAM1958 LOC150135 3'	GCCTGGCAGGTCACCTGGCCC 38846	C GT_ GGTT
	GGGCCAGG G C GC CAGGT	

CCGGTCC C G CG GTCCG
 A TG A ____
 GAM1958 LOC150139 5' CCTGGAATTTTTGGCCC 38857 CG CGCGG
 GGGCCAGG GT TTCAGG
 ||||| || |||||
 CCGGT TT TA AGGTCC
 TT ____
 GAM1958 LOC150150 5' ACCGCGTGGCCACTTGGCTT 41133 C ____
 GGGCCAGG GGT CGCGGT
 ||||| || |||||
 TTCGGTTC CCG GCGCCA
 A GT
 GAM1958 LOC150157 5' ACCTTTGCTAGCTGCCTGGTCC 41140 CGC TC
 GGGCCAGGCGGT GGT AGGT
 ||||| || |||||
 CCTGGTCCGTCG TCG TCCA
 A__ TT
 GAM1958 LOC150166 5' GCCTGAGCCCACCGTGCCTGGC 41148 ____ CGC
 CT GGGCCAGGC GGT GTTCAGGT
 ||||| || |||||
 TCCGGTCCG CCA CCGAGTCCG
 TG C__
 GAM1958 LOC150406 3' GCCATGGCTCTTGGCCT 38964 C C
 GGGCCAGG GGTCTG GGT
 ||||| ||||| |||||
 TCCGGTTC TCGGT CCG
 _ A
 GAM1958 LOC150445 3' ACTTTTCCTGCTGCCTGGCCT 38971 T C TTC
 GGGCCAGGCGG CG GG AGGT
 ||||| || || |||||
 TCCGGTCCGTC GT CC TTCA
 _ _ TT_
 GAM1958 LOC150465 5' GCCTTCTCGGCCGCTGGTCC 38973 C TTC
 GGGCCAGGCGGTCTG GG AGGT
 ||||| || || |||||
 CCTGGTCCGCCGGC CT TCCG
 T ____
 GAM1958 LOC150568 5' GCCTGGGTCTAAGCCAGGTCT 41205 A GGTCGC TT
 GGGCC GGC GG CAGGT
 ||||| || || |||||
 TCTGG CCG CT GTCCG
 A AAT__ GG
 GAM1958 LOC150577 3' ATTTGGGCTCTGACATCTGGCC 41215 CG C
 T GGGCCAGG GTCG GTTCAGGT
 ||||| || |||||
 TCCGGTCT CAGT TCGGGTTTA
 A_ C
 GAM1958 LOC150587 3' ACTTGGATTAAACATGTCTGCC 41212 C GTCGC
 T GGGC AGGCG GTTCAGGT
 ||||| || |||||

		TCCG TCTGT TTAGGTTCA		
		— ACAA		
GAM1958	LOC150696 3'	ACCTGGACTCACAGCCTGGCT 29529	G	CGC
		GGCCAGGC GT GGTTTCAGGT		
		TCGGTCCG CA TCAGGTCCA		
		A C_		
GAM1958	LOC150837 3'	GCTTGGGCTGTGGCAAGCT 39015	G_	
		GGC GTCGCGGTTTCAGGT		
		TCG CGGTGTCGGGTTTCG		
		AA		
GAM1958	LOC150886 5'	TGAATGTGACCGCTGTGGTTT 41268	—	G
		GGGCCA GGCGGTCGCG TTCA		
		TTTGGT TCGCCAGTGT AAGT		
		G —		
GAM1958	LOC151361 3'	GCCTTTGGCCGACTGTCTGCTC 41331	C	GC C_
		GGGC AGGCGGTC GGTT AGGT		
		CTCG TCTGTCAG CCGG TCCG		
		— — TT		
GAM1958	LOC151438 3'	GCCTGCCCTGATTGCCTGCCC 41349	C	C TT
		GGGC AGGCGGTCG GG CAGGT		
		CCCG TCCGTTAGT CC GTCCG		
		— — C_		
GAM1958	LOC151457 5'	GCTTGAATTGGATTTGTTGGTT 39116	GC	G
	T	GGGCCAG GGTC CGGTTTCAGGT		
		TTTGGTT TTAG GTTAAGTTTCG		
		GT —		
GAM1958	LOC151568 5'	GCCTGAGTCAGGACACCTGGCT 28838	CG	GC GT
	T	GGGCCAGG GTC G TCAGGT		
		TTCGGTCC CAG C AGTCCG		
		A_ GA TG		
GAM1958	LOC151647 3'	TCTGAGTCCTGATTGGCTT 39158	GGCG	C GT
		GGGCCA GTCG G TCAGG		
		TTCGGT TAGT C AGTCT		
		— C TG		
GAM1958	LOC152286 5'	GTTTGAGCTTCCCCACTGCCTG 41462	C	CGC_ GG
	ACCC	GG CAGGCGGT GGTTCA T		
		CC GTCCGTCA TCGAGT G		
		A CCCCT TT		
GAM1958	LOC152317 5'	ATCTGAGCTGCGGGAGGGCCC 41464	AGGCGG	
		GGGCC TCGCGGTTTCAGGT		

C C C G G G G C G T C G A G T C T A
 G A G _ _
 GAM1958 LOC152343 3' ACCAGCATTGCTTGGCTT 39260 C _
 G G G C C A G G C G G T G C G G T
 ||||| || |||
 T T C G G T T C G T T A C G C C A
 _ A
 GAM1958 LOC152426 5' G C T T C G A C T G T C T C G C C C 41500 C C
 G G G C A G G C G G T C G G G T
 ||| ||||| |||
 C C C G T C T G T C A G C T C G
 C T
 GAM1958 LOC152441 5' T C T G A A C T G C C A T A C T C T G C C C 41506 C C G C G T
 G G G C A G G G T G C G G T T C A G
 ||| || || |||||
 C C C G T C T T A C G T C A A G T C
 _ C A C T G
 GAM1958 LOC152453 5' G C C T G A G A G G T T T C T T G G C T C 39277 C G G T C G G
 G G G C C A G G G C T T C A G G T
 ||||| || |||||
 C T C G G T T C T G G A G T C C G
 T T _ _ G A
 GAM1958 LOC152667 3' T G A A T G T G T T G T T T G G T T C 39300 T G
 G G G C C A G G C G G C G C G T T C A
 ||||| ||| |||
 C T T G G T T T G T T G T G T A A G T
 _ _
 GAM1958 LOC152926 5' G C T T T G A C T G C T T G C T T 39342 C C
 G G G C A G G C G G T C G G G T
 ||| ||||| |||
 T T C G T T C G T C A G T T C G
 _ T
 GAM1958 LOC152992 3' G C C C C C A G C T G A C T G C C T G G C T 39350 _ _ T T C A
 T G G G C C A G G C G G T C G C G G G T
 ||||| || || |||
 T T C G G T C C G T C A G C G C C C C G
 T A C _ _
 GAM1958 LOC153505 3' C C T G A A C G C C A C C T G G C C C 39381 C C G C G
 G G G C C A G G G G T G T T C A G G
 ||||| || |||||
 C C C G G T C C C C G C A A G T C C
 A _ _
 GAM1958 LOC153811 3' G C C T G G G C T T C C A G G C C T G G T T 39417 _ T C G C
 C G G G C C A G G C G G G G T T C A G G T
 ||||| || |||||
 C T T G G T C C G C C T C G G G T C C G
 G A T _ _
 GAM1958 LOC153914 5' A C C T G G G C T G C G A C G T G G 39434 G G C G
 C C A G T C G C G G T T C A G G T
 ||| |||||

GGT CAGCGTCGGGTCCA
G____
GAM1958 LOC154007 3' ATTTGGATCAGATTGGCTGTTA 39452 AG C____
GGCTT CC GCGGTCG GGTTCAGGT
|| ||||| |||||
GG TGTCGGT CTAGGTTTA
AT TAGA
GAM1958 LOC154222 3' CTGGGGACTGCCTGTTTC 41691 GC GCGG
GG CAGGCGGTC TTCAG
|| ||||| ||||
CT GTCCGTCAG GGGTC
TT _____
GAM1958 LOC154739 5' CCTGAGCCTGCATGGCCT 41718 G GTCGC
GGGCCA GCG GGTTCAGG
||||| ||| |||||
TCCGGT CGT CCGAGTCC
A _____
GAM1958 LOC154877 5' CCTATCTGGGTCGCTTGGCCT 41741 GT G TTC T
GGGCCAGGCG C CGG AGG
||||||| | ||| |||
TCCGGTTCGC G GTC TCC
TG_ TA_ C
GAM1958 LOC155006 3' CTGAAGAGATTGCCTGGTTC 39525 GCGG
GGGCCAGGCGGTC TTCAG
||||||| ||||
CTTGGTCCGTTAG AAGTC
AG____
GAM1958 LOC155036 5' GCTTGAGTCTGGTCTGAGTCT 41754 _ GGTCG _
GGGC CAGGC CGG TTCAGGT
||||| ||| |||||
TCTG GTCTG GTC GAGTTCG
A _____ T
GAM1958 LOC155434 3' TCTGAGCTGATTCTGTTTGCTC 41772 C TCG GT
GGGC AGGCGG CGGTTTCAG
||||| |||||
CTCG TTTGTC GTCGAGTC
_ TTA TG
GAM1958 LOC155435 3' CCTGGCAGCCCTCTGGCCT 39570 C C GGTT
GGGCCAGG GGT GC CAGG
||||| ||| ||| ||||
TCCGGTCT CCG CG GTCC
C A _____
GAM1958 LOC157273 3' ACTTGAAGTCTGTTTGGCTT 41779 GGT C
GGGCCAGGC CG GGTTCAGGT
||||| || |||||
TTCGGTTTG GT TCAAGTTCA
_____ C
GAM1958 LOC157556 5' ACCTGGATTAAATCCTGGCTT 41820 CCGTCGC
GGGCCAGG GGTTCAGGT
||||| |||||

TTCGGTCC TTAGGTCCA
 TAAAT__
 GAM1958 LOC157623 5' GCTTGGGCTCTGGGTTTGACCC 39616 C GG C
 GGG CAGGC TCG GGTTCAGGT
 ||| |||| ||| |||||
 CCC GTTTG GGT TCGGGTTCG
 A _ C
 GAM1958 LOC157753 3' CCTGAGTCATGATTGGCTC 39660 GGCG C GT
 GGGCCA GTCG G TCAGG
 ||||| ||||| |||||
 CTCGGT TAGT C AGTCC
 _____ A TG
 GAM1958 LOC157860 3' ATCTCTCTCTGTGGCTGTTGGG 41858 AG TTC_
 CCC GGGCC GCGGTCGCGG AGGT
 ||||| ||||| |||
 CCCGG TGTCGGTGTC TCTA
 GT TCTC
 GAM1958 LOC157922 5' CTGTGGTGGGCCTCTGGCCC 41888 C G GTT
 GGGCCAGG GGTC CG CAG
 ||||||| ||||| || |||
 CCCGGTCT CCGG GT GTC
 _ _ GGT
 GAM1958 LOC157927 5' GCCTGGGCTCAGAGTCAGGCTT 41907 A GG GC
 GGGCC GGC TC GGTTCAGGT
 ||||| ||| || |||||
 TTCGG CTG AG TCGGGTCCG
 A _ AC
 GAM1958 LOC158046 5' CTTGAGGTTGCCTGGCT 29800 GT GCGGT
 GGCCAGGCG C TCAGG
 ||||||| | |||||
 TCGGTCCGT G AGTTC
 TG _____
 GAM1958 LOC158308 5' ATCTGCCCTGTGCCGCCTGGTT 41940 T TT
 C GGGCCAGGCGG CGCGG CAGGT
 ||||||| ||||| |||||
 CTTGGTCCGCC GTGTC GTCTA
 _ CC
 GAM1958 LOC158310 5' GCCTGGAAACATGCTTGGCTC 41947 GTCGCGG
 GGGCCAGGCG TTCAGGT
 ||||||| |||||
 CTCGGTTCGT AGGTCCG
 ACAA__
 GAM1958 LOC158427 5' GCCATGACGTGTCTGCTTGGCT 29247 T GT _
 C GGGCCAGGCGG CGCG TCA GGT
 ||||||| ||||| ||| |||
 CTCGGTTCGTC GTGC AGT CCG
 T _ A
 GAM1958 LOC158563 3' GCCTGAACCAGAGCTATGGCTC 39870 _ GG GC
 GGGCCA GGC TC GGTTCAGGT
 ||||| ||| || |||||

CTCGGT TCG AG CCAAGTCCG
A _ A_
GAM1958 LOC158856 5' CCTGAGCCCCGCTCGGCCT 42034 AG TCGC
GGGCC GCGG GGTTCAAG
||||| ||| |||||
TCCGG CGCC CCGAGTCC
CT _
GAM1958 LOC158969 3' ATTTGGGTTGTTACCAGGTTT 39918 AGGC C TT
GGGCC GGT GCGG CAGGT
||||| ||| ||| |||||
TTTGG CCA TGTT GTTTA
A _ T GG
GAM1958 LOC158969 3' CCCACCGCCACTGCTTGGCTT 39920 C TCA T
GGGCCAGGCGGT GCGGT GG
||||||| ||| ||
TTCGGTTCGTCA CGCCA CC
C CC_ T
GAM1958 LOC159148 5' ATTTGGAAGTTCCTTTGTCTTG 42076 _ TC _
GTTC GGCCAGG CGG GCG GTTCAGGT
||||||| ||| ||| |||||
TTGGTTC GTT CGT CAGGTTTA
T TC T
GAM1958 LOC159148 5' TCTGGAAACTCCTGGTTT 42080 C CGCGG
GGGCCAGG GGT TTCAGG
||||||| ||| |||||
TTTGGTCC TCA AGGTCT
_ AA_
GAM1958 LOC159199 5' ACTTGGAAGCGTATGGCCTGGC 39978 G _ GG
CC GGGCCAGGC GT CGC TTCAGGT
||||||| ||| ||| |||||
CCCGGTCCG TA GCG AGGTTCA
G T A_
GAM1958 LOC159723 5' GAACCCCTTGGCTT 39984 C TCGC
GGGCCAGG GG GTTC
||||||| ||| |||||
TTCGGTTC CC CCAAG
_ _
GAM1958 LOC161877 5' TCTGGGGGTTGCTTTGCTT 40042 C GT GCGG
GGGC AGGCG C TTCAGG
||||| ||||| | |||||
TTCG TTCGT G GGTCT
T TG_
GAM1958 LOC163412 5' ACCTGGAAGTGTGGTGGGCTC 39950 AG GGT
GGGCC GC CGCGGTTCAAGT
||||| ||| |||||
CTCGG TG GTGTCAGGTCCA
G_ _
GAM1958 LOC165246 5' ACTTGCTGTATGGCTT 40125 G C
GGGCCA GCGGTCG GGT
||||| ||||| |||

	TTCGGT TGTCGGT TCA	
	A _	
GAM1958 LOC169225 5'	ACCTGGGCCCCAGCGTCAGGCTT 42204	A GTCGC
	GGGCC GGCG GGTTTCAGGT	
	TTCGG CTGC CCGGGTCCA	
	A GAC__	
GAM1958 LOC170425 5'	ATCTGAGTTAGGCTTGGCC 37549	GGT GC GT
	GGCCAGGC C G TCAGGT	
	CCGGTTCG G T AGTCTA	
	__A_TG	
GAM1958 LOC196027 3'	TTGAGACCAGCCTGGCCC 42307	_ G
	GGGCCAGGC GGTC CGG	
	CCCGGTCCG CCAG GTT	
	A A	
GAM1958 LOC196205 3'	CTGTGGACTGTCTGACTC 42325	C _
	GGG CAGGCGGTC GCGG	
	CTC GTCTGTCAG TGTC	
	A G	
GAM1958 LOC196337 3'	TCTGAGCAGGTTCTGGCCC 42360	CGGTC G_
	GGGCCAGG GC GTTCAGG	
	CCCGGTCT TG CGAGTCT	
	__GA	
GAM1958 LOC196738 3'	CTTTGATGGTTGCCTGCTT 42287	C GTC G C
	GGGC AGGCG GC GTT AGG	
	TTCG TCCGT TG TAG TTC	
	_ __G T	
GAM1958 LOC196812 3'	ACCTGGATTCTAGTTCTGGCTT 43132	_GGTCGC
	GGGCCAGG C GGTTTCAGGT	
	TTCGGTCT G TTAGGTCCA	
	T ATC__	
GAM1958 LOC196955 5'	ATCTGAGCAGGGATCGATCTGG 37929	_ GCG
CCT	GGGCCAGG CGGTC GTTCAGGT	
	TCCGGTCT GCTAG CGAGTCTA	
	A GGA	
GAM1958 LOC197350 5'	CTGAGCGGCTGCCGGGCCC 42503	A GGT
	GGGCC GGCGGTCGC TCAG	
	CCCGG CCGTCGGCG AGTC	
	G __	
GAM1958 LOC197350 5'	GCCTGAGCCGGCCCCCGGTCC 42504	A C CG
	GGGCC GG GGT CGGTTTCAGGT	

	CCTGG CC CCG GCCGAGTCCG	
	C _ _	
GAM1958 LOC199800 5'	ACTTGCCCTGCATTGCCTGGCC 43248	C TT
C	GGGCCAGGCGGT GCGG CAGGT	
	CCCGGTCCGTTA CGTC GTTCA	
	_ CC	
GAM1958 LOC199858 5'	ATTTGAGAGACAACTCTTGGCC 42630	C CGCGG
T	GGGCCAGG GGT TTCAGGT	
	TCCGGTTC TCA GAGTTTA	
	_ ACAGA	
GAM1958 LOC199858 5'	ATTTGGGTGTATTACTCTGGCC 42631	_CG C G TT
C	GGGCCAG G GT GC G CAGGT	
	CCCGGTC C TA TG T GTTTA	
	T AT _ _ GG	
GAM1958 LOC199907 3'	ACTTGATCAGTCGTTTGACCT 42656	C GTC GGT
	GGG CAGGCG GC TCAGGT	
	TCC GTTTGC TG AGTTCA	
	A _ _ ACT	
GAM1958 LOC200325 5'	CCTGGGGGTGGCCTGGTCC 43289	GGT GG
	GGGCCAGGC CGC TTCAGG	
	CCTGGTCCG GTG GGGTCC	
	_ _ G_	
GAM1958 LOC200470 5'	GCCTGAGCCGTGACCAGAGGTC 43308	AGGC
C	GGGCC GGTGCGGTTTCAGGT	
	CCTGG CCAGTGCCGAGTCCG	
	AGA_	
GAM1958 LOC200597 3'	GCCTGGGCCGTGGCAGCCGCCT 42824	CA G
	GGGC GGC GTCGCGGTTTCAGGT	
	TCCG CCG CGGTGCCGGGTCCG	
	_ A	
GAM1958 LOC200853 5'	GCCTGGATTCCAGTCCTGGCTC 42867	_ _ TCGC
	GGGCCAGG C GG GTTCAGGT	
	CTCGGTCC G CC TTAGGTCCG	
	T A _ _	
GAM1958 LOC201191 3'	CTTGGGCTAGCCTGGTCC 43216	GGTCGC
	GGGCCAGGC GTTCAGG	
	CCTGGTCCG TCGGTTC	
	A_ _ _	
GAM1958 LOC201627 3'	ATTTGAAAGAAATCGTTTGCCT 42895	C CGCGG
	GGGC AGGCGGT TTCAGGT	

TCCG TTTGCTA AAGTTTA
 _ AAGA_
 GAM1958 LOC202052 3' GCCTGGGCTGTGTGGTTCTGGG 43407 G _ G T
 CC GG CCAGG C G CGCGGTTTCAGGT
 || ||||| || |||||
 CC GGTCT G T GTGTCGGGTCCG
 G T G_
 GAM1958 LOC202451 5' GCCTTGGCTCCTGGCTT 43439 C C
 GGGCCAGG GGTCG GGT
 ||||| ||||| ||
 TTCGGTCC TCGGT CCG
 _ T
 GAM1958 LOC203078 3' ACTTGGATCACGGCTTGGTTC 43005 G CGC
 GGGCCAGGC GT GGTTCAGGT
 ||||| || |||||
 CTTGGTTCG CA CTAGGTTCA
 G _
 GAM1958 LOC203246 3' ACCTGGGTTTGCCTCTTGGCTC 43015 C CGC TT
 GGGCCAGG GGT GG CAGGT
 ||||| || || |||||
 CTCGGTTC CCG TT GTCCA
 T T_ GG
 GAM1958 LOC203276 3' CCTGAGCCTGCATGGCCT 43484 G GTCGC
 GGGCCA GCG GGTTCAGG
 ||||| || |||||
 TCCGGT CGT CCGAGTCC
 A _
 GAM1958 LOC203305 3' CCTGAGCCTGCATGGCCT 43508 G GTCGC
 GGGCCA GCG GGTTCAGG
 ||||| || |||||
 TCCGGT CGT CCGAGTCC
 A _
 GAM1958 LOC203350 3' GTTGAACCCAGGTCTGCCT 43537 _ GC_ GG
 AGGCGG TC GGTTC A T
 ||||| || ||||| |
 TCCGTC GG CCAAGT G
 T ACC TT
 GAM1958 LOC203378 5' ATTTGAACCTGTGTTCTTGGTT 43548 CGGT _
 C GGGCCAGG CGC GGTTCAGGT
 ||||| || |||||
 CTTGGTTC GTG CCAAGTTTA
 TT_ T
 GAM1958 LOC204161 5' ACCTGGCCCATCGCCGTGGCCT 43578 _ CGC TT
 GGGCCA GGCGGT GG CAGGT
 ||||| ||||| || |||||
 TCCGGT CCGCTA CC GTCCA
 G _ CG
 GAM1958 LOC204804 3' ACTTGGATTTCTGACTTGGCTC 43098 _ TCGC
 GGGCCAGG CGG GGTTCAGGT
 ||||| || |||||

		CTCGGTTC GTC TTAGGTTCA		
		A T__		
GAM1958	LOC204970 5'	GCCTGGGCCGCGGTCGTGGTCC 43070	AG	GT
		GGGCC GCG CGCGGTTCAAGT		
		CCTGG TGC GCGCCGGGTCCG		
		__ TG		
GAM1958	LOC205327 3'	GCTTGAGCCCAGGCTGTGTGGT 43105	G	GC
	TC	GGGCCA GCGGTC GGTTCAGT		
		CTTGGT TGTCGG CCGAGTTCG		
		G AC		
GAM1958	LOC219404 3'	CTGAGCATATGCCTGGCT 44908	GTCGCG	
		GGCCAGGCG GTTCAG		
		TCGGTCCGT CGAGTC		
		ATA__		
GAM1958	LOC219686 5'	GCTTCAAGATGGCCGCTTGGCT 43673	CGG	C
	C	GGGCCAGGCGGTCG TT AGGT		
		CTCGGTTGCGCCGGT AA TTCG		
		AG_ C		
GAM1958	LOC219848 3'	CTGAGCCTGAGGTTTGCTC 43985	C	GG C
		GGGC AGGC TCG GGTCAG		
		CTCG TTTG AGT CCGAGTC		
		_ G_ _		
GAM1958	LOC219942 3'	CTGAGCCTGCCCTGGCTT 44825	CGGTC	_
		GGGCCAGG GC GGTCAG		
		TTCGGTCC CG CCGAGTC		
		_____ T		
GAM1958	LOC220045 5'	GCCTGCCCCCACTGTCTGGCCT 44861	CGC	TT
		GGGCCAGGCGGT GG CAGGT		
		TCCGGTCTGTCA CC GTCCG		
		C_ CC		
GAM1958	LOC220143 3'	CTGGCTGTCCCTGGCCT 44953	C GTC	T
		GGGCCAGG G GCGGT CAG		
		TCCGGTCC C TGTCG GTC		
		- - -		
GAM1958	LOC220739 3'	CCTGGCGGTCCCTTGGCCT 44657	C GT	GGTT
		GGGCCAGG G CGC CAGG		
		TCCGGTTC C GCG GTCC		
		_ TG _____		
GAM1958	LOC220776 3'	TTTGAGTCCAGGCCTGCCT 33939	_ GC	_
		AGGC GGTC GG TTCAGG		

TCCG CCGG CC GAGTTT
 T A_ T
 GAM1958 LOC220929 5' ACCTCCCCGACTGCTGGGCCC 43928 A C TTC
 GGGCC GGCGGTTCG GG AGGT
 |||| ||||| || ||||
 CCCGG TCGTCAGC CC TCCA
 G _ C__
 GAM1958 LOC221002 3' GTTGGGCTGCGGTGAGTCC 43977 _ GGCGG GG
 GGGC CA TCGCGTTCA T
 ||| || ||||| |
 CCTG GT GCGTCGGGT G
 A _____ TT
 GAM1958 LOC221042 3' CTGGGCAGCTGTCTGCCT 44753 C CGCG
 GGGC AGGCGGT GTTCAG
 ||| ||||| |||||
 TCCG TCTGTCTG CGGGTC
 _ A__
 GAM1958 LOC221042 3' CTGGGCCTCCCTGGCTT 44754 C TCGC
 GGGCCAGG GG GTTCAG
 ||||| || |||||
 TTCGGTCC CT CCGGGTC
 _ _____
 GAM1958 LOC221463 3' ACCTGCCGGGGGACTGCCGTGGC 44198 _ _ G TT
 TT GGGCCA GGCGGT C CGG CAGGT
 |||| ||||| | ||| ||||
 TTCGGT CCGTCA G GCC GTCCA
 G G G _
 GAM1958 LOC221477 3' ACTTGAATGGCCTGTTTGTCT 44249 C TC G
 GGGC AGGCGG GC GTTCAGGT
 ||| ||||| || |||||
 TCTG TTTGTC CG TAAGTTCA
 _ _ G
 GAM1958 LOC221477 3' ACTTTGGCCTCTGGTTC 44250 C C
 GGGCCAGG GGTCG GGT
 ||||| ||||| |||
 CTTGGTCT CCGGT TCA
 _ T
 GAM1958 LOC221583 3' ATCTGAATAGCAACTGTCTGAC 44243 C C G
 TT GGG CAGGCGGT GC GTTCAGGT
 ||| ||||| || |||||
 TTC GTCTGTCA CG TAAGTCTA
 A A A
 GAM1958 LOC221687 5' CCTGGAAGATTTCTGGTTT 44304 C GCGG
 GGGCCAGG GGTC TTCAGG
 ||||| ||| |||||
 TTTGGTCT TTAG AGGTCC
 _ A__
 GAM1958 LOC221935 3' TTTAAATGTGTCATTGTTTGGT 44503 C CAGGT
 TT GGGCCAGGCGGT GCGGTT
 ||||| ||||| |||||

	TTTGGTTTGTTA TGTTAA		
	C AATTTA		
GAM1958 LOC222237 3'	CTGGAGTGCTTGGCTT 45269	G	GCGGTT
	GGGCCAGGCG TC CAG		
	TTCGGTTCGT AG GTC		
	G _____		
GAM1958 LOC253019 5'	GTTTGAATTGTGGCTGAGAGGT 45669	AGG	GG
TT	GGGCC CGGTCGCGGTTCA T		
	TTTGG GTCGGTGTAAAGT G		
	AGA TT		
GAM1958 LOC253502 3'	CTGCGGGGTCTGCCTGGCCT 45380	___	
	GGGCCAGGCGG TCGCGG		
	TCCGGTCCGTC GGCCTC		
	TGG		
GAM1958 LOC253664 5'	GTCTGGACCCTGGCTTATCTGG 45450	C_ C	GT
TTC	GGGCCAGG GGTCG GGTTCAAG		
	CTTGGTCT TCGGT CCAGGTC		
	AT C TG		
GAM1958 LOC253975 5'	GTTTGAATTGTGGCTGAGAGGT 45936	AGG	GG
TT	GGGCC CGGTCGCGGTTCA T		
	TTTGG GTCGGTGTAAAGT G		
	AGA TT		
GAM1958 LOC253981 3'	GCTTGAGCCACTGCGCCCGGCC 45866	A	GTCGC
T	GGGCC GGCG GGTTCAAGT		
	TCCGG CCGC CCGAGTTCG		
	C GTCA_		
GAM1958 LOC254015 3'	CTGAGTCTGGGTCTGGGTC 46243	G	GG C GT
	GG CCAGGC TCG G TCAG		
	CT GGTCTG GGT C AGTC		
	G _ _ TG		
GAM1958 LOC254015 3'	GCTTGGGTCTGAGTCTGGGTC 46245	G	GG C TT
	GG CCAGGC TCG GG CAGGT		
	CT GGTCTG AGT CT GTTCG		
	G _ _ GG		
GAM1958 LOC254041 5'	GCCTCTGGCTGCTGGTTT 45481	G	C_
	GGGCCAG CGGTCG GGT		
	TTTGGTC GTCGGT CCG		
	_ CT		
GAM1958 LOC254243 3'	CCTGAGCCTGCATGGCCT 46510	G	GTCGC
	GGGCCA GCG GGTTCAAG		

TCCGGT CGT CCGAGTCC
A _____
GAM1958 LOC254531 5' GCCTGAGCCGCCTGCT 45540 TC
GGCGG GCGGTTCAAGT
||||| ||||||||
TCGTC CGCCGAGTCCG

GAM1958 LOC254532 5' ACTTGGATTGCATTTGGCT 46207 CGGTC
GGCCAGG GCGGTTCAAGT
||||| ||||||||
TCGGTTT CGTTAGGTTCA
A _____
GAM1958 LOC255057 3' GCCTGAAGGGTTCTGCTGTGGT 45661 _ TC GG
CC GGGCCA GGCGG GC TTCAGGT
||||| |||| || |||||||
CCTGGT TCGTC TG AAGTCCG
G T_ GG
GAM1958 LOC255082 5' CTTGATGCTGCTTGGGCC 46118 G CGCGGT
GG CCAGGCGGT TCAGG
|| ||||||| ||||
CC GGTTCTGTCG AGTTC
G T _____
GAM1958 LOC255082 5' TGCAGGGCTGCGGGCGCTTGGT 46120 G AGGT
TC GGGCCAGGCG TCGCGGTTT
||||||||| |||||||
CTTGGTTTCGC GGCGTCGGG
G ACGTC
GAM1958 LOC255452 3' GCTTGGGCACAGTGCCCTGGCT 46575 CG T G_
C GGGCCAGG G CGC GTTCAGGT
||||||| | ||| |||||||
CTCGGTCC C GTG CGGGTTTCG
_ _ ACA
GAM1958 LOC255645 3' GCTTGGAGTTGCTGTCCTGGCC 46222 _ C GG
C GGGCCAGG CGGT GC TTCAGGT
||||||| |||| || |||||||
CCCGGTCC GTCG TG AGGTTTCG
T T _
GAM1958 LOC255995 5' CCTGAACCAGCCTGGTCC 46324 GGTCGC
GGGCCAGGC GTTCAGG
||||||| |||||||
CCTGGTCCG CCAAGTCC
A _____
GAM1958 LOC256158 5' TTGTGGTCGGCCTGGCCC 46636 _ GT
GGGCCAGGC G CGCGG
||||||| | ||||
CCCGGTCCG C GTGTT
G TG
GAM1958 LOC256790 5' CTAATGGTGACTGCTTGGC 45460 G C
GCCAGGCGGTCTGC GTT AG
||||||||||| ||| ||

CGGTTCGTCAGTG TAA TC
G _
GAM1958 LOC256848 5' CCTGGGTAAGTCTGGTTC 46570 G CG GGT
GGGCCAG CGGT C TCAGG
||||| ||| | ||||
CTTGGTC GTCA G GGTCC
_ AT _
GAM1958 LOC257054 3' ACTTGCGTGGTGGCCCCTGGCC 45779 C G TT
C GGGCCAGG GGTCGC G CAGGT
||||| ||||| | ||||
CCCGGTCC CCGGTG T GTTCA
_ G GC
GAM1958 LOC257054 5' TCTGAGCCCTAGGATTTGGCCC 45784 GCGG GC_ GT
GGGCCAG TC GTTCAG
||||| || |||||
CCCGGTT GG CCGAGTC
TA_ ATC TG
GAM1958 LOC257096 5' ATCTGAATCAGAAGTTTGCTC 45911 C GG GC
GGGC AGGC TC GTTCAGGT
||| ||| || |||||
CTCG TTTG AG CTAAGTCTA
_ A_ A_
GAM1958 LOC257354 3' ACTTGAAGCCTGATCTGGCCT 45575 GCG C _
GGGCCAG GTCG GGTT CAGGT
||||| ||| ||| |||||
TCCGGTC TAGT CCGA GTTCA
_ _ A
GAM1958 LOC257451 3' GCCTGGATTGCTCACTGTTT 45743 C_
AGGCGGT GCGGTT CAGGT
||||| |||||
TTTGTCA CGTTAGGTCCG
CT
GAM1958 LOC257463 5' GTTTGTACAGATATGTTTGGCC 35210 GTCGCG T GG
C GGGCCAGGCG GT CA T
||||||| || || |
CCCGGTTTGT CA GT G
ATAGA_ T TT
GAM1958 LOC257472 3' ATCTTACTGGTTGTTAGGCCT 45593 AG GT GC TC
GGGCC GCG C GGT AGGT
|||| ||| | ||| ||||
TCCGG TGT G TCA TCTA
AT TG_ T_
GAM1958 LOC257472 3' GCCTGAATAGGCTCCTGGCCC 45594 C GCG
GGGCCAGG GGTC GTTCAGGT
||||| ||| |||||
CCCGGTCC TCGG TAAGTCCG
_ A_
GAM1958 LOC51185 3' ACTTGAATCTGATAGGCCGCC 18422 A G_ C
T GGGCC GGC GTCG GGTT CAGGT
|||| ||| ||| |||||

		TCCGG CCG TAGT CTAAGTTCA		
		GA		
GAM1958	LOC51219	5' GTTTGAGCTGTGGCAGAAGCAC 18545	CAGGCG	GG
	C	GG GC GTCGCGGTTCA T		
		CC CG CGGTGTCGAGT G		
		A AAGA TT		
GAM1958	LOC51236	3' GCCTGGGCCACTCCTCCCTGGC 18571	C TCGC	
	CT	GGGCCAGG GG GTTCAGGT		
		TCCGGTCC CC CCGGGTCCG		
		CT TCA		
GAM1958	LOC51279	3' TGATAAGATTTTGGCTGTTTGG 18618	CG CAGGT	
	TTT	GGGCCAGGCGGTTCG GTT		
		TTTGGTTTGTCCGT TAG		
		TT AATAGTT		
GAM1958	LOC51644	3' ACCTGTGGGATCGTTGCCTGGT 18129	GTC	
	TT	GGCCAGGCG GCGGTT CAGGT		
		TTGGTCCGT TGCTAG GTCCA		
		GGT		
GAM1958	LOC54499	3' ACTTGATAGTGCTTTTGGTCC 34965	C T GGT	
		GGGCCAGG GG CGC TCAGGT		
		CCTGGTTT TC GTG AGTTCA		
		AT		
GAM1958	LOC55580	5' ACTTGGGTAAACGTTTGGAC 18994	GTCGC TT	
	CT	GGG CCAGGCG GG CAGGT		
		TCC GGTTTGC TT GTTCA		
		A AAAA GG		
GAM1958	LOC56181	5' CCAGTGCGCTGCCTTGTCC 45739	C	
		GGGC AGGCGGTCGC GG		
		CCTG TCCGTCCGTG CC		
		T A		
GAM1958	LOC56270	3' GCCATACGTGGTTGTCTGCTT 21231	C GT GTTCA	
		GGGC AGGCG CGCG GGT		
		TTCG TCTGT GTGC CCG		
		TG ATA		
GAM1958	LOC56899	5' GCCTTCTTCTGCTGCCTGGTTT 21336	GTC TTC	
		GGGCCAGGCG GCGG AGGT		
		TTTGGTCCGT CGTC TCCG		
		TTCT		
GAM1958	LOC57826	3' ACCTGGGTTGCAGAACTGAGCC 22158	GCGGTC TT	
	T	GGGC CAG GCGG CAGGT		

TCCG GTC CGTT GTCCA
 A AAGA__ GG
 GAM1958 LOC64744 5' GCCTGGGCTGAGGGTCTCTGGC 30952 C GT G_
 CC GGGCCAGG G C CGGTTCAAGT
 ||||| | | |||||
 CCCGGTCT C G GTCGGGTCCG
 _TG GA
 GAM1958 LOC90038 3' CCTGAGCCTGCATGGCCT 30647 G GTCGC
 GGGCCA GCG GGTTCAAG
 ||||| || |||||
 TCCGGT CGT CCGAGTCC
 A ____
 GAM1958 LOC90092 5' ATCTTGACCTCTGGCTT 30781 C C
 GGGCCAGG GGTCG GGT
 ||||| ||||| |||||
 TTCGGTCT CCAGT CTA
 _ T
 GAM1958 LOC90133 3' GCCTGGGCTCCAGCTTTGGCTC 30868 _ _ TCGC
 GGGCCAG GC GG GGTTCAAGT
 ||||| || || |||||
 CTCGGTT CG CC TCGGGTCCG
 T A ____
 GAM1958 LOC90148 5' ATTTGAACCCAGGTCTGCCC 30891 C GGTCGC
 GGGC AGGC GGTTCAAGT
 ||| ||| |||||
 CCCG TCTG CCAAGTTTA
 _ GAC____
 GAM1958 LOC90170 5' GGCTGTGTTGTTTGCTC 30912 C T
 GGGC AGGCGG CGCGGT
 ||| ||||| |||||
 CTCG TTTGTT GTGTCCG
 _ _
 GAM1958 LOC90170 5' GTCTGAACCTGCCGTGTTCTTG 30914 ____ T C GT
 GCTT CCAGG CGG CG GGTTCAAG
 |||| ||| || |||||
 GGTTG GCC GT CCAAGTC
 TTGT _ _ TG
 GAM1958 LOC90198 5' CCTGAACTGTGGGTGGCTG 30958 G G
 CAG CG TCGCGGTTCAAG
 ||| || |||||
 GTC GT GGTGTCAAGTCC
 G G
 GAM1958 LOC90233 3' CCTGGAACTGCTTGGTGC 28743 G CGCGG
 G GCCAGGCGGT TTCAGG
 | ||||| |||||
 C TGGTTCGTCA AGGTCC
 G A____
 GAM1958 LOC90249 5' GCCTCATCGCCGTGGCCGTCTG 31012 C TC____
 CCT GGC AGGCGGTGCGGT AGGT
 ||| ||||| ||||| |||||

CCG TCTGCCGGTGCCG TCCG
 _ CTAC
 GAM1958 LOC90288 3' GCCTGAGCTGTCTTGTCTGTGT 31109 _ TC
 TT GGC CAGGCGG GCGGTTCAAGT
 ||| ||||| |||||
 TTTG GTCTGTT TGTCGAGTCCG
 T C_
 GAM1958 LOC90288 3' GCTTGGAAGTGTCTCTGTCT 31110 TC__
 AGGCGG GCGGTTCAAGT
 ||||| |||||
 TCTGTC CGTCAGGTTCG
 TCTT
 GAM1958 LOC90355 5' TCTGGATTGTGCAGACTGGTGC 27064 G GCG T GT
 G GCCAG G CGCGGTTCAAG
 | |||| | |||||
 C TGGTC C GTGTAGGTC
 G AGA _ TG
 GAM1958 LOC90485 3' GCCTGAGCTACGGTGCCTGGCC 31554 G CG
 GGCCAGGCG TCG GTTCAGGT
 ||||| ||| |||||
 CCGGTCCGT GGC CGAGTCCG
 _ AT
 GAM1958 LOC90632 5' GCTTGAGCTGAGATGGACTGGT 31829 GCG G
 CT GGGCCAG GTC CGGTTCAAGT
 ||||| || |||||
 TCTGGTC TAG GTCGAGTTTCG
 AGG A
 GAM1958 LOC90777 3' CTTTCCTGACCTCTGGTTT 31993 C C TTC
 GGGCCAGG GGTCG GG AGG
 ||||| ||||| || |||
 TTTGGTCT CCAGT CC TTC
 _ _ T_
 GAM1958 LOC90784 5' ACCTGGGTAAGTGCCTGG 32002 CG GGT
 CCAGGCGGT C TCAGGT
 ||||| | |||||
 GGTCCGTCA G GGTCCA
 AT _
 GAM1958 LOC90786 5' ACCTGGGCCACAGTGCCTGCCT 32011 C GTCGC
 GGGC AGGCG GTTCAGGT
 ||| |||| |||||
 TCCG TCCGT CCGGGTCCA
 _ GACA_
 GAM1958 LOC90826 5' TTTGAGCAGTTGTCTGGTCC 32053 GTC G T
 GGGCCAGGCG GC GTTCAGG
 ||||| || |||||
 CCTGGTCTGT TG CGAGTTT
 _ A T
 GAM1958 LOC90906 5' ACTTGAATTGCTTGATACTTTG 32147 CG _
 GTTT GGCAGG GTC GCGGTTCAAGT
 ||||| ||| |||||

		TTGGTTT TAG CGTTAAGTTCA		
		CA TT		
GAM1958	LOC91050	3' CCAGTGGTGGTCTGGTTT 32333	G	_
		GGGCCAGGC GTCGC GG		
		TTTGGTCTG TGGTG CC		
		G A		
GAM1958	LOC91097	3' GCTTTGATTCTTGGTTC 32369	C	C
		GGGCCAGG GGTCG GGT		
		CTTGGTTC TTAGT TCG		
		_ T		
GAM1958	LOC91149	5' ACTTGCCGGCGGTTGCTTGCTC 32453	C	GT _ TT
		GGGC AGGCG CGC GG CAGGT		
		CTCG TTCGT GCG CC GTTCA		
		_ TG G _		
GAM1958	LOC91301	5' GCCTGGGCTTTATGGGTCTCTG 32650	C	GT GC _
		GCCC GCCAGG G C GGTTCAGGT		
		CGGTCT C G TCGGGTCCG		
		_ TG GTATT		
GAM1958	LOC91355	5' ACTTGATGGGTACGTTTGGTCC 32701		GTCGCGGT
		GGGCCAGGCG TCAGGT		
		CCTGGTTTGC AGTTCA		
		ATGGGT _		
GAM1958	LOC91445	3' ACTTGAATGACTTCCTGGTTT 30365	C	GCG
		GGGCCAGG GGTC GTTCAGGT		
		TTTGGTCC TCAG TAAGTTCA		
		T _		
GAM1958	LOC91531	5' ATTTGGACAGATGCCTGACTC 32972	C	GTCGCG
		GGG CAGGCG GTTCAGGT		
		CTC GTCCGT CAGGTTTA		
		A AGA _		
GAM1958	LOC91632	5' GCTTGGACCGCGATGGGGCTGG 33164	A	G _
		GCCC GGCC GGC GTCGCGGTTTCAGGT		
		CCGG TCG TAGCGCCAGGTTTCG		
		G GGG		
GAM1958	LOC91759	3' ACCTGGGTGTGGTGCTGCCTGG 33300		_ G TT
		C GCCAGGCGGT CGC G CAGGT		
		CGGTCCGTCG GTG T GTCCA		
		TG _ GG		
GAM1958	LOC91812	5' CCTGGGCCAGCTCTGGCTT 33391	CGGTC	_
		GGGCCAGG GC GGTTCAGG		

TTCGGTCT CG CCGGGTCC
_____ A
GAM1958 LOC91813 5' ACTTGCTGTGCGCCTTTGGCTT 33394 C _ TT
GGGCCAGG GGTCG CGG CAGGT
||||||| ||||| ||| |||||
TTCGGTTT CCGGC GTC GTTCA
_ T _
GAM1958 LOC91813 5' CCTGGGCCAGCTCTGGCTT 33399 CGGTC _
GGGCCAGG GC GGTTCAAGG
||||||| || |||||
TTCGGTCT CG CCGGGTCC
_____ A
GAM1958 LOC91974 5' GCCTCCTGTTGACCAGCCTGGT 33654 _ _ TTC
TT GGGCCAGGC GGTCG CGG AGGT
||||||| ||||| ||| |||||
TTTGGTCCG CCAGT GTC TCCG
A T C_
GAM1958 LOC92249 5' ACCTGAGCTGGGGCCTGTGCTT 34018 _ GGT G
GGGC CAGGC C CGGTTCAAGT
||| |||| | |||||
TTCG GTCCG G GTCGAGTCCA
T _ G
GAM1958 LOC92360 5' CCTGGACCCAGTTGGCTC 34240 G GGTCGC
GGGCCA GC GGTTCAAGG
||||| || |||||
CTCGGT TG CCAGGTCC
_ AC_
GAM1958 LOC92492 5' GTTTGGGGAGCAGCCCCTGGCT 34453 C C GG GG
C GGGCCAGG GGT GC TTCA T
||||||| ||| || ||| |
CTCGGTCC CCG CG GGGT G
_ A AG TT
GAM1958 LOC92499 5' GCCTCTGGCTGCTGGTTT 34462 G C_
GGGCCAG CGGTGCG GGT
||||||| ||||| |||
TTTGGTC GTCGGT CCG
_ CT
GAM1958 LOC92973 5' GTTGAATCGGGGCCTTTGTTC 35186 GC C G GG
G CAGG GGTC CGGTTCA T
| ||||| ||||| ||||| |
C GTTT CCGG GCTAAGT G
TT _ G TT
GAM1958 LOC93017 3' ACCTGGGAAATTTGATTTGGTT 35252 _ TCGCGG
T GGGCCAGG CGG TTCAGGT
||||||| ||| |||||
TTTGGTTT GTT GGGTCCA
A TAAA_
GAM1958 LOC93052 5' GCTTGGGAGCCCATCGTCCTGG 35303 _ C_ GG
CTC GGCCAGG CCGT GC TTCAGGT
||||||| ||||| || |||||

TCGGTCC GCTA CG GGGTTCG
T CC A_

GAM1958 LOC93613 5' GCTGGACGCGGTCGGCCTGGTC 35996 _GT G GT
C GGGCCAGGC G CGCG TTCAG
||||||| | ||| |||||
CCTGGTCCG C GCGC AGGTC
G TG _ G

GAM1958 LOC96597 3' ACCTGGACACAGACTTGCCGGC 33226 A _ GCG
TC GGGCC GGCG GTC GTTCAGGT
||||| ||| ||| |||||
CTCGG CCGT CAG CAGGTCCA
_ T ACA

GAM1959 ACCN2 3' TTCTGGTGAGGTGGGTTTGGGA 21298 G GT T G GT
G TTC CAG CT CC TC CAGGG
||| ||| ||| ||| |||||
GAG GTT GG GG AG GTCTT
G TG T _ TG

GAM1959 ACK1 3' CCCTGGTCCTGGGCGGGGCCTG 12359 TT G____
TGG GCAGGTC CCGTC TCAGGG
||||||| ||||| |||||
TGTCCGG GGCGG GGTCCC
_ GTCCT

GAM1959 ADAM19 3' CCTTCCCCAGGGGAGCCTGCGA 27096 TC GTCGTC G
A TTCGCAGG TTCC AGG
||||||| ||||| |||
AAGCGTCC GGGG TCC
GA ACCCCT

GAM1959 ADAMTS13 3' CCTGGGAGCCGGCGGGAGGTCT 29129 GT ____ G
GC CAG CTTCGTCG TCAGG
||| ||||| |||||
GTC GAGGGCGGC GGTCC
TG CGAG

GAM1959 ADCY6 3' TCAGGAGGTGGGAGGCCGTGG 21978 A GT G AG
TCGC GGTCTTCC C TC GG
||||| ||||| | |||
GGTG CCGGAGGG G AG CT
_ TG _ GA

GAM1959 ADCY6 3' TCAGGAGGTGGGAGGCCGTGG 17591 A GT G AG
TCGC GGTCTTCC C TC GG
||||| ||||| | |||
GGTG CCGGAGGG G AG CT
_ TG _ GA

GAM1959 ADD2 5' TTCTGACGGCAGGGCTGTGAG 18934 G TCC
TTCGCAG TCT GTCGTCAGGG
||||||| ||| |||||
GAGTGTC GGA CGGCAGTCTT
G ____

GAM1959 ADD2 5' TTCTGACGGCAGGGCTGTGAG 18936 G TCC
TTCGCAG TCT GTCGTCAGGG
||||||| ||| |||||

			GAGTGTC GGA CGGCAGTCTT		
			G ____		
GAM1959	ADD2	5'	TTCTGACGGCAGGGCTGTGAG 18939	G	TCC
			TTCGCAG TCT GTCGTCAGGG		
			GAGTGTC GGA CGGCAGTCTT		
			G ____		
GAM1959	ADD2	5'	TTCTGACGGCAGGGCTGTGAG 18941	G	TCC
			TTCGCAG TCT GTCGTCAGGG		
			GAGTGTC GGA CGGCAGTCTT		
			G ____		
GAM1959	ADD2	5'	TTCTGACGGCAGGGCTGTGAG 18944	G	TCC
			TTCGCAG TCT GTCGTCAGGG		
			GAGTGTC GGA CGGCAGTCTT		
			G ____		
GAM1959	ADD2	5'	TTCTGACGGCAGGGCTGTGAG 18947	G	TCC
			TTCGCAG TCT GTCGTCAGGG		
			GAGTGTC GGA CGGCAGTCTT		
			G ____		
GAM1959	ADD2	5'	TTCTGACGGCAGGGCTGTGAG 18949	G	TCC
			TTCGCAG TCT GTCGTCAGGG		
			GAGTGTC GGA CGGCAGTCTT		
			G ____		
GAM1959	ADM	3'	CTGACAGCCCTGCGGA 6793	TCTTCC	C
			TTCGCAGG GT GTCAG		
			AGGCGTCC CG CAGTC		
			_____ A		
GAM1959	ADORA1	3'	CCTGCAGGAGGCCTGGGAG 6327	G	T GTCGT
			TTC CAGGTCT CC CAGG		
			GAG GTCCGGA GG GTCC		
			G _ AC__		
GAM1959	AGPAT2	3'	TCCTGCTGGCCTGGAAGACTCT 32746	_	_ T
	GTGG		GCAG GTCTTCC GTCG CAGGG		
			TGTC CAGAAGG CGGT GTCCT		
			T TC C		
GAM1959	AGPAT2	3'	TCCTGCTGGCCTGGAAGACTCT 13119	_	_ T
	GTGG		GCAG GTCTTCC GTCG CAGGG		
			TGTC CAGAAGG CGGT GTCCT		
			T TC C		
GAM1959	AGRP	5'	CCCTGTCCTGTGGAAATTTGTG 6805	C	TCGT_
	GA		TTCGCAGGT TTCCG CAGGG		

			AGGTGTTTA AAGGT GTCCC		
			_ GTCCT		
GAM1959	AKAP1	5'	TAGCACGTGGGGGAGCTGCGGA 9580	G	T CAGGG
			TTCGCAG TCTTCCG CGT		
			AGGCGTC AGGGGGT GCA		
			G _ CGATC		
GAM1959	ALK	5'	CTCTGTTCGGAGGGTCGCGG 36320	A GT	TCGT
			TCGC G CTTCCG CAGGG		
			GGCG C GGAGGC GTCTC		
			_TG TT__		
GAM1959	AMFR	3'	CCCAGTGAGGTGGAAGACTTCG 29065	C	GT G _
	AG		TTCG AGGTCTTCC C TCA GGG		
			GAGC TTCAGAAGG G AGT CCC		
			_ TG _ GA		
GAM1959	ANK1	3'	CCCTGGCCGCGGGGCCTGTGAG 21731	TT	C
			TTCGCAGGTC CCGT GTCAGGG		
			GAGTGTCCGG GGCG CGGTCCC		
			_ C		
GAM1959	ANK1	3'	CCCTGCCGCGGGGCCTGTGAG 30282	TT	T T
			TTCGCAGGTC CCG CG CAGGG		
			GAGTGTCCGG GGC GC GTCCC		
			_ _ C		
GAM1959	ANK1	3'	CCCTGGCCGCGGGGCCTGTGAG 5478	TT	C
			TTCGCAGGTC CCGT GTCAGGG		
			GAGTGTCCGG GGCG CGGTCCC		
			_ C		
GAM1959	APLP2	3'	CCCTGAAACTGAGTCTGTGGA 43700	T	CCGTCG
			TTCGCAGG CTT TCAGGG		
			AGGTGTCT GAG AGTCCC		
			_ TCAA__		
GAM1959	APOL1	3'	TCCTGATGATGGTCATTGGGG 9734	G	GTCTT
			TC CAG CCGTCGTCAGGG		
			GG GTT GGTAGTAGTCCT		
			G ACT__		
GAM1959	ARHGAP6	3'	TCCTGGACCAAGGCTTGGGAA 6849	G	CC GT
			TTC CAGGTCTT GTC CAGGG		
			AAG GTTCGGAA CAG GTCCT		
			G C_ _		
GAM1959	ATP1B2	3'	TCTGGTGACTCTGTGAG 7395	TCTTCC	GT
			TTCGCAGG GTC CAGG		

			GAGTGTCT	CAG GTCT		
			_____ TG			
GAM1959	ATP2A3	3'	TTCTGGCCTGGGAGGTCTGT	11674	GT TC	
			GCAG CTTCCG GTCAGGG			
			TGTC GAGGGT CGGTCTT			
			TG C_			
GAM1959	ATP7B	3'	TTCTGATGACGCCTGTCTGTG	5510	TCTTC	
			CGCAGG CGTCGTCAGGG			
			GTGTCT GCAGTAGTCTT			
			GTCC_			
GAM1959	ATP8B2	5'	CCCTGGTGCTCTGGATTTTGG	32512	C TCC T GT	
	A		TTCG AGGTCT G C CAGGG			
			AGGT TTTAGG C G GTCCC			
			T TCT_ TG			
GAM1959	BCL6	5'	CTCTGCTTATGAGGACCTCGAA	7429	C CGTC T	
			TTCG AGGTCTTC G CAGGG			
			AAGC TCCAGGAG C GTCTC			
			_ TATT _			
GAM1959	BCL7A	3'	CTTGATGGCCGGCCTCGAA	21992	C TTCC	
			TTCG AGGTC GTCGTCAGG			
			AAGC TCCGG CGGTAGTTC			
			_ C_			
GAM1959	BCRP2	3'	CCTGATAAGCTCTGTGAA	31273	GT CCGTC	
			TTCGCAG CTT GTCAGG			
			AAGTGTC GAA TAGTCC			
			TC _____			
GAM1959	BLAME	3'	CCTGGTGGATTTGTGGG	21308	TTCCGT GT	
			TTCGCAGGTC C CAGG			
			GGGTGTTTAG G GTCC			
			_____ TG			
GAM1959	BNC	3'	TCCTGGGGAAGAAGACTCTGTG	7451	_ CG G	
	GA		TTCGCAG GTCTTC TC TCAGGG			
			AGGTGTC CAGAAG AG GGTCCCT			
			T A_ G			
GAM1959	BTG2	3'	CCCTGGGTCCCAGGAGGGTCTG	13623	G GT GTCG_	
	GAG		TC CAG CTTCC TCAGGG			
			AG GTC GGAGG GGTCCC			
			_ TG ACCCTG			
GAM1959	BTG2	3'	CCCTGGTGCTCAGAGCACCTGT	13624	_ CCGT GT	
	GG		TCGCAGGT CTT C CAGGG			

GGTGTCCA GAG G GTCCC
C ACTC TG
GAM1959 CARD15 3' TCTGGTTGATGCCTGTGAA 22719 CT CGTCG
TTCGCAGGT TC TCAGG
||||||| || |||||
AAGTGTCCG AG GGTCT
T_ TT__
GAM1959 CASP10 3' TTCTGACCCATGGGAGATTTGG 26834 G C_
AG TTC CAGGTCTTCCGT GTCAGGG
||| ||||||||| |||||||
GAG GTTTAGAGGGTA CAGTCTT
_ CC
GAM1959 CCNF 3' CTCTGCTGTGGGGGCCCGTGG 7526 A T T T
TCGC GGTCT CCG CG CAGGG
||||| ||||| ||| || |||||
GGTG CCGGG GGT GT GTCTC
C _ _ C
GAM1959 CDH5 3' TCTGGAGAAGGCCTGGAA 7549 G CGTCG
TTC CAGGTCTTC TCAGG
||| ||||||| |||||
AAG GTCCGGAAG GGTCT
_ A____
GAM1959 CDK10 3' TCCTGGTGATGGGTTACTGTGA 27556 GTCT GT
G TTCGCAG TCCGTC CAGGG
||||||| ||||||| |||||
GAGTGTC GGGTAG GTCCT
ATT_ TG
GAM1959 CDR2 3' CCTGAAAAGGACCAGTGGA 37428 A CCGTCG
TTCGC GGTCTT TCAGG
||||| ||||||| |||||
AGGTG CCAGGA AGTCC
A AA____
GAM1959 CEACAM1 3' CCTTGGGAAATGGGGCTGTGAG 7441 G TCCG G
TTCGCAG TCT TC TCAGGG
||||||| ||| || |||||||
GAGTGTC GGG AG GGTTC
G TAA_ _
GAM1959 CELSR3 3' CCTGCAGAGGGTCGGTGGA 7103 A GT CGTC T
TTCGC G CTTC G CAGG
||||| | ||||| | |||||
AGGTG C GGAG C GTCC
G TG A____
GAM1959 CEP2 5' CTCTGGCTACCTAGGGACCTGT 14043 CC_ C
GG TCGCAGGTCTT GT GTCAGGG
||||||||| || |||||||
GGTGTCCAGGG CA CGGTCTC
ATC T
GAM1959 CGB 5' CCTTGGCGCTGGACCAGTGAG 6394 A TCCGT
TTCGC GGTCT CGTCAGGG
||||| ||||| |||||||

			GAGTG CCAGG GCGGTTCC	
			A TC__	
GAM1959	CGTHBA	3'	CCCTGGTGGTTCCGCTGTGG 14356	GTCTT TCG
			TTCGCAG CCG TCAGGG	
			GGTGTC GGT GGTCCC	
			GCCTT __	
GAM1959	CHD2	3'	TTTTGATGTCCTTGTCTGCGAA 6938	TCTTCCGT
			TTCGCAGG CGTCAGGG	
			AAGCGTCT GTAGTTTT	
			GTTCTT__	
GAM1959	CHRNE	3'	CTCTGGTGGCTGCCAGCTTGTG 5522	CTTCC GT
	AG		TTCGCAGGT GTC CAGGG	
			GAGTGTTTCG CGG GTCTC	
			ACCGT TG	
GAM1959	CNP	3'	CTCTGAGAAGGGGAGGACCTCT 26977	C G__ G
	GG		TCG AGGTCTTCC TC TCAGGG	
			GGT TCCAGGAGG AG AGTCTC	
			C GGA _	
GAM1959	CNTN2	3'	TCCTGGTATTGGGAGGTTTCTG 11526	G __ TCG
	GG		C CAGG TCTTCCG TCAGGG	
			G GTCT GGAGGGT GGTCTT	
			G TT TAT	
GAM1959	COL1A1	3'	TTTTGTGGATGGGGACTTGTGA 5540	T GT
	A		TTCGCAGGTCT CCGTC CAGGG	
			AAGTGTTTCAGG GGTAG GTTTT	
			_ GT	
GAM1959	COX11	3'	TCTAAATGTAGGAAGGCCTGTG 10594	GT CA
	AA		TTCGCAGGTCTTCC CGT GGG	
			AAGTGTCGGAAGG GTA TCT	
			AT AA T	
GAM1959	CRMP1	3'	TTCTGAATTCAAAGCTTGTGAA 6999	T CCGTCG
			TTCGCAGG CTT TCAGGG	
			AAGTGTTTC GAA AGTCTT	
			_ ACTTA_	
GAM1959	CXCL16	3'	CCAAGAATGGAAGCTTGTGAG 22597	T CG AG
			TTCGCAGG CTTCCGT TC GG	
			GAGTGTTTC GAAGGTA AG CC	
			_ _ AA	
GAM1959	CXorf6	3'	CTTTGATGGTTTCTATCTGC 11991	CTTCCG
			GCAGGT TCGTCAGGG	

		CGTCTA GGTAGTTTC	
		TCTTT_	
GAM1959 DBN1	5'	CTCTGACCTGGGGGCTTCTGGA 28123	G T_ TC
		TC CAGG CTTCCG GTCAGGG	
		AG GTCT GGGGGT CAGTCTC	
		_ TC C_	
GAM1959 DLG5	3'	CCTTGGTGGCACCTCTCCTGGA 40335	G TCTTCC GT
A		TTC CAGG GTC CAGGG	
		AAG GTCC CGG GTTCC	
		_ TCTCCA TG	
GAM1959 DMD	5'	CTCTGGTGACACAACCTGTGG 10192	CTTCC GT
		TCGCAGGT GTC CAGGG	
		GGTGTCCA CAG GTCTC	
		ACA_ TG	
GAM1959 DMD	5'	CTCTGGTGACACAACCTGTGG 10219	CTTCC GT
		TCGCAGGT GTC CAGGG	
		GGTGTCCA CAG GTCTC	
		ACA_ TG	
GAM1959 DMD	5'	CTCTGGTGACACAACCTGTGG 10231	CTTCC GT
		TCGCAGGT GTC CAGGG	
		GGTGTCCA CAG GTCTC	
		ACA_ TG	
GAM1959 DNM2	3'	GGTGGTGGCGGGGGGTCTTGG 11387	C GT GT GGG
		TCG AG CTTCCGTC CA	
		GGT TC GGGGGCGG GT	
		_ TG TG GGT	
GAM1959 DXS1283E	5'	CCTTGGTGGCGGAATGGCGTTG 35061	_ _ GT
		CAG GTC TTCCGTC CAGGG	
		GTT CGG AAGGCGG GTTCC	
		G T TG	
GAM1959 EFNB1	5'	CTGGACAGCAGTGGGAGGTTTG 10710	GT TC ____ GG
TGAG		GCAG CTTCCG GT CAG	
		TGTT GAGGGT CG GTC	
		TG GA ACAG	
GAM1959 EFNB1	3'	CTTGGGCTGGGGCCTGGAA 10711	G CC GT
		TTC CAGGTCTT GTC CAGG	
		AAG GTCCGGGG CGG GTTC	
		_ T_ _	
GAM1959 EGFL3	3'	CTTTGAGGGCCGTGGAGGGCTG 31375	G _ _ G
TGGA		TCGCAG TCTTC CG TC TCAGGG	

GGTGTC GGAGG GC GG AGTTTC
G T C G

GAM1959 EGLN2 5' TCCTGTTCGGAGGTCTATGG 18992 C T TCGT
TCG AGG CTTCCG CAGGG
||||| ||||
GGT TCT GGAGGC GTCCT
A _ TT_

GAM1959 EHHADH 3' TGATGGAAAAATCTTGAA 7695 C C_
TTCG AGGT TTCCGTCG
||||| |||||
AAGT TCTA AAGGTAGT
_ AA

GAM1959 ELAVL3 3' CTCTGGGGTGGGAGGGTCTGC 7119 GT GTCG
GCAG CTTCC TCAGGG
||||| |||||
CGTC GGAGG GGTCTC
TG GTGG

GAM1959 ENDOG 5' CTTGGCAGTGTGTTGTGAG 10720 TCTTC TC
TTCGCAGG CG GTCAGG
||||| || |||||
GAGTGTTT GT CGGTTC
_ GA

GAM1959 EPS15 3' TCTGATGATAGCCAGTGAG 7712 A T TCC
TTCGC GG CT GTCGTCAGG
||||| || |||||
GAGTG CC GA TAGTAGTCT
A _ _

GAM1959 ETV5 3' TCTGATGAGGTTTCTGGG 10750 G TCTT G
C CAGG CC TCGTCAGG
| ||| || |||||
G GTCT GG AGTAGTCT
G TT_ _

GAM1959 EVC 3' TCTGAAAGCATCTGTGGA 15896 CTTCC CG
TTCGCAGGT GT TCAGG
||||| || |||||
AGGTGTCTA CG AGTCT
_ AA

GAM1959 EXT1 5' GCGCGGGGGCCTGCGAA 5603 T T
TTCGCAGGTCT CCG CGT
||||| || |||||
AAGCGTCCGGG GGC GCG
_ _

GAM1959 EZH1 3' TCCTGGCTCGCTGGATTTGTGG 7718 TC TC
TCGCAGGTCT CG GTCAGGG
||||| || |||||
GGTGTTTAGG GC CGGTCCT
TC T_

GAM1959 FANCF 3' CCTTGGTGGCTGCCCTGTGGA 22921 TCTTCC GT
TTCGCAGG GTC CAGGG
||||| || |||||

			AGGTGTCC	CGG GTTCC		
			CGT__	TG		
GAM1959	FASN	3'	CCCGCTGAGTGGGGGGTCGTGG	10316	A GT	_ TCA
			TCGC G	CTTCCG TCG GGG		
			GGTG C	GGGGGT AGT CCC		
			TG	G CG		
GAM1959	FGF23	3'	CCTTCCACAGGAGGTCCTGTGA	21792	T	GTCGTC G
	G		TTCGCAGG	CTTCC AGG		
			GAGTGTCC	GGAGG TCC		
			T	ACACCT		
GAM1959	FLNB	3'	CCAGACGGAGGACCTGGAA	31140	G	GTCA
			TTC CAGGTCTTCCGTC	GG		
			AAG GTCCAGGAGGCAG	CC		
			_	A__		
GAM1959	FLNB	3'	CCTTGCGCGGTGGAAGGCCCCAG	31141	A__	GT
	C		GC GGTCTTCC	CGTCAGGG		
			CG	CCGGAAGG GCGGTTCC		
			ACC	TG		
GAM1959	FOXM1	3'	TTTTGATAGAAGGGAAGACCTG	22484	G_ _	
	C		GCAGGTCTTCC	TC GTCAGGG		
			CGTCCAGAAGG	AG TAGTTTT		
			GA	A		
GAM1959	FSTL3	3'	CCTGACGATATCCTGGAA	12468	G	TCTTCC
			TTC CAGG	GTCGTCAGG		
			AAG GTCC	TAGCAGTCC		
			_	TA__		
GAM1959	FXYD6	3'	TCTTGGGACCTGGGAAGGTTTG	22553	GT	_ G
	C		GCAG CTTCC	GTC TCAGGG		
			CGTT GAAGG	CAG GGTCT		
			TG	GTC _		
GAM1959	GAN	3'	TTCTGGGGTAGTACCTGTGGA	22566	_ T	GTCG
			TTCGCAGGT	CT CC TCAGGG		
			AGGTGTCCA	GA GG GGTCTT		
			T T	__		
GAM1959	GATA2	3'	CTCTGGGGGCAGATTTGTGG	7803	TCC	G
			TGCAGGTCT	GTC TCAGGG		
			GGTGTTTAGA	CGG GGTCTC		
			_	G		
GAM1959	GATA2	3'	TGACGGGCCAGGCCTGGAG	7807	G	_
			TTC CAGGTCT	TCCGTCG		

			GAG GTCCGGA GGGCAGT		
			— CC		
GAM1959	GEM	3'	TTTGATGGCCCTTGTGAA 11767	—	TCTTCC
			TTCG CAGG GTCGTCAGG		
			AAGT GTTC CGGTAGTTT		
			T C_____		
GAM1959	GLO1	3'	CTCTAGTGGAAGACCTTTGGA 13528	C	TCGTC
			TTCG AGGTCTTCCG AGGG		
			AGGT TCCAGAAGGT TCTC		
			T GA_____		
GAM1959	GNAI3	3'	TCCTGGAAATGAGACCTGGTGG 13242	—	TC CG
	A		TTCGC AGGTCT CGT TCAGGG		
			AGGTG TCCAGA GTA GGTCT		
			G — AA		
GAM1959	GPR44	3'	TTGATGTGCCTGTGAA 11176		CTTCCGT
			TTCGCAGGT CGTCAG		
			AAGTGTCCG GTAGTT		
			T_____		
GAM1959	GPRK7	3'	CCTGAAGGAGACCTATGG 29227	C	CGTCG
			TCG AGGTCTTC TCAGG		
			GGT TCCAGAGG AGTCC		
			A A_____		
GAM1959	GPRK7	3'	TCCACACGTGGAAATCTGTGGA 29230	C	T CA
			TTCGCAGGT TTCCG CGT GGG		
			AGGTGTCTA AAGGT GCA CCT		
			— — CA		
GAM1959	GRM6	3'	CCCTGAATAAAGTTTTGTGG 6507	T	CCGTCG
			TCGCAGG CTT TCAGGG		
			GGTGTTC GAA AGTCCC		
			T ATA_____		
GAM1959	HDAC4	3'	CCCTGCAAATGGATGGCTTGTG 12661	T	CGT
	AA		TTCGCAGGTC TCCGT CAGGG		
			AAGTGTTCGG AGGTA GTCCC		
			T AAC		
GAM1959	HDAC7A	3'	TCCTGGCGATGCCCTGGTGG 17714	—	TCTTC
			TTCGC AGG CGTCGTCAGGG		
			AGGTG TCC GTAGCGGTCCT		
			G C_____		
GAM1959	HDAC7A	3'	TCCTGGCGATGCCCTGGTGG 18684	—	TCTTC
			TTCGC AGG CGTCGTCAGGG		

		AGGTG TCC GTAGCGGTCCT	
		G C____	
GAM1959 HTR1D	5'	CCAAATGTGTGGAGGTCTGTGG 6528	GT _ T CA G
		TGCGAG CTTC CG CGT GG	
		GGTGTC GAGG GT GTA CC	
		TG T _ AA	
GAM1959 IFNAR2	3'	CTTGAGTGGGCCCTGTGAG 6555	TCT TCG
		TTCGCAGG TCCG TCAGG	
		GAGTGTCC GGGT AGTTC	
		C__ G__	
GAM1959 IGFBP5	5'	TTCTGACCCGCTCAGGCTTGAG 6203	G TC_ TC
G		TC CAGGTCT CG GTCAGGG	
		GG GTTCGGA GC CAGTCTT	
		A CTC C_	
GAM1959 IL2RB	3'	CCCTGATGCTGCCAGGCCTGGG 6571	G TC T
A		TC CAGGTCT CG CGTCAGGG	
		AG GTCCGGA GT GTAGTCCC	
		G CC C	
GAM1959 IL2RB	3'	CCTTGGGAGCAGGTGCTTGTGG 6572	CTT _ CG
A		TTCGCAGGT CC GT TCAGGG	
		AGGTGTTCC GG CG GGTTC	
		T__ A AG	
GAM1959 IRF1	3'	CTTTGGCTGAGGGGCTTGGGAA 32173	G TC TC
		TTC CAGGTCT CG GTCAGGG	
		AAG GTTCGGG GT CGGTTTC	
		G GA _	
GAM1959 IRTA1	3'	TTTTGGTGAATTGGGATTTGC 25305	CCG GT
		GCAGGTCTT TC CAGGG	
		CGTTAGGG AG GTTTT	
		TTA TG	
GAM1959 ISLR	3'	TTCTGATGATTTGGGGGCTTGG 12073	G C_
GAG		TTC CAGGTCTTC GTCGTCAGGG	
		GAG GTTCGGGGG TAGTAGTCTT	
		G TT	
GAM1959 ITK	3'	CTCTGACGGTGGAGAACCATGT 12075	_ CT GT
G		CGCA GGT TCC CGTCAGGG	
		GTGT CCA AGG GCAGTCTC	
		A AG TG	
GAM1959 ITPR3	3'	TTTTGGCGGCTGCGGCCTCTGG 8001	C TTCC
		TCG AGGTC GTCGTCAGGG	

			GGT TCCGG CGGCGGTTTT		
			C CGT_		
GAM1959	ITSN1	3'	TTTTGGCTCGGAGGCCTGTGA 8958	T TC	
			TCGCAGGTCT CCG GTCAGGG		
			AGTGTCCGGA GGC CGGTTTT		
			_ T_		
GAM1959	KCNJ10	3'	CTCTGATGGTCACTTTGTGG 8026	TCTTCCG	
			TCGCAGG TCGTCAGGG		
			GGTGTTT GGTAGTCTC		
			CACT__		
GAM1959	KCNK1	5'	TTTGCGGCGGCGGTGGA 8033	AGGTCTT	
			TTCGC CCGTCGTCAGG		
			AGGTG GGCGGCGGTTT		
			GC__		
GAM1959	KCNK5	3'	TCCTGACTCACAGGGCCTGGAA 9829	G CCGTC	
			TTC CAGGTCTT GTCAGGG		
			AAG GTCCGGA CAGTCCT		
			_ CACT_		
GAM1959	KCNS2	3'	TTCCATTGGACTGGAGGCTTGT 33901	C GTCA	
	GG		TCGCAGGTCTTC GTC GGG		
			GGTGTTCCGAGG CAG CCT		
			T GTTA TT		
GAM1959	KDR	3'	CCTGGAAGAGGCTTGTGA 8053	CCGTCG	
			TCGCAGGTCTT TCAGG		
			AGTGTTCCGAG GTTCC		
			AA__		
GAM1959	KIAA0857	3'	TCTTCAGGAGAGGGCCTGTGG 33121	CG GTC	
			TCGCAGGTCTTC TC AGGG		
			GGTGTCGGGAG GG TTCT		
			A_ AC_		
GAM1959	KIF5C	3'	CTTGTCGGGGGGTTTGAGG 10854	G GT TCGT	
			TC CAG CTTCCG CAGG		
			GG GTT GGGGGC GTTC		
			A TG CT__		
GAM1959	KIFC3	5'	CCCTCGCTGCGGGGCCTGTGGA 12081	TT C C	
			TTCGCAGGTC CCGT GT AGGG		
			AGGTGTCCGG GGCG CG TCCC		
			_ T C		
GAM1959	LAMC1	3'	TCCTGATGATCCTAACCTGC 8078	CTTCC	
			GCAGGT GTCGTCAGGG		

		CGTCCA TAGTAGTCCT		
		ATCC_		
GAM1959 LBR	3'	TCTTGATCCAAAGTTTGTGAA 29854	T	CCGTC
		TTCGCAGG CTT GTCAGGG		
		AAGTGTTT GAA TAGTTCT		
		_ ACC_		
GAM1959 LFNG	3'	CTCTGCTCCGAGGGCCAGTGG 44509	A	C TC T
		TCGC GGTCTTC G G CAGGG		
		GGTG CCGGGAG C C GTCTC		
		A _CT_		
GAM1959 LIF	3'	CCTCTGGGAGATTGTGGA 8095	G	TCGTC
		TTCGCAG TCTTCCG AGG		
		AGGTGTT AGAGGGT TCC		
		_ C_		
GAM1959 LIFR	3'	CTTGGAGGGATCCTGTGAA 8104	TCT	G GT
		TTCGCAGG TCC TC CAGG		
		AAGTGTC AGG AG GTTC		
		T_ G_		
GAM1959 LIFR	3'	TTCTGAGCTTTATGATCTGTGG 8106	TTCC_	CG
A		TTCGCAGGTC GT TCAGGG		
		AGGTGTCTAG CG AGTCTT		
		TATTT _		
GAM1959 LIMK1	3'	CCTGAGGGCCTGCGGA 18797	TCCGTCG	
		TTCGCAGGTCT TCAGG		
		AGGCGTCCGGG AGTCC		

GAM1959 LTB	3'	CCCTGGCGGCGGGGACC 14315	T	
		GGTCT CCGTCGTCAGGG		
		CCAGG GGCGGCGGTCCC		
		-		
GAM1959 M6PR	5'	CTCTGGGACCGGGGTCTGCGG 8164	T	C G
		TCGCAGG CTTC GTC TCAGGG		
		GGCGTCT GGGG CAG GGTCTC		
		_ C _		
GAM1959 MADH5	5'	CTTTGAGTTACAGGAAGGTCTC 12523	C GT	_ CG_
CGAA		TCG AG CTTCC GT TCAGGG		
		AGC TC GAAGG CA AGTTTC		
		C TG A TTG		
GAM1959 MAML1	3'	CCTGGGCAGGGTCTGTGG 16497	GT	_ GTCGT
		TCGCAG CTT CC CAGG		

GGTGTC GGA GG GTCC
TG C _____

GAM1959 MAP1A 3' TCTTGGACAGAGGATCTGGGAG 8187 G C GT
TTC CAGGTCTTC GTC CAGGG
||| ||||| ||| |||||
GAG GTCTAGGAG CAG GTTCT
G A _

GAM1959 MBD3 3' CCCTGATGGGGCCTGACCGCGG 10018 A TT_ G
TCGC GGTC CC TCGTCAGGG
||| ||| || |||||
GGCG CCAG GG GGTAGTCCC
_ TCC _

GAM1959 MBP 3' CTCTGGTGGTGTGTGCTTGCGG 43221 CTTC GT GT
A TTCGCAGGT C C CAGGG
||| ||| | | |||
AGGCGTTCG G G GTCTC
TGT_ TG TG

GAM1959 MEF2C 3' TCTTGAATGTGAAGATCTGTC 8214 _ _ CG
GA TCG CAGGTCTTC CGT TCAGGG
||| ||||| ||| |||||
AGC GTCTAGAAG GTA GGTTC
T T A_

GAM1959 MEF2D 3' CCCTGGGGATGGGGTGGTCTGT 46307 GT_ G
GAA TTCGCAG C TTCCGTC TCAGGG
||| ||| | ||||| |||||
AAGTGTC G GGGGTAG GGTCCC
TG T G

GAM1959 METTL1 3' CTTTGGACCATAGGGGATCTTT 23307 C CG C _
GGA TTCG AGGTCTTC T GTC AGGG
||| ||||| | ||| |||
AGGT TCTAGGGG A CAG TTTC
T AT C G

GAM1959 METTL1 3' CTTTGGACCATAGGGGATCTTT 23312 C CG C _
GGA TTCG AGGTCTTC T GTC AGGG
||| ||||| | ||| |||
AGGT TCTAGGGG A CAG TTTC
T AT C G

GAM1959 MHC2TA 3' CCTTGAAC TGGGTACTTGTGGA 5778 CT TCG
TTCGCAGGT TCCG TCAGGG
||| ||| ||| |||||
AGGTGTTCA GGGT AGTTCC
T_ CA_

GAM1959 MLC1 3' CCCTGCCAGGGGGTTTGAGGA 17523 G T GTC T
TTC CAGG CTTCC G CAGGG
||| ||| |||| | |||||
AGG GTTT GGGGG C GTCCC
A _ AC_

GAM1959 MLC1 3' CCCTGCCAGGGGGTTTGAGGA 29217 G T GTC T
TTC CAGG CTTCC G CAGGG
||| ||| |||| | |||||

			AGG GTTT GGGGG C GTCCC		
			A _ AC__		
GAM1959	MMP16	3'	TTTTGTCAGGTGGGAGATTTGG 12580	G	GT GT_
	AA		TTC CAGGTCTTCC C CAGGG		
			AAG GTTTAGAGGG G GTTTT		
			_ TG ACT		
GAM1959	MTCP1	5'	CCCAGGGTGGGAGACCTGGAA 15486	G	GT GTCA
			TTC CAGGTCTTCC C GGG		
			AAG GTCCAGAGGG G CCC		
			_ TG GA__		
GAM1959	MTMR8	3'	TCCATGGGTGGAACTTGTGAG 17747	C	GT GT _
			TTCGCAGGT TTCC C CA GGG		
			GAGTGTTCA AAGG G GT CCT		
			_ TG __ A		
GAM1959	MVK	3'	CCTGAGAGGTTTGTGGA 30425	GT	CCGTCG G
			TTCGCAG CTT TCAGG		
			AGGTGTT GAG AGTCC		
			TG _____ A		
GAM1959	NAGA	3'	CCCTGGTGGCTCTCCCCTTTGG 5799	C	TCTTCC GT
	A		TTCG AGG GTC CAGGG		
			AGGT TCC CGG GTCCC		
			T CCTCT_ TG		
GAM1959	NAGA	3'	CTCTGAAATCAGGATTTGGAA 5802	G	CCGTCG
			TTC CAGGTCTT TCAGGG		
			AAG GTTTAGGA AGTCTC		
			_ CTAA__		
GAM1959	NCOA6	5'	CCTTGAAAAATTGGAAGATCTG 15289		TCG__
	T		GCAGGTCTTCCG TCAGGG		
			TGTCTAGAAGGT AGTTCC		
			TAAAA		
GAM1959	NPC1	3'	CTTTGAACGTAGCGCCTGTGAA 5814	C C	CG
			TTCGCAGGT TT CGT TCAGGG		
			AAGTGTCCG GA GCA AGTTTC		
			C T _		
GAM1959	NPTX2	3'	TTCTGATGATGGAATTC 44425	TC	
			GG TTCCGTCGTCAGGG		
			CT AAGGTAGTAGTCTT		
			TT		
GAM1959	NR3C2	3'	CCCGCTTGGGGCATTGTGG 6595	C	TCGTCA
			TCGCAGGT TTCCG GGG		

GGTGTTTA GGGGT CCC
C TCG____

GAM1959 Nrap 3' TCCTCCATGGAGGGCCTGC 29239 CGTC
GCAGGTCTTCCGT AGGG
||||||| |||
CGTCCGGGAGGTA TCCT
CC__

GAM1959 NRIP1 3' TCTTGATCGTTGTGGAAGGTTT 30121 G GT T__ _
GGAG C CAG CTTCCG CG TCAGGG
| || |||| | |||||
G GTT GAAGGT GC AGTTCT
_ TG GTT T

GAM1959 OGG1 5' TCTTGGTGAAGACAGGGTTCGT 18811 A GT CCG_ GT
GG TCGC G CTT TC CAGGG
|||| | || | |||||
GGTG T GGA AG GTTCT
C TG CAGA TG

GAM1959 OGG1 5' TCTTGGTGAAGACAGGGTTCGT 18816 A GT CCG_ GT
GG TCGC G CTT TC CAGGG
|||| | || | |||||
GGTG T GGA AG GTTCT
C TG CAGA TG

GAM1959 OGG1 5' TCTTGGTGAAGACAGGGTTCGT 8394 A GT CCG_ GT
GG TCGC G CTT TC CAGGG
|||| | || | |||||
GGTG T GGA AG GTTCT
C TG CAGA TG

GAM1959 OGT 5' TCTGATGATGCGCTGTGA 9663 GTCTTC
TCGCAG CGTCGTCAGG
||||| |||||
AGTGTC GTAGTAGTCT
GC____

GAM1959 OSM 3' CCCTGGTGGTGGATCCTGGAA 21754 G TCT GT GT
TTC CAGG TCC C CAGGG
||| ||| || | |||||
AAG GTCC AGG G GTCCC
_ T__ TG TG

GAM1959 P2RY6 3' CTCTGGCCCAGACCCTGTGG 10355 _ TCCGTC
TCGCAGG TCT GTCAGGG
||||| ||| |||||
GGTGTCC AGA CGGTCTC
C CC____

GAM1959 PCDH11X 3' TTCTGATTATCAGATTTGT 26795 TCC C
GCAGGTCT GT GTCAGGG
||||| || |||||
TGTTTAGA TA TAGTCTT
C__ T

GAM1959 PCDH11X 3' TTCTGATTATCAGATTTGT 26810 TCC C
GCAGGTCT GT GTCAGGG
||||| || |||||

			TGTTTAGA TA TAGTCTT		
			C__ T		
GAM1959	PCDH11Y	3'	TCCTCATATCTGGAAACTTGTG 26827	C	TC_ C
	AA		TTCGCAGGT TTCCG GT AGGG		
			AAGTGTTCA AAGGT TA TCCT		
			_ CTA C		
GAM1959	PCDH11Y	3'	TTCTGATTATCAGATTTGT 26829	TCC	C
			GCAGGTCT GT GTCAGGG		
			TGTTTAGA TA TAGTCTT		
			C__ T		
GAM1959	PEA15	3'	TCCTGGCCCCCTGGGCTTGTGA 9851	TCCGTC	
	A		TTCGCAGGTCT GTCAGGG		
			AAGTGTTCTGGG CGGTCCT		
			TCCCC_		
GAM1959	PFKFB3	3'	TCTTGCCCTGGGGGGCTTGGA 40319	G	TC T
			TTC CAGGTCTTCCG G CAGGG		
			AAG GTTCGGGGGGT C GTTCT		
			_ CC _		
GAM1959	PHB	3'	TCCTGTCACTGATGGAAGGTTT 8494	GT	_ _
	GCGGA		GCAG CTTCCGTC GT CAGGG		
			CGTT GAAGGTAG CA GTCCT		
			TG T CT		
GAM1959	PIG8	3'	CCGTTGGTGGTGGGAGGCCAGC 11315	A	GT GT _
	GG		TCGC GGTCTTCC C CAG GG		
			GGCG CCGGAGGG G GTT CC		
			A TG TG G T		
GAM1959	PIK3C2B	3'	TCCTGATTTAAAGAGATCTGTG 8509	CCGTC	
			CGCAGGTCTT GTCAGGG		
			GTGTCTAGAG TAGTCCT		
			AAATT		
GAM1959	PKD1	3'	TCCTGGCGGGGGTGGGCCGTGG 5842	A	T G
	A		TTCGC GGTCT CC TCGTCAGGG		
			AGGTG CCGGG GG GGCGGTCCT		
			_ T G		
GAM1959	PMM2	3'	CTTGATGGGGGCTGTGAG 35679	GTCTT	G
			TTCGCAG CC TCGTCAGG		
			GAGTGTC GG GGTAGTTC		
			_ _ G		
GAM1959	PPARGC1	3'	TCTTGGTGATGGAGTGTGCGTG 14932	G C_	GT
	TG		CGCA GT TTCCGTC CAGGG		

		GTGT CG GAGGTAG GTTCT		
		G TGT TG		
GAM1959 PPIG	5'	TTCTGGCGGCGGTAGATTTG 11202	T	
		CAGGTCT CCGTCGTCAGGG		
		GTTTAGA GGCGGCGGTCTT		
		T		
GAM1959 PRDM4	3'	CCTGATGAGTACATGTGGA 14785	G	CTTCCG
		TTCGCA GT TCGTCAGG		
		AGGTGT CA AGTAGTCC		
		A TG__		
GAM1959 PReX1	3'	CTCTGGAGCTGGGATTTGGGAG 21885	G	TT TCG
		TTC CAGGTC CCG TCAGGG		
		GAG GTTTAG GGT GGTCTC		
		G _ CGA		
GAM1959 PROK1	3'	CCTTCACGTGAGGTCTGTGAG 26199	GT	TC CGTC
		TTCGCAG CT CGT AGG		
		GAGTGTC GA GCA TCC		
		TG GT CT__		
GAM1959 PSAP	3'	CCTTGTTTGGGGTTCTGTGG 34373	TC	TCGT
		TCGCAGG TTCCG CAGGG		
		GGTGTCT GGGGT GTTCC		
		T_ TT__		
GAM1959 PTGFRN	3'	CCTTGCCCCGGGCCTGTGG 33363	CTT	TC
		TCGCAGGT CCG GTCAGGG		
		GGTGTCCG GGC CGGTTCC		
		_ C_		
GAM1959 PTGS1	3'	TTCTGGCCAAGGGGTGGGCCTG 27901	_	GTC
TGAA		TCGCAGGTCT TCC GTCAGGG		
		AGTGTCCGGG GGG CGGTCTT		
		TG AAC		
GAM1959 PTGS1	3'	TTCTGGCCAAGGGGTGGGCCTG 6680	_	GTC
TGAA		TCGCAGGTCT TCC GTCAGGG		
		AGTGTCCGGG GGG CGGTCTT		
		TG AAC		
GAM1959 PTK2B	3'	CCTGAGGGAGGACCTGGGG 10310	G	GTCG
		TC CAGGTCTTCC TCAGG		
		GG GTCCAGGAGG AGTCC		
		G G__		
GAM1959 PTPRG	5'	CCGAGCGCGGGGGGCCCGTGGA 8726	A	T CA
		TTCGC GGTCTTCCG CGT GG		

			AGGTG CCGGGGGGC GCG CC		
			C _ AG		
GAM1959	RAD9	3'	TTTGGCGCTGACTTGAA 10932 G	TTCCGT	
			TTC CAGGTC CGTCAGG		
			AAG GTTCAG GCGGTTT		
			_ TC__		
GAM1959	RALBP1	3'	CTCTGATGCTCTGAGGCTTCTG 13659 C	CCGT	
	G		TCG AGGTCTT CGTCAGGG		
			GGT TTCGGAG GTAGTCTC		
			C TCTC		
GAM1959	RANBP3	5'	CTCTGAAGAGGAAGCCTGTGAG 14237 T G G		
			TTCGCAGG CTTCC TC TCAGGG		
			GAGTGTCC GAAGG AG AGTCTC		
			_ _ A		
GAM1959	RASSF1	3'	CCCTGGGCCAGGGTCTGTG 14038 GT CC GT		
			CGCAG CTT GTC CAGGG		
			GTGTC GGA CGG GTCCC		
			TG C_ _		
GAM1959	RBBP5	3'	CTCTCAGGAATGAAGATTTGTG 11486 CG GTC		
	AA		TTCGCAGGTCTTC TC AGGG		
			AAGTGTTTAGAAG AG TCTC		
			TA GAC		
GAM1959	RENT1	3'	CCTTTGGAAGATTTGGTGGA 8814 _ TCGTC		
			TTCGC AGGTCTTCCG AGG		
			AGGTG TTTAGAAGGT TCC		
			G T__		
GAM1959	RGS3	3'	CCCTGCTGCGGAGACCGCGGA 29306 A T C T		
			TTCGC GGTCT CCGT G CAGGG		
			AGGCG CCAGA GGCG C GTCCC		
			_ _ T _		
GAM1959	RGS3	3'	CCCTGCTGCGGAGACCGCGGA 29308 A T C T		
			TTCGC GGTCT CCGT G CAGGG		
			AGGCG CCAGA GGCG C GTCCC		
			_ _ T _		
GAM1959	RGS3	3'	CCCTGCTGCGGAGACCGCGGA 28282 A T C T		
			TTCGC GGTCT CCGT G CAGGG		
			AGGCG CCAGA GGCG C GTCCC		
			_ _ T _		
GAM1959	RGS3	3'	CCCTGCTGCGGAGACCGCGGA 28668 A T C T		
			TTCGC GGTCT CCGT G CAGGG		

			AGGCG CCAGA GGCG C GTCCC		
			— — T —		
GAM1959	RGS3	3'	CCCTGCTGCGGAGACCGCGGA 19423	A	T C T
			TTCGC GGTCT CCGT G CAGGG		
			AGGCG CCAGA GGCG C GTCCC		
			— — T —		
GAM1959	RGS3	3'	CCCTGCTGCGGAGACCGCGGA 22088	A	T C T
			TTCGC GGTCT CCGT G CAGGG		
			AGGCG CCAGA GGCG C GTCCC		
			— — T —		
GAM1959	RNF4	3'	CCCTGACAGCACAGGGCCTGGG 8841	G	CC C
	G		TC CAGGTCTT GT GTCAGGG		
			GG GTCCGGGA CG CAGTCCC		
			G CA A		
GAM1959	RP42	3'	TCCTGTCTTGAAGATTTTGAG 21803	C	CGTCGT
			TTCG AGGTCTTC CAGGG		
			GAGT TTTAGAAG GTCCT		
			— TTCT —		
GAM1959	RPE	3'	CCTGGAAGGATCTGGGAA 31153	G	CCGTCG
			TTC CAGGTCTT TCAGG		
			AAG GTCTAGGA GGTCC		
			G AA —		
GAM1959	SCD	3'	TTTGGCTGAGACCTGGGA 11499	G	CCGTC
			TC CAGGTCTT GTCAGG		
			AG GTCCAGAG CGGTTT		
			G T —		
GAM1959	SCN1A	5'	CCTGATCCAGTCTGTGAA 42834	T	TCCGTC
			TTCGCAGG CT GTCAGG		
			AAGTGTCT GA TAGTCC		
			— CC —		
GAM1959	SDHD	3'	CTTTGAGGAAAAGGTTTGAGAG 8896	G	GT CCG G
			TTC CAG CTT TC TCAGGG		
			GAG GTT GAA AG AGTTTC		
			A TG A — G		
GAM1959	SERPINB5	3'	TCCTATAAGGAAGATTTGGAA 8495	G	GTC C
			TTC CAGGTCTTCC GT AGGG		
			AAG GTTTAGAAGG TA TCCT		
			— AA —		
GAM1959	SF1	5'	CCCTCCCCCGGGAGGCTTGCG 11001		TCGTC
	AA		TTCGCAGGTCTTCCG AGGG		

			AAGCGTTCGGAGGGC	TCCC	
			CCCC		
GAM1959	SH3BP2	3'	TCTGATGGTCGTTGTGG	8951	GTCTTC _
			TCGCAG CG TCGTCAGG		
			GGTGTT GC GGTAGTCT		
			_____ T		
GAM1959	SIM2	3'	CTCTGGCCCCACACAGATCTGT	11518	TCCGTC
			GCAGGTCT GTCAGGG		
			TGTCTAGA CGGTCTC		
			CACACC		
GAM1959	SIM2	3'	CTATGGTGGAAATTTGTGG	14311	C GT C
			TCGCAGGT TTCC CGT AG		
			GGTGTTTA AAGG GTA TC		
			_ TG _		
GAM1959	SLC1A5	3'	TTTTGGCGGCTGTAGTTGTGG	38404	GT TCC
			TCGCAG CT GTCGTCAGGG		
			GGTGTT GA CGGCGGTTTT		
			_ TGT		
GAM1959	SLC1A5	3'	TTTTGGCGGCTGTAGTTGTGG	12144	GT TCC
			TCGCAG CT GTCGTCAGGG		
			GGTGTT GA CGGCGGTTTT		
			_ TGT		
GAM1959	SLC30A3	5'	CTCTGGTGGCCCCGCCGCCCTG	9525	TCTTCC_ GT
	CGG		TCGCAGG GTC CAGGG		
			GGCGTCC CGG GTCTC		
			CGCCGCCC TG		
GAM1959	SLC6A8	3'	TGAGGGTGGCGGGCCTGCGG	12153	T GT G
			TCGCAGGTCT CC C TCA		
			GGCGTCCGGG GG G AGT		
			C TG G		
GAM1959	SLC7A6	3'	TCCTGATAACAAGACTCTGTGG	10133	_ CC CG
			TCGCAG GTCTT GT TCAGGG		
			GGTGTC CAGAA CA AGTCCT		
			T _ AT		
GAM1959	SOX12	3'	TCCTGGTGAAGCATGGCTTCGG	13831	C TTCCG GT
			TCG AGGTC TC CAGGG		
			GGC TTCGG AG GTCCT		
			_ TACGA TG		
GAM1959	SRGAP2	3'	CTCTGGTGCTCCTAACACCTGT	36879	CTTCCGT_ GT
	GAG		TTCGCAGGT C CAGGG		

			GAGTGTCCA	G	GTCTC	
			CAATCCTC	TG		
GAM1959	STAM	3'	TCTTGGTGGCAGATACCTGC	9542	CT C	GT
			GCAGGT TC GTC CAGGG			
			CGTCCA AG CGG GTTCT			
			T_ A	TG		
GAM1959	SUPT6H	5'	TTTGATGACCGCCTGGAG	30293	G	CTTCC
			TTC CAGGT GTCGTCAGG			
			GAG GTCCG CAGTAGTTT			
			_ C_			
GAM1959	TAF1C	5'	TCCAAACCGGAAGACCGTGG	12237	A	TC CA
			TCGC GGTCTTCCG GT GGG			
			GGTG CCAGAAGGC CA CCT			
			_ _ AA			
GAM1959	TAF7	5'	CCCGGACGGAGGGCCGGCGAG	12175	A	GTCA
			TTCGC GGTCTTCCGTC GGG			
			GAGCG CCGGGAGGCAG CCC			
			G G_			
GAM1959	TAF7	5'	CTTTGTTCCGGGAGAGTTTGTG	12177	_	TCGT
	AG		TTCGCAGG TCTTCCG CAGGG			
			GAGTGTTT AGAGGGC GTTTC			
			G CTT_			
GAM1959	TAL1	3'	TCCAACGTTTGAAGATCCTGT	9171	_	T_ CA
	GAG		TCGCAGG TCTTCCG CGT GGG			
			AGTGTCC AGAAGGT GCA CCT			
			T TT A_			
GAM1959	TCF2	3'	TTCTGATGAGAAAGGCCTGAGG	13204	G	CCG
			TC CAGGTCTT TCGTCAGGG			
			GG GTCCGGAA AGTAGTCTT			
			A AG_			
GAM1959	TCF2	3'	TTTTGTTTGGGGGCTTTGTGGA	13205	T	TCGT
			TTCGCAGG CTTC CG CAGGG			
			AGGTGTTT GGGGGT GTTTT			
			C TT_			
GAM1959	TCF3	3'	CCCTGCATTGAGGCCTTGTGGA	35007	T	C C T
			TTCGCAGG CTTC GT G CAGGG			
			AGGTGTTT GGAG TA C GTCCC			
			C T _ _			
GAM1959	TCF4	5'	TCTTGGCTGTGTGTCTGCGGA	9187	TCTTC	TC
			TTCGCAGG CG GTCAGGG			

AGGCGTCT GT CGGTTCT
 GT__ GT
 GAM1959 TCIRG1 5' TCCTGCCCCGGGGGGCCTGGTGG 12690 _ TC T
 TCGC AGGTCTTCCG G CAGGG
 |||| ||||| | ||||
 GGTG TCCGGGGGGG C GTCCT
 G C__
 GAM1959 THRA 5' GGGGGTGGGTGGCCTGTGG 9258 T GT G
 TCGCAGGTC TCC C TC
 ||||| || | ||
 GGTGTCCGG GGG G GG
 T TG G
 GAM1959 TIC 3' TCTGGGCAGGGACCTCGG 14830 C CC GT
 TCG AGGTCTT GTC CAGG
 || ||||| || ||||
 GGC TCCAGGG CGG GTCT
 _ A_ _
 GAM1959 TIM3 3' TCTTGACGTGGGGTCTCTGGA 26526 G TC T
 TC CAGG TTCCG CGTCAGGG
 || |||| |||||
 AG GTCT GGGGT GCAGTTCT
 _ CT _
 GAM1959 TOMM22 3' TTTTGGCTGTTAGACCTGTG 21517 TC TC
 CGCAGGTCT CG GTCAGGG
 ||||| || |||||
 GTGTCCAGA GT CGGTTTT
 TT _
 GAM1959 TOP3B 5' TTGGCCGGCGGAGGACCCGCGA 10039 A _ GG
 G TTCCG GGTCTTCCGTCG TCAG
 |||| ||||| ||||
 GAGCG CCAGGAGGCGGC GGTT
 C C
 GAM1959 TRIM9 3' TCTCAGTAATGGGAGATCTTGA 17520 C CG CA
 G TTCG AGGTCTTCCGT T GGG
 |||| ||||| | |||
 GAGT TCTAGAGGGTA G TCT
 _ AT AC
 GAM1959 TRPM6 5' CTTTGGGAGCAGGGCCTGC 19199 CC CG
 GCAGGTCTT GT TCAGGG
 ||||| || |||||
 CGTCCGGGA CG GGTTTC
 _ AG
 GAM1959 UBE2L3 3' CCCGAAATGGGGGGCCTGC 9358 CG A
 GCAGGTCTTCCGT TC GGG
 ||||| || |||
 CGTCCGGGGGGTA AG CCC
 A_ _
 GAM1959 UBE2V1 3' CCTTGGTGGTTGAACTTGAG 9370 G CT CG GT
 TTC CAGGT TC TC CAGGG
 || |||| || || ||||

			GAG GTTCA AG GG GTTCC		
			— — TT TG		
GAM1959	UBE2V1	3'	CTCTAGCCTGGGGGGCTTGT 9372		TC TC
			GCAGGTCTTCCG G AGGG		
			TGTTCGGGGGGT C TCTC		
			C_ GA		
GAM1959	UBE2V1	3'	CCTTG GTGGTTGAACTTGGAG 22769	G	CT CG GT
			TTC CAGGT TC TC CAGGG		
			GAG GTTCA AG GG GTTCC		
			— — TT TG		
GAM1959	UBE2V1	3'	CTCTAGCCTGGGGGGCTTGT 22771		TC TC
			GCAGGTCTTCCG G AGGG		
			TGTTCGGGGGGT C TCTC		
			C_ GA		
GAM1959	UBE2V1	3'	CCTTG GTGGTTGAACTTGGAG 22522	G	CT CG GT
			TTC CAGGT TC TC CAGGG		
			GAG GTTCA AG GG GTTCC		
			— — TT TG		
GAM1959	UBE2V1	3'	CTCTAGCCTGGGGGGCTTGT 22524		TC TC
			GCAGGTCTTCCG G AGGG		
			TGTTCGGGGGGT C TCTC		
			C_ GA		
GAM1959	UQCRC1	5'	CCCTGGGCTCGAACCTGCGGA 9391		CT C_ GT
			TTCGCAGGT TC GTC CAGGG		
			AGGCGTCCA AG CGG GTCCC		
			— CT —		
GAM1959	USP11	5'	CCCTCAAGGAGGACTGGTGGGA 11020	A	GTCGTC
			TTCGC GGTCTTCC AGGG		
			AGGTG TCAGGAGG TCCC		
			G AAC_		
GAM1959	VANGL2	3'	CCCTGATGATGTAACACCTGCG 35478		C C
	A		TCGCAGGT TT CGTCGTCAGGG		
			AGCGTCCA AA GTAGTAGTCCC		
			C T		
GAM1959	VIPR2	3'	CCCTGGT GATGGGGTTACGTGG 9413	G G C_	GT
	GG		TC CA GT TTCCGTC CAGGG		
			GG GT CA GGGGTAG GTCCC		
			G G TT TG		
GAM1959	VLDLR	3'	CTTTGACCTCAATGGAGGTTTG 34451	T	C_
	C		GCAGG CTTCCGT GTCAGGG		

			CGTTT GGAGGTA CAGTTTC		
			ACTC		
GAM1959	WWP2	3'	CTCTGATGATGGAGATGAAGTG 30623	AG_ T	
	AA		TTCGC GTCT CCGTCGTCAGGG		
			AAGTG TAGA GGTAGTAGTCTC		
			AAG _		
GAM1959	ZNF132	5'	CCCTGATGATGGCCCTGT 9485	TCTT	
			GCAGG CCGTCGTCAGGG		
			TGTCC GGTAGTAGTCCC		
			C__		
GAM1959	ZNF24	5'	TTTGCGCCGAGTGCCTGTGAA 13839	C T T	
			TTCGCAGGT TTCCG CG CAGG		
			AAGTGTCCG GAGGC GC GTTT		
			T C _		
GAM1959	ZNF266	5'	TTTTGATGATCTGGCTGTGGA 42601	G TTCC	
			TTCGCAG TC GTCGTCAGGG		
			AGGTGTC GG TAGTAGTTTT		
			_ TC__		
GAM1959	ZNF268	5'	TCTGGCTGCAGATCTGGAG 31502	G TCC C	
			TTC CAGGTCT GT GTCAGG		
			GAG GTCTAGA CG CGGTCT		
			_ _ T		
GAM1959	ZNF35	3'	CCTTGGTATTGTAAAGATCTGG 9464	G C_ TCG	
	GGA		TTC CAGGTCTT CG TCAGGG		
			AGG GTCTAGAA GT GGTTC		
			G AT TAT		
GAM1959	A4GALT	3'	CCAGTGGGAGGCTGTGGA 18895	G TCGTCA	
			TTCGCAG TCTTCCG GG		
			AGGTGTC GGAGGGT CC		
			_ GA__		
GAM1959	ACAS2	5'	CCTTGACAGCCAGTCTGTGAA 29265	T TCC C	
			TTCGCAGG CT GT GTCAGGG		
			AAGTGTCT GA CG CAGTTCC		
			_ C_ A		
GAM1959	ACTR1A	3'	TCTTGAGTCGGAGTGTTCGCA 31534	TC TCG	
	G		TTCGCAGG TTCCG TCAGGG		
			GAGCGTTT GAGGC AGTTCT		
			GT TG_		
GAM1959	AF053356_CDS3	5'	CCCTGGGCCTGGGTCTGCGG 23428	GT TCC GT	
			TTCGCAG CT GTC CAGGG		

			GGCGTC GG CGG GTCCC	
			TG TC_ _	
GAM1959	AKAP7	3'	TCTGGTGCAATCTGTGAA 11254	CTTCC T GT
			TTCGCAGGT G C CAGG	
			AAGTGTCTA C G GTCT	
			A_ _ _TG	
GAM1959	AKAP7	3'	TCTGGTGCAATCTGTGAA 28907	CTTCC T GT
			TTCGCAGGT G C CAGG	
			AAGTGTCTA C G GTCT	
			A_ _ _TG	
GAM1959	AKAP7	3'	TCTGGTGCAATCTGTGAA 18517	CTTCC T GT
			TTCGCAGGT G C CAGG	
			AAGTGTCTA C G GTCT	
			A_ _ _TG	
GAM1959	AMOTL2	3'	CCCACCTGGAGGGTTTGGGAG 18294	G GT TC CA
			TTC CAG CTTCCG GT GGG	
			GAG GTT GGAGGT CA CCC	
			G TG C_ _	
GAM1959	AP3D1	3'	CTTGGGCAGGACCTGTGAG 10045	_ GTCGT
			TTCGCAGGTCTT CC CAGG	
			GAGTGTCCAGGA GG GTTC	
			C _ _ _	
GAM1959	AP3D1	3'	TCCTGGGCCAGGGCCTGATGG 10050	_ CC GT
			TCG CAGGTCTT GTC CAGGG	
			GGT GTCCGGGA CGG GTCCT	
			A C_ _	
GAM1959	APCL	5'	GCCACCGATGGAGGGTCGTGG 12502	A GT TCA G
			TCGC G CTTCCGTCG GG	
			GGTG C GGAGGTAGC CC	
			_ TG CA_ GA	
GAM1959	API5	3'	AAAACAACAGATGGGGGGTTTG 13360	GT _ CAGGG
	TGGA		TCGCAG CTTCCGTC GT	
			GGTGTT GGGGGTAG CA	
			TG A AAAAAAT	
GAM1959	APOARGC	3'	TTTGGCACAACTTGCGAG 23690	CTTCC C
			TTCGCAGGT GT GTCAGG	
			GAGCGTTCA CA CGGTTT	
			A_ _ _	
GAM1959	APOL3	3'	CTTGATGATGGCGGTGGA 15675	AGGTCTT
			TTCGC CCGTCGTCAGG	

AGGTG GGTAGTAGTTC
 GC____
 GAM1959 ASAH 3' CTTTGACATTTGGGGATCTGGT 10517 _ T TC_
 GG TCGC AGGTCT CCG GTCAGGG
 ||| ||||| ||| |||||
 GGTG TCTAGG GGT CAGTTTC
 G _ TTA
 GAM1959 ATIP1 3' TTTTGATGCAGGTCTGC 21863 GT TCC T
 GCAG CT G CGTCAGGG
 ||| || | |||||
 CGTC GA C GTAGTTTT
 TG ____
 GAM1959 ATP9A 3' CTTGGTGTCTCGGTTTGGGAG 31083 G TCTT T GT
 TTC CAGG CCG C CAGG
 ||| ||| ||| | |||
 GAG GTTT GGC G GTTC
 G ____ T TG
 GAM1959 ATP9A 3' TTTTGATGATGGTTGTGTGA 31089 GGTCTT
 TCGCA CCGTCGTCAGGG
 ||||| |||||
 AGTGT GGTAGTAGTTTT
 GTT____
 GAM1959 BANP 5' CTCTGAAAATGAAGATTTGGAA 32912 G C CG
 TTC CAGGTCTTC GT TCAGGG
 ||| ||||| || |||||
 AAG GTTTAGAAG TA AGTCTC
 _ _ AA
 GAM1959 BLR1 3' TCCAGGGGATGGGAGGTTGTGG 26778 A GT G A
 TCGC G CTTCCGTC TC GGG
 |||| | ||||| || |||
 GGTG T GAGGGTAG GG CCT
 _ TG G A
 GAM1959 BLR1 3' TCCAGGGGATGGGAGGTTGTGG 7448 A GT G A
 TCGC G CTTCCGTC TC GGG
 |||| | ||||| || |||
 GGTG T GAGGGTAG GG CCT
 _ TG G A
 GAM1959 C(27)-3BETA-HSD 3' TCCTGATGGCCGCTTGGTGAG 24849 _ CTTCC
 TTCGC AGGT GTCGTCAGGG
 ||||| ||| |||||
 GAGTG TTCG CGGTAGTCCT
 G C____
 GAM1959 C11orf11 3' CTCTGGGCCCTGGGATCTGGAA 44786 G CC_ GT
 TTC CAGGTCTT GTC CAGGG
 ||| ||||| ||| |||||
 AAG GTCTAGGG CGG GTCTC
 _ TCC ____
 GAM1959 C15orf5 5' TTTGAAATGTGGAGGATTTTGA 25216 C TCG_ G
 A TTCG AGGTCTTCCG TCAGG
 ||||| ||||| |||||

			AAGT TTTAGGAGGT AGTTT		
			— GTAA		
GAM1959	C1QR1	3'	TCTTGTTTGGGGGATCTTGG	14339	C TCGT
			TCG AGGTCTTCCG CAGGG		
			GGT TCTAGGGGGT GTTCT		
			— TT—		
GAM1959	C20orf100	5'	TCTGGCTGAGAGCTGTGGA	26705	G CCGTC
			TTCGCAG TCTT GTCAGG		
			AGGTGTC AGAG CGGTCT		
			G T—		
GAM1959	C20orf108	3'	CTTTGGCGAGGGTCTGTGGG	28084	TCTT G
			TTCGCAGG CC TCGTCAGGG		
			GGGTGTCT GG AGCGGTTTC		
			— G		
GAM1959	C20orf162	5'	CTTTGGAAAAAGATCTGGGAA	27915	G CCGTCG
			TTC CAGGTCTT TCAGGG		
			AAG GTCTAGAA GGTTTC		
			G AAAA—		
GAM1959	C20orf162	5'	TCCTGGTGGATGGACCTCGG	27918	C TCCG GT
			TCG AGGTCT TC CAGGG		
			GGC TCCAGG GG GTCCT		
			— TA— TG		
GAM1959	C20orf98	3'	CTCTGCCATGAGGGCTTTGGA	35414	C C C T
			TTCG AGGTCTTC GT G CAGGG		
			AGGT TTCGGGAG TA C GTCTC		
			— — C—		
GAM1959	C21orf108	3'	CCCTGATGACCAGAGCCTCGAG	42768	C T CC
			TTCG AGG CTT GTCGTCAGGG		
			GAGC TCC GAG CAGTAGTCCC		
			— — AC		
GAM1959	C5orf5	3'	CTCTGATGGTGCTCAGATTTGT	18696	TC_GT
	G		CGCAGGTCT C CGTCAGGG		
			GTGTTTAGA G GTAGTCTC		
			CTC TG		
GAM1959	CACNG4	3'	TTTTGATGCCTCAGGGTCTCTG	15747	C GT CCGT
	AA		TTCG AG CTT CGTCAGGG		
			AAGT TC GGA GTAGTTTT		
			C TG CTCC		
GAM1959	CAT56	3'	CCCAACATGGGAGAATTGTGAA	24932	G C CA
			TTCGCAG TCTCCGT GT GGG		

AAGTGTT AGAGGGTA CA CCC
 A _ A_
 GAM1959 CDC14B 3' CTCTGACTCTAGTTCTGCGGA 27169 GT TCCGTC
 TTCGCAG CT GTCAGGG
 ||||| || |||||
 AGGCGTC GA CAGTCTC
 TT TCT__
 GAM1959 CGB5 5' CCTTGGCGCTGGACCAGTGAG 26931 A TCCGT
 TTCGC GGTCT CGTCAGGG
 |||| |||| |||||
 GAGTG CCAGG GCGGTTCC
 A TC__
 GAM1959 CGB8 5' CCTTGGCGCTGGACCAGTGAG 27046 A TCCGT
 TTCGC GGTCT CGTCAGGG
 |||| |||| |||||
 GAGTG CCAGG GCGGTTCC
 A TC__
 GAM1959 CHERP 3' TTTGACTTGACTTGCGAA 13093 TTCCGTC
 TTCGCAGGTC GTCAGG
 ||||| ||||
 AAGCGTTCAG CAGTTT
 TT____
 GAM1959 CSE-C 5' TCCTGAGGTCGCGGGAGGCTGC 43981 G T ____
 GAG CGCAG TCTTCCG CG TCAGGG
 |||| ||||| || |||||
 GCGTC GGAGGGC GC AGTCCT
 _ _ TGG
 GAM1959 CSEN 3' CCCTGGGGAAGAGGCCTTGG 15090 C CCG G
 TCG AGGTCTT TC TCAGGG
 || ||||| || |||||
 GGT TCCGGAG AG GGTCCC
 _ A_ G
 GAM1959 CTNNBIP1 3' CCTGGCAGGGACCTGAGAG 21543 G CCGTC
 TTC CAGGTCTT GTCAGG
 || ||||| ||||
 GAG GTCCAGGG CGGTCC
 A A____
 GAM1959 CXYorf1 5' CTCGGCTCGGGAGGCCTGGGA 39906 G TC AG
 TC CAGGTCTTCCG GTC G
 || ||||| || ||
 AG GTCCGGAGGGC CGG C
 G T_ CT
 GAM1959 CXYorf1 3' TCTGGGAAAGGACCTGGGG 39913 G TCCG G
 TC CAGGTCT TC TCAGG
 || ||||| || ||||
 GG GTCCAGG AG GGTCT
 G AA__ _
 GAM1959 D4ST-1 3' CTCTGGCTCTGGGGCTTGGGG 28227 G TT TC
 TC CAGGTC CCG GTCAGGG
 || ||||| || |||||

			GG GTTCGG GGT CGGTCTC		
			G _ CT		
GAM1959	DAPK3	3'	GCCCGGAGGAGGGTTTGCGG 7029	GT	GT TCA G
			TCGCAG CTTCC CG GG		
			GGCGTT GGAGG GC CC		
			TG AG _ GG		
GAM1959	DDX34	3'	CCCTACCACTGCGAGGCCTGCG 16160	C _ C C	
	G		TCGCAGGTCTT C GT GT AGGG		
			GGCGTCCGGAG G CA CA TCCC		
			C T C _		
GAM1959	DDX34	3'	TCCTGGCGGCTTCCCTGCGG 16166	TCTTCC	
			TCGCAGG GTCGTCAGGG		
			GGCGTCC CGGCGGTCCT		
			CTT__		
GAM1959	DJ465N24.2.1	5'	TCCTGAGTTGAGGCTTGCGG 21581	CCGTCG	
			TCGCAGGTCTT TCAGGG		
			GGCGTTCGGAG AGTCCT		
			TTG__		
GAM1959	DKFZP434B195	5'	CCTGGCGCTGGCCGTGG 25308	A TTCCGT	
			TCGC GGTC CGTCAGG		
			GGTG CCGG GCGGTCC		
			_ TC__		
GAM1959	DKFZp434C0923	3'	CCTTGGCGCTCAGATTTGAGAG 19064	G TCC T	
			TTC CAGGTCT G CGTCAGGG		
			GAG GTTTAGA C GCGGTTCC		
			A CT__		
GAM1959	DKFZp434C0923	3'	TCTGGTGGGACCCGTGAA 19067	A TCCGT GT	
			TTCGC GGTCT C CAGG		
			AAGTG CCAGG G GTCT		
			C _ TG		
GAM1959	DKFZP434C131	3'	CCCTGGTGGTGCAGGCTGTGAA 34243	G TC GT GT	
			TTCGCAG TCT C C CAGGG		
			AAGTGTC GGA G G GTCCC		
			_ C_ TG TG		
GAM1959	DKFZP434C212	3'	CTCACCGTGGAAGTTTGTGAG 34169	T TC C	
			TTCGCAGG CTTCCG GT AG		
			GAGTGTTT GAAGGT CA TC		
			_ GC C		
GAM1959	DKFZP434I092	3'	TTCTGGCCTCAGTTCTGTGAG 33676	GT TCCGTC	
			TTCGCAG CT GTCAGGG		

	GAGTGTC GA CGGTCTT		
	TT CTC___		
GAM1959 DKFZP434I2117 3'	CCCACGTAGGGCAGGAGGGCTT 25555	_ G _	
GTGG	CGCAGGTCTTCC GTC TCAG GG		
	GTGTTCTGGGAGG CGG AGTC CC		
	A G A C		
GAM1959 DKFZP434K1772 5'	CCCATACTGGGAGGCTGGCGAG 33631	A TC CA	
	TTCGC GGTCTTCCG GT GGG		
	GAGCG TCGGAGGGT CA CCC		
	G _ TA		
GAM1959 DKFZP434K1772 5'	TCCTGATGGCTGTGGAGTCTGT 33634	T _ _	
GG	TCGCAGG CTTC C GTCGTCAGGG		
	GGTGTCT GAGG G CGGTAGTCCT		
	_ TT		
GAM1959 DKFZP434L1435 5'	CGAAAGGTGGAGAGATCTGTGA 44268	_ GT GTCAGGG	
G	TTCGCAGGTCT TCC C		
	GAGTGTCTAGA AGG G		
	G TG AAAGC		
GAM1959 DKFZp434N2435 5'	TTTGACCCGTGGGACTTGTGG 46090	TC TC	
	TCGCAGGTCT CG GTCAGG		
	GGTGTTTCAGG GC CAGTTT		
	GT C_		
GAM1959 DKFZp434O0320 3'	CCCTGCAAATGGAGACCTGTG 40703	T CGT	
	CGCAGGTCT CCGT CAGGG		
	GTGTCCAGA GGTA GTCCC		
	_ AAC		
GAM1959 DKFZP434O047 5'	GAGGGTGGGAGGCCTCGG 17866	C GT G	
	TCG AGGTCTTCC C TC		
	GGC TCCGGAGGG G AG		
	_ TG G		
GAM1959 DKFZP434P1750 3'	TCCTGGTGATGGGAGTCAGC 17795	A T GT	
	GC GG CTTCCGTC CAGGG		
	CG CT GAGGGTAG GTCCT		
	A _ TG		
GAM1959 DKFZP564F013 3'	CTTTGATGATAAACTTGT 45201	C CC	
	GCAGGT TT GTCGTCAGGG		
	TGTTCA AA TAGTAGTTTC		
	A _		
GAM1959 DKFZP564J157 3'	CTTGTGATTGGGGAGGTTTGTG 20529	GT _ T G	
GA	TTCGCAG CTTC GTCG CAGG		

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AGGTGTT GAGGG TAGT GTTC
TG  GT  _
GAM1959 DKFZP564P1916 5' CCTGAAGAGGACCTGC 17899 CGTCG
GCAGGTCTTC TCAGG
||||||| ||||
CGTCCAGGAG AGTCC
A____
GAM1959 DKFZp566H0824 5' TCCTGAAGAAATTGGGATACTT 18978 C ____ G
GTGG GCAGGT TTCCG TC TCAGGG
||||| |||| || |||||
TGTTCAGGAGT AG AGTCCT
T TAA A
GAM1959 DKFZp586I021 3' CTCTGAGGAGAGGCCTGGGG 26024 G CCG G
TC CAGGTCTT TC TCAGGG
|| ||||| || |||||
GG GTCCGGAG AG AGTCTC
G ____ G
GAM1959 DKFZP586M1120 3' CCCTGGTCAGAAAAAGCTTGCG 25320 T CCG G__
GA TTCGCAGG CTT TC TCAGGG
||||||| || || |||||
AGGCGTTC GAA AG GGTCCC
_ AA_ ACT
GAM1959 DKFZP761D0211 3' TTTGACCAGGTCCTGTGAG 25738 TCTT GTC
TTCGCAGG CC GTCAGG
||||||| || |||||
GAGTGTCC GG CAGTTT
T__ AC_
GAM1959 DKFZp762M136 3' CTTTGGTGCTAGAAAGCCTGCGG 32303 T CGT GT
TCGCAGG CTTT C CAGGG
||||||| |||| | |||||
GGCGTCC GAAG G GTTTC
_ ATC TG
GAM1959 DKFZp762P2111 3' CTTTGAGCTAGGTCTTGTGAG 41756 T CC CG
TTCGCAGG CTT GT TCAGGG
||||||| |||| || |||||
GAGTGTTT GGA CG AGTTTC
T T_ __
GAM1959 DLAT 3' CTGATGAAACCTTGAA 33502 C CTTCCG
TTCG AGGT TCGTCAG
|||| |||| |||||
AAGT TCCA AGTAGTC
_ A____
GAM1959 DRIL2 3' CTGGGTGGGGGTCTGTGG 13187 T GT GT
TCGCAGG CTTCC C CAG
||||||| |||| | |||
GGTGTCT GGGGG G GTC
_ TG__
GAM1959 DT1P1A10 3' TTTTGAGGATTGCAGACCTGTG 30860 TCC G
GA TTCGCAGGTCT GTC TCAGGG
||||||| |||| |||||

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			AGGTGTCCAGA TAG AGTTTT		
			CGT G		
GAM1959	DVS27	3'	TGATGGAAACCTGTGAG 27251	C	
			TTCGCAGGT TTCCGTCG		
			GAGTGTCCA AAGGTAGT		
			—		
GAM1959	EPB41L1	3'	CCTGGTGCAGGCCGGTGG 34940	A	TCC T GT
			TCGC GGTCT G C CAGG		
			GGTG CCGGA C G GTCC		
			G ——— TG		
GAM1959	FBXO27	3'	CCCTGATCCTCAAGGACCTGT 36835		CCGTC
			GCAGGTCTT GTCAGGG		
			TGTCCAGGA TAGTCCC		
			ACTCC		
GAM1959	FKBP14	3'	CTTTGAATAGAAGACTTCTGGA 19644	C	CGTCG
			TTCG AGGTCTTC TCAGGG		
			AGGT TTCAGAAG AGTTTC		
			C ATA—		
GAM1959	FKBP5	3'	TCTGGCGTGAGTTGTGAA 10325	G	TTCCGT
			TTCGCAG TC CGTCAGG		
			AAGTGTT AG GCGGTCT		
			G T——		
GAM1959	FKBP9	5'	TGATGGATATTTGGAA 45145	G	CT
			TTC CAGGT TCCGTCG		
			AAG GTTTA AGGTAGT		
			— T—		
GAM1959	FKSG28	3'	TTGAAAAGACCTGGAA 25203	G	CCGTCG
			TTC CAGGTCTT TCAG		
			AAG GTCCAGAA AGTT		
			— A——		
GAM1959	FLJ00026	3'	CCCTGGAGAAGGACTTGC 32426		CCG GT
			GCAGGTCTT TC CAGGG		
			CGTTCAGGA AG GTCCC		
			— AG		
GAM1959	FLJ00060	5'	CTCTGAAGTGAAGATCTGGAA 30629	G	CGTCG
			TTC CAGGTCTTC TCAGGG		
			AAG GTCTAGAAG AGTCTC		
			— TGA—		
GAM1959	FLJ10159	3'	TTTTGATGGCGGAGAGGGGTGG 19750	AGG	T
			TCGC TCT CCGTCGTCAGGG		

GGTG AGA GGCGGTAGTTTT
GGG _
GAM1959 FLJ10656 3' TGATCCAAGGCCTTGTGAG 19990 _ CC
TTCGCA GGTCTT GTCG
||||| ||||| |||
GAGTGT CCGGAA TAGT
T CC
GAM1959 FLJ10724 3' CCAACAGTGATTGAGGATTTGT 20050 C TCAG_
GG TCGCAGGTCTTC GTCG GG
||||||| ||| ||
GGTGTTTAGGAG TAGT CC
T GACAA
GAM1959 FLJ10737 3' GTCTTGGCTGGGTCTGGAGGTG 20066 GT_ _ _
TCTGTGGA G CTTCCG TC GTCAGGG T
| ||||| || ||||| |
C GGAGGT GG CGGTTCT G
TGT CTG T
GAM1959 FLJ10803 3' CCTCATGGAGGACTTGGAG 20151 G CGTC
TTC CAGGTCTTCCGT AGG
||| ||||| |||
GAG GTTCAGGAGGTA TCC
_ C_
GAM1959 FLJ11252 3' CTTTGGTGGTGGAAGAAAGAA 33567 GCAGG GT GT
TTC TCTTCC C CAGGG
||| ||||| | |||||
AAG AGAAGG G GTTTC
AA_ TG TG
GAM1959 FLJ11710 3' CTTACGAGGAGGAGGGCTTGTGA 24274 GT C G
G TTCGCAGGTCTTCC CGT AGG
||||||| ||| |||
GAGTGTTCTGGGAGG GCA TTC
AG C
GAM1959 FLJ12122 3' CCTGGCCAAGCCTGTGGA 24539 T CCGTC
TTCGCAGG CTT GTCAGG
||||||| ||| |||||
AGGTGTCC GAA CGGTCC
_ C_
GAM1959 FLJ12190 3' CTTGGAGAGGACTTTGAA 24668 C CGTCG
TTCG AGGTCTTC TCAGG
||| ||||| |||||
AAGT TTCAGGAG GGTTC
_ A_
GAM1959 FLJ12287 5' CCTGGTGACAGTCTGTGG 22754 T TCC GT
TCGCAGG CT GTC CAGG
||||||| || ||| |||
GGTGTCT GA CAG GTCC
_ _ TG
GAM1959 FLJ12443 3' CCCTGGCCTGCGGGGACCTGC 24223 T C_
GCAGGTCT CCGT GTCAGGG
||||||| ||| |||||

		CGTCCAGG GGCG CGGTCCC	
		— TC	
GAM1959	FLJ12517 3'	CCCTGCCTTTGCAGGGCCTGTG 23268	C TCGT
	GA	TTCGCAGGTCTT CG CAGGG	
		AGGTGTCCGGGA GT GTCCC	
		C TTCC	
GAM1959	FLJ12547 3'	CTCTGGGTCTGGGTCTGTGAG 24548	GT TCCGTCG
		TTCGCAG CT TCAGGG	
		GAGTGTC GG GGTCTC	
		TG TCTG__	
GAM1959	FLJ12650 3'	TTTTGGTGGAAAGTGGGCCTTGA 23724	C __ GT TCAGGG
	A	TCG AGGTCT TCC CG	
		AGT TCCGGG AGG GT	
		— TGA TG TTT	
GAM1959	FLJ12687 3'	CCCTGGTGGTGGGCACCTGT 24445	CT GT GT
		GCAGGT TCC C CAGGG	
		TGTCCA GGG G GTCCC	
		C_ TG TG	
GAM1959	FLJ12800 3'	CCCTGGGTGGTGGACCTGTGGA 23190	T GT GT
		TTCGCAGGTCT CC C CAGGG	
		AGGTGTCCAGG GG G GTCCC	
		T TG__	
GAM1959	FLJ12895 5'	CCCTGCAGGCAGGTCTGTGG 23404	GT T GTCGT
		TCGCAG CT CC CAGGG	
		GGTGTC GA GG GTCCC	
		TG C AC__	
GAM1959	FLJ13072 5'	TTTTGATCACTGGGAAGACTGT 43239	G __ C
	GAA	TCGCAG TCTTCC GT GTCAGGG	
		AGTGTC AGAAGG CA TAGTTTT	
		— GT C	
GAM1959	FLJ13158 3'	CCCTGCCCTGGGAGACCTGGGG 24409	G TC T
		TC CAGGTCTTCCG G CAGGG	
		GG GTCCAGAGGGT C GTCCC	
		G CC_	
GAM1959	FLJ13181 5'	CCTGAGTAGATCTGTGG 24828	TCCGTCG
		TTCGCAGGTCT TCAGG	
		GGTGTCTAGA AGTCC	
		TG__	
GAM1959	FLJ13544 5'	CCCAGGAGTGGAGGGCTCTGTG 24579	_ TCG A
	AG	TTCGCAG GTCTTCCG TC GGG	

		GAGTGTC CGGGAGGT GG CCC	
		T GA_ A	
GAM1959	FLJ13910	3' CTTGAGAGTGT TTTGTGAA 23056	TC CGTCG
		TTCGCAGG TTC TCAGG	
		AAGTGTTT GAG AGTTC	
		GT _____	
GAM1959	FLJ14084	3' CCTGT TAGAAGTCTGTGAG 22284	T CGTCGT
		TTCGCAGG CTTC CAGG	
		GAGTGTCT GAAG GTCC	
		_ ATT_	
GAM1959	FLJ14213	3' TCTTGATGGCATTTCCTTCTG 24256	C_ TCTTCC
	AG	TTCG AGG GTCGTCAGGG	
		GAGT TCC CGGTAGTTCT	
		CT CTTTA_	
GAM1959	FLJ14213	3' TTTTGACCCAGGAGGGCCGCGA 24257	A GTC
	G	TTCGC GGTCTTCC GTCAGGG	
		GAGCG CCGGGAGG CAGTTTT	
		_ ACC	
GAM1959	FLJ14442	3' CTCTGAGGAAGAGGGTCTGTGG 26536	GT CG G
		TCGCAG CTTC TC TCAGGG	
		GGTGTC GGAG AG AGTCTC	
		TG A_ G	
GAM1959	FLJ14641	3' TCTTGGAATTGGGACCTTTGGA 26589	C TT TCG
		TTCG AGGTC CCG TCAGGG	
		AGGT TCCAG GGT GGTTC	
		T _ TAA	
GAM1959	FLJ14681	3' CTGATAGGTGGCAGGCCTGTGG 26597	T GT_ GG
		TCGCAGGTCT CC C GTCAG	
		GGTGTCCGGA GG G TAGTC	
		C TG A	
GAM1959	FLJ14743	3' TTTTGGCTTTCGAGGGCCTGT 33764	CGTC
		GCAGGTCTTC GTCAGGG	
		TGTCCGGGAG CGGTTTT	
		CTTT	
GAM1959	FLJ14816	3' CTCTGACCCCCAAGAGGCCTGT 26639	CCGTC_
	GAG	TTCGCAGGTCTT GTCAGGG	
		GAGTGTCCGGAG CAGTCTC	
		AACCCC	
GAM1959	FLJ14957	3' CCCAATAGGGTGGGGGCCTGTG 26681	T GT GTCA_
	G	TCGCAGGTCT CC C GGG	

GGTGTCCGGG GG G CCC
 _ TG GATAA
 GAM1959 FLJ14957 3' TCTTGAAAGCTGGGGGATGTGT 26684 G _ CG
 GG TCGCA GTCTTCC GT TCAGGG
 ||||| ||||| || |||||
 GGTGT TAGGGGGG CG AGTTCT
 G T AA
 GAM1959 FLJ20150 3' CTTTGAGTGCTGGGTACCTGTG 19243 CT T _
 G TCGCAGGT TCCG CG TCAGGG
 ||||| ||||| || |||||
 GGTGTCCA GGGT GT AGTTTC
 T_ C G
 GAM1959 FLJ20209 3' TCCTGGCCCCAAGGGGCCTGTG 41405 CCGTC
 G TCGCAGGTCTT GTCAGGG
 ||||| |||||
 GGTGTCCGGGG CGGTCCT
 AACCC
 GAM1959 FLJ20297 3' CCTTGGGCTGAGAGGACCTGGG 19651 G _ _ GT
 AA TTC CAGGTCTTC C GTC CAGGG
 ||| ||||| ||| |||||
 AAG GTCCAGGAG G CGG GTTCC
 G A T _
 GAM1959 FLJ20297 3' CCTTGGGCTGAGAGGACCTGGG 19360 G _ _ GT
 AA TTC CAGGTCTTC C GTC CAGGG
 ||| ||||| ||| |||||
 AAG GTCCAGGAG G CGG GTTCC
 G A T _
 GAM1959 FLJ20360 3' CCTTTGAAAACTTGTGAA 43680 C TCGTC
 TTCGCAGGT TTCCG AGG
 ||||| ||||| |||
 AAGTGTTC AAGGT TCC
 A T _
 GAM1959 FLJ20477 5' CCTCTGGGAGGCCTGAGG 19502 G TCGTC
 TC CAGGTCTTCCG AGG
 || ||||| |||
 GG GTCCGGAGGGT TCC
 A C _
 GAM1959 FLJ20509 5' CCCTGACGGCCCATTTGTCCGCG 19523 A TCTTCC_
 G TCGC GG GTCGTCAGGG
 |||| || |||||
 GGCG CC CGGCAGTCCC
 _ TGTTACC
 GAM1959 FLJ21276 5' TCTTGAAAAATGAGGATCTCTG 23904 C CGTCG
 AG TTCG AGGTCTTC TCAGGG
 |||| ||||| |||||
 GAGT TCTAGGAG GGTTCT
 C TAAAA
 GAM1959 FLJ21313 3' CCCTGGTCAAGAATCTGTGAG 23408 _ CCGTCG
 TTCGCAGGT CTT TCAGGG
 ||||| ||| |||||

GAGTGTCTA GAA GGTCCC
 A CT____
 GAM1959 FLJ21551 3' TCCTGGTGA CTGAACTTCTGGG 24180 G TC C GT
 C CAGG TTC GTC CAGGG
 ||||| ||| ||| |||||
 G GTCT AAG CAG GTCCT
 G TC T TG
 GAM1959 FLJ21865 3' CTCTGCAGTGGGGGTTGTGG 23000 GT TC T
 TCGCAG CTTCCG G CAGGG
 ||||| ||||| | |||||
 GGTGTT GGGGGT C GTCTC
 ____ GA ____
 GAM1959 FLJ22035 3' TTCTGATGGTGTGCATGTGAG 23725 G CTTC GT
 TTCGCA GT C CGTCAGGG
 ||||| || | |||||
 GAGTGT CG G GTAGTCTT
 A T____ TG
 GAM1959 FLJ22233 3' CCTTGCCGTGGGGACCTTGGA 24515 C T T T
 TTCG AGGTCT CCG CG CAGGG
 ||| ||||| ||| || |||||
 AGGT TCCAGG GGT GC GTTCC
 ____ _ _ C
 GAM1959 FLJ22341 3' TTCTGGGGCGTGAGGCCTGTGA 23849 TC G
 G
 TTCGCAGGTCT CGTC TCAGGG
 ||||| ||||| ||||| |||||
 GAGTGTCCGGA GCGG GGTCTT
 GT ____
 GAM1959 FLJ22474 3' TCCTGATGAGGGCGTTGTGG 24050 GTCTT G
 TCGCAG CC TCGTCAGGG
 ||||| || |||||
 GGTGTT GG AGTAGTCCT
 GC____ G
 GAM1959 FLJ22479 3' TCTGGCTGAGGCTTGC 24387 CCGTC
 GCAGGTCTT GTCAGG
 ||||| |||||
 CGTTCGGAG CGGTCT
 T____
 GAM1959 FLJ22679 5' CCCTGGTGTCTGGAGGGGGGTT 25949 G ____ T_ GT
 GTGG GCAG TCT TCCG C CAGGG
 ||||| ||| ||||| | |||||
 TGTT GGG AGGT G GTCCC
 G GG CT TG
 GAM1959 FLJ22761 5' TCCTGGTGGACCTGGGTCTGGA 24773 G GT TCCG GT
 A
 TTC CAG CT TC CAGGG
 ||| ||| || || |||||
 AAG GTC GG GG GTCCT
 ____ TG TCCA TG
 GAM1959 FLJ22940 5' GGAGGACGCGGAAGGCCTGCGA 23798 T AGGG
 G
 TTCGCAGGTCTTCCG CGTC
 ||||| ||||| ||||| |||||

GAGCGTCCGGAAGGC GCAG
 _ GAGGC
 GAM1959 FLJ23091 3' TGACGGTAGCTTTTGA 24418 C T T
 TTCG AGG CT CCGTCG
 |||| ||| || |||||
 AGGT TTC GA GGCAGT
 T _ T
 GAM1959 FLJ23309 3' TCTTGAAAGGTGGTCTGTGGA 24380 GT TT GTCG
 TTCGCAG C CC TCAGGG
 |||||| | || |||||
 AGGTGTC G GG AGTTCT
 TG T_ AA_
 GAM1959 FLJ23499 3' TCTTGGTGGCGGGCGCCTGT 23007 CT GT
 GCAGGT TCCGTC CAGGG
 ||||| ||||| |||||
 TGTCCG GGGCGG GTTCT
 C_ TG
 GAM1959 FLJ23556 3' TCTTGGTGATGGTCAACTCTG 24320 _ CTT GT
 CAG GT CCGTC CAGGG
 ||| || ||||| |||||
 GTC CA GG TAG GTTCT
 T ACT TG
 GAM1959 FLJ25442 5' TCCTGACTTTCGGTGGCTTGTG 29641 TT TC_
 GA TTCGCAGGTC CCG GTCAGGG
 ||||||| ||| |||||
 AGGTGTTCCG GGC CAGTCCT
 T_ TTT
 GAM1959 FLJ31709 3' TTTTGATGATCAGAGGTCTTGA 29460 C GT CC
 G TTCG AG CTT GTCGTCAGGG
 |||| || ||| |||||
 GAGT TC GAG TAGTAGTTTT
 _ TG AC
 GAM1959 FLJ31951 3' TCTGATGAACACTTTGGA 29551 C CTTCCG
 TTCG AGGT TCGTCAGG
 |||| |||| |||||
 AGGT TTCA AGTAGTCT
 _ CA_
 GAM1959 FLJ32334 3' TCCTGGCCCAGGCCTGGCGG 29369 _ TCCGTC
 TCGC AGGTCT GTCAGGG
 |||| ||||| |||||
 GGCG TCCGGA CGGTCCT
 G CC_
 GAM1959 FOXO3A 5' GGGGGTGACGGGGGGGTCGCGGA 7190 A GT GT AGGG
 TTCGC G CTTCCGTC C
 ||||| | ||||| |
 AGGCG C GGGGGCAG G
 _ TG TG GGGG
 GAM1959 FREQ 3' TCTGACCTGGGGTCTGGGG 15564 G GT TT TC
 TC CAG C CCG GTCAGG
 || ||| | ||| |||||

			GG GTC G GGT CAGTCT		
			G TG__ C_		
GAM1959	FUSIP1	3'	TTCTGGTTCCTATGAAGATTTG 27625	G	CGTCG__
	GAA		TC CAGGTCTTC TCAGGG		
			AG GTTTAGAAG GGTCTT		
			_ TATCCTT		
GAM1959	GFPT1	3'	TGTGGAGGACTTTGAA 7820	C	T
			TTCG AGGTCTTCCG CG		
			AAGT TTCAGGAGGT GT		
			- -		
GAM1959	GGTLA4	5'	TCCTGGGGAGCCACGGAAGGTT 28142	A GT	__ G
	GTGG		C G CTTCCG TC TCAGGG		
			G T GAAGGC AG GGTCTT		
			_ TG ACCG G		
GAM1959	GNG11	5'	TCCTGGGTTGCAGGGACTTGAG 10333	G	CC CG_
	AA		TTC CAGGTCTT GT TCAGGG		
			AAG GTTCAGGG CG GGTCTT		
			A A_ TTG		
GAM1959	GPT2	3'	CCTGACCGAGCCTGTGAG 28523	T	CCGTC
			TTCGCAGG CTT GTCAGG		
			GAGTGTCC GAG CAGTCC		
			_ C__		
GAM1959	GR6	5'	CCTTGGCGCGTGGCTCGTGGA 14282	AG	TTC T
			TTCGC GTC CG CGTCAGGG		
			AGGTG CGG GC GCGGTTCC		
			CT T__ _		
GAM1959	GRIN3A	3'	CTCTGTGCGAGAGATCTGTGAA 28533		TC T T
			TTCGCAGGTCT CG CG CAGGG		
			AAGTGTCTAGA GC GT GTCTC		
			GA _ _		
GAM1959	GS3955	3'	TTTTGAACAATGAGGGTTTGTG 22306	GT	CGTCG
			CGCAG CTTC TCAGGG		
			GTGTT GGAG AGTTTT		
			TG TAACA		
GAM1959	GTF3C1	3'	CCCTGGCCTTGGGTCTGC 7260	TCT	TC
			GCAGG TCCG GTCAGGG		
			CGTCT GGGT CGGTCCC		
			_ TC		
GAM1959	HCCA2	5'	CCCTGGTGAGGAAGATCTGC 33203	G	GT
			GCAGGTCTTCC TC CAGGG		

			CGTCTAGAAGG AG GTCCC	
			_ TG	
GAM1959	HEMK	3'	CCTTGATTTTAAGCCCTGTGAA 18267	T CCGTC
			TTCGCAGG CTT GTCAGGG	
			AAGTGTCC GAA TAGTTCC	
			C TTT__	
GAM1959	HEMK	3'	TTCTGGAGGGGAGGGTCTGGAG 18274	G GT G GT
			TTC CAG CTTCC TC CAGGG	
			GAG GTC GGAGG GG GTCTT	
			_ TG _ AG	
GAM1959	HIC2	3'	TTTGAAGTCTGGAAGGTCTGGGG 32535	G GT TCG
			TC CAG CTTCCG TCAGG	
			GG GTC GAAGGT AGTTT	
			G TG CA_	
GAM1959	HN1L	3'	CCTGGCAGGGACTTCTGGG 29376	G TC GTC
			C CAGG TTCC GTCAGG	
			G GTCT AGGG CGGTCC	
			G TC A__	
GAM1959	HPIP	3'	TTTTGGGGTGGGGTCTGGGGA 21740	G GT TT GT G
			TTC CAG C CC C TCAGGG	
			AGG GTC G GG G GGTTTT	
			G TG __ TG _	
GAM1959	HRIHFB2122	3'	CCCTGGCCCAGAGGTCTGGCGG 13898	A T CGTC
	A		TTCGC GG CTTC GTCAGGG	
			AGGCG TC GGAG CGGTCCC	
			G T ACC_	
GAM1959	HS6ST	3'	TTCTGACCCACTGGGATTTGC 31073	CCGTC
			GCAGGTCTT GTCAGGG	
			CGTTTAGGG CAGTCTT	
			TCACC	
GAM1959	HSP105B	5'	CCCAGAGGTGCGGAGCGACCTGC 13438	_ T GT A_
	GGA		TCGCAGGTC TTCCG C C GGG	
			GGCGTCCAG GAGGC G G CCC	
			C _ TG AG	
GAM1959	HT002	3'	TTCTGAGGAAAGTCCTGTGG 15284	T CCG G
			TTCGAGG CTT TC TCAGGG	
			GGTGTCC GAA AG AGTCTT	
			T __ G	
GAM1959	HU-K4	5'	TTCTGGCGGTTGTGGGCTTCGG 14592	C TCCG
	A		TTCG AGGTCT TCGTCAGGG	

		AGGC TTCGGG GGCGGTCTT		
		— TGTT		
GAM1959	ITGA10	3' CCCTGAAACCTGAGACCTGT 29861	CC	CG
		GCAGGTCTT GT TCAGGG		
		TGTCCAGAG CA AGTCCC		
		TC A_		
GAM1959	JM11	3' TCCTGGTGGAGGGGATCTTGG 27331	C	T GT GT
		TCG AGGTCT CC C CAGGG		
		GGT TCTAGG GG G GTCCT		
		— — AG TG		
GAM1959	KCNJ9	5' CCTTCGGGGGGGCCCGTGG 11430	A	TCGTC
		TCGC GGTCTTCCG AGG		
		GGTG CCGGGGGGC TCC		
		C T_		
GAM1959	KCNT1	3' TACTACATGGAGGGCTCTGTGG 30978	—	C C GG
	A	TTCGCAG GTCTTCCGT GT AG		
		AGGTGTC CGGGAGGTA CA TC		
		T — — ATC		
GAM1959	KHDRBS1	3' TTCTGAAGTAAAGGCTTGT 13330	CCGTCG	
		GCAGGTCTT TCAGGG		
		TGTTCGGAA AGTCTT		
		ATGA_		
GAM1959	KIAA0052	3' TGGTGGAAGGCTTGGAG 33692	G	GT
		TTC CAGGTCTTCC CG		
		GAG GTTCGGAAGG GT		
		— TG		
GAM1959	KIAA0057	3' CCTTGGTGGTCCTCATGTGGA 14618	GGTCTT	TCG
		TTCGCA CCG TCAGGG		
		AGGTGT GGT GGTTC		
		ACTCCT _		
GAM1959	KIAA0087	3' CTTTGCGACGGGAACTT 16557	C	
		AGGT TTCCGTCGTCAGGG		
		TTCA AGGGCAGCGTTTC		
		A		
GAM1959	KIAA0140	3' CCCTGGTGGTGGGGGCTGT 16108	GT	GT GT
		GCAG CTTCC C CAGGG		
		TGTC GGGGG G GTCCC		
		_ TG TG		
GAM1959	KIAA0146	5' TTCTGGTACAAGATGCCTGTGG 39584	CT	CGTCG
	A	TTCGCAGGT TC TCAGGG		

		AGGTGTCCG AG GGTCTT		
		T_ AACAT		
GAM1959	KIAA0218	3' TCCTGCTTGGAAGACTTGGGG 16519	G	TC T
		TC CAGGTCTTCCG G CAGGG		
		GG GTTCAGAAGGT C GTCCT		
		G T_		
GAM1959	KIAA0247	3' CCTTGGCCGAGGATGGAAGATT 16374		_____
	TGGAG	CAGGTCTTCCGTC GTCAGGG		
		GTTTAGAAGGTAG CGGTTCC		
		GAGC		
GAM1959	KIAA0261	3' TTTTGGTGAACCTGACTTGTGG 33838		TTCCG GT
		TCGCAGGTC TC CAGGG		
		GGTGTTTCTAG AG GTTTT		
		TCCA_ TG		
GAM1959	KIAA0286	3' TTTTGGTGACTTAAGCTTATGA 33909	C T CC GT	
	A	TTCG AGG CTT GTC CAGGG		
		AAGT TTC GAA CAG GTTTT		
		A _ TT TG		
GAM1959	KIAA0316	3' TCTGGGCAGAAGACCTGCGAG 34531		C GT
		TTCGCAGGTCTTC GTC CAGG		
		GAGCGTCCAGAAG CGG GTCT		
		A _		
GAM1959	KIAA0323	3' CCTAACCTGGAAGCCTGTGAG 31691	T	TC C
		TTCGCAGG CTTCCG GT AGG		
		GAGTGTCC GAAGGT CA TCC		
		_ C_ A		
GAM1959	KIAA0326	3' TCTTGCTTCCGGAAGCTTGCGA 32160	T	TCGT
	A	TTCGCAGG CTTCCG CAGGG		
		AAGCGTTC GAAGGC GTTCT		
		_ CTC		
GAM1959	KIAA0342	3' TTCTGATGAGTCTCTGCTTGC 34961		CTTCCG
		GCAGGT TCGTCAGGG		
		CGTTCTG AGTAGTCTT		
		TCTCTG		
GAM1959	KIAA0418	3' TTTGTCTGAAGGCCTGTGG 15999		TCCG T
		TCGCAGGTCT TCG CAGG		
		GGTGTCCGGA AGC GTTT		
		_____ T		
GAM1959	KIAA0444	3' CTCTGTTACCACTGGGGGGCCT 31240		TC_ _
	GTGG	GCAGGTCTTCCG GT CAGGG		

		TGTCCGGGGGGT CA GTCTC		
		GAC TT		
GAM1959 KIAA0450	5'	TCCATGCTGGGGGACCGTGG 16033	A	T CA
		TCGC GGTCTTCCG CGT GGG		
		GGTG CCAGGGGGT GTA CCT		
		— C —		
GAM1959 KIAA0469	3'	CCTGGCTGGGAGTCCTGTGG 16889	T	TC
		TCGCAGG CTTCCG GTCAGG		
		GGTGTCC GAGGGT CGGTCC		
		T —		
GAM1959 KIAA0495	5'	CTTTACTGCAGGGCCTGCGAG 31357		CC C C
		TTCGCAGGTCTT GT GT AGG		
		GAGCGTCCGGGA CG CA TTC		
		— T T		
GAM1959 KIAA0514	5'	CCCTGGTGAACCTAGCGCTGTG 16205	_T	TCCG GT
G		TCGCAG G CT TC CAGGG		
		GGTGTC C GA AG GTCCC		
		G_ TCCA TG		
GAM1959 KIAA0775	5'	TCCTGAACTCTGGGATCCTGCG 16321	TC	TCG_
G		TCGCAGG TTCCG TCAGGG		
		GGCGTCC AGGGT AGTCCT		
		T_ CTCA		
GAM1959 KIAA0794	3'	TCTTGGAATTAGGGGATTTGG 39186	G	CGTC_
GAA		TTC CAGGTCTTC GTCAGGG		
		AAG GTTTAGGGG CGGTTCT		
		G ATTAA		
GAM1959 KIAA0802	5'	GAGATGGAGGACATGCGG 31350	G	G
		TCGCA GTCTTCCGTC TC		
		GGCGT CAGGAGGTAG AG		
		A —		
GAM1959 KIAA0802	5'	TCTTGGGCCCGGAAGATCGTGGA 31353	A	TCG
		TTCGC GGTCTTCCG TCAGGG		
		AGGTG CTAGAAGGC GGTCT		
		— CG_		
GAM1959 KIAA0892	3'	GCGGTGAAGATCTGTGGA 35170	C GT	
		TTCGCAGGTCTT C CGT		
		AGGTGTCTAGAA G GCG		
		_TG		
GAM1959 KIAA0918	3'	GCTGCGCGGGTGACCTGTGAA 36198	T T T	GG
		TTCGCAGGTC TCCG CG CAG		

		AAGTGTCCAG GGGC GC GTC	
		T _ _ GT	
GAM1959	KIAA0924	3' CCTTGA CTTGAGACTTGTGG 17064	CCGTC
		TCGCAGGTCTT GTCAGGG	
		GGTGTTCAGAG CAGTTCC	
		TT__	
GAM1959	KIAA0939	3' GAGATGGGGGACCTGTGG 31064	G
		TCGCAGGTCTTCCGTC TC	
		GGTGTCCAGGGGGTAG AG	
		-	
GAM1959	KIAA0945	3' CCCTGGCCCTGAGACTCTGTGA 17292	_ CCGTC
	G	TTCGCAG GTCTT GTCAGGG	
		GAGTGTC CAGAG CGGTCCC	
		T TCC__	
GAM1959	KIAA0945	3' CCCTGGGTGGAGATTTCCGAA 17293	C T GT GT
		TTCG AGGTCT CC C CAGGG	
		AAGC TTTAGA GG G GTCCC	
		C _ TG__	
GAM1959	KIAA0978	5' TCTTGATGAAACATCTTCGAA 34889	C CTTCCG
		TTCG AGGT TCGTCAGGG	
		AAGC TCTA AGTAGTTCT	
		T CAA__	
GAM1959	KIAA0981	3' CTTTGTTTTTTGATACCTGTGG 30798	CT CGTCG
	A	TTCGCAGGT TC TCAGGG	
		AGGTGTCCA AG GGTTC	
		T_ TTTTT	
GAM1959	KIAA0982	3' CTTTGCTGGGAAGACTGTGAG 15249	G GT T
		TTCGCAG TCTTCC CG CAGGG	
		GAGTGTC AGAAGG GT GTTTC	
		_ _ C	
GAM1959	KIAA1016	5' CTTGAACCGGGGTCTGGAG 44086	G GT TT TCG
		TTC CAG C CCG TCAGG	
		GAG GTC G GGC AGTTC	
		_ TG__ CA_	
GAM1959	KIAA1024	3' TTTTGATGATGTTTCATGGTGG 34238	AGGTCTTC
		TCGC CGTCGTCAGGG	
		GGTG GTAGTAGTTTT	
		GTACTTT_	
GAM1959	KIAA1026	3' TTTTGATCCAAAGGATCTGTGG 35280	CCGTC
		TCGCAGGTCTT GTCAGGG	

		GGTGTCTAGGA TAGTTTT		
		AACC_		
GAM1959	KIAA1032	3' CCTTGGGGTTGGGGAGATCTGC 32877	G__ G	
		GCAGGTCTTCC TC TCAGGG		
		CGTCTAGAGGG GG GGTTC		
		GTT _		
GAM1959	KIAA1052	3' CCTGAGCAGGGGCTTGGGG 17311 G	CC CG	
		TC CAGGTCTT GT TCAGG		
		GG GTTCGGGG CG AGTCC		
		G A_ _		
GAM1959	KIAA1068	3' CCTTGTTATTTGGGAGACTTTG 17643 C	TCGT_	
	AG	TTCG AGGTCTTCCG CAGGG		
		GAGT TTCAGAGGGT GTTCC		
		_ TTATT		
GAM1959	KIAA1130	3' CCTTCAGAGCGAGGATCTGTGG 31283	CG GTC G	
		TCGCAGGTCTTC TC AGG		
		GGTGTCTAGGAG AG TCC		
		CG ACT		
GAM1959	KIAA1185	3' TTCTGGTGGTGGAGCAGGTCCG 31372	CA GT _ GT GT	
	G	TCG G CT TCC C CAGGG		
		GGC C GA AGG G GTCTT		
		_ TG CG TG TG		
GAM1959	KIAA1190	3' TCCTCATCTTGGAGGGTTTGGG 35224	G GT TC C	
	GA	TTC CAG CTTCCG GT AGGG		
		AGG GTT GGAGGT TA TCCT		
		G TG TC C		
GAM1959	KIAA1199	3' TCTTGGCAGCAGACCAGTGG 35900	A TCC C	
		TCGC GGTCT GT GTCAGGG		
		GGTG CCAGA CG CGGTTCT		
		A _ A		
GAM1959	KIAA1233	3' CTTGGTTTAGTCTGTGAA 31589	T TCCGTCG	
		TTCGCAGG CT TCAGG		
		AAGTGTCT GA GGTTC		
		_ TTT_		
GAM1959	KIAA1247	5' CCCAGGCCGGAGATCTGCGAG 30988	T TC A	
		TTCGCAGGTCT CCG GTC GGG		
		GAGCGTCTAGA GGC CGG CCC		
		_ _ A		
GAM1959	KIAA1280	5' CTTTGATGATAAAACAAGACTT 34553	CC_	
	GT	GCAGGTCTT GTCGTCAGGG		

		TG TTCAGAA TAGTAGTTTC CAAAA	
GAM1959 KIAA1322	3'	CCCTGGCATCGGTCCTGCGGA 36023 TTCGCAGG CCG GTCAGGG AGGCGTCC GGC CGGTCCC T__ TA	TCTT TC
GAM1959 KIAA1332	3'	CCCTGGCGAAGCTGGTGCTGTG 35255 AG TTCGCAG CT TCGTCAGGG GAGTGTC GG AGCGGTCCC GT TCGA	GT TCCG
GAM1959 KIAA1399	3'	CAGAGGGTGGGGGACCTGGCGG 34796 TCGC AGGTCTTCC C TC GGCG TCCAGGGGG G AG G TG G AC	_ GT G AGGG
GAM1959 KIAA1449	3'	TCTTG TAGGAAGATCTGT 21899 GCAGGTCTTCC CAGGG TGTCTAGAAGG GTTCT AT__	GTCGT
GAM1959 KIAA1458	5'	CCTGGCGGTGGGGCCTG 34204 CAGGTC CC CGTCAGG GTCCGG GG GCGGTCC _ TG	TT GT
GAM1959 KIAA1465	3'	CCTTGCGCGCTGAGCCTGTGGA 30502 TTCGCAGGT TC GTCGTCAGGG AGGTGTCCG AG CGGCGGTTCC _ T	CT C
GAM1959 KIAA1467	3'	CCCTGATGGTTGCAAAGGCTTG 35451 GGAA TC CAGGTCTT TCGTCAGGG AG GTTCGGAA GG TAGTCCC G ACGTT	G CCG__
GAM1959 KIAA1509	3'	CTCTGCACCAGGGGGTTTGGGG 30877 A TTC CAGG CTTCC GT CAGGG AGG GTTT GGGGG CA GTCTC G _ AC_ C	G T GTC _
GAM1959 KIAA1576	3'	CTCTGATGAGAACAATTGC 32772 GCAGGT TTC TCGTCAGGG CGTTCA AAG AGTAGTCTC C _	C CG
GAM1959 KIAA1580	5'	TTTTGGTGGTGGTGGCTGTTGG 34412 TCG GGTC CC C CAGGG 	CA TT GT GT

	GGT TCGG GG G GTTTT	
	TG T_ TG TG	
GAM1959 KIAA1656	3' CTCTGGGGCACAGACCTGTGAG 32732	TCC G
	TTCGCAGGTCT GTC TCAGGG	
	GAGTGTCCAGA CGG GGTCTC	
	CA_ _	
GAM1959 KIAA1679	3' TTCTGGGAAAAACAGACCTGTG 34754	TCCG_ G
AA	TTCGCAGGTCT TC TCAGGG	
	AAGTGTCCAGA AG GGTCTT	
	CAAAA _	
GAM1959 KIAA1729	3' TCTGGAGAGAGCCTGTGAA 42950	T CCG GT
	TTCGCAGG CTT TC CAGG	
	AAGTGTCC GAG AG GTCT	
	_ _ _ AG	
GAM1959 KIAA1755	3' TCCTGGTGGTTGGGGACCGTGG 30752	A CG GT
	TCGC GGTCTTC TC CAGGG	
	GGTG CCAGGGG GG GTCCT	
	_ TT TG	
GAM1959 KIAA1789	5' TCTGATGTAGTTTGTGGA 33313	T TCCGT
	TTCGCAGG CT CGTCAGG	
	AGGTGTTT GA GTAGTCT	
	_ T _ _	
GAM1959 KIAA1798	5' ACCGTCGCGGAGAGGTTTGTGG 30401	GT _ T TCA G
A	TTCGCAG CT TCCG CG GG	
	AGGTGTT GA AGGC GC CC	
	TG G _ TG_ AC	
GAM1959 KIAA1805	3' TTCTGGTGAGTAAGACCTGGGG 39002	G CCG GT
A	TTC CAGGTCTT TC CAGGG	
	AGG GTCCAGAA AG GTCTT	
	G TG_ TG	
GAM1959 KIAA1870	5' CTCTGGTGACTGCCTGCGGG 26709	CTTCC GT
	TTCGCAGGT GTC CAGGG	
	GGGCGTCCG CAG GTCTC	
	T _ _ TG	
GAM1959 KIAA1904	3' CCCTGGGCTCTGAACCTGTGAA 36374	CTTCC GT
	TTCGCAGGT GTC CAGGG	
	AAGTGTCCA CGG GTCCC	
	AGTCT _	
GAM1959 KIAA1906	3' CTCTGATGGCAGTGCTTGACGG 36229	_ _ TCC
	TCG CAGGT CT GTCGTCAGGG	

GGC GTTCG GA CGGTAGTCTC
A T ____
GAM1959 KIAA1908 5' TTCTGGTCCCGAGACTTGGGG 36340 G T TC
TC CAGGTCT CCG GTCAGGG
|| ||||| || |||||
GG GTTCAGA GGC TGGTCTT
G _ CC
GAM1959 KIAA1924 3' CTTGATGAGCTGCTGCGAG 36476 GTCTTCCG
TTCGCAG TCGTCAGG
||||| |||||
GAGCGTC AGTAGTTC
GTCG____
GAM1959 KIAA1941 3' TTGGCGATGTTCTGGA 36954 G TCTTC
TC CAGG CGTCGTCAG
|| ||| |||||
AG GTCT GTAGCGGTT
_ T____
GAM1959 KIAA1948 5' CCCAATCAGGAGATTTGTGG 40079 T GTCGTCA
TCGCAGGTCT CC GGG
||||||| || |||
GGTGTTTAGA GG CCC
_ ACTAA____
GAM1959 KIAA1950 3' CAGCCTGTGGTGGAGGGTCTCT 44486 C GT GT T G
GG TCG AG CTTCC CG CAGG
||| || |||| || ||||
GGT TC GGAGG GT GTCC
C TG TG _ GACT
GAM1959 KIAA1977 5' CTTTGGTGAACCCACATGCGA 36745 G CTTCCG GT
G TTCGCA GT TC CAGGG
||||| || || |||||
GAGCGT CA AG GTTTC
A CCCCCA_ TG
GAM1959 KIAA1981 3' CCCTGATGCTGGCCTGTGAG 42608 TTCCGT
TTCGCAGGTC CGTCAGGG
||||||| |||||
GAGTGTCCGG GTAGTCCC
TC____
GAM1959 KIAA1981 3' TCCTGGTGCCGCAGAGGCCTCG 42611 C C_ T GT
GA TTCG AGGTCTT CG C CAGGG
|||| ||||| || |||||
AGGC TCCGGAG GC G GTCCT
_ AC C TG
GAM1959 KIF13B 3' TTTTGGTTTCTAGGAAGGTCTT 40310 C GT GTCG____
TGG TCG AG CTTCC TCAGGG
||| || |||| |||||
GGT TC GAAGG GGTTTT
T TG ATCTTT
GAM1959 KIF13B 3' TTTTGGTTTCTAGGAAGGTCTT 17583 C GT GTCG____
TGG TCG AG CTTCC TCAGGG
||| || |||| |||||

		GGT TC GAAGG GGT TTT		
		T TG ATCTTT		
GAM1959	L3MBTL2	3' CTGGACGGTGGAGGACCTGC 42788	GT	A G
		GCAGGTCTTCC CGTC GG		
		CGTCCAGGAGG GCAG TC		
		TG G		
GAM1959	LANCL2	3' CTTTGTGGGGAGACTTCTGGA 20778	C	GT T
		TTCG AGGTCTTCC CG CAGGG		
		AGGT TTCAGAGGG GT GTTTC		
		C _ T		
GAM1959	LASP1	3' CTGGAATGGGAGACCTGT 12795	CG	
		GCAGGTCTTCCGT TCAG		
		TGTCCAGAGGGTA GGTC		
		A_		
GAM1959	LATS1	3' TCCATCAGGGAGACCTGGAA 30239	G	GTCGTCA
		TTC CAGGTCTTCC GGG		
		AAG GTCCAGAGGG CCT		
		_ ACTA_		
GAM1959	LIMK2	3' CCTGGCAGTGGATTGTGG 18784	GTCT	TC
		TCGCAG TCCG GTCAGG		
		GGTGTT AGGT CGGTCC		
		_ GA		
GAM1959	LIMK2	3' CCTGGCAGTGGATTGTGG 12094	GTCT	TC
		TCGCAG TCCG GTCAGG		
		GGTGTT AGGT CGGTCC		
		_ GA		
GAM1959	MAP2K3	5' TCCTGGTGCAAGGCCGGTGGGA 8637	A	CC T GT
		TTCGC GGTCTT G C CAGGG		
		AGGTG CCGGAA C G GTCCT		
		G _ _ TG		
GAM1959	MAPK8IP2	3' CCTTACGCTTGTGGGGGTCTGC 18552	GT	_ T_ C G
	GG	TCGCAG CTTC CG CGT AGG		
		GGCGTC GGGG GT GCA TCC		
		TG T TC T		
GAM1959	MAPK8IP2	3' CCTTACGCTTGTGGGGGTCTGC 14704	GT	_ T_ C G
	GG	TCGCAG CTTC CG CGT AGG		
		GGCGTC GGGG GT GCA TCC		
		TG T TC T		
GAM1959	MAPK8IP2	3' CCTTACGCTTGTGGGGGTCTGC 29155	GT	_ T_ C G
	GG	TCGCAG CTTC CG CGT AGG		

	GGCGTC GGGG GT GCA TCC	
	TG T TC T	
GAM1959 MAPK8IP3 3'	TCTTGGTGGCGTCCCTTTCTGT 27222	TCTTC_ GT
GAG	TTCGCAGG CGTC CAGGG	
	GAGTGTCT GCGG GTTCT	
	TTCCCT TG	
GAM1959 MGC10471 5'	TCTTCGCAGGGAAGCCTGTGGA 25147	T GTC C
	TTCGCAGG CTTCC GT AGGG	
	AGGTGTCC GAAGG CG TTCT	
	_ GA_ C	
GAM1959 MGC10715 3'	CTCTGTGGGCAGGGCTTGTGG 23614	CC GT
	TCGCAGGTCTT GTC CAGGG	
	GGTGTTCGGGA CGG GTCTC	
	_ GT	
GAM1959 MGC12760 3'	CCTGCCGTCGTAGGGAGGCTTG 26448	GT___ T G
CGGA	CGCAGGTCTTCC CG CAGG	
	GCGTTCGGAGGG GC GTCC	
	ATGCT C	
GAM1959 MGC13114 3'	CCCTCCTGGAGGACCTGGGAA 26151	G TCGTC
	TTC CAGGTCTTCCG AGGG	
	AAG GTCCAGGAGGT TCCC	
	G CC___	
GAM1959 MGC13114 3'	CCCTGCGCTGCACGGAGGTCTG 26152	T ___ T
TGG	GCAGG CTTCCGT CG CAGGG	
	TGTCT GGAGGCA GC GTCCC	
	_ CGTC _	
GAM1959 MGC15429 3'	TCCTGCTCTGAGGCTTGTGG 26486	CCGTC T
	TCGCAGGTCTT G CAGGG	
	GGTGTTCGGAG C GTCCT	
	TCT___	
GAM1959 MGC15873 3'	CCCTGGTGACACCTGGACCTTG 26741	C TCC_ GT
GA	TTCG AGGTCT GTC CAGGG	
	AGGT TCCAGG CAG GTCCC	
	_ TCCA TG	
GAM1959 MGC2306 3'	CTCTGGGGGCAGATTTGTGG 26352	TCC G
	TCGCAGGTCT GTC TCAGGG	
	GGTGTTTAGA CGG GGTCTC	
	_ G	
GAM1959 MGC2721 3'	CCCAGGAGCCGGGAGGCCTGCG 26462	TCG A
G	TCGCAGGTCTTCCG TC GGG	

GGCGTCCGGAGGGC GG CCC
CGA A
GAM1959 MGC3222 3' TTCTGAAACCAGAGATCTGT 23643 CC CG
GCAGGTCTT GT TCAGGG
||||||| || |||||
TGTCTAGAG CA AGTCTT
AC A_

GAM1959 MGC4415 3' TTCTGTTTGAAGATTTGGGG 25574 G CGTCGT
TC CAGGTCTTC CAGGG
|| ||||| |||||
GG GTTTAGAAG GTCTT
G TTT__

GAM1959 MGC4796 3' CTTTGGCCAGAGAGACCTGTGA 30832 CCGTC
G TTCGCAGGTCTT GTCAGGG
||||||| |||||
GAGTGTCCAGAG CGGTTTC
AGAC_

GAM1959 MGC8407 3' CTCTGGTGTGTGAAGGTCGGTG 23480 A GT _ T GT
G TCGC G CTTC CG C CAGGG
|||| | |||| | |||||
GGTG C GAAG GT G GTCTC
G TG T _ TG

GAM1959 MIDORI 3' TCTGGTGTGGTTGGAGGTCTGT 36531 GT _ T GT G
GGA CGCAG CTT CCG C CAGG
|||| ||| ||| |||||
GTGTC GAG GGT G GTCT
TG GTT _ TG

GAM1959 MRF2 5' CCTTGGCGACTTTTTCTTTGT 37601 TCTTCC
GCAGG GTCGTCAGGG
|||| |||||
TGTTT CAGCGGTTCC
CTTTTT

GAM1959 MY038 5' TTCTGACGAACCCCTGCTTGTG 26345 CTTCCG
G TCGCAGGT TCGTCAGGG
||||| |||||
GGTGTTCTG AGCAGTCTT
TCCCCA

GAM1959 MY038 5' TTCTGAGTATCGGGGGGTCTCT 26346 C GT TCG_
GGA TTCG AG CTTCCG TCAGGG
|||| || ||||| |||||
AGGT TC GGGGGC AGTCTT
C TG TATG

GAM1959 NAF1 3' TCTGTGAGGAGCTGTGG 12703 G CGTCGT
TCGCAG TCTTC CAGG
||||| ||||| |||||
GGTGTC AGGAG GTCT
G T____

GAM1959 NDRG4 3' CCCATCATGGGAGGCTTTTGGGA 23212 C C CA
TTCG AGGTCTTCCGT GT GGG
|||| ||||| ||||| |||

AGGT TTCGGAGGGTA TA CCC
 T C _
 GAM1959 NDRG4 3' CCCATCATGGGAGGCTTTTGGA 21697 C C CA
 TTCG AGGTCTTCCGT GT GGG
 |||| ||||| || |||
 AGGT TTCGGAGGGTA TA CCC
 T C _
 GAM1959 NLI-IF 3' CCTTTGGGGGATCTGT 22173 TCGTC
 GCAGGTCTTCCG AGG
 ||||| || |||
 TGTCTAGGGGGT TCC
 T _
 GAM1959 NUDEL 3' CTCTGATGGTGTCTCCTCTGG 25123 C TCTTC GT
 TCG AGG C CGTCAGGG
 ||| || | |||||
 GGT TCC G GTAGTCTC
 C TCCT_ TG
 GAM1959 NXN 3' TTTTGGTGAAGGATCTGC 22813 CCG GT
 GCAGGTCTT TC CAGGG
 ||||| || |||||
 CGTCTAGGA AG GTTTT
 _ TG
 GAM1959 OAZ2 3' TTTTGGTTATTAAGACTTGTG 8377 CC CG
 CGCAGGTCTT GT TCAGGG
 ||||| || |||||
 GTGTTTCAGAA TA GGTTTT
 T_ TT
 GAM1959 OBSCN 3' CCCTGATGACCCTCCCTGCGAG 34989 TCTTCC
 TTCGCAGG GTCGTCAGGG
 ||||| |||||
 GAGCGTCC CAGTAGTCCC
 CTCC_
 GAM1959 OLFM3 5' TCTGAGAATGCCTGCGGA 39962 C CGTCG
 TTCGCAGGT TTC TCAGG
 ||||| || |||||
 AGGCGTCCG AAG AGTCT
 T _
 GAM1959 p25 3' CCTGATCCGGTCTGTGG 13891 TCTT TC
 TCGCAGG CCG GTCAGG
 ||||| || |||||
 GGTGTCT GGC TAGTCC
 _ C_
 GAM1959 P2RXL1 3' CCCTGGGGGTGGGAGGCTGTGG 11930 G GT G
 TCGCAG TCTTCC C TCAGGG
 ||||| ||||| | |||||
 GGTGTC GGAGGG G GGTCCC
 _ TG G
 GAM1959 P2RXL1 3' TTTTGCCATGGAGGTCTGGGAG 11934 G T C T
 TTC CAGG CTTCCGT G CAGGG
 ||| ||| ||||| | |||||

GAG GTCT GGAGGTA C GTTTT
 G _ C _
 GAM1959 PAXIP1L 3' TCTTGGTGGAGAGGTTGCGGA 34740 GT CG GT
 TTCGCAG CTTC TC CAGGG
 ||||| ||| || |||||
 AGGCGTT GGAG GG GTTCT
 _ A_ TG
 GAM1959 PCQAP 3' TTCTGCCTTGGGGACCTGC 18035 T TC T
 GCAGGTCT CCG G CAGGG
 ||||| ||| | |||||
 CGTCCAGG GGT C GTCTT
 _ TC _
 GAM1959 PDE11A 3' GGTTTTGGATCCAAGGACCTGT 18867 _ TCGTCAGGG
 GGA GCAGGTCT TCCG
 ||||| |||
 TGTCCAGG AGGT
 AACCT TTT GGG
 GAM1959 PDE4DIP 3' CTCTGATTTCAATTGAGGATCTT 16051 C C C _
 GG TCG AGGTCTTC GT GTCAGGG
 || ||||| || |||||
 GGT TCTAGGAG TA TAGTCTC
 _ T CTT
 GAM1959 PIF1 3' CTTGGAGGGGACTGGTGG 30587 A TT G GT
 TCGC GGTC CC TC CAGG
 ||| ||| || |||
 GGTG TCAG GG AG GTTC
 G _ G _
 GAM1959 PINK1 3' CTCTGTGTCGTGATGGTCTGTG 26194 GT T _ T T
 AA TTCGCAG C TC CG CG CAGGG
 ||||| | || || |||||
 AAGTGTC G AG GC GT GTCTC
 TG T T T _
 GAM1959 PISD 5' CCTGGCGATCTTCTGGGG 15655 G TCTTCC
 TC CAGG GTCGTCAGG
 || ||| |||||
 GG GTCT TAGCGGTCC
 G TC _
 GAM1959 PLCL2 3' TTTTGGTGGCATGCTTGCTGAG 33796 _ CTTCC GT
 TTC GCAGGT GTC CAGGG
 || ||||| || |||||
 GAG CGTTCC CGG GTTTT
 T TA _ TG
 GAM1959 PM5 5' TCTGGCGGCGGCGGTGGG 30498 AGGTCTT
 TTCGC CCGTCGTCAGG
 |||| |||||
 GGGTG GGCGGCGGTCT
 GC _
 GAM1959 PP3501 3' TCCTGCCAGAAGGCCTCTGAG 22333 C CGTC T
 TTCG AGGTCTTC G CAGGG
 ||| ||||| | |||||

GAGT TCCGGAAG C GTCCT
 C AC__
 GAM1959 PPFIBP1 3' TCCGCGGTATGGAGGATTTGAG 9686 G CA
 GA TTC CAGGTCTTCCGT CGT GGG
 ||| ||||| ||| |||
 AGG GTTTAGGAGGTA GCG CCT
 A TG _
 GAM1959 PPP4R1L 5' CTGACGGCCCAGCGGA 38817 A TCTTCC
 TTCGC GG GTCGTCAG
 ||||| || |||||
 AGGCG CC CGGCAGTC
 A _
 GAM1959 PRC1 3' CTTTGTCTGGAGATCTGGAA 10120 G T T T
 TTC CAGGTCT CCG CG CAGGG
 ||| ||||| ||| ||| |||||
 AAG GTCTAGA GGT GC GTTTC
 _ _ _ T
 GAM1959 PRO2405 5' CCCGTTGTTGGAGGATTTGATG 20698 _ T TCA
 AG TTCG CAGGTCTTCCG CG GGG
 ||||| ||||| ||| |||
 GAGT GTTTAGGAGGT GT CCC
 A T TG_
 GAM1959 PRO2405 5' CCCTGATGATGGCCTACACTGT 20699 _ CTT
 G CGCAG GT CCGTCGTCAGGG
 ||||| || ||||| |||||
 GTGTC CA GGTAGTAGTCCC
 A TCC
 GAM1959 PRPF8 5' TCTTGTGTGAGGGCCTGTGG 30687 CGT T
 TCGCAGGTCTTC CG CAGGG
 ||||| || |||||
 GGTGTCCGGGAG GT GTTCT
 T _ _
 GAM1959 PRRDH 5' CCCTGCAGGGGATCTGTGG 17935 T GTCGT
 TCGCAGGTCT CC CAGGG
 ||||| || |||||
 GGTGTCTAGG GG GTCCC
 _ AC_ G
 GAM1959 PRRDH 5' CCCTGCAGGGGATCTGTGGG 17936 T GTCGT
 TTCGCAGGTCT CC CAGGG
 ||||| || |||||
 GGTGTCTAGG GG GTCCC
 _ AC_
 GAM1959 PTPRR 3' TTTTGATGATGGAGGTATG 28383 GGT
 CA CTTCCGTCGTCAGGG
 || ||||| |||||
 GT GGAGGTAGTAGTTTT
 AT_
 GAM1959 PTPRR 3' TTTTGATGATGGAGGTATG 8743 GGT
 CA CTTCCGTCGTCAGGG
 || ||||| |||||

			GT GGAGGTAGTAGTTTT		
			AT_		
GAM1959	QSCN6	3'	CCCTGCCTTGGGAGGTGTGTGG 8697	GG	TC T
	A		TTCGCA TCTTCCG G CAGGG		
			AGGTGT GGAGGGT C GTCCC		
			GT TC_		
GAM1959	RAB-R	3'	CTCTGGTGACCACTTGCCTGTG 12721	CTTCC	GT
	G		TCGCAGGT GTC CAGGG		
			GGTGTCCG CAG GTCTC		
			TTCAC TG		
GAM1959	RAB3D	3'	CCCGGTGGGAGGCTGCGGA 10495	G	GT TCA
			TTCGCAG TCTTCC CG GG		
			AGGCGTC GGAGGG GC CC		
			_ TG _		
GAM1959	RAI	3'	CCTTAGCCTTGGGAGGTCTGGG 13469	G GT	TC TC
	AA		TTC CAG CTTCCG G AGGG		
			AAG GTC GAGGGT C TTCC		
			G TG TC GA		
GAM1959	RAI17	3'	TCCTGCTTGGGGACTGGTGG 43864	A T	TC T
			TCGC GGTCT CCG G CAGGG		
			GGTG TCAGG GGT C GTCCT		
			G _ T__		
GAM1959	RASGRP4	3'	TCTCAGGAGGACTTTGAG 27506	C	GTCGTC
			TTCG AGGTCTTCC AGG		
			GAGT TTCAGGAGG TCT		
			_ AC_		
GAM1959	RGS12	3'	CCTGGGTGAGGCCTGGGG 8830	G	_ GTCGT
			TC CAGGTCTT CC CAGG		
			GG GTCCGGAG GG GTCC		
			G T _		
GAM1959	RLUCL	5'	CCCTGGAGGGGAGGGTCTGTGG 27754	GT	G GT
	G		TTCGCAG CTTCC TC CAGGG		
			GGGTGTC GGAGG GG GTCCC		
			TG _ AG		
GAM1959	RPP14	3'	CTTTGGTGGGGTGGGCTTCGGA 29926	C	T G GT
			TTCG AGGTCT CC TC CAGGG		
			AGGC TTCGGG GG GG GTTTC		
			_ T _ TG		
GAM1959	SAMHD1	3'	TGGGGAAGATCTGAGAG 30737	G	G
			TTC CAGGTCTTCC TCG		

			GAG GTCTAGAAGG GGT		
			A _		
GAM1959	SEMA4F	3'	CCTGGTCTTGGCCTGTGAA 10456		TTCCGTCG
			TTCGCAGGTC TCAGG		
			AAGTGTCCGG GGTCC		
			TTCT__		
GAM1959	SEMA4F	3'	CTTGGCAGCAGCCTGTGAA 10458		T TCC C
			TTCGCAGG CT GT GTCAGG		
			AAGTGTCC GA CG CGGTTC		
			_ _ A		
GAM1959	SEPT3	3'	CCTGTATGGAGACCTTGA 21182	C T	CGT
			TTCG AGGTCT CCGT CAGG		
			AGGT TCCAGA GGTA GTCC		
			_ _ T_		
GAM1959	SLC39A3	3'	CCCTGATGACACCCTGCGAG 29357		TCTTCC
			TTCGCAGG GTCGTCAGGG		
			GAGCGTCC CAGTAGTCCC		
			CA__		
GAM1959	SMC1L1	3'	CCTGGTAAGCGGAGGGCCTGAG 35618	G	CG_ G
	GA		TTC CAGGTCTTCCGT TCAGG		
			AGG GTCCGGGAGGCG GGTCC		
			A AAT		
GAM1959	SNTG1	3'	TCTGGATGACATCTGTGAA 21041	CTTCC	_
			TTCGCAGGT GTCGTC AGG		
			AAGTGTCTA CAGTAG TCT		
			_ _ G		
GAM1959	SR-BP1	3'	CCTGAAGGAAGACCTGCGGA 12485		GTCG
			TTCGCAGGTCTTCC TCAGG		
			AGGCGTCCAGAAGG AGTCC		
			A_		
GAM1959	SSB-3	3'	CCCTGAGCCCCAGGTCTTGTGG 28102	T CC_ CG	
			TGCGAGG CTT GT TCAGGG		
			GGTGTTC GGA CG AGTCCC		
			T CCC _		
GAM1959	SSH2	3'	TTTTGATGGTGGATAAGAT 31190	_ GT	
			GTCT TCC CGTCAGGG		
			TAGA AGG GTAGTTTT		
			AT TG		
GAM1959	STX3A	3'	CTCTGACATTGAGGCCTGGGG 10387	G CC C	
			TC CAGGTCTT GT GTCAGGG		

GG GTCCGGAG TA CAGTCTC
G T_ _
GAM1959 SULT1C2 5' CCTGAGTCGGGAGGCCTGC 13353 TCG
GCAGGTCTTCCG TCAGG
||||| ||||
CGTCCGGAGGGC AGTCC
TG_
GAM1959 TBX4 3' CTTTGA CT TCTGGAGAGTCTGT 20546 TC TC_
GAG TTCGCAGG TTCCG GTCAGGG
||||| |||| |||||
GAGTGTCT GAGGT CAGTTTC
GA CTT
GAM1959 TEX27 3' CTCTGGTAGGTGAGGGCCTGAG 22459 G CGTCG
G TC CAGGTCTTC TCAGGG
|| ||||| ||||
GG GTCCGGGAG GGTCTC
A TGGAT
GAM1959 TIGD1 5' TTCTGAAAACAAATGGAGGGTT 42848 GT CG____
TGTGG CAG CTTCCGT TCAGGG
||| ||||| ||||
GTT GGAGGTA AGTCTT
TG AACAAA
GAM1959 TNFAIP3 3' CTTTGGACTTGGAAGGTGTGCG 12979 GG TCG
G TCGCA TCTTCCG TCAGGG
|||| ||||| ||||
GGCGT GGAAGGT GGTTC
GT TCA
GAM1959 TREX1 5' TCCTGATGTGACGGACTGTGAA 18521 GTCT _
TTCGCAG TCCGTC GTCAGGG
||||| ||||| |||||
AAGTGTC AGGCAG TAGTCCT
_ TG
GAM1959 TREX1 5' TCCTGATGTGACGGACTGTGAA 27341 GTCT _
TTCGCAG TCCGTC GTCAGGG
||||| ||||| |||||
AAGTGTC AGGCAG TAGTCCT
_ TG
GAM1959 TREX1 5' TCCTGATGTGACGGACTGTGAA 27348 GTCT _
TTCGCAG TCCGTC GTCAGGG
||||| ||||| |||||
AAGTGTC AGGCAG TAGTCCT
_ TG
GAM1959 TRIM11 3' TTTTGGCCACTTGAGGACCTG 36056 G TC_
GGAG TC CAGGTCTTCCG GTCAGGG
|| ||||| ||||
AG GTCCAGGAGGT CGGTTTT
G TCAC
GAM1959 UBCE7IP5 3' CCTTGGGAGCAGTGGGGGTGTC 17271 GT_ TC _
TGTGGA CAG CTTCCG GT CAGGG
||| ||||| || ||||

		GTC GGGGGT CG GTTCC	
		TGT GA AGG	
GAM1959 UXS1	5'	TTGTAAATGGAAGGTTTCGAG 24677	C GT CGT
		TTCG AG CTTCCGT CAG	
		GAGC TT GAAGGTA GTT	
		_ TG AAT	
GAM1959 VI	3'	TTCTGGCCAATCAAGGCTTGC 15110	CCGTC
		GCAGGTCTT GTCAGGG	
		CGTTCGGAA CGGTCTT	
		CTAAC	
GAM1959 VLCS-H1	5'	CCCTGAGTAGTGAGGATCTGCG 15260	CGTCG
G		TCGCAGGTCTTC TCAGGG	
		GGCGTCTAGGAG AGTCCC	
		TGATG	
GAM1959 WDR7	3'	CCTTGATCTGTATATACTTGTG 17610	CTTCCGTC
AG		TTCGCAGGT GTCAGGG	
		GAGTGTTCA TAGTTCC	
		TATATGTC	
GAM1959 ZDHC8	3'	CCTTGGTGTGACGGACCTGAGA 31962	G TT GT_ GT
G		TTC CAGGTC CC C CAGGG	
		GAG GTCCAG GG G GTTCC	
		A _ ACT TG	
GAM1959 ZFP95	5'	TTTGGTGATGCTGTGCGAG 15923	_ CTTCC GT
		TTCGCA GGT GTC CAGG	
		GAGCGT TCG TAG GTTT	
		G _ _ _ TG	
GAM1959 ZID	3'	TCTTGGTGTATAGTTCTGTGAA 13416	GT TCCGT GT
		TTCGCAG CT C CAGGG	
		AAGTGTC GA G GTTCT	
		TT TAT_ TG	
GAM1959 ZNF17	3'	TTTTGGTGGTGGGGGGGTTGCG 40070	G GT GT
		CGCAG TCTTCC C CAGGG	
		GCGTT GGGGGG G GTTTT	
		G TG TG	
GAM1959 ZNF317	3'	CCATAGGAGGTTTGTGAG 35635	T GTCGTCA
		TTCGCAGG CTTCC GG	
		GAGTGTTT GGAGG CC	
		_ ATA_	
GAM1959 LOC115051	3'	TTCTGACCCACTGGGATTTGC 30161	CCGTC
		GCAGGTCTT GTCAGGG	

	CGTTTAGGG CAGTCTT		
	TCACC		
GAM1959 LOC115110 5'	CTCTGAATGAAGAGGAACCTGC 35509	_ CG _	
GG	TCGCAGGT CTTC TCGT CAGGG		
	GGCGTCCA GGAG AGTA GTCTC		
	A A_ A		
GAM1959 LOC115343 5'	CCCAGGAGGCGGGGCGCCTGTG 35666	C GT A	
G	TCGCAGGT TTCCGTC C GGG		
	GGTGTCCG GGGGCGG G CCC		
	C AG A		
GAM1959 LOC115708 3'	CCCTGTGCTGGGGGCCTTGAG 36405	C T T T	
	TTCG AGGTCT CCG CG CAGGG		
	GAGT TCCGGG GGT GT GTCCC		
	_ _ C _		
GAM1959 LOC120772 5'	CCTGGTGACGGGGCTGGC 36628	A TT GT	
	GC GGTC CCGTC CAGG		
	CG TCGG GGCAG GTCC		
	G _ TG		
GAM1959 LOC122792 3'	CTTTGGGGAAGGTGATTTGTGG 29763	TT G G	
	TCGCAGGTC CC TC TCAGGG		
	GGTGTTTAG GG AG GGTTTC		
	T_ A G		
GAM1959 LOC124145 3'	TCTGGTGAAGTTTGTGAA 36735	T TCCG GT	
	TTCGCAGG CT TC CAGG		
	AAGTGTTT GA AG GTCT		
	_ _ _ TG		
GAM1959 LOC124245 3'	CCTGGTCAGGCCTGTGGA 29418	TCCGTCG	
	TTCGCAGGTCT TCAGG		
	AGGTGTCCGGA GGTCC		
	CT_		
GAM1959 LOC124538 3'	CTTTGGTGGTTAAGGTTTGTGA 37257	GT CCG GT	
	TCGCAG CTT TC CAGGG		
	AGTGTT GAA GG GTTTC		
	TG TT_ TG		
GAM1959 LOC124842 3'	CCCTGTGCAGGGGGTTCTGTGG 37259	GT GT T	
	TCGCAG CTTC CG CAGGG		
	GGTGTC GGGGG GT GTCCC		
	TT AC _		
GAM1959 LOC126917 3'	TCTTGGGAGTGAGGACTTGGGG 36874	G CG G	
	TC CAGGTCTTC TC TCAGGG		

	GG GTTCAGGAG AG GGTTCT		
	G _ TG _		
GAM1959 LOC126917 3'	TCTTGGGGTGGGGATCTGAGG 36875	G	T GT G
	TC CAGGTCT CC C TCAGGG		
	GG GTCTAGG GG G GGTTCT		
	A _ TG _		
GAM1959 LOC127534 3'	CTCTGACGGTGGGAGGGTCACG 37169	CAGG	GT
G	TCG TCTTCC CGTCAGGG		
	GGC GGAGGG GCAGTCTC		
	ACTG TG		
GAM1959 LOC132671 3'	CCCTGTGCTGGAGGTTTGAGG 29776	G T	T T
	TC CAGG CTTCCG CG CAGGG		
	GG GTTT GGAGGT GT GTCCC		
	A _ C _		
GAM1959 LOC133308 5'	TCCTGGCCCCAGAAGCCTGCGG 37036	T	CGTC
A	TTCGCAGG CTTC GTCAGGG		
	AGGCGTCC GAAG CGGTCCT		
	_ ACCC		
GAM1959 LOC133923 5'	CTCTGAGTCACGGTCTGTGAG 37382	TCTT	CG_
	TTCGCAGG CCGT TCAGGG		
	GAGTGTCT GGCA AGTCTC		
	_____ CTG		
GAM1959 LOC139296 5'	CCGTGTGGGAGATCTGTGAG 37339	TCGT	G
	TTCGCAGGTCTTCCG CA GG		
	GAGTGTCTAGAGGGT GT CC		
	_____ G		
GAM1959 LOC143146 5'	CCTGACTTGGGAGGCCGCGGA 30195	A	TC
	TTCGC GGTCTTCCG GTCAGG		
	AGGCG CCGGAGGGT CAGTCC		
	G T_		
GAM1959 LOC143279 5'	TCCTGGTGGTGGAGGTGGGGG 37600	G GGT	GT GT
	TTC CA CTTCC C CAGGG		
	GGG GT GGAGG G GTCCT		
	G _ TG TG		
GAM1959 LOC143425 5'	CCTGGCGGTGAGCGCGGA 42352	AG	CTTC GT
	TTCGC GT C CGTCAGG		
	AGGCG CG G GCGGTCC		
	_ A_ TG		
GAM1959 LOC143719 5'	TCCTGTATGGAGATTTGAGAA 30405	G	T CGT
	TTC CAGGTCT CCGT CAGGG		

AAG GTTTAGA GGTA GTCCT
 A _ T_
 GAM1959 LOC144182 3' CTTGATGATAACCAAGTGA 29167 A CTTCC
 TTCGC GGT GTCGTCAGG
 ||||| ||| |||||
 AGGTG CCA TAGTAGTTC
 A A_
 GAM1959 LOC144266 5' CCTAGTTGGGAGGTCTGACGGA 37709 _ GT TCGTC
 TTCG CAG CTTCCG AGG
 ||||| ||| ||||| |||
 AGGC GTC GAGGGT TCC
 A TG TGA_
 GAM1959 LOC144305 5' CCTGAGCCGGGATCTGGGG 40399 G TT TCG
 TC CAGGTC CCG TCAGG
 || ||||| ||| |||||
 GG GTCTAG GGC AGTCC
 G _ CG_
 GAM1959 LOC144317 3' CTCTGATGGCAATCTTTGGA 37717 C CTTCC
 TTCG AGGT GTCGTCAGGG
 ||||| ||| |||||
 AGGT TCTA CGGTAGTCTC
 T A_
 GAM1959 LOC144501 3' CTTTGGTGCACCAGGCCTTGGA 40427 C TCC _ GT
 TTCG AGGTCT GT C CAGGG
 ||||| ||||| ||| |||||
 AGGT TCCGGA CA G GTTTC
 _ C_ C TG
 GAM1959 LOC144535 3' CTTGTTTGAAGACTTGTGGA 37762 CGTCGT
 TTCGCAGGTCTTC CAGG
 ||||| ||||| ||||| |||||
 AGGTGTTTCAAG GTTC
 TTT_
 GAM1959 LOC144871 3' CCCTGGTGATGGGCGTTGC 40468 _ CTT GT
 GCAG GT CCGTC CAGGG
 ||||| ||| ||||| |||||
 CGTT CG GG TAG GTCCC
 G _ TG
 GAM1959 LOC145317 5' CTCTGTGACTGAAGGGCCTGCG 40530 _ C T
 GA TTCGCAGGTC TTC GTCG CAGGG
 ||||| ||| ||||| |||||
 AGGCGTCCGG AAG CAGT GTCTC
 G T _
 GAM1959 LOC145622 5' CTCTGATGGTGAGACTTGAGGA 37907 G TC GT
 TTC CAGGTCT C CGTCAGGG
 ||| ||||| ||| |||||
 AGG GTTCAGA G GTAGTCTC
 A _ TG
 GAM1959 LOC145622 3' CTGAAAAGACTGTGGA 37908 G CCGTCG
 TTCGCAG TCTT TCAG
 ||||| ||||| |||||

		AGGTGTC AGAA AGTC		
		— A —		
GAM1959	LOC145622 5'	TCTGATGGTAAGCCTGGAG 37915	G T	CCG
		TTC CAGG CTT TCGTCAGG		
		GAG GTCC GAA GGTAGTCT		
		— — T —		
GAM1959	LOC145725 3'	CCGGGTGGGGGATTTTGG 37949	C	GT GTCA
		TCG AGGTCTTCC C GG		
		GGT TTTAGGGGG G CC		
		— TG G —		
GAM1959	LOC145732 3'	CCGGGTGGGGGATTTTGG 37958	C	GT GTCA
		TCG AGGTCTTCC C GG		
		GGT TTTAGGGGG G CC		
		— TG G —		
GAM1959	LOC145761 5'	CCCGAGTTGGGGGATTTGAGAG 40583	G	TCG A
		TTC CAGGTCTTCCG TC GGG		
		GAG GTTTAGGGGGT AG CCC		
		A TG —		
GAM1959	LOC145815 5'	CCTTGATGGTGAATGACCGGG 40604	A —	GT
	T	GC GGTC TTCC CGTCAGGG		
		TG CCAG AAGG GTAGTTCC		
		GG T TG		
GAM1959	LOC146237 3'	CTTGAAACAGAAGGCCTGTGG 40667	C CG	G
		TCGCAGGTCTTC GT TCAGG		
		GGTGTCCGGAAG CA GGTTT		
		A AA		
GAM1959	LOC146332 5'	TCTGAGCCAGGCCTGTGAG 38130	TCC	CG
		TTCGCAGGTCT GT TCAGG		
		GAGTGTCCGGA CG AGTCT		
		C — —		
GAM1959	LOC146452 3'	CTCTGGTGATGGCTGTGAG 38164	GTCTT	GT
		TTCGCAG CCGTC CAGGG		
		GAGTGTC GGTAG GTCTC		
		— TG		
GAM1959	LOC146488 3'	TGAGGGTGGTGGGCCTGCGG 35050	T GT	G
		TCGCAGGTCT CC C TCA		
		GGCGTCCGGG GG G AGT		
		T TG G		
GAM1959	LOC146513 5'	CCTTGATGCCCGTGCCTGTGAA 40709	CTTC	T —
		TTCGCAGGT CG CGTCAGGG		

		AAGTGTCCG GC GTAGTTCC		
		T__ CC		
GAM1959	LOC146714 5'	CCACAGAGGCGGAAGACCAGCG 40720	A	GTCAG
	AG	TTCGC GGTCTTCCGTC GG		
		GAGCG CCAGAAGGCGG CC		
		A AGACA		
GAM1959	LOC146894 3'	CCTTCAGGAAGCCTGTGAA 29780	T	GTCGTC
		TTCGCAGG CTTCC AGG		
		AAGTGTCC GAAGG TCC		
		_ ACT__		
GAM1959	LOC146957 3'	CCCTGGGGCAGAGATTTGTGAG 38277		CC G
		TTCGCAGGTCTT GTC TCAGGG		
		GAGTGTTTAGAG CGG GGTCCC		
		A_ _		
GAM1959	LOC147054 5'	CCCTGGTGACACCTTGATCTTG 40789	C	TTCC_ GT
	GA	TTCG AGGTC GTC CAGGG		
		AGGT TCTAG CAG GTCCC		
		_ TTCCA TG		
GAM1959	LOC147136 3'	CCTTGATGGGCAGGCTTGGA 38303	G	T GT
		TTC CAGGTCT CC CGTCAGGG		
		AAG GTTCGGA GG GTAGTTCC		
		_ C _		
GAM1959	LOC147165 3'	TCCTGGCAGGAGGACCTGGAG 40815	G	GTC
		TTC CAGGTCTTCC GTCAGGG		
		GAG GTCCAGGAGG CGGTCCT		
		_ A_		
GAM1959	LOC147178 3'	CCCTGGTGACCCGGGGTCAGCG 30743	A GT	CC GT
	GA	TTCGC G CTT GTC CAGGG		
		AGGCG C GGG CAG GTCCC		
		A TG CC TG		
GAM1959	LOC147694 5'	CCTGGCTGGGCTGGCGGA 38371	A	TCCGTC
		TTCGC GGTCT GTCAGG		
		AGGCG TCGGG CGGTCC		
		G T__		
GAM1959	LOC147859 5'	CTTTGGGACCCAGGGCCTGC 42151		CC G
		GCAGGTCTT GTC TCAGGG		
		CGTCCGGGA CAG GGTTTC		
		CC _		
GAM1959	LOC147993 5'	CCTTGGCCTCTCGGAGGCCTCT 42153	C	T TC__
	GG	TCG AGGTCT CCG GTCAGGG		

	GGT TCCGGA GGC CGGTTCC	
	C _ TCTC	
GAM1959 LOC148089 3'	CCCTGCAGTGGGGACTTCGTGG 38450	_ T TC T
	TCGC AGGTCT CCG G CAGGG	
	GGTG TTCAGG GGT C GTCCC	
	C _ GA _	
GAM1959 LOC148397 3'	CCCTGGTGACAAAGCCTTTGGA 38528	C T CC GT
	TTCG AGG CTT GTC CAGGG	
	AGGT TCC GAA CAG GTCCC	
	T _ A_ TG	
GAM1959 LOC148710 3'	CTCTGTAGTGTGAGGGTCTGTG 40894	GT _ TC T
G	TCGCAG CTTC CG G CAGGG	
	GGTGTC GGAG GT T GTCTC	
	TG T GA _	
GAM1959 LOC148918 5'	TGATGGAAATTAGTGAG 38614	AG C
	TTCGC GT TTCCGTCG	
	GAGTG TA AAGGTAGT	
	AT _	
GAM1959 LOC148936 3'	TCCTGATTCTGAGACTTTGG 40932	C CCGTC
	TCG AGGTCTT GTCAGGG	
	GGT TTCAGAG TAGTCCT	
	_ TCT__	
GAM1959 LOC148938 3'	TCCTGATTCTGAGGCTTTGG 40925	C CCGTC
	TCG AGGTCTT GTCAGGG	
	GGT TTCGGAG TAGTCCT	
	_ TCT__	
GAM1959 LOC148979 5'	CCCTCTGACGGGAGATCTGGGG 40942	G TC
	TC CAGGTCTTCCGTCG AGGG	
	GG GTCTAGAGGGCAGT TCCC	
	G C_	
GAM1959 LOC149132 5'	TCTACCATGAAAGACTTGTGAA 38645	C C C
	TTCGCAGGTCTT CGT GT AGG	
	AAGTGTTTCAGAA GTA CA TCT	
	A C _	
GAM1959 LOC149171 5'	CCTTGCCCTGGAGGGTTTTGAG 38666	C GT TC T
	TTCG AG CTTCCG G CAGGG	
	GAGT TT GGAGGT C GTTCC	
	_ TG CC _	
GAM1959 LOC149194 5'	CTCTGGTGGTGGGCACCTGT 38669	CT GT GT
	GCAGGT TCC C CAGGG	

	TGTCCA GGG G GTCTC	
	C_ TG TG	
GAM1959 LOC149267 5'	CCTGATGACCCTCTGCGG 28831	TCTTCC
	TCGCAGG GTCGTCAGG	
	GGCGTCT CAGTAGTCC	
	CC____	
GAM1959 LOC149276 5'	TCTGATTTGGTTTGTGG 40978	TCTT TC
	TCGCAGG CCG GTCAGG	
	GGTGTTT GGT TAGTCT	
	T__ T_	
GAM1959 LOC149506 3'	CTCTGGCGATAATCACCTGAG 41008	G TCTTCC
AG	TTC CAGG GTCGTCAGGG	
	GAG GTCC TAGCGGTCTC	
	A CACTAA	
GAM1959 LOC149603 3'	CCTTGGTGCGATGTCTGTGAG 34971	TCTTC _
	TTCGCAGG CGTCGT CAGGG	
	GAGTGTCT GTAGCG GTTCC	
	_____ TG	
GAM1959 LOC149620 5'	CTGAAGTATGGGAGGCTTCTGA 38788	C CG_ GG
G	TTCG AGGTCTTCCGT TCAG	
	GAGT TTCGGAGGGTA AGTC	
	C TGA	
GAM1959 LOC149650 3'	CCGTGTTACAGGAGGCTTGTGA 38793	C CGT G
G	TTCGCAGGTCTTC GT CA GG	
	GAGTGTTCCGGAGG CA GT CC	
	A TT_ G	
GAM1959 LOC149657 3'	TGACGGGAGATTTGCTGAG 41037	_
	TTC GCAGGTCTTCCGTCG	
	GAG CGTTTAGAGGGCAGT	
	T	
GAM1959 LOC150142 5'	CGAAGGAAGGCCTGAGAA 38851	G G
	TTC CAGGTCTTCC TCG	
	AAG GTCCGGAAGG AGC	
	A A	
GAM1959 LOC150150 5'	CCTTGGATAAAAGATTTGC 41136	CC GT
	GCAGGTCTT GTC CAGGG	
	CGTTTAGAA TAG GTTCC	
	AA _	
GAM1959 LOC150372 5'	CTGGCGTGGGAGGTCTGGGG 38938	G GT T
	TC CAG CTTCCG CGTCAG	

GG GTC GAGGGT GCGGTC
G TG _
GAM1959 LOC150421 3' CTGGGTATGGAGGGTCTTGAG 41204 C GT CG
TTCG AG CTTCCGT TCAG
|||| || ||||| |||
GAGT TC GGAGGTA GGTC
_ TG TG
GAM1959 LOC150776 3' CCTTGGGCTGAGAGGACCTGGG 31677 G _ _ GT
AA TTC CAGGTCTTC C GTC CAGGG
||| ||||| | ||| |||||
AAG GTCCAGGAG G CGG GTTCC
G A T _
GAM1959 LOC150819 3' TTTTGGGGGTGGGGGTTGCGGA 41249 GT GT G
TTCGCAG CTTCC C TCAGGG
||||| |||| | |||||
AGGCGTT GGGGG G GGTTTT
_ TG G
GAM1959 LOC150935 3' TCCTGGTGATGACATCTTGAGA 39021 G TCTTC GT
G TTC CAGG CGTC CAGGG
||| ||| ||| |||||
GAG GTTC GTAG GTCCT
A TACA_ TG
GAM1959 LOC151201 3' TTCTCATTGTGTAGGATTTGTG 41327 C TC C
AA TTCGCAGGTCTT CG GT AGGG
||||||| || || |||||
AAGTGTTTAGGA GT TA TCTT
T GT C
GAM1959 LOC151507 3' TTCTGACGGTTCCTTCTCTGTG 39127 TCTTCCG
AA TTCGCAGG TCGTCAGGG
||||| |||||
AAGTGTCT GGCAGTCTT
CTTCCTT
GAM1959 LOC151877 3' TCTTGATGGTATCATTTGC 41397 CTTCCG
GCAGGT TCGTCAGGG
||||| |||||
CGTTTA GGTAGTTCT
CTAT_
GAM1959 LOC152078 3' CTTGACTTAAGACTTGGA 39211 G CCGTC
TTC CAGGTCTT GTCAGG
||| ||||| |||||
AAG GTTCAGAA CAGTTC
_ TT_
GAM1959 LOC152441 5' GTCCTGACAAGGATTGAGAGGA 41505 _ _ _
TTTGTGG GGTCTTC CG TC GTCAGGG T
||||| || || ||||| |
TTAGGAG GT AG CAGTCCT G
A T GAA
GAM1959 LOC152765 5' CTCTGGCATTGGGGTCTGC 39315 GT CC C
GCAG CTT GT GTCAGGG
|||| ||| || |||||

	CGTC GGG TA CGGTCTC	
	TG TT _	
GAM1959 LOC153020 3'	CCTTGATGGCGATAATCTGTGA 39354	CT C
G	TTCGCAGGT TC GTCGTCAGGG	
	GAGTGTCTA AG CGGTAGTTCC	
	AT _	
GAM1959 LOC153339 5'	TGGGGGAAAATTTGTGGA 41615	C G
	TTCGCAGGT TTCC TCG	
	AGGTGTTTA AAGG GGT	
	A G	
GAM1959 LOC153442 5'	TCTTGGCTAGAGAAAACCTGTG 41636	C CGTC
G	TCGCAGGT TTC GTCAGGG	
	GGTGTCCA AAG CGGTTCT	
	A AGAT	
GAM1959 LOC153577 3'	CCCTGAGGAGGGGCCTGC 41643	CTT G G
	GCAGGT CC TC TCAGGG	
	CGTCCG GG AG AGTCCC	
	_ G G	
GAM1959 LOC153688 3'	TCCTGGCTCAGGCCTGGCGAG 41661	_ TCCGTC
	TTCGC AGGTCT GTCAGGG	
	GAGCG TCCGGA CGGTCCT	
	G CT__	
GAM1959 LOC153811 3'	CCCTGCATCAGAATGCCTGCGA 39415	C CGTC T
A	TTCGCAGGT TTC G CAGGG	
	AAGCGTCCG AAG C GTCCC	
	T ACTA _	
GAM1959 LOC154442 3'	CCTTGACTGCAGGCTTGGGAG 41705	G TCC C
	TTC CAGGTCT GT GTCAGGG	
	GAG GTTCGGA CG CAGTTCC	
	G _ T	
GAM1959 LOC157556 3'	CCTGACCAGTTTTTGCGG 41821	T TCCGTC
	TCGCAGG CT GTCAGG	
	GGCGTTT GA CAGTCC	
	T C__	
GAM1959 LOC157623 5'	CTTGACAGGAAGGCTGTGAG 39615	G GTCGT
	TTCGCAG TCTTCC CAGG	
	GAGTGTC GGAAGG GTTC	
	_ AC__	
GAM1959 LOC157638 5'	CCCTGTCCGGGGACCTGTG 39623	T TCGT
	CGCAGGTCT CCG CAGGG	

		GTGTCCAGG GGC GTCCC		
		_ CT_		
GAM1959	LOC157657 3'	TCCTGACATCACTGAGATCTGA 39626	G	CCGTC_
		GGA TTC CAGGTCTT GTCAGGG		
		AGG GTCTAGAG CAGTCCT		
		A TCACTA		
GAM1959	LOC157773 5'	TTCTGATGAGACTGAGACTTTG 39670	C	CCG_
		AA TTCG AGGTCTT TCGTCAGGG		
		AAGT TTCAGAG AGTAGTCTT		
		_ TCAG		
GAM1959	LOC157848 3'	CCTGGCTGCAGCCTGCGG 39672	T TCC C	
		TCGCAGG CT GT GTCAGG		
		GGCGTCC GA CG CGGTCC		
		_ _ _ T		
GAM1959	LOC157860 3'	TCCTGGTGATGGGGGGTTCCT 41861	_	GT
		AGG TCTTCCGTC CAGGG		
		TCC GGGGGGTAG GTCCT		
		TT TG		
GAM1959	LOC158056 5'	TCTTGCCTGCGGGGACCTGTG 39720	T	CGT
		CGCAGGTCT CCGT CAGGG		
		GTGTCCAGG GGCG GTTCT		
		_ TCC		
GAM1959	LOC158156 3'	CCTTGGCACCTCAGATTCTGTG 39739	_	TCC C
		G TCGCAGG TCT GT GTCAGGG		
		GGTGTCT AGA CA CGGTTCC		
		T CTC _		
GAM1959	LOC158332 3'	TCCTGGTAATGGACCTGC 39825	TCT	CG
		GCAGG TCCGT TCAGGG		
		CGTCC AGGTA GGTCCT		
		_ AT		
GAM1959	LOC158476 5'	CTTTGACTAGCAAGGCTTGT 41999		CCGTC
		GCAGGTCTT GTCAGGG		
		TGTTCGGAA CAGTTTC		
		CGAT_		
GAM1959	LOC158549 3'	TCTTGGCGGCGGGGGGATC 42012	_	
		GGTCTTCC GTCGTCAGGG		
		CTAGGGGG CGGCGGTTCT		
		G		
GAM1959	LOC160336 5'	CTTGAGAAAGCTTGTGAA 39996	T	CGTCG
		TTCGCAGG CTTC TCAGG		

	AAGTGTTC GAAG GGTTC	
	— A —	
GAM1959 LOC160414 5'	CTTTGATGGCCATGACTTCGTG 42103	— TTCC
GA	TTCGC AGGTC GTCGTCAGGG	
	AGGTG TTCAG CGGTAGTTTC	
	C TAC_	
GAM1959 LOC160484 5'	TCCTGATGGACAACTATGTGAG 39998	— CT GTC
	TTCGCA GGT TCC GTCAGGG	
	GAGTGT TCA AGG TAGTCCT	
	A AC —	
GAM1959 LOC160717 5'	CCTGAGGAGATTCTGTGAG 40006	TC GTCG
	TTCGCAGG TTCC TCAGG	
	GAGTGTCT GAGG AGTCC	
	TA —	
GAM1959 LOC162333 5'	TCTTGGTGCCGTGAAGACCTGT 42135	— T GT
GAG	TTCGCAGGTCTTC CG C CAGGG	
	GAGTGTCCAGAAG GC G GTTCT	
	T C TG	
GAM1959 LOC163682 3'	CCCTGCCAGAGGCCCTGTGG 42090	T CGTC T
	TTCGAGG CTTC G CAGGG	
	GGTGTCC GGAG C GTCCC	
	C AC__	
GAM1959 LOC165908 5'	TCTTGGTGGCAAGAGCTGTG 40196	G CC GT
	CGCAG TCTT GTC CAGGG	
	GTGTC AGAA CGG GTTCT	
	G — TG	
GAM1959 LOC166793 5'	CCTGGCCCCAGCCTGTGAA 29806	CTTCCGTC
	TTCGCAGGT GTCAGG	
	AAGTGTCCG CGGTCC	
	ACC_	
GAM1959 LOC166983 5'	CCCTGGCAGGGGGCTTCTGGA 42198	C CGTC
	TTCG AGGTCTTC GTCAGGG	
	AGGT TTCGGGGG CGGTCCC	
	C A_	
GAM1959 LOC170082 3'	TTTTGCTTTGGGGGTTTGTG 40173	T TC T
	CGCAGG CTTCCG G CAGGG	
	GTGTTT GGGGGT C GTTTT	
	— TT —	
GAM1959 LOC170221 3'	CCTAAGGTGGACCTGTGAG 40182	T GTCGTC
	TTCGCAGGTCT CC AGG	

		GAGTGTCCAGG GG	TCC		
		T AA__			
GAM1959	LOC170394 5'	CTCTGTTCCGGGACCCTGTGAG	40313	TC	TCGT
		TTCGCAGG TTCCG CAGGG			
		GAGTGTCC GGGGC GTCTC			
		CA TT__			
GAM1959	LOC195977 3'	TCTGAGCCAGGACTTGGAG	42302	G	CC CG
		TTC CAGGTCTT GT TCAGG			
		GAG GTTCAGGA CG AGTCT			
		_ C_ __			
GAM1959	LOC196337 3'	TCTGGTGAGGAGCTGCGAA	42361	G	TCCG GT
		TTCGCAG TCT TC CAGG			
		AAGCGTC AGG AG GTCT			
		G ____ TG			
GAM1959	LOC196478 5'	CCTAGTTGGAACTTGTGGA	42378	C	TCGTC
		TTCGCAGGT TTCCG AGG			
		AGGTGTTCA AAGGT TCC			
		_ TGA__			
GAM1959	LOC196510 3'	CCCTGCTTGAGAAGGTTTTGG	42394	C GT	CG T_
		TCG AG CTTC TCG CAGGG			
		GGT TT GAAG AGT GTCCC			
		_ TG _ TC			
GAM1959	LOC196812 3'	CCCTGATGATAAGGTTGGTGG	43133	A GT	CC
		TCGC G CTT GTCGTCAGGG			
		GGTG T GAA TAGTAGTCCC			
		G TG _			
GAM1959	LOC196860 5'	CTCTGGTGGTTTGGCTTTGAA	43153	C	TT_ TCG
		TTCG AGGTC CCG TCAGGG			
		AAGT TTCGG GGT GGTCTC			
		_ TTT _			
GAM1959	LOC196872 3'	TTCTGGCGGTGGGGAAACGGC	42419	AGG_	T GT
		GC TCT CC CGTCAGGG			
		CG AGG GG GCGGTCTT			
		GCAA _ TG			
GAM1959	LOC196957 3'	CCGGGTGGGGGATTTTGG	42430	C	GT GTCA
		TCG AGGTCTTCC C GG			
		GGT TTTAGGGGG G CC			
		_ TG G__			
GAM1959	LOC196961 3'	CCGGGTGGGGGATTTTGG	42439	C	GT GTCA
		TCG AGGTCTTCC C GG			

GGT TTTAGGGGG G CC
_ TG G_
GAM1959 LOC197138 3' CCGGGTGGGGGATTTTGG 42457 C GT GTCA
TCG AGGTCTTCC C GG
||| ||||| | ||
GGT TTTAGGGGG G CC
_ TG G_
GAM1959 LOC197273 5' CTAAAAGATGGAATATTTGCGG 33472 C GTCA G
TCGCAGGT TTCCGTC GG
||||| ||||| ||
GGCGTTTA AAGGTAG TC
T AAAA
GAM1959 LOC197342 3' AAGTGGTGGCGGGGGGCCTGTG 42485 GT GGG
G TCGCAGGTCTTCCGTC CA
||||||| ||
GGTGTCCGGGGGGCGG GT
TG GAAT
GAM1959 LOC199704 3' TCTGGAGAGGGCCTCTGAG 42605 C CGTCG
TTCG AGGTCTTC TCAGG
||| ||||| ||||
GAGT TCCGGGAG GGTCT
C A_
GAM1959 LOC199733 3' CCCATGGTGGGGGTCTGTGAG 43245 T GT CA
TTCGCAGG CTTCC CGT GGG
||||| |||| ||| |||
GAGTGTCT GGGGG GTA CCC
_ TG _
GAM1959 LOC199858 3' CCTGGCTGTGTCTGTGAG 42635 TCTTC TC
TTCGCAGG CG GTCAGG
||||| || |||||
GAGTGTCT GT CGGTCC
_ GT
GAM1959 LOC199920 3' TTTTGAGATGGTGGGAATCTGTG 42662 _ T G
GA TTCGCAGGT CT CCGTC TCAGGG
||||||| || ||||| |||||
AGGTGTCTA GG GGTA AGTTTT
A T _
GAM1959 LOC199990 3' CCCTGAGTCATGGAGGCCTGGG 42680 G T CG_
G TC CAGGTCT CCGT TCAGGG
|| ||||| |||| |||||
GG GTCCGGA GGTA AGTCCC
G _ CTG
GAM1959 LOC200059 3' TTCTGGCGGTGCTGTGCTTGA 42702 G CTTC GT
A TTC CAGGT C CGTCAGGG
||| |||| | |||||
AAG GTTCG G GCGGTCTT
_ TGTC TG
GAM1959 LOC200093 5' CTCGGCTCGGGAGGCCTGGGA 31599 G TC AG
TC CAGGTCTTCCG GTC G
|| ||||| ||| |

AG GTCCGGAGGGC CGG C
 G T_ CT
 GAM1959 LOC200093 3' TCTGGGAAAGGACCTGGGG 31605 G TCCG G
 TC CAGGTCT TC TCAGG
 || ||||| || |||||
 GG GTCCAGG AG GGTCT
 G AA__ _
 GAM1959 LOC200205 3' CCCATGCTGGAGGCTTGTGGA 42736 T T CA
 TTCGCAGGTCT CCG CGT GGG
 ||||| ||| ||| |||
 AGGTGTTGGA GGT GTA CCC
 _ C _
 GAM1959 LOC200220 3' CCCTGCTTGAGAAGGTTTTGG 42743 C GT CG T_
 TCG AG CTTC TCG CAGGG
 ||| || ||| ||| |||||
 GGT TT GAAG AGT GTCCC
 _ TG _ TC
 GAM1959 LOC200953 5' ACAGCGGGAGGCCTGGGA 43366 G C
 TC CAGGTCTTCCGT GT
 || ||||| ||| ||
 AG GTCCGGAGGGCG CA
 G A
 GAM1959 LOC201382 5' CCCTGATCTTTGGGTCTTGGA 42573 G TCT TC_
 TC CAGG TCCG GTCAGGG
 || ||| ||| |||||
 AG GTTC GGGT TAGTCCC
 _ T_ TTC
 GAM1959 LOC201627 3' TCTTATGAGAGACTTGTGG 42897 CCG C
 TCGCAGGTCTT TCGT AGG
 ||||| ||| |||
 GGTGTTGAGAG AGTA TCT
 _ T
 GAM1959 LOC201911 5' TTCTCCGGGGGGGACTTGCGGA 43392 G TC
 TTCGCAGGTCTTCC TCG AGGG
 ||||| ||| ||| |||
 AGGCGTTCAGGGGG GGC TCTT
 _ C_
 GAM1959 LOC204804 3' CCCTGATCCTGGGGTCTGGGGA 43099 G GT TT TC
 TTC CAG C CCG GTCAGGG
 ||| ||| | ||| |||||
 AGG GTC G GGT TAGTCCC
 G TG _ CC
 GAM1959 LOC204820 3' TTTTGACGTGTCTTGAGCCTG 43584 T CGT_
 TGG CGCAGG CTTC CGTCAGGG
 ||||| ||| |||||
 GTGTCC GAGG GCAGTTTT
 _ TTCTGT
 GAM1959 LOC206463 5' CTTTGATGGCACCAAGATCGTG 43123 A CC_
 G TCGC GGTCTT GTCGTCAGGG
 ||| ||||| |||||

GGTG CTAGAA CGGTAGTTTC
_ CCA
GAM1959 LOC219793 5' CCTTGGCAGGAGGATTTGGGG 43916 G GTC
TC CAGGTCTTCC GTCAGGG
|| ||||| |||||
GG GTTTAGGAGG CGGTTCC
G A_

GAM1959 LOC220018 5' CTCTGGCCACCAAGAATTTGTG 44854 _ CC C
AA TTCGCAGGT CTT GT GTCAGGG
||||| || || |||||
AAGTGTTTA GAA CA CGGTCTC
A C_ C

GAM1959 LOC220020 5' CCTTGGCAGAGGGGTCTGGAG 44864 G TCT G _
TTC CAGG TCC TC GTCAGGG
|| ||| || || |||||
GAG GTCT GGG AG CGGTTCC
_ _ G A

GAM1959 LOC220705 3' CTTTGGGGCCGGGAAC TTGCGG 43833 C _ G
TCGCAGGT TTCCG TC TCAGGG
||||| |||| || |||||
GGCGTTCA AGGGC GG GGTTTC
_ C _

GAM1959 LOC220766 5' TCCTGGA ACTCAAGACTTGC 43657 CC CG
GCAGGTCTT GT TCAGGG
||||| || |||||
CGTTCAGAA CA GGTCCT
CT A_

GAM1959 LOC221143 3' CTTTGGTCCACCTGGAGGCCCG 44943 A C_ CG_
TGAA TCGC GGTCTTC GT TCAGGG
|||| ||||| || |||||
AGTG CCGGAGG CA GGTTTC
C TC CCT

GAM1959 LOC221178 5' CTGATGGCCCCTGGAG 44928 G TCTTCC
TTC CAGG GTCGTCAG
|| ||| |||||
GAG GTCC CGGTAGTC
_ C_

GAM1959 LOC221415 5' TTTTGGCGGCGCCCTCTGC 45064 TCTTC
GCAGG CGTCGTCAGGG
|||| |||||
CGTCT GCGGCGGTTTT
CCC_

GAM1959 LOC221496 3' TCTTGGCGGCGGGAGAGGCG 44177 AGG
CGC TCTTCCGTCGTCAGGG
|| |||||
GCG AGAGGGCGGCGGTTCT
G_

GAM1959 LOC221692 3' CTCTGACGGTGGCAGCTGT 44297 GT T GT
GCAG CT CC CGTCAGGG
||| || || |||||

	TGTC GA GG GCAGTCTC		
	__ C TG		
GAM1959 LOC221756 5'	TCTGGCGAGGGCTGCGG 44241	GTCTT G	
	TCGCAG CC TCGTCAGG		
	GGCGTC GG AGCGGTCT		
	_____ G		
GAM1959 LOC221922 5'	CCCTGGTCTGGGAGTGGCCTGT 44533	_ GTCG	
GG	TCGCAGGTC TTCC TCAGGG		
	GGTGTCCGG GAGG GGTCCC		
	T GTCT		
GAM1959 LOC222060 5'	TTCTGCTCAGGAGTTCTGTGAG 45162	TC GTC T	
	TTCGCAGG TTCC G CAGGG		
	GAGTGTCT GAGG C GTCTT		
	T_ ACT_		
GAM1959 LOC222134 5'	TCCTGGTTCTCTGGGATCTGCG 45171	CCGTCCG	
G	TCGCAGGTCTT TCAGGG		
	GGCGTCTAGGG GGTCCT		
	TCTCTT		
GAM1959 LOC222602 5'	TTTGGCTACACTTGTGAA 44618	CTTCC C	
	TTCGCAGGT GT GTCAGG		
	AAGTGTTC CA CGGTTT		
	_____ T		
GAM1959 LOC245727 3'	CCGGGTGGGGGATTTTGG 43798	C GT GTCA	
	TCG AGGTCTTCC C GG		
	GGT TTTAGGGGG G CC		
	_ TG G_		
GAM1959 LOC245728 5'	CCTTATTAATACGGGGATCTGT 43802	T C_ C G	
GAG	CGCAGGTCT CCGT GT AGG		
	GTGTCTAGG GGCA TA TCC		
	_ TAAT T		
GAM1959 LOC245771 5'	CCTTGGGAGAGAGGGCTTCGG 44636	C CG G	
	TCG AGGTCTTC TC TCAGGG		
	GGC TTCGGGAG AG GGTTC		
	_ AG _		
GAM1959 LOC253001 3'	TCCTGATGGCTAATGCCTCTGA 46060	C CTTCC	
G	TTCG AGGT GTCGTCAGGG		
	GAGT TCCG CGGTAGTCCT		
	C TAAT_		
GAM1959 LOC253216 3'	TCCTGACGTGGCGGAGCTGTGG 45521	G T T	
A	TTCGCAG TCT CCG CGTCAGGG		

	AGGTGTC AGG GGT GCAGTCCT	
	G C _	
GAM1959 LOC253539 5'	TTTGAGGTGGGGCCTGGAG 45939	G TT GT G
	TTC CAGGTC CC C TCAGG	
	GAG GTCCGG GG G AGTTT	
	_ _ TG _	
GAM1959 LOC254228 3'	CCTTGGCTAAAGGTCTGGGGA 45921	G GT CCGTC
	TTC CAG CTT GTCAGGG	
	AGG GTC GAA CGGTTCC	
	G TG AT__	
GAM1959 LOC255452 5'	CCTTGATGAGACTGACTGTGG 46574	G TTCCG
	TCGCAG TC TCGTCAGGG	
	GGTGTC AG AGTAGTTCC	
	_ TCAG_	
GAM1959 LOC255458 5'	CCTTGATCTTGGACTTGC 46407	TCCGTC
	GCAGGTCT GTCAGGG	
	CGTTCAGG TAGTTCC	
	TTC__	
GAM1959 LOC255535 5'	CTCTGAGTGCAGGGCCTGC 45807	CC CG
	GCAGGTCTT GT TCAGGG	
	CGTCCGGGA CG AGTCTC	
	_ TG	
GAM1959 LOC255743 5'	TTTTGACCATGGACTTTGTGGA 45902	TCT C
	TTCGCAGG TCCGT GTCAGGG	
	AGGTGTTT AGGTA CAGTTTT	
	C_ C	
GAM1959 LOC256158 5'	CCCTGGTGAGCAGGCCTGGGGA 46622	G TCCG GT
	TTC CAGGTCT TC CAGGG	
	AGG GTCCGGA AG GTCCC	
	G CG_ TG	
GAM1959 LOC256158 5'	CCCTGGTGCTAAAAGGCCTGAG 46623	G CCGT GT
G	TC CAGGTCTT C CAGGG	
	GG GTCCGGA G GTCCC	
	A AATC TG	
GAM1959 LOC256158 5'	TCCTGGTGGCTGAAGGCTTGGG 46632	G C GT
A	TC CAGGTCTTC GTC CAGGG	
	AG GTTCGGAAG CGG GTCCT	
	G T TG	
GAM1959 LOC256306 3'	TCTTGGTGGCATCAAGCTTGTG 46239	T CC_ GT
	CGCAGG CTT GTC CAGGG	

		GTGTTC GAA CGG GTTCT			
		_ CTA TG			
GAM1959	LOC256307 5'	TGGGATGACGGAAGACCTGGGG	46370	G	AGGG
	A	TTC CAGGTCTTCCGTCGTC			
		AGG GTCCAGAAGGCAGTAG			
		G GGT			
GAM1959	LOC256492 5'	TCCTGATGATGGAATAATCC	46592	TC__	
		GG TTCCGTCGTCAGGG			
		CC AAGGTAGTAGTCCT			
		TAAT			
GAM1959	LOC256781 5'	CCCTGCAACAGAAGGCCTTTGA	46602	C C C T	
	A	TTCG AGGTCTTC GT G CAGGG			
		AAGT TCCGGAAG CA C GTCCC			
		T A A _			
GAM1959	LOC256867 5'	CCTGGTGACGGGGCTGGC	45473	A TT GT	
		GC GGTC CCGTC CAGG			
		CG TCGG GGCAG GTCC			
		G _ TG			
GAM1959	LOC256867 5'	TCCTGGAAGGAAGATCTTGG	45476	C GTCG	
		TCG AGGTCTTCC TCAGGG			
		GGT TCTAGAAGG GGTCCT			
		_ AA_			
GAM1959	LOC257364 3'	CCCTGGTGACACCTTCCTGGAG	45523	G TCTTCC GT	
		TTC CAGG GTC CAGGG			
		GAG GTCC CAG GTCCC			
		_ TTCCA_ TG			
GAM1959	LOC51308 3'	TCTGGAAGGGGCTTGAA	18710	G TT GTCG	
		TTC CAGGTC CC TCAGG			
		AAG GTTCGG GG GGTCT			
		_ _ AA_			
GAM1959	LOC51334 5'	CGTGGAGGATTTGGAA	18751	G T	
		TTC CAGGTCTTCCG CG			
		AAG GTTTAGGAGGT GC			
		- -			
GAM1959	LOC85028 5'	TTCTGGTGATCGAGGACTTCCG	27585	C C GT	
	G	TCG AGGTCTTC GTC CAGGG			
		GGC TTCAGGAG TAG GTCTT			
		C C TG			
GAM1959	LOC90249 3'	CCCTGCCCGGCGGGGCCTGTGA	31008	TT T_	
	A	TTCGCAGGTC CCGTCG CAGGG			

AAGTGTCCGG GGCGGC GTCCC
 _ CC
 GAM1959 LOC90342 5' TTCTGGGGCAAGGAGAGCTTGT 31257 TC _ G
 GG TCGCAGG TTCC GTC TCAGGG
 ||||| ||| |||||
 GGTGTTT GAGG CGG GGTCTT
 GA AA _
 GAM1959 LOC90826 5' TCCTGATGATGAAGTGATTTGC 32050 TTC_
 GCAGGTC CGTCGTCAGGG
 ||||| |||||
 CGTTTAG GTAGTAGTCCT
 TGAA
 GAM1959 LOC91040 5' CTCGGCTCGGGAGGCTTGGA 32316 G TC AG
 TC CAGGTCTTCCG GTC G
 || ||||| ||| |
 AG GTTCGGAGGGC CGG C
 G T_ CT
 GAM1959 LOC91040 3' TCTGGGAAAGGACCTGGGG 32322 G TCCG G
 TC CAGGTCT TC TCAGG
 || ||||| |||||
 GG GTCCAGG AG GGTCT
 G AA__ _
 GAM1959 LOC91355 5' TCTTGGTGCCCTGGGCTTCGG 32704 C TCCGT GT
 A TTCG AGGTCT C CAGGG
 ||| ||||| | |||||
 AGGC TTCGGG G GTTCT
 _ TCCCC TG
 GAM1959 LOC91355 5' TTCTGATGGCCTAGCTGTGTGG 32705 _ T TCC
 A TTCGCA GG CT GTCGTCAGGG
 ||||| ||| |||||
 AGGTGT TC GA CGGTAGTCTT
 G _ TC_
 GAM1959 LOC91409 3' TTCTGGTGATCCCTGAGTTTGC 32808 _ TTCC GT
 GG TCGCAGG TC GTC CAGGG
 ||||| || ||| |||||
 GGCGTTT AG TAG GTCTT
 G TCCC TG
 GAM1959 LOC91450 5' CTCTGAGGATGGGGCTTGT 32854 TT G
 GCAGGTC CCGTC TCAGGG
 ||||| ||||| |||||
 TGTTCGG GGTAG AGTCTC
 _ G
 GAM1959 LOC91464 5' CCCTGGGTCAGGCGCTTGTGGA 32874 CTT GTCG
 TTCGCAGGT CC TCAGGG
 ||||| || |||||
 AGGTGTTCG GG GGTCCC
 C_ ACTG
 GAM1959 LOC91565 5' CTCTGATGGGCTGCTAGTGG 33023 A CT GTC
 TCGC GGT TCC GTCAGGG
 ||| ||| ||| |||||

GGTG TCG GGG TAGTCTC
A TC ____

GAM1959 LOC91782 3' CTTTGAGGGACTGGGGGACTTG 33336 G _ _ G
GGG TC CAGGTCTTCC GT C TCAGGG
|| ||||| || |||||
GG GTTCAGGGGG CA G AGTTTC
G T G G

GAM1959 LOC91828 5' CCCTGGTGACGGCCACCTGC 33407 CTT GT
GCAGGT CCGTC CAGGG
|||| | ||| ||||
CGTCCA GGCAG GTCCC
CC_ TG

GAM1959 LOC91828 5' TCCTGGCGCCGGACGTGTGG 33409 G TCT T
TCGCA G TCCG CGTCAGGG
|||| | ||| |||||
GGTGT C AGGC GCGGTCCT
G _ C

GAM1959 LOC91960 3' CTCTGGGACTAAGCCTGCGAG 33610 T CC G
TTCGCAGG CTT GTC TCAGGG
||||| || | |||||
GAGCGTCC GAA CAG GGTCTC
_ T _

GAM1959 LOC92162 5' CCCTCCCCGGAGGCGCCTGTGG 33921 _ TCGTC
A TTCGCAGGT CTTCCG AGGG
||||| |||| | |||
AGGTGTCCG GGAGGC TCCC
C CCC_

GAM1959 LOC92230 5' CTTTGGGAGTTTGTGAA 34007 T TCGTC
TTCGCAGG CTTCCG AG
||||| |||| | ||
AAGTGTTT GAGGGT TC
_ T _

GAM1959 LOC93109 3' CCCTGTGCTGGGGGGCCTTGG 35374 C T T
TCG AGGTCTTCCG CG CAGGG
|| | ||||| || |||||
GGT TCCGGGGGGT GT GTCCC
_ C _

GAM1959 LOC93444 3' CCCTGGCTGTTAGGGTCTGGGA 35844 G GT CCGTC
G TTC CAG CTT GTCAGGG
|| | || | |||||
GAG GTC GGA CGGTCCC
G TG TTGT_

GAM1959 LOC95702 5' TCCTGACGTGGCGGAGCTGTGG 31384 G T T
A TTCGCAG TCT CCG CGTCAGGG
||||| || | |||||
AGGTGTC AGG GGT GCAGTCCT
G C _

GAM1959 LOC96597 5' TCTTGGTCAAAGGGGCTTGGGG 33233 G CCGTCG
A TTC CAGGTCTT TCAGGG
|| | ||||| |||||

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AGG GTTCGGGG  GGTTC
G  AACT_
GAM1960 AGTR1  3' GATTGTTCTGTCCAGTTT  6342  GTC
GAAC ACGGAGCAATC
||||| |||||
TTTG TGTCTTGTTAG
ACC
GAM1960 AGTR1  3' GATTGTTCTGTCCAGTTT  11243  GTC
GAAC ACGGAGCAATC
||||| |||||
TTTG TGTCTTGTTAG
ACC
GAM1960 AGTR1  3' GATTGTTCTGTCCAGTTT  14309  GTC
GAAC ACGGAGCAATC
||||| |||||
TTTG TGTCTTGTTAG
ACC
GAM1960 AGTR1  3' GATTGTTCTGTCCAGTTT  25594  GTC
GAAC ACGGAGCAATC
||||| |||||
TTTG TGTCTTGTTAG
ACC
GAM1960 AGTR1  3' GATTGTTCTGTCCAGTTT  25769  GTC
GAAC ACGGAGCAATC
||||| |||||
TTTG TGTCTTGTTAG
ACC
GAM1960 AKAP13 3' GGTTGTTTTGGTGGTCTTTTTT 43179  CG _
AAAGAA TCAC GGAGCAATC
||||| ||| |||||
TTTTTT GGTG TTTTGTTGG
CT G
GAM1960 ARHGEF6 3' GGTTGTTTCATTTTTTTTTTCAA 33848  CGTCACG
TTGAAAGAA GAGCAATC
||||| |||||
AACTTTTTT CTTGTTGG
TTTTA__
GAM1960 ATRX 3' GTTTTAATGTTCTTTTGA 28685 TG CAC
T AAAGAACGT GGAGC
| ||||| |||||
A TTTCTTGTA TTTTG
GT A__
GAM1960 ATRX 3' GTTTTAATGTTCTTTTGA 6096 TG CAC
T AAAGAACGT GGAGC
| ||||| |||||
A TTTCTTGTA TTTTG
GT A__
GAM1960 CA2 3' GGTTGCTTTGTGTCTAGTTTTC 5514 AACGT
GAAAG CACGGAGCAATC
||||| |||||

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		CTTTT GTGTTTCGTTGG	
		GATCT	
GAM1960 CALD1	3'	GGTTGTTTTGTGGATTCTTT 26992	CG
		AAAGAA TCACGGAGCAATC	
		TTTCTT GGTGTTTTGTTGG	
		TA	
GAM1960 CALD1	3'	GGTTGTTTTGTGGATTCTTT 27010	CG
		AAAGAA TCACGGAGCAATC	
		TTTCTT GGTGTTTTGTTGG	
		TA	
GAM1960 DDEF2	3'	GATTGCAAAACAGTTCTTTTAA 9966	GTCACGGA
		TTGAAAGAAC GCAATC	
		AATTTTCTTG CGTTAG	
		ACAAAA__	
GAM1960 DPYSL2	3'	GGTTGTTTTGGTTGTTTTCTTA 7064	A TCA
A		TTGA AGAACG CGGAGCAATC	
		AATT TTTTGT GTTTTGTTGG	
		C TG_	
GAM1960 E2F3	3'	GATTGTTGTGTGTTTTGTT 7668	T__ G
		AACG CACG AGCAATC	
		TTGT GTGT TTGTTAG	
		TTT G	
GAM1960 F2R	3'	GATTGCTCAAATCAGGTTTTCT 7723	CG ACG__
TTTAA		AAAGAA TC GAGCAATC	
		TTTCTT GG CTCGTTAG	
		TT ACTAAA	
GAM1960 FBXL2	3'	TCGATGTGATTTTTTTTCAA 14454	C G_____
		TTGAAAGAA GTCAC GA	
		AACTTTTTT TAGTG CT	
		T TAG	
GAM1960 GPC1	3'	GTGACGTGTGTTCTTTTGA 7875	TG T GA
		T AAAGAACG CACG GC	
		A TTTCTTGT GTGC TG	
		GT _ AG	
GAM1960 HFE	3'	GGTTGTGAAGAGGTGTTTTTC 5985	GT ACGGA
		GAAAGAAC C GCAATC	
		CTTTTTTG G TGTTGG	
		TG AGAAG	
GAM1960 HFE	3'	GGTTGTGAAGAGGTGTTTTTC 29099	GT ACGGA
		GAAAGAAC C GCAATC	

			CTTTTTTG G TGTTGG		
			TG AGAAG		
GAM1960	HIVEP2	3'	GCTATTGTGAGTTTTTCAA 13585	G	_
			TTGAAAGAAC TCACGG AGC		
			AACTTTTTTG AGTGTT TCG		
			_ A		
GAM1960	KIF5C	3'	GATTGTTTTAGATTCTTC 10855	AC	AC
			GAAAGA GTC GGAGCAATC		
			CTTTCT TAG TTTTGTTAG		
			_ A_		
GAM1960	LETM1	3'	GATTGCTTTGTGGTGATTCTCA 14698	AA	_ GT
	G		TTGA GAA C CACGGAGCAATC		
			GA CT CTT G GTGTTTCGTTAG		
			_ A TG		
GAM1960	LILRB4	3'	TTGTTGGTGGTTTTTCAA 13717	GT	G G
			TTGAAAGAAC CAC GA CAA		
			AACTTTTTTG GTG TT GTT		
			_ G _		
GAM1960	MADH4	3'	GATTTGATGTGACTTTTTTTGG 11834	TG	C GAGC
			T AAAGAA GTCACG AATC		
			G TTTTTT CAGTGT TTAG		
			GT _ AGT_		
GAM1960	MGAM	3'	TCTGTGGGTTCTTTCAA 35827	G	
			TTGAAAGAAC TCACGGA		
			AACTTTCTTG GGTGTCT		
			-		
GAM1960	NET1	3'	GGTTGTTCTTTTTTCTTTTTTT 12474	CGTCAC	
	AA		TTGAAAGAA GGAGCAATC		
			AATTTTTT TCTTGTTGG		
			CTTTT		
GAM1960	NTRK2	3'	GGTTGTTCCTTTTTCTTTTTTT 12847	CGTCAC	
	AA		TTGAAAGAA GGAGCAATC		
			AATTTTTT CCTTGTTGG		
			CTTTT		
GAM1960	P4HA1	3'	CTTACTTTGTGGGTTCTTTTAA 6625	G	CAATC
			TTGAAAGAAC TCACGGAG		
			AATTTTCTTG GGTGTTTC		
			_ ATTCG		
GAM1960	PDL2	5'	GATTGTTTTGTTTTCTTTTG 24923	TG	AACGTC
	G		T AAAG ACGGAGCAATC		

G TTTC TGTTTTGTTAG
 GT CTTTT_
 GAM1960 PSCDBP 3' ACAATCGATTGTGGTGCCTTT 10500 A GT G_____ GCAA
 CAA GAAAG AC CAC GA T
 ||||| || ||| || |
 CTTTC TG GTG CT A
 C TG TTAG AACG
 GAM1960 SFRP1 3' TTTGTGTTGTTTTTTTAA 8935 T
 TTGAAAGAACG CACGGA
 ||||| |||||
 AATTTTTTTGT GTGTTT
 T
 GAM1960 TIMP3 3' GATTGCTCTCTGTCTCTTTTTT 5930 CGT_ C
 CAG TTGAAAGAA CA GGAGCAATC
 ||||| || |||||
 GACTTTTTT GT TCTCGTTAG
 CTCT C
 GAM1960 TPM4 3' TCGATGTGATGTTCTTTT 9301 G_____
 GAAAGAACGTCAC GA
 ||||| ||
 TTTTCTTGTAGTG CT
 TAG
 GAM1960 ZNF14 3' GATTGTTCCAGTTTCTTTTGA 22018 TG CGTC _
 T AAAGAA AC GGAGCAATC
 | |||| || |||||
 A TTTCTT TG CCTTGTTAG
 GT _ A
 GAM1960 ARFGAP3 3' GATTGTTTTGCTACTTTTCA 15924 AC CA
 TGAAAGA GT CGGAGCAATC
 ||||| || |||||
 ACTTTTT CA GTTTTGTTAG
 _ TC
 GAM1960 B7-H1 3' GGTTGTGAATGATTTCTTTTGA 15424 TG C CGGA
 T AAAGAA GTCA GCAATC
 | |||| ||| |||||
 A TTTCTT TAGT TGTTGG
 GT _ AAG_
 GAM1960 C1orf17 3' GGTTGATTTTTGTGGTGTGTTTG 33855 _ GT _
 TTAA AA AGAAC CACGGAG CAATC
 || |||| ||||| |||||
 TT TTTG GTGTTT GTTGG
 G TG TA
 GAM1960 CACNG4 3' GGTTGTTCTGTCTTTTTTTTAA 15746 CGTC
 TTGAAAGAA ACGGAGCAATC
 ||||| |||||
 AATTTTTT TGTCTTGTTGG
 TC_
 GAM1960 COE2 3' GGTTGCTCTGGTCTTTTTTGA 32129 TG ACGTCA
 T AAAGA CGGAGCAATC
 | |||| |||||

A TTTT GTCTCGTTGG
 GT CTG____
 GAM1960 CYYR1 3' GATTGCTTTGTGAAGCTCTT 27513 ACG
 AAGA TCACGGAGCAATC
 ||| |||||
 TTCT AGTGTTTCGTTAG
 CGA
 GAM1960 DKFZp434C0328 3' TTTTGTGATGTTTATTTAA 19017 A
 TTGAA GAACGTCACGGAG
 ||| |||||
 AATTT TTTGTAGTGTTTT
 A
 GAM1960 DKFZp434K1210 3' TCGATGTGACTTTTTTCAG 19103 C G____
 TTGAAAGAA GTCAC GA
 ||||| ||| ||
 GACTTTTTT CAGTG CT
 _ TAG
 GAM1960 EIF4B 3' GTTCTTGATGTCTTTTGG 37400 TG A C
 T AAAGA CGTCA GGAGC
 | ||| ||| |||
 G TTTCT GTAGT CTTTG
 GT _ T
 GAM1960 FLJ20094 3' TTCTGTGATGTCTTTTTAA 19209 GA
 TTGAAA ACGTCACGGAG
 |||| |
 AATTT TGTAGTGTCTT
 TC
 GAM1960 FLJ21106 3' TTCTGATGTTTTTTCAG 24738 C
 TTGAAAGAACGTCA GGA
 ||||| |||
 GACTTTTTTGTAGT CTT
 _
 GAM1960 FPGT 3' TTTGTCAGTGTGTTTTTTAA 9930 T GGA TC
 TTGAAAGAACG CAC GCAA
 ||||| ||| |||
 AATTTTTTTGT GTG TGTT
 _ AC_ TA
 GAM1960 KIAA0368 3' GGTTGAAGTGGTGGTGTCTTT 32488 G GT GGAG_
 GAA TT AAAGAAC CAC CAATC
 || ||||| ||| |||
 AA TTTCTTG GTG GTTGG
 G TG GTGAA
 GAM1960 KIAA0427 3' GGTTGCTTTGAAGTCTCTTT 16579 _ GTCA
 AAAGA AC CGGAGCAATC
 |||| || |||||
 TTTCT TG GTTTCGTTGG
 C AA_
 GAM1960 KIAA0534 3' TCTGTGGGGTTTTTTTGG 35387 TG G
 T AAAGAAC TCACGGA
 | ||||| |||||

G TTTTTTG GGTGTCT
 GT G
 GAM1960 KIAA0644 3' GGTTGCTCCTGTGGCTTTTTTA 16785 AC _
 A TTGAAAGA GTCAC GGAGCAATC
 ||||| ||| |||||
 AATTTTT CGGTG CCTCGTTGG
 _ T
 GAM1960 KIAA0961 3' TTCCATGATGTTCTTTTAA 17075 C
 TTGAAAGAACGTCA GGAG
 ||||| |||
 AATTTTCTTGTAGT CCTT
 A
 GAM1960 KIAA0984 3' GTTGTGTGGGCTTTTTTTGA 32644 TG CG G
 T AAAGAA TCACG AGC
 | |||| |||||
 A TTTTTT GGTGT TTG
 GT CG G
 GAM1960 KIAA1136 3' GATTGCTCTCATTTTCTT 43883 C CAC
 AAGAA GT GGAGCAATC
 |||| || |||||
 TTCTT TA TCTCGTTAG
 T C_
 GAM1960 KIAA1300 3' GGTTGGAGGCTGAGTTCTTTTG 31481 TG G CGGAG
 A T AAAGAAC TCA CAATC
 | |||| || |||||
 A TTTCTTG AGT GTTGG
 GT _ CGGAG
 GAM1960 KIAA1598 3' GATTGTTTCAAAATTGGTGTTT 20331 A GT C____
 ATTTAA A GAAC CA GGAGCAATC
 | ||| || |||||
 T TTTG GT CTTTGTTAG
 A TG TAAAA
 GAM1960 KIAA1676 3' GCCCTGTGATTTTTTTTAA 44727 C A
 TTGAAAGAA GTCACGG GC
 ||||| ||||| ||
 AATTTTTTT TAGTGTC CG
 _ C
 GAM1960 KIAA1889 3' GGTCAAAGTGATGTGTCTTTTA 36389 _ GGA_ AATC
 G TTGAAAGA ACGTCAC GC
 ||||| ||||| ||
 GATTTTCT TGTAGTG TG
 G AAAC G
 GAM1960 L3MBTL2 3' GCTTGTATGTTCTTTTGG 42791 TG C G
 T AAAGAACGT ACG AGC
 | ||||| ||| |||
 G TTTCTTGTA TGT TCG
 GT _ _
 GAM1960 LIN-7-C 3' TTCATCTTTTGTGATTTCTTTT 20372 C CAATC
 AA TTGAAAGAA GTCACGGAG
 ||||| |||||

AATTTTCTT TAGTGTTTT
 _ CTACTTT
 GAM1960 MESDC1 3' TCGAGCGTGTGTTTTTTTAA 22885 T _____
 TTGAAAGAACG CACG GA
 ||||| ||| ||
 AATTTTTTTGT GTGC CT
 _ GAG
 GAM1960 MGC12335 3' GGTGCTCATCCATTTTTTTCA 26478 CGTCACG
 G TTGAAAGAA GAGCAATC
 ||||| |||||
 GACTTTTT CTCGTTGG
 TACCTA_
 GAM1960 RNF38 3' TCTTTGGTGTGTTTTTTTAA 23064 GT C
 TTGAAAGAAC CA GGA
 ||||| |||
 AATTTTTTTG GT TCT
 TG T
 GAM1960 SLC6A14 3' GATTGTATAATGTGATTTTTTT 14101 C GA_
 TAG TGAAAGAA GTCACG GCAATC
 ||||| ||||| |||||
 ATTTTTTT TAGTGT TGTTAG
 _ AATA
 GAM1960 SS18L1 3' TTTGTGTGTTTTTTTAA 32567 T
 TTGAAAGAACG CACGGA
 ||||| |||||
 AATTTTTTTGT GTGTTT
 _
 GAM1960 STAM2 3' TCGGTGTGTTGTTTTTTTAA 12460 T G_____
 TTGAAAGAACG CAC GA
 ||||| ||| ||
 AATTTTTTTGT GTG CT
 T TGG
 GAM1960 TRAP150 5' TGCTGCGGGTGTCTTTTGG 11603 TG GT A G
 T AAAGAAC C CG AGCA
 | ||||| | |||||
 G TTTCTTG G GC TCGT
 GT TG _ G
 GAM1960 USP8 3' GATTGCTTTTTTTCTTTCAG 11631 CGTCAC
 TTGAAAGAA GGAGCAATC
 ||||| |||||
 GACTTCTT TTTCGTTAG
 TT_____
 GAM1960 ZNF294 3' GATTGCTTTGTAAATGTTT 35058 C_
 GAACGT ACGGAGCAATC
 ||||| |||||
 TTTGTA TGTTTCGTTAG
 AA
 GAM1960 ZNF33A 3' GTTCACTGATGTGTTTTTGA 43899 TG A CG
 T AAAG ACGTCA GAGC
 | ||||| |||||

A TTTT TGTAGT CTTG
 GT G CA
 GAM1960 LOC112616 3' TTTGTGTGTTTTTTTAA 28776 T
 TTGAAAGAACG CACGGA
 ||||| |||||
 AATTTTTTTGT GTGTTT
 —
 GAM1960 LOC113763 3' GATTGCTCAGAGTTCCTTTAG 28804 A GTCACG
 TTGAA GAAC GAGCAATC
 |||| ||| |||||
 GATTT CTTG CTCGTTAG
 C AGA__
 GAM1960 LOC134266 3' GCCTATGTGGTTTTTTTTCAG 37070 CG GA_
 TTGAAAGAA TCACG GC
 ||||| |||| ||
 GACTTTTTT GGTGT CG
 TT ATC
 GAM1960 LOC139673 3' GTTCTTGATGTCTTTTGG 37405 TG A C
 T AAAGA CGTCA GGAGC
 | |||| |||| ||||
 G TTTCT GTAGT CTTTG
 GT _ T
 GAM1960 LOC144747 5' TTCTGTGTGTGTTTTTTTAG 37785 GT_
 TTGAAAGAAC CACGGAG
 ||||| |||||
 GATTTTTTTG GTGTCTT
 TGT
 GAM1960 LOC146856 3' GATTGTTGTGTGTTTTGTT 40299 T__ G
 AACG CACG AGCAATC
 ||| ||| |||||
 TTGT GTGT TTGTTAG
 TTT G
 GAM1960 LOC147990 3' GATTGTTTTGTGAAACTTTTAA 40863 AACG
 TTGAAAG TCACGGAGCAATC
 ||||| |||||
 AATTTTC AGTGTTTGTAG
 AA__
 GAM1960 LOC152018 5' GATTGATGAGTGTTCTTTTAA 41421 _ CGGAG
 TTGAAAGAACG TCA CAATC
 ||||| ||| |||||
 AATTTTCTTGT AGT GTTAG
 G A____
 GAM1960 LOC157798 5' GATTGTTCTGTGAATTGTTGTT 41850 G ____
 AA AACG TCACGGAGCAATC
 || ||| |||||
 TT TTGT AGTGTCTTGTTAG
 G TA
 GAM1960 LOC158709 3' GGTTGGCTGGTGATGCTCTTTC 39882 A _ AG
 AA
 TTGAAAGA CGTCAC GG CAATC
 ||||| ||||| || |||||

AACTTTCT GTAGTG TC GTTGG
 C G G_
 GAM1960 LOC203365 3' GTAAGCCTGTGGTAGTTTTTTT 43034 TG GT_ A AATC
 GA T AAAGAAC CACGG GC
 | ||||| ||||| ||
 A TTTTTTG GTGTC CG
 GT ATG _ AATGG
 GAM1961 ITPR1 3' TATGTAATAAATGGTTAA 7985 G
 TTAAC ATTTATTATATA
 ||||| ||||| |||||
 AATTG TAAATAATGTAT
 G
 GAM1962 AKAP10 3' TAAAGATACAAAATGGTATTGT 14056 AAA_
 TTA TAAACAATACTA TATCTTTA
 ||||| ||||| |||||
 ATTTGTTATGGT ATAGAAAT
 AAAAC
 GAM1962 C11orf23 3' TGTTTTCTGTATTGTTTAA 20304 T_
 TTAAACAATAC AAAATA
 ||||| ||||| |||||
 AATTGTTATG TTTTGT
 TC
 GAM1962 C20orf180 3' AAAGAACCCGTTAGTATTGTTT 20494 AATA_
 A TAAACAATACTAA TCTTT
 ||||| ||||| |||||
 ATTTGTTATGATT AGAAA
 GCCCA
 GAM1963 RP2 3' ATATAGAATTTGATAATA 13790
 TATTATCAGATTCTATAT
 ||||| ||||| |||||
 ATAATAGTTTAAAGATATA
 GAM1963 caspr5 3' TCAAATATATGATTGCTGATAG 28267 AT_ T C
 TA TATTATCAG TC ATATATT GA
 ||||| || ||||| ||
 ATGATAGTC AG TATATAA CT
 GTT _ A
 GAM1963 FLJ11252 3' CAATATATAGTGATAATG 33566 GATT C
 TATTATCA CTATATATT G
 ||||| ||||| |||||
 GTAATAGT GATATATAA C
 _ A
 GAM1964 B3GNT3 3' CCAGTATGTTTTACAGATTA 15533 TTTA_
 TGATCTGTAAAAC GG
 ||||| ||||| |||||
 ATTAGACATTTTG CC
 TATGA
 GAM1964 MAP7 3' CTTATCTTTCCTTACTGATCA 10118 T AACTTT
 TGATC GTAA AGGATAAG
 ||||| ||||| |||||

		ACTAG CATT TTCTATTC		
		T CCGT__		
GAM1964	RPE65	3' CTTGAAAGCATTACAGATCA 5872	AA	_
		TGATCTGTAA CTT TAGG		
		ACTAGACATT GAA GTTC		
		AC A		
GAM1964	ERp44	3' CCTGTAAAAGTTTTATAAATCA 39722	C	___
		TGAT TGTAAAACTT TAGG		
		ACTA ATATTTTGAA GTCC		
		A AAT		
GAM1964	KIAA0266	3' CTTATTTTTCAGCTTTACAGACA 22309	A	A TT
		TG TCTGTAAA CT AGGATAAG		
		AC AGACATTT GA TTTTATTC		
		_ C C_		
GAM1964	LOC113523	3' CTTGAAGTCTTACAGTCA 36152	T	A
		TGA CTGTAA ACTTTAGG		
		ACT GACATT TGAAGTTC		
		_ C		
GAM1964	LOC145786	5' CTTAAGTTCTGCAGATCA 40591	A	T
		TGATCTGTA AACTT AG		
		ACTAGACGT TTGAA TC		
		C T		
GAM1964	LOC146332	3' CTTACCCTTTTCACACAGATCA 38128	AAA	ACTTT A
		TGATCTGT AGG TAAG		
		ACTAGACA TCC ATTC		
		CACTT__ C		
GAM1964	LOC158527	5' TTAAAGTTCCACAGATC 39865	AA	
		GATCTGT AACTTTAGG		
		CTAGACA TTGAAATTT		
		CC		
GAM1964	LOC91408	3' CCAAAGTTTTACAGACA 32792	A	A
		TG TCTGTAAAACTTT GG		
		AC AGACATTTTGAAA CC		
		- -		
GAM1965	ABCD4	3' TAAATGGATTTTAAAGTGAAAT 21583	GTT	
	T	AGTTTCAT GGGGTCCATTTA		
		TTAAAGTG TTTTAGGTAAAT		
		AAT		
GAM1965	ABCD4	3' TAAATGGATTTTAAAGTGAAAT 21585	GTT	
	T	AGTTTCAT GGGGTCCATTTA		

		TTAAAGTG TTTTAGGTAAAT	
		AAT	
GAM1965 ABCD4	3'	TAAATGGATTTTAAAGTGAAAT 21588	GTT
T		AGTTTCAT GGGGTCCATTTA	
		TTAAAGTG TTTTAGGTAAAT	
		AAT	
GAM1965 ABCD4	3'	TAAATGGATTTTAAAGTGAAAT 21591	GTT
T		AGTTTCAT GGGGTCCATTTA	
		TTAAAGTG TTTTAGGTAAAT	
		AAT	
GAM1965 ACPT	3'	TGGCACTCAGCTTGGGGCTG 28046	TT T GT
		TAGT CA GTTGGG CCA	
		GTCG GT CGACTC GGT	
		GG T AC	
GAM1965 ACPT	3'	TGGCACTCAGCTTGGGGCTG 28049	TT T GT
		TAGT CA GTTGGG CCA	
		GTCG GT CGACTC GGT	
		GG T AC	
GAM1965 ACTR1B	3'	TAGATGCCCTGGTGTAGGGCTG 35054	TC TG TG TC
		TAGTT A T GGG CATTTA	
		GTCGG T G CCC GTAGAT	
		GA GT GT _ G	
GAM1965 ADCY6	3'	TGAGTGGACTCTGTGCTCACTG 21979	TT_ GTT
		TAGT CAT GGGGTCCATTTA	
		GTCA GTG TCTCAGGTGAGT	
		CTC _	
GAM1965 ADCY6	3'	TGAGTGGACTCTGTGCTCACTG 17592	TT_ GTT
		TAGT CAT GGGGTCCATTTA	
		GTCA GTG TCTCAGGTGAGT	
		CTC _	
GAM1965 AKAP13	3'	TGAATGGGCTTCAAGTGG 43182	G
		TCAT TTGGGGTCCATTTA	
		GGTG AACTTCGGGTAAGT	
		-	
GAM1965 ALDH1A3	3'	AATGTCTTTAATATGAAAT 6350	TC
		GTTTCATGTTGGGG CATT	
		TAAAGTATAATTTT GTAA	
		T_	
GAM1965 AMD1	3'	ACTCTTGCTGTGAAATTG 7346	_ T
		TAGTTTCAT GT GGGGT	

		GTAAAGTG CG TCTCA		
		T T		
GAM1965	AMT	3' TGGCTCAGGGTGGGGCTG 6091	TT G	GT
		TAGT CAT TTGGG CCA		
		GTCG GTG GACTC GGT		
		GG G _		
GAM1965	ANKRD3	3' TGTCCCCTCCAGGTGAAGCTG 21798	GTT_	TC
		TAGTTTCAT GGGG CA		
		GTCGAAGTG TCCC GT		
		GACC CT		
GAM1965	AP1B1	3' GTGGCTGTGATGTGGGGTTA 6798	TT	G T
		TAG TCATGTTG GG CCAT		
		ATT GGTGTAGT TC GGTG		
		GG G _		
GAM1965	APC	3' AATTGTGTCTCAACAGAACTA 5479	A	TC TTTA
		TAGTTTC TGTTGGGG CA		
		ATCAAAG ACAACTCT GT		
		_ GT TAAG		
GAM1965	APPL	3' TGCCCGGCCCTAAATGAAATT 14401	G	CATTTA
	A	TAGTTTCAT TTGGGGTC		
		ATTAAAGTA AATCCCGG		
		A CCCGT		
GAM1965	ARCN1	3' TAAATGGCTGTGTGTGGAATTG 7368	TG TGG	T
		TAGTTTCA T GG CCATTTA		
		GTTAAGGT G TC GGTAAT		
		GT TG_ _		
GAM1965	ARF3	3' GGTATTCTAATGAGGAGCTG 7380	A	_
		TAGTTTC TGTTGGGGT CC		
		GTCGAGG GTAATCTTA GG		
		A T		
GAM1965	ARHGEF7	3' TGAAGACCAGTTCTGAGGTGAA 9986	G TG ____	CATTTA
	GCTG	TTTCAT T G GGTC		
		GAAGTG A C CCAG		
		G GT TTGA AAGT		
GAM1965	ATP10C	3' GGACTCCCAGCTGGAGCTG 23688	T	_
		TAGTTTCA GTTGGG GTCC		
		GTCGAGGT CGACCC CAGG		
		_ T		
GAM1965	ATP11A	3' AAGAAGACATTTTCAGTGTGAGA 37799	TG GG CCA	A
	TT	AGTTTCA TTG GT TTT		

		TTAGAGT GAC TA AAG		
		GT TT CAG AAA		
GAM1965 ATP2C1	3'	TGGCAGTCCCAAATGAAATTA 15718	G	T__
		TAGTTTCAT TTGGGG CCA		
		ATTAAAGTA AACCT GGT		
		_ GAC		
GAM1965 ATP8B2	3'	TGGATGGGCTGCAGTGAGGT 32519	TT	GT G
		G TCAT TG GGTCCATTTA		
		T AGTG AC TCGGGTAGGT		
		GG _ G		
GAM1965 AVPR1A	5'	TGGATAGTAAAGTGGAATTA 6376	G	GG
		TAGTTTCAT TTG GTCCA		
		ATTAAGGTG AAT TAGGT		
		A GA		
GAM1965 BACE TA	3'	TGGGACCTGCTAAGTGTGGAAT 29089	TG G__	ATTTA
		AGTTTCA TT GGGTCC		
		TTAAGGT GA TCCAGG		
		GT ATCG GT		
GAM1965 BACE TA	3'	TGGGACCTGCTAAGTGTGGAAT 14421	TG G__	ATTTA
		AGTTTCA TT GGGTCC		
		TTAAGGT GA TCCAGG		
		GT ATCG GT		
GAM1965 BAZ2A G	5'	TGGGTGGTCCCAGCCTGGAGCT 15122	T	T
		TAGTTTCA GTTGGGG CCATTTA		
		GTCGAGGT CGACCCT GGTGGGT		
		C _		
GAM1965 BAZ2B TA	5'	TAAATGGGTCAATAAATGGAAG 15125	G	GTTGG GT
		TA TTTCAT G CCATTTA		
		AT AAGGTA C GGTAAT		
		G AATAA TG		
GAM1965 BCL2L2	3'	TGGATGGGTGGGCATGGAAC 10264	GGGG	
		GTTTCATGTT TCCATTTA		
		CAAGGTACGG GGGTAGGT		
		GT__		
GAM1965 BCL7A	3'	GAGTGGGCCGGGGAGGCTG 21993	ATGTTGG	
		TAGTTTC GGTCCATT		
		GTCGGAG CCGGGTGAG		
		GGG__		
GAM1965 BCRP2	3'	GGAGCCCAGCTGGGATTG 31274	TT T	G
		TAGT CA GTTGGG TCC		

			GTTA GT CGACCC AGG		
			GG _ G		
GAM1965	BMPR1A	3'	TAAGTGGGTTTTTATGAACTG 10529	T TT GT	
			TAGTT CATG GGG CCATTTA		
			GTCAA GTAT TTT GGTGAAT		
			_ _ TG		
GAM1965	BSN	3'	TGGATGGGACAGGAAGCTG 9522	A GGG	
			TAGTTTC TGTT GTCCA		
			GTCGAAG ACAG TAGGT		
			G GG_		
GAM1965	BTG1	3'	TGGGTGGGCTCCTCTTGGGGAT 7466	TT ATGTT	
			GT C GGGGTCCATTTA		
			TA G CCTCGGGTGGGT		
			GG GTTCT		
GAM1965	C11orf8	3'	TAAATGGATGCAATGGAAGCTA 7303	A GG	
			TAGTTTC TGTTG GTCCATTTA		
			ATCGAAG GTAAC TAGGTAAAT		
			_ G_		
GAM1965	C1D	3'	TGAATTTTGGCATGATGACTG 13033	_ TG C	
			TAGTT TCATGT GGGT CA		
			GTCAG AGTACG TTTA GT		
			T GT A		
GAM1965	C5R1	3'	TGGGTGGATCACCTGAGG 7475	TGTT _	
			TTTCA GG GGTCCATTTA		
			GGAGT CC CTAGGTGGGT		
			_ _ A		
GAM1965	CALU	3'	TGGTTTCACATGAAATTG 6887	T GG T	
			TAGTTTCATGT G G CCA		
			GTAAAGTACA C T GGT		
			_ TT _		
GAM1965	CASP3	3'	GAACCACTATGAAGCTA 26872	T GG	
			TAGTTTCATG TGG TC		
			ATCGAAGTAT ACC AG		
			C A_		
GAM1965	CASP3	3'	GAACCACTATGAAGCTA 10541	T GG	
			TAGTTTCATG TGG TC		
			ATCGAAGTAT ACC AG		
			C A_		
GAM1965	CCNF	3'	GTTTGGGGCTTCAGTGGGGAGC 7528	A GT ATTTA	
	TG		TAGTTTC T TGGGGTCC		

			GTCGAGG G ACTTCGGG	
			G TG GTTTGG	
GAM1965	CD28	3'	TAAGTGGGCTTCCATTCCATGG 12782	T__ _
	A		TTCATG TGGG GTCCATTTA	
			AGGTAC ACCT CGGGTGAAT	
			CTT T	
GAM1965	CD69	3'	TAAATGGACAAATGCTTATGAA 7539	TTGGG__
	ACTA		AGTTTCATG GTCCATTTA	
			TCAAAGTAT CAGGTAAAT	
			TCGTAAA	
GAM1965	CDH2	3'	GGCTTTGGCATAGGCTG 7543	C TG
			TAGTTT ATGT GGGTC	
			GTCGGA TACG TTCGG	
			_ GT	
GAM1965	CDH6	3'	TGGATAAACAAACATTGAGATTA 11377	_ GG_
			TAGTTTCA TGTTG GTCCA	
			ATTAGAGT ACAAC TAGGT	
			T AAA	
GAM1965	CDKN1A	3'	TGGGCTCATATGGGGCTG 27784	TT TG
			TAGT CATGT GGGTCCA	
			GTCG GTATA CTCGGGT	
			GG _	
GAM1965	CEACAM6	3'	TGAATGGTCTCTCTTTGGCTGG 8311	T ____ T
	AATTA		TTCA GTT GGGG CCATTTA	
			AGGT CGG TCTC GGTAAGT	
			_ TTTC T	
GAM1965	CENTD1	5'	ATCCCATACATGAAATTA 29198	_
			TAGTTTCATGT TGGGGT	
			ATTAAAGTACA ACCCTA	
			T	
GAM1965	CERD4	3'	TGCTTTTCAGCCATGAAACTA 14352	_ GG TC
			TAGTTTCATG TTG G CA	
			ATCAAAGTAC GAC T GT	
			C TT TC	
GAM1965	CERD4	3'	TGGGTGGGCTTTGGCAGGTGGC 14353	TCA TG
	T		AGTT TGT GGGTCCATTTA	
			TCGG ACG TTCGGGTGGGT	
			TGG GT	
GAM1965	CGTHBA	3'	GGTGGTTCCGCTGTGGGGCTG 14365	TT GT T
			TAGT CAT TGGGG CCATT	

			GTCG GTG GCCTT GGTGG		
			GG TC _		
GAM1965	CHRNA4	3'	TGGGGAGACCGAGTGTGGAGCT 6399		TG G G_ ATTTA
	G		TAGTTTCA TT GG TCC		
			GTCGAGGT GA CC AGG		
			GT G AG GGT		
GAM1965	CHRNA5	5'	AGGCTGCTGTCCCGGCGGGAGC 30057	A	TC_ TTTA
	TG		TAGTTTC TGTTGGGG CA		
			GTCGAGG GCGGCCCT GT		
			_ GTC CGGAG		
GAM1965	CHRNA2	3'	TGGGTGGGCCCCACAGTGG 6403	GT	
			TCAT TGGGGTCCATTTA		
			GGTG ACCCCGGGTGGGT		
			AC		
GAM1965	CLASP1	3'	TGGCTTTTCAGCGTAGAATTG 32542	TC	GG T
			TAGTT ATGTTG G CCA		
			GTAA TGCGAC T GGT		
			GA TT C		
GAM1965	CLASP2	3'	TGGTTTCCTTTTACCATGAAAT 32271	TT__	T_ TTTA
	TG		GTTTCATG GGGG CCA		
			TAAAGTAC TCCT GGT		
			CATTT TT A		
GAM1965	CLN2	3'	ATCTTGTTTCTGATATGGACTA 5963	T	TG T TTTA
			TAGTT CATGT GGG CCA		
			ATCAG GTATA CTT GGT		
			_ GT _ TCTAA		
GAM1965	CNP	3'	TGGGCCTCCTCTAACAGGGGCT 26978	TT A	__ TTTA
	G		GT C TGTTGG GGTCCA		
			CG G ACAATC CCGGGT		
			GG_ TCCT A		
GAM1965	COL4A1	3'	TGAACCTCCAAATGGAATTA 7579	G	_ C
			TAGTTTCAT TTGG GGT CA		
			ATTAAGGTA AACC CCA GT		
			_ T A		
GAM1965	CPD	3'	TAAATGCCCACTTGAATGAAGC 6986	GTTG__	TC
	TG		TAGTTTCAT GGG CATTTA		
			GTCGAAGTA CCC GTAAAT		
			AGTTCA _		
GAM1965	CPN1	5'	TAGGTGGACCTTGGATTTTGGC 6991	TCATG TG	
			GTT T GGGTCCATTTA		

		CGG G TCCAGGTGGAT		
		TTTTA GT		
GAM1965 CREBL2	3'	TGAGCCATTCCAGCATAAGCTG 6996	C	___ TC
		TAGTTT ATGTTGG GG CA		
		GTCGAA TACGACC CC GT		
		___ TTA GA		
GAM1965 CTGF	3'	GACTTGACAGTGGA ACTA 7625	___	TG G
		TAGTTTCA TGT GG TC		
		ATCAAGGT ACA TC AG		
		G GT ___		
GAM1965 CXorf6	3'	TGGGTGTGCAACTTGAGGCTG 11995	T	GGG_
		TAGTTTCA GTTG TCCA		
		GTCGGAGT CAAC GGGT		
		T GTGT		
GAM1965 DAZ	3'	TAGTTTTATCTTAACACTGAAA 10283	___	CCATTTA
CTG		TAGTTTCA TGTTGGGGT		
		GTCAAAGT ACAATTCTA		
		C TTTTGAT		
GAM1965 DAZ	3'	TGGATGAAACTGAGATTG 39946	T	GGG
		TAGTTTCA GTT GTCCA		
		GTTAGAGT CAA TAGGT		
		___ AG_		
GAM1965 DAZ	3'	TGGATGAAACTGAGATTG 39945	T	GGG
		TAGTTTCA GTT GTCCA		
		GTTAGAGT CAA TAGGT		
		___ AG_		
GAM1965 DBT	3'	GACTTCTTAATATGGTGCTG 7633	T	___
		TAGT TCATGTTGGG GTC		
		GTCG GGTATAATTC CAG		
		T TT		
GAM1965 DCTN1	5'	TGGCTCAGTGTGAGATTG 10286	TG	GT
		TAGTTTCA TTGGG CCA		
		GTTAGAGT GACTC GGT		
		GT ___		
GAM1965 DFFB	3'	GAACCACGTGAAACTG 42244	T	GG
		TAGTTTCATGT GG TC		
		GTCAAAGTGCA CC AG		
		___ A_		
GAM1965 DGKG	3'	TGAATGGACTTAGGGCCCATGA 7027	TT	TTG___
GGTTG		TCATG GGGTCCATTTA		

		AGTAC TTCAGGTAAGT		
		GG CCGGGA		
GAM1965 DHCR24	3'	GGATTCTCACCGTGGGGCTG 16526	TT T _	
		TAGT CATG TG GGGTCC		
		GTCG GTGC AC CTTAGG		
		GG C T		
GAM1965 DHFR	3'	ATTCCAGCTATGGAGCTA 6446	_	
		TAGTTTCAT GTTGGGGT		
		ATCGAGGTA CGACCTTA		
		T		
GAM1965 DLG3	5'	TGGAATCCGGCGTGGGCTG 22095	T GG	
		TAGTT CATGTTGG TCCA		
		GTCGG GTGCGGCC AGGT		
		_ TA		
GAM1965 DLG5	3'	TGGAACCTCAATGGGGGCTG 40342	TT A _	
		TAGT C TGTTGGGGT CCA		
		GTCG G GTA ACTCCA GGT		
		GG _ A		
GAM1965 DPYD	3'	TGGCATCTTCAATATGAATCTA 30319	T T__	
		TAG TTCATGTTGGGG CCA		
		ATC AAGTATAACTTC GGT		
		T TAC		
GAM1965 DRD2	3'	TGGGGCTTGGCGTGGAGC 6467	TG G	
		GTTTCATGT GG TCCA		
		CGAGGTGCG TC GGGT		
		GT G		
GAM1965 DSC3	3'	AATCTCAA ACTCCAGCACTGGA 23662	_ CCATTTA	
ATTA		AGTTTCA TGTTGGGGT		
		TTAAGGT ACGACCTCA		
		C AACTCTAAA		
GAM1965 DSC3	3'	AATCTCAA ACTCCAGCACTGGA 7651	_ CCATTTA	
ATTA		AGTTTCA TGTTGGGGT		
		TTAAGGT ACGACCTCA		
		C AACTCTAAA		
GAM1965 E2F3	3'	TGAGGTCTGCTAATATGGAAT 7672	_ T ATTTA	
		GTTTCATGTTGG GG CC		
		TAAGGTATAATC TC GG		
		G T AGT		
GAM1965 EDN3	3'	TAAGTGGA CTCCAAGCTAACT 5582	TCATG	
		AGTT TTGGGGTCCATTTA		

		TCAA AACCTCAGGTGAAT	
		TCG__	
GAM1965 EDNRA	3'	GGTTTTTCAGTATGAACCTA 32057	T GG T
		TAG TTCATGTTG G CC	
		ATC AAGTATGAC T GG	
		C TT T	
GAM1965 EIF1A	3'	TAGGTGGAATGCATCTGAGACT 42725	__ TGGGG
A		TAGTTTCA TGT TCCATTTA	
		ATCAGAGT ACG AGGTGGAT	
		CT TA__	
GAM1965 EIF2S3	3'	TGAATGGATTTCGAATGAAATTG 7113	GTTG
		TAGTTTCAT GGGTCCATTTA	
		GTAAAGTA CTTAGGTAAGT	
		AG__	
GAM1965 ERBB4	3'	TGGAATTTCTAGTATGAGACTA 11747	__ TTTA
		TAGTTTCATGTTGGGG TCCA	
		ATCAGAGTATGATCTT AGGT	
		TA A	
GAM1965 EXT2	3'	TGGAGGTCTGAATGTGAGGCTG 5976	G __
		TAGTTTCATGTT GGG TCCA	
		GTCGGAGTGTA TCT AGGT	
		G GG	
GAM1965 FACL3	3'	ACAAGGGTATTGATATGAAATT 10759	TG GG ATTTA
A		TAGTTTCATGT G TCC	
		ATTAAAGTATA T GGG	
		GT AT AACAT	
GAM1965 FCN2	3'	TGGACCGTGAGTGTGGGGCTG 17955	TT TG _ G
		TAGT CA TT G GGTCCA	
		GTCG GT GA T CCAGGT	
		GG GT G G	
GAM1965 FDX1	3'	TGAGTGGACTTCATATTATGAC 30260	TCATGT
TA		TAGTT TGGGGTCCATTTA	
		ATCAG ACTTCAGGTGAGT	
		TATTAT	
GAM1965 FZD7	3'	TAATGTTCACTTGAGTGGAAC T 9599	G TG GTC_ TA
G		TAGTTTCAT T GG CATT	
		GTCAAGGTG A TC GTAA	
		_GT ACTT T	
GAM1965 G2A	5'	GAGTGGAGCACGTGAGAC 14989	T GGG
		GTTTCATGT G TCCATTT	

		CAGAGTGCA C AGGTGAG		
		_ G _		
GAM1965	GAB2	3' TGGATGGGGGTGATGCAGGGAC 14655	TT A TGGGG_	
	TG	TAGT C TGT TCCATTTA		
		GTCA G ACG GGGTAGGT		
		GG _ TAGTGG		
GAM1965	GAB2	3' TGGATGGGGGTGATGCAGGGAC 27850	TT A TGGGG_	
	TG	TAGT C TGT TCCATTTA		
		GTCA G ACG GGGTAGGT		
		GG _ TAGTGG		
GAM1965	GABPA	5' GATTCCGGAGTGGGACTG 7793	TT G	
		TAGT CAT TTGGGGTC		
		GTCA GTG GGCCTTAG		
		GG A		
GAM1965	GABPB1	3' TGGACTGATGCTGGAATTA 11762	T TGG	
		TAGTTTCA GT GGTCCA		
		ATTAAGGT CG TCAGGT		
		_ TAG		
GAM1965	GALNT3	3' TGTTTCCTTAACATGAAACTG 10805	_ TC	
		TAGTTTCATGTT GGGG CA		
		GTCAAAGTACAA TCCT GT		
		AT TT		
GAM1965	GALNT7	5' TGAATGGGCTTTCAGAAGGC 27652	CA TT	
		GTTT TG GGGGTCCATTTA		
		CGGA AC TTTCGGGTAAGT		
		AG _		
GAM1965	GAS7	3' TGGAGAGGTCAGGATGGAACTA 9718	G GG_	
		TAGTTTCAT TTGG TCCA		
		ATCAAGGTA GACT AGGT		
		G GGAG		
GAM1965	GBAS	3' GATGTTTCAATGTGAGAC 7227	GG TC	
		GTTTCATGTTG G CATT		
		CAGAGTGTAAC T GTAG		
		TT _		
GAM1965	GEMIN5	5' GCCACCAGCTCCGACGATGGGA 42973	TT _ CCATTTA	
	CTG	TAGT CAT GTTGGGGT		
		GTCA GTA CAGCCTCG		
		GG G ACCACCGT		
GAM1965	GGCX	3' GACGCAATGTGAAACTG 6482	GG	
		TAGTTTCATGTTG GTC		

			GTCAAAGTGTAAC CAG		
			G _		
GAM1965	GJB3	3'	TGGCTCGGGGTGGAGCTA 23442	G	GT
			TAGTTTCAT TTGGG CCA		
			ATCGAGGTG GGCTC GGT		
			G _		
GAM1965	GNAI1	3'	TGGTCCTGCAGTGTGAAACTG 7842	TG	_ T
			TAGTTTCA TTG GGG CCA		
			GTCAAAGT GAC TCC GGT		
			GT G T		
GAM1965	GNG2	5'	TAGGTGGTTGAAGATATTGAAA 45502	_	GGGGT
	TTG		TAGTTTCA TGTT CCATTTA		
			GTAAAGT ATAG GGTGGAT		
			T AAGTT		
GAM1965	GPC1	3'	TGGGCTCTGCCAATGTGGGCTG 7876	T	_
			TAGTT CATGTTGG GGTCCA		
			GTCGG GTGTAACC TCGGGT		
			_ GTC		
GAM1965	GPR85	5'	TGAGACTTGACTGAGGCTG 21044	T	TG G _
			TAGTTTCA GT GG TC CA		
			GTCGGAGT CA TC AG GT		
			_ GT _ A		
GAM1965	GRLF1	3'	TGAGATTCAGGGTGGGGCTG 38417	TT	G G _
			TAGT CAT TTGGG TC CA		
			GTCG GTG GACTT AG GT		
			GG G _ A		
GAM1965	GRM6	3'	TGGTTTTGACCGTGGGACTA 6511	TT	_ TG T
			TAGT CATG T GGG CCA		
			ATCA GTGC A TTT GGT		
			GG C GT _		
GAM1965	HCS	3'	TGGGTGACGAGTGAAACTG 21017	G	GG
			TAGTTTCAT TTG GTCCA		
			GTCAAAGTG AGC TGGGT		
			_ AG		
GAM1965	HIP1	3'	TAGATGGACCCCAGCATTTAAG 11811	G	TC
	TG		TA TT ATGTTGGGGTCCATTTA		
			GT AA TACGACCCCAGGTAGAT		
			G TT		
GAM1965	HNRPD	3'	TAGGTGACGAGTTGACATTGAG 11955	_	TG G _ C
	ATTG		GTTTCA TGT G GTC ATTTA		

			TAGAGT ACA T CAG TGGAT		
			T GT GAG _		
GAM1965	HOXB9	3'	TGAAGGTATCTTAGGTGGAGCT 23448	G	_ ATTTA
	A		TAGTTTCAT TTGGGGT CC		
			ATCGAGGTG GATTCTA GG		
			_ T AAGT		
GAM1965	HRH1	3'	TGAGCCCTCCTGGAATGGAGCT 6527	GTT__	TC TTTA
	G		AGTTTCAT GGGG CA		
			TCGAGGTA TCCC GT		
			AGGTCC GA A		
GAM1965	HSPA5	3'	TGGATGGTGACATTGAAACTA 11822	_	GG
			TAGTTTCA TGTTG GTCCA		
			ATCAAAGT ACAGT TAGGT		
			T GG		
GAM1965	ICOS	3'	TGAGATGTTGATGTGAACTG 14392	T	TG G _
			TAGTT CATGT G GTC CA		
			GTCAA GTGTA T TAG GT		
			_ GT G A		
GAM1965	ID3	3'	TGGGTGGGGGCAGCGTGGGGC 38612	TT	GGG
			GT CATGTTG TCCATTTA		
			CG GTGCGAC GGGTGGGT		
			GG GG_		
GAM1965	IHPK1	3'	GACCTTAGCATGGGGCTA 45824	TT	
			TAGT CATGTTGGGGTC		
			ATCG GTACGATTCCAG		
			GG		
GAM1965	IHPK1	3'	GACCTTAGCATGGGGCTA 45825	TT	
			TAGT CATGTTGGGGTC		
			ATCG GTACGATTCCAG		
			GG		
GAM1965	IL11	3'	GATGTCCTGACATGAAAC 6280	TG	TC
			GTTTCATGT GGG CATT		
			CAAAGTACA CCT GTAG		
			GT _		
GAM1965	IL18	5'	TGGACAGTCAGCAAGGAATTG 7292	A	G_
			TAGTTTC TGTTGG GTCCA		
			GTTAAGG ACGACT CAGGT		
			A GA		
GAM1965	IL1R1	3'	TGGTCTCCCTCCAGCTGGAATT 6567	T	T__ TTTA
	G		GTTTCA GTTGGGG CCA		

			TAAGGT CGACCTC	GGT	
			— CCTCT	A	
GAM1965	IL1RAPL2	5'	GCCCTGGACATGGAACTA	18874	— TG
			TAGTTTCATG T	GGGT	
			ATCAAGGTAC G	CCCG	
			A GT		
GAM1965	IL21R	3'	GGATGGGCCTTTGAGCCTG	22355	T TGTT
			TAG TTCA	GGGGTCCATTT	
			GTC GAGT	TTCCGGGTAGG	
			C	—	
GAM1965	ILF1	3'	TGAGTGGGTCTCCCAAGACTA	10844	CA TT GT
			TAGTTT TG	GGG CCATTTA	
			ATCAGA AC CTC	GGTGAGT	
			— C_	TG	
GAM1965	IRS1	5'	TGGGCCCGGATGGGGCTG	12070	TT TG G
			TAGT CA TT	GGGTCCA	
			GTCG GT AG	CCCGGGT	
			GG	— G	
GAM1965	IRS2	3'	GGGGTCAATGTGATGCTG	30034	T G G
			TAGT TCATGTTG G	TCC	
			GTCG AGTGTAAC T	GGG	
			T	— G	
GAM1965	ISL1	3'	AAAGTTGACTTTAACAAGGGGT	7958	TT A C A
	TA		TAG TC TGTTGGGGTC	ATTT	
			ATT GG ACAATTTTCAG	TGAA	
			GG A	T AT	
GAM1965	ITGA5	3'	GCCTGCAGTGTGAGGCTG	30722	TG —
			TAGTTTCA TTG	GGGT	
			GTCGGAGT GAC	TCCG	
			GT	G	
GAM1965	ITPR1	3'	TGGATGAAAAATATGAAAT	7987	GGG_
			GTTTCATGTT	GTCCA	
			TAAAGTATAA	TAGGT	
			AAAG		
GAM1965	JAG1	3'	GGGCTGCTGTGAAGCTG	5711	— TGG
			TAGTTTCAT GT	GGTCC	
			GTCGAAGTG CG	TCGGG	
			T	—	
GAM1965	JAK2	3'	TGAATGTGTTTTTTAAATGGAA	11417	GTT_ TC
	CTA		TAGTTTCAT	GGGG CATTTA	

		ATCAAGGTA TTTT GTAAGT	
		AATT GT	
GAM1965 JJAZ1	3'	AAGATGTGTTTAACTGTGAGGC 17652	_ GTC A
	TA	TAGTTTCAT GTTGGG CATT	
		ATCGGAGTG CAATTT GTAGA	
		T GT_ AT	
GAM1965 KCNA5	3'	AGTCAGAGATCTTGGTATGGGC 30027	T TT CATT
	TG	TAGTT CATG GGGGTC	
		GTCGG GTAT TTCTAG	
		_ GG AGACTGAG	
GAM1965 KCNK6	3'	TGGGTGTGCCTGGCCTGGGACT 11240	TT T TG G TC
	G	TAGT CA GT G G CATT	
		GTCA GT CG C C GTGGGT	
		GG C GT_ GT	
GAM1965 KCNS2	3'	AACCCAGGGGTCTGAGCATGGA 33895	G GT ATT
	GCTA	TAGTTTCATGTT GG CC	
		ATCGAGGTACGA TC GG	
		G TG GACCCAAG	
GAM1965 KDR	3'	AATGCGGGAGGTTCAATGTGAA 8051	G_ ATT
	GCTG	AGTTTCATGTTGGG TCC	
		TCGAAGTGTAAGTT AGG	
		GG GCGTAAG	
GAM1965 KIAA0857	3'	TGAGTCTGCTTCAGTCTGGAGC 33122	TG CC
	TG	TAGTTTCA TTGGGGT ATT	
		GTCGAGGT GACTTCG TGAGT	
		CT TC	
GAM1965 KIF3B	3'	TGGGTGGACCACCTGAGGTTA 11219	TT TGTT _
		TAG TCA GG GGTCCATT	
		ATT AGT CC CCAGGTGGGT	
		GG _ A	
GAM1965 KLRG1	3'	TGAATGAACCAATGTGTGATTG 12393	T GGTC
		TAGTT CATGTTGG CATT	
		GTTAG GTGTAACC GTAAGT	
		T AA_	
GAM1965 LAMP2	3'	TGGGTGGATCACTTGAGGC 15187	T TGG
		GTTTCA GT GGTCCATT	
		CGGAGT CA CTAGGTGGGT	
		T _	
GAM1965 LEP	3'	TAGATGGGTCTGGCTGAGCTG 5741	T T G GT
		TAGTT CA GTTG G CCATT	

GTCGA GT CGGT C GGTAGAT
 _ _ _ TG
 GAM1965 LHX5 5' TCGCGCCCGTGGCATGAGGTTG 22751 TT _ _
 TAG TCATGTTG GGGTC CA
 ||| ||||| ||||| ||
 GTT AGTACGGT CCCGG GT
 GG G C
 GAM1965 LOH11CR2A 5' GATTCCCAGCATGGCATTG 15987 T _
 TAGT TCATGTTGGGG TC
 |||| ||||| ||||| ||
 GTTA GGTACGACCCT AG
 C T
 GAM1965 LOH11CR2A 5' TGGGGATGCCTAACATGAAGC 15991 _ ATTAA
 GTTTCATGTTGGG GTCC
 ||||| ||||| ||||| |||||
 CGAAGTACAATCC TAGG
 G GGT
 GAM1965 LRAT 3' TAAATGGATATAGGATTGAAGT 30183 GT TGTGTTGGG
 TA TA TTCA GTCCATTTA
 || |||| ||||| |||||
 AT AAGT TAGGTAAAT
 TG TAGGATA
 GAM1965 LRP1 5' GGCTCCGAGATGGGGCTG 8139 TT G
 TAGT CAT TTGGGGTC
 |||| ||| ||||| |||||
 GTCG GTA AGCCTCGG
 GG G
 GAM1965 LRP8 3' TGAATGGGTTTCTATATATGGG 27133 T T__ GT
 TCTG AG TTCATGT GGG CCATTTA
 || ||||| ||| ||||| |||||
 TC GGGTATA CTT GGTAAGT
 T TAT TG
 GAM1965 LRP8 3' TGAATGGGTTTCTATATATGGG 11009 T T__ GT
 TCTG AG TTCATGT GGG CCATTTA
 || ||||| ||| ||||| |||||
 TC GGGTATA CTT GGTAAGT
 T TAT TG
 GAM1965 MADH7 3' GACTTTAACATAAGCTA 12524 C
 TAGTTT ATGTTGGGGTC
 ||||| ||||| ||||| |||||
 ATCGAA TACAATTCAG
 _
 GAM1965 MAP2K1 3' AATGTTTCTTAAATGGAATTA 8633 G TC
 TAGTTTCAT TTGGGG CATT
 ||||| ||||| ||||| |||||
 ATTAAGGTA AATTCT GTAA
 _ TT
 GAM1965 MAP3K7IP2 3' TGAGTGCTTAGAATGGGGCTA 17488 TT G GTC
 TAGT CAT TTGGG CATTTA
 |||| ||| ||||| |||||

			ATCG GTA GATTC GTGAGT		
			GG A ____		
GAM1965	MASP1	3'	TGGTTTCTAACATTGAACTG 29160	C	T
			TAGTTT ATGTTGGGG CCA		
			GTCAAG TACAATCTT GGT		
			T T		
GAM1965	MEIS2	3'	GACACTTAATATGAAATT 21348	—	
			AGTTTCATGTTGGG GTC		
			TTAAAGTATAATTC CAG		
			A		
GAM1965	MEN1	5'	TAGATGGGCTCTTCTGGA 44846	TGTT	
			TTCA GGGGTCCATTTA		
			AGGT TCTCGGGTAGAT		
			CT__		
GAM1965	MEN1	5'	TAGGTGGTTGATTTGAACTG 44847	T TG GGT	
			TAGTTTCA GT G CCATTTA		
			GTCAAAGT TA T GGTGGAT		
			T GT__		
GAM1965	MEOX1	3'	GACTCTTGGATATGAACTG 15189	—	
			TAGTTTCATGTT GGGGTC		
			GTCAAAGTATAG TCTCAG		
			GT		
GAM1965	MEOX1	3'	GACTCTTGGATATGAACTG 10865	—	
			TAGTTTCATGTT GGGGTC		
			GTCAAAGTATAG TCTCAG		
			GT		
GAM1965	METTL1	3'	TGGGTCTTCCCAGTTGAGACTG 23309	TGT	—
			TAGTTTCA TGGGG TCCA		
			GTCAGAGT ACCCT GGGT		
			TG_ TCT		
GAM1965	METTL1	3'	TGGGTCTTCCCAGTTGAGACTG 23314	TGT	—
			TAGTTTCA TGGGG TCCA		
			GTCAGAGT ACCCT GGGT		
			TG_ TCT		
GAM1965	MGAM	3'	GGACAGCCAAGTGGAGCTA 35825	G G_	
			TAGTTTCAT TTGG GTCC		
			ATCGAGGTG AACC CAGG		
			_ GA		
GAM1965	MGAM	3'	TGAATGGGTCTCTAGACTGGGA 35828	TT T _ GT	
C			GT CA GTT GGG CCATTTA		

		CA GT CAG CTC GGTAAGT	
		GG _ AT TG	
GAM1965 MGEA5	3'	TAAGGGTTCTGAGCATGAAGCT 14517	_ GG ATTTA
G		TAGTTTCATGTT GG TCC	
		GTCGAAGTACGA TC GGG	
		G TT AAT	
GAM1965 MMP11	3'	TGGGCACCAGGCATGGGACTG 12579	TT TG _
		TAGT CATGT GG GTCCA	
		GTCA GTACG CC CGGGT	
		GG GA A	
GAM1965 MNT	3'	TGAGTGGGCCCTGCCCGGGGAG 21568	A TT_
CT		AGTTTC TG GGGGTCCATTTA	
		TCGAGG GC TCCCGGGTGAGT	
		G CCG	
GAM1965 MUC4	3'	TGGATGGGTCTCCTCACGCAGAC 28712	CA T GT
		GTTT TGT GGG CCATTTA	
		CAGA GCA TCC GGTAGGT	
		C_ C TG	
GAM1965 MYCBP	3'	GACTTAATTATGAGACTG 14725	TTG
		TAGTTTCATG GGGTC	
		GTCAGAGTAT TTCAG	
		TAA	
GAM1965 NAPB	3'	TGGCTCTCAACTGGAATTG 34768	T GT
		TAGTTTCA GTTGGG CCA	
		GTTAAGGT CAACTC GGT	
		_ TC	
GAM1965 NCALD	3'	ACCCTCTGGGGTGAGGCTA 25743	G _
		TAGTTTCAT TT GGGGT	
		ATCGGAGTG GG TCCCA	
		G TC	
GAM1965 NDUFA6	3'	GACATTGGGCATGAGGCTG 8313	G _
		TAGTTTCATGTT GG GTC	
		GTCGGAGTACGG TT CAG	
		G A	
GAM1965 NEBL	3'	ATCTCGTGTCATGAAGCTG 13097	_
		TAGTTTCATGT TGGGGT	
		GTCGAAGTACG GCTCTA	
		T	
GAM1965 NFIA	3'	TGGTCTGTTTTGACAGAACTG 34843	A TG _ T
		TAGTTTC TGT G GG CCA	

GTCAAAG ACA T TC GGT
 _ GT TTG T
 GAM1965 NOVA1 3' TGAATGTAGATTTTACTGTGAA 13219 GT _
 GCTA AGTTTCAT TGGGGTC CATTTA
 ||||| ||||| |||||
 TCGAAGTG ATTTTAG GTAAGT
 TC AT
 GAM1965 NOVA1 3' TGAATGTAGATTTTACTGTGAA 8350 GT _
 GCTA AGTTTCAT TGGGGTC CATTTA
 ||||| ||||| |||||
 TCGAAGTG ATTTTAG GTAAGT
 TC AT
 GAM1965 NPHP1 3' TGGGTGGATCACCTGAGG 31316 TGTT _
 TTTCA GG GTCCATTTA
 |||| |||||
 GGAGT CC CTAGGTGGGT
 _ A
 GAM1965 NPY1R 5' TAAATGGATTCCAATATCGGGA 6608 TT _
 T C ATGTTGGGGTCCATTTA
 | | |||||
 A G TATAACCTTAGGTAAAT
 GG C
 GAM1965 NRCAM 5' TGAGTCTCAGCAGGAGTTA 11453 GT A TC
 TA TTC TGTTGGGG CA
 || ||||| ||
 AT AGG ACGACTCT GT
 TG _ GA
 GAM1965 NRCAM 3' TGGACATTGTTGTGAAATTG 11454 TTGGG
 TAGTTTCATG GTCCA
 ||||| ||||
 GTTAAAGTGT CAGGT
 TGTTA
 GAM1965 NRF1 3' GAAACCCGCATGGAATTA 30189 T GG
 TAGTTTCATGT GG TC
 ||||| || ||
 ATTAAGGTACG CC AG
 C AA
 GAM1965 NRF1 3' GGAAAGAGGCTCCAGCATGGGG 30190 TT CA A
 T CATGTTGGGGTC TTT
 | ||||| |||
 G GTACGACCTCGG AAA
 GG AG GGA
 GAM1965 OCLN 3' AGGAAGGTTCTGGTGTGAACTA 8378 T TG TG T A A
 TAGTT CA T GGG CC TTT
 |||| || | ||| |||
 ATCAA GT G CTT GG AGG
 _ GT GT _ A AA
 GAM1965 OCLN 3' TGAAGTCTCTGAAGTGAAACTG 8383 G TG TCCA
 TAGTTTCAT T GGG TTTA
 ||||| | || |||

GTCAAAGTG A CTC AAGT
 A GT TG__
 GAM1965 OSR1 5' TGGCCCGTGC GTGGGGCTG 11592 TT TG T
 TAGT CATGT GGG CCA
 ||| ||| ||| |||
 GTCG GTGCG CCC GGT
 GG TG _
 GAM1965 PAFAH1B1 3' TGTTTTTCAACATGAATCTG 6014 T GG TC
 TAG TTCATGTTG G CA
 ||| ||| ||| ||| | ||
 GTC AAGTACAAC T GT
 T TT TT
 GAM1965 PAX5 3' GGAGTGATTTTGACATGGGGGT 18791 G TT TG C A
 G TA T CATGT GGGTC ATTT
 || ||| ||| ||| |||
 GT G GTACA TTTAG TGAG
 G GG GT _ GG
 GAM1965 PCDH11X 3' TGGGTGGATCACCTGAGG 26782 TGTT _
 TTTCA GG GGTCCATTTA
 ||| ||| ||| ||| ||| |||
 GGAGT CC CTAGGTGGGT
 _ A
 GAM1965 PCTP 3' GGATTTATTAATGTGGGAT 22194 TT _
 GT CATGTTGG GGTCC
 || ||| ||| ||| ||| |||
 TA GTGTAATT TTAGG
 GG AT
 GAM1965 PDE4C 3' TGCACTCCAGCCTGGGGCTG 6635 TT T C
 TAGT CA GTTGGGGT CA
 ||| ||| ||| ||| ||| |||
 GTCG GT CGACCTCA GT
 GG C C
 GAM1965 PDGFRB 3' TAAATGTGCCAGTGTGGAG 32817 TG G TC
 TTTCA TTGG G CATTTA
 ||| ||| ||| ||| ||| |||
 GAGGT GACC T GTAAAT
 GT G__
 GAM1965 PLA2G2D 3' TGTTCCCTCAGCATGGAGCT 14774 TC
 AGTTTCATGTTGGGG CA
 ||| ||| ||| ||| ||| ||| ||| |||
 TCGAGGTACGACTCC GT
 TT
 GAM1965 PPARBP 3' TAAATGGCATGGCTTTGACATC 11164 C TG _
 AAGCTG TT ATGT GGGT CCATTTA
 || ||| ||| ||| ||| ||| |||
 AA TACA TTCG GGTAAT
 C GT GTAC
 GAM1965 PPP2R4 3' GGGTGGGCCCAAGGTG 30377 G G_
 CAT TT GGGTCCATT
 ||| ||| ||| ||| ||| ||| ||| |||

		GTG AA CCCGGGTGGG	
		G GA	
GAM1965	PPP2R5A	3' TAAATGGAAAAATATATGGACT 12912	T TGGGG
	A	TAGTT CATGT TCCATTTA	
		ATCAG GTATA AGGTAAAT	
		_ TAAAA	
GAM1965	PPP2R5E	3' TAGATGGACTTCTCAGAACT 12923	CA TT
		AGTTT TG GGGGTCCATTTA	
		TCAAG AC CTTCAGGTAGAT	
		_ T_	
GAM1965	PRDM2	3' GAACTGGCTCCTCGTCATGGGA 18004	TT T T_ TTTA
	CTG	TAGT CATG TGGGG CCA	
		GTCA GTAC GCTCC GGT	
		GG T TC CAAGT	
GAM1965	PRKAB1	3' GGCCTGGCTATGGA ACTA 12931	_ TG GT
		TAGTTTCAT GT GG CC	
		ATCAAGGTA CG CC GG	
		T GT _	
GAM1965	PROS1	3' TAGATGGATGTATACGAAGCTG 42256	A TGGG
		TAGTTTC TGT GTCCATTTA	
		GTCGAAG ATA TAGGTAGAT	
		C TG_	
GAM1965	PRX	3' AAAGTCCCTGACATGAAGCT 21932	TG TCCA A
		AGTTTCATGT GGG TTT	
		TCGAAGTACA CCC AAA	
		GT TG_ G	
GAM1965	PRX	3' GATCCCCGAGGTGGAGCTG 21938	G _
		TAGTTTCAT TTGGGG TC	
		GTCGAGGTG AGCCCC AG	
		G T	
GAM1965	PSG1	3' GAACCAATATGAACTG 13784	T GG
		TAGTT CATGTTGG TC	
		GTCAA GTATAACC AG	
		_ A_	
GAM1965	PTTG1IP	3' TGAGTGGGCTTCTCTGGGAGCT 10538	ATGTT
		AGTTTC GGGGTCCATTTA	
		TCGAGG CTTCGGGTGAGT	
		GTCT_	
GAM1965	PUM2	3' TGAGTGGAGACCTATCAGA 17635	A T G_
		TC TG TGGG TCCATTTA	

AG AC ATCC AGGTGAGT
 _ T AG
 GAM1965 RAB5B 3' TGGTGTTCCTCCCTAATCGTGGG 8774 TT TT_ TC_ TA
 GTTG G TCATG GGGG CATT
 | |||| ||| |||
 T GGTGC CCCC GTGG
 GG TAAT TTT T
 GAM1965 RAD54B 3' TGAATGGCAGATGTGGAGCTA 28679 GGGGT
 TAGTTTCATGTT CCATTTA
 ||||| |||||
 ATCGAGGTGTAG GGTAAGT
 AC_
 GAM1965 RALBP1 3' TGGCTCCGGTGGGAACTG 13667 ATG T
 TAGTTTC TTGGGG CCA
 ||||| ||||| |||
 GTCAAGG GGCCTC GGT
 GT_ _
 GAM1965 RANBP2L1 3' TAGGTGGGCCCACCACTTGAG 11483 T TG_
 TTCA GT GGGTCCATTTA
 ||| || |||||
 GAGT CA CCCGGGTGGAT
 T CCA
 GAM1965 RGL 3' TGAAGTGCAGATTGTAACATGG 17509 G _ A
 AGCTA GTTTCATGTTG GGTC CATT
 ||||| ||| |||||
 CGAGGTACAAT TTAG GTGAA
 G AC GT
 GAM1965 RNPEPL1 3' GGGCCTCCAGCCTGGGACTG 20162 TT T _
 TAGT CA GTTGG GGTCC
 ||| || ||||| |||||
 GTCA GT CGACC CCGGG
 GG C T
 GAM1965 RRM2B 3' CAGATGCCTTAATGTGAAGCT 33688 TC A
 AGTTTCATGTTGGGG CATT
 ||||| ||||| |||||
 TCGAAGTGTAATTCC GTAGA
 _ CA
 GAM1965 RXRA 3' GGTGTCCCTGTCGTGGAGCTG 8872 T TC
 TAGTTTCATG TGGGG CATT
 ||||| ||||| |||||
 GTCGAGGTGC GTCCC GTGG
 T T_
 GAM1965 SACS 3' AAGTGGATCCTCTTGGA 45496 TGTT
 TTCA GGGGTCCATT
 ||| |||||
 AGGT TCCTAGGTGAA
 TC_
 GAM1965 SCAP2 3' AAAATATTCCTCTGATGTGAAA 10027 TG_ TCC A
 TTA TAGTTTCATGT G GG ATTT
 ||||| ||| |||

		ATTAAAGTGTA C CC TAAA	
		GT T TTA AT	
GAM1965	SCN1A	3' TGGGGTTGTTTAACATGAAAC 42836	___ G
		GTTTCATGTTGG G TCCA	
		CAAAGTACAATT T GGGT	
		TGT G	
GAM1965	SDHD	3' TGGGAATCTCTAATGTGAAA 8897	___ ATTTA
		TTTCATGTTGGGG TCC	
		AAAGTGTAACTC AGG	
		TA GT	
GAM1965	SEDL	3' TGTATCCTTGTGTGAAATTG 15917	TG T C
		TAGTTTCA T GGGGT CA	
		GTAAAGT G TCCTA GT	
		GT T T	
GAM1965	SFPA2	3' TGGCCTTTGGCATGAGAT 13811	TG T
		GTTTCATGT GGG CCA	
		TAGAGTACG TTC GGT	
		GT C	
GAM1965	SHMT2	3' TGGACATTTATTGTGAAATTA 11881	GT _
		TAGTTTCAT TGGG GTCCA	
		ATTAAAGTG ATTT CAGGT	
		TT A	
GAM1965	SIM2	3' TGGGTAACAGAGTGAGACTG 14313	G GG
		TAGTTTCAT TTG GTCCA	
		GTCAGAGTG GAC TGGGT	
		A AA	
GAM1965	SLA	3' TGGCTTAGGATGGAATTA 13598	G GT
		TAGTTTCAT TTGGG CCA	
		ATTAAGGTA GATTC GGT	
		G _	
GAM1965	SLA	3' GGTGCCCTGAATGGAATA 13597	G TG _
		TAGTTTCAT T GGGT CC	
		ATCAAGGTA A CCCG GG	
		_GT T	
GAM1965	SLC10A2	5' TAAGTGTCACCTTAAGTAAATT 6066	T GTC
	A	TAGTTTCA GTTGGG CATTTA	
		ATTAAAGT CAATTC GTGAAT	
		_ ACT	
GAM1965	SLC13A4	5' TGGCACCTAGAATGAAGTTA 14820	GT G GT
		TA TTCAT TTGGG CCA	

	AT AAGTA GATCC GGT	
	TG A AC	
GAM1965 SLC14A1	3' TGGGTGACAAGAGTGAAACTG 17998	G_ GG
	TAGTTTCAT TTG GTCCA	
	GTCAAAGTG AAC TGGGT	
	AG AG	
GAM1965 SLC14A1	3' TGTGCTCTGGTATGGAATT 17999	TT TC
	AGTTTCATG GGGG CA	
	TTAAGGTAT TCTC GT	
	GG GT	
GAM1965 SLC14A1	3' TGATGTGCTCTGGTATGGAATT 17997	TT TC TA
	AGTTTCATG GGGG CATT	
	TTAAGGTAT TCTC GTAG	
	GG GT T	
GAM1965 SLC17A4	3' TAGGATTCAATTCAATGTGGAA 11999	____ ATT TA
C	TTTCATGTTG GGGTCC	
	AAGGTGTAAC CTTAGG	
	TTAA AT A	
GAM1965 SLC1A1	3' TGAACCGTCAATGTGAAAT 10381	_ C
	GTTTCATGTTGG GGT CA	
	TAAAGTGTAAC CCA GT	
	G A	
GAM1965 SLC21A3	3' AAATTTGTTCTTTGATATTGGA 28672	_ TG TC TT TA
ATTA	AGTTTCA TGT GGG CA	
	TTAAGGT ATA TTC GT	
	T GT TT TTAAAT	
GAM1965 SLC21A3	3' AAATTTGTTCTTTGATATTGGA 22075	_ TG TC TT TA
ATTA	AGTTTCA TGT GGG CA	
	TTAAGGT ATA TTC GT	
	T GT TT TTAAAT	
GAM1965 SLC24A1	3' GAATGTGATCTGAGACTA 11101	TGTTGG _
	TAGTTTCA GGTC CATT	
	ATCAGAGT CTAG GTAAG	
	_____ T	
GAM1965 SLC4A7	3' TGAATGGGGTTGTGAAACTG 9672	GTTG G
	TAGTTTCAT GG TCCATT TA	
	GTCAAAGTG TT GGGTAAGT	
	_____ G	
GAM1965 SLC8A2	3' GGGTG GGGGGGATGGGACTG 32969	TT G GGGG
	TAGT CAT TT TCCATT	

			GTCA GTA GG GGGTGGG		
			GG G ____		
GAM1965	SMARCA3	3'	TGGAATAATAATGTGGGATTA 29133	TT	GGG_
			TAGT CATGTTG TCCA		
			ATTA GTGTAAT AGGT		
			GG AATA		
GAM1965	SMARCA3	3'	TGGAATAATAATGTGGGATTA 9038	TT	GGG_
			TAGT CATGTTG TCCA		
			ATTA GTGTAAT AGGT		
			GG AATA		
GAM1965	SNAI2	3'	TGAATGAGTTCTGTATGAACT 9032	TT	G C
	G		TAGTTTCATG GGG TC ATTTA		
			GTCAAAGTAT CTT AG TAAGT		
			GT G _		
GAM1965	SNRPN	5'	TAAGTGGGATCTGTGGATCTG 23084	T	GTT GT
			TAG TTCAT GGG CCATTTA		
			GTC AGGTG TCT GGTGAAT		
			T ____ AG		
GAM1965	SNX9	3'	TAGATGGAAAAGTGTAGGGACT 18332	TT_	TG GGGG
	G		TAGT C A TT TCCATTTA		
			GTCA G T GA AGGTAGAT		
			GG A GT AA__		
GAM1965	SORD	3'	TGGGTGGGCTCTGATGCAGAAC 9070	CA	TG
	T		AGTTT TGT GGGTCCATTTA		
			TCAAG GTA CTCGGGTGGGT		
			AC GT		
GAM1965	SRP46	5'	TGGAGTATTTGGCCTGAAATTG 25793	T	TG G__
			TAGTTTCA GT GG TCCA		
			GTAAAGT CG TT AGGT		
			C GT ATG		
GAM1965	SUFU	3'	TGAATGGGTCTCAAAGACT 18260	CATG	GT
			AGTTT TTGGG CCATTTA		
			TCAGA AACTC GGTAAGT		
			____ TG		
GAM1965	SYT1	3'	TAAATGACACTATTATGAAGCT 12172	T	G C
	A		TAGTTTCATG TGG GTC ATTTA		
			ATCGAAGTAT ATC CAG TAAAT		
			T A _		
GAM1965	SYT5	5'	ATCCCTTTAGGATGGAATA 9152	G	__
			TAGTTTCAT TT GGGGT		

		ATCAAGGTA GA CCCTA	
		G TTT	
GAM1965 TACC1	3'	ATGGTTATAGTTCTAATATGGA 12961	GG _____ TTTA
G		TTCATGTTGG T CCA	
		AGGTATAATC G GGT	
		TT ATATT AT	
GAM1965 TACC1	3'	TAAGTGGGGAATGCAACGTGAG 12968	GGG__
GC		GTTTCATGTTG TCCATTTA	
		CGGAGTGCAAC GGGTGAAT	
		GTAAG	
GAM1965 TAL1	3'	GAATGGGATCATGAAAGTA 9169 G	TTGGGG
		TA TTTTCATG TCCATTT	
		AT AAAGTAC GGGTAAG	
		G TA_____	
GAM1965 TAL1	3'	TGGATGGGTTTTATGAGAT 9172	TTG GT
		GTTTCATG GG CCATTTA	
		TAGAGTAT TT GGTAGGT	
		____ TG	
GAM1965 TCEB1L	3'	TAAATGTTCTGAGTGGAGCTA 9186	G TG TC
		TAGTTTCAT T GGG CATTTA	
		ATCGAGGTG A CTT GTAAAT	
		_GT _	
GAM1965 THRA	5'	TGGAGGGCATCCTGGATGGAAT 9259	G TG _ A
TG		TAGTTTCAT T GGGT CC TTTA	
		GTTAAGGTA G CCTA GG AGGT	
		_GT C G	
GAM1965 TMEM1	3'	ATGGTTCTACTCCCAGGATGAA 9288	G _ _____ TTTA
ATTA		TTCAT TTGGG GT CCA	
		AAGTA GACCC CA GGT	
		G T TCTT AT	
GAM1965 TMPRSS2	3'	TGGATGAGCATGGAGCTG 12195	GGG
		TAGTTTCATGTT GTCCA	
		GTCGAGGTACGA TAGGT	
		G__	
GAM1965 TNF	3'	TGGGGGACCCAATGTAGGAGCT 43772	_ GT ATTTA
G		TAGTTTC ATGTTGGG CC	
		GTCGAGG TGTAACCC GG	
		A AG GGT	
GAM1965 TOX	3'	TGGGTGTTTATATGAAACTA 16329	TG GG
		TAGTTTCATGT G TCCA	

		ATCAAAGTATA T GGGT	
		TT GT	
GAM1965 TP53	3'	TGAGCCACCACGTGGAGCTG 6153	T _ TC
		TAGTTTCATGT GG GG CA	
		GTCGAGGTGCA CC CC GT	
		_ A GA	
GAM1965 TRIM14	3'	TGGCACTTTTGATATGAGAC 16671	TG _ _
		GTTTCATGT GG GT CCA	
		CAGAGTATA TT CA GGT	
		GT T C	
GAM1965 TRPC6	3'	TGGACATTAAGTGGAACTG 10980	T G
		TAGTTTCA GTTGG GTCCA	
		GTCAAGGT CAATT CAGGT	
		_ A	
GAM1965 TSLP	5'	TGGGAAGAGTTTAGTGTGAAAC 26929	TG G CATTTA
TG		TAGTTTCA TTGGG TC	
		GTCAAAGT GATTT AG	
		GT G AAGGGT	
GAM1965 TSNAX	3'	TAGATGATTACTTGTGATGTGA 12616	_ C__
AACTG		TTTCATGTTG GGGT CATTTA	
		AAAGTGTAGT TTCA GTAGAT	
		G TTA	
GAM1965 UBL1	3'	GATGTTCTAGCATGTGATTA 9379	T TC
		TAGTT CATGTTGGGG CATT	
		ATTAG GTACGATCTT GTAG	
		T _	
GAM1965 UC28	3'	TGGGTGGATCACCTGAGG 22281	TGTT _
		TTTCA GG GGTCCATTTA	
		GGAGT CC CTAGGTGGGT	
		_ A	
GAM1965 VANGL2	3'	ATGGATTCAAGTCTGGTGTGTG 35476	T TG TG ____ TTTA
ATTG		T CA T GG GTCCA	
		G GT G CC TAGGT	
		T GT GT TGA CT AT	
GAM1965 VANGL2	3'	TGAGTCCCTTCCAAGTGAGATT 35487	GTT__ TC TTTA
G		AGTTTCAT GGGG CA	
		TTAGAGTG CCCT GT	
		AACCTT GA A	
GAM1965 VDR	3'	TAGGTGGATCACCTGAGG 5949	TGTT _
		TTTCA GG GGTCCATTTA	

			GGAGT CC CTAGGTGGAT		
			_____ A		
GAM1965 WDR3	3'	CCTGATGGAATTCCAACATGAG 13654		_____ TA	
	ATTA	AGTTTCATGTTGGGGT CCATT			
		TTAGAGTACAACCTTA GGTAG			
		A TCCG			
GAM1965 WHSC1	3'	TGGGCCCGATTCTGATATGAG 14253	_____ TTTA		
		TTCATGTTG GGGTCCA			
		GAGTATAGT CCCGGGT			
		CTTAG A			
GAM1965 WNT10B	3'	TGAATGGACTAAGATGAAAT 9431	G GG		
		GTTTCAT TT GGTCCATTTA			
		TAAAGTA AA TCAGGTAAGT			
		G _____			
GAM1965 WNT5B	3'	TAGATGGGTTCCGTAAGAGGC 25059	ATGT GG		
		GTTTC TGG TCCATTTA			
		CGGAG GCC GGGTAGAT			
		AAT_ TT			
GAM1965 WNT5B	3'	TAGATGGGTTCCGTAAGAGGC 26361	ATGT GG		
		GTTTC TGG TCCATTTA			
		CGGAG GCC GGGTAGAT			
		AAT_ TT			
GAM1965 WNT8B	3'	TGAATGGACTTTACTAGTGGGG 29985	TT GT_		
	C	GT CAT TGGGGTCCATTTA			
		CG GTG ATTCAGGTAAGT			
		GG ATC			
GAM1965 XRCC3	3'	TGGAAGCCCAACTGGGGTTG 11910	TT T G_		
		TAG TCA GTTGGG TCCA			
		GTT GGT CAACCC AGGT			
		GG _ GA			
GAM1965 XT3	3'	TGGAATGTCTCGGTGTAAAGCT 21448	C TG _____ TTTA		
	G	AGTTT A TTGGGG TCCA			
		TCGAA T GGCTCT AGGT			
		A GT GTA A			
GAM1965 XT3	3'	TGGGTGGATCACTTGAGG 21449	T TGG		
		TTTCA GT GGTCCATTTA			
		GGAGT CA CTAGGTGGGT			
		T _____			
GAM1965 YWHAZ	3'	AGGTGGCCAATATGGGG 9442	TT GGT		
		T CATGTTGG CCATT			

G GTATAACC GGTGGA
 GG ____
 GAM1965 ZNF124 5' TGAGGATCAAATTTTCAGCATGA 9483 ____ ATTTA
 AATT TCATGTTGG GGTCC
 ||||| ||||
 AGTACGACT CTAGG
 TTAAA AGT A
 GAM1965 ZNF137 3' GAGTGGATAATGGAACTG 9493 ATGTTGGG
 TAGTTTC GTCCATTT
 ||||| |||||
 GTCAAAG TAGGTGAG
 GTAA____
 GAM1965 ZNF202 3' TAAGTGGAGCACAGGGTATGGG 9510 TT __ GGG
 GTTA AG TCATG TTG TCCATTTA
 || |||| || |||||
 TT GGTAT GAC AGGTGAAT
 GG GG ACG
 GAM1965 ZNF74 3' GACCCTGTGTGAAATTA 9474 TG T
 TAGTTTCA T GGGGTC
 ||||| | |||||
 ATTAAAGT G TCCCAG
 GT_
 GAM1965 ZNF74 5' TGAGTGCGCCGAGCATGGGGCT 9476 TT G GTC
 G TAGT CATGTT GG CATTTA
 ||| ||||| || |||||
 GTCG GTACGA CC GTGAGT
 GG G GC_
 GAM1965 AF020591 3' TGGGTGGATCACCTGAAG 15827 TGTT _
 TTTCA GG GGTCCATTTA
 |||| || |||||
 GAAGT CC CTAGGTGGGT
 ____ A
 GAM1965 AKAP8 3' TAGGTGGAATAATCCAACATAA 12466 C G____
 ATTG GTTT ATGTTGGG TCCATTTA
 ||| ||||| |||||
 TAAA TACAACCT AGGTGGAT
 _ AATA
 GAM1965 AP4E1 3' TAAATGGAAGGGGAGACATGAAA 14277 GGGG_
 TTG TAGTTTCATGTT TCCATTTA
 ||||| |||||
 GTTAAAGTACAG AGGTAAAT
 AGGGA
 GAM1965 APOL4 5' TGTGTCCTAGTTGAGGCTA 24978 TGT TC
 TAGTTTCA TGGGG CA
 ||||| |||| ||
 ATCGGAGT ATCCT GT
 TG_ GT
 GAM1965 APOL6 3' TGAATGGATTCTGGGTGGAGAT 24972 ATG TG
 GTTTC T GGGTCCATTTA
 |||| | |||||

			TAGAG G CTTAGGTAAGT		
			GTG GT		
GAM1965	ARHGAP10	3'	ATAGTGGATCCTGGATGGA	21886	G TG TA
	G		TAGTTTCAT T GGGTCCATT		
			GTCAAGGTA G CCTAGGTGA		
			_ GT TAG		
GAM1965	ATP6V0A1	3'	GATGTCTTCAGTGTGGGACTG	11677	TT TG TC
			TAGT CA TTGGGG CATT		
			GTCA GT GACTTC GTAG		
			GG GT T_		
GAM1965	B3GNT5	3'	TGGTGCTCCAGTGTAGGGCTA	25765	TC TG _
			TAGTT A TTGGGGT CCA		
			ATCGG T GACCTCG GGT		
			GA GT T		
GAM1965	BDG-29	3'	GGCTTTGGTACTGAAACTG	35817	_ TT
			TAGTTTCA TG GGGGTC		
			GTCAAAGT AT TTTCGG		
			C GG		
GAM1965	BDG-29	3'	AAATCCTATTTCAACACTGAAA	35812	_ GG CCATTTA
	TTG		TAGTTTCA TGTTG GT		
			GTTAAAGT ACAAC TA		
			C TT TCCTAAAT		
GAM1965	BLOV1	3'	TAGATGGTTTCCCAGTGTGAGA	37522	TG T_
	TT		AGTTTCA TTGGGG CCATTTA		
			TTAGAGT GACCCT GGTAGAT		
			GT TT		
GAM1965	BLR1	3'	TGGATGCTCCTTCCAACAGGAG	26779	A _ TC
	CTG		AGTTTC TGTTGG GG CATTTA		
			TCGAGG ACAACC CC GTAGGT		
			_ TT TC		
GAM1965	BLR1	3'	TGGATGCTCCTTCCAACAGGAG	7449	A _ TC
	CTG		AGTTTC TGTTGG GG CATTTA		
			TCGAGG ACAACC CC GTAGGT		
			_ TT TC		
GAM1965	BOP	5'	AAAATATTTTCAAAGTGAAGCT	41206	G GG TCC A
	G		TAGTTTCAT TTG G ATTT		
			GTCGAAGTG AAC T TAAA		
			A TT TA_ AA		
GAM1965	BTBD1	3'	TAAGCCTCAGTTAAATGGAATT	24920	GT_ CCATTTA
	A		AGTTTCAT TGGGGT		

TTAAGGTA ACTCCG
 AATTG AAT A
 GAM1965 BTN1A1 3' TGGGTCAGGTTAGCATGGGGTT 7470 TT ____GT TTTA
 G AG TCATGTTGG G CCA
 || ||||| | |||
 TT GGTACGATT C GGT
 GG GGA TG A
 GAM1965 C14orf4 5' TGGCGTCTCGGCGTGGAAC 33446 _
 GTTTCATGTTGGGGT CCA
 ||||| |||
 CAAGGTGCGGCTCTG GGT
 C
 GAM1965 C16orf7 3' GAGCTACGTGGAGCTG 11346 TG G
 TAGTTTCATGT GG TC
 ||||| |||
 GTCGAGGTGCA TC AG
 _ G
 GAM1965 C17orf26 3' TGAATGGACTCTCTTTCAGTG 29188 TT GTT____
 GGATTA CAT GGGGTCCATTTA
 || |||||
 GTG TCTCAGGTAAGT
 GG ACTTCTC
 GAM1965 C1orf16 3' TGGAGTTAGTGTGGAAC 16860 TG G G
 AGTTTCA TTG G TCCA
 ||||| ||| |||
 TCAAGGT GAT T AGGT
 GT _ G
 GAM1965 C1orf24 3' TAAGTGCTTGTCTAGCATAAA 27535 C GG C__
 TTA AGTTT ATGTTGG T CATTTA
 |||| ||||| | |||||
 TTAAA TACGATC G GTGAAT
 _ TT TTC
 GAM1965 C1orf25 3' TAAATGCTTATCAGCATGAAAT 35911 GGTC
 GTTTCATGTTGG CATTTA
 ||||| |||||
 TAAAGTACGACT GTAAAT
 ATTC
 GAM1965 C1orf34 3' TGGGTGGGCACCCGTCAGGCTG 30440 TCA T _
 TAGTT TG TGGG GTCCATTTA
 |||| || ||| |||||
 GTCGG AC GCCC CGGGTGGGT
 _ T A
 GAM1965 C20orf12 5' TGGAAAAGCTAACCATGAAATT 19961 _ GG__ TTTA
 G AGTTTCATG TTGG TCCA
 ||||| ||| |||
 TTAAAGTAC AATC AGGT
 C GAAA A
 GAM1965 C20orf121 3' GACCAAATGTGAGACTG 23631 GG
 TAGTTTCATGTT GGTC
 ||||| |||

GTCAGAGTGTA CCAG
 A_
 GAM1965 C20orf124 5' TGGATGATGAGCCTGACGTGGA 24145 TG G _
 ACT AGTTTCATGT GG TC CATTTA
 ||||| || ||
 TCAAGGTGCA CC AG GTAGGT
 GT G TA
 GAM1965 C20orf126 3' TGAGGTCCCAGTATGAACTG 25136 T GT _
 TAGTT CATGTTGGG C CA
 |||| ||||| | ||
 GTCAA GTATGACCC G GT
 _ TG A
 GAM1965 C20orf162 5' TGGATGGACCTCGGGTGCAGCT 27920 T G
 G TAGTT CAT TTGGGGTCCATTTA
 |||| || |||||
 GTCGA GTG GGCTCCAGGTAGGT
 C _
 GAM1965 C20orf39 3' TGGATGGATTCTGGTGGATGAA 24370 _ TT
 TTCAT G GGGGTCCATTTA
 |||| | |||||
 AAGTA T TCTTAGGTAGGT
 GG GG
 GAM1965 C20orf43 3' TGGCCACTCTTGATGTGAGGC 30114 TG _ _
 GTTTCATGT GG GT CCA
 ||||| || || ||
 CGGAGTGTA TC CA GGT
 GT T CC
 GAM1965 C20orf60 3' GATCTCTAATGTGGAGGTG 27541 G _
 TA TTTTCATGTTGG GGTC
 || ||||| ||||
 GT GAGGTGTAATC CTAG
 G T
 GAM1965 C20orf60 3' TGGCACAGTCCTGGTGTGGTGC 27542 T TG TG _ _ TTTA
 TG GT TCA T GG GT CCA
 || || | || ||||
 CG GGT G CC CA GGT
 T GT GT TGA C A
 GAM1965 C20orf98 3' TAAATGGGCTCTCTCAGAGGC 35417 A TT
 GTTTC TG GGGGTCCATTTA
 |||| || |||||
 CGGAG AC TCTCGGGTAAAT
 _ TC
 GAM1965 C21orf100 3' TGAATGAACCAGCTATGGAATT 29649 _ GGTC
 G TAGTTTCAT GTTGG CATTTA
 ||||| |||| ||||
 GTTAAGGTA CGACC GTAAGT
 T AA_
 GAM1965 C21orf41 3' GAACCTAGAATGAGACTG 28731 G G
 TAGTTTCAT TTGGG TC
 ||||| |||| ||

GTCAGAGTA GATCC AG
 A A
 GAM1965 C21orf7 3' TAAATGAGATCATTAACGTGAA 21363 _ _
 ACTA AGTTTCATGTTGG GGTC CATTTA
 ||||| ||| |||||
 TCAAAGTGCAATT CTAG GTAAAT
 A A
 GAM1965 C5orf7 3' TGATTTCCAACATGAGGTT 31943 TT TC
 AG TCATGTTGGGG CA
 || ||||| ||
 TT AGTACAACCTT GT
 GG TA
 GAM1965 C6orf9 3' TGGGTGGGCACCTGAGAGATTA 22655 ATG TG _
 TAGTTTC T GG GTCCATTTA
 ||||| | |||||
 ATTAGAG A CC CGGGTGGGT
 _ GT A
 GAM1965 C8orf14 5' GGATGGAGGCAGGGGGCTG 27641 TT A GGGG
 TAGT C TGTT TCCATTT
 ||| ||| |||||
 GTCG G ACGG AGGTAGG
 GG G _
 GAM1965 C8orf7 3' TAAGTGGGTAAATTGAGAC 39649 T GG GT
 GTTTCA GTT G CCATTTA
 ||||| ||| | |||||
 CAGAGT TAA T GGTGAAT
 _ A TG
 GAM1965 C9orf7 3' TGGCCTCTCTGACCGTGAGGCT 19037 TT _ T TTTA
 G GTTTCATG GGGG CCA
 ||||| ||| |||
 CGGAGTGC CTCC GGT
 CAGTCT _ A
 GAM1965 CAPN13 3' GGGCCTTACGTGGGATTG 29381 TT T
 TAGT CATGT GGGGTCC
 ||| ||||| |||||
 GTTA GTGCA TTCCGGG
 GG _
 GAM1965 CBX6 3' TGGAGGGTCAGCCCCAACAGGG 15578 A _ A
 AGCTG TTTC TGTTGGGGT CC TTTA
 ||| ||||| || |||
 GAGG ACAACCCCG GG AGGT
 G ACT G
 GAM1965 CCR6 5' TGGGGCCCCGAGTGAGGCTG 10581 G G
 TAGTTTCAT TTGGG TCCA
 ||||| ||||| |||
 GTCGGAGTG GGCCC GGGT
 A G
 GAM1965 CCR6 3' TGGGTGGATCACTTGAGG 10582 T TGG
 TTTCA GT GGTCCATTTA
 ||||| || |||||

			GGAGT CA CTAGGTGGGT		
			T _		
GAM1965 CCR6	5'	TGGGGCCCCGGAGTGAGGCTG	25376	G	G
		TAGTTTCAT TTGGG TCCA			
		GTCGGAGTG GGCCC GGGT			
		A G			
GAM1965 CCR6	3'	TGGGTGGATCACTTGAGG	25377	T	TGG
		TTTCA GT GGTCCATTTA			
		GGAGT CA CTAGGTGGGT			
		T _			
GAM1965 CDV-1	5'	GATGTTCTGGCTGAGATTG	25541	T	TG TC
		TAGTTTCA GT GGG CATT			
		GTTAGAGT CG CTT GTAG			
		_ GT _			
GAM1965 CDV-1	5'	TGAGTTTCTTCAGGATGAAACT	25542	G	TCC
G		TAGTTTCAT TTGGGG ATTTA			
		GTCAAAGTA GACTTC TGAGT			
		G TT_			
GAM1965 CG012	5'	CCTTTGGTTCTGGCATGGCATT	40487	T	TG T TTTA
A		TAGT TCATGT GGG CCA			
		ATTA GGTACG CTT GGT			
		C GT _ TTCCG			
GAM1965 CHL1	3'	TATGACCCTGATTTTAATTGTG	13395	_____	TG CATTTA
AAATTA		CAT GT GGGTC			
		GTG TA CCCAG			
		TTAATTT GT T ATT			
GAM1965 CHRFAM7A	3'	AATGTCTAGCATGGGAACTA	45551	_	GTC
		TAGTTTC ATGTTGGG CATT			
		ATCAAGG TACGATCT GTAA			
		G _			
GAM1965 CHST3	3'	GATATGATTTTCAGCTTGAGC	10483	T	GG TC TTA
TG		TAGTTTCA GTTG G CAT			
		GTCGAGGT CGAC T GTA			
		T TT TA TAGG			
GAM1965 CLDN15	3'	TGAGCTCCCAGTAGGGGCTG	28794	TT A	_ TC
		TAGT C TGTTGGG G CA			
		GTCG G ATGACCC C GT			
		GG_ T GA			
GAM1965 CLECSF9	3'	TGAATGGATCTCACCAGA	15689	A	T
		TC TG TGGGGTCCATTTA			

			AG AC ACTCTAGGTAAGT		
			_ C		
GAM1965 CLIC5	3'	TGGAGAGCCCACATATGGGATT 18848	TT _ G_ TTTA		
G		AGT CATGT TGGG TCCA			
		TTA GTATA ACCC AGGT			
		GG C GAG A			
GAM1965 CNNM4	3'	TGGGTGCAGCAGGAGCTG 21429	A GGG		
		TAGTTTC TGTTG TCCA			
		GTCGAGG ACGAC GGGT			
		_ GT_			
GAM1965 CNOT3	5'	TGTTCTCAGTATGGGGCTG 15844	TT TC		
		TAGT CATGTTGGGG CA			
		GTCG GTATGACTCC GT			
		GG TT			
GAM1965 CSMD1	3'	TGGGATCAACAGAACTG 36195	A GG		
		TAGTTTC TGTTGG TCCA			
		GTCAAAG ACAACT GGGT			
		_ A_			
GAM1965 DAMS	5'	TGGATCCATAAATGTGAACTG 22544	G_		
		TAGTTTCATGTT GGGTCCA			
		GTCAAAGTGTA CCTAGGT			
		ATA			
GAM1965 DCAMKL1	3'	TGGACCGTGTGAAGCTA 11118	TG TGG		
		TAGTTTCA T GGTCCA			
		ATCGAAGT G CCAGGT			
		GT _			
GAM1965 DEGS	3'	TGGGTGGATCACCTGAGG 9770	TGTT _		
		TTTCA GG GGTCCATTTA			
		GGAGT CC CTAGGTGGGT			
		_ A			
GAM1965 DIM1	3'	TGGAGCACCTCTGAGATGGAAT 13527	G TG _ TTTA		
TG		GTTTCAT T GGG TCCA			
		TAAGGTA A CTC AGGT			
		G GT CACG A			
GAM1965 DJ122O8.2	3'	TAGGTGGATCACTTGAGG 21703	T TGG		
		TTTCA GT GGTCCATTTA			
		GGAGT CA CTAGGTGGAT			
		T _			
GAM1965 DKFZP434A043	3'	AAATCTTTCCTGCATGAAGCTA 17698	T TCC A		
		TAGTTTCATGT GGGG ATTT			

ATCGAAGTACG CCTT TAAA
 T TC_ A
 GAM1965 DKFZP434A043 3' TGGGCTTACCCTTGACAGGAAC 17705 A _ _ TTTA
 TG TTTC TGTT GGG GTCCA
 |||| ||| ||||
 AAGG ACAG CCC CGGGT
 _ TT ATT A
 GAM1965 DKFZp434B0417 3' TGAATGGAATGCATGCGACTG 15031 T TGGGG
 TAGTT CATGT TCCATTTA
 |||| |||| |||||
 GTCAG GTACG AGGTAAGT
 C TA__
 GAM1965 DKFZP434B1727 3' TAGGTATCAAGTCAACATGAAA 25831 _ _ ATTTA
 TTG TTTTCATGTTGG GGT CC
 ||||| ||| ||
 AAAGTACA ACT CTA GG
 GAA T AT A
 GAM1965 DKFZP434D193 3' GGAACCTGGTATAAACTA 42853 C TT G
 TAGTTT ATG GGG TCC
 |||| ||| ||| ||
 ATCAAA TAT TCC AGG
 A GG A
 GAM1965 DKFZp434E0519 3' TGATGTGCTTTGATGTGAGTCT 25984 T TG TC TA
 G TAG TTCATGT GGG CATT
 || ||||| ||| ||||
 GTC GAGTGTA TTC GTAG
 T GT GT T
 GAM1965 DKFZP434F0318 3' TGGCTTGGCCTGAGACTG 25145 T TG GT
 TAGTTTCA GT GG CCA
 ||||| || || |||
 GTCAGAGT CG TC GGT
 C GT _
 GAM1965 DKFZP434F0318 3' AGTCCTGCTCCCTCACATGAAG 25138 T TC TTTA
 CTG TAGTTTCATGT GGGG CA
 ||||| |||| ||| ||
 GTCGAAGTACA TCCC GT
 C TC CCTGAA
 GAM1965 DKFZp434F054 5' TGGAAGTCAGACATGAAACTG 26003 _ GG
 TAGTTTCATGT TGG TCCA
 ||||| ||| ||||
 GTCAAAGTACA ACT AGGT
 G GA
 GAM1965 DKFZp434G171 3' TGGGTGGATCACCTGAGG 38778 TGTT _
 TTTCA GG GGTCCATTTA
 |||| || ||||| ||||
 GGAGT CC CTAGGTGGGT
 _ A
 GAM1965 DKFZP434H204 5' TGCATCCGCAGCGTGGGGCTG 33017 TT _ C
 TAGT CATGTTG GGGT CA
 ||| ||||| |||| ||

GTCG GTGCGAC CCTA GT
 GG G C
 GAM1965 DKFZP434I1735 3' TAAATATGACTCTAGTGTAAT 42422 C TG C_
 TA TAGTTT A TTGGGGTC ATTTA
 ||||| | ||||| ||||
 ATTAAA T GATCTCAG TAAAT
 _GT TA
 GAM1965 DKFZP434K1210 3' TAGGTGGGCTTTTAGAACTA 19102 ATGTT
 TAGTTTC GGGGTCCATTTA
 ||||| |||||
 ATCAAAG TTTCGGGTGGAT
 AT__
 GAM1965 DKFZP434L187 5' TGGATGGATCTCTTGAGG 34125 TGTT
 TTTCA GGGGTCCATTTA
 |||| |||||
 GGAGT CTCTAGGTAGGT
 T__
 GAM1965 DKFZP434O047 5' TGGGTGGATCCTAGGTGCAT 17870 ____
 ATGT TGGGGTCCATTTA
 ||| |||||
 TACG ATCCTAGGTGGGT
 TGG
 GAM1965 DKFZP434P0111 3' ATGGCCACATTTTGGCATGAG 33451 ____ _ T TTTA
 GGTG TCATGT TG GGG CCA
 ||||| || |||
 AGTACG AC CCC GGT
 GTTTT A _ AT
 GAM1965 DKFZP547L112 3' TGGATGGATTTGATGTAAAATT 33060 C TG G
 A TAGTTT ATGT GG TCCATTTA
 ||||| ||| || |||||
 ATTAAA TGTA TT AGGTAGGT
 A GT _
 GAM1965 DKFZP564B1162 3' TGTTTCCCTCTGAGTGAACTG 25340 GTT__ TC
 TAGTTTCAT GGGG CA
 ||||| ||| ||
 GTCAAAGTG CCCT GT
 AGTCT TT
 GAM1965 DKFZP564F013 3' TGGTACACTCTAGTGTAGGCTA 45204 C TG ____
 TAGTTT A TTGGGGT CCA
 ||||| | ||||| |||
 ATCGGA T GATCTCA GGT
 _GT CAT
 GAM1965 DKFZP564I052 3' TAAATGGGTGAGATGGAAC 33140 G GGG
 GTTTCAT TTG TCCATTTA
 ||||| ||| |||||
 CAAGGTA AGT GGGTAAAT
 G ____
 GAM1965 DKFZP564I052 3' TGGGTGGATCACTTGAAG 33141 T TGG
 TTTCA GT GGTCCATTTA
 ||||| || |||||

	GAAGT CA CTAGGTGGGT	
	T ____	
GAM1965 DKFZP564I122 3'	TGGGTGACAGTGTGAGACT 31647	TG GG
	AGTTTCA TTG GTCCA	
	TCAGAGT GAC TGGGT	
	GT AG	
GAM1965 DKFZP564M182 3'	TGGGTGACAGTGTGAGATT 38221	TG GG
	AGTTTCA TTG GTCCA	
	TTAGAGT GAC TGGGT	
	GT AG	
GAM1965 DKFZP564O1863 3'	TGAATGGGGTGGATGAGACTG 34043	GTTGGGG
	TAGTTTCAT TCCATTTA	
	GTCAGAGTA GGGTAAGT	
	GGTG____	
GAM1965 DKFZP566F2124 3'	TAGATGGACTTTTTGGTAAAT 17888	C GTT
	GTTT AT GGGGTCCATTTA	
	TAAA TG TTTCAGGTAGAT	
	_ GTT	
GAM1965 DKFZP566F2124 3'	TGAATGGATTTTAAAAATAAT 17890	TCATG
T	AGTT TTGGGGTCCATTTA	
	TTAA AATTTTAGGTAAGT	
	TAAAA	
GAM1965 DKFZP586D2223 3'	TGGGTGGATCACCTGAGG 20646	TGTT _
	TTTCA GG GGTCCATTTA	
	GGAGT CC CTAGGTGGGT	
	____ A	
GAM1965 DKFZp586I021 3'	TGAGTGGGGGGGCATGGGGC 26030	TT GGGG
	GT CATGTT TCCATTTA	
	CG GTACGG GGGTGAGT	
	GG GG__	
GAM1965 DKFZP727M111 5'	TGGCCCCTGACGTGGACCTG 17801	T TG T
	TAG TTCATGT GGG CCA	
	GTC AGGTGCA CCC GGT	
	C GT C	
GAM1965 DKFZp761F2014 3'	TGGATGGGAGTGTGGGGCTG 21464	TT TG GGGG
	TAGT CA TT TCCATTTA	
	GTCG GT GA GGGTAGGT	
	GG GT ____	
GAM1965 DKFZP761F241 3'	TGAGTGGGTCCCAGCTGTGTGA 25479	T _ GT
TT	AGTT CAT GTTGGG CCATTTA	

TTAG GTG CGACCC GGTGAGT
 T T TG
 GAM1965 DKFZp761G0313 3' TAGATGGTACCTGGCATGGACT 32743 T TG GT
 G TAGTT CATGT GG CCATTTA
 ||||| ||||| || |||||
 GTCAG GTACG CC GGTAGAT
 _ GT AT
 GAM1965 DKFZP761G1913 3' TGGGTGGATCACTTGAGG 25547 T TGG
 TTTCA GT GGTCCATTTA
 ||||| || |||||
 GGAGT CA CTAGGTGGGT
 T _
 GAM1965 DKFZp761G2113 3' TGAATGGGTCCGGTGCTTGGAG 34645 T TG_ GT
 CTG TAGTTTCA GT GG CCATTTA
 ||||| || || |||||
 GTCGAGGT CG CC GGTAAGT
 T TGG TG
 GAM1965 DKFZp761O0113 5' TAGATGGATTTTATATGA 20448 T
 TCATGT GGGGTCCATTTA
 ||||| |||||
 AGTATA TTTTAGGTAGAT
 _
 GAM1965 DKFZp761P1010 3' TGAGCCCTACATGTGGGGTTG 20480 TT _ TC
 TAG TCATGT TGGGG CA
 ||| ||||| ||||| ||
 GTT GGTGTA ATCCC GT
 GG C GA
 GAM1965 DKFZp762L0311 3' TGCACCTCCAGCAGAGGCTA 20801 A C
 TAGTTTC TGTTGGGGT CA
 ||||| ||||| ||
 ATCGGAG ACGACCTCA GT
 C
 GAM1965 DRF1 3' TGGGTGGACCACTTGAGGC 24750 T TGG
 GTTTCA GT GGTCCATTTA
 ||||| || |||||
 CGGAGT CA CCAGGTGGGT
 T _
 GAM1965 DSCR1L1 3' GATTATTGGGATGAAGCTA 12429 G TG_
 TAGTTTCAT T G GGTC
 ||||| || |||||
 ATCGAAGTA G T TTAG
 G GT A
 GAM1965 EFNA5 3' TAAATGGACTCCAGATGAAA 7687 G
 TTTTCAT TTGGGGTCCATTTA
 ||||| |||||
 AAAGTA GACCTCAGGTAAAT
 _
 GAM1965 EML4 3' TGGGTGGGGTTATGAAATTG 21146 TTGG G
 TAGTTTCATG G TCCATTTA
 ||||| || |||||

		GTAAAGTAT T GGGTGGGT	
		____ G	
GAM1965 ENAH	3'	TACGTGTTCTGAATGAAGCTG 20128	G TG TC TTA
		TAGTTTCAT T GGG CAT	
		I	
		GTCGAAGTA A CCT GTG	
		_ GT T_ CATA	
GAM1965 ENPP4	3'	TGAGTGGATTTTATATAGGAT 17241	TC T
		GTT ATGT GGGGTCCATTTA	
		TAG TATA TTTTAGGTGAGT	
		GA _	
GAM1965 EPLIN	3'	AAGCAGGTATCCCAGCATGAAA 18495	_ ATTTA
T		GTTTCATGTTGGGGT CC	
		TAAAGTACGACCCTA GG	
		T ACGAAT	
GAM1965 ERMAP	3'	AAGTGGATACATAAGATTA 20604	C TGGG
		TAGTTT ATGT GTCCATTT	
		ATTAGA TACA TAGGTGAA	
		A _____	
GAM1965 ET	3'	TGGGTGGATCGCCTGAGG 23605	TGTT _
		TTTCA GG GGTCCATTTA	
		GGAGT CC CTAGGTGGGT	
		____ G	
GAM1965 FADS2	3'	GGACCAGGGTGGAGCTG 10468	G GG
		TAGTTTCAT TT GGTCC	
		GTCGAGGTG GA CCAGG	
		G _	
GAM1965 FBX30	3'	TAGATGGGTACCAGGTGGGGTT 27043	TT G GG
A		TAG TCAT TTGG TCCATTTA	
		ATT GGTG GACC GGGTAGAT	
		GG _ AT	
GAM1965 FBXO8	3'	TATTTGATTCTGATCTGAAACT 14467	T TG CATTTA
A		TAGTTTCA GT GGGTC	
		ATCAAAGT TA CTTAG	
		C GT TTTAT	
GAM1965 FGD3	3'	TGAGTGGCAGGCGCATGAGATT 36093	TGGG T
		AGTTTCATGT G CCATTTA	
		TTAGAGTACG C GGTGAGT	
		CGGA _	
GAM1965 FLJ00001	3'	GCCCTGGTTGTGAGATTG 39781	_ TT
		TAGTTTCAT G GGGGT	

	GTTAGAGTG T TCCCG		
	T GG		
GAM1965 FLJ00001	3' GGACCTTGTTCATGGGACTG 39784	TT	T
	TAGT CATG TGGGGTCC		
	GTCA GTAC GTTCCAGG		
	GG T		
GAM1965 FLJ00007	3' GGCCCCCAGCCTGAGACTG 35311	T	T
	TAGTTTCA GTTGGGG CC		
	GTCAGAGT CGACCCC GG		
	C C		
GAM1965 FLJ00007	3' TGATGGGAAGATGAGATTA 35314	G	GGGG TA
	TAGTTTCAT TT TCCATT		
	ATTAGAGTA AA GGGTAG		
	G ____ TG		
GAM1965 FLJ10290	3' TGGTGTCTGGCATGAAATTA 19799	TG	GT
	TAGTTTCATGT GG CCA		
	ATTAAGTACG CT GGT		
	GT GT		
GAM1965 FLJ10420	3' TGGATGCTGTTGTCATGGAGCT 19859	TT__	G TTTA
G	AGTTTCATG GG GTCCA		
	TCGAGGTAC TC TAGGT		
	TGTTG G A		
GAM1965 FLJ10460	3' TAGGTGGGCAGATCATGAGG 19868	TTGGG	
	TTTCATG GTCCATTTA		
	GGAGTAC CGGGTGGAT		
	TAGA_		
GAM1965 FLJ10460	3' TGGGTGGATCACCTGAGG 19870	TGTT	_
	TTTCA GG GGTCCATTTA		
	GGAGT CC CTAGGTGGGT		
	____ A		
GAM1965 FLJ10508	3' TGGATGGATCAAGTGAAG 19895	GTTGG	
	TTTCAT GGTCCATTTA		
	GAAGTG CTAGGTAGGT		
	AA__		
GAM1965 FLJ10520	3' TAAAGCCTTCCCCATGTGAAGC 19907	T	TCCA_
TG	TAGTTTCATGT GGGG TTTA		
	GTCGAAGTGTA CCCC AAAT		
	_ TTCCG		
GAM1965 FLJ10535	3' TGGCCCAGAGTGGAGCTA 19923	GTTG	T
	TAGTTTCAT GGG CCA		

		ATCGAGGTG	CCC GGT		
		AGA_ _			
GAM1965	FLJ10539	3'	TGGGTTGTTTCCAGTTTGGGGC	19925	TT TG ____ TTTA
		TG	GT CA TTGGGG TCCA		
			CG GT GACCTT GGGT		
			GG TT TGTT A		
GAM1965	FLJ10547	3'	TGAGTGGATCACCTGAGG	19932	TGTT _
			TTTCA GG GGTCCATTTA		
			GGAGT CC CTAGGTGAGT		
			____ A		
GAM1965	FLJ10579	5'	TGAGTGGATCTCCTGCCAGGC	19947	CAT T _
			GTTT GT GG GGTCCATTTA		
			CGGA CG CC CTAGGTGAGT		
			C_ T T		
GAM1965	FLJ10619	3'	GGAATAGCCCTTAACATGAAAT	19968	_ CC A
		T	AGTTTCATGTTG GGGT ATTT		
			TTAAAGTACAAT CCGG TAAG		
			T A_ GG		
GAM1965	FLJ10704	3'	TGGATTCTTGACATGTAATTG	20036	T TG _
			TAGTT CATGT GGG TCCA		
			GTTAA GTACA TCT AGGT		
			T GT T		
GAM1965	FLJ10895	3'	GCTTTGTGACATGAAGCTA	21159	_
			TAGTTTCATGTT GGGGT		
			ATCGAAGTACAG TTTCG		
			TG		
GAM1965	FLJ10904	5'	TGGGCTGACTGGGGCTG	20241	TT T GG
			TAGT CA GTT GGTCCA		
			GTCG GT CAG TCGGGT		
			GG _ _		
GAM1965	FLJ10922	3'	TGACCCCCAGCATGGGATTG	20258	TT TC
			TAGT CATGTTGGGG CA		
			GTTA GTACGACCCC GT		
			GG CA		
GAM1965	FLJ10936	5'	CCCGTGGGCTCCGGCGTGAGGC	20269	TTA
			GTTTCATGTTGGGGTCCAT		
			CGGAGTGCGGCCTCGGGTG		
			CCCC		
GAM1965	FLJ11210	3'	TGAGTGGGCTTCACCAGCTA	29976	TTCA T
			TAGT TG TGGGGTCCATTTA		

			ATCG	AC	ACTTCGGGTGAGT			
			___	C				
GAM1965	FLJ11539	3'	TGGATGGACTCCTGCAGGC	24089	TCA	T		
			GTT TGT GGGGTCCATTTA					
			CGG ACG CCTCAGGTAGGT					
			___	T				
GAM1965	FLJ12057	3'	GGCTCCCTGGTAGAAGCTG	24128	A	TT	T_	
			TAGTTTC TG GGGG CC					
			GTCGAAG AT TCCC GG					
			_	GG	TC			
GAM1965	FLJ12363	3'	GCCTTAACAGTGGAGTTG	25869	GT	_		
			TA TTCA TGTTGGGGT					
			GT AGGT ACAATTCCG					
			TG G					
GAM1965	FLJ12363	3'	TGGGTGGATCACCTGAGG	25870	TGTT	_		
			TTTCA GG GGTCCATTTA					
			GGAGT CC CTAGGTGGGT					
			___	A				
GAM1965	FLJ12425	3'	TGGCTTTTCCGATATGGAAC	41562	T	_		
			GTTTCATGTTGGGG CCA					
			CAAGGTATAGCCTT GGT					
			TTC					
GAM1965	FLJ12425	3'	TGGGTGGGTTTTCTCTGCAGAC	41563	TCA	T	___	
	TA		AGTT TGT GGGG TCCATTTA					
			TCAG ACG CTCT GGGTGGGT					
			___	T	TTT			
GAM1965	FLJ12547	3'	TCAAAGGCCTCATTGTGGAGCT	24550	GT	CATTTA		
	G		TAGTTTCAT TGGGGTC					
			GTCGAGGTG ACTCCGG					
			TT	AACT				
GAM1965	FLJ12552	3'	AAAATCATCCTTGACATGAAAC	23113	TG	TCC	A	
			GTTTCATGT GGG ATTT					
			CAAAGTACA TCC TAAA					
			GT TAC AT					
GAM1965	FLJ12587	3'	TGGTGCCCTGACAGGGACTG	22854	TT	A	TG	_
			TAGT C TGT GGGT CCA					
			GTCA G ACA CCCG GGT					
			GG_	GT	T			
GAM1965	FLJ12592	3'	TGGGTGACCGAGTGAGACTG	25876	G	GG_		
			TAGTTTCAT TTGG TCCA					

GTCAGAGTG AGCC GGGT
 _ AGT
 GAM1965 FLJ12687 3' TGAGTGATCATCAGATGAGATT 24448 G _ C
 A TAGTTTCAT TTGG GGTC ATTGA
 ||||| ||| ||| ||||
 ATTAGAGTA GACT CTAG TGAGT
 _ A _
 GAM1965 FLJ12747 3' TGGCTTTTAATATGAACTG 25882 T T
 TAGTT CATGTTGGGG CCA
 |||| ||||| |||
 GTCAA GTATAATTTT GGT
 _ C
 GAM1965 FLJ12770 3' GAACTGGCTTTGACCATGAAAC 25886 _TG T TTGA
 TG TAGTTTCATG T GGG CCA
 ||||| | ||| |||
 GTCAAAGTAC A TTC GGT
 C GT _ CAAGG
 GAM1965 FLJ12770 3' TGGTTAATCCTGCATGGGATTA 25887 TT T GT_
 TAGT CATGT GGG CCA
 ||| |||| ||| |||
 ATTA GTACG CCT GGT
 GG T AATT
 GAM1965 FLJ12903 3' TGTCAGTTTCAATTATGAAACT 22985 _ GG CCATTGA
 G TAGTTTCATG TTGG T
 ||||| ||| |
 GTCAAAGTAT AACT G
 T TT ACTGT
 GAM1965 FLJ12994 3' TAAATGTTGATTTTAATATGGA 23133 _
 GCTA AGTTTCATGTTGGGGTC CATTGA
 ||||| ||||| |||||
 TCGAGGTATAATTTTAG GTAAAT
 TT
 GAM1965 FLJ12994 3' TAAATGTTGATTTTAATATGGA 37975 _
 GCTA AGTTTCATGTTGGGGTC CATTGA
 ||||| ||||| |||||
 TCGAGGTATAATTTTAG GTAAAT
 TT
 GAM1965 FLJ13162 3' TGGGTGGATCACCTGAAG 24575 TGTT _
 TTTCA GG GGTCCATTGA
 |||| || ||||| |||||
 GAAGT CC CTAGGTGGGT
 _ A
 GAM1965 FLJ13612 3' TAATGGTGGGTCTTAATGGAGG 24865 A GT TA
 CTG TAGTTTC TGTTGGG CCATT
 ||||| ||||| |||||
 GTCGGAG GTAATTC GGTGG
 _ TG TAATG
 GAM1965 FLJ13614 3' TGAATGGATTATTGTATGAGCT 29150 T TTGG
 A TAGTT CATG GGTCCATTGA
 |||| ||| ||||| |||||

ATCGA GTAT TTAGGTAAGT
 _ GTTA
 GAM1965 FLJ13646 3' TGGGTTCTACGACATTGAAGTT 23816 GT _ _ GG TTTA
 G A TTCA TGTTG G TCCA
 | ||| |||| | ||||
 T AAGT ACAGC C GGGT
 TG T ATTT A
 GAM1965 FLJ13693 3' TGGATGGCCCTGCCCTGACTGG 24189 TT T TG ____
 GGCTG CA GT GGGT CCATTTA
 || || ||| |||||
 GT CA CCCG GGTAGGT
 GG _ GT TCCC
 GAM1965 FLJ13902 3' GGAGATGGCCTCAGCTGTGGGG 23952 TT _ T A
 CTG AGT CAT GTTGGGG CCATT
 ||| ||| ||||| |||||
 TCG GTG CGACTCC GGTAGA
 GG T _ GGA
 GAM1965 FLJ13952 3' TGGGTGGATCACCTGAGG 24176 TGTT _
 TTTCA GG GGTCCATTTA
 |||| | |||||
 GGAGT CC CTAGGTGGGT
 _ A
 GAM1965 FLJ14054 3' TGAGTGGATGCAGACATGAGAG 23787 G GGG
 TA TA TTTCATGTT GTCCATTTA
 || ||||| |||||
 AT AGAGTACAG TAGGTGAGT
 G ACG
 GAM1965 FLJ14084 3' TGAAGAGAATCCTGATATGAAA 22287 TG _ CA
 C GTTTCATGT GGGT C TTTA
 ||||| ||| | |||
 CAAAGTATA CCTA G AAGT
 GT A AG
 GAM1965 FLJ14356 5' TGAGTGGGTTCCCTCGTG GGG 25154 TT TT GG
 T CATG GG TCCATTTA
 | ||| || |||||
 G GTGC CC GGGTGAGT
 GG TC TT
 GAM1965 FLJ14431 3' GGGAATCACATTTCAACATGAG 26527 GG CC_ A
 ATT AGTTTCATGTTG GT ATTT
 ||||| || |||
 TTAGAGTACAAC TA TAAG
 TT CAC GGT
 GAM1965 FLJ14525 3' GATTATCAACAATGGGGCTA 26550 TT _ _
 TAGT CAT GTTGG GGTC
 ||| ||| ||| |||
 ATCG GTA CAACT TTAG
 GG A A
 GAM1965 FLJ14751 3' TAGGTGGAAAACATGGAATT 26611 GGGG
 AGTTTCATGTT TCCATTTA
 ||||| |||||

		TTAAGGTACAA AGGTGGAT		
		A___		
GAM1965	FLJ14871	3' TGGGACTCGGCTGGAGCTG 26653	T	GT
		TAGTTTCA GTTGGG CCA		
		GTCGAGGT CGGCTC GGT		
		_ AG		
GAM1965	FLJ14888	3' TGAGTGGGTCTCATGGGAAC 26656	ATGT	GT
		GTTTC TGGG CCATTTA		
		CAAGG ACTC GGTGAGT		
		GT__ TG		
GAM1965	FLJ20034	3' TGGCCTCGGGGTGGGATTG 19138	TT G	T
		TAGT CAT TTGGGG CCA		
		GTTA GTG GGCTCC GGT		
		GG G _		
GAM1965	FLJ20139	3' GATAGTAGATATGAGACTA 19235	GGG_	
		TAGTTTCATGTT GTC		
		ATCAGAGTATAG TAG		
		ATGA		
GAM1965	FLJ20150	3' TGGCCCCCTCTGACATAAACTG 19244	C _	T
		TAGTTT ATGTT GGGG CCA		
		GTCAAA TACAG CCCC GGT		
		_ TCT C		
GAM1965	FLJ20232	5' TGGATGGGCTCCCCACGACTG 21089	TCAT T	_
		TAGTT GT GGG GTCCATTTA		
		GTCAG CA CCC CGGGTAGGT		
		_ C T		
GAM1965	FLJ20308	3' TAAGTGGGGCTGTATCAGGCTG 33198	C TTG	G
		TAGTTT ATG GG TCCATTTA		
		GTCGGA TAT TC GGGTGAAT		
		C G_ G		
GAM1965	FLJ20343	3' TACCAGCATCCAGCATGAAGTT 19400	GT	_ CCATTTA
	G	TA TTCATGTTGGG GT		
		GT AAGTACGACCT CG		
		TG A ACCAT		
GAM1965	FLJ20413	3' TGCACTCCAGCGTGGGCTA 19454	T	C
		TAGTT CATGTTGGGGT CA		
		ATCGG GTGCGACCTCA GT		
		_ C		
GAM1965	FLJ20511	5' TAGGGTCCTGTCCGGCTTGGGG 19530	TT T	_ T ATTTA
	CTG	GT CA GTTGG GG CC		

	CG GT CGGCC CC GG		
	GG T TGT T GAT		
GAM1965 FLJ20666 5'	TACTGATTTTCAGTACTGAGATT 19584	_	GG CATTTA
A	TAGTTTCA TGTTG GTC		
	ATTAGAGT ATGAC TAG		
	C TT TCAT		
GAM1965 FLJ20686 3'	TGGGTGGATCACTTGAGGC 19596	T	TGG
	GTTTCA GT GGTCCATTTA		
	CGGAGT CA CTAGGTGGGT		
	T _		
GAM1965 FLJ20689 3'	TGAGTTGAGACCTGTATGGAAT 19600	TT	GG C
TG	TAGTTTCATG GG TC ATTTA		
	GTTAAGGTAT CC AG TGAGT		
	GT AG T		
GAM1965 FLJ20689 3'	TGAGTTGAGACCTGTATGGAAT 19704	TT	GG C
TG	TAGTTTCATG GG TC ATTTA		
	GTTAAGGTAT CC AG TGAGT		
	GT AG T		
GAM1965 FLJ20986 5'	TGGTGTCTAGCAGGAGACTA 23727	A	GT_
	TAGTTTC TGTTGGG CCA		
	ATCAGAG ACGATCC GGT		
	G TGT		
GAM1965 FLJ22004 3'	TATAGCCCAGCTTGATAATGGA 24817	_____	GTCCATTTA
ACTA	TTCAT GTTGGG		
	AGGTA CGACCC		
	ATAGTT GAT ATT		
GAM1965 FLJ22301 5'	GGGATGAGCTCCAGCATGGGG 24242	TT	TC A
	T CATGTTGGGG CATT		
	G GTACGACCTC GTAGG		
	GG GA GT		
GAM1965 FLJ22761 5'	GAGTTCGACAGGGAGCTG 24772	A	G
	TAGTTTC TGTTGGG TC		
	GTCGAGG ACAGCTT AG		
	G G		
GAM1965 FLJ23040 3'	TGGGCCTCCCAGTGCTGGAATT 24809	_GT _	TTTA
A	AGTTTCA T TGGG GTCCA		
	TTAAGGT G ACCC CGGGT		
	C TG TC A		
GAM1965 FLJ23119 3'	CCCCAGGTCTCAGATGGAATTA 23949	G	GT CATTTA
	TAGTTTCAT TTGGG C		

ATTAAGGTA GACTC G
 _ TG ACCCCT
 GAM1965 FLJ23311 3' TGGGGATTTGTTCAATGTGAAA 23993 ____ ATTTA
 T GTTTCATGTTGGG GTCC
 ||||| |||
 TAAAGTGTAAC TT TAGG
 GTT GGT
 GAM1965 FLJ23342 3' TGAGTTTCATATGAAATTG 23899 T GG TC
 TAGTTTCATGT G G CA
 ||||| | | ||
 GTTAAAGTATA C T GT
 _ TT GA
 GAM1965 FLJ23462 3' TAGATAACTCCAGCAGGAAACT 24268 A CC
 G TAGTTTC TGTTGGGGT ATTTA
 ||||| ||||| |||||
 GTCAAAG ACGACCTCA TAGAT
 G A_
 GAM1965 FLJ23499 3' TGGGTGGATCACCTGAGG 23008 TGTT _
 TTTCA GG GGTCCATTTA
 |||| |||||
 GGAGT CC CTAGGTGGGT
 _ A
 GAM1965 FLJ23556 3' TGGATGCTGGAGTAAGTGGAAT 24321 G__ TG G TTTA
 TG GTTTCAT T G GTCCA
 ||||| | | |||||
 TAAGGTG G C TAGGT
 AATGA GT G A
 GAM1965 FLJ23590 3' TATACCCACTTACTAATGTGGA 23942 ____ CCATTTA
 ATTA TTCATGTTG GGGT
 ||||| |||
 AGGTGTAAT CCA
 CATTCA T ATT
 GAM1965 FLJ25415 3' GAATCAACAGTTGAAACTG 29534 _ GG
 TAGTTTCA TGTTGG TC
 ||||| ||||| ||
 GTCAAAGT ACAACT AG
 TG A_
 GAM1965 FLJ30294 3' GATCCCAGCATAAAGTTA 29450 GT C
 TA TT ATGTTGGGGTC
 || || |||||
 AT AA TACGACCCTAG
 TG A
 GAM1965 FLJ30567 3' TGGGTAGCTTCAGGATGGGGCT 29634 TT G _ TTTA
 G AGT CAT TTGGGGT CCA
 || || ||||| ||
 TCG GTA GACTTCG GGT
 GG G ATG A
 GAM1965 FLJ31890 3' ATGGGCCCGATTCCAGCATGG 43893 T _ TTTA
 GGC CATGT TGGGGTCCA
 |||| |||||

		GTACG GCCCCGGGT	
		G ACCTTA AT	
GAM1965	FLJ32865	3' GAGTCACAGAAATGGAGCTA 29428	G _ G
		TAGTTTCAT TTG GG TC	
		ATCGAGGTA GAC CT AG	
		A A G	
GAM1965	FLJ32894	3' TGGCCTACTCAACATGAAG 29486	GT__
		TTTCATGTTGGG CCA	
		GAAGTACAAC TC GGT	
		ATCC	
GAM1965	FLJ33069	3' TGATGGTTAATATGAAA 29476	GGT TA
		TTTCATGTTGG CCATT	
		AAAGTATAATT GGTAG	
		__ TA	
GAM1965	FOXH1	5' GGAGCTTGGCATGGGCTA 10012	T TG G
		TAGTT CATGT GG TCC	
		ATCGG GTACG TC AGG	
		_ GT G	
GAM1965	FRSB	3' TGGTGTCTGTGTGTGAAGCTG 12247	TG_ GT
		TAGTTTCA T TGGG CCA	
		GTCGAAGT G GTCT GGT	
		GT T GT	
GAM1965	GAB3	3' GTCCTGCATTCTGACTGAGATT 27929	T TG C TTTA
	G	TAGTTTCA GT GGGT CA	
		GTTAGAGT CA CTTA GT	
		_ GT C CCTGG	
GAM1965	GAPCENA	3' TGGGTGACTTGACTGTGAGACT 14496	_ TG GT_ ATTTA
	G	TAGTTTCAT GT GG CC	
		GTCAGAGTG CA TC GG	
		T GT AGT GT	
GAM1965	GDAP1L1	3' GGTCTCAAGATGGAAGT 23466	G GT
		TAGTTTCAT TTGGG C	
		GTCAAGGTA AACTC G	
		G TG	
GAM1965	GENX-3414	3' TGAGTGGGGTTGGGCATAGGCT 10060	C G G
	G	TAGTTT ATGTT GG TCCATTTA	
		GTCGGA TACGG TT GGGTGAGT	
		_ G G	
GAM1965	GGA2	3' TGGGTGGGTTTCTACCTTTGAA 28927	T__ T GT
	ACTG	AGTTTCA GT GGG CCATTTA	

			TCAAAGT CA CTT GGTGGGT		
			TTC T TG		
GAM1965	GGA2	3'	TGGGTGGGTTTCTACCTTTGAA 17405	T__ T GT	
	ACTG		AGTTTCA GT GGG CCATTTA		
			TCAAAGT CA CTT GGTGGGT		
			TTC T TG		
GAM1965	GMEB2	3'	TGGTTTCGGCGTGATGTTG 14742	TT GG T	
			TAG TCATGTTG G CCA		
			GTT AGTGCGGC T GGT		
			GT TT _		
GAM1965	GOLGA2LY	5'	TGGCATTCCAGCAGGAGCTA 32145	A _	
			TAGTTTC TGTTGGGGT CCA		
			ATCGAGG ACGACCTTA GGT		
			_ C		
GAM1965	GP5	3'	TGGAGCAGTTAACATGTGACTG 10820	T G__	
			TAGTT CATGTTGG G TCCA		
			GTCAG GTACAATT C AGGT		
			T GA G		
GAM1965	GPS2	5'	TGGATGGAGAGGATATGGGGC 10828	TT GGGG	
			GT CATGTT TCCATTTA		
			CG GTATAG AGGTAGGT		
			GG GAG_		
GAM1965	GPS2	5'	GACTTTGCCAACATGGAGCTG 42149	___	
			TAGTTTCATGTTGG GGTC		
			GTCGAGGTACAACC TCAG		
			GTT		
GAM1965	GPS2	5'	TGGATGAATTCAACAATGGGGT 42150	TT _ _ TTTA	
	TG		G TCAT GTTGGG GTCCA		
			T GGTA CAACTT TAGGT		
			GG A AAG A		
GAM1965	GRIN3A	5'	TAAGTGGGTCTCGCCTGGGC 28538	T T T GT	
			GTT CA GT GGG CCATTTA		
			CGG GT CG CTC GGTGAAT		
			_ C _ TG		
GAM1965	GTPBP2	3'	TGGCCCAGGCGTGGGGCTA 21174	TT TG T	
			TAGT CATGT GGG CCA		
			ATCG GTGCG CCC GGT		
			GG GA _		
GAM1965	GTSE1	3'	TAAATGGACTTATTGAAGC 18547	TGTTG	
			GTTTCA GGGTCCATTTA		

		CGAAGT TTCAGGTAAAT	
		TA__	
GAM1965 H326	3'	TAGGTGGGGCAGGCTGGGGCTG 17940	TT T GGGG
		TAGT CA GTT TCCATTTA	
		GTCG GT CGG GGGTGGAT	
		GG _ ACG_	
GAM1965 HCA127	3'	GATGTCCTGATGTGAAAC 20757	TG TC
		GTTTCATGT GGG CATT	
		CAAAGTGTA CCT GTAG	
		GT _	
GAM1965 HIG2	3'	TGGGTGGATCACCTGAGG 14979	TGTT _
		TTTCA GG GGTCCATTTA	
		GGAGT CC CTAGGTGGGT	
		_ A	
GAM1965 HSPC065	3'	TGGCAGCCCCAGTGTGCAACTA 15456	T TG _
		TAGTT CA TTGGGGT CCA	
		ATCAA GT GACCCCG GGT	
		C GT AC	
GAM1965 HT002	3'	GAATGGAGAGCATGGA 15280	GGGG
		TTCATGTT TCCATT	
		AGGTACGA AGGTAAG	
		G__	
GAM1965 HT007	5'	TGGTGTTTCGGGTATGAGGCTG 20543	G GG _
		TAGTTTCATGTT G T CCA	
		GTCGGAGTATGG C G GGT	
		G TT T	
GAM1965 HUMNPIIY20	3'	GGCGCGGCCTTCAGCGTGGGGC 40538	TT T ATTTA
TG		TAGT CATGTTGGGG CC	
		GTCG GTGCGACTTC GG	
		GG C CGCGGG	
GAM1965 HYA22	3'	TGGATACACATGGAGCTG 12390	T GG
		TAGTTTCATGT G GTCCA	
		GTCGAGGTACA C TAGGT	
		_ A_	
GAM1965 IDN3	5'	TGGATGCATTGGCTGAAATTG 28513	T TG G__
		TAGTTTCA GT G GTCCA	
		GTAAAGT CG T TAGGT	
		_ GT ACG	
GAM1965 IDN3	5'	TGGATGCATTGGCTGAAATTG 17685	T TG G__
		TAGTTTCA GT G GTCCA	

		GTAAAGT CG T TAGGT		
		_ GT ACG		
GAM1965	IL-23R	3' TGGGTGGATCACCTGAGG	29525	TGTT _
		TTTCA GG GGTCCATTTA		
		GGAGT CC CTAGGTGGGT		
		_____ A		
GAM1965	IL1RAPL1	5' TAGGGAAGATCTGTATGGAATT	15555	TT GG_ ATTTA
	A	TAGTTTCATG GG TCC		
		ATTAAGGTAT CT AGG		
		GT AGA GAT		
GAM1965	IMAGE:4907098	3' AGTGGAGCTGGAGCTG	44059	TGTTGG G
		TAGTTTCA G TCCATT		
		GTCGAGGT C AGGTGA		
		_____ G		
GAM1965	IMPACT	3' TAGATGGGAATTGCAGAAGCTG	20504	A TGGGG
		TAGTTTC TGT TCCATTTA		
		GTCGAAG ACG GGGTAGAT		
		_ TTAA_		
GAM1965	jdp2	3' TGGAAGTCAGAATGAACTG	28231	G G
		TAGTTTCAT TTGGG TCCA		
		GTCAAAGTA GACTC AGGT		
		A A		
GAM1965	KCNS1	3' GAGCCTACCATGAGGCTG	8043	T G
		TAGTTTCATG TGGG TC		
		GTCGGAGTAC ATCC AG		
		C G		
GAM1965	KIAA0040	3' TAAATGAAAGTAGGATGAAGCT	16097	G GGGTC
	A	TAGTTTCAT TTG CATTTA		
		ATCGAAGTA GAT GTAAAT		
		G GAAA_		
GAM1965	KIAA0061	3' TGGATCCAACCCAGATGAGACT	33893	G _____ TTTA
	G	GTTTCAT TTGGG GTCCA		
		CAGAGTA GACCC TAGGT		
		_ AACC A		
GAM1965	KIAA0090	3' TAAGTGTTAGAGACTTTAATGT	42654	C _____
	AAGCTA	T ATGTTGGGGTC CATTTA		
		A TGTAATTTTCAG GTGAAT		
		_ AGATT		
GAM1965	KIAA0092	3' TAAATCTCCCTGGCATGAGGT	16156	TT TG TCC
		G TCATGT GGG ATTTA		

		T AGTACG CCC TAAAT	
		GG GT TC_	
GAM1965 KIAA0102	5'	AGTGGCTTTGATTGGGATTA 16476	TT T TG T
		TAGT CA GT GGG CCATT	
		ATTA GT TA TTC GGTGA	
		GG T GT _	
GAM1965 KIAA0133	3'	AAAATTGACCCTGGGATGAGAT 16608	G TG C A
	TA	TAGTTTCAT T GGGTC ATTT	
		ATTAGAGTA G CCCAG TAAA	
		G GT T AG	
GAM1965 KIAA0161	3'	TAGGGGCCTCTTGGCAGAGGCT 16433	A _ ATTTA
	G	TAGTTTC TGTT GGGGTCC	
		GTCGGAG ACGG CTCCGGG	
		_ TT GAT	
GAM1965 KIAA0173	3'	TAGGTGGGTTTCAGGAGC 16043	ATGT GT
		GTTTC TGGG CCATTTA	
		CGAGG ACTT GGTGGAT	
		_ TG	
GAM1965 KIAA0186	3'	TGGGCACCTTGATTGAGATTG 22039	TGTT _
		TAGTTTCA GGG GTCCA	
		GTTAGAGT TCC CGGGT	
		TAGT A	
GAM1965 KIAA0227	3'	GAAGCCAACATAGAGACTG 30453	_ GG
		TAGTTTC ATGTTGG TC	
		GTCAGAG TACAACC AG	
		A GA	
GAM1965 KIAA0232	5'	TGGCCTCAATGTGAAATTA 36039	T
		TAGTTTCATGTTGGGG CCA	
		ATTAAAGTGTA ACTCC GGT	
		_	
GAM1965 KIAA0247	3'	TAGGGCATTCCAGCAAGAGGCT 16378	A _ ATTTA
	G	TAGTTTC TGTTGGG GTCC	
		GTCGGAG ACGACCT CGGG	
		A TA AT	
GAM1965 KIAA0258	3'	GATTTTGGGATGAACTG 16646	G TG
		TAGTTTCAT T GGGTC	
		GTCAAAGTA G TTTAG	
		G GT	
GAM1965 KIAA0265	3'	TGGATGCCAAATGAGACTG 34631	G G
		TAGTTTCAT TTGG GTCCA	

GTCAGAGTA AACC TAGGT
 _ G
 GAM1965 KIAA0326 3' TGGGAACTGGGTGGAAGT 32161 G TG GG
 TAGTTTCAT T G TCCA
 ||||| | | |||
 GTCAAGGTG G C GGGT
 _ GT AA
 GAM1965 KIAA0336 3' TAGGTGGGCCCACCACTTGAG 16012 T TG_
 TTCA GT GGGTCCATTTA
 ||| || |||||
 GAGT CA CCCGGGTGGAT
 T CCA
 GAM1965 KIAA0349 3' TGAGCCTGTCTAAGGTGGGGCT 44342 TT G ____ TC TTAA
 A AGT CAT TTGG GG CA
 ||| ||| ||| |||
 TCG GTG AATC CC GT
 GG G TGT GA A
 GAM1965 KIAA0352 3' TGGTCCCTCCCCAGCTGAAGTT 16825 GT T T____ TTAA
 A TTCA GTTGGGG CCA
 ||| ||||| |||
 AAGT CGACCCC GGT
 TG _ TCCCT A
 GAM1965 KIAA0354 3' TAAGTGGACTTTGCTTTTGGGG 16999 TT TGT_ GG
 CT AGT CA T GGTCCATTTA
 ||| || | |||||
 TCG GT G TCAGGTGAAT
 GG TTTC TT
 GAM1965 KIAA0365 5' TGGATGCCAGTGGTGAGGCTG 38471 _GT G
 TAGTTTCA T TGG GTCCA
 ||||| | ||| |||
 GTCGGAGT G ACC TAGGT
 G TG G
 GAM1965 KIAA0375 5' ATGGAACAGTGTCTCAGCTGGA 35177 T _____ TTAA
 ACTG TCA GTTGGGG TCCA
 ||| ||||| |||
 GGT CGACTCT AGGT
 _ GTGACA AT
 GAM1965 KIAA0410 3' AGACTGCTTTCTAATAGTGAAA 16612 _ TC TTAA
 CTA TAGTTTCA TGTTGGGG CA
 ||||| ||||| |||
 ATCAAAGT ATAATCTT GT
 G TC CAGAT
 GAM1965 KIAA0419 3' TGGGTGGATCACCTGAGG 16261 TGTT _
 TTTC A GG GGTCCATTTA
 |||| |||||
 GGAGT CC CTAGGTGGGT
 ____ A
 GAM1965 KIAA0446 5' TAGATGCTTGGCATGAGGTT 34153 TT TG GTC
 AG TCATGT GG CATTTA
 || ||||| || |||||

	TT AGTACG TC GTAGAT	
	GG GT ____	
GAM1965 KIAA0449 5'	TGGATGGGGCCAAGGTGGAGCT 19056	G G G
G	TAGTTTCAT TTG G TCCATTTA	
	GTCGAGGTG AAC C GGGTAGGT	
	G _ G	
GAM1965 KIAA0449 3'	TGGCTCTGTCCAAAGTGAGATT 19057	G ____ T TTTA
G	GTTTCAT TTGG GG CCA	
	TAGAGTG AACC TC GGT	
	A TGTC _ A	
GAM1965 KIAA0450 5'	TGAGTGGGCCCTGGGGACACTG 16034	T ATG TG
	TAGT TC T GGGTCCATTTA	
	GTCA AG G CCCGGGTGAGT	
	C G__ GT	
GAM1965 KIAA0450 3'	TGGGACTTGGGTGGAGCTG 16035	G TG GT
	TAGTTTCAT T GG CCA	
	GTCGAGGTG G TC GGT	
	_ GT AG	
GAM1965 KIAA0478 3'	TGAGTGGGCTCCGCACTGGCTG 16989	TCA T
	TAGTT TGT GGGGTCCATTTA	
	GTCGG ACG CCTCGGGTGAGT	
	TC_ _	
GAM1965 KIAA0478 3'	TGGAAGTGTTTAATGTGAGGC 16990	GG__
	GTTTCATGTTGG TCCA	
	CGGAGTGTAATT AGGT	
	TGTGA	
GAM1965 KIAA0527 3'	ATGGGCCCTGTTTCCAGTGTGA 45842	TG _____ TTTA
GG	TCA TTGG GGTCCA	
	AGT GACC CCGGGT	
	GT TTTGTC AT	
GAM1965 KIAA0527 3'	CCTCTGTCTCAGCATTGGGACT 45845	TT _ TC TTTA
G	TAGT CA TGTTGGGG CA	
	GTCA GT ACGACTCT GT	
	GG T _ CTCCA	
GAM1965 KIAA0537 3'	GGTCTGGCTGCGTGGAGCTG 16867	TGG_ T
	TAGTTTCATGT GG CC	
	GTCGAGGTGCG TC GG	
	TCGG T	
GAM1965 KIAA0563 5'	GGA ACTTA ACTTGGGGCTA 16843	TT T G
	TAGT CA GTTGGG TCC	

ATCG GT CAATTC AGG
 GG T A
 GAM1965 KIAA0565 3' GCCTCAGTCATGAAATTG 33219 _
 TAGTTTCATG TTGGGGT
 ||||| |||||
 GTTAAAGTAC GACTCCG
 T
 GAM1965 KIAA0565 3' TGGGTGGATCACCTGAGG 33221 TGTT _
 TTTCA GG GGTCCATTTA
 |||| || |||||
 GGAGT CC CTAGGTGGGT
 ____ A
 GAM1965 KIAA0570 3' TGGGTGGATTGCTTGAAAC 16256 T TGG
 GTTTCA GT GGTCCATTTA
 |||| || |||||
 CAAAGT CG TTAGGTGGGT
 T ____
 GAM1965 KIAA0574 3' TGGGTGGGCCCTGCGGTGAAC 34350 T GT
 GTT CAT TGGGGTCCATTTA
 ||| ||| |||||
 CAA GTG GTCCCGGGTGGGT
 _ GC
 GAM1965 KIAA0607 3' GGCTCCAGCAGGGACTA 35927 TT A
 TAGT C TGTTGGGGTC
 |||| | |||||
 ATCA G ACGACCTCGG
 GG _
 GAM1965 KIAA0685 3' TGGCCCAGTGTGATGCTG 16150 T TG GT
 TAGT TCA TTGGG CCA
 |||| ||| |||| |||
 GTCG AGT GACCC GGT
 T GT _
 GAM1965 KIAA0703 5' ATGGGTATATACCCCAAAGTGG 16928 G ____ TTTA
 AATTG TCAT TTGGGGT CCA
 |||| ||||| |||
 GGTG AACCCCA GGT
 A TATATG AT
 GAM1965 KIAA0712 5' TGGGACCTAACTTGAAGTTA 16268 GT T GT
 TA TTCA GTTGGG CCA
 || |||| ||||| |||
 AT AAGT CAATCC GGT
 TG T AG
 GAM1965 KIAA0792 3' TGAGTGGGAATGCGTTGGGACT 16216 TT _ TGGGG
 G TAGT CA TGT TCCATTTA
 |||| || ||| |||||
 GTCA GT GCG GGGTGAGT
 GG T TAA__
 GAM1965 KIAA0794 3' TGAGTGTTAAATATGGAGC 39187 GGGGTC
 GTTTCATGTT CATTTA
 ||||| |||||

	CGAGGTATAA GTGAGT	
	ATT___	
GAM1965 KIAA0798	3' TGGGTGGATCACTTGAGG 16073	T TGG
	TTTCA GT GGTCCATTTA	
	GGAGT CA CTAGGTGGGT	
	T ___	
GAM1965 KIAA0825	3' TAAATGGATTTCAGGTGCTGCT 30593	TT G GG
A	TAGT CAT TTG GTCCATTTA	
	ATCG GTG GAC TAGGTAAAT	
	TC _ TT	
GAM1965 KIAA0847	5' TGGAAGTCCAGCCTGGAGCTG 38049	T _
	TAGTTTCA GTTGGGGT CCA	
	GTCGAGGT CGACCTCA GGT	
	C A	
GAM1965 KIAA0854	3' CAGTGAAGTCCAAGTGGAACTA 17253	G C TA
	TAGTTTCAT TTGGGGTC ATT	
	ATCAAGGTG AACCTCAG TGA	
	_ _ CC	
GAM1965 KIAA0869	3' TGGCTGCCCAACGTGGAGC 35094	GT_
	GTTTCATGTTGGG CCA	
	CGAGGTGCAACCC GGT	
	GTC	
GAM1965 KIAA0870	3' TGAGTCTGCCAAGTGGAACTG 39610	GTTGG CC
	TAGTTTCAT GGT ATTTA	
	GTCAAGGTG CCG TGAGT	
	AA___ TC	
GAM1965 KIAA0884	3' TGGGTAACAGAGTGAGACTG 34778	G GG
	TAGTTTCAT TTG GTCCA	
	GTCAGAGTG GAC TGGGT	
	A AA	
GAM1965 KIAA0889	3' TGGGTGGATCGCCTGAGAT 17681	TGTT _
	GTTTCA GG GGTCCATTTA	
	TAGAGT CC CTAGGTGGGT	
	___ G	
GAM1965 KIAA0930	3' TGGGTGGATCACCTGAGAT 34918	TGTT _
	GTTTCA GG GGTCCATTTA	
	TAGAGT CC CTAGGTGGGT	
	___ A	
GAM1965 KIAA0937	3' TGGTCCCCGGCATTAGATTG 44020	C T
	TAGTTT ATGTTGGGG CCA	

	GT TAGA TACGGCCCC GGT	
	T T	
GAM1965 KIAA0939	3' TGGGCTGGCTGGCATGAGGC 31069	TG__
	GTTTCATGT G GGTCCA	
	CGGAGTACG C TCGGGT	
	GT GG	
GAM1965 KIAA0953	3' TAAATGATAGAGCATGAGGCTG 33170	GGG C
	TAGTTTCATGTT GTC ATTTA	
	GTCGGAGTACGA TAG TAAAT	
	GA_ _	
GAM1965 KIAA0971	3' TGGCCTGTGTGAAGCTG 17225	TG TG T
	TAGTTTCA T GGG CCA	
	GTCGAAGT G TCC GGT	
	GT_ _	
GAM1965 KIAA1013	3' TGGATTTAATTATGAGGCTA 42861	TTG
	TAGTTTCATG GGGTCCA	
	ATCGGAGTAT TTTAGGT	
	TAA	
GAM1965 KIAA1023	3' TGAGTGACCTGACTGAGACTA 19098	T TG GTC
	TAGTTTCA GT GG CATTTA	
	ATCAGAGT CA CC GTGAGT	
	_ GT A__	
GAM1965 KIAA1029	3' TGGAACCCCCAAGTGAGGCTG 14147	GTT _
	TAGTTTCAT GGGGT CCA	
	GTCGGAGTG CCCC A GGT	
	AAC A	
GAM1965 KIAA1037	3' GATGCTGCTCAACATGGGCTA 17385	T GTC
	TAGTT CATGTTGGG CATT	
	ATCGG GTACAACTC GTAG	
	_ GTC	
GAM1965 KIAA1040	3' TAAATGCCAGTCTTAGTGTGAA 35742	TG TC__
GC	GTTTCA TTGGGG CATTTA	
	CGAAGT GATTCT GTAAAT	
	GT GACC	
GAM1965 KIAA1054	3' AGATGGGTCCTAGCCTGA 33951	T GT
	TCA GTTGGG CCATTT	
	AGT CGATCC GG TAGA	
	C TG	
GAM1965 KIAA1055	3' GAGTGGGCTCGGGATGCTG 32853	T ATGT G
	TAGT TC T GGGTCCATTT	

GTCG AG G CTCGGGTGAG
 T ____ G
 GAM1965 KIAA1110 3' TGGGCAGCAGCATGAGGCTG 30986 GG
 TAGTTTCATGTTG GTCCA
 ||||| ||||
 GTCGGAGTACGAC CGGGT
 GA
 GAM1965 KIAA1161 5' ATGGATCGCGACTCTGTGTGGG 39748 TT ____ G TTTA
 GCTA CAT GTTG GGTCCA
 || ||| ||||
 GTG CAGC CTAGGT
 GG TGTCT G AT
 GAM1965 KIAA1161 3' TAAATGAGAGGACATGAGATT 39755 GGGG _
 AGTTTCATGTT TC CATTTA
 ||||| || ||||
 TTAGAGTACAG AG GTAAAT
 G__ A
 GAM1965 KIAA1163 3' TGGATGGATCTTTGCAGGAGC 38561 A TG
 GTTTC TGT GGGTCCATTTA
 |||| || |||||
 CGAGG ACG TCTAGGTAGGT
 _ TT
 GAM1965 KIAA1189 3' TGAATTAAACCCATTGTGAGGT 35652 TT GT GTCC
 TG TAG TCAT TGGG ATTTA
 || ||| ||| ||||
 GTT AGTG ACCC TAAGT
 GG TT AAAT
 GAM1965 KIAA1191 3' TGCACCTTTAAAGTGAGATTA 21684 G C
 TAGTTTCAT TTGGGGT CA
 ||||| ||||| ||
 ATTAGAGTG AATTTCA GT
 A C
 GAM1965 KIAA1198 3' GGGTGGGTCCCAGAAGTGA 31712 G_ GT
 TCAT TTGGG CCATTT
 ||| |||| ||||
 AGTG GACCC GGTGGG
 AA TG
 GAM1965 KIAA1254 3' TGAAAAGATCACCTTAAGTGAA 34698 GTT_ _ CA
 ATTA AGTTTCAT GG GGTC TTTA
 ||||| || ||| ||||
 TTAAAGTG CC CTAG AAGT
 AATT A AA
 GAM1965 KIAA1265 3' TAAATGGACTTTGGGGAGAC 35033 ATG TG
 GTTTC T GGGTCCATTTA
 |||| | |||||
 CAGAG G TTCAGGTAAAT
 G__ GT
 GAM1965 KIAA1266 3' TGGGTGGACGTGCAGAGACTG 32868 A TGGG
 TAGTTTC TGT GTCCATTTA
 ||||| || |||||

GTCAGAG ACG CAGGTGGGT
 _ TG_
 GAM1965 KIAA1280 5' TAAATGGGAGGGATTGAGGCTA 34555 T GGGG
 TAGTTTCA GTT TCCATTTA
 ||||| || |||||
 ATCGGAGT TAG GGGTAAAT
 _ GGA_
 GAM1965 KIAA1322 3' AAGTTTGATTCTAACACTGGA 36019 GT _ TC TTTA
 GTTG A TTCA TGTTGGGG CA
 | ||| ||||| ||
 T AGGT ACAATCCT GT
 TG C TA TTGAAT
 GAM1965 KIAA1332 3' TGTGTTTTAACAGGGGCTG 35262 TT A TC
 TAGT C TGTTGGGG CA
 ||| | ||||| ||
 GTCG G ACAATTTT GT
 GG _ GT
 GAM1965 KIAA1337 3' GGGTGGGGGACAGGAGCTG 35985 A GGGG
 TAGTTTC TGTT TCCATT
 ||||| ||| |||||
 GTCGAGG ACAG GGGTGGG
 _ G_
 GAM1965 KIAA1363 3' ATGGCTTTAAAATGGAGCTA 34332 G T
 TAGTTTCAT TTGGGG CCAT
 ||||| ||||| |||||
 ATCGAGGTA AATTTC GGTA
 A _
 GAM1965 KIAA1389 3' TGAATGTAACCTCCTGGTGTGAA 34571 TG TG _ C_
 G TTTCA T GG GT CATTTA
 |||| | || |||||
 GAAGT G CC CA GTAAGT
 GT GT T AT
 GAM1965 KIAA1404 3' CCCCTGGGCCCTGAATGGAGCT 31050 G TG TTTA
 A TAGTTTCAT T GGGTCCA
 ||||| | |||||
 ATCGAGGTA A CCCGGGT
 _GT CCCCCA
 GAM1965 KIAA1463 3' TGGGGTTTGTTAACATGGAAC 35774 _ G TTTA
 A AGTTTCATGTTGG G TCCA
 ||||| ||| |||||
 TCAAGGTACAATT T GGGT
 GTT G A
 GAM1965 KIAA1484 3' GGACTCTAAGTGAGACTG 34679 G
 TAGTTTCAT TTGGGGTCC
 ||||| |||||
 GTCAGAGTG AATCTCAGG
 _
 GAM1965 KIAA1559 3' TGGGTGGATCACTTGAGGC 36166 T TGG
 GTTTCA GT GGTCCATTTA
 ||||| || |||||

CGGAGT CA CTAGGTGGGT
T ____

GAM1965 KIAA1579 3' TGAGTTCACTGAATATGAAATT 20120 G GTCC
G TAGTTTCATGTT GG ATTTA
||||||| || ||||
GTTAAAGTATAA TC TGAGT
G ACT_

GAM1965 KIAA1622 3' AGATATACCGTGTGAAGCTA 27763 TG TGG CC
TAGTTTCA T GGT ATTT
|||||| | ||| ||||
ATCGAAGT G CCA TAGA
GT ____ TA

GAM1965 KIAA1649 5' TGAGTGGGATAGTGTGGGGC 26112 TT TG GGG
GT CA TTG TCCATTTA
|| || || |||||
CG GT GAT GGGTGAGT
GG GT A_

GAM1965 KIAA1649 5' TGGAGGCTGATGTGAGCTG 26113 T TG GG
TAGTT CATGT G TCCA
|||| |||| | ||||
GTCGA GTGTA C AGGT
_ GT GG

GAM1965 KIAA1671 3' TGGGTGGGCTCAGGAAG 32694 ATGTTG
TTTC GGGTCCATTTA
||| |||||
GAAG CTCGGGTGGGT
GA_

GAM1965 KIAA1676 3' TGAATGGACTTCTTAAGCTG 44729 CATGTT
TAGTTT GGGGTCCATTTA
|||| |||||
GTCGAA CTTCAGGTAAGT
TT_

GAM1965 KIAA1679 5' GACGGCTCAGCATGGACTG 34752 T _
TAGTT CATGTTGGG GTC
|||| ||||| |||
GTCAG GTACGACTC CAG
_ GG

GAM1965 KIAA1706 3' TGAATGGAAAAATATGAAAGTA 44578 G GGGG
TA TTTTCATGTT TCCATTTA
|| ||||| |||||
AT AAAGTATAA AGGTAAGT
G AA_

GAM1965 KIAA1706 3' TGGCTTCTCTGACCTGGAGCTG 44579 T TG T_
TAGTTTCA GT GGG CCA
|||||| || ||| |||
GTCGAGGT CA CTC GGT
C GT TTC

GAM1965 KIAA1710 3' TGGTTTTTCTAATAGAACTG 31333 A T_
TAGTTTC TGTTGGGG CCA
|||||| ||||| |||

GTCAAAG ATAATCTT GGT
 _ TTT
 GAM1965 KIAA1727 3' TGAGTGGATTGCTTGAGCCTA 32038 T T TGG
 TAG TTCA GT GGTCCATTTA
 ||| ||| || |||||
 ATC GAGT CG TTAGGTGAGT
 C T _
 GAM1965 KIAA1729 3' GATTCCAGTAGATGGAATTG 42949 G_
 TAGTTTCAT TTGGGGTC
 ||||| |||||
 GTTAAGGTA GACCTTAG
 GAT
 GAM1965 KIAA1754 3' TAGGAAGCCTTCCAGTGTGAGC 31681 T TG _ ATTTA
 TG GTT CA TTGGGG TCC
 ||| || ||||| |||
 CGA GT GACCTT AGG
 _ GT CCGA AT
 GAM1965 KIAA1765 3' TAAATGGATTACACTGGGGCT 34957 TT T T GG
 AGT CA GT G GTCCATTTA
 ||| ||| |||||
 TCG GT CA C TAGGTAAAT
 GG _ _ AT
 GAM1965 KIAA1789 5' TAATTGGTCTGACATGGAGTTG 33312 GT TG GT T
 TA TTCATGT GG CCA TTA
 || ||||| || |||||
 GT AGGTACA CT GGT AAT
 TG GT _ T
 GAM1965 KIAA1804 3' TGAATTTCAAAATGAAGCTG 34588 G GG C
 TAGTTTCAT TTG GT CA
 ||||| ||| |||
 GTCGAAGTA AAC TA GT
 A TT A
 GAM1965 KIAA1804 3' TGGTGTGCCCTTGAGTGAGGC 34591 GTT_ TC TA
 TA TAGTTTCAT GGGG CATT
 ||||| ||| |||
 ATCGGAGTG CCCC GTGG
 AGTT GT T
 GAM1965 KIAA1813 5' TGGAAACTGGTATGAGCCTG 34815 T TT GG
 TAG TTCATG GG TCCA
 ||| ||||| || |||
 GTC GAGTAT TC AGGT
 C GG AA
 GAM1965 KIAA1813 5' CCCCAGGGCCCGGCTGGGGTT 34809 TT T ATTTA
 G TAG TCA GTTGGGGTCC
 ||| ||| |||||
 GTT GGT CGGCCCCGGG
 GG _ GCCCG
 GAM1965 KIAA1829 3' TGGGTGGGCTCTAAATTTGG 31036 TG_
 TCA TTGGGGTCCATTTA
 ||| |||||


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GGT AATCTCGGGTGGGT
TTA
GAM1965 KIAA1858 3' GGGTTCCTCGTATGGAAGT 33330 TT GG
TAGTTTCATG GG TCC
||||||| || |||
GTCAAGGTAT CC GGG
GC TT
GAM1965 KIAA1872 3' TGGGTGGATCACCTGAGG 31522 TGTT _
TTTCA GG GGTCCATTTA
|||| || |||||
GGAGT CC CTAGGTGGGT
_____ A
GAM1965 KIAA1887 5' GACCCCGGGTGGGGCTG 37715 TT G
TAGT CAT TTGGGGTC
||| || |||||
GTCG GTG GGCCCCAG
GG _
GAM1965 KIAA1908 5' TGAGTGGACACCAGTGAAG 36339 GT G
TTTCAT TGG GTCCATTTA
|||| || |||||
GAAGTG ACC CAGGTGAGT
_ A
GAM1965 KIAA1908 3' AAGTGGACACATAAAATTA 36326 C TGGG
TAGTTT ATGT GTCCATT
|||| || |||||
ATTAAA TACA CAGGTGAA
A _____
GAM1965 KIAA1932 3' TGGCCCTCCATGTGAGGTTG 36352 TT T T
TAG TCATGT GGGG CCA
|| |||| ||| |||
GTT AGTGTA CTCC GGT
GG C C
GAM1965 KIAA1987 3' TGGATGGATTTGCCGATTCTGA 42502 T_ _
AATTG TTTCA GTTGG GGTCCATTTA
|||| ||| |||||
AAAGT TAGCC TTAGGTAGGT
CT GT
GAM1965 KLHL6 3' GGGTCTGTATATGAAGCTG 28212 _ GG
TAGTTTCATGT TGG TCC
||||||| || |||
GTCGAAGTATA GTC GGG
T TT
GAM1965 KLHL8 3' TGGGTGGACCACCTGAGAT 31478 TGTT _
GTTTCA GG GGTCCATTTA
|||| || |||||
TAGAGT CC CCAGGTGGGT
_____ A
GAM1965 KRTHB2 3' TAGATGGAGGAGGTGTGGGCTG 26924 T TG GGGG
TAGTT CA TT TCCATTTA
|||| || || |||||

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		GTCGG GT GG AGGTAGAT	
		_ GT AGG_	
GAM1965 Kv6.3	3'	TGAATATTATCCAACATGGG 28567	GTCC
		TTCATGTTGGG ATTTA	
		GGGTACAACCT TAAGT	
		ATTA	
GAM1965 LASP1	3'	TGGGTGGGGTTATGTGAGGGTA 12804	G TG G
		TA TTTTCATGT GG TCCATTTA	
		AT GGAGTGTA TT GGGTGGGT	
		G _ G	
GAM1965 LATS1	3'	GAGAGATATCCTGGCTGAAGCT 30236	T TG CCA A
G		TAGTTTCA GT GGGT TTT	
		GTCGAAGT CG CCTA AGA	
		_ GT TAG GA	
GAM1965 LIN-7-C	3'	TAAAAGGCAGCTATTAGTGTGG 20369	TT TG _ _ A
GACTG		T CA TTGG GGT CC TTTA	
		A GT GATT TCG GG AAAT	
		GG GT A AC A	
GAM1965 LRRN3	5'	TGGGCTAGCACTGAAACTG 34403	_ GG
		TAGTTTCA TGTT GGTCCA	
		GTCAAAGT ACGA TCGGGT	
		C _	
GAM1965 MADHIP	3'	TAGATGGGAAGTCCATGGAGAC 14244	ATGT G_
TA		TAGTTTC TGGG TCCATTTA	
		ATCAGAG ACCT GGGTAGAT	
		GT_ GAA	
GAM1965 MAN1	3'	TGGGTTTGCAGCATGAAC 15619	T _ GT
		AGTT CATGTTG GG CCA	
		TCAA GTACGAC TT GGT	
		_ G TG	
GAM1965 MAP3K3	3'	GGGCCCGCGATGTGGAAC 8223	_
		TAGTTTCATGTTG GGGTCC	
		GTCAAGGTGTAGC CCCGGG	
		G	
GAM1965 MAWBP	3'	TGGGTGGATCACCTGAGG 22682	TGTT _
		TTTCA GG GGTCCATTTA	
		GGAGT CC CTAGGTGGGT	
		_ A	
GAM1965 MBD2	3'	GGACCCTAAGATGAAGCTG 17947	G
		TAGTTTCAT TTGGGGTCC	

			GTCGAAGTA AATCCCAGG		
			G		
GAM1965	MESDC2	3'	TGTCCCAGTGGAAAGCTG 35896	ATG	TC
			TAGTTTC TTGGGG CA		
			GTCGAAG GACCCT GT		
			GT_ _		
GAM1965	MESDC2	3'	TGGGTGGATCAGTTGAGG 35895	TGTTGG	
			TTTCA GGTCCATTTA		
			GGAGT CTAGGTGGGT		
			TGA_		
GAM1965	MGC10200	5'	TGGGCTTCCAACGGAGACTG 29696	A	_
			TAGTTTC TGTTGGG GTCCA		
			GTCAGAG GCAACCT CGGGT		
			_ T		
GAM1965	MGC10814	5'	TGGGTGGATCACCTGAGG 26396	TGTT	_
			TTTCA GG GGTCCATTTA		
			GGAGT CC CTAGGTGGGT		
			_ A		
GAM1965	MGC10960	3'	TAAGTGGATTTCAAACTGTG 26383	_ _	GG
			CAT GTT G GTCCATTTA		
			GTG CAA C TAGGTGAAT		
			T A TT		
GAM1965	MGC11034	3'	GGCATTCTAATGTGAAAT 25471		_
			GTTTCATGTTGGGGT CC		
			TAAAGTGTAATCTTA GG		
			C		
GAM1965	MGC11115	3'	GGCCTGGGCCTTGCTGTGGGAC 26097	TT	TT TTTA
			TG TAGT CATG GGGGTCCA		
			GTCA GTGT TTCCGGGT		
			GG CG CCGGT		
GAM1965	MGC11115	3'	GGTCCCAGCTGGAATTA 26098	T	GT
			TAGTTTCA GTTGGG C		
			ATTAAGGT CGACCC G		
			_ TG		
GAM1965	MGC13071	3'	TGAATGAAGACAATGTGGAAT 26409	GGGTC	
			GTTTCATGTTG CATTTA		
			TAAGGTGTAAC GTAAGT		
			AGAA_		
GAM1965	MGC13114	3'	TGGACGTGACGTGGGGCTG 26155	TT	GGG
			TAGT CATGTT GTCCA		

GTCG GTGCAG CAGGT
 GG TG_
 GAM1965 MGC14407 3' TGGGTGGATCACTTGAGGC 26730 T TGG
 GTTTCA GT GGTCCATTTA
 ||||| || |||||
 CGGAGT CA CTAGGTGGGT
 T ____
 GAM1965 MGC15873 3' TGGGTGGGCCCTGATCCAAGCT 26744 CAT TG
 G TAGTTT GT GGGTCCATTTA
 ||||| || |||||
 GTCGAA TA CCCGGGTGGGT
 CC_ GT
 GAM1965 MGC15873 3' TTATGCCCTCTGTTTCGATAGG 26745 A _____ CCATTTA
 AAGCTG C TGTTG GGGT
 | |||| |||
 G ATAGC CCCG
 G TTTGTCT T ATTT
 GAM1965 MGC16025 3' GGTATCCAGATGAGGCTA 26749 G GT_
 TAGTTTCAT TTGGG CC
 ||||| ||||| ||
 ATCGGAGTA GACCT GG
 _ ATT
 GAM1965 MGC2603 3' TAGGTGGGAAGGTGGCATGGGA 23471 TT GGGG_
 T GT CATGTT TCCATTTA
 || ||||| |||||
 TA GTACGG GGGTGGAT
 GG TGGAA
 GAM1965 MGC2668 3' GAATGGACCTGAGTAGCTG 30380 TCATG G
 TAGTT TT GGGTCCATTT
 |||| || |||||
 GTCGA GA TCCAGGTAAG
 T____ G
 GAM1965 MGC2848 3' AGGTGTTTTTGGATGAGACTA 26735 G TG TC A
 TAGTTTCAT T GGG CATTT
 ||||| | || |||||
 ATCAGAGTA G TTT GTGGA
 GT T A
 GAM1965 MGC5576 3' TGGAGTGATGTGGAGCTA 23493 GGG
 TAGTTTCATGTTG TCCA
 ||||| ||||| |||||
 ATCGAGGTGTAGT AGGT
 G_
 GAM1965 MIDORI 3' ATGGATGGAGACTTTCCAAATA 36526 _ ____
 TGGA ACTA CATGTT GGGG TCCATTTA T
 ||||| ||||| ||||| |
 GTATAA CCTT AGGTAGGT A
 A TCAG
 GAM1965 MKP-7 3' TAGTACACCTTAGCGCTGAGAC 33010 _ CCATTTA
 TG TAGTTTCA TGTTGGGGT
 ||||| |||||

			GTCAGAGT GCGATTCCA		
			C CATGAT		
GAM1965 MKP-7	3'	TGGCTCTCTTCAGCATGTAATT 33011	T	T__	TTTA
G		AGTT CATGTTGGGG CCA			
		TTAA GTACGACTTC GGT			
		T TCTC A			
GAM1965 MORF4	5'	TGAGTGGGTTCCGGAGAGC 43644	CATG	GG	
		GTTT TTGG TCCATTTA			
		CGAG GGCC GGGTGAGT			
		A__ TT			
GAM1965 MRPL56	3'	TGGGTGGATCACCTGAGG 26660	TGTT	_	
		TTTCA GG GGTCCATTTA			
		GGAGT CC CTAGGTGGGT			
		__ A			
GAM1965 MTCH1	3'	TGAATGGGAAATCATGCAACTA 15662	T	TTGGGG	
		TAGTT CATG TCCATTTA			
		ATCAA GTAC GGGTAAGT			
		C TAAA__			
GAM1965 MY014	5'	TGGTGTGTCCGACGTAGAGCTG 25192	TC	GT__	
		TAGTT ATGTTGGG CCA			
		GTCGA TGCAGCCT GGT			
		GA GTGT			
GAM1965 My015	3'	TGGTATCCTACATGGAATTA 33109	T	_	
		TAGTTTCATGT GGGGT CCA			
		ATTAAGGTACA TCCTA GGT			
		_ T			
GAM1965 N4BP2	3'	TAGGTGGATCGCCTGAGG 20005	TGTT	_	
		TTTCA GG GGTCCATTTA			
		GGAGT CC CTAGGTGGAT			
		__ G			
GAM1965 N4BP3	3'	TGGATGGTCGGGATTGAGGCTG 32940	T	GG T	
		TAGTTTCA GTT GG CCATTTA			
		GTCGGAGT TAG CT GGTAGGT			
		_ GG _			
GAM1965 NIBAN	3'	TAAGTGCTTGTCTAGCATAAA 22631	C	GG C__	
TTA		AGTTT ATGTTGG T CATTTA			
		TTAAA TACGATC G GTGAAT			
		_ TT TTC			
GAM1965 NMT1	3'	TGGACAACTGCATGGAGCTG 22050	TGGG		
		TAGTTTCATGT GTCCA			

		GTCGAGGTACG CAGGT	
		TCAA	
GAM1965 NMT1	3'	TGGAGCTCTTGGCTGGGGCTG 22051	TT T TG __
		TAGT CA GT GG G TCCA	
		GTCG GT CG TC C AGGT	
		GG _ GT T G	
GAM1965 NMT2	3'	TGGGTGACAGAGCGTGAGACT 11231	GGG C
		AGTTTCATGTT GTC ATTTA	
		TCAGAGTGCGA CAG TGGGT	
		GA_ _	
GAM1965 NX-17	3'	TGGATGGATAAAAAATGGAATTA 21835	GTTGGG
		TAGTTTCAT GTCCATTTA	
		ATTAAGGTA TAGGTAGGT	
		AAAA_	
GAM1965 NXP-2	3'	GAAAGTGTATTTTTTGGTATGAA 35230	TT TC_ A
		GCTG AGTTTCATG GGGG CATTT	
		TCGAAGTAT TTTT GTGAA	
		GG TAT AGT	
GAM1965 NXPH3	3'	TGAGCATGGCATGAGGCTG 32721	GG TC
		TAGTTTCATGTTG G CA	
		GTCGGAGTACGGT C GT	
		A_ GA	
GAM1965 NXPH3	3'	TGGTCCCAACCTGAAGCTG 32723	T T
		TAGTTTCA GTTGGGG CCA	
		GTCGAAGT CAACCCT GGT	
		C _	
GAM1965 ORC6L	3'	TGGGTGGATCACCTGAGG 15621	TGTT _
		TTTCA GG GGTCCATTTA	
		GGAGT CC CTAGGTGGGT	
		_ A	
GAM1965 OSBPL10	3'	TGGATGGGGGTTGGCAGGAAGC 19417	A TG GG
		TG TAGTTTC TGT G TCCATTTA	
		GTCGAAG ACG T GGGTAGGT	
		G GT GG	
GAM1965 P11	3'	TGAATGGGCTGGGGGTGGGG 12643	TT G G G
		T CAT TT GG TCCATTTA	
		G GTG GG TC GGGTAAGT	
		GG G G _	
GAM1965 P2RX1	3'	TGGGTGCAGCGTGAGGCT 33359	GGG
		AGTTTCATGTTG TCCA	

			TCGGAGTGCGAC GGGT		
			GT_		
GAM1965	P5-1	3'	GGATGTTAACATGGGATT 13500	TT	G
			AGT CATGTTGG GTCC		
			TTA GTACAATT TAGG		
			GG G		
GAM1965	PADI3	3'	TGGGTGGGTACTAGGGAGACTG 18347		ATGT GG
			TAGTTTC TGG TCCATTTA		
			GTCAGAG ATC GGGTGGGT		
			GG_ AT		
GAM1965	PANK	3'	TGGTTTCAAATGAACTA 28715		G GG T
			TAGTTTCAT TTG G CCA		
			ATCAAAGTA AAC T GGT		
			_ TT _		
GAM1965	PDE2A	3'	GGAGTCCCAGCAGAGGCTA 8462		A _
			TAGTTTC TGTTGGGG TCC		
			ATCGGAG ACGACCCT AGG		
			_ G		
GAM1965	PDGFC	5'	TGGATGGGATTATGTGGAACT 18303		ATGT GG
	A		TAGTTTC TGG TCCATTTA		
			ATCAAAG ATT GGGTAGGT		
			GTGT A_		
GAM1965	PDK2	3'	GAGTGGGGAATGAGGCTG 8474		GTTGGGG
			TAGTTTCAT TCCATT		
			GTCGGAGTA GGGTGAG		
			AG_____		
GAM1965	PDZD2	5'	TGAATGGGCAGCTGATGGTTGG 39398	T _	TG G_
			AGTTG TTCA TGT G GTCCATTTA		
			AGGT GTA C CGGGTAAGT		
			G TG GT GA		
GAM1965	PDZD2	3'	TAAGTGCATAATATGAAAT 39394		GG TC
			GTTTCATGTTG G CATTTA		
			TAAAGTATAAT C GTGAAT		
			AA _		
GAM1965	PEX12	3'	TGGTTTCAGCATGGTATTG 5833	T	GG T
			TAGT TCATGTTG G CCA		
			GTTA GGTACGAC T GGT		
			T TT _		
GAM1965	PGR1	3'	GGATGACAGTATGGAAGT 27124		GG
			TAGTTTCATGTTG GTCC		

			GTCAAGGTATGAC TAGG		
			AG		
GAM1965	PHYHIP	3'	TGGGGCCTGGCATGGAAC 16514	TG G	
			GTTTCATGT GG TCCA		
			CAAGGTACG CC GGGT		
			GT G		
GAM1965	PIP5K2B	3'	TGGGAGGGCTTTAGCAATGAGA 9616	_	ATTTA
	CTG		TAGTTTCAT GTTGGGGTCC		
			GTCAGAGTA CGATTTCGGG		
			A AGGGT		
GAM1965	POF1B	3'	TCAAATAGGTCTTGATATGAAG 24455	TG GT C	A
	CTA		TAGTTTCATGT GG C ATTT		
			ATCGAAGTATA TC G TAAA		
			GT TG A CTT		
GAM1965	POLM	3'	TGAGTGGGGCCACATCGTGGA 43785	T_ G	
	GCTG		AGTTTCATG TGGG TCCATTTA		
			TCGAGGTGC ACCC GGGTGAGT		
			TAC G		
GAM1965	PP1057	3'	TGGTTTGACTTGGA ACTA 25312	T TG GT	
			TAGTTTCA GT GG CCA		
			ATCAAGGT CA TT GGT		
			T GT _		
GAM1965	PPFIA4	3'	GGCCCTGGCATAAGCTG 34820	C TG	
			TAGTTT ATGT GGGTC		
			GTCGAA TACG CCCGG		
			_ GT		
GAM1965	PPI5PIV	3'	TGAGTGGGCCCCAGAGCCCAGC 21279	TCATG	
	TG		TAGTT TTGGGGTCCATTTA		
			GTCGA GACCCCGGGTGAGT		
			CCCGA		
GAM1965	PPP4R1L	5'	TAGAGCTGCTTCTGAGTGAGGC 38818	GTT CCA	
	TG		TAGTTTCAT GGGGT TTTA		
			GTCGGAGTG CTTCG AGAT		
			AGT TCG		
GAM1965	PRO0233	5'	GAGTCCTGATCTGGA ACTG 15375	T TG _	
			TAGTTTCA GT GGG TC		
			GTCAAGGT TA CCT AG		
			C GT G		
GAM1965	PRO0245	5'	TAAATGACATTA ACTTGAAATT 15378	T G C	
	A		TAGTTTCA GTTGG GTC ATTTA		

		ATTAAAGT CAATT CAG TAAAT	
		T A _	
GAM1965	PRO0246	5' TAAATGGACCTCTGTACGGCTG 15380	TCA TT
		TAGTT TG GGGGTCCATTTA	
		GTCGG AT CTCCAGGTAAAT	
		C_ GT	
GAM1965	PRO0456	3' TGGATGGATCACCTGAGCCTG 15395	T TGTT _
		TAG TTCA GG GGTCCATTTA	
		GTC GAGT CC CTAGGTAGGT	
		C _ _ _ A	
GAM1965	PRO0899	5' TGAAGTTCAGCATGAGCTG 20649	T C
		TAGTT CATGTTGGGGT CA	
		GTCGA GTACGACTTCA GT	
		_ A	
GAM1965	PRO1048	3' GATTCCAATGCGGAGCTG 20558	AT
		TAGTTTC GTTGGGGTC	
		GTCGAGG TAACCTTAG	
		CG	
GAM1965	PRO1866	5' GCCTCATGTGTGAAATTA 20581	TG _
		TAGTTTCA T TGGGGT	
		ATTAAAGT G ACTCCG	
		GT T	
GAM1965	PRO2198	3' GGATTATCAATGTGAACTG 20696	T _
		TAGTT CATGTTGG GGTCC	
		GTCAA GTGTAAGT TTAGG	
		_ A	
GAM1965	PRO2198	5' TGGGTGGATCACTTGAGG 20697	T TGG
		TTTCA GT GGTCCATTTA	
		GGAGT CA CTAGGTGGGT	
		T _ _	
GAM1965	PRO2859	5' TGAAGTCAACCAATGTGGAAC 20617	_ _ C
		GTTTCATGTTGG G GT CA	
		CAAGGTGTAACC C CA GT	
		A T A	
GAM1965	PRO2859	3' AAAATCCTACTGGATATGAAAC 20614	G GTCC A
	TG	TAGTTTCATGTT GG ATTT	
		GTCAAAGTATAG TC TAAA	
		G ATCC AT	
GAM1965	PRO2964	5' TAAATGGACACGATAGGAAACT 20632	A GG
	A	TAGTTTC TGTTG GTCCATTTA	

		ATCAAAG ATAGC CAGGTAAAT	
		G A_	
GAM1965	PRRG1	3' TAAATGGGTTGCCAACATAAGC 6655	C _ GT
	TG	TAGTTT ATGTTGG G CCATTTA	
		GTCGAA TACAACC T GGTAAT	
		_ G TG	
GAM1965	PSTPIP2	3' TAAAGCCTACAAGTGTGAAATT 23682	_ _ CCATTTA
	A	TAGTTTCATG TTG GGGT	
		ATTAAAGTGT AAC TCCG	
		G A AAAT	
GAM1965	QSCN6	3' TGGGTGGGCTGGAATGGAAC 8700	GTTGG
		AGTTTCAT GGTCCATTTA	
		TCAAGGTA TCGGGTGGGT	
		AGG_	
GAM1965	RA-GEF-2	3' TGGAAGGCCAAATGAAGCTG 18468	G GG_
		TAGTTTCAT TTGG TCCA	
		GTCGAAGTA AACC AGGT	
		_ GGA	
GAM1965	RAB17	3' TAGGTGGATTCTGATTCACTG 22788	TTCAT TG
		TAGT GT GGGTCCATTTA	
		GTCA TA CTTAGGTGGAT	
		CT_ GT	
GAM1965	RAB33B	3' TGGTTTTTCAGGTGAGATTG 25333	G GG T
		TAGTTTCAT TTG G CCA	
		GTTAGAGTG GAC T GGT	
		_ TT T	
GAM1965	RAB35	3' TGGACCTGATGTGAAATT 13734	TG G
		AGTTTCATGT GG TCCA	
		TTAAAGTGTA CC AGGT	
		GT _	
GAM1965	Rabip4R	3' TGGATTCAACCAACATGGA 19718	___
		TTCATGTTGG GGTCCA	
		AGGTACAACC TTAGGT	
		AAC	
GAM1965	RAN	3' TGAGTGGGCTTCGGAGTGAA 13019	G
		TTCAT TTGGGGTCCATTTA	
		AAGTG GGCTTCGGGTGAGT	
		A	
GAM1965	RAN	3' TGAATGTTAGATGCTTAGTGTG 13018	TG _ _
	AAGTTG	TTCA TTGGG GTC CATTTA	

AAGT GATTG TAG GTAAGT
 GT G ATT
 GAM1965 RANBP6 5' ATGGTTTCAGCATGGGCTA 30885 T GG T
 TAGTT CATGTTG G CCAT
 |||| ||||| | ||||
 ATCGG GTACGAC T GGTA
 _ TT _
 GAM1965 RANBP6 5' GATTCGGAATGGAATA 30886 G G
 TAGTTTCAT TT GGGTC
 ||||| || ||||
 ATCAAGGTA AG CTTAG
 _ G
 GAM1965 RASSF2 3' GTGGTCTTAACGTAGACTG 16396 C T
 TAGTTT ATGTTGGGG CCAT
 |||| ||||| ||||
 GTCAGA TGCAATTCT GGTG
 _ _
 GAM1965 RASSF2 3' TGGATGGACTTCAACTTGGAGT 16397 GT T
 TG TA TTCA GTTGGGGTCCATTTA
 || ||| ||||| |||||
 GT AGGT CAACTTCAGGTAGGT
 TG T
 GAM1965 Rpo1-2 3' TGAACATCAAAGTGAAACTG 25937 G GG C
 TAGTTTCAT TTG GT CA
 ||||| || ||||
 GTCAAAGTG AAC CA GT
 A TA A
 GAM1965 RYK 3' TGAATGGGCTTTCTAAATAGCT 40206 TCATG _
 A TAGTT TTGG GGTCCATTTA
 |||| ||| |||||
 ATCGA AATC TCGGGTAAGT
 TA__ TT
 GAM1965 SBB103 3' TAGGTGTGATTATTTTAATATG 12367 _ _
 AAGGTG TTCATGTTGGG GTC CATTTA
 ||||| ||| |||||
 AAGTATAATTT TAG GTGGAT
 TAT T
 GAM1965 SC65 3' TGGGTGGATCACTTGAGGC 13175 T TGG
 GTTTCA GT GGTCCATTTA
 |||| || |||||
 CGGAGT CA CTAGGTGGGT
 T _
 GAM1965 SCAMP5 3' TGGGCTGCACGTGGAGCTG 29078 T G
 TAGTTTCATGT G GGTCCA
 ||||| | |||||
 GTCGAGGTGCA C TCGGGT
 _ G
 GAM1965 SCYA5 3' TGGGTGGATCACTTGAGG 8883 T TGG
 TTTCA GT GGTCCATTTA
 |||| || |||||

		GGAGT CA CTAGGTGGGT	
		T _	
GAM1965	SDCCAG3	3' TGGGTGTTCTCAGCATGAAGCT 13437	TC
		AGTTTCATGTTGGGG CATTTA	
		TCGAAGTACGACTCT GTGGGT	
		T_	
GAM1965	SE57-1	3' TGGATGGACTCTTCAAAACT 24893	CA TT
		AGTTT TG GGGGTCCATTTA	
		TCAA AC TCTCAGGTAGGT	
		_ T_	
GAM1965	SEC24A	3' AAGTGGATTTTATTTGG 40231	TGT
		TCA TGGGGTCCATT	
		GGT ATTTTAGGTGAA	
		TT_	
GAM1965	SEMA3E	3' TGGATGGATCTTCTCTGAACT 14810	T TGTT
		AGTT CA GGGGTCCATTTA	
		TCAA GT TTCTAGGTAGGT	
		_ CTC_	
GAM1965	SEMA4B	3' AAAAAACAATTCCAAATGTGAA 34224	_ CCATTTA
	ACTA	AGTTTCATGTT GGGGT	
		TCAAAGTGTA CCTTA	
		A ACAAAAAAT	
GAM1965	SEMA4G	5' TGGCACCTGATGTGAGACTG 45415	TG GT
		TAGTTTCATGT GG CCA	
		GTCAGAGTGTA CC GGT	
		GT AC	
GAM1965	SERPINB7	3' TAGATGGTAAAAAATGTGAAAT 9874	GGGGT
	TG	TAGTTTCATGTT CCATTTA	
		GTAAAGTGTA GGTAGAT	
		AAAAT	
GAM1965	SFXN5	3' ATTTCTGGGCCTTATGTGGGGT 29385	TT T TTTA
	TG	TAG TCATGT GGGGTCCA	
		GTT GGTGTA TTCCGGGT	
		GG _ CTTTAC	
GAM1965	SIAT9	5' TGAGTACACCTATGTGAAACTG 9978	TG CC
		TAGTTTCATGT GGGT ATTTA	
		GTCAAAGTGTA TCCA TGAGT	
		_ CA	
GAM1965	SIMRP7	3' TGGACACCAGCCAGCTGGAGCT 44374	T_ G TTTA
	G	AGTTTCA GTTGG GTCCA	

			TCGAGGT CGACC CAGGT		
			CGAC A A		
GAM1965	SIRPB1	3'	TAAATGTATCCAGATGAGGTTG 12709	TT G	GTC
			TAG TCAT TTGGG CATTTA		
			GTT AGTA GACCT GTAAAT		
			GG _ AT_		
GAM1965	SLC7A11	3'	AAAATATCTCTTCAGATGAAAC 15644	G	TCC_ A
	TG		TAGTTTCAT TTGGGG ATTT		
			GTCAAAGTA GACTTC TAAA		
			_ TCTA AT		
GAM1965	SLK	3'	ACCTCTTTTGGCATGAGCTA 16280	T	_____
			TAGTT CATGTT GGGGT		
			ATCGA GTACGG CTCCA		
			_ TTTT		
GAM1965	SNAPC1	3'	TGTTTTCCAGCATGGTATTA 9057	T	TC
			TAGT TCATGTTGGGG CA		
			ATTA GGTACGACCTT GT		
			T TT		
GAM1965	SP192	5'	GGATCCTGGCCATGAGGTTG 22297	TT	_TG
			TAG TCATG T GGGTCC		
			GTT AGTAC G CCTAGG		
			GG C GT		
GAM1965	SPEC1	3'	TAAATGGGGTAGGTGGGTGAGA 21515		GTTGGGG_
	TTA		TAGTTTCAT TCCATTTA		
			ATTAGAGTG GGGTAAAT		
			GGTGGATG		
GAM1965	SPINLW1	3'	TGAGTGTATACCCAGTAATGGG 21667	TT GTTG	C_
	ATTG		AGT CAT GGGT CATTTA		
			TTA GTA CCCA GTGAGT		
			GG ATGA TAT		
GAM1965	SSH2	3'	TGGAAGCTCCTAGTAGAGGCTG 31188	A	_____
			TAGTTTC TGTTGGGG TCCA		
			GTCGGAG ATGATCCT AGGT		
			_ CGA		
GAM1965	SSH2	3'	TAAGTGGGTATACGCTGAAGCT 31186	_	TGGG
	G		TAGTTTCA TGT GTCCATTTA		
			GTCGAAGT GCA TGGGTGAAT		
			C TA_		
GAM1965	STK38L	3'	TGAATGGAAAATAAGTGTGGAG 34293	TG	GGGG_
			TTTCA TT TCCATTTA		

GAGGT GA AGGTAAGT
 GT ATAAA
 GAM1965 STMN3 3' TGAGACCACCTGGCGTGAGGT 18041 TT _ _ _ TTTA
 G TCATGTT GG GGTC CA
 | ||||| || |||||
 T AGTGCGG CC CCAG GT
 GG T A A A
 GAM1965 STOML1 3' TGAATGGAGGCTGCAGGAGGCT 11234 A T GG
 G TAGTTTC TGT GG TCCATTTA
 ||||| ||| || |||||
 GTCGGAG ACG TC AGGTAAGT
 G _ GG
 GAM1965 SUPT4H1 3' TGGATTAACAGATGGAATTG 9146 G GG_
 TAGTTTCAT TTG GTCCA
 ||||| ||| |||||
 GTTAAGGTA GAC TAGGT
 _ AAT
 GAM1965 SV2 3' TCCCAGTTTTGAGATGAAGCTG 16886 G_____
 TAGTTTCAT T TGGGG
 ||||| | |||||
 GTCGAAGTA A ACCCT
 G GTTTTG
 GAM1965 SYNCOILIN 3' TAAATAAAACCCATCAGCATGG 25081 TT _ CCATTTA
 GGTTA G TCATGTTG GGGT
 | ||||| |||||
 T GGTACGAC CCCA
 GG TA AAATAAAT
 GAM1965 TAO1 3' ATGGGAGCCCCTCTCAGCTGTG 11189 _ _ _ ATTTA
 GGGCTG CAT GTT GGGG TCC
 ||| ||| |||||
 GTG CGA CCCC AGG
 T CTCT G GT AT
 GAM1965 TBL1Y 5' TGGCCTCAGTGTGGCATTG 27100 T TG T
 TAGT TCA TTGGGG CCA
 |||| ||| ||||| |||||
 GTTA GGT GACTCC GGT
 C GT _
 GAM1965 TBL1Y 5' TGGCCTCAGTGTGGCATTG 28611 T TG T
 TAGT TCA TTGGGG CCA
 |||| ||| ||||| |||||
 GTTA GGT GACTCC GGT
 C GT _
 GAM1965 TED 3' TGAATGGGAGGGCGGGCCTGGA 17922 T GGGG_
 GCTG AGTTTCA GTT TCCATTTA
 ||||| ||| |||||
 TCGAGGT CGG GGGTAAGT
 C GCGGGA
 GAM1965 TERE1 5' AGCCGTGGGCTCTAACGCGGGG 14966 TT A TTA
 CTG TAGT C TGTTGGGGTCCAT
 |||| | ||||| |||||

GTCG G GCAATCTCGGGTG
 GG C CCGAC
 GAM1965 TIP47 3' TAAGTGGGCCTCCTGGGGAT 12418 TT ATGTT
 GT C GGGGTCCATTTA
 || | |||||
 TA G CTCCGGGTGAAT
 GG GTC__
 GAM1965 TOMM34 3' GAGCTAAGCGTGAAGCTG 13681 G G
 TAGTTTCATGTT GG TC
 ||||| || ||
 GTCGAAGTGCGA TC AG
 A G
 GAM1965 TOPK 3' ATGGATAACTATTTCTAATATG 20553 _____ TTTA
 AAAT CATGTTGGG GTCCA
 ||||| ||||
 GTATAATCT TAGGT
 TTATCAA AT
 GAM1965 TRIM2 3' ATGTCCTAACATGGAGTTA 17599 GT TC
 TA TTCATGTTGGGG CAT
 || ||||| |||
 AT AGGTACAATCCT GTA
 TG ____
 GAM1965 UBCE7IP5 3' TGGGTGGATCACTTGAGG 17274 T TGG
 TTTCA GT GGTCCATTTA
 |||| || |||||
 GGAGT CA CTAGGTGGGT
 T ____
 GAM1965 UQCR 3' TGAGGAAGGCTCAACTGGGGCT 13712 TT T G__ ATTTA
 G TAGT CA GTTGGG TCC
 |||| || ||||| |||
 GTCG GT CAACTC AGG
 GG _ GGA AGT
 GAM1965 VIT1 5' TGGGTGGATCATTTGAGG 20768 TGTTGG
 TTTCA GGTCCATTTA
 |||| |||||
 GGAGT CTAGGTGGGT
 TTA__
 GAM1965 VPS4B 3' TGGGTGGATCACCTGAGG 11295 TGTT _
 TTTCA GG GGTCCATTTA
 |||| || |||||
 GGAGT CC CTAGGTGGGT
 ____ A
 GAM1965 WBSCR17 3' GGGTGCCCCCGATGGGAGGCTG 39547 AT TC A
 TAGTTTC GTTGGGG CATT
 ||||| ||||| |||||
 GTCGGAG TAGCCCC GTGGG
 GG C_ G
 GAM1965 WIT-1 3' TGGAATTCCAGTCTGAGGTTA 17993 TT TG _
 TAG TCA TTGGGGT CCA
 ||| ||| ||||| |||

		ATT AGT GACCTTA GGT		
		GG CT A		
GAM1965 WSB1	3'	TAAATGGATTTTCAGTATAGCT 28618	TC	GG
		AGTT ATGTTG GTCCATTTA		
		TCGA TATGAC TAGGTAAAT		
		— TT		
GAM1965 ZAK	3'	ACCTTCTAATTGAGACTA 18777	T	—
		TAGTTTCA GTTGG GGT		
		ATCAGAGT TAATC CCA		
		— TT		
GAM1965 ZDHC7	3'	CGTGTGGGCTTCAGTGTGAGGC 19331	TG	TTA
T		AGTTTCA TTGGGGTCCAT		
		TCGGAGT GACTTCGGGTG		
		GT TGCG		
GAM1965 ZER6	3'	TGAGTGGAATTTCAAGCATTTGC 31746	TTC	_GG
		GT ATGTT G GTCCATTTA		
		CG TACGA C TAGGTGAGT		
		TT_ A TT		
GAM1965 ZID	3'	AAAATTATACCATTTGGCATGAA 13413	TG_	CCATTTA
GCTG		AGTTTCATGT G GGT		
		TCGAAGTACG T CCA		
		GT A TATTAAAT		
GAM1965 ZNF237	5'	TGAGGCTTTGGCAGAAATTA 15506	A TG	_
		TAGTTTC TGT GGGTC CA		
		ATTAAAG ACG TTCGG GT		
		_ GT A		
GAM1965 ZNF237	3'	TGGATGTATAACATGAAGCTG 15507	GG_	
		TAGTTTCATGTTG GTCCA		
		GTCGAAGTACAAT TAGGT		
		ATG		
GAM1965 ZNF287	5'	TGTGACTCTAGCATGAGACT 21820	—	
		AGTTTCATGTTGGGGTC CA		
		TCAGAGTACGATCTCAG GT		
		T		
GAM1965 ZNF297B	3'	TGGGTGGATCACCTGAGG 15223	TGTT	_
		TTTCA GG GGTCCATTTA		
		GGAGT CC CTAGGTGGGT		
		— A		
GAM1965 ZNF31	5'	TGAAGAACTCCTGATTGTGAAA 32423	TT_	CCATTTA
CTG		AGTTTCATG GGGGT		

	TCAAAGTGT CCTCA	
	TAGT AGAAGT	
GAM1965 ZNF33A 3'	TGGGTGACAGAATGAGACTG 43901	G GG
	TAGTTTCAT TTG GTCCA	
	GTCAGAGTA GAC TGGGT	
	A AG	
GAM1965 LOC113523 3'	GGTGCCAACATGAAGCTA 36154	G T
	TAGTTTCATGTTGG G CC	
	ATCGAAGTACAACC T GG	
	G _	
GAM1965 LOC113523 3'	TGGATGGTAGCATGAGCTG 36155	T GG
	TAGTT CATGTTG GTCCA	
	GTCGA GTACGAT TAGGT	
	_ GG	
GAM1965 LOC114932 3'	GATGACCTCGATATGGA 36007	C
	TTCATGTTGGGGTC ATT	
	AGGTATAGCTCCAG TAG	
	_	
GAM1965 LOC115297 3'	GAGTCCATCACTGTGAAATTG 36071	_ _ G
	TAGTTTCAT GT TGGG TC	
	GTAAAGTG CA ACCT AG	
	T CT G	
GAM1965 LOC116166 3'	TGGGTGGGCTCTGATGCAGAAC 30061	CA TG
T	AGTTT TGT GGGTCCATTTA	
	TCAAG GTA CTCGGGTGGGT	
	AC GT	
GAM1965 LOC120196 3'	AATGGACTGGAATTG 37217	ATGTTGG
	TAGTTTC GGTCCATT	
	GTAAAG TCAGGTAA	
	G _	
GAM1965 LOC120526 3'	TGAGTGGGCTGAGCATGTAGAC 36624	_ G G
TA	TAGTTT CATGTT GG TCCATTTA	
	ATCAGA GTACGA TC GGGTGAGT	
	T G _	
GAM1965 LOC121219 5'	GTGGGTGGGGGGAGCTTGGAGC 36651	T GGGG
TG	TAGTTTCA GTT TCCATTTA	
	GTCGAGGT CGA GGGTGGGT	
	T GGG_ GG	
GAM1965 LOC121601 5'	GGAATTTGGTATGGAATT 36673	TT G
	AGTTTCATG GGG TCC	

	TTAAGGTAT TTT AGG	
	GG A	
GAM1965 LOC122786 3'	TAAAGTTCTCCAGATGGAGCTA 36700	G TCCA
	TAGTTTCAT TTGGGG TTTA	
	ATCGAGGTA GACCTC AAAT	
	_ TTG_	
GAM1965 LOC124145 3'	ACCTTAATATTGAACTA 36734	_
	TAGTTTCA TGTTGGGGT	
	ATCAAAGT ATAATTCCA	
	T	
GAM1965 LOC124446 5'	GTCTGGGCTCTGGCTGGA ACTA 36752	T TG TTTA
	TAGTTTCA GT GGGTCCA	
	ATCAAGGT CG CTCGGGT	
	_ GT CTGT	
GAM1965 LOC124944 5'	TGAGTGGGGGCGAGCACGGGGC 36778	TT A GGGG
TG	TAGT C TGTT TCCATTTA	
	GTCG G ACGA GGGTGAGT	
	GG C GCGG	
GAM1965 LOC126167 5'	TGAGGCGTCCCGGCGAGGAGCT 36814	A _ _ TTTA
G	AGTTTC TGTTGGG GTC CA	
	TCGAGG GCGGCCCG CGG GT	
	A TG A A	
GAM1965 LOC126917 3'	TGAATGGCTTGAGTGGGACTG 36876	TT G TG GT
	TAGT CAT T GG CCATTTA	
	GTCA GTG A TC GGTAAGT	
	GG _ GT _	
GAM1965 LOC126964 3'	TGGAACCTGGTATGAGAT 36885	TT G
	GTTTCATG GGG TCCA	
	TAGAGTAT TCC AGGT	
	GG A	
GAM1965 LOC127162 3'	TGGGAATCTCTAATGTGAAA 36887	_ ATTTA
	TTTCATGTTGGGG TCC	
	AAAGTGTAATCTC AGG	
	TA GT	
GAM1965 LOC127281 3'	GGAGACCTGACTGGA ACTG 36889	T TG G_
	TAGTTTCA GT GG TCC	
	GTCAAGGT CA CC AGG	
	_ GT AG	
GAM1965 LOC127534 3'	TAGGTGGACCTCAGAGAGGA 37173	ATG
	TTC TTGGGGTCCATTTA	

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AGG GACTCCAGGTGGAT
AGA
GAM1965 LOC127841 5' TAGGTGGGCCAAGTCCTGGCAG 36910 A TG _____
GAGCTG TC TGT GG GTCCATTTA
|| ||| || |||||
GG ACG CC CGGGTGGAT
_ GT TGAAC
GAM1965 LOC128077 3' TAGATGGGGGTTATGGTTGAAA 36919 TGT_ GG
CTG TAGTTTCA TGG TCCATTTA
||||| ||| |||||
GTCAAAGT ATT GGGTAGAT
TGGT GG
GAM1965 LOC129198 5' TAAATGGACTTATTGAAGC 37465 TGTTG
GTTTCA GGGTCCATTTA
||||| |||||
CGAAGT TTCAGGTAAAT
TA__
GAM1965 LOC133022 3' TAAATGGGAATTCATGAAATTA 37376 TTGGGG
TAGTTTCATG TCCATTTA
||||| |||||
ATTAAAGTAC GGGTAAAT
TTAA__
GAM1965 LOC133088 5' GGACCTCAGTGTGAAGCT 37032 TG
AGTTTCA TTGGGGTCC
||||| |||||
TCGAAGT GACTCCAGG
GT
GAM1965 LOC133584 3' TGGGTGGGCAACTTGGGGAGCT 37048 ATGTTGGG
G TAGTTTC GTCCATTTA
||||| |||||
GTCGAGG CGGGTGGGT
GGTTCAA_
GAM1965 LOC134121 3' TGATTTTCAGCTGGAATTA 37065 T GG TC
TAGTTTCA GTTG G CA
||||| ||| | ||
ATTAAGGT CGAC T GT
_ TT TA
GAM1965 LOC134147 3' TGGGTGGATCACCTGAGG 29033 TGTT _
TTTCA GG GGTCCATTTA
||||| |||||
GGAGT CC CTAGGTGGGT
_ A
GAM1965 LOC134147 3' TGGGTGGATCACTTGAGG 29034 T TGG
TTTCA GT GGTCCATTTA
||||| |||||
GGAGT CA CTAGGTGGGT
T _
GAM1965 LOC135293 3' TAGGTGGACCTGCTTGAGGT 37496 TT T TG
G TCA GT GGGTCCATTTA
| ||| || |||||

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	T AGT CG TCCAGGTGGAT	
	GG T _	
GAM1965 LOC135818 3'	TGGATGGATTACAAAGAAA 37096	A TG
	TTTC TGT GGGTCCATTTA	
	AAAG ACA CTTAGGTAGGT	
	A _	
GAM1965 LOC139221 3'	GGCTTAACATGAAACTG 37333	GT
	TAGTTTCATGTTGGG CC	
	GTCAAAGTACAATTC GG	
	—	
GAM1965 LOC139248 5'	TACCACCATCCCAGCTGTGAGG 37338	_ CCATTTA
CTG	TAGTTTCAT GTTGGGGT	
	GTCGGAGTG CGACCCTA	
	T CCACCAT	
GAM1965 LOC139770 3'	GAATGGAATTGTGAAGC 37146	TTGGGG
	GTTTCATG TCCATT	
	CGAAGTGT AGGTAAG	
	TA _	
GAM1965 LOC139770 3'	TGAATGGATGGATGAATGGAAT 37148	GTTGGG
TG	TAGTTTCAT GTCCATTTA	
	GTTAAGGTA TAGGTAAGT	
	AGTAGG	
GAM1965 LOC139770 3'	TGGATGGATGAATGGAATTG 37149	GTTGGG
	TAGTTTCAT GTCCATTTA	
	GTTAAGGTA TAGGTAGGT	
	AG _	
GAM1965 LOC142973 5'	TGAATGACCACAACGTGAAGT 30240	GT _ G C
TA	TA TTCAT GTTG GGTC ATTTA	
	AT AAGTG CAAC CCAG TAAGT	
	TG T A _	
GAM1965 LOC143188 5'	TGAGTGGGTTCACAGGAAAC 40328	A T GG
	GTTTC TGT GG TCCATTTA	
	CAAAG ACA CC GGGTGAGT	
	G _ TT	
GAM1965 LOC143465 5'	TGAGTGGATCCTGGTAAATAC 40365	TTCA TT
	GT TG GGGGTCCATTTA	
	CA AT TCCTAGGTGAGT	
	TAA_ GG	
GAM1965 LOC144245 3'	TAGGTGGAAAACATGGAATT 35051	GGGG
	AGTTTCATGTT TCCATTTA	

	TTAAGGTACAA AGGTGGAT		
	A____		
GAM1965 LOC144266 5'	AAGTGCAGCATGGGACTA 37707	TT	GGGTC
	TAGT CATGTTG CATTT		
	ATCA GTACGAC GTGAA		
	GG _____		
GAM1965 LOC144512 5'	GACTTCTAGTGTGGAAGTG 40430	G	TG _
	TA TTTCA TTGGG GTC		
	GT AAGGT GATCT CAG		
	G GT T		
GAM1965 LOC144512 5'	GAGTGCAAGCATGGAAC 40431		GGGGTC
	GTTTCATGTT CATTT		
	CAAGGTACGA GTGAG		
	AC_____		
GAM1965 LOC144524 3'	TAAGTGGATCACCTGAGG 40434	TGTT	_
	TTTCA GG GGTCCATTTA		
	GGAGT CC CTAGGTGAAT		
	____ A		
GAM1965 LOC144920 3'	ACTCTCAATGTGATGATTA 40464	_	-
	TAGTT TCATGTTGGG GT		
	ATTAG AGTGTA ACTC CA		
	T T		
GAM1965 LOC145082 5'	TGGGTGGATCACCTGAGAT 40495	TGTT	_
	GTTTCA GG GGTCCATTTA		
	TAGAGT CC CTAGGTGGGT		
	____ A		
GAM1965 LOC145231 3'	TGGGTGACAGTGTGAAACT 40522	TG	GG
	AGTTTCA TTG GTCCA		
	TCAAAGT GAC TGGGT		
	GT AG		
GAM1965 LOC145231 3'	TGGGTGGGTCCCTTAGGGAGC 40523	ATGTT	GT
	GTTTC GGG CCATTTA		
	CGAGG TCC GGTGGGT		
	GAT__ TG		
GAM1965 LOC145368 5'	TAAATGGACTTCATGAGGAAAT 37829	ATGT	
	GTTTC TGGGGTCCATTTA		
	TAAAG ACTTCAGGTAAAT		
	GAGT		
GAM1965 LOC145497 5'	GGATGCCCCCAGATGAGATTG 37874	G	TC A
	TAGTTTCAT TTGGGG CATTT		

GTTAGAGTA GACCCC GTAGG
 _ C_ G
 GAM1965 LOC145547 3' ATCTTGCCATGAAACTG 37891 _ TG
 TAGTTTCATG T GGGT
 ||||| | |||
 GTCAAAGTAC G TCTA
 C GT
 GAM1965 LOC145662 3' TGGGTGGATCACCTGAGG 37918 TGTT _
 TTTC A GG GGTCCATTTA
 ||| || |||||
 GGAGT CC CTAGGTGGGT
 _ A
 GAM1965 LOC145761 5' GGCCCTGGCAGGAGATTA 40585 A TG
 TAGTTTC TGT GGGTC
 |||| | |||
 ATTAGAG ACG CCCGG
 G GT
 GAM1965 LOC145955 5' TGGGTGGGCTTCAGGCTGGGGC 40646 TT TG
 TG TAGT CA TTGGGGTCCATTTA
 ||| || |||||
 GTCG GT GACTTCGGGTGGGT
 GG CG
 GAM1965 LOC145988 5' TGGATGGACTGTTGGGTACTG 38043 _ TGTG
 TAGT TTCA GGTCCATTTA
 ||| ||| |||||
 GTCA GGGT TCAGGTAGGT
 T TG____
 GAM1965 LOC146108 5' TAAGTGGGCCTGCTTGAAGTTG 38063 GT T TG
 TA TTCA GT GGGTCCATTTA
 || ||| || |||||
 GT AAGT CG TCCGGGTGAAT
 TG T _
 GAM1965 LOC146315 5' TGGGTGGACAGACAGGGGCTG 30535 TT A GGG
 TAGT C TGTT GTCCATTTA
 ||| | ||| |||||
 GTCG G ACAG CAGGTGGGT
 GG _ A_
 GAM1965 LOC146336 3' TGGGCACTGACAGTGAGGCTG 38134 _ TG G
 TAGTTTCA TGT G GTCCA
 ||||| || | |||
 GTCGGAGT ACA C CGGGT
 G GT A
 GAM1965 LOC146445 3' TGGGTTGACGTGCATGGAGCTG 40699 _ G_ GT
 TAGTTTCATGT TG G CCA
 ||||| || | |||
 GTCGAGGTACG GC T GGT
 T AG TG
 GAM1965 LOC146745 5' TGCCCTCCAATGTGGGGCTG 38232 TT TC
 TAGT CATGTTGGGG CA
 ||| ||||| ||

	GTCG GTGTAACCTC GT	
	GG CC	
GAM1965 LOC146756 3'	TGAATGTGAGCCGATATGCAGC 40740	T G G _
TG	TAGTT CATGTTG G TC CATTTA	
	GTCGA GTATAGC C AG GTAAGT	
	C _ G T	
GAM1965 LOC146802 3'	TGGTCATCCGCCGTGGGGCTG 38248	TT T GT_
	TAGT CATG TGGG CCA	
	GTCG GTGC GCCT GGT	
	GG C ACT	
GAM1965 LOC146839 5'	GACCCGAAATGAGGCTA 40755	G G
	TAGTTTCAT TT GGGTC	
	ATCGGAGTA AA CCCAG	
	_ G	
GAM1965 LOC146880 3'	GAGGTCAATGTGGAGCTG 38262	GG
	TAGTTTCATGTTGG TC	
	GTCGAGGTGTA ACT AG	
	GG	
GAM1965 LOC146880 3'	TGAGAACTAGGTGAACTG 38263	G GG _
	TAGTTTCAT TTGG TC CA	
	GTCAAAGTG GATC AG GT	
	_ AA A	
GAM1965 LOC147071 5'	GGAACCTTA ACTTGGGGCTA 36138	TT T G
	TAGT CA GTTGGG TCC	
	ATCG GT CAATTC AGG	
	GG T A	
GAM1965 LOC147077 3'	TAAATTGACTTCAGTGGTGAGA 38292	_ GT C
CTG	TAGTTTCA T TGGGGTC ATTTA	
	GTCAGAGT G ACTTCAG TAAAT	
	G TG T	
GAM1965 LOC147160 5'	TGGATGGGCCCCACCGCGGGG 40811	TT A T
	T C TG TGGGGTCCATTTA	
	G G GC ACCCCGGGTAGGT	
	GG C C	
GAM1965 LOC147229 5'	TGGCCCTGGTGAGAGGCTA 38323	A TT T
	TAGTTTC TG GGGG CCA	
	ATCGGAG GT TCCC GGT	
	A GG _	
GAM1965 LOC148029 5'	GGACTAGGGTGAGGCTG 38446	G GG
	TAGTTTCAT TT GGTCC	

GTCGGAGTG GA TCAGG
 G _
 GAM1965 LOC148223 3' AAGTGGCTTTGACGTGGGGC 38493 TT TG T A
 GT CATGT GGG CCATTT
 || |||| || ||||
 CG GTGCA TTC GGTGAA
 GG GT _ G
 GAM1965 LOC148394 3' TGGGTGGACTCCAGCCTCCCCA 40882 TCAT_
 GC GTT GTTGGGGTCCATTTA
 || |||||
 CGA CGACCTCAGGTGGGT
 CCCCTC
 GAM1965 LOC148479 3' TGTGACTTTAGAATGGAAGT 38543 G _
 TAGTTTCAT TTGGGGTC CA
 ||||| ||||| ||
 GTCAAGGTA GATTTCAG GT
 A T
 GAM1965 LOC148823 3' TGAATGGACCCTCTTCTAGGC 29796 CATGTT
 GTTT GGGGTCCATTTA
 ||| |||||
 CGGA TCCCAGGTAAGT
 TCTTC_
 GAM1965 LOC148887 5' TGGGTGGGCTCTGCCAGAG 40912 A TT
 TTC TG GGGGTCCATTTA
 ||| || |||||
 GAG AC TCTCGGGTGGGT
 _ CG
 GAM1965 LOC149010 5' GACCCTCAGGTGAGACTA 38628 G _
 TAGTTTCAT TTG GGGTC
 ||||| || ||||
 ATCAGAGTG GAC CCCAG
 _ T
 GAM1965 LOC149013 3' TGGATGGTGGTGACATGGACT 38634 T GGGGT
 AGTT CATGTT CCATTTA
 ||| |||| |||||
 TCAG GTACAG GGTAGGT
 _ TGGT_
 GAM1965 LOC149086 3' TGGGTGGGCCAGGATGGCACTG 40947 T G GG
 TAGT TCAT TT GGTCCATTTA
 ||| ||| || |||||
 GTCA GGTA GA CCGGGTGGGT
 C G _
 GAM1965 LOC149127 3' GAGTGGAGTATGGGGCTG 40950 TT TTGGGG
 TAGT CATG TCCATTT
 ||| ||| |||||
 GTCG GTAT AGGTGAG
 GG G____
 GAM1965 LOC149153 3' TGGGCATTGGTATGGAAT 40966 TT G
 GTTTCATG GG GTCCA
 ||||| || ||||

TAAGGTAT TT CGGGT
 GG A
 GAM1965 LOC149175 3' TGGGGTTCAGCTGAGGTTG 38664 TT T G
 TAG TCA GTTGGG TCCA
 ||| ||| ||||| ||||
 GTT AGT CGACTT GGGT
 GG _ G
 GAM1965 LOC149175 3' TGGGTGGGCCGTCAGGCATGGG 38665 TT _ _
 CCTG AG TCATGT TGG GGTCCATTTA
 || ||||| ||| |||||
 TC GGTACG ACT CCGGGTGGGT
 CG G G
 GAM1965 LOC149182 5' TGGGTGGGGCACATGGGAC 40972 TT T GGG
 GT CATGT G TCCATTTA
 || ||||| ||| |||||
 CA GTACA C GGGTGGGT
 GG _ G_
 GAM1965 LOC149271 3' TGGGTGGATCACCTGAGG 38684 TGTT _
 TTTCA GG GGTCCATTTA
 |||| ||| |||||
 GGAGT CC CTAGGTGGGT
 _ A
 GAM1965 LOC149271 3' TGAGCTCCAGATGGAGCTA 38683 G TC
 TAGTTTCAT TTGGGG CA
 ||||| ||||| ||
 ATCGAGGTA GACCTC GT
 _ GA
 GAM1965 LOC149317 3' TGGATGGTGGTGACATGGACT 38710 T GGGGT
 AGTT CATGTT CCATTTA
 ||| ||||| |||||
 TCAG GTACAG GGTAGGT
 _ TGGT_
 GAM1965 LOC149319 3' TGGGTGGATCACCTGAGG 38713 TGTT _
 TTTCA GG GGTCCATTTA
 |||| ||| |||||
 GGAGT CC CTAGGTGGGT
 _ A
 GAM1965 LOC149464 3' TGGGTGGATCACCTGAGG 40995 TGTT _
 TTTCA GG GGTCCATTTA
 |||| ||| |||||
 GGAGT CC CTAGGTGGGT
 _ A
 GAM1965 LOC149464 5' TGGGTGGATTGCTTGAGTCTA 40996 T T TGG
 TAG TTCA GT GGTCCATTTA
 ||| ||| ||| |||||
 ATC GAGT CG TTAGGTGGGT
 T T _
 GAM1965 LOC149566 3' TGGTTTCTCAACATGAGG 41018 T_
 TTTCATGTTGGGG CCA
 ||||| |||

	GGAGTACAACTCT GGT	
	TT	
GAM1965 LOC149606 3'	TGGATGGGTCCTTTGGA ACT 38785	TGTT GT
	AGTTTCA GGG CCATTTA	
	TCAAGGT TCC GGTAGGT	
	T__ TG	
GAM1965 LOC149684 5'	GGGCTCCAGCAGAGGCTG 41049	A
	TAGTTTC TGTTGGGGTCC	
	GTCGGAG ACGACCTCGGG	
	—	
GAM1965 LOC149692 3'	TGGATGGGTCCCTGAAA 41041	TGTT GT
	TTTCA GGG CCATTTA	
	AAAGT CCC GGTAGGT	
	__ TG	
GAM1965 LOC149711 5'	TGGGACCTGACTTGAACTA 41076	T TG GT
	TAGTTTCA GT GG CCA	
	ATCAAAGT CA CC GGT	
	T GT AG	
GAM1965 LOC149722 5'	TGAATGGGTATTTTGTGAAAT 41045	TT GG
	GTTTCATG GG TCCATTTA	
	TAAAGTGT TT GGGTAAGT	
	T_ AT	
GAM1965 LOC149773 5'	TGGATCACCGGGATGAAGCTG 38801	G _
	TAGTTTCAT TTGG GGTCCA	
	GTCGAAGTA GGCC CTAGGT	
	G A	
GAM1965 LOC150150 5'	GGA CTCCAACGTGGGCT 41137	T
	AGTT CATGTTGGGGTCC	
	TCGG GTGCAACCTCAGG	
	—	
GAM1965 LOC150299 3'	TGAATGCACTTTGATGTGAGAC 41183	TG C
	GTTTCATGT GGGT CATTTA	
	CAGAGTGTA TTCA GTAAGT	
	GT C	
GAM1965 LOC150365 5'	TGAGCTTCTGTTATGAAGCTG 38913	TT_ TC
	TAGTTTCATG GGGG CA	
	GTCGAAGTAT CTTC GT	
	TGT GA	
GAM1965 LOC150423 5'	TAAATGGACTTCATGAGGAAAT 38969	ATGT
	GTTTC TGGGGTCCATTTA	

	TAAAG ACTTCAGGTAAAT	
	GAGT	
GAM1965 LOC150468 3'	TGAATGGACCTTGACAGATGGC 38976	TCA TG
	GTT TGT GGGTCCATTTA	
	CGG ACA TCCAGGTAAGT	
	TAG GT	
GAM1965 LOC150848 5'	TGGTTTTTCAGATGAAATTG 41259	G GG T
	TAGTTTCAT TTG G CCA	
	GTAAAGTA GAC T GGT	
	_ TT T	
GAM1965 LOC150933 3'	TAAGTGGGTCTTTTAAACT 41272	CATGTT GT
	AGTTT GGG CCATTTA	
	TCAA TTC GGTGAAT	
	TT___ TG	
GAM1965 LOC150998 3'	TGGGTGGAGAGATGTGTAAGT 41288	T GGGG
	TAGTT CATGTT TCCATTTA	
	GTCAA GTGTAG AGGTGGGT	
	T AG__	
GAM1965 LOC151124 5'	TGGCCTCTGATGTGAAAGTG 41303	G TG T
	TA TTTTCATGT GGG CCA	
	GT AAAGTGTA CTC GGT	
	G GT C	
GAM1965 LOC151126 3'	TGGGTGTATTCTAGTGTGGAAC 39059	TG C
	GTTTCA TTGGGGT CATTTA	
	CAAGGT GATCTTA GTGGGT	
	GT T	
GAM1965 LOC151146 5'	TGGGCTTAGTTGGCTGGGATTG 39062	TT T TG__
	TAGT CA GT G GGTCCA	
	GTTA GT CG T TCGGGT	
	GG _ GT GAT	
GAM1965 LOC151201 3'	TGAATTCTCTTTAGCATAAAGC 41322	C TCC
TG	TAGTTT ATGTTGGGG ATTTA	
	GTCGAA TACGATTTC TAAGT	
	A TCT	
GAM1965 LOC151405 5'	TAGATGGGCTTTAGTAAAGACT 41340	CA
G	TAGTTT TGTTGGGGTCCATTTA	
	GTCAGA ATGATTTCGGGTAGAT	
	A_	
GAM1965 LOC151446 5'	TGAATGGCAGGATATGAAGC 41352	GGG T
	GTTTCATGTT G CCATTTA	

CGAAGTATAG C GGTAAGT
GA__

GAM1965 LOC151568 5' TGGGTGGGCTGAGTGGAGGTG 28839 G GTTGG
TA TTTTCAT GGTCCATTTA
|| ||||| |||||
GT GAGGTG TCGGGTGGGT
G AG__

GAM1965 LOC151602 3' TAAGTGGGTCTCCAAAGTGGGG 39140 TT G _
CT AGT CAT TTGGGG TCCATTTA
||| ||| ||||| |||||
TCG GTG AACCTC GGGTGAAT
GG A T

GAM1965 LOC151643 3' AAATGGAACCAGAGGTTA 39152 TT ATGT GG
TAG TC TGG TCCATTT
||| || ||| |||||
ATT AG ACC AGGTAAA
GG ____ A_

GAM1965 LOC151904 5' TGCCCTGACTCCGATGGTGAAA 39174 _ CATTTA
CTG TAGTTTCAT GTTGGGGTC
||||||| |||||
GTCAAAGTG TAGCCTCAG
G TCCCGT

GAM1965 LOC151959 3' TGGGCTGATTTGGAAGT 41410 T GG
TAGTTTCA GTT GGTCCA
||||||| ||| |||||
GTCAAGGT TAG TCGGGT
T _

GAM1965 LOC152018 3' TGCACTCTGATATCAGACTG 41423 C TG C
TAGTTT ATGT GGGT CA
||||||| ||||| |||||
GTCAGA TATA CTCA GT
C GT C

GAM1965 LOC152137 3' TAAATTAATTCAACATGAAGTT 39223 GT GTCC
G TA TTCATGTTGGG ATTTA
|| ||||| |||||
GT AAGTACAACCTT TAAAT
TG AAT_

GAM1965 LOC152315 5' ACTCCAGGCTCTAACCTGGAGC 39255 T CATTTA
TG TAGTTTCA GTTGGGGTC
||||||| |||||
GTCGAGGT CAATCTCGG
C ACCTCAA

GAM1965 LOC152345 3' TGGTTCTCCAGCAGGAACTG 39268 A T_
TAGTTTC TGTTGGGG CCA
||||||| ||||| |||
GTCAAGG ACGACCTC GGT
_ TT

GAM1965 LOC152627 5' TAAGTTGAAGCCAATATGAA 39296 GG C
TTCATGTTGG TC ATTTA
||||||| || |||||

	AAGTATAACC AG TGAAT	
	GA T	
GAM1965 LOC152804 3'	TAAGTGGGCCTCCTGAAAC 41557	TGTT
	GTTTCA GGGGTCCATTTA	
	CAAAGT CTCCGGGTGAAT	
	C__	
GAM1965 LOC152804 3'	TGGATGGATCACCTGAGG 41558	TGTT _
	TTTCA GG GGTCCATTTA	
	GGAGT CC CTAGGTAGGT	
	____ A	
GAM1965 LOC152845 5'	AAGTGCCAATGTGAAATT 30256	GGTC
	AGTTTCATGTTGG CATTT	
	TTAAAGTGTAACC GTGAA	

GAM1965 LOC152860 3'	TGGAGGTTGATGTGAGCTG 39326	T TG GG
	TAGTT CATGT G TCCA	
	GTCGA GTGTA T AGGT	
	_ GT GG	
GAM1965 LOC153516 5'	TGGACAATCAGCATGGAAT 28843	G_
	GTTTCATGTTGG GTCCA	
	TAAGGTACGACT CAGGT	
	AA	
GAM1965 LOC153688 3'	TGTCTCCCAGCAGAGACTA 41662	A TC
	TAGTTTC TGTTGGGG CA	
	ATCAGAG ACGACCCT GT	
	_ CT	
GAM1965 LOC153810 3'	TGGATGTGAGACATGGAAT 39413	GGG_
	GTTTCATGTT GTCCA	
	TAAGGTACAG TAGGT	
	AGTG	
GAM1965 LOC153811 3'	TGGAAGCCAGAGTGGGGCTG 39419	TT G GG
	TAGT CAT TTGG TCCA	
	GTCG GTG GACC AGGT	
	GG A GA	
GAM1965 LOC153910 5'	GAATGGATTAATGGAAC 39440	GTTGGG
	GTTTCAT GTCCATT	
	CAAGGTA TAGGTAAG	
	AT__	
GAM1965 LOC154222 3'	TGGAGCAATTTCCAGCAGAAAGT 41694	T A ____ TTTA
TG	TTC TGTTGGGG TCCA	

	AAG ACGACCTT AGGT	
	G _ TAACG A	
GAM1965 LOC154739 5'	AAATGGATTCTCAGTTTG 41710	TG _
	CA TTG GGGTCCATTT	
	GT GAC CTTAGGTAAA	
	TT T	
GAM1965 LOC155060 3'	TGGTTCCTAGCTGTGGGGCTG 41751	TT _ GT
	TAGT CAT GTTGGG CCA	
	GTCG GTG CGATCC GGT	
	GG T TT	
GAM1965 LOC155179 3'	TGAGTGACCTGACTGAGACTA 39561	T TG GTC
	TAGTTTCA GT GG CATTTA	
	ATCAGAGT CA CC GTGAGT	
	_ GT A_	
GAM1965 LOC157381 3'	TAAGTGGGCTCTAGGGGAAGGT 41791	G ATG
A	TA TTTC TTGGGGTCCATTTA	
	AT GAAG GATCTCGGGTGAAT	
	G GG_	
GAM1965 LOC157506 3'	TGGATGGACTCTTATCTAGAAT 39602	CATGTT
	GTTT GGGGTCCATTTA	
	TAAG TCTCAGGTAGGT	
	ATCTAT	
GAM1965 LOC157621 3'	TGGATGGACTCCAGAGGG 41825	ATG
	TC TTGGGGTCCATTTA	
	GG GACCTCAGGTAGGT	
	GA_	
GAM1965 LOC157624 5'	TGAGTTTCAAATGTGGAAGT 41827	_ GG TC
	TAGTTTCATGTT G G CA	
	GTCAAGGTGTAA C T GT	
	A TT GA	
GAM1965 LOC158055 3'	TGGTGCTTGCTGTGAGACTG 39707	_ T G T
	TAGTTTCAT GT GG G CCA	
	GTCAGAGTG CG TC T GGT	
	T T G _	
GAM1965 LOC158056 5'	GAGTGGGTCTGAGGCTG 39715	TGTTGG GT
	TAGTTTCA G CCATTT	
	GTCGGAGT C GGTGAG	
	_____ TG	
GAM1965 LOC158301 3'	TAAATGCTGACCTAATGTGGA 39812	GTC_
	TTCATGTTGGG CATTTA	

	AGGTGTAATCC GTAAAT		
	AGTC		
GAM1965 LOC158308 5'	TGGCCTCCAGCATGAGCCTG 41942	T	T
	TAG TTCATGTTGGGG CCA		
	GTC GAGTACGACCTC GGT		
	C C		
GAM1965 LOC158332 3'	TGGACCTGCCAGCGTGTGAACT 39826	_	_ TTTA
G	AGTTT CATGTTGG GGTCCA		
	TCAAG GTGCGACC CCAGGT		
	T GT A		
GAM1965 LOC158382 5'	TGGGGATCAAATTTCAACATGA 41969	_____	ATTTA
GGTT	TCATGTTGG GGTCC		
	AGTACAACT CTAGG		
	TTAAA GGT A		
GAM1965 LOC158427 5'	TGGCTCCCTGATATAAGCTG 29248	C	TG T_
	TAGTTT ATGT GGG CCA		
	GTCGAA TATA CCC GGT		
	_ GT TC		
GAM1965 LOC158490 3'	CCATGGTTCTGACAGAGACTG 39849	A	TG T TTA
	TAGTTTC TGT GGG CCAT		
	GTCAGAG ACA CTT GGTA		
	_ GT _ CCA		
GAM1965 LOC158527 5'	TGAAGATCTCTGACATGGTGCT 39864	T	TG_ CATTTA
G	TAGT TCATGT G GGTC		
	GTCG GGTACA C CTAG		
	T GT T AAGT		
GAM1965 LOC158987 3'	TGAATGGACTCCTCTGAAAACCT 42051	_	TGTT
A	TAGTTT CA GGGGTCCATTTA		
	ATCAAA GT CCTCAGGTAAGT		
	A CT_		
GAM1965 LOC161527 5'	TGGCATTCCAGCAGGAGCTA 40020	A	_
	TAGTTTC TGTTGGGGT CCA		
	ATCGAGG ACGACCTTA GGT		
	_ C		
GAM1965 LOC161829 5'	GAAGTTGTTTTTTGGGCATGAG 40036	_	TG TC TTTA
ATTG	AGTTTCATG T GGG CA		
	TTAGAGTAC G TTT GT		
	G GT TT TGAAGT		
GAM1965 LOC161829 5'	TGAGATTGTGAATGTGGAACCTA 40041	_	G _
	TAGTTTCATGTT G GGTC CA		

	ATCAAGGTGTAA T TTAG GT	
	G G A	
GAM1965 LOC162137 5'	GACTTCAGCGAGAACTG 42114	A
	TAGTTTC TGTTGGGGTC	
	GTCAAAG GCGACTTCAG	
	A	
GAM1965 LOC162333 5'	TGGTTCATTACGTGTGAGACT 42139	TG_ GT_ TTTA
G	AGTTTCA T TGGG CCA	
	TCAGAGT G ACTT GGT	
	GT C ACTT A	
GAM1965 LOC170106 5'	GACCTTTTGGCTGGAATTG 40175	T TG_
	TAGTTTCA GT G GGTC	
	GTTAAGGT CG T CCAG	
	_ GT TT	
GAM1965 LOC170409 3'	TGTCCTTCAAAATGAACTG 40316	G TC
	TAGTTTCAT TTGGGG CA	
	GTCAAAGTA AACTTC GT	
	A CT	
GAM1965 LOC196477 3'	TGGAAGTGAATTTGAGGCTA 42377	T TG GG
	TAGTTTCA GT G TCCA	
	ATCGGAGT TA C AGGT	
	T GT A_	
GAM1965 LOC196484 5'	CCATGGTTCTGACAGAGACTG 31486	A TG T TTA
	TAGTTTC TGT GGG CCAT	
	GTCAGAG ACA CTT GGTA	
	_ GT _ CCA	
GAM1965 LOC196955 5'	TGGATATCCCTCCAGGTGGGGC 37939	TT G _ TTTA
TG	T CAT TTGGGG TCCA	
	G GTG GACCTC AGGT	
	GG _ CCTAT A	
GAM1965 LOC197196 5'	TGGACATCAGCTGGGGCTG 43203	TT T GG
	TAGT CA GTTG GTCCA	
	GTCG GT CGAC CAGGT	
	GG _ TA	
GAM1965 LOC197201 3'	TGGGTGGATCTCCAGAAAT 42466	A TT
	GTTTC TG GGGGTCCATTTA	
	TAAAG AC CTCTAGGTGGGT	
	_ C_	
GAM1965 LOC197342 3'	TGGATGGCGGCAGCGTGGAG 42490	GG T
	TTTCATGTTG G CCATTTA	

GAGGTGCGAC C GGTAGGT
 GG _
 GAM1965 LOC199858 5' TGGATGGACCTCTCTGAGTG 42644 GTT__
 CAT GGGGTCCATTTA
 ||| |||||
 GTG CTCCAGGTAGGT
 AGTCT
 GAM1965 LOC199858 5' TGGGCTTTGGTGGAACTG 42645 ATG TG
 TAGTTTC T GGGTCCA
 ||||| | |||||
 GTCAAAG G TTCGGGT
 GT_ GT
 GAM1965 LOC200382 3' TGAGTGGATCCTGAAATG 42808 G TG
 CAT T GGGTCCATTTA
 ||| | |||||
 GTA A CCTAGGTGAGT
 A GT
 GAM1965 LOC200488 5' TAGATGCCACATTTGACTGTGA 43314 _ TG _ C_
 AATTA TTTTCAT GT GG GT CATTTA
 ||||| || || || |||||
 AAAGTG CA TT CA GTAGAT
 T GT A CC
 GAM1965 LOC200830 5' TGAGTGGGTTCTGGCTGCTGGC 43349 TCAT TG GG
 TG TAGTT GT G TCCATTTA
 |||| || | |||||
 GTCGG CG C GGGTGAGT
 TCGT GT TT
 GAM1965 LOC200953 5' TGGGTGGGCTTGGTGGGG 43368 TT GTTG
 T CAT GGGTCCATTTA
 | ||| |||||
 G GTG TTCGGGTGGGT
 GG G__
 GAM1965 LOC201173 5' GGAACCTTAACCTGGGGCTA 42217 TT T G
 TAGT CA GTTGGG TCC
 |||| || ||||| |||
 ATCG GT CAATTC AGG
 GG T A
 GAM1965 LOC201203 3' TGGAGTTTGGCAATGAACTG 42537 _ TG G
 TAGTTTCAT GT GG TCCA
 ||||| || || |||||
 GTCAAAGTA CG TT AGGT
 A GT G
 GAM1965 LOC201220 5' GGAACCTTAACCTGGGGCTA 42226 TT T G
 TAGT CA GTTGGG TCC
 |||| || ||||| |||
 ATCG GT CAATTC AGG
 GG T A
 GAM1965 LOC201243 5' TGCCCTCCAATGTGGGGCTG 42554 TT TC
 TAGT CATGTTGGGG CA
 |||| ||||| ||

	GTCG GTGTAACCTC GT		
	GG CC		
GAM1965 LOC201626 3'	GATGTCTTCGTTATGAACTG 42888	T TC	
	TAGTTTCATG TGGGG CATT		
	GTCAAAGTAT GCTTC GTAG		
	T T_		
GAM1965 LOC201895 3'	TGGGTGGATCACTTGAGG 42928	T TGG	
	TTTCA GT GGTCCATTTA		
	GGAGT CA CTAGGTGGGT		
	T _		
GAM1965 LOC202134 5'	TGGGTGGATCACCTGAGG 43415	TGTT _	
	TTTCA GG GGTCCATTTA		
	GGAGT CC CTAGGTGGGT		
	_ A		
GAM1965 LOC203235 5'	TGGGTGGGCCTCACCCTGCTG 43479	TTCATGT	
	TAGT TGGGGTCCATTTA		
	GTCG ACTCCGGGTGGGT		
	TCCC_		
GAM1965 LOC203248 3'	TAGATGAGATAGCTGAGGCTA 43019	T GGG _	
	TAGTTTCA GTT GTC CATTTA		
	ATCGGAGT CGA TAG GTAGAT		
	_ _ A		
GAM1965 LOC203339 3'	TAGGGAGGTCAATTGTGGGGCT 43526	TT _ GG ATTTA	
A	TAGT CATG TTGG TCC		
	ATCG GTGT AACT AGG		
	GG T GG GAT		
GAM1965 LOC203378 3'	TGAGCACCAACATGACACTA 43559	T G TC	
	TAGT TCATGTTGG G CA		
	ATCA AGTACAACC C GT		
	C A GA		
GAM1965 LOC203504 3'	ATGGACCCAGGTCCTGAATGAA 43567	GTTG_____ TTTA	
GCTG	TTCAT GGGTCCA		
	AAGTA CCCAGGT		
	AGTCCTGGA AT		
GAM1965 LOC205251 5'	TGGAATTAATTATGAGACTG 43591	_ GG	
	TAGTTTCATG TTGG TCCA		
	GTCAGAGTAT AATT AGGT		
	T A_		
GAM1965 LOC219540 5'	TGAGGCTATATGGGGCTG 44959	TT TGG _	
	TAGT CATGT GGTC CA		

	GTCG GTATA TCGG GT		
	GG ____ A		
GAM1965 LOC219627 5'	TGGTCCTCCAGCGTGAGCTA 44275	T	_ T
	TAGTT CATGTTGG GG CCA		
	ATCGA GTGCGACC CC GGT		
	____ T T		
GAM1965 LOC219690 3'	TGGGACCAGCACGGGGCTG 44707	TT A	GG
	TAGT C TGTTGG TCCA		
	GTCG G ACGACC GGGT		
	GG C A_		
GAM1965 LOC219735 3'	TAAGTGGATCTCACCAGA 44722	A T	
	TC TG TGGGGTCCATTTA		
	AG AC ACTCTAGGTGAAT		
	____ C		
GAM1965 LOC219920 5'	TGGGTGGACTCCGGTAGGCCAG 44813	TCA_ TT	
CT	AGTT TG GGGGTCCATTTA		
	TCGA AT CCTCAGGTGGGT		
	CCGG GG		
GAM1965 LOC219942 3'	CACAGTGACCCCGACGTTGGGC 44823	TC	C TA
TG	TAGTT ATGTTGGGGTC ATT		
	GTCGG TGCAGCCCCAG TGA		
	GT ____ CACG		
GAM1965 LOC220073 5'	CCATGGTTCTGACAGAGACTG 44875	A TG T TTA	
	TAGTTTC TGT GGG CCAT		
	GTCAGAG ACA CTT GGTA		
	____ GT ____ CCA		
GAM1965 LOC220143 3'	TGGGTGGGAGATGGACGTTAGG 44955	C	GGGG_
CTG	TAGTTT ATGTT TCCATTTA		
	GTCGGA TGCAG GGGTGGGT		
	T GTAGA		
GAM1965 LOC220692 3'	TAGGTGGGCCCACCACTTGAG 43832	T TG_	
	TTCA GT GGGTCCATTTA		
	GAGT CA CCCGGGTGGAT		
	T CCA		
GAM1965 LOC221002 3'	GAGATGAACTCTGAGTATGAAG 43974	_ TG C A	
CTG	TAGTTTCATG T GGGT CATTT		
	GTCGAAGTAT A CTCA GTAGA		
	G GT A GT		
GAM1965 LOC221002 3'	TAGGCAGCGCCCTAATTGGAAT 43978	T	____ ATTTA
TG	GTTTCA GTTGGGGT CC		

	TAAGGT TAATCCCG GG	
	CGAC AT	
GAM1965 LOC221143 3'	TGGATGTTTCTAGTGGGAGCTG 44946	ATG ____
	TAGTTTC TTGGG GTCCA	
	GTCGAGG GATCT TAGGT	
	GT_ TTG	
GAM1965 LOC221178 3'	TGGGTGGATCCTACTTGGA 44930	T T
	TTCA GT GGGGTCCATTTA	
	AGGT CA TCCTAGGTGGGT	
	T _	
GAM1965 LOC221288 3'	TGAAGGCACTCTGGCATAGGCT 44971	C TG _ ATTTA
G	TAGTTT ATGT GGGT CC	
	GTCGGA TACG CTCA GG	
	_ GT C AAGT	
GAM1965 LOC221421 3'	TAGATGGGCTTGACGGAGC 44324	AT TG G
	GTTTC GT GG TCCATTTA	
	CGAGG CA TC GGGTAGAT	
	_ GT _	
GAM1965 LOC221466 5'	GGATGGCTTGACCTGGGATTG 44995	TT T TG GT A
	TAGT CA GT GG CCATTT	
	GTTA GT CA TC GGTAGG	
	GG C GT _ A	
GAM1965 LOC221495 3'	GCTCCTGGCATGGAAGT 45059	TG _
	TAGTTTCATGT GG GT	
	GTCAAGGTACG CC CG	
	GT T	
GAM1965 LOC221495 3'	GGCCCTGGGTGGAATTG 45060	G TG
	TAGTTTCAT T GGGTC	
	GTTAAGGTG G CCCGG	
	_ GT	
GAM1965 LOC221495 5'	TGGATGGGCTTCTATCAGA 45061	A TT_
	TC TG GGGGTCCATTTA	
	AG AC CTTCGGGTAGGT	
	_ TAT	
GAM1965 LOC221543 3'	TGGGTGGATCACCTGAGGTTA 45015	TT TGTT _
	TAG TCA GG GGTCCATTTA	
	ATT AGT CC CTAGGTGGGT	
	GG _ A	
GAM1965 LOC221641 5'	TGGGTGGATCACTTGAGG 45010	T TGG
	TTTCA GT GGTCCATTTA	

	GGAGT CA CTAGGTGGGT	
	T ____	
GAM1965 LOC221662 3'	GAGTGGAACTGTGGAAC 44389	GTT GG
	GTTTCAT GG TCCATTT	
	CAAGGTG TC AGGTGAG	
	____ A_	
GAM1965 LOC221712 5'	ATGGATTCCGTATTTTGATATG 44974	_____ TTTA
AA	CATGTT GGGGTCCA	
	GTATAG CCTTAGGT	
	TTTTATG AT	
GAM1965 LOC221760 5'	TGGATGGAGGGAGCGTGTGAGA 45033	TG TGGGG_
T	GTTTCA T TCCATTTA	
	TAGAGT G AGGTAGGT	
	GT CGAGGG	
GAM1965 LOC221773 3'	GCTTTAACAGTGGAGCTG 43765	_
	TAGTTTCA TGTTGGGGT	
	GTCGAGGT ACAATTTG	
	G	
GAM1965 LOC221955 3'	GGATGGATCCCTTGGCTG 29193	TCATGTT
	TAGTT GGGGTCCATTT	
	GTCGG CCCTAGGTAGG	
	TT_____	
GAM1965 LOC221955 3'	TGGATGTACAAATGGAACGTG 29194	G GG_
	TAGTTTCAT TTG GTCCA	
	GTCAAGGTA AAC TAGGT	
	_ ATG	
GAM1965 LOC222112 3'	TGGAGATGGATATGAGACTA 44583	GGGG
	TAGTTTCATGTT TCCA	
	ATCAGAGTATAG AGGT	
	GTAG	
GAM1965 LOC222128 5'	TAAATGGACTAATGATGGGATT 44540	TT GTTGG
G	TAGT CAT GGTCCATTTA	
	GTTA GTA TCAGGTAAAT	
	GG GTAA_	
GAM1965 LOC222256 3'	TGAGTGGCAAAGCGTGGGCTG 45250	T GGG T
	TAGTT CATGTT G CCATTTA	
	GTCGG GTGCGA C GGTGAGT	
	_ AA__	
GAM1965 LOC222671 5'	TGGTGTTTGGCGCTGGAATTA 44604	_ TG GT
	TAGTTTCA TGT GG CCA	

ATTAAGGT GCG TT GGT
 C GT GT
 GAM1965 LOC253216 5' TGCATCCGCAGCGTGGGGCTG 45522 TT _ C
 TAGT CATGTTG GGGT CA
 ||| ||||| ||| ||
 GTCG GTGCGAC CCTA GT
 GG G C
 GAM1965 LOC253264 5' TGAATGGATTTTAACAAATGGA 45418 CA_
 CT AGTTT TGTTGGGGTCCATTTA
 |||| |||||
 TCAGG ACAATTTTAGGTAAGT
 TAA
 GAM1965 LOC253612 3' TGGGTGGATCACCTGAGG 46257 TGTT _
 TTTCA GG GGTCCATTTA
 |||| |||||
 GGAGT CC CTAGGTGGGT
 _ A
 GAM1965 LOC253758 5' GATCCTAGCGCGGAGCTG 46320 A
 TAGTTTC TGTTGGGGTC
 ||||| |||||
 GTCGAGG GCGATCCTAG
 C
 GAM1965 LOC253912 3' TGGGTGGGCTTAGGGACGCTG 46485 T ATGTTG
 TAGT TC GGGTCCATTTA
 ||| || |||||
 GTCG AG TTCGGGTGGGT
 C GGA_
 GAM1965 LOC253926 5' TAGATGCACAGCAGTGGGAATTG 45500 _ GGGTC
 TAGTTTCA TGTTG CATTTA
 ||||| |||| |||||
 GTTAAGGT ACGAC GTAGAT
 G AC_
 GAM1965 LOC254015 3' TGAATGTGAGCCGATATGCAGC 46247 T G G _
 TG TAGTT CATGTTG G TC CATTTA
 |||| ||||| || |||||
 GTCGA GTATAGC C AG GTAAGT
 C _ G T
 GAM1965 LOC254143 5' GACTTCTAGTGTGGAAGTG 46159 G TG _
 TA TTTCA TTGGG GTC
 || |||| |||| |||
 GT AAGGT GATCT CAG
 G GT T
 GAM1965 LOC254143 5' GAGTGCAAGCATGGAAC 46160 GGGGTC
 GTTTCATGTT CATT
 ||||| |||||
 CAAGGTACGA GTGAG
 AC_
 GAM1965 LOC254196 3' TGGGTGGACTCCAGCCTCCCCA 46477 TCAT_
 GC GTT GTTGGGGTCCATTTA
 || |||||

	CGA CGACCTCAGGTGGGT	
	CCCCTC	
GAM1965 LOC254266 5'	GTGGGCCCCAGTGAGAGACTG 46482	A GT
	TAGTTTC T TGGGGTCCAT	
	I	
	GTCAGAG G ACCCCGGGTG	
	A TG	
GAM1965 LOC254351 3'	TGCACTCCAGCCTGGGACTG 45543	TT T C
	TAGT CA GTTGGGGT CA	
	GTCA GT CGACCTCA GT	
	GG C C	
GAM1965 LOC254413 5'	TGGATTCGTAAGGTGAGGCTG 46405	G _
	TAGTTTCAT TTG GGGTCCA	
	GTCGGAGTG AAT CTTAGGT	
	G G	
GAM1965 LOC254719 5'	ACCTCATAGTATGAAATTA 45952	T__
	TAGTTTCATG TGGGGT	
	ATTAAAGTAT ACTCCA	
	GAT	
GAM1965 LOC254896 5'	ACCCATGGCATGGAGCTG 45988	_
	TAGTTTCATGTTG GGGT	
	GTCGAGGTACGGT CCCA	
	A	
GAM1965 LOC254896 5'	TGGCTTCCCCCAGCGTGAGACT 45990	T__ TTTA
	AGTTTCATGTTGGGG CCA	
	TCAGAGTGCGACCCC GGT	
	CTTC A	
GAM1965 LOC254947 5'	TGGCATTCCAGCAGGAGCTA 46192	A _
	TAGTTTC TGTTGGGGT CCA	
	ATCGAGG ACGACCTTA GGT	
	_ C	
GAM1965 LOC255104 3'	TAAATGGAAGGAATTGGAAGT 45685	TGTTGGGG
	TAGTTTCA TCCATTTA	
	GTCAAGGT AGGTAAAT	
	TAAGGA__	
GAM1965 LOC255177 3'	TAAATGAATAGTGATGTGGAGC 46202	GG C
	GTTTCATGTTG GT CATTTA	
	CGAGGTGTAGT TA GTAAAT	
	GA A	
GAM1965 LOC255252 3'	TGAGAGGCTGGCATGGATCTA 45548	T TG GG _
	TAG TTCATGT G TC CA	

ATC AGGTACG C AG GT
 T GT GG A
 GAM1965 LOC255320 5' AGTGGCTTTGATTTGGGATTA 45544 TT T TG T
 TAGT CA GT GGG CCATT
 |||| || || ||||
 ATTA GT TA TTC GGTGA
 GG T GT _
 GAM1965 LOC255327 5' TGGATGGAAAAGTTGTGGAAC 46023 TTGGGG
 GTTTCATG TCCATTTA
 ||||| |||||
 CAAGGTGT AGGTAGGT
 TGAAA_
 GAM1965 LOC255338 5' TAGGTGGGAATATGTTGTGGG 45913 TT TTGGGG_
 ATTA AGT CATG TCCATTTA
 || ||| |||||
 TTA GTGT GGGTGGAT
 GG TGGTATAA
 GAM1965 LOC255426 3' GACCCACGTGGAACCTG 46410 TG
 TAGTTTCATGT GGGTC
 ||||| ||||
 GTCAAGGTGCA CCCAG
 _
 GAM1965 LOC255533 5' TAAATGGGCTTTAATTTTG 46332 T_
 CA GTTGGGGTCCATTTA
 || |||||
 GT TAATTCGGGTAAAT
 TT
 GAM1965 LOC255975 5' TAAGTGGATTCCAGAGGGG 45892 ATG
 TTC TTGGGGTCCATTTA
 || |||||
 GGG GACCTTAGGTGAAT
 GA_
 GAM1965 LOC256096 5' TAATGCTTTCTAACATGAAG 46420 TC TA
 TTTTCATGTTGGGG CATT
 ||||| ||||
 GAAGTACAATCTT GTAA
 TC T
 GAM1965 LOC256207 3' TGGGTGGATCACCTGAGG 45622 TGTT _
 TTTCA GG GGTCCATTTA
 |||| || |||||
 GGAGT CC CTAGGTGGGT
 _ A
 GAM1965 LOC256337 3' ATGGAAGAAATCCCAGCAGG 45420 A _ TTTA
 AGCTG C TGTTGGGG TCCA
 | ||||| ||||
 G ACGACCCT AGGT
 _ AAAAGAA AT
 GAM1965 LOC256867 5' TGGGTGGGGGGCAGTGGGGGCT 45477 TT ATG GGG
 G TAGT C TTG TCCATTTA
 |||| | || |||||

	GTCG G GAC GGGTGGGT		
	GG GT_ GGG		
GAM1965 LOC256905 3'	TGAATGTGGCTACCTAATGTGG 46298	—	—
AAC	TTTCATGTTGGG GTC CATTTA		
	AAGGTGTAATCC CGG GTAAGT		
	AT T		
GAM1965 LOC257302 5'	TGGGTGGGCCTGTCCTGGGGC 46064	TT	TGTTG
	GT CA GGGTCCATTTA		
	CG GT TCCGGGTGGGT		
	GG CCTG_		
GAM1965 LOC257358 3'	TAGATGGACCCCAAACTGA 46389	TG_	
	TCA TTGGGGTCCATTTA		
	AGT AACCCCAGGTAGAT		
	CAA		
GAM1965 LOC257431 5'	TGGCATTCCAGCAGGAGCTA 39947	A	—
	TAGTTTC TGTTGGGGT CCA		
	ATCGAGG ACGACCTTA GGT		
	— C		
GAM1965 LOC257464 5'	GGGCCAGCCGTGAGGCTA 43167	TTGG	
	TAGTTTCATG GGTCC		
	ATCGGAGTGC CCGGG		
	CGA_		
GAM1965 LOC257476 3'	GACCTTAGCATGGGGCTA 30716	TT	
	TAGT CATGTTGGGGTC		
	ATCG GTACGATTCCAG		
	GG		
GAM1965 LOC257476 3'	GACCTTAGCATGGGGCTA 30717	TT	
	TAGT CATGTTGGGGTC		
	ATCG GTACGATTCCAG		
	GG		
GAM1965 LOC257551 3'	TGGGGGACCCAATGTAGGAGCT 46646	—	GT ATTTA
G	TAGTTTC ATGTTGGG CC		
	GTCGAGG TGTAACCC GG		
	A AG GGT		
GAM1965 LOC257596 3'	TGGGTGGATCACCTGAGGTTA 46755	TT	TGTT _
	TAG TCA GG GGTCCATTTA		
	ATT AGT CC CTAGGTGGGT		
	GG _ A		
GAM1965 LOC257601 3'	TGGGGGACCCAATGTAGGAGCT 46697	—	GT ATTTA
G	TAGTTTC ATGTTGGG CC		

	GTCGAGG TGTAACCC GG	
	A AG GGT	
GAM1965 LOC257615 5'	TGGTGTTTGGCGCTGGAATTA 46744	_ TG GT
	TAGTTTCA TGT GG CCA	
	ATTAAGGT GCG TT GGT	
	C GT GT	
GAM1965 LOC51134 3'	TGGTTCCAAGCATGGAACTA 18212	G GT
	TAGTTTCATGTT GG CCA	
	ATCAAGGTACGA CC GGT	
	A TT	
GAM1965 LOC51134 5'	TGAGTGGGTGCCTGTGGTTGGA 18211	TGTT_ G
GCTG	AGTTTCA GG GTCCATTTA	
	TCGAGGT CC TGGGTGAGT	
	TGGTGT G	
GAM1965 LOC51200 3'	TAGGTGGGTCTCAAAGATGA 18482	G_ GT
	TCAT TTGGG CCATTTA	
	AGTA AACTC GGTGGAT	
	GA TG	
GAM1965 LOC51301 3'	TAAATGGAGTCAGTGTGGAATT 18672	TG G G
G	TAGTTTCA TTG G TCCATTTA	
	GTTAAGGT GAC T AGGTAAAT	
	GT _G	
GAM1965 LOC51308 3'	GGATGGAAGACAGGGATTG 18709	TT A GGGG
	TAGT C TGTT TCCATT	
	GTTA G ACAG AGGTAGG	
	GG _ A__	
GAM1965 LOC51580 5'	GGAAGCTATGTGAAATTA 18016	T GG
	TAGTTTCATGT GG TCC	
	ATTAAAGTGTA TC AGG	
	_ GA	
GAM1965 LOC51696 3'	TGGATGGGCTCCATTAAAAC 18316	CATGT
	GTTT TGGGGTCCATTTA	
	CAAA ACCTCGGGTAGGT	
	ATT__	
GAM1965 LOC56920 3'	TAAATGGATTTAGGAAGACTG 21383	_ATGTTG
	TAGTTT C GGGTCCATTTA	
	GTCAGA G TTTAGGTAAAT	
	A GA__	
GAM1965 LOC57805 3'	TAGAAAGAGCTCAGTGTGGGC 22150	TC TG G CA
TG	TAGTT A TTGGG TC TTTA	

	GTCGG T GACTC AG AGAT	
	GT GT G AA	
GAM1965 LOC58525 3'	TGGGTGGGGGCCAGTGGGGTTG 38460	TT GT GG
	TAG TCAT TGG TCCATTTA	
	GTT GGTG ACC GGGTGGGT	
	GG _ GG	
GAM1965 LOC90019 3'	GGGTGGGCCTGGACGGCTG 28874	TTCA G
	TAGT TGTT GGGTCCATTT	
	GTCG GCAG TCCGGGTGGG	
	_ G	
GAM1965 LOC90019 3'	GGGTGGGCCTGGGCAGCTG 28875	TTCA G
	TAGT TGTT GGGTCCATTT	
	GTCG ACGG TCCGGGTGGG	
	_ G	
GAM1965 LOC90019 3'	GGGTGGGCCTGGGCAGCTG 28876	TTCA G
	TAGT TGTT GGGTCCATTT	
	GTCG ACGG TCCGGGTGGG	
	_ G	
GAM1965 LOC90072 3'	TGGGTGGATCGCCTGAGAT 30731	TGTT _
	GTTTCA GG GGTCCATTTA	
	TAGAGT CC CTAGGTGGGT	
	_ G	
GAM1965 LOC90092 5'	ATGGTCCTCATCCCGATGGGAA 30782	AT _ TTTA
ACTG	TTC GTTGGGGT CCA	
	AAG TAGCCCTA GGT	
	GG CTCCT AT	
GAM1965 LOC90092 5'	TGGCCACTTTGACCTGGGGCTG 30793	TT T TG _
	TAGT CA GT GGGT CCA	
	GTCG GT CA TTCA GGT	
	GG C GT CC	
GAM1965 LOC90170 5'	GTCTCAGATCTTGATGTGTGAC 30913	T TG CATTTA
TA	TAGTT CATGT GGGTC	
	ATCAG GTGTA TCTAG	
	T GT ACTCTGG	
GAM1965 LOC90246 3'	TAAATGGATGTTGCTTGAAGCT 31003	T T G
G	TAGTTTCA GT GG GTCCATTTA	
	GTCGAAGT CG TT TAGGTAAAT	
	T _ G	
GAM1965 LOC90379 5'	TGGGTGGGCCTCCCCATTGAAA 31338	G _ TT
GTG	TA TTTCA TG GGGGTCCATTTA	

GT AAAGT AC CTCCGGGTGGGT
 G T CC
 GAM1965 LOC90459 3' TGGATCATTCCAATTGAAGTTG 31493 GT T ____
 TA TTCA GTTGG GGTCCA
 || ||| |||| |||||
 GT AAGT TAACC CTAGGT
 TG _ TTA
 GAM1965 LOC90509 5' TAAATGTGTCTTGGTATGAA 31610 TT TC
 TTCATG GGGG CATTTA
 ||||| ||| |||||
 AAGTAT TTCT GTAAAT
 GG GT
 GAM1965 LOC90529 3' AGTGGTTTTGGTGGAGGCTG 31639 ATG TG T
 TAGTTTC T GGG CCATT
 ||||| | ||| |||||
 GTCGGAG G TTT GGTGA
 GT_ GT _
 GAM1965 LOC90538 3' TGGAAATCATCAGCATGAGAT 31660 GG__ TTTA
 GTTTCATGTTGG TCCA
 ||||| |||
 TAGAGTACGACT AGGT
 ACTAA A
 GAM1965 LOC90670 3' TGAACCACTAATTGAGATTA 31884 T _ C
 TAGTTTCA GTTGG GGT CA
 ||||| |||| ||| ||
 ATTAGAGT TAATC CCA GT
 _ A A
 GAM1965 LOC90750 3' TGAATGGTAACTTTTAAATGTG 31970 _ _
 AAAC TTCATGTTGG GGT CCATTTA
 ||||| ||| |||||
 AAGTGTAATT TCA GGTAAGT
 TT AT
 GAM1965 LOC90918 5' TGGGTGGATCACCTGAGG 32177 TGTT _
 TTTCA GG GGTCCATTTA
 |||| |||||
 GGAGT CC CTAGGTGGGT
 _ A
 GAM1965 LOC91040 3' TGGCCTCCCCAGCGTGGGGCT 32324 TT T__
 AGT CATGTTGGGG CCA
 || ||||| |||
 TCG GTGCGACCCC GGT
 GG TCC
 GAM1965 LOC91069 3' CCATGGTTCTGACAGAGACTG 32347 A TG T TTA
 TAGTTTC TGT GGG CCAT
 ||||| ||| ||| |||
 GTCAGAG ACA CTT GGTA
 _ GT _ CCA
 GAM1965 LOC91149 3' TGAATGGACTTTGCACCAGTG 32459 _ _ GG
 CAT GT T GGTCCATTTA
 || ||| |||||

	GTG CA G TCAGGTAAGT		
	AC C TT		
GAM1965 LOC91408 3'	TGGAAGCTGGCATGGACTA 32793	T	TG GG
	TAGTT CATGT G TCCA		
	ATCAG GTACG C AGGT		
	_ GT GA		
GAM1965 LOC91445 3'	TGGTTTCCTGGCATAAATTA 30373	C	TG T_
	TAGTTT ATGT GGG CCA		
	ATTAAA TACG CCT GGT		
	_ GT TT		
GAM1965 LOC91464 5'	GACTCCTTTGATGTCAAAGT 32875	C	___
	TAGTTT ATGTT GGGGTC		
	GTCAAA TGTA G CCTCAG		
	C TTT		
GAM1965 LOC91948 3'	TGGGTGGATCACTTGAAGC 33576	T	TGG
	GTTTCA GT GGTCCATTTA		
	CGAAGT CA CTAGGTGGGT		
	T ___		
GAM1965 LOC92078 3'	TGAGTGGATCACCTGAGG 33748	TGTT	_
	TTTCA GG GGTCCATTTA		
	GGAGT CC CTAGGTGAGT		
	___ A		
GAM1965 LOC92140 3'	ATGGACAGCTTTCCTAACAAGA 33888	A	___ TTTA
GATTA	TC TGTTGGG GTCCA		
	AG ACAATCC CAGGT		
	A TTTCGA AT		
GAM1965 LOC92181 3'	TAGGTGGGAAAACCATGGTGCT 33945	T	TTGGGG
G	TAGT TCATG TCCATTTA		
	GTCG GGTAC GGGTGGAT		
	T CAAAA_		
GAM1965 LOC92249 5'	TGGACACAGTCCAACGTGAGCT 34026	T	___ TTTA
	GTT CATGTTGGG GTCCA		
	CGA GTGCAACCT CAGGT		
	_ GACA A		
GAM1965 LOC92267 3'	GCCTTAACAGTGGAGTTG 34056	GT	_
	TA TTCA TGTTGGGGT		
	GT AGGT ACAATTCCG		
	TG G		
GAM1965 LOC92267 3'	TGGGTGGGTCACCTGAGG 34059	TGTT	_ GT
	TTTCA GG G CCATTTA		

GGAGT CC C GGTGGGT
____ A TG
GAM1965 LOC92340 3' TGGGACCAGTGTGTAGCTG 34201 T TG GG
TAGTT CA TTGG TCCA
||||| || ||| ||||
GTCGA GT GACC GGGT
T GT A_
GAM1965 LOC92379 3' GATGGAATGTGAAGC 34267 TGGGG
GTTTCATGT TCCATT
||||||| |||||
CGAAGTGTA AGGTAG

GAM1965 LOC92661 3' GGATGGGCTGAAGGGGCTG 34723 TT ATGT GG
TAGT C T GGTCCATTT
||| | | |||||
GTCG G A TCGGGTAGG
GG ____ AG
GAM1965 LOC92771 3' ATGGAGCTAGTGTCCAGCTGA 27248 T ____ TTTA
AGCTA CA GTTGGGG TCCA
|| ||||| |||
GT CGACCCT AGGT
_ GTGATCG AT
GAM1965 LOC93052 5' ATGGGGTTTCCCTGGATGTGGG 35301 TT G ____ TTTA
GCTG CATGTT GGG TCCA
||||| ||| |||
GTGTAG TCC GGGT
GG G CTTTG AT
GAM1965 LOC93070 5' CCCGTGGGCTCCGGCGTGAGGC 35324 TTA
GTTTCATGTTGGGGTCCAT
|||||||
CGGAGTGCGGCCTCGGGTG
CCCC
GAM1965 LOC93622 3' TGAATGCGACTTTGGATGAGAT 28949 G TG _
TA TAGTTTCAT T GGGTC CATTTA
||||||| | |||||
ATTAGAGTA G TTCAG GTAAGT
_ GT C
GAM1965 LOC93624 5' GGAGCTTATTGTGAGATTG 36015 GT G
TAGTTTCAT TGGG TCC
||||||| ||| |||
GTTAGAGTG ATTC AGG
TT G
GAM1966 SURF6 3' AGAAAAGAAGTCTTAAGAT 13608 _ _
ATCTTAAGATT CTTT CT
||||||| ||| ||
TAGAATTCTGA GAAA GA
A A
GAM1967 DUOX1 3' GCACCCCAGTCTAACAC 18888 AAA C_
GTGTT GGA CTGGG GC
||||| ||||| ||

CACAA TCTGACCC CG
____ CA
GAM1967 GDF2 5' TGCCCGCTAACACAGCA 18299 C AAGGAC
TGC GTGTTA TGGGCG
||| ||||| |||||
ACG CACAAT GCCCGT
A C____
GAM1967 JUNB 5' GCACCCAGTCCGGTCACCGCA 8011 C TTAAA C
TGC GTG GGA CTGGG GC
||| ||| ||||| |||
ACG CAC CCTGACCC CG
C TGG__ A
GAM1967 PPT2 3' GCACCATTGTTTTAATACGGCA 29062 GAC _
TGCCGTGTAAAG TGG GC
||||||| |||
ACGGCATAATTTT ACC CG
GTT A
GAM1967 RRM2 3' CAGTCCTTTAACCAGCA 6698 CGT
TGC GTTAAAGGACTG
||| |||||
ACG CAATTCCTGAC
AC_
GAM1967 DKFZP434I2117 3' GCGCCCAGTCCCTCACCATCGG 25556 _ TTAAA
C GCCG TG GGA CTGGGCGC
||| ||| |||||
CGGC AC CCTGACCCGCG
T CACTC
GAM1967 DKFZp564A176 3' GCTGTCCTTTAACACCGCA 25979 C TG
TGC GTGTAAAGGAC GGC
||| ||||| |||
ACG CACAATTCCTG TCG
C _
GAM1967 GNB4 5' GCGCCCAGCGGACACCGGCA 22270 _ AAAGGA
TGCCG TGTT CTGGGCGC
||||| ||| |||||
ACGGC ACAG GACCCGCG
C GC____
GAM1967 KIAA0323 3' CCTAGATTTTAACACTGCA 31692 C GA
TGC GTGTAAAG CTGGG
||| ||||| |||
ACG CACAATTTT GATCC
T A_
GAM1967 SARM 3' CCCAGTCCACTGGCA 17456 T TAAA C
TGCCG GT GGA CTGGG G
||||| ||| |||||
ACGGT CA CCTGACCC C
_ ____ A
GAM1967 LOC149345 5' GCGCCCAGCCCCCACCATGCCA 38715 C TTAAA A
TG CGTG GG CTGGGCGC
|| ||| || |||||

		AC GTAC CC GACCCGCG			
		C CACCC _			
GAM1967	LOC152275 3'	CGTCCCAGTCCTTCAACAC 41457	A		_
		GTGTT AAGGACTGGG CG			
		CACAA TTCCTGACCC GC			
		C T			
GAM1967	LOC152286 3'	TTTGGTCCTTTAACCGACA 41463	C T		TG
		TG CG GTTAAAGGAC GG			
		AC GC CAATTCCTG TT			
		A _ GT			
GAM1967	LOC160646 5'	GCACCCAGTCCTGTACGC 40004	TAA		C
		GTGT AGGACTGGG GC			
		CGCA TCCTGACCC CG			
		TG_ A			
GAM1967	LOC84548 3'	GCACCACGTGTTTAGACACAGC 35297	C A G _ _		
	A	TGC GTGTT AAG AC TGG GC			
		ACG CACAG TTT TG ACC CG			
		A A G C A			
GAM1968	AP1G1 3'	GTAAAAAGAGCTTTTGTT 6801	C GA		
		GACGAAGGCTCT TT AGC			
		TTGTTTTCGAGA AA TTG			
		A A_			
GAM1968	ASIC4 3'	GTGGGAAGGGAGCCTTCTCA 20748	C		GAA
		TGA GAAGGCTCTCTT GC			
		ACT CTTCCGAGGGAA TG			
		_ GGG			
GAM1968	ATP7B 3'	GCAGTTTTAGCAGCACTTTTG 5505	CT C		
		CGAAGG CT TTGAAGCTGC			
		GTTTTC GA GATTTTGACG			
		AC C			
GAM1968	BCL6 5'	GTGGCTTTGAGGGCTTTTG 7432	TT TG		
		CGAAGGCTCTC GAAGC C			
		GTTTTCGGGAG TTTCG G			
		_ GT			
GAM1968	BLAME 3'	GGGTGCACCAGGGCCTTGTT 21310	G		CT AA TG
		GAC AAGGCTCT TG GC C			
		TTG TTCCGGGA AC TG G			
		_ CC G_ GT			
GAM1968	BRCA1 3'	GGGTGAAGGAGCTTTCATCA 14203	C		T GAA TG
		TGA GAAGGCTC CTT GC C			

		ACT CTTTCGAG GAA TG G		
		A _ G_ GT		
GAM1968	BSN	3' GTGGCTTCAAGCTAAGTTTC 9518	G CT_ TG	
		GAAG CT CTTGAAGC C		
		CTTT GA GAACTTCG G		
		_ ATC GT		
GAM1968	BUB3	3' GCAGTTTTGAGAATCAGTTTT 11095	C_ TG	
		AAGGCT TCT AAGCTGC		
		TTTTGA AGA TTTGACG		
		CTA GT		
GAM1968	CCND1	5' CTACAGGGGAGTTTTGTT 27599	G A	
		GACGAAG CTCTCTTG AG		
		TTGTTTT GAGGGGAC TC		
		_ A		
GAM1968	CIAO1	5' GCGGAACGGGGAGCCTCTGTC 11226	A TGAAG	
		GACG AGGCTCTCT CTGC		
		CTGT TCCGAGGGG GGCG		
		C CAA_		
GAM1968	CORO1C	3' GTAGCTTTGTTTTCTTTGT 15630	CTCTCT	
		ACGAAGG TGAAGCTGC		
		TGTTTCC GTTTCGATG		
		TTTT_		
GAM1968	CPD	3' GCAGTTTTGAACTTCCCTTCCT 6984	C CTCTC TG	
	TA	TGA GAAGG T AAGCTGC		
		ATT CTTCC A TTTGACG		
		C CTTCA GT		
GAM1968	CPD	3' GTGGCTTTAGTATTTTTCTTTG 6985	CTCTC_ TG	
	TT	GACGAAGG TTGAAGC C		
		TTGTTTCT GATTTG G		
		TTTTAT GT		
GAM1968	CYP7A1	3' GTAGTTTTTCTGTCATTGTTA 6423	A TCTCTT	
		TGACGA GGC GAAGCTGC		
		ATTGTT CTG TTTTGATG		
		A TCT_		
GAM1968	D1S155E	3' GCGGTTTTATCTTCCCCCTTGT 14005	A CTCTCT	
	C	GACGA GG TGAAGCTGC		
		CTGTT CC ATTTTGGCG		
		C CCTTCT		
GAM1968	DDEF2	3' TAGTTTTTTGTTTTGTT 9967	TCTCTT	
		GACGAAGGC GAAGCTG		

		TTGTTTTTG	TTTTGAT		
		TT____			
GAM1968	DDX3	5'	GCAGTTCTCCCGTGAGAGGGCC 7035	_____	-
		TTCGCG	AAGGCTCTCTT GA AGCTGC		
			TTCCGGGAGAG CT TTGACG		
			TGCC C		
GAM1968	DDX3	3'	GCAGTTTTAGTCAGTTTTAGTT 7036	G	CT T
			GAC AAGGCT CT GAAGCTGC		
			TTG TTTTGA GA TTTTGACG		
			A CT _		
GAM1968	DDX3	5'	GCAGTTCTCCCGTGAGAGGGCC 23432	_____	-
		TTCGCG	AAGGCTCTCTT GA AGCTGC		
			TTCCGGGAGAG CT TTGACG		
			TGCC C		
GAM1968	DGKB	3'	GGGTTTAACAGTTTTTGTTA 44449		CTCTTG TG
			TGACGAAGGCT AAGC C		
			ATTGTTTTTGA TTTG G		
			CAA____ GT		
GAM1968	DNAJB1	3'	GCCCAGGGAGGGCTTTCGT 12789		GAA
			ACGAAGGCTCTCTT GC		
			TGCTTTCGGGAGGG CG		
			ACC		
GAM1968	DNASE1	5'	GGGCTTTGGCCTCTTTGTC 11715	___	CTCTT TG
			GACGA AGGCT GAAGC C		
			CTGTT TCCGG TTTG G		
			TC _____ GT		
GAM1968	EFNB1	3'	GCAGTCGGAAGGGTTTTTGT 10712		CT AA
			GACGAAGGCTCT TG GCTGC		
			TTGTTTTTGGGA GC TGACG		
			AG _		
GAM1968	ERBB2	3'	GCACTGGGGAGTCTTTGT 10746		TGAA
			ACGAAGGCTCTCT GC		
			TGTTTCTGAGGGG CG		
			TCA_		
GAM1968	FUT5	3'	GGGTTTTATTGCTGTTGTTA 7789	A	TCTCT TG
			TGACGA GGC TGAAGC C		
			ATTGTT TCG ATTTTG G		
			G TT____ GT		
GAM1968	GAS7	3'	GCAGCTTCGGGGGGTCCT 9715		CT
			AGG CTCTTGAAGCTGC		

TCC GGGGGCTTCGACG
 TG
 GAM1968 GSPT1 5' GCGGCGACGCCGGGGATCTTTG 7883 _ CT AA
 TC GACGAAGG CTCT TG GCTGC
 ||||| ||| || |||||
 CTGTTTCT GGGG GC CGGCG
 A CC AG
 GAM1968 GSTM5 3' GGGTTTTTTGTCTTCTGTT 6520 _ TCTCTT TG
 GAC GAAGGC GAAGC C
 ||| ||||| ||||| |
 TTG CTTCTG TTTTG G
 T TT___ GT
 GAM1968 H3F3B 3' GTGGGGAGTCTTGTCA 11795 G TGAA
 TGAC AAGGCTCTCT GC
 ||| ||||| ||
 ACTG TTCTGAGGGG TG
 _ _
 GAM1968 HMGA2 3' GTAGTTTCTCATGACGGCTTTT 9568 C TT___
 GTCA GACGAAGGCT TC GAAGCTGC
 ||||| || |||||
 CTGTTTTCGG AG CTTTGATG
 C TACT
 GAM1968 HR 5' GCCCCGGGGGAGCCTCTGTC 11616 A AA
 GACG AGGCTCTCTTG GC
 ||| ||||| ||
 CTGT TCCGAGGGGGC CG
 C CC
 GAM1968 HS2ST1 3' CAGCTTTGTGGCCTTTGCA 14573 A CTCT
 TG CGAAGGCT TGAAGCTG
 || ||||| |||||
 AC GTTTCGG GTTTCGAC
 _ T___
 GAM1968 KCNJ15 5' ACAGTGAGAGAGTTTTCTTCA 8029 C GAA C
 TGA GAAGGCTCTCTT GCTG
 ||| ||||| |||||
 ACT CTTTGGAGAGAG TGAC
 T ___ AA
 GAM1968 KIF2 3' CAGTTTTAAATCCTTTGCG 10848 A CTCTC
 TG CGAAGG TTGAAGCTG
 || ||||| |||||
 GC GTTTC AATTTTGAC
 _ TA___
 GAM1968 LTK 5' GCGACCGCAAGGGCTTTTGTT 8143 CT AA_
 GACGAAGGCTCT TG GC
 ||||| || ||
 TTGTTTTCGGGA GC CG
 AC CAG
 GAM1968 MAP3K7 3' GCAGTTTTACCGGATTTTGTTA 9164 GC CT
 TGACGAAG TCT TGAAGCTGC
 ||||| ||| |||||

		ATTGTTTT AGG ATTTTGACG	
		__ CC	
GAM1968 MMP14	3'	AAAAC TCAGAGAGGGTCTTCGT 11433	GA CTGC
T		GACGAAGGCTCTCTT AG	
		TTGCTTCTGGGAGAG TC	
		AC AAAAG	
GAM1968 MYLK	3'	GCAGCTTCAGACATTTGGTTA 46358	G GCTC T
		TGAC AAG TCT GAAGCTGC	
		ATTG TTT AGA CTTCGACG	
		G AC__	
GAM1968 NDRG3	3'	GTGGTTTTAGACACGCTTTC 25723	TC_ T TG
		GAAGGC TCT GAAGC C	
		CTTTCG AGA TTTTG G	
		CAC _ GT	
GAM1968 NDRG3	3'	GTGGTTTTAGACACGCTTTC 22847	TC_ T TG
		GAAGGC TCT GAAGC C	
		CTTTCG AGA TTTTG G	
		CAC _ GT	
GAM1968 NEURL	3'	GTGGTTTTGGGTTTTTTTGT 10416	CTCT TG TG
		GACGAAGG CT AAGC C	
		TTGTTTTT GG TTTG G	
		TTT_ GT GT	
GAM1968 NFKBIL2	5'	CAGCTTCGGGAGCGCGCT 15086	_ T
		AG GC CTCTTGAAGCTG	
		TC CG GAGGGCTTCGAC	
		G C	
GAM1968 NUP98	3'	GCAGGCAGAGGGCCTTTG 18443	T AAG
		CGAAGGCTCTCT G CTGC	
		GTTTCCGGGAGA C GACG	
		_ G_	
GAM1968 OIP2	5'	GCGGGCCAGGGACCTTTCGTC 37794	C T AAG
		GACGAAGG TC CTTG CTGC	
		CTGCTTTC AG GGAC GGCG	
		C _ CG_	
GAM1968 PABPN1	3'	GTGGTAGGAGGGTTTTTTTA 11018	C AA
		TGA GAAGGCTCTCTTG GC	
		ATT TTTTGGGAGGAT TG	
		T GG	
GAM1968 PDGFB	3'	GTGGCTTCTTTTCGTTTCGTT 8470	TCTCTT TG
		GACGAAGGC GAAGC C	

			TTGCTTTTG	CTTCG	G		
			CTTTT_	GT			
GAM1968	PGF	3'	GTGGTTGCCTGGGGGCTTTTGC	8493	A	TTGA	TG
	CA		TG CGAAGGCTCTC	AGC	C		
			AC GTTTTCGGGGG	TTG	G		
			C	TCCG	GT		
GAM1968	PIK3R3	3'	GGGTTTCTGAAGCTTTTGCA	30606	A	C TT	TG
			TG CGAAGGCT TC	GAAGC	C		
			AC GTTTTCGA AG	CTTTG	G		
			_	T_	GT		
GAM1968	PNN	3'	GCAGCTTTGAGGGGAACAGTT	35233		GAAGG	TG
			GAC	CTCTCT	AAGCTGC		
			TTG	GGGGGA	TTCGACG		
			ACAA_	GT			
GAM1968	POLH	5'	GCAGTTTTGCCAGGTGTTTGTT	13251		G T CT	
	A		TGACGAA GC CT	TGAAGCTGC			
			ATTGTTT TG GA	GTTTGTACG			
			G	_	CC		
GAM1968	PRKY	5'	GCATGGGGAGCCTCCGTT	8647	A	TGAA	
			GACG AGGCTCTCT	GC			
			TTGC TCCGAGGGG	CG			
			C	TA_			
GAM1968	RAB5A	3'	GTGGGGAGGGGGGCTTTTGTT	10372		GAA	
			GACGAAGGCTCTCTT	GC			
			TTGTTTTCGGGGGAG	TG			
			GGG				
GAM1968	RENT1	3'	GCGGCCGGAGGAGTTTGTGTT	8815		G T GAA	
			GACGAAG CTC CTT	GCTGC			
			TTGTTTT GAG GAG	CGGCG			
			_	_	GC_		
GAM1968	SH3BP2	3'	GCACAGGGAGCTTCTGTT	8947	A	TGAA	
			GACG AGGCTCTCT	GC			
			TTGT TTCGAGGGA	CG			
			C	CA_			
GAM1968	SUSP1	3'	TTAGGAAGCTTTTGTTA	17844		C	
			TGACGAAGGCT TCTTGA				
			ATTGTTTTCGA	AGGATT			
			-				
GAM1968	TBL1X	3'	GCAGGGCAGGGGGCCTTT	12185		AAG	
			GAAGGCTCTCTTG	CTGC			

			TTTCCGGGGGGGAC GACG			
			GG_			
GAM1968	TBL1X	3'	GCAGTTTTTATTGTCTGTGTCA 12186	A	TCTCTT	
			TGACG AGGC GAAGCTGC			
			ACTGT TCTG TTTTGACG			
			G TTAT_			
GAM1968	TFCP2	5'	GTAGTTTTCTTGGTTTGCGTTA 12191	A	CTCTT	
			TGACG AGGCT GAAGCTGC			
			ATTGC TTTGG TTTTGATG			
			G TTC_			
GAM1968	TMEPAI	3'	GGGCTTTCTCTAGCCTTGTCA 21407	G	CTCTT	TG
			TGAC AAGGCT GAAGC C			
			ACTG TTCCGA TTTCG G			
			_ TCTC_ GT			
GAM1968	TRRAP	3'	GCAGCTTCGTGCTTTTGTACA 9589	_	TCTCT	
			TG ACGAAGGC TGAAGCTGC			
			AC TGTTTTCG GCTTCGACG			
			A T_			
GAM1968	UCP3	3'	GCCTTGAGAGAGATTTTGTGTC 9385	G	TG A	
			GACGAAG CTCTCT A GC			
			CTGTTTT GAGAGG T CG			
			A GT C			
GAM1968	WASF3	3'	GCAGGATGGTGATGGGGGTTTT 13442	_	AAG_	
	TGTTA		CGAAGGCTCTC TTG CTGC			
			GTTTTTGGGGG AGT GACG			
			T GGTAG			
GAM1968	YWHAE	3'	GTGGTTTGGGGAGGGACTTCGT 13614	G	G	TG
	T		GACGAAG CTCTCTT AAGC C			
			TTGCTTC GGGAGGG TTTG G			
			A G GT			
GAM1968	AD-020	3'	GTAGCTTTAATGATTTTGTGTT 21340	C	TC	
			GACGAAGG TC TTGAAGCTGC			
			TTGTTTTT AG AATTTCGATG			
			_ T_			
GAM1968	AD-020	3'	GTAGCTTTAATGATTTTGTGTT 29870	C	TC	
			GACGAAGG TC TTGAAGCTGC			
			TTGTTTTT AG AATTTCGATG			
			_ T_			
GAM1968	AP3D1	5'	GGGCTTCAGGGGCTCCTGTC 10046	GA	CT	TG
			GAC AGG CTCTGAAGC C			

			CTG TCC GGGGACTTCG G		
			___ TC GT		
GAM1968	AP3D1	3'	GGGCTTCAGGGGCTCCTGTC 10047	GA CT	TG
			GAC AGG CTCTTGAAGC C		
			CTG TCC GGGGACTTCG G		
			___ TC GT		
GAM1968	BCAA	5'	CGGGGGGGGATTTTTCGTC 18509	___	
			GACGAAGG CTCTCTTG		
			CTGCTTTT GGGGGGGC		
			TA		
GAM1968	BRD1	5'	GTGGTTTTCTCGAGTCTTTGGT 15939	_	TCTT TG
	CA		TGAC GAAGGCTC GAAGC C		
			ACTG TTTCTGAG TTTTG G		
			G CTC_ GT		
GAM1968	C17orf31	3'	GCTGAGGGAGGGCCTTCTC 19006	C	GA
			GA GAAGGCTCTCTT AGC		
			CTCTTCCGGGAGGG TCG		
			_ AG		
GAM1968	C19orf7	3'	GCAGTGTGTGGTTTTTGTT 30636		CTCTTGAA
			GACGAAGGCT GCTGC		
			TTGTTTTTGG TGACG		
			TGTTG___		
GAM1968	C20orf100	3'	GGGTTTTGGGGTTTCGTT 26704	GCTC TG	TG
			GACGAAG TCT AAGC C		
			TTGCTTT GGG TTTG G		
			___ GT GT		
GAM1968	C21orf25	3'	GGGCTTGAGGGCTTTTGTT 31801	TTG TG	
			GACGAAGGCTCTC AAGC C		
			TTGTTTTCGGGAG TTCG G		
			___ GT		
GAM1968	C21orf59	5'	AGCCGGGGCCTTCTCA 19501	C	CTTGAA
			TGA GAAGGCTCT GCT		
			ACTCTTCCGGGG CGA		
			_ C___		
GAM1968	CCR6	3'	GCTGAAGACTTTTGTTA 25370	CTC	GA
			TGACGAAGG TCTT AGC		
			ATTGTTTTC AGAA TCG		
			___ G_		
GAM1968	CCR6	3'	GCTGAAGACTTTTGTTA 10577	CTC	GA
			TGACGAAGG TCTT AGC		

ATTGTTTTTC AGAA TCG
 ____ G_
 GAM1968 CRSP3 3' GCAGTTTTATTACCTTTG 30411 CTCTCT
 CGAAGG TGAAGCTGC
 ||||| |||||
 GTTTCC ATTTTGACG
 ATT____
 GAM1968 DJ37E16.5 3' GCTCGAAGGGGGGCTTTTCGT 21576 GA_
 ACGAAGGCTCTCTT AGC
 ||||| |||||
 TGCTTTCGGGGGGA TCG
 AGC
 GAM1968 DKFZP434E2135 3' GCAGCTTGATGAGTTTTTGTG 25115 _ TTG
 GACGAAGGCTC TC AAGCTGC
 ||||| || |||||
 TTGTTTTTGAG AG TTCGACG
 T ____
 GAM1968 DKFZP434F091 3' GTAGCTTAATTAGTATTTTGTG 17739 GCT CTTG
 GACGAAG CT AAGCTGC
 ||||| || |||||
 TTGTTTT GA TTCGATG
 AT_ TTAA
 GAM1968 DKFZP564B1162 5' TCAGGGGACTTTTTGTCA 25337 C
 TGACGAAGG TCTCTTGA
 ||||| |||||
 ACTGTTTTT AGGGGACT
 C
 GAM1968 DKFZP586A0522 3' GCGGTTTTTTTGGTTTGTGTT 15262 _ CTCTT
 GACGA AGGCT GAAGCTGC
 ||||| |||||
 TTGTT TTTGG TTTTGGCG
 G TTT____
 GAM1968 FBXO21 3' GGGTTTTCACACCTCTTGTTA 27324 _ CTCTCT TG
 TGACGA AGG TGAAGC C
 ||||| || ||||| |
 ATTGTT TCC ACTTTG G
 C AC____ GT
 GAM1968 FLJ10199 5' AGCGCATTAAAGGGGTTTTTGT 35285 T _ T
 T GACGAAGGCTC CTTGAA GC GC
 ||||| ||||| || ||
 TTGTTTTTGGG GAATTT CG CG
 _ A _ AG
 GAM1968 FLJ11269 3' GAATATTTGGGCAGGGTTTTTG 35954 _ TG GCTGC
 TTA TGACGAAGGCTCT CT AA
 ||||| || || ||
 ATTGTTTTTGGGA GG TT
 C GT ATAAG
 GAM1968 FLJ12783 3' GCAGAAGAGAGGGTTTTCTCA 25418 C GAAG
 TGA GAAGGCTCTCTT CTGC
 || ||||| ||||| |||||

		ACT CTTTGGGAGAG	GACG	
		— AA—		
GAM1968	FLJ13441	3'	GCACGTGTAGAGTTTTGTCA	23393 CTTGAA _
			TGACGAAGGCTCT GC TGC	
			ACTGTTTTTGAGA TG ACG	
			TG— C	
GAM1968	FLJ13646	3'	GTAGCTTTAACAACCTTTCTGT	23813 _ CTCTC
	TA		TGAC GAAGG TTGAAGCTGC	
			ATTG CTTT AATTCGATG	
			T CAAC—	
GAM1968	FLJ14803	3'	GTAGTTTTAATTTGGGTTTTAG	26627 G TC_
	TTA		TGAC AAGGCTC TTGAAGCTGC	
			ATTG TTTTGGG AATTTGATG	
			A TTT	
GAM1968	FLJ20445	3'	GCAGGAGGGAGGGTTTTT	19481 GAAG
			GAAGGCTCTCTT CTGC	
			TTTTTGGGAGGG GACG	
			AG—	
GAM1968	FLJ20548	3'	GCATTAGAAGAGGGTCTTT	19545 GA C
			GAAGGCTCTCTT AG TGC	
			TTTCTGGGAGAA TT ACG	
			GA _	
GAM1968	FLJ22479	3'	GCAGTTTTGTGAGGCTTTTGT	24386 T T
			ACGAAGGC CTC TGAAGCTGC	
			TGTTTTCG GAG GTTTTGACG	
			— T	
GAM1968	FLJ22679	3'	GCAGCAGGCTTAGGATTTTTGT	25950 CT CTTGAA
	CA		TGACGAAGG CT GCTGC	
			ACTGTTTTT GA CGACG	
			AG TTCGGA	
GAM1968	FLJ22679	3'	GCAGCAGGCTTAGGATTTTTGT	19263 CT CTTGAA
	CA		TGACGAAGG CT GCTGC	
			ACTGTTTTT GA CGACG	
			AG TTCGGA	
GAM1968	FOXP1	5'	GTGTCCAGAAAGCTTTTGTT	26404 C T_ A
			GACGAAGGCT TCT GA GC	
			TTGTTTTCGA AGA CT TG	
			— CC G	
GAM1968	GS3955	3'	CGGCTTCACCCTTCGT	22301 CTCTCT
			ACGAAGG TGAAGCTG	

			TGCTTCC	ACTTCGGC		
			C_____			
GAM1968	HCA4	3'	GTAGCTTTAGGATGTGTTTGCA	38024	A G TC	
			TG CGAA GC TCTTGAAGCTGC			
			AC GTTT TG AGGATTTTCGATG			
			_ G T_			
GAM1968	HDAC9-PENDING	5'	GCAGGACTGAGGGTTTTTGCA	27728	A	TTGAAG
			TG CGAAGGCTCTC CTGC			
			AC GTTTTTGGGAG GACG			
			_ TCAG_			
GAM1968	HDAC9-PENDING	5'	GCAGGACTGAGGGTTTTTGCA	27729	A	TTGAAG
			TG CGAAGGCTCTC CTGC			
			AC GTTTTTGGGAG GACG			
			_ TCAG_			
GAM1968	HDAC9-PENDING	5'	GCAGGACTGAGGGTTTTTGCA	16251	A	TTGAAG
			TG CGAAGGCTCTC CTGC			
			AC GTTTTTGGGAG GACG			
			_ TCAG_			
GAM1968	IL-17RC	3'	GCGGCTTCAAGAGAGAGCG	26456	AAGG	
			CG CTCTCTTGAAGCTGC			
			GC GAGAGAACTTCGGCG			
			GA_			
GAM1968	KCNT1	3'	GCGGAAGAAGAGGGCCTTCTC	30976	C	GAAG
			GA GAAGGCTCTCTT CTGC			
			CT CTTCCGGGAGAA GGCG			
			_ GAA_			
GAM1968	KIAA0057	3'	GTAGTTGTAGGGTACTTTGTCA	14622	GCT TGA	
			TGACGAAG CTCT AGCTGC			
			ACTGTTTC GGGA TTGATG			
			AT_ TG_			
GAM1968	KIAA0335	3'	GCAGCTTCAAGAGAAGAATTT	16732	GG _	
			GAA CT CTCTTGAAGCTGC			
			TTT GA GAGAACTTCGACG			
			AA A			
GAM1968	KIAA0446	3'	GCAGTTTTAAGGGTGATGTGT	34150	AAGGCT	
			ACG CTCTTGAAGCTGC			
			TGT GGGAATTTTGACG			
			GTAGT_			
GAM1968	KIAA0534	3'	TAGTTTTAGGAGAGTTTTTCTT	35385	C	C
	A		TGA GAAGGCTCTCTTGAAGCTG			

ATT TTTTGTGAGAGGATTTTGAT
 C A
 GAM1968 KIAA0843 3' GCGAGATTGAAGGGCTTTTGTT 17260 _TTGAA_ TGC
 A TGACGAAGGCTCT C GC
 ||||| | ||
 ATTGTTTTCGGGA G CG
 A TTAGAG
 GAM1968 KIAA0892 3' GTTTTAGGTCTTGTCA 35172 G CTCT
 TGAC AAGGCT TGAAGC
 ||| ||||| |||||
 ACTG TTCTGG ATTTTG
 — —
 GAM1968 KIAA0894 3' GCAGTTTCCATGTCTTTTTT 17056 C TCTCTT
 GA GAAGGC GAAGCTGC
 || ||||| |||||
 TT TTTCTG CTTTGACG
 T TAC—
 GAM1968 KIAA0981 3' GCAGTTTTAATACTGCTGTGTC 30799 AA TCTC
 A TGACG GGC TTGAAGCTGC
 |||| ||| |||||
 ACTGT TCG AATTTTGACG
 G_ TCAT
 GAM1968 KIAA1157 3' GCATGACAGAGGGTCTTTGTT 35751 TGAA_
 GACGAAGGCTCTCT GC
 ||||| ||||| ||
 TTGTTTCTGGGAGA CG
 CAGTA
 GAM1968 KIAA1274 3' GCGGAGTTGGGAGCCTTT 43911 TT AG
 GAAGGCTCTC GA CTGC
 ||||| || |||||
 TTTCCGAGGG TT GGCG
 — GA
 GAM1968 KIAA1529 5' GGGCTTCGAGGGATGGCGGCG 34947 AAG _ TG
 CG GC TCTCTTGAAGC C
 || || ||||| |
 GC CG AGGGAGCTTCG G
 GG_ GT GT
 GAM1968 KIAA1538 5' TTGGGAGACCTTTGTCA 35437 C TG
 TGACGAAGG TCTCT A
 ||||| ||||| |
 ACTGTTTCC AGAGG T
 — GT
 GAM1968 KIAA1576 3' GGGCTTTAGAGCTTTTGTTA 32775 CTT TG
 TGACGAAGGCTCT GAAGC C
 ||||| ||||| |
 ATTGTTTTCGAGA TTTCG G
 — GT
 GAM1968 KIAA1821 3' CAGTTTCTTGCTTTCTTCA 35551 C TCTCTT
 TGA GAAGGC GAAGCTG
 ||| ||||| |||||

ACT CTTTCG CTTTGAC
 T TT____
 GAM1968 KIAA1894 3' GTAGCTTCAGTATGTTTCCTCA 36561 C G TCTC
 TGA GAAG C TTGAAGCTGC
 ||| ||| | |||||
 ACT CTTT G GACTTCGATG
 C _TAT_
 GAM1968 MAFB 3' GCAGCAAGCTGAGGGTCTTTGT 11943 TTGAA
 T GACGAAGGCTCTC GCTGC
 ||||| ||||
 TTGTTTCTGGGAG CGACG
 TCGAA
 GAM1968 MAP2K6 5' CAGCTTGCATCTTTGTT 8641 CTCTCT _
 GACGAAGG TG AAGCTG
 ||||| || |||||
 TTGTTTCT AC TTCGAC
 _____ G
 GAM1968 MGC2628 3' GTGGTTCTGTAGGGACCTTTGT 23511 C _GA TG
 CA TGACGAAGG TCTCT T AGC C
 ||||| |||| | ||| |
 ACTGTTTCC AGGGA G TTG G
 _ TTC GT
 GAM1968 MGC30052 3' GCAGCTTTAGAATAGCTTC 29544 G CTC
 GAAG CT TTGAAGCTGC
 ||| || |||||
 CTTC GA GATTCGACG
 _ TAA
 GAM1968 MGC4294 5' GCAGCCATAGAGGAGAGCTTTC 23608 GAA__
 GAAGGCTCTCTT GCTGC
 ||||| ||||
 CTTTCGAGAGGA CGACG
 GATAC
 GAM1968 OSBPL5 3' GTGGCTTTGTTTCCAGTTTTTG 35991 CTCT_ TG
 T ACGAAGGCT TGAAGC C
 ||||| |||| |
 TGTTTTTGA GTTTCG G
 CCTTT GT
 GAM1968 pcnp 3' GCAGCTTCAGACTGTTTT 21628 TC T
 AAGGC TCT GAAGCTGC
 |||| ||| |||||
 TTTTG AGA CTTCGACG
 TC _
 GAM1968 PDZD2 5' CAGATGGGGATTTTTGTCA 39391 C TGAAG C
 TGACGAAGG TCTCT CTG
 ||||| |||| |||
 ACTGTTTTT AGGGG GAC
 _ TA__ A
 GAM1968 PNMA3 3' GTGGCTGTGAAGGGAAGTCTTT 15010 _ GA_ TG
 GTT GACGAAGGCT CTCTT AGC C
 ||||| |||| ||| |

			TTGTTTCTGA GGGAA TCG G		
			A GTG GT		
GAM1968	PTRF	5'	GCGGCGCTGGAGCTTTCGTC 31784		CTTGAA
			GACGAAGGCTCT GCTGC		
			CTGCTTTCGAGG CGGCG		
			TCG__		
GAM1968	RAB14	3'	GTAGTTTTGGGGAACCTTT 18448		C T TG
			GAAGG TC CT AAGCTGC		
			TTTTC AG GG TTTGATG		
			A _ GT		
GAM1968	RASGRP4	3'	GCAGTCACAGGGGGCCTGTGTC 27504		A T AA
	A		TGACG AGGCTC CTTG GCTGC		
			ACTGT TCCGGG GGAC TGACG		
			G _ AC		
GAM1968	RBBP1	3'	GTGAGTAGGGGGTTTATGTT 23261		A TGAA
			GACG AGGCTCTCT GC		
			TTGT TTTGGGGGA TG		
			A TGAG		
GAM1968	RBBP1	3'	GTGAGTAGGGGGTTTATGTT 8800		A TGAA
			GACG AGGCTCTCT GC		
			TTGT TTTGGGGGA TG		
			A TGAG		
GAM1968	RHOBTB1	3'	CAGCAGGGGAGCTTTCGT 43950		GAA C
			ACGAAGGCTCTCTT GCTG		
			TGCTTTCGAGGGGA CGAC		
			__ A		
GAM1968	RNAH	3'	TAGCTTCAAGAATTTCTT 31039		CTC
			AAGG TCTTGAAGCTG		
			TTCT AGAACTTCGAT		
			TTA		
GAM1968	RNF11	3'	GGGTTTTGATCTTTTGTC 15705		C TCTT TG
			TGACGAAGG TC GAAGC C		
			ACTGTTTTC AG TTTTG G		
			T __ GT		
GAM1968	RNF11	3'	GTAGTTTAAAGCTTGTT 15706		TCT
			AGGC CTTGAAGCTGC		
			TTTG GAATTTTGATG		
			TTC		
GAM1968	RRN3	3'	GTAGTAAGTGGGGTCTTTGT 20489		_ GAA
			ACGAAGGCTCT CTT GCTGC		

TGT TTTCTGGGG GAA TGATG
 T ____
 GAM1968 SAST 5' GCTTGGAGGTGGCCTTCGTTA 31542 CT G
 TGACGAAGGCT CTT AAGC
 ||||| |||||
 ATTGCTTCCGG GAG TTCG
 TG G
 GAM1968 SEMA6B 3' GCAGTTTTGTTTTCTTTTGCG 25801 A CTCTC TG
 TG CGAAGG T AAGCTGC
 || ||||| | |||||
 GC GTTTC G TTTGACG
 _ TTT__GT
 GAM1968 SLC6A14 3' TAGTTAAAAGTTTTTGTC A 14103 CTC GA
 TGACGAAGGCT TT AGCTG
 ||||| || |||||
 ACTGTTTTGA AA TTGAT
 _ A_
 GAM1968 STAT2 5' GCGGCTGCGAGGGACTTTGTCA 45371 GC A
 TGACGAAG TCTCTTG AGCTGC
 ||||| ||||| |||||
 ACTGTTTC AGGGAGC TCGGCG
 _ G
 GAM1968 STAT2 5' GCGGCTGCGAGGGACTTTGTCA 9960 GC A
 TGACGAAG TCTCTTG AGCTGC
 ||||| ||||| |||||
 ACTGTTTC AGGGAGC TCGGCG
 _ G
 GAM1968 STIM2 3' GTGGGTTGTATAAGGGTAGCTT 21916 _ _ G TG
 TTGTT GAAGGCT CTCTTG AA C C
 ||||| ||||| || |
 TTTTCGA GGGAAT TT G G
 T ATG G GT
 GAM1968 TA-PP2C 3' GGGCTTTATGTCTTTGTTA 29283 TCTCT TG
 TGACGAAGGC TGAAGC C
 ||||| ||||| |
 ATTGTTTCTG ATTCG G
 T__ GT
 GAM1968 TBLR1 3' GTAGTTTTGGGTTTTTTGTT 23966 CTCT TG
 GACGAAGG CT AAGCTGC
 ||||| || |||||
 TTGTTTTT GG TTTGATG
 T__ GT
 GAM1968 TIP-1 5' GCGGGCCGAGCGGGGCGGCCTT 15968 C AA__ _
 TGTTA CGAAGGCT TCTTG GCT GC
 ||||| ||||| ||| ||
 GTTTCGG GGGGCG CGG CG
 C GAGC G
 GAM1968 TOLLIP 3' CCATCGATTGGGGGTGGTTTTT 21091 _ TG AGCTGC
 GTCA GACGAAGGCT CTCT A
 ||||| ||||| |

		CTGTTTTTGG GGGG T		
		T GT AGCTACCG		
GAM1968	TRIM4	3' GTAGAAGAAACAGAGTTTTTGT 26904	C	GAAG
	T	GACGAAGGCTCT TT CTGC		
		TTGTTTTTGAGA AA GATG		
		C AGAA		
GAM1968	TRIP-Br2	3' CATGGTTTTTGAGGAGGGCTTT 16483	—	C
	TGTCA	ACGAAGGCTCTCTT GAAGCTG		
		TGTTTTCGGGAGGA TTTTGGT		
		GT ACG		
GAM1968	TSPAN-5	5' CGGCTTCCCTGCTTTCTC 12276	C	TCTCTT
		GA GAAGGC GAAGCTG		
		CT CTTTCG CTTCGGC		
		— TCC—		
GAM1968	LOC115073	3' AAATTTTAAGGGAGTTTCGTT 36233	G	CTGC
		GACGAAG CTCTCTTGAAG		
		TTGCTTT GAGGGAATTTT		
		— AAAT		
GAM1968	LOC115219	5' GTGGTCAAAGGAGAGAGTCTTT 36281	GAA—	TG
	GTCA	GACGAAGGCTCTCTT GC C		
		CTGTTTCTGAGAGAG TG G		
		GAAAC GT		
GAM1968	LOC118709	5' GCAGTTTCAGGGGAGGTGTC 36600	AAGG	
		GACG CTCTCTTGAAGCTGC		
		CTGT GAGGGGACTTTGACG		
		G—		
GAM1968	LOC126353	3' GCTGGAGGGGGGTCTTTGTC 36830	GA	
		GACGAAGGCTCTCTT AGC		
		CTGTTTCTGGGGGA TCG		
		GG		
GAM1968	LOC126661	3' GCTTTAAGAATTTTTTG 36853	CTC	
		CGAAGG TCTTGAAGC		
		GTTTTT AGAATTCG		
		TA—		
GAM1968	LOC132321	3' TAGCTTGTGAGCTTTCTCA 37027	C	TCTTG
		TGA GAAGGCTC AAGCTG		
		ACT CTTTCGAG TTCGAT		
		— TG—		
GAM1968	LOC133686	3' GTAGTTTTGGAATTGCCTTCCT 37053	C	TCTC TG
	TA	TGA GAAGGC T AAGCTGC		

	ATT CTTCCG G TTTGATG		
	C TTAAGT		
GAM1968 LOC144317 3'	GCAGTGTCTAGAATTTTGTTA 37718	C	CTT A
	TGACGAAGG TCT GA GCTGC		
	ATTGTTTTT AGA CT TGACG		
	A T__ G		
GAM1968 LOC144848 3'	GGGCTTCGAAGCCTTCATCA 36421	C	CTC TG
	TGA GAAGGCT TTGAAGC C		
	ACT CTTCCGA AGCTTCG G		
	A ____ GT		
GAM1968 LOC145317 5'	GTGGTGGGGACCAGGGGATCTT 40531	C	AA____ TG
	CGTCA GAAGG TCTCTTG GC C		
	CTTCT AGGGGAC TG G		
	_ CAGGGG GT		
GAM1968 LOC145844 3'	GTTTATTGGGGGGGCTTTTTTT 38001	C	TG AGCTGC
	A TGA GAAGGCTCTCT A		
	ATT TTTTCGGGGGG T		
	T GT ATTTG		
GAM1968 LOC150185 3'	GCAGCACCCAGAGCTTATTGTT 41152	_	CTTGAA
	A TGACGA AGGCTCT GCTGC		
	ATTGTT TTCGAGA CGACG		
	A CCCA__		
GAM1968 LOC150407 3'	GTGGTTTTTAAGAGAGAGGATC 38952	AGG_	TG
	GA CTCTCTTGAAGC C		
	CT GAGAGAATTTTG G		
	AGGA GT		
GAM1968 LOC151405 5'	GTAGTTTCAAACCTTTTG 41339	CTCTC	
	CGAAGG TTGAAGCTGC		
	GTTTCT AACTTTGATG		
	CA__		
GAM1968 LOC157660 3'	GTGGTTGGGCAAGAGAGTGTCT 41830	_	AA__ TG
	TTGTT GAAG GCTCTCTTG GC C		
	TTTC TGAGAGAAC TG G		
	TG GGGT GT		
GAM1968 LOC158434 5'	GTGGCTTCCTTGGCTTGTCGTC 41986	_	CTCTT TG
	GACGA AGGCT GAAGC C		
	CTGCT TTCGG CTTCG G		
	G TTC__ GT		
GAM1968 LOC164173 3'	TAGTTATGGAGTTTTTGCA 39975	A	CTTGA
	TG CGAAGGCTCT AGCTG		

		AC GTTTTTGAGG	TTGAT		
		—	TA—		
GAM1968	LOC165741 3'	GCTGATTCAGGAGAGCCTGCGT	42192	A	GCT
	T	GACG AGGCTCTCTTGA	GC		
		TTGC TCCGAGAGGACTT	CG		
		G	AGT		
GAM1968	LOC196047 5'	GCAGCCTCCAAGGGGAGCCTTT	43145	—	A
	G	CGAAGGCTCTCTT	GA GCTGC		
		GTTTCCGAGGGGA	CT CGACG		
		AC	C		
GAM1968	LOC196529 3'	GCGGTTTTTTTGGTTTGTGTT	42409	—	CTCTT
		GACGA AGGCT	GAAGCTGC		
		TTGTT TTTGG	TTTTGGCG		
		G	TTT—		
GAM1968	LOC200942 3'	TTGGGTTAGGGGAGCCTTTGTC	42873		AG C
		GACGAAGGCTCTCTTGA	CTG		
		CTGTTTCCGAGGGGATT	GGT		
		G_	TC		
GAM1968	LOC201685 5'	GTAGGAAAAGAGGGTCTTGTC	43386	G	GAAG
		TGAC AAGGCTCTCTT	CTGC		
		ACTG TTCTGGGAGAA	GATG		
		—	AAG—		
GAM1968	LOC202020 3'	GGGCTTCTGAGCTTTCTTCA	42954	C	TCTT TG
		TGA GAAGGCTC	GAAGC C		
		ACT CTTTCGAG	CTTCG G		
		T	T— GT		
GAM1968	LOC202934 5'	TTTTGGGAGACTTTTTGTTA	43469	C	TG
		TGACGAAGG TCTCT	AAG		
		ATTGTTTTT AGAGG	TTT		
		C	GT		
GAM1968	LOC220672 3'	GTAGCTTTAGCCCTTTGTT	30309		CTCTC
		GACGAAGG	TTGAAGCTGC		
		TTGTTTCC	GATTTCGATG		
		C—			
GAM1968	LOC254158 5'	CGGCTTCGAAAGCTTCGCA	46082	A	G CTC
		TG CGAAG CT	TTGAAGCTG		
		AC GCTTC GA	AGCTTCGGC		
		—	— A—		
GAM1968	LOC255045 3'	GTAGCTTTAACAACCTTTTCTGT	46033	—	CTCTC
	TA	TGAC GAAGG	TTGAAGCTGC		

	ATTG CTTTT AATTTGATG		
	T CAAC_		
GAM1968 LOC256536 3'	GCAGCAATAGGGTTTTTCATCA 45428	C	C GAA
	TGA GAAGGCTCT TT GCTGC		
	ACT CTTTTGGGA AA CGACG		
	A T ____		
GAM1968 LOC257017 5'	GTAGTTTCCTTAGTTTTTGT 46496		CTCTT
	ACGAAGGCT GAAGCTGC		
	TGTTTTTGA CTTTGATG		
	TTC__		
GAM1968 LOC56912 5'	GCGTGGAGAGCCTTCGCG 21365	A	TGAA
	TG CGAAGGCTCTCT GC		
	GC GCTTCCGAGAGG CG		
	_ TG__		
GAM1968 LOC85414 3'	GCGGTTTCCCAAGCCTTTGTC 26952		CTCTT
	GACGAAGGCT GAAGCTGC		
	CTGTTTCCGA CTTTGGCG		
	ACC__		
GAM1968 LOC90183 3'	GCAGCAAGCTGAGGGTCTTTGT 30926		TTGAA
T	GACGAAGGCTCTC GCTGC		
	TTGTTTCTGGGAG CGACG		
	TCGAA		
GAM1968 LOC91272 5'	GTATCAGAGGGGGCCTTCGCCG 32612	A	_ A
	TG CGAAGGCTCTCT TGA GC		
	GC GCTTCCGGGGGA ACT TG		
	C G A		
GAM1968 LOC91301 5'	GCGGTTTGAGGTCCTTCGTTA 32651		CT TTG
	TGACGAAGG CTC AAGCTGC		
	ATTGCTTCC GAG TTTGGCG		
	TG ____		
GAM1968 LOC91516 5'	GCATCCCTGAGGGAGCCTTTG 32956		__ A TGC
	CGAAGGCTCTCTT GA GC		
	GTTTCCGAGGGAG CT CG		
	TCC A		
GAM1968 LOC91585 3'	GTAGTTTTGAGTAGTATTTTGT 33076		GCT _ TG
T	GACGAAG CT CT AAGCTGC		
	TTGTTTT GA GA TTTGATG		
	AT_ T GT		
GAM1968 LOC93166 3'	GCAGAGTGAGAGCCTTCG 35462		TTGAAG
	CGAAGGCTCTC CTGC		

GCTTCCGAGAG GACG
 TGA____
 GAM1969 FLJ21432 3' GATGGCTCATGTCACAGGC 23767 CG
 GCC GTGACGTGAGCCATC
 ||| |||||
 CGG CACTGTACTCGGTAG
 A_
 GAM1969 KIAA1538 3' TGATGGTTTCTCCCAGACTAG 35432 CCC T CGT
 CTAG GG GA GAGCCATCA
 ||| || || |||||
 GATC CC CT TTTGGTAGT
 AGA _ C_
 GAM1969 LOC143914 5' GATGGCTTTGCCACACCAGGC 37635 C ACGT_
 GCC GGTG GAGCCATC
 ||| ||| |||||
 CGG CCAC TTCGGTAG
 A ACCGT
 GAM1969 LOC146795 5' ATGGCTTGGACCAGGCCAG 38243 A C GA GT
 CT GCC GGT C GAGCCAT
 || ||| ||| | |||||
 GA CGG CCA G TTCGGTA
 C A G_ _
 GAM1969 LOC154860 3' CTCCGCCACCGGGCTAG 41736 A T
 CTAGCCCGGTG CG GAG
 ||||| || |||
 GATCGGGCCAC GC CTC
 C _
 GAM1970 CSNK1G2 3' AGCTTGTCTCCCTCGATC 7006 T C T A
 GATCGAGG AG AC GG CT
 ||||| || || ||
 CTAGCTCC TC TG TC GA
 C _ T _
 GAM1970 ZNF200 3' TGGTGCTGCCTCAACCTGA 9504 ATC
 TCAG GAGGTAGCACTG
 ||| |||||
 AGTC CTCCGTCGTGGT
 CAA
 GAM1970 BLP1 3' AGTCCAGTGCCATGCCTT 25686 _
 GAGGTA GCACTGGACT
 |||| |||||
 TTCCGT CGTGACCTGA
 AC
 GAM1970 GFR 3' AGTCCAGTTTTCAATATGA 14633 G C TAGC
 TCA AT GAGG ACTGGACT
 ||| || ||| |||||
 AGT TA CTTT TGACCTGA
 A A _ _
 GAM1970 IL1RAPL1 3' AGTCCAGTGCCTGGAAC 15551 A G GTA
 AG TC AG GCACTGGACT
 || || || |||||

		TC AG TC CGTGACCTGA		
		A G _ _		
GAM1970	LOC143187 3'	TAGTCCAGCTCTGTGATCTGA 29746	A T	AC
		TCAGATCG GG AGC TGGACTA		
		AGTCTAGT TC TCG ACCTGAT		
		G _ _ _		
GAM1970	LOC149711 5'	CAGCTGCCACCCTGATCTGA 41070	A A	_
		TCAGATCG GGT GCA CTG		
		AGTCTAGT CCA CGT GAC		
		C C C		
GAM1970	LOC90906 3'	CTGGGGGCTACCTGATCTGA 32151	G	A TG
		TCAGATC AGGTAGC C G		
		AGTCTAG TCCATCG G C		
		_ G GT		
GAM1971	AR 5'	GGTGGAAGATTCAGCCAAGCTC 5487	A	AA
	A	TGAGCT GGCT GAA CTTCCACC		
		ACTCGA CCGA CTT GAAGGTGG		
		A _ A _		
GAM1971	INSRR 3'	GGTGAATGAGCTGGCCAGCCCA 33962	A	AAACTTC
		TG GCTGGCTAG CACC		
		AC CGACCGGTC GTGG		
		C GAGTAA _		
GAM1971	PFKFB4 3'	GGTGTTCACTCTCGCCAGCTCA 10910	T	AAACTTC
		TGAGCTGGC AGA CACC		
		ACTCGACCG TCT GTGG		
		C CACTT _		
GAM1971	PMM2 3'	GTGAAAGCAGCCAGCTCA 35682	AGAAAA	C
		TGAGCTGGCT CTT CAC		
		ACTCGACCGA GAA GTG		
		C _ _ A		
GAM1971	PRKCABP 5'	GGCAGTTAGCCAGCCCA 14788	A	GAAA T
		TG GCTGGCTA ACT CC		
		AC CGACCGAT TGA GG		
		C _ _ C		
GAM1971	PTHLH 3'	TGGTTTCTACCAGCTCA 8687	C	ACTT
		TGAGCTGG TAGAAA CCA		
		ACTCGACC ATCTTT GGT		
		_ _ _ _		
GAM1971	C2orf6 5'	GGTCCGCTCCCTCTAGCCAGCT 20142	AAACTTCC	
	C	GAGCTGGCTAGA ACC		

		CTCGACCGATCT	TGG		
		CCCTCGCC			
GAM1971	DKFZp547l014	5'	GTGAAAGTTTGGTCAGTCTCA	21467	_ GAA C
			TGAG CTGGCTA AACTT CAC		
			ACTC GACTGGT TTGAA GTG		
			T _ A		
GAM1971	EDR2	5'	GTGGCCCTCCAGCCCAGCTCA	30339	_ A AAACCTT
			TGAGCTGG CT GA CCAC		
			ACTCGACC GA CT GGTG		
			C C CCC_		
GAM1971	FLJ10700	3'	GGCCATTTCCAGCCAGCTC	20020	A ACTT
			GAGCTGGCT GAAA CC		
			CTCGACCGA CTTT GG		
			C ACC_		
GAM1971	FLJ11160	3'	TGGAAGTCCCCTGGCATGGTCA	20353	G _ AAA
			TGA CTG GCTAG ACTTCCA		
			ACT GGT CGGTC TGAAGGT		
			_ A CCC		
GAM1971	FLJ12270	5'	GTGGAATATCTAGCCGCCCA	24954	A T AAAC
			TG GC GGCTAGA TTCCAC		
			AC CG CCGATCT AAGGTG		
			C _ AT_		
GAM1971	FLJ12294	5'	GTGGAAGCTCCGTGAGACCA	24746	AG G TA AAA
			TG CT GC GA CTTCCAC		
			AC GA TG CT GAAGGTG		
			CA G C_ C_		
GAM1971	FLJ14297	3'	GGTGGAAGCTCTCAAGCTC	24392	GGCT AAA
			GAGCT AGA CTTCCACC		
			CTCGA TCT GAAGGTGG		
			AC_ C_		
GAM1971	FLJ22329	3'	GTGGTGTCCAGCCAGCTC	23958	A AAACCTT
			GAGCTGGCT GA CCAC		
			CTCGACCGA CT GGTG		
			C GT_		
GAM1971	IKKE	5'	GGCAGAAGGTGACCAGCCAGCT	15202	AGAAAA CA
	CA		TGAGCTGGCT CTTC CC		
			ACTCGACCGA GAAG GG		
			CCAGTG AC		
GAM1971	KIAA1344	3'	TGGAAACCTCCTCTTCCAGCTT	35874	CT AAAC_
	A		TGAGCTGG AGA TTCCA		

			ATTCGACC TCT AAGGT		
			T_ CCTCCA		
GAM1971	MAP	3'	GGTAGAAGTTTTCTACTCAGCT 23097	GC	C
			AGCTG TAGAAACTTC ACC		
			TCGAC ATCTTTTGAAG TGG		
			TC A		
GAM1971	MGC13061	3'	TGGAAGGGGACTAGCCAGCTC 26130		AAAA
			GAGCTGGCTAG CTTCCA		
			CTCGACCGATC GAAGGT		
			AGGG		
GAM1971	MGC1842	3'	GGCAGTTAGCCAGCTCA 32688	GAAA	T
			TGAGCTGGCTA ACT CC		
			ACTCGACCGAT TGA GG		
			_____ C		
GAM1971	PRO0943	5'	TGGAAATGATCAACCAGCTCA 20651	CTA	AAAC
			TGAGCTGG GA TTCCA		
			ACTCGACC CT AAGGT		
			AA_ AGTA		
GAM1971	SEC14L1	3'	GGAAGCTGCCAGCTC 8903	T	AAAA
			GAGCTGGC AG CTTCC		
			CTCGACCG TC GAAGG		

GAM1971	SLC26A9	3'	GGTGGAAGTCCTCCAG 27494	CT	AAA
			CTGG AG ACTTCCACC		
			GACC TC TGAAGGTGG		
			_____ C_____		
GAM1971	SLC26A9	3'	GGTGGAAGTCCTCCAG 28632	CT	AAA
			CTGG AG ACTTCCACC		
			GACC TC TGAAGGTGG		
			_____ C_____		
GAM1971	ZNF271	5'	GTAAAAGTTTTAGCCAGC 45637	AA	CC
			GCTGGCTAGA ACTT AC		
			CGACCGATTT TGAA TG		
			_____ AA		
GAM1971	ZNF387	5'	TGGAAACTCTCCAGTTCA 16180	CT	AAAC
			TGAGCTGG AGA TTCCA		
			ACTTGACC TCT AAGGT		
			_____ CA_____		
GAM1971	LOC153688	3'	GTGGAGATCTAGCCAGGTCA 41660	G	AAAC
			TGA CTGGCTAGA TTCCAC		

		ACT GACCGATCT	GAGGTG		
		G	A__		
GAM1971	LOC154428 5'	GTGGCTCCAGCCAGCTC	41703	A	AAACTT
		GAGCTGGCT GA	CCAC		
		CTCGACCGA CT	GGTG		
		C C__			
GAM1971	LOC157273 3'	GGCAAAGTGCAACTGCAGCCAG	41786	__	AAA_ __
	CTCA	TGAGCTGGCT AG	ACTT CC		
		ACTCGACCGA TC	TGAA GG		
		CG AACG	AC		
GAM1971	LOC163255 5'	TGGAAGCCCTCATTGCCAGTCA	40109	G	TA_ AAA
		TGA CTGGC GA	CTTCCA		
		ACT GACCG CT	GAAGGT		
		_ TTA CCC			
GAM1971	LOC220020 3'	GGCAGAAGCTCCACTAGCTCA	44867	CTA	AAA CA
		TGAGCTGG GA	CTTC CC		
		ACTCGATC CT	GAAG GG		
		AC_ C_	AC		
GAM1971	LOC91266 5'	TGGAAGTTCTCCAATAGTGGCT	32604	G	__ A
		AGCTG CTA GA	AACTTCCA		
		TCGGT GAT CT	TTGAAGGT		
		_ AAC C			
GAM1972	BCL10 3'	TATCTTGGCCTAAACCTCA	10009	G	ATCT
		TGAGGTTT AG	CTAAGATA		
		ACTCCAAA TC	GGTTCTAT		
		_ C__			
GAM1972	GOCAP1 3'	CTCAGAGATTTTTCTTCA	22939	TTT	A
		TGAGG GAGATCTCT AG			
		ACTTC TTTTAGAGA TC			
		T_ C			
GAM1972	GPR86 3'	ATATCCCACCATCACCTCAAAC	23387	A	ATCTCTAA__
	CCA	TG GGTGAG	GATAT		
		AC CCAA	CTC CTATA		
		_ CACTACCACC			
GAM1972	NR3C1 3'	ATATCCCAGAAATTAGAAACCT	5685	GA	C AA
	TA	TGAGGTTT GAT TCT	GATAT		
		ATTCCAAA TTA AGA	CTATA		
		GA A CC			
GAM1972	CALN1 3'	CTGCCCTGTCTCAAATCTCA	25515	CTCTA	
		TGAGGTTTGAGAT AG			

		ACTCTAAACTCTG	TC	
		TCCCG		
GAM1972	IDI1	3' ATATCTCAGATTTGAAACCTCA	33285	G CTA
		TGAGGTTT AGATCT	AGATAT	
		ACTCCAAA TTTAGA	TCTATA	
		G	C__	
GAM1973	ABL1	3' CCCCACCTCCTCTAAGACAA	11638	TCACA
		TTGTCTTA	AGTGGGG	
		AACAGAAT	TCACCCC	
		CTCC_		
GAM1973	ABL1	3' CCCCACCTCCTCTAAGACAA	14227	TCACA
		TTGTCTTA	AGTGGGG	
		AACAGAAT	TCACCCC	
		CTCC_		
GAM1973	CHRNA3	3' CCCCACCTTCTATCTAAGACAA	6396	TCACAA__
	T	ATTGTCTTA	GTGGGG	
		TAACAGAAT	CACCCC	
		CTATCTTC		
GAM1973	KNSL3	5' CCCTCTGATTGATAAGACA	11823	CA_ T
		TGTCTTATCA	AG GGG	
		ACAGAATAGT	TC CCC	
		TAG T		
GAM1973	KNSL3	5' CCCTCTGATTGATAAGACA	24961	CA_ T
		TGTCTTATCA	AG GGG	
		ACAGAATAGT	TC CCC	
		TAG T		
GAM1973	CHL1	3' CCCACTCGTGATAAGTCAA	13392	T A
		TTG CTTATCAC	AGTGGG	
		AAC GAATAGTG	TCACCC	
		T	C	
GAM1973	CREG	3' CCCCACCTAAGTCGAGACAGTA	9947	ATCACAA
		TATTGTCTT	GTGGGG	
		ATGACAGAG	CACCCC	
		CTGAATC		
GAM1973	FLJ22794	5' CCCAAAATAGGACAATA	44027	CACAAG
		TATTGTCTTAT	TGGG	
		ATAACAGGATA	ACCC	
		AA__		
GAM1973	KIAA0522	3' CCCCACCTACAACCTGAAGACAA	35622	ATCACAA__
	TG	TATTGTCTT	GTGGGG	

		GTAACAGAA	CACCCC	
		GTCAACATC		
GAM1973	KIAA0532	3'	CCCCACTTAGAGACAATG	35023 ATCAC
			TATTGTCTT AAGTGGGG	
			GTAACAGAG TTCACCCC	
			A_____	
GAM1973	MIL1	3'	CCCCACTTGTGAGTGCAA	17666 CTTA
			TTGT TCACAAGTGGGG	
			AACG AGTG TTCACCCC	
			TG_____	
GAM1974	FZD10	3'	ATAAAATATGTTCTTTAG	14050 A
			CTAAA AACATATTTTAT	
			GATTT TTGTATAAAATA	
			C	
GAM1974	FLJ13621	5'	ATAAACTTGTTTTAGAAGAC	24580 AA TA
			GTCTTCTAAA ACA TTTTAT	
			CAGAAGATTT TGT AAAATA	
			_____ TC	
GAM1974	KIAA0781	3'	AAATGTGTTCTAAGAAGACA	33497 AAAA
			TGTCTTCT AACATATTT	
			ACAGAAGA TTGTGTAAA	
			ATCC	
GAM1974	KLF5	3'	AGTAAGTTTTTTTAGAAGACA	7460 _ A
			TGTCTTCTAAAAAA C TATT	
			ACAGAAGATTTTTT G ATGA	
			T A	
GAM1974	NAALAD2	3'	ATAAAATATGTTTCTATTTAGA	11962 _____
			TCTAAA AACATATTTTAT	
			AGATTT TTTGTATAAAATA	
			ATC	
GAM1974	LOC148266	3'	TAAATATGTTGAAAGGCA	38515 CTAAAA
			TGTCTT AACATATTTTA	
			ACGGAA TTGTATAAAAT	
			AG_____	
GAM1975	FGF7	3'	AGGGGCCTCCATCCCTCT	7748 G ATATA
			AGAGGGATGG AG TTCCT	
			TCTCCCTACC TC GGGGA	
			_ C_____	
GAM1975	MASP1	3'	AATGCCTCTCCCATCCTCT	7604 G TA
			AGAGG ATGGGAGA TATT	

		TCTCC TACCCTCT GTAA	
		— CC	
GAM1975	METTL1	3' GAAGAATACAAGATCCCGTCC 23308	GATA_ C
		GGATGGGA TATTC TC	
		CCTGCCCT ATAAG AG	
		AGAAC A	
GAM1975	METTL1	3' GAAGAATACAAGATCCCGTCC 23313	GATA_ C
		GGATGGGA TATTC TC	
		CCTGCCCT ATAAG AG	
		AGAAC A	
GAM1975	MYH11	3' AGGAATATAAAAACCACCACCC 23140	A GAGA__
	T	AGGG TGG TATATTCCT	
		TCCC ACC ATATAAGGA	
		— ACCAAAA	
GAM1975	MYH11	3' AGGAATATAAAAACCACCACCC 8298	A GAGA__
	T	AGGG TGG TATATTCCT	
		TCCC ACC ATATAAGGA	
		— ACCAAAA	
GAM1975	NGFR	3' GAGGAATGCTCCCCCATCCT 8334	A TA
		GGGATGGG GA TATTCCTC	
		TCCTACCC CT GTAAGGAG	
		C C_	
GAM1975	NPR2L	3' GAGTAACCCTCCCATCCC 13300	ATA
		GGGATGGGAG TATTC	
		CCCTACCCTC ATGAG	
		CCA	
GAM1975	PMX1	5' AGGGGGTCCCCCACCCTCT 13777	A A ATA
		AGAGGG TGGG GAT TTCCT	
		TCTCCC ACCC CTG GGGGA	
		— C —	
GAM1975	PMX1	5' AGGGGGTCCCCCACCCTCT 22912	A A ATA
		AGAGGG TGGG GAT TTCCT	
		TCTCCC ACCC CTG GGGGA	
		— C —	
GAM1975	TNFSF4	3' TATATTCCTCCATCCCTCT 9335	A
		AGAGGGATGGGAG TATA	
		TCTCCCTACCCTT ATAT	
		—	
GAM1975	CNTNAP1	3' GAGGATATTCCCCCATCCC 9694	A T T
		GGGATGGG GA ATAT CCTC	

CCCTACCC CT TATA GGAG
 C _ _
 GAM1975 DKFZP434P1750 3' GAAATGTCCCCATCTCCCT 17792 A A A
 AG GGGATGGG GATAT TTC
 || ||||| |||| |||
 TC CTCTACCC CTGTA AAG
 C C _
 GAM1975 FLJ10687 3' AATATATTCTCTCATCCCTCT 20006 _
 AGAGGGATGGGAGA TATATT
 ||||| ||||| |||||
 TCTCCCTACTCTCT ATATAA
 T
 GAM1975 FLJ11286 3' AGGAATCTGGACTCCCCATCCC 20412 _ A_ T
 GGGATGGG AG TA ATTCCT
 ||||| || || |||||
 CCCTACCC TC GT TAAGGA
 C AG C
 GAM1975 FLJ14154 3' GAGGAGTGCCCCCACTCCTC 24272 GA AGATA
 GAGG TGGG TATTCCTC
 ||| ||| |||||
 CTCC ACCC GTGAGGAG
 TC CCG_
 GAM1975 FLJ20619 3' GAAGAGTCCTCCCATCCCCT 19570 A ATATA
 AG GGGATGGGAG TTC
 || ||||| |||
 TC CCCTACCCTC AAG
 _ CTGAG
 GAM1975 HN1L 3' GAAGCCTCTGCCCATCCCCCT 29377 A _ TATA
 AG GGGATGGG AGA TTC
 || ||||| ||| |||
 TC CCCTACCC TCT AAG
 C G CCG_
 GAM1975 KCNS1 3' AATATATCCCTATACTC 8040 GG A
 GAG ATGGG GATATATT
 ||| |||| |||||
 CTC TATCC CTATATAA
 A_ _
 GAM1975 KIAA0435 3' GAATACATTTCCCCTCCCT 16720 T A
 AGGGA GGGAGAT TATTC
 |||| ||||| |||||
 TCCCT CCCTTTA ATAAG
 C C
 GAM1975 KIAA0544 3' GAGGTTGGCATCCCCATCCC 35112 A ATATT
 GGGATGGG GAT CCTC
 ||||| ||| |||
 CCCTACCC CTA GGAG
 C CGGTT
 GAM1975 KIAA0556 3' GAGGACAATCCCCATCTC 34251 A ATAT
 GGGATGGG GAT TCCTC
 ||||| ||| |||||

CTCTACCC CTA AGGAG
 C AC__
 GAM1975 KIAA0848 3' AGAAATATATCCCTTGCTCCCT 17212 T__ A C
 TT AGAGGGA GGG GATATATT CT
 ||||| || ||||| ||
 TTTCCCT TCC CTATATAA GA
 CGT _ A
 GAM1975 MGC2574 3' GATTCAGCTCCCATCCCTC 23539 ATAT
 GAGGGATGGGAG ATT
 ||||| ||
 CTCCTACCCTC TAG
 GACT
 GAM1975 N4BP3 3' GAGGAAGCATTCCCCACCCC 32936 A A TATA
 GGG TGGG GA TTCCTC
 || ||| || |||||
 CCC ACCC CT AAGGAG
 C _ TACG
 GAM1975 SARM 3' AATGGCTCTCCCTCCCCCT 17450 A T TA
 AG GGA GGGAGA TATT
 || ||| ||||| ||
 TC CCCT CCCTCT GTAA
 C _ CG
 GAM1975 SCYA16 3' AATATATTTACATCCTTCT 10933 G
 AGAGGGATG GAGATATATT
 ||||| |||||
 TCTTCCTAC CTTTATATAA
 A
 GAM1975 SYTL2 5' AGGAATACAGCATCCTTCT 26757 GGAGATA
 AGAGGGATG TATTCCT
 ||||| |||||
 TCTTCCTAC ATAAGGA
 GAC__
 GAM1975 XT2 3' AGAAATATATCTCTATCTCTCT 22721 G C
 AGAGGGATGG AGATATATT CT
 ||||| ||||| ||
 TCTCTCTATC TCTATATAA GA
 _ A
 GAM1975 LOC145195 5' AGGAACACATCTCCTGCACTTC 40511 GA ATA
 T AGAGG TGGGAGAT TTCCT
 |||| ||||| ||||
 TCTTC GTCCTCTA AAGGA
 AC CAC
 GAM1975 LOC148137 3' AGGAAATGCCCCCATCCT 29512 AGA A
 GGGATGGG TAT TTCCT
 ||||| || ||||
 TCCTACCC GTA AAGGA
 CCC _
 GAM1975 LOC158116 3' AGGGGCCTCCATCCCTCT 30251 G ATATA
 AGAGGGATGG AG TTCCT
 ||||| || ||||

			TCTCCCTACC TC	GGGGA		
			_ C _			
GAM1975	LOC160646	3'	GAGGTCCTCTCCCCATCCCTC	40003	A	TATATT
			GAGGGATGGG GA	CCTC		
			CTCCCTACCC CT	GGAG		
			C CTCCT_			
GAM1975	LOC51200	3'	AGGTCTCTCCCTCCCTC	18479	T	TATATT
			GAGGGA GGGAGA	CCT		
			CTCCCT CCCTCT	GGA		
			_ CT _			
GAM1975	LOC51267	3'	AGAAATATATCCCCATCTCC	18590	_	A C
			GG GATGGG GATATATT CT			
			CC CTACCC CTATATAA GA			
			T _ A			
GAM1975	LOC81558	3'	GATAGATCCCCATCCTCT	25110	G	A A
			AGAGG ATGGG GAT TATT			
			TCTCC TACCC CTA ATAG			
			_ C G			
GAM1976	DMD	3'	TGGTTTTTGTTGCTTTTT	5574	_	
			AAAAA CAACAAAAACCA			
			TTTTT GTTGTTTTTGGT			
			C			
GAM1976	DMD	3'	TGGTTTTTGTTGCTTTTT	10157	_	
			AAAAA CAACAAAAACCA			
			TTTTT GTTGTTTTTGGT			
			C			
GAM1976	DMD	3'	TGGTTTTTGTTGCTTTTT	10164	_	
			AAAAA CAACAAAAACCA			
			TTTTT GTTGTTTTTGGT			
			C			
GAM1976	DMD	3'	TGGTTTTTGTTGCTTTTT	10170	_	
			AAAAA CAACAAAAACCA			
			TTTTT GTTGTTTTTGGT			
			C			
GAM1976	DMD	3'	TGGTTTTTGTTGCTTTTT	10178	_	
			AAAAA CAACAAAAACCA			
			TTTTT GTTGTTTTTGGT			
			C			
GAM1976	DMD	3'	TGGTTTTTGTTGCTTTTT	10183	_	
			AAAAA CAACAAAAACCA			

		TTTTT GTTGT TTTTGGT	
		C	
GAM1976 DMD	3'	TGGTTTTTGTGCTTTT 10188	—
		AAAAA CAACAAAAACCA	
		TTTTT GTTGT TTTTGGT	
		C	
GAM1976 DMD	3'	TGGTTTTTGTGCTTTT 10199	—
		AAAAA CAACAAAAACCA	
		TTTTT GTTGT TTTTGGT	
		C	
GAM1976 DMD	3'	TGGTTTTTGTGCTTTT 10205	—
		AAAAA CAACAAAAACCA	
		TTTTT GTTGT TTTTGGT	
		C	
GAM1976 DMD	3'	TGGTTTTTGTGCTTTT 10210	—
		AAAAA CAACAAAAACCA	
		TTTTT GTTGT TTTTGGT	
		C	
GAM1976 DMD	3'	TGGTTTTTGTGCTTTT 10215	—
		AAAAA CAACAAAAACCA	
		TTTTT GTTGT TTTTGGT	
		C	
GAM1976 DMD	3'	TGGTTTTTGTGCTTTT 10226	—
		AAAAA CAACAAAAACCA	
		TTTTT GTTGT TTTTGGT	
		C	
GAM1976 DMD	3'	TGGTTTTTGTGCTTTT 10238	—
		AAAAA CAACAAAAACCA	
		TTTTT GTTGT TTTTGGT	
		C	
GAM1976 IL20RA	3'	TTGTGGATATTTGGCTGTTTTT 15792	A_ AA_
A		TAAAAACA CAAA CCACAA	
		ATTTTGT GTTT GGTGTT	
		CG ATA	
GAM1976 PCDH11X	3'	GTATTTTTTGTGTTTTTA 26792	CC
		TAAAAACAACAAAAA AC	
		ATTTTGTGTTTTT TG	
		TA	
GAM1976 PCDH11X	3'	GTATTTTTTGTGTTTTTA 26807	CC
		TAAAAACAACAAAAA AC	

		ATTTTGTGTTTTT TG		
		TA		
GAM1976	PCDH11Y	3' GTATTTTTGTGTTTTTA 26825		CC
		TAAAAACAACAAAAA AC		
		ATTTTGTGTTTTT TG		
		TA		
GAM1976	PDAP1	3' TTGAATGTTTTTGCTGTTTTTA 44422	A	CA_
		TAAAAACA CAAAAAC CAA		
		ATTTTGT GTTTTG GTT		
		C TAA		
GAM1976	PIGA	3' TGGGGGGTTTTTGTTTTTTA 21714	C	ACAA
		TAAAAA AACAAAAACC CTA		
		ATTTT TTGTTTTTGG GGT		
		GG_		
GAM1976	PIGA	3' TGGGGGGTTTTTGTTTTTTA 21721	C	ACAA
		TAAAAA AACAAAAACC CTA		
		ATTTT TTGTTTTTGG GGT		
		GG_		
GAM1976	PIGA	3' TGGGGGGTTTTTGTTTTTTA 8501	C	ACAA
		TAAAAA AACAAAAACC CTA		
		ATTTT TTGTTTTTGG GGT		
		GG_		
GAM1976	SMARCA1	3' TAGTTGTATTATTGTTGTTTCA 9033	A	A CC
		A AAACAACAA AA ACAACTA		
		A TTTGTTGTT TT TGTGAT		
		C A A_		
GAM1976	SMARCA1	3' TAGTTGTATTATTGTTGTTTCA 29132	A	A CC
		A AAACAACAA AA ACAACTA		
		A TTTGTTGTT TT TGTGAT		
		C A A_		
GAM1976	STAU2	3' TAGAATTTGTTTTTGTTGTTTT 15723		CACAA
		AAAACAACAAAAAC CTA		
		TTTTGTTGTTTTTG GAT		
		TTTAA		
GAM1976	DKFZP566K023	3' GTGTTTTTGTGTTTTTG 17758		C
		TAAAAACAACAAAAA CAC		
		GTTTTTGTGTTTTT GTG		
		T		
GAM1976	FLJ14117	3' GTGGTTTTTGCCATTTTTA 23050		CAA
		TAAAAA CAAAAACCAC		

ATTTT GTTTTGGTG
 ACC
 GAM1976 FLJ14751 3' TTGTGGTTTTTGCCATTG 26613 ____
 CAA CAAAAACCACAA
 ||| |||||
 GTT GTTTTGGTGTT
 ACC
 GAM1976 FLJ23153 3' TGAGGTTTTTGTGTTTTT 23909 A
 AAAACAACAAAAACC CA
 ||||| ||
 TTTTGTGTTTTTGG GT
 A
 GAM1976 HSPC195 5' TAGTTGCTTTTTGTGTTTTT 39425 CCA
 AAAACAACAAAA CAACTA
 ||||| ||||
 TTTTGTGTTTTT GTTGAT
 C_
 GAM1976 KIAA0562 3' ATAGTTACAGGGGGTTTTTTTG 16239 ____ AC____ |||
 TTGTTTT AACAAAA ACC AACTA T
 ||||| || |||| |
 TTGTTTT TGG TTGAT A
 TT GGGACA |||
 GAM1976 KIAA0923 3' GGATTTTTGTGTTTTTG 15242 _
 TAAAAACAACAAAA CC
 ||||| ||
 GTTTTGTGTTTTT GG
 A
 GAM1976 KIAA1327 3' AGTTGTGGCTCTGTTTTT 35763 ACAAAAA
 AAAACA CCACAAC
 ||||| |||||
 TTTTGT GGTGTTGA
 CTC_
 GAM1976 MRPL20 3' AGCTGGGTTTTTGCTGTTTTTA 19694 A A A
 TAAAAACA CAAAAACC CA CT
 ||||| ||||| || ||
 ATTTTGT GTTTTGG GT GA
 C _ C
 GAM1976 PFDN4 3' AGTTGTGTCATGTTGTTT 8486 AAAC
 AAACAACA CACAAC
 ||||| |||||
 TTTGTTGT GTGTTGA
 ACT_
 GAM1976 RAB14 3' TAGTTACAGTGGGTTTTATTGT 18449 C A ____
 TTTTG TAAAAACAA AAAA CCAC AACTA
 ||||| ||| ||| ||||
 GTTTTGT TTTT GGTG TTGAT
 A G ACA
 GAM1976 RYK 3' AGTTGGAGGCTTTTGCTGTTTT 40203 A A A_
 TA TAAAAACA CAAAA CC CAACT
 ||||| ||||| || ||||

	ATTTTGT GTTT GG GTTGA	
	C C AG	
GAM1976 WNT16	3' GTGGTCTTCTTGTTTTTA 27675	C A
	TAAAAACAA AAA ACCAC	
	ATTTTGT TTT TGGTG	
	C C	
GAM1976 WNT16	3' GTGGTCTTCTTGTTTTTA 18171	C A
	TAAAAACAA AAA ACCAC	
	ATTTTGT TTT TGGTG	
	C C	
GAM1976 LOC134266	3' AGTTTTTTTGTGTTTTT 37066	CCAC
	AAAAACAACAAAAA AACT	
	TTTTTGTGTTTT TTGA	

GAM1976 LOC144245	3' TTGTGGTTTTTGCCATTG 35052	_____
	CAA CAAAAACCACAA	
	GTT GTTTTTGGTGTT	
	ACC	
GAM1976 LOC148697	3' TGGTTTTGTGTTTTTA 38576	A
	TAAAAACAACAAAA CCA	
	ATTTTGTGTTTT GGT	
	—	
GAM1976 LOC150933	3' TGGTTGATTTTTGTGTT 41273	CCA
	AACAACAAAA CAACTA	
	TTGTTGTTTT GTTGGT	
	A_	
GAM1976 LOC152580	3' TGGTCGTTGCTGTTTTTA 41524	A AA
	TAAAAACA CAA ACCA	
	ATTTTGT GTT TGGT	
	C GC	
GAM1976 LOC152925	3' TAGTTCTTTTTTTGTGTT 39334	CCAC
	AACAACAAAAA AACTA	
	TTGTTGTTTT TTGAT	
	TTCT	
GAM1976 LOC219404	3' GGCCTTTGTGTTTTTA 44909	A_
	TAAAAACAACAAA ACC	
	ATTTTGTGTTT TGG	
	CC	
GAM1976 LOC221738	3' AGTTGTTATTGTGTTTTTG 45027	AAACC
	TAAAAACAACAA ACAACT	

		GTTTTTGTGTT TGTTGA	
		AT__	
GAM1976	LOC51068	3' TTGTTCTTTTGTGTTTTG 18060	ACC
		TAAAAACAACAAAA ACAA	
		GTTTTTGTGTTTT TGTT	
		CT_	
GAM1976	LOC93380	3' TTGGGTTTTTATTGTTGTTT 35729	__ A
		AAACAACAA AAACC CAA	
		TTTGTTGTT TTTGG GTT	
		ATT _	
GAM1977	ARCN1	3' AAATATAGTTATATTTTCATACT 7363	TTTA_
	T	AGGTATGAAAT TATATTT	
		TTCATACTTTA ATATAAA	
		TATTG	
GAM1977	FLJ12888	3' ATGAAATTTTCATAGCTTA 24494	G
		TAAG TATGAAATTTTAT	
		ATTC ATACTTTAAAGTA	
		G	
GAM1978	BLTR2	5' TCCAGTTTTGCCAGATGTGCT 21245	C_ CTAA_
	A	TAGCACATC GGC GGA	
		ATCGTGTAG CCG CCT	
		AC TTTTGA	
GAM1978	CERD4	3' TGTCTCTGTTGGGATGTGC 14354	GG TTA
		GCACATCC CC AGGACA	
		CGTGTAGG GG TCCTGT	
		_ TC_	
GAM1978	CYP1B1	3' TGTCAACCAGGTCCAGATGTGC 5567	C _ TAAG
	TA	TAGCACATC GG CCT GACA	
		ATCGTGTAG CC GGA CTGT	
		A T CCAA	
GAM1978	GJA1	3' GTCCTTAAGTCCCTGCTA 5678	CATCC C
		TAGCA GG CTTAAGGAC	
		ATCGT CC GAATTCCTG	
		C__ T	
GAM1978	HTR2C	3' TCCTCAAGTTGTGTGCTA 6536	TC C A
		TAGACA CGGC TT AGGA	
		ATCGTGT GTTG AA TCCT	
		_ _ C	
GAM1978	PAFAH1B3	5' GTCCTCCGCGGGTGTGCTA 8433	G CTTA
		TAGCACATCCG C AGGAC	

		ATCGTGTGGGC G TCCTG	
		_ CC _	
GAM1978	PDGFRA	3' TGCCTTAAATGTGGTCTGC 12887	C _ GCC
		GCA ATC CG TTAAGGACA	
		CGT TGG GT AATTCCTGT	
		C T AA _	
GAM1978	PPP1CB	3' GCCTTCTATATGTGCTA 8561	CC CCTT A
		TAGCACAT GG AAGG C	
		ATCGTGTA TC TTCC G	
		TA _ _ C	
GAM1978	TRIP15	3' GTCCTTAAGGCAACAGTGC 10431	ATCCG
		GCAC GCCTTAAGGAC	
		CGTG CGGAATTCCTG	
		ACAA _	
GAM1978	HSPC065	3' TGTCCCCAAGGCTGGAGTGC 15457	A AA
		GCAC TCCGGCCTT GGACA	
		CGTG AGGTCGGAA CCTGT	
		_ CC	
GAM1978	KIAA0153	3' TGTCCCCAAACCTGTGCT 17500	TCC CC AA
		AGCACAT GG TT GGACA	
		TCGTGT CC AA CCTGT	
		_ AA CC	
GAM1978	MGC10870	5' GTCCTGTCGCGGGTGTGC 26082	G CTTA
		GCACATCCG C AGGAC	
		CGTGTGGGC G TCCTG	
		_ CTG _	
GAM1978	LOC144231	5' TGCCCTGGGCCATATGTGCTA 40396	CC TA A
		TAGCACAT GGCCT AGG CA	
		ATCGTGTA CCGGG TCC GT	
		TA _ _ C	
GAM1978	LOC163231	5' TGTCCTGGACAGATGTGTTA 40103	CGG TTA
		TAGCACATC CC AGGACA	
		ATTGTGTAG GG TCCTGT	
		ACA _	
GAM1978	LOC205313	5' TGTCCTCAAGTTGTTCTGCTA 43595	CATC C A
		TAGCA CGGC TT AGGACA	
		ATCGT GTTG AA TCCTGT	
		CCTT _ C	
GAM1978	LOC58525	3' CCTTGGGGGCCGGGCACACTA 38456	CACA _
		TAG TCCGGCCTT AAGG	

ATC GGGCCGGGG TTCC
 ACAC G
 GAM1978 LOC91650 5' TGTCCTTAAGTTGGGAGC 33201 ACA C
 GC TCCGGC TTAAGGACA
 || ||||| |||||
 CG GGGTTG AATTCCTGT
 A__ _
 GAM1979 PPP2R5E 3' CATCCTCCTCTGGATAACT 12921 C A
 AGTT TCCAGAGGA GATG
 ||| ||||| |||
 TCAA AGGTCTCCT CTAC
 T C
 GAM1979 PYCR1 3' CTCCTCTAGAGCTCG 34730 T CC
 A AGTTCT AGAGGAAG
 | |||| |
 G TCGAGA TCTCCTTC
 C _
 GAM1979 TTC3 3' CTCCTCTGCCTTTGTTCA 9314 TTCTC
 TGAATAG CAGAGGAAG
 ||||| |||||
 ACTTGTT GTCTCCTTC
 TCC__
 GAM1979 CASPR3 3' TCCTCAAGAAACTATTTA 24316 C CA
 TGAATAGTT TC GAGGA
 ||||| || |||
 ATTTATCAA AG CTCCT
 A AA
 GAM1979 CHL1 3' TTCCTAGAGAACTGTCCA 13397 A CAG
 TG ATAGTTCTC AGGAA
 || ||||| |||
 AC TGTCAAGAG TCCTT
 C A__
 GAM1979 FLJ20060 3' ATCTTAGAGAACTATACA 19149 A CAGAGG
 TG ATAGTTCTC AAGAT
 || ||||| |||
 AC TATCAAGAG TTCTA
 A A____
 GAM1979 FLJ22569 5' TCCTGATGGAAGTATTCA 23402 TC G_
 TGAATAGT TCCA AGGA
 ||||| ||| |||
 ACTTATCA AGGT TCCT
 _ AG
 GAM1979 KIAA0367 3' TCTATGGAAACTACTCA 33426 A C GA
 TGA TAGTT TCCA GGA
 ||| |||| ||| |||
 ACT ATCAA AGGT TCT
 C A A_
 GAM1979 MGC10200 3' TCCTCCTGCCTCAGCTACTCA 29695 A CTC_ _
 TGA TAGTT CAG AGGA
 ||| |||| ||| |||

ACT ATCGA GTC TCCT
 C CTCC C
 GAM1979 TINF2 3' TCTCTGGAAACTATCA 14835 A C
 TGA TAGTT TCCAGAGG
 ||| |||| |||||
 ACT ATCAA AGGTCTCT
 _ A
 GAM1979 LOC162333 5' ATTTTCCAGAGAACTTTCA 42125 T CAGA
 TGAA AGTTCTC GGAAGAT
 |||| ||||| |||||
 ACTT TCAAGAG CCTTTTA
 _ A__
 GAM1980 LPIN1 3' CTAAACTTCCACATCACTGC 33466 TCA A_
 GCA ATG GAAGTTTAAG
 ||| ||| |||||
 CGT TAC CTTCAAATTC
 CAC AC
 GAM1980 PSEN1 3' ATTTCTCATCAATTCTCTA 5455 C CA
 TAGAG AT ATGAGAAGT
 ||||| || |||||
 ATCTC TA TACTCTTTA
 T AC
 GAM1980 PSEN1 3' ATTTCTCATCAATTCTCTA 14233 C CA
 TAGAG AT ATGAGAAGT
 ||||| || |||||
 ATCTC TA TACTCTTTA
 T AC
 GAM1980 FLJ20666 5' GCTGTCATTGATGCTCTA 19582 GA
 TAGAGCATCAATGA AGT
 ||||| ||||| |||
 ATCTCGTAGTTACT TCG
 G_
 GAM1980 KIAA1203 3' AAACCTCTCATTTTTGTTT 35465 TC A
 GAGCA AATGAGA GTTT
 ||||| ||||| |||||
 TTTGT TTA CTCT CAAA
 TT C
 GAM1980 PIPPIN 3' AAGCCCCACTGATGCTCTG 38908 A AGAA
 TAGAGCATCA TG GTTT
 ||||| || |||||
 GTCTCGTAGT AC CGAA
 C CC__
 GAM1980 PRO0529 5' TTTCTCATTGCTGCTCTA 15302 T
 TAGAGCA CAATGAGAAG
 ||||| |||||
 ATCTCGT GTTACTCTTT
 C
 GAM1981 HLCS 5' ACAGAGATCATCCTCTT 5987 TCAT
 AAGAG ATGATCTCTGT
 ||||| |||||

		TTCTC TACTAGAGACA		
		C__		
GAM1981	LIG4	5' AGATGTCACAGACTCTTT 8107	ATA	C
		AAAGAGTC TGAT TCT		
		TTTCTCAG ACTG AGA		
		AC_ T		
GAM1981	MAPRE2	3' ACAGAAAAATCTATGACTC 15543	T	C__
		GAGTCATA GAT TCTGT		
		CTCAGTAT CTA AGACA		
		_ AAA		
GAM1981	PLA2G10	5' ACAGAGATCAGGACGCCTTTG 9617	A_	ATA
		CAAAG GTC TGATCTCTGT		
		GTTTC CAG ACTAGAGACA		
		CG G__		
GAM1981	PLAG1	3' ACAAAGATCATATTTTTTTGTG 8514	GTC	C
		TACAAAGA ATATGATCT TGT		
		GTGTTTTT TATACTAGA ACA		
		____ A		
GAM1981	STAU	3' ACAAAGATCATATCCATGTGTA 10939	AAGAGTC	C
		TACA ATATGATCT TGT		
		ATGT TATACTAGA ACA		
		GTACC__ A		
GAM1981	STAU	3' ACAAAGATCATATCCATGTGTA 18924	AAGAGTC	C
		TACA ATATGATCT TGT		
		ATGT TATACTAGA ACA		
		GTACC__ A		
GAM1981	STAU	3' ACAAAGATCATATCCATGTGTA 18912	AAGAGTC	C
		TACA ATATGATCT TGT		
		ATGT TATACTAGA ACA		
		GTACC__ A		
GAM1981	STAU	3' ACAAAGATCATATCCATGTGTA 18918	AAGAGTC	C
		TACA ATATGATCT TGT		
		ATGT TATACTAGA ACA		
		GTACC__ A		
GAM1981	FLJ11259	3' CAGAGATACACCTTTGTA 20383	A	CATATG
		TACAAAG GT ATCTCTG		
		ATGTTTC CA TAGAGAC		
		_ CA__		
GAM1981	FLJ13910	3' CAGAGACAAACTCTTTG 23053	CATA	A
		CAAAGAGT TG TCTCTG		

GTTTCTCA AC AGAGAC
 A__ _
 GAM1981 FLJ20086 3' ACAGAATATTTGAATCTTTGTA 19189 G T ATC
 TACAAAGA TCA ATG TCTGT
 ||||| ||| ||| ||||
 ATGTTTCT AGT TAT AGACA
 A T A__
 GAM1981 KIAA0931 3' ACAGAAAACCTATACTCTTTG 33480 C TGATC
 CAAAGAGT ATA TCTGT
 ||||| ||| ||||
 GTTTCTCA TAT AGACA
 _ CCAA
 GAM1981 KIAA0953 3' CAGAGATCGCCCTTTG 33166 A CATAT
 CAAAG GT GATCTCTG
 |||| || |||||
 GTTTC CG CTAGAGAC
 C ____
 GAM1981 KIAA1323 5' CAGAGATCACTGCCCTGTG 31560 A A CATA
 CA AG GT TGATCTCTG
 || ||| |||||
 GT TC CG ACTAGAGAC
 G C TC__
 GAM1981 RAI17 3' ACAGAAACCATCATCGTCTTTG 43855 GTCAT C__
 TA TACAAAGA ATGAT TCTGT
 ||||| ||| ||||
 ATGTTTCT TACTA AGACA
 GC__ CCAA
 GAM1981 SEC24B 3' GGAACACAAAACCTCTTTGTA 13015 CATA A
 TACAAAGAGT TG TCT
 ||||| |||
 ATGTTTCTCA AC AGG
 AAAC A
 GAM1981 SIAT4A 5' ACAGAGATTAATGACCCCTT 8977 A_ A
 AAG GTCAT TGATCTCTGT
 || |||| |||||
 TTC CAGTA ATTAGAGACA
 CC _
 GAM1982 KIAA0553 3' CCATGACACTGACAAGAGGAAT 34636 AACCTA
 TA TAATT TCAGTGT CATGG
 |||| |||||
 ATTAAG AGTCACAGTACC
 GAGAAC
 GAM1982 MST4 3' ACACAAAGGTAAATTA 18607 ATCA
 TAATTTAACCT GTGT
 ||||| |||
 ATTAAATTGGA CACA
 AA__
 GAM1983 AVPR2 5' TCAATCTTCCCTGCCCA 5511 A TACTA
 TG GGTA GAAGATTGA
 || ||| |||||

		AC CCGT CTTCTAACT	
		— CC__	
GAM1983	HMGA2	3' AGTCCCAGTATACCTCA 9563	AGAA
		TGAGGTATACT GATT	
		ACTCCATATGA CTGA	
		CC__	
GAM1983	MTMR2	3' TAGTCTCTGCATACCTCA 18244	AC A
		TGAGGTAT TAGA GATTG	
		ACTCCATA GTCT CTGAT	
		C_ _	
GAM1983	VCAM1	3' CTTTCAGGTAATAACCTCA 27984	AC AAGA
		TGAGGTAT TAG TTGAAAG	
		ACTCCATA ATC GACTTTC	
		A_ ATG_	
GAM1983	VCAM1	3' CTTTCAGGTAATAACCTCA 6738	AC AAGA
		TGAGGTAT TAG TTGAAAG	
		ACTCCATA ATC GACTTTC	
		A_ ATG_	
GAM1983	ACVR2	3' TCAACAAGGTATACCTCA 7321	AGAAGA
		TGAGGTATACT TTGA	
		ACTCCATATGG AACT	
		AAC__	
GAM1983	SPEC1	3' GTTGCTCTAAAATACCTCA 21514	AC A_
		TGAGGTAT TAGA GAT	
		ACTCCATA ATCT TTG	
		AA CG	
GAM1983	LOC89932	5' CTTCTGCCCTGTATACCTCA 30492	_____
		TGAGGTATAC TAGAAG	
		ACTCCATATG GTCTTC	
		TCCC	
GAM1984	SCG3	3' TGTTTCAGAAAACATAAT 14904	C AG
		ATTATGTTT CT AACA	
		TAATACAAA GA TTGT	
		A CT	
GAM1984	FLJ20086	3' GTTCAGAAAACATAATC 19192	C A
		GATTATGTTT CT GAAC	
		CTAATACAAA GA CTTG	
		A _	
GAM1984	JAM1	3' CAGCTGTTCTAGAGCGGGAATT 29321	A_ TC A
	A	TGATT TGTT CTAGAACA CTG	

			ATTAAGCGAGATCTTGTGAC			
			GG _ C			
GAM1984	JAM1	3'	CAGCTGTTCTAGAGCGGGAATT 29328	A_	TC	A
	A		TGATT TGTT CTAGAACA CTG			
			ATTAAGCGAGATCTTGTGAC			
			GG _ C			
GAM1984	JAM1	3'	CAGCTGTTCTAGAGCGGGAATT 18861	A_	TC	A
	A		TGATT TGTT CTAGAACA CTG			
			ATTAAGCGAGATCTTGTGAC			
			GG _ C			
GAM1984	JAM1	3'	CAGCTGTTCTAGAGCGGGAATT 29337	A_	TC	A
	A		TGATT TGTT CTAGAACA CTG			
			ATTAAGCGAGATCTTGTGAC			
			GG _ C			
GAM1984	JAM1	3'	CAGCTGTTCTAGAGCGGGAATT 29348	A_	TC	A
	A		TGATT TGTT CTAGAACA CTG			
			ATTAAGCGAGATCTTGTGAC			
			GG _ C			
GAM1984	SETBP1	3'	GTTGTGAAACATACTCA 17826	T	CTAGA	
			TGA TATGTTTC ACAAC			
			ACT ATACAAAG TGTTG			
			C _ _ _ _			
GAM1984	YAP1	3'	CAGCTGTTCTAGAGTTTCAGTC 12750	ATGT	C	A
	A		TGATT TTC TAGAACA CTG			
			ACTGA GAG ATCTTGT GAC			
			CTTT _ C			
GAM1985	CDKN2A	3'	AGTCATGATGATGGGCAGCG 27757	A	A C	
			CG TGCCCATCA TA TGA CT			
			GC ACGGGTAGT GT ACTGA			
			G A _			
GAM1985	CKTSF1B1	3'	AGTCAGTAGGGACATTG 15023	_	ATCAA	
			CGATG CCC TACTGACT			
			GTTAC GGG ATGACTGA			
			A _ _ _ _			
GAM1985	HKE4	3'	GGAGTCGGGGATAAACATC 13841	CCC	AATA	
			GATG ATC CTGACTCC			
			CTAC TAG GGCTGAGG			
			AAA G _ _ _			
GAM1985	LFG	3'	GGAGTCAGGATGGGACA 37695	_	AATA	
			TG CCCATC CTGACTCC			

AC GGGTAG GACTGAGG
 A ____
 GAM1985 PKD1 3' GAGTCGGAGTGGACACCG 5840 A C CAATA
 CG TG CCAT CTGACTC
 || || ||| |||||
 GC AC GGTG GGCTGAG
 C A A____
 GAM1985 RAB27A 3' AGATTAATGGGCATTGT 10927 C A
 ACGATGCCCAT AAT CT
 ||||| ||| ||
 TGTTACGGGTA TTA GA
 A _
 GAM1985 RB1CC1 3' TCATATTGATGAAATCGT 16633 GCC C
 ACGAT CATCAATA TGA
 |||| ||||| |||
 TGCTA GTAGTTAT ACT
 AA_ _
 GAM1985 AP3M2 3' GAGTGTAGCGGGCATCG 13676 ATCAA TG
 CGATGCCC TAC ACTC
 ||||| ||| |||
 GCTACGGG ATG TGAG
 CG_ _
 GAM1985 C17orf26 3' GGAGTCAGGTATGCAGGCATTG 29186 CAT ATA
 CGATGCC CA CTGACTCC
 ||||| || |||||
 GTTACGG GT GACTGAGG
 AC_ ATG
 GAM1985 FLJ20584 3' GGAACCAGCACAAAGTGTGTC 19563 _ CAATA_ AC
 ATCG CGATGCC CAT CTG TCC
 ||||| || ||| |||
 GCTACGG GTG GAC AGG
 TT AAACAC CA
 GAM1985 TRIAD3 3' GAGTCAGCTGAGCATC 45348 CCA ATA
 GATGC TCA CTGACTC
 |||| ||| |||||
 CTACG AGT GACTGAG
 _ C_
 GAM1985 LOC126267 5' GAATCAGTGTGGGACTC 37271 TG TCA C
 GA CCCA ATACTGA TC
 || ||| ||||| ||
 CT GGGT TGTGACT AG
 CA _ A
 GAM1985 LOC147229 5' GGAGGGGACTGCATGGGCATC 38320 _ ATA GA
 GATGCCCAT CA CT CTCC
 ||||| || || |||
 CTACGGGTA GT GG GAGG
 C CA_ G_
 GAM1985 LOC163081 5' TCAGTATTGATTCTGCATC 40087 CC_
 GATGC ATCAATACTGA
 |||| |||||

		CTACG TAGTTATGACT		
		TCT		
GAM1985	LOC166424 5'	GAGTCAGTTTTGAGCTTC	42194	T CCA T
		GA GC TCAA ACTGACTC		
		CT CG AGTT TGA CTGAG		
		T ____ T		
GAM1985	LOC255242 5'	GAGTTGCGACGGGCGTCG	45905	A AATAC
		CGATGCCC TC TGACTC		
		GCTGCGGG AG GTTGAG		
		C C ____		
GAM1986	XRCC3 3'	ACACTGTGGCCAGGCCTTA	11905	ACA TATGA
		TAAG CTGGCCAT TGT		
		ATTC GACCGGTG ACA		
		CG_ TC_		
GAM1986	HEMK 3'	CAAAATGGCAGTGTCTTA	18264	G A
		TAAGACACTG CCATT TG		
		ATTCTGTGAC GGTA AC		
		_ A		
GAM1986	LGALS8 3'	CACTGTCATAACCA GTGCTCT	13243	_ CCA _
		AGA CACTGG TTATGAT GTG		
		TCT GTGACC AATACTG CAC		
		C ____ T		
GAM1986	PPP1R3B 3'	CAGATTACACAACCA GTGTCT	23857	CCATTA G
		AGACACTGG TGAT TG		
		TCTGTGACC ATTA AC		
		AACAC_ G		
GAM1986	SCAND2 3'	CACACCAGGCACCA GTGTCTT	27355	CCATTA A
		AAGACACTGG TG TGTG		
		TTCTGTGACC AC ACAC		
		ACGG_ C		
GAM1986	LOC113763 3'	CACATGCTCATGGCCAGAATCT	28800	CA TATG
	TA	TAAGA CTGGCCAT ATGTG		
		ATTCT GACCGGTA TACAC		
		AA CTCG		
GAM1986	LOC137964 3'	CACATCACGTTCA GTGTTT	37110	CCATTA
		AGACACTGG TGATGTG		
		TTTGTGACT ACTACAC		
		TGC_		
GAM1986	LOC150577 3'	CACAATGGCAAGTGTCTTA	41216	G A
		TAAGACACT GCCATT TG		

	ATTCTGTGA CGGTAA AC	
	A C	
GAM1986 LOC199863 3'	CACACCACCCTGTCCAGTGTCT 43254	C TTA A
TG	TAAGACACTGG CA TG TGTG	
	GTTCTGTGACC GT AC ACAC	
	T CCC C	
GAM1986 LOC253897 3'	CACATCACGTTCAAGTGTTC 45967	CCATTA
	AGACACTGG TGATGTG	
	TTTGTGACT ACTACAC	
	TGC__	
GAM1987 KIAA1467 3'	CTCAGTGACCCATCTCTGA 35455	AGATAAT _
	TCAGAGAT TCA TGAG	
	AGTCTCTA AGT ACTC	
	CCC__ G	
GAM1987 MGC11061 3'	CTCACAAAATATATTTCTGATA 26116	GATAATTCA
	TATCAGAGATA TGAG	
	ATAGTCTTTAT ACTC	
	ATAAAAC__	
GAM1987 SNAP91 3'	CATAAATTATCTTTTCTTCTG 16869	_ T_ C
	CAGA GA AGATAATT ATG	
	GTCT CT TCTATTAA TAC	
	T TT A	
GAM1987 LOC120406 3'	TCATGATCCATCTCTGG 37220	A TAAT
	TCAGAGAT GA TCATGA	
	GGTCTCTA CT AGTACT	
	C ____	
GAM1987 LOC93349 3'	CTCAGGGACACCTCCTCTGATA 28769	AT ATAA A
	TATCAGAG AG TTC TGAG	
	ATAGTCTC TC AGG ACTC	
	C_ CAC_ G	
GAM1988 APC 3'	CCCATCCCAACTTCCTTTAATT 5481	TT A CA
	GATTG GGAAGTTG GA GG	
	TTAAT CCTTCAAC CT CC	
	TT C AC	
GAM1988 PKIB 5'	CCTGTCTCAGAAATAACAA 26229	GAAG
	TTGTTG TTGAGACAGG	
	AACAAT GACTCTGTCC	
	AAA_	
GAM1988 SCNN1G 3'	CCTGTCTCTCACCAACAA 6704	AAGTT
	TTGTTGG GAGACAGG	

		AACAACC CTCTGTCC	
		ACT__	
GAM1988 TCF1	3'	CCTGCCCCAACTCCTTCCAGC 6147	___ AGA
		GTTGGA AGTTG CAGG	
		CGACCT TCAAC GTCC	
		TCC CCC	
GAM1988 BLOV1	3'	CCTGTCTCAACTAATAATA 37520	GA
		TGTTG AGTTGAGACAGG	
		ATAAT TCAACTCTGTCC	
		AA	
GAM1988 FLJ00058	5'	CCTGCCTCCACCCTTTCCAACA 38508	___ T A
A		TTGTTGGAA GT GAG CAGG	
		AACAACCTT CA CTC GTCC	
		TCC C C	
GAM1988 FLJ10276	3'	CTCAACTCCCCTGTAGTTTA 19790	TT A_
		TAGATTG GG AGTTGAG	
		ATTTGAT CC TCAACTC	
		GT CC	
GAM1988 FLJ10803	3'	CCTGTCTCAAAAAACAAATC 20153	_ GGAAG
		GATT GTT TTGAGACAGG	
		CTAA CAA AACTCTGTCC	
		A AA__	
GAM1988 FLJ11142	3'	CTCATCACCTCCAACAATCT 20343	A _
		AGATTGTTGGA GT TGAG	
		TCTAACAACCT CA ACTC	
		C CT	
GAM1988 KIAA0997	3'	CCTGACAAACTTCCATCAA 17280	T GAGA
		TTG TGGAAGTT CAGG	
		AAC ACCTTCAA GTCC	
		T ACA_	
GAM1988 KIAA1069	3'	CCTGTGTGCCCCAGCAATCTA 33723	AA TGAG
		TAGATTGTTGG GT ACAGG	
		ATCTAACGACC CG TGTCC	
		C_ TG__	
GAM1988 NUDEL	3'	CCTGCCCTCCTCCAACAA 25122	AGTT A_
		TTGTTGGA GAG CAGG	
		AACAACCT CTC GTCC	
		C__ CC	
GAM1988 LOC151178	5'	CCTGTCTCTGGACAACAATC 39071	GAAGTT
		GATTGTTG GAGACAGG	

CTAACAAC CTCTGTCC
 AGGT__
 GAM1988 LOC199786 3' CCTGTCTCAAAAAACAAAATC 42618 G GAAG
 GATT TTG TTGAGACAGG
 ||| ||| |||||
 CTAA AAC AACTCTGTCC
 _ AAAA
 GAM1988 LOC255975 5' CTGCCTCACAACAACCT 45890 A GAAGT A
 AG TTGTTG TGAG CAG
 || ||||| ||| |||
 TC AACAAC ACTC GTC
 C _ C
 GAM1989 DPH2L1 3' ATCCATCCTGCAAAGGC 7053 CTAATC
 GCCTTTGCAG TGGAT
 ||||| |||
 CGGAAACGTC ACCTA
 CT__
 GAM1989 RNMT 3' CCAGTGCAAAGGCTA 9882 GCTAAT
 TAGCCTTTGCA CTGG
 ||||| |||
 ATCGGAAACGT GACC

 GAM1989 TCF19 3' CCTATCAGTTGCAAAAGC 46658 C A CT
 GC TTTGCAGCT AT GG
 || ||||| || ||
 CG AAACGTTGA TA CC
 A C T_
 GAM1989 TCF19 3' CCTATCAGTTGCAAAAGC 46707 C A CT
 GC TTTGCAGCT AT GG
 || ||||| || ||
 CG AAACGTTGA TA CC
 A C T_
 GAM1989 ACAA2 5' CCAGGAGGACGCAGAGGCTA 44093 AG AA
 TAGCCTTTGC CT TCTGG
 ||||| || |||
 ATCGGAGACG GG GGACC
 CA A_
 GAM1989 FLJ20374 5' CCAGACTCGCCAGGAAAGGCTA 19429 GCA_ TAA
 TAGCCTTT GC TCTGG
 ||||| || |||
 ATCGGAAA CG AGACC
 GGAC CTC
 GAM1989 FLJ25415 3' CCAGAGCCTGCAGAAGGCTA 29533 _ CTAA
 TAGCCT TTGCAG TCTGG
 ||||| ||||| |||
 ATCGGA GACGTC AGACC
 A CG_
 GAM1989 KIAA0798 5' GATCCAGAGGAGACAAAG 16068 CAG AA
 CTTTG CT TCTGGATC
 |||| || |||||

GAAAC GA AGACCTAG
 A__ GG
 GAM1989 KIAA1281 3' AGTGTTAGCCACAAAAGGCTA 42961 GCA_ _
 TAGCCTTT GCTAAT CT
 ||||| ||||| ||
 ATCGGAAA CGATTG GA
 ACAC T
 GAM1989 MACMARCKS 3' GATCTCTAAGCTGCAAAAAGT 23273 CC AATCT
 TAG TTTGCAGCT GGATC
 || ||||| |||||
 GTC AAACGTCGA TCTAG
 AA ATC__
 GAM1989 MGC10812 3' GATCCAGACCAGCGTCTGGC 25412 TTT A AA
 GCC GC GCT TCTGGATC
 || || || |||||
 CGG TG CGA AGACCTAG
 TC_ _ CC
 GAM1989 MGC2628 3' GATGCAGCCCTAACTGCAAAAG 23509 C C AT_ G
 T GC TTTGCAG TA CTG ATC
 || ||||| || || |||||
 TG AAACGTC AT GAC TAG
 A A CCC G
 GAM1989 SYPL 3' GATTTTTTTTTTAATTGCAAAGA 44645 C C TCT_
 CTA TAG CTTTGCAG TAA GGATC
 || ||||| || |||||
 ATC GAAACGTT ATT TTTAG
 A A TTTT
 GAM1989 LOC143310 5' ATCCATCATCTTCAAAGGCTA 37605 C CTAATC
 TAGCCTTTG AG TGGAT
 ||||| || |||||
 ATCGGAAAC TC ACCTA
 T TACT__
 GAM1989 LOC169577 5' ATCCAGAAGAGCAAAGGC 40283 AG AA
 GCCTTTGC CT TCTGGAT
 ||||| || |||||
 CGGAAACG GA AGACCTA
 A_ __
 GAM1989 LOC219920 5' ATCCAGAAGAGCAGAAGGCTA 44803 GCA AA
 TAGCCTTT GCT TCTGGAT
 ||||| || |||||
 ATCGGAAG CGA AGACCTA
 A_ GA
 GAM1990 TNFRSF6 3' AATGTCTATCCACAGGCTA 5484 _ T
 TAGCCTGT ATAG CATT
 ||||| |||||
 ATCGGACA TATC GTAA
 CC T
 GAM1990 PREI3 3' GCTTACAGATTATACCTCA 32965 A GC T
 TGAG TATA CTGTA AGT
 ||||| ||||| |||||

		ACTC ATAT GACAT TCG	
		C TA _	
GAM1990	USP25	3' AATGACTATACAGACTTTAGTC 15046	AT_ C
		GAT AG CTGTATAGTCATT	
		CTG TC GACATATCAGTAA	
		ATT A	
GAM1990	LOC146092	5' GCTGAGGGCATATCTCA 40652	A GTA
		TGAGATAT GCCT TAGT	
		ACTCTATA CGGG GTCG	
		_ A _	
GAM1990	LOC92181	3' ACTATGTAATGGCTATATTTCA 33941	TG__
		TGAGATATAGCC TATAGT	
		ACTTTATATCGG GTATCA	
		TAAT	
GAM1991	METTL1	3' AGGGTGGAGTATGTATCA 23306	TG AATC
		TGATG T ACTCCACCCT	
		ACTAT A TGAGGTGGGA	
		GT ____	
GAM1991	METTL1	3' AGGGTGGAGTATGTATCA 23311	TG AATC
		TGATG T ACTCCACCCT	
		ACTAT A TGAGGTGGGA	
		GT ____	
GAM1991	SLC21A3	5' AGGGTAGAAGTAAGACATATCA 22076	AATC _ C
		TGATGTGT ACT C ACCCT	
		ACTATACA TGA G TGGGA	
		GAA_ A A	
GAM1991	SLC21A3	5' AGGGTAGAAGTAAGACATATCA 28673	AATC _ C
		TGATGTGT ACT C ACCCT	
		ACTATACA TGA G TGGGA	
		GAA_ A A	
GAM1991	SUFU	3' AGAGGGTGAGGTTGAGCACATC 18250	AATC TC
	A	TGATGTGT AC CACCCTCT	
		ACTACACG TG GTGGGAGA	
		ACT_ GA	
GAM1991	ABCC13	3' AGGGTGGAGTAATTTGTCCA 28970	TG TC_
		TG TAA ACTCCACCCT	
		AC GTT TGAGGTGGGA	
		CT TAA	
GAM1991	C5orf4	3' GAGGATGGAGTGAGAGACA 26181	AA_ C
		TGT TCACTCCA CCTC	

	ACA AGTGAGGT GGAG	
	GAG A	
GAM1991 DJ12208.2 3'	AGAGCAAAGGAAAAACACATCA 21702	AATCAC ACC_
	TGATGTGT TCC CTCT	
	ACTACACA AGG GAGA	
	AAA__ AAAC	
GAM1991 DKFZp547I224 5'	GGTGGATATACATCA 21479	ATCAC
	TGATGTGTA TCCACC	
	ACTACATAT AGGTGG	

GAM1991 FLJ10759 3'	AGAGGGTGGAGTCCACATC 20100	TAATC
	GATGTG ACTCCACCCTCT	
	CTACAC TGAGGTGGGAGA	
	C_____	
GAM1991 FLJ21432 3'	AGGATGGAGTGCATCA 23764	TGTAAT C
	TGATG CACTCCA CCT	
	ACTAC GTGAGGT GGA	
	_____ A	
GAM1991 KIAA1034 3'	GTGAAGTGAACAATCA 31311	G AA C
	TGAT TGT TCACT CAC	
	ACTA ACA AGTGA GTG	
	_ AA A	
GAM1991 MGC3020 5'	AGAGGGTGAGAGCCACCATCA 23481	T AATCA _
	TGATG GT CTC CACCCTCT	
	ACTAC CA GAG GTGGGAGA	
	_ CC__ A	
GAM1991 PRO2435 5'	AGAGCTCAAATGATTACACATC 20599	CTCCACC
	GATGTGTAATCA CTCT	
	CTACACATTAGT GAGA	
	AAACTC_	
GAM1991 LOC143310 5'	AGGGTGGAAGAACCATCA 37604	T AA AC
	TGATG GT TC TCCACCCT	
	ACTAC CA AG AGGTGGGA	
	_ _ A_	
GAM1991 LOC143465 5'	AGGATAGAGTGTGTGCATCA 40360	TG AT CAC
	TGATG TA CACTC CCT	
	ACTAC GT GTGAG GGA	
	GT _ ATA	
GAM1991 LOC154877 3'	AGGATGGCCTGGACCACACACA 41738	A AA ACT_ C
	TG TGTGT TC CCA CCT	

		AC ACACA AG GGT GGA	
		_ CC GTCC A	
GAM1991	LOC196527 3'	AGAAGGTGCAGTATTACACATC 42398	C C C
	A	TGATGTGTAAT ACT CACC TCT	
		ACTACACATTA TGA GTGG AGA	
		_ C A	
GAM1991	LOC221738 5'	AGAGGGTGGAGTGAGGATGCA 45026	AA
		TGTGT TCACTCCACCCTCT	
		ACGTA AGTGAGGTGGGAGA	
		GG	
GAM1992	TCEA1 3'	AAATAATTTTGTCCCAAGTCTT 39201	C ATT
	A	TAAGATT GG TAGGATTATTT	
		ATTCTGA CC GTTTAATAAAA	
		A CT_	
GAM1992	LOC203084 3'	AAATAATTTTGTCCCAAGTCTT 42279	C ATT
	A	TAAGATT GG TAGGATTATTT	
		ATTCTGA CC GTTTAATAAAA	
		A CT_	
GAM1993	ZNF333 3'	AACTCTGTCTCAAAAATAATA 26202	TGT A
		TGTTATTTTGA GATA AGTT	
		ATAATAAAACT CTGT TCAA	
		_ C	
GAM1994	HSPA5 3'	CTAGTAGAACTGGATCCCA 11821	AT_
		TGGGA GTTCTACTAG	
		ACCCT CAAGATGATC	
		AGGT	
GAM1994	CSEN 3'	GGAACATTCCCACATAATA 15092	GA
		TATTA TGGGAATGTTCT	
		ATAAT ACCCTTACAAGG	
		AC	
GAM1994	KIAA1509 3'	AGTAGAACACTCATTTG 30872	AA
		TAGATGGG TGTTCTACT	
		GTTTACTC ACAAGATGA	
		_	
GAM1994	LOC148760 3'	GTATTAACATTCTCCATCTAAT 40897	_ C_
	A	TATTAGATGG GAATGTT TAC	
		ATAATCTACC CTTACAA ATG	
		T TT	
GAM1994	LOC168667 3'	CTAGAGGAGTCCCATC 44566	ATG A
		GATGGGA TTCT CTAG	

			CTACCCT GAGG GATC		
			___ A		
GAM1994	LOC253842	3'	CTAGCCCAGTTCCCATCTAG 46503		GTTCTA
			TTAGATGGGAAT CTAG		
			GATCTACCCTTG GATC		
			ACCC__		
GAM1995	ANK1	3'	AGAGCAGGCAGAGATGA 30279 C		AGTAC
			TCA CTCTGTCT CTCT		
			AGT GAGACGGA GAGA		
			A C__		
GAM1995	APM1	3'	GAGAGGGATGAAGAGGTGA 11211		G TAGTA
			TCACCTCT TC CCTCTC		
			AGTGGAGA AG GGAGAG		
			_ TAG__		
GAM1995	COL1A2	3'	AGGTGCTGACCTAGACAGAGAT 5541 C		_____
	GA		TCA CTCTGTCT AGTACCT		
			AGT GAGACAGA TCGTGGA		
			A TCCAG		
GAM1995	F7	3'	GAGAGAGACAGAGACAGAG 5607		A_ AC
			CTCTGTCT GT CTCTC		
			GAGACAGA CA GAGAG		
			GA GA		
GAM1995	F7	3'	GAGAGAGACAGAGACAGAG 21236		A_ AC
			CTCTGTCT GT CTCTC		
			GAGACAGA CA GAGAG		
			GA GA		
GAM1995	ICA1	3'	AGGTGCTGACAAAGATGA 22736 C C T		
			TCA CT TGTC AGTACCT		
			AGT GA ACAG TCGTGGA		
			A A _		
GAM1995	KCNJ8	5'	GGAGAGGCAGGTGAGAGGGA 11429 A		GT AGTA
			TC CCTCT CT CCTCTCC		
			AG GGAGA GG GGAGAGG		
			_ GT AC__		
GAM1995	NT5C2	3'	AGAGTGGGAAGAGGTGA 14525		GT GTAC
			TCACCTCT CTA CTCT		
			AGTGGAGA GGT GAGA		
			AG _____		
GAM1995	PAK4	3'	TGGAGAGAACACTAAGAGGTGA 12507		GTC AC_
			TCACCTCT TAGT CTCTCCA		

			AGTGGAGA ATCA GAGAGGT		
			___ CAA		
GAM1995 PUM2	3'	AGTAGGAACCATAGAGATGA 17633	C A A _		
		TCA CTCTGTCT GT CCT CT			
		AGT GAGATAGA CA GGA GA			
		A C A T			
GAM1995 RLB1	5'	TGGAGAGGCCAGGACAGAG 5869	AGTA		
		CTCTGTCT CCTCTCCA			
		GAGACAGG GGAGAGGT			
		ACC_			
GAM1995 TIC	3'	GGAGAGGATAGAGAGGT 14828	TG GTA		
		ACCTC TCTA CCTCTCC			
		TGGAG AGAT GGAGAGG			
		_ A_			
GAM1995 USP9Y	5'	GGAATAGTAGAAGAGGTGA 32017	G G CCTC		
		TCACCTCT TCTA TA TCC			
		AGTGGAGA AGAT AT AGG			
		_ G A_			
GAM1995 C20orf54	3'	GGAGGCAACAGAGGTGA 27229	CTAGTA		
		TCACCTCTGT CCTCT			
		AGTGGAGACA GGAGG			
		AC_			
GAM1995 CDT1	3'	TGGAGAAGCTGGGCAGG 38069	ACC		
		TCTGTCTAGT TCTCCA			
		GGACGGGTCG AGAGGT			
		A_			
GAM1995 COVA1	3'	GGAAAGTAAACAGAGAGGA 36266	AC C GTAC C		
		TC CTCTGT TA CT TCC			
		AG GAGACA AT GA AGG			
		GA A _ A			
GAM1995 CSR1	3'	TGGAGATGGGAGACAGAGG 18361	AGTA _		
		CCTCTGTCT CC TCTCCA			
		GGAGACAGA GG AGAGGT			
		G_ T			
GAM1995 DIO2	3'	AGAGGGAGACAGAGATG 15164	C AGTA		
		CA CTCTGTCT CCTCT			
		GT GAGACAGA GGAGA			
		A G_			
GAM1995 DIO2	3'	AGAGGGAGACAGAGATG 6454	C AGTA		
		CA CTCTGTCT CCTCT			

		GT GAGACAGA GGAGA		
		A G__		
GAM1995	DJ667H12.2	3' GAGAGGTGTTATACAGGGCGA	21217	A T C
		TC CC CTGT TAGTACCTCTC		
		AG GG GACA ATTGTGGAGAG		
		C _ T		
GAM1995	DOK4	3' TGGAGTTTTAAGCAGAGGTGA	19883	TC TACCT
		TCACCTCTG TAG CTCCA		
		AGTGGAGAC ATT GAGGT		
		GA TT__		
GAM1995	FLJ10079	3' AGAGCTACACAGAGGTGA	30215	CTA C
		TCACCTCTGT GTA CTCT		
		AGTGGAGACA CAT GAGA		
		_ C		
GAM1995	FLJ10300	5' AGAGACAGACAGAGGGA	19810	A A AC
		TC CCTCTGTCT GT CTCT		
		AG GGAGACAGA CA GAGA		
		- - -		
GAM1995	FLJ10904	3' GAAAGGTACAAATAGAGGT	20240	CTA C
		ACCTCTGT GTACCT TC		
		TGGAGATA CATGGA AG		
		AA_ A		
GAM1995	FLJ10986	5' GAGAGGTACTATGTGGGTG	20281	CTGTC
		CACCT TAGTACCTCTC		
		GTGGG ATCATGGAGAG		
		TGT__		
GAM1995	FLJ12969	5' GGAAAGGGGACAGAGTGA	23125	C AGTA C
		TCAC TCTGTCT CCT TCC		
		AGTG AGACAGG GGA AGG		
		- _ A		
GAM1995	FLJ32356	3' TGGAGAAGCACAGCCAGAG	29493	T A ACC
		CTCTG CT GT TCTCCA		
		GAGAC GA CA AGAGGT		
		C _ CGA		
GAM1995	ITGA10	5' GGAGAGGGACAGAGG	29864	TAGTA
		CCTCTGTC CCTCTCC		
		GGAGACAG GGAGAGG		
		- - -		
GAM1995	KIAA0318	3' TGGAGAGGTAGGGCCAGAGG	34189	T AG
		CCTCTG CT TACCTCTCCA		

GGAGAC GG ATGGAGAGGT
C G_
GAM1995 KIAA0416 3' AGGCAGCACAGAGGTGA 17830 _ AGTA
TCACCTCTGT CT CCT
||||||| || |||
AGTGGAGACA GA GGA
C C__
GAM1995 KIAA0426 3' TGGAAACTTGTATAGACAGAG 16314 G CTC__
CTCTGTCTA TAC TCCA
||||||| ||| ||||
GAGACAGAT ATG AGGT
_ TTCAA
GAM1995 KIAA0459 3' TGGATTCCCTAGTCAGAGGTGA 30581 T TACCTC
TCACCTCTG CTAG TCCA
||||||| |||| ||||
AGTGGAGAC GATC AGGT
T CTT__
GAM1995 KIAA0711 5' TGGAGAGGAGAGGGCAAAGGCG 16960 A C AGTA
A TC CCT TGTCT CCTCTCCA
|| ||| |||| |||||
AG GGA ACGGG GGAGAGGT
C A AGA_
GAM1995 KIAA1199 3' TGGAGAAATCACAGAGAGGT 35901 TG A ACC_
ACCTC TCT GT TCTCCA
||||| ||| || |||||
TGGAG AGA CA AGAGGT
_ _ CTAA
GAM1995 KIAA1950 3' GAGATTAAACAGAGGTGA 44489 C AC
TCACCTCTGT TAGT CTC
||||||| |||| |||
AGTGGAGACA ATTA GAG
A _
GAM1995 LSR7 5' AGAAAAGTGACAAGGGCAGAGA 20642 C AG__ C__
TGA TCA CTCTGTCT TAC TCT
||| ||||| ||| |||
AGT GAGACGGG GTG AGA
A AACA AAA
GAM1995 MAPK8IP3 3' GAGAGGCTGGGCAGAGG 27221 TA
CCTCTGTCTAG CCTCTC
||||||| |||||
GGAGACGGGTC GGAGAG
_
GAM1995 PDE8A 3' TGGAAAGGACTGGACGAAATGA 31380 CC T A C
TCA TC GTCTAGT CCT TCCA
||| || ||||| ||| ||||
AGT AG CAGGTCA GGA AGGT
AA _ _ A
GAM1995 PDZD2 5' GAGAGGTCAGAAGTGG 39393 C TCTAGT
TCAC TCTG ACCTCTC
||||| |||| |||||

GGTG AGAC TGGAGAG
A _____

GAM1995 PEG10 3' TGGAAAGACCTGGGCAGAAATG 17433 CC TAC C
G TCA TCTGTCTAG CT TCCA
||| ||||| || |||
GGT AGACGGGTC GA AGGT
AA CA_ A

GAM1995 PRO0233 3' GAGAAGGATAGAGAGGT 15374 TG GTA _
ACCTC TCTA CCT CTC
|||| ||| ||| |||
TGGAG AGAT GGA GAG
_ A_ A

GAM1995 SEC24C 3' GAGAGGCACACTGTCAGAGGTG 11357 TC A_
A TCACCTCTG TAGT CCTCTC
||||| ||| |||||
AGTGGAGAC GTCA GGAGAG
T_ CAC

GAM1995 SMC1L1 3' GAGAGGAACAGAGGTGA 35620 CTAGTA C
TCACCTCTGT CCTCT C
||||||| |||||
AGTGGAGACA GGAGA G
A_____ A

GAM1995 USP24 3' AGAGAAACGGACAGAGGCGA 43813 A A AC
TC CCTCTGTCT GT CTCT
|| ||||| || |||
AG GGAGACAGG CA GAGA
C _ AA

GAM1995 WDR9 3' TGGAGAGGTGGAAAGA 21033 G AGT
TCT TCT ACCTCTCCA
||| ||| |||||
AGA AGG TGGAGAGGT
A _____

GAM1995 LOC124470 3' GGAAAGGCAGGCAGAGGGA 37256 A AGTA C
TC CCTCTGTCT CCT TCC
|| ||||| ||| |||
AG GGAGACGGA GGA AGG
_ C_ A

GAM1995 LOC146489 5' GAAAGGTA CTGTAGGCAG 35038 _ C
CTGTCT AGTACCT TC
||||| ||||| ||
GACGGA TCATGGA AG
TG A

GAM1995 LOC147650 5' GAGAGGAGGACAGAGATGA 38348 C AGTA
TCA CTCTGTCT CCTCTC
||| ||||| |||||
AGT GAGACAGG GGAGAG
A A_

GAM1995 LOC162333 5' AGAGAAGGACAGAGGTGG 42123 AGTAC
TCACCTCTGTCT CTCT
||||||| |||

		GGTGGAGACAGG	GAGA		
		AA__			
GAM1995	LOC167040 5'	GAGAAGGAAGAAAGGTGA	42201	CTG	AGTA _
		TCACCT TCT CCT CTC			
		AGTGGA AGA GGA GAG			
		A__ A__ A			
GAM1995	LOC201283 3'	AGAGATGATCCAGACAGAGATG	30302	C	AG__ C
		CA CTCTGTCT TA CTCT			
		GT GAGACAGA GT GAGA			
		A CCTA A			
GAM1995	LOC202460 5'	GAAAGGTGATGACAGAGG	42983	TAG	C
		CCTCTGTC TACCT TC			
		GGAGACAG GTGGA AG			
		TA__ A			
GAM1995	LOC206327 5'	AGAGCCAGACAGAGGAGA	43613	A	A TAC
		TC CCTCTGTCT G CTCT			
		AG GGAGACAGA C GAGA			
		A C__			
GAM1995	LOC221474 5'	TGGAAACTGAAAACAGAGGTGA	44383	C__	ACCTC
		TCACCTCTGT TAGT TCCA			
		AGTGGAGACA GTCA AGGT			
		AAA A__			
GAM1995	LOC51170 3'	GAGAAATACCTTTAGAGGTGA	18363	TCTA	CC
		TCACCTCTG GTA TCTC			
		AGTGGAGAT CAT AGAG			
		TTC_ AA			
GAM1995	LOC90333 3'	TGAAGAGAAACCATACAGAGGT	31227	CTA AC	C
		ACCTCTGT GT CTCT CA			
		TGGAGACA CA GAGA GT			
		TAC AA A			
GAM1995	LOC92568 5'	AGAGAAGCTAGACAGAAGG	34574	_	AC
		CCT CTGTCTAGT CTCT			
		GGA GACAGATCG GAGA			
		A AA			
GAM1996	AXL 3'	AAGGAAGGGGTTGGATTGCAAT	7417	CA	GAA
	A	TAT TAATCCAATTT TCCTT			
		ATA GTTAGGTTGGG AGGAA			
		AC GA_			
GAM1996	AXL 3'	AAGGAAGGGGTTGGATTGCAAT	22438	CA	GAA
	A	TAT TAATCCAATTT TCCTT			

		ATA GTTAGGTTGGG AGGAA		
		AC GA_		
GAM1996 BCAT1	3'	AGGATTCAACTCGTGATA 32895	AATCCAAT	
		TATCAT TTGAATCCT		
		ATAGTG AACTTAGGA		
		CTC_____		
GAM1996 KMO	3'	AAGGACGAACTTGGATTA 9778	_ AA	
		TAATCCAA TTTG TCCTT		
		ATTAGGTT AAGC AGGAA		
		C _		
GAM1996 GRSF1	3'	GATCCAGTTTGGGATTATGA 7880	AAT_ A	
		TCATAATCC TTG ATC		
		AGTATTAGG GAC TAG		
		GTTT C		
GAM1996 KIAA1467	3'	AAGGATTCTAGAAAATTATGA 35450	CCAATTT	
		TCATAAT GAATCCTT		
		AGTATTA CTTAGGAA		
		AAAGAT_		
GAM1996 RYK	3'	AAGGATTTGTTTTATATTATGA 40202	CC TT	
		TCATAAT AA TGAATCCTT		
		AGTATTA TT GTTTAGGAA		
		TA TT		
GAM1996 SLC19A3	3'	TTTTAATTGGATTTTGATA 24925	T T	
		TATCA AATCCAATT GAA		
		ATAGT TTAGGTTAA TTT		
		T T		
GAM1996 LOC256277	5'	AAGGATGTGATATTAAAGTTAT 45423	CC_ TTGA_	
		GATA TATCATAAT AAT ATCCTT		
		ATAGTATTG TTA TAGGAA		
		AAA TAGTG		
GAM1997 FLJ14547	3'	TTTACTTCCAATATTTTA 26562	A	
		TAGAATATTGGAA TAGA		
		ATTTTATAACCTT ATTT		
		C		
GAM1997 SMBP	3'	ACATCTATTTCCATTGATC 35705	A T C	
		GA TA TGGAAATAGA GT		
		CT GT ACCTTTATCT CA		
		A T A		
GAM1998 ANGPT1	3'	TCTTGAAGATGACAAAAGT 29291	C AATC	
		GC TTTGTTAT TCAAGA		

			TG AAACAGTA AGTTCT		
			A GA__		
GAM1998	BLNK	5'	CTTGAGACCAGAGGCT	14963	TTATAA
			AGCCTTTG TCTCAAG		
			TCGGAGAC AGAGTTC		
			C_____		
GAM1998	F8	3'	TCTTGAAATTTGTGATGGC	5619	TTT TC_
			GCC GTTATAA TCAAGA		
			CGG TAGTGTT AGTTCT		
			_____ TAA		
GAM1998	FBXL7	3'	TCATGGGCAACAGAGGC	14673	ATAAT A
			GCCTTTGTT CTCA GA		
			CGGAGACAA GGGT CT		
			C_____ A		
GAM1998	LRR2	3'	CTTGAAGAAACAAAGGCTGG	23705	ATAA _
			TCAGCCTTTGTT TCT CAAG		
			GGTCGGAAACAA AGA GTTC		
			_____ A		
GAM1998	NOL3	3'	CTTGAGTAGACAAAGGC	10063	ATAAT
			GCCTTTGTT CTCAAG		
			CGGAAACAG GAGTTC		
			AT_____		
GAM1998	SERPINA5	3'	TCCTGAAATCATATAGAAAGGC	6240	G _ C A
			TGG TCAGCCTTT TTATA AT TCA GA		
			GGTCGGAAA GATAT TA AGT CT		
			_ AC A C		
GAM1998	DKFZP434N178	3'	GAGGGCAGCTAACAAGGGCTGA	35597	TAA__
			TCAGCCTTTGTTA TCTC		
			AGTCGGGAACAAT GGAG		
			CGACG		
GAM1998	FLJ10458	3'	GAGAACAAAGGCTGA	19866	TATAA
			TCAGCCTTTGT TCTC		
			AGTCGGAAACA AGAG		

GAM1998	KIAA0326	3'	AGATGGTAGCAGAACTGA	32157	CC A
			TCAG TTTGTTAT ATCT		
			AGTC AGACGATG TAGA		
			AA G		
GAM1998	KIAA0420	3'	TGAGCCACAAAGGCTGG	31730	TATAAT
			TCAGCCTTTGT CTCA		

	GGTCGGAAACA	GAGT	
	CC_____		
GAM1998 KIAA0494	3' CTTGAGATTTTACCTAGAGGCT 16589		TTAT_
	AGCCTTTG AATCTCAAG		
	TCGGAGAT TTAGAGTTC		
	CCATT		
GAM1998 KIAA0552	3' CTTGAAGAACAAGGCTGA 16346		T ATAATC
	TCAGCCTT GTT TCAAG		
	AGTCGGAA CAA AGTTC		
	_ GA_____		
GAM1998 KIAA0970	3' CTTAAAATTGTATAAGGCTGA 17204		TGT CTC
	TCAGCCTT TATAAT AAG		
	AGTCGGAA ATGTTA TTC		
	T_ AAA		
GAM1998 LOC145453	3' TCTTTAGGGCACAATAAAGGCT 37838		ATAA C
	AGCCTTTGTT TCT AAGA		
	TCGGAAATAA GGA TTCT		
	CACG T		
GAM1998 LOC155064	3' TGAGACTACAGTGGGGCTGA 39532		T TG A A
	TCAGCC T TT TA TCTCA		
	AGTCGG G GA AT AGAGT		
	_ GT C C		
GAM1998 LOC221738	3' TCTTGAGATAATGAAAAGTGA 45030		GC G A
	TCA CTTT TTAT ATCTCAAGA		
	AGT GAAA AGTA TAGAGTTCT		
	_ _ A		
GAM1998 LOC257354	3' TGAGCCACAAAGGCTGG 45583		TATAAT
	TCAGCCTTTGT CTCA		
	GGTCGGAAACA GAGT		
	CC_____		
GAM1998 LOC51236	3' TGAGACCTGGCCTCAAAGGGCT 18574		_____ TAA
	GA TCAGCCTT GTTA TCTCA		
	AGTCGGGAA CGGT AGAGT		
	ACTC CC_		
GAM1998 LOC90268	3' CTTGAGATTATGAGACTGA 31042		C TGTT
	TCAG CTT ATAATCTCAAG		
	AGTC GAG TATTAGAGTTC		
	A _____		
GAM1999 FER	5' AAGGCATGACCAGCAATGA 11754	AGT	A
	TCA TTGCT GTCATGCCTT		

AGT AACGA CAGTACGGAA
 ____ C
 GAM1999 FLJ13385 3' AGGGACTTCTAGCAAACCTG 24283 A TCATG
 CA GTTTGCTAG CCTT
 || ||||| |||
 GT CAAACGATC GGGA
 C TTCA_
 GAM1999 KIAA0555 3' AAGGCTTGGAGCAAACCTGA 16677 A AG T
 TCA GTTTGCT TCA GCCTT
 ||| ||||| ||| |||||
 AGT CAAACGA GGT CGGAA
 _ _ T
 GAM1999 PDZD2 3' AAGGCATGACTAGTATTTCT 39385 TT_
 AG TGCTAGTCATGCCTT
 || ||||| |||||
 TC ATGATCAGTACGGAA
 TTT
 GAM1999 LOC203411 3' AAGACATGCAGTTAAACTTGA 43563 _ A T C
 TCAAGTTTG CT G CATG CTT
 ||||| ||| ||| |||
 AGTTCAAAT GA C GTAC GAA
 T _ _ A
 GAM1999 LOC54499 3' GGCAGCCAGCAAACCTTGATA 34966 A CA
 TATCAAGTTTGCT GT TGCC
 ||||| ||| |||
 ATAGTTCAAACGA CG ACGG
 C _
 GAM2000 CYP4F3 3' CATGTTATACGTACACTT 6590 A AGAAT
 AAGTGTAC TATAA TG
 ||||| ||| ||
 TTCACATG ATATT AC
 C GT_
 GAM2000 MHC2TA 3' TCAATTCTCATTTGTACACAC 5782 _ TATAA
 TTTG TAAAGTGT ACA AGAATTGA
 ||||| ||| |||||
 GTTTCACA TGT TCTTAACT
 CAC TTAC_
 GAM2000 KLF3 3' TTTTACATGTACATTTTA 18595 A
 TAAAGTGTACAT TAAAG
 ||||| ||| |||
 ATTTTACATGTA ATTTT
 C
 GAM2000 LOC201626 3' TCAAAGCTTATATGTAAACTT 42890 G A AA
 AAGT TACATATAA G TTGA
 ||| ||||| ||| |||
 TTCA ATGTATATT C AACT
 A _ GA
 GAM2001 RNF12 5' GGAAACTCAGATTCCAA 18202 TC A
 TTGGA CT AGTTTTTC
 |||| ||| |||||

			AACCT GA TCAAAAGG		
			TA C		
GAM2001	KIAA0680	3'	TAATAAAAACTTGAATCCAA 16286	CC	C
			TTGGAT TAAGTTTTT TTA		
			AACCTA GTTCAAAAA AAT		
			A_ T		
GAM2002	FGF2	3'	ACCTGAAACCAAGATTGGCT 7731	ATCTG	
			AGCCAGTCTTG AGGT		
			TCGGTTAGAAC TCCA		
			CAAAG		
GAM2002	FSTL3	3'	TAAACCACAGCCTCAGACCAGC 12471	CA	T T_ A
	T		AGC GTCT GA CTG GGTTTA		
			TCG CAGA CT GAC CCAAAT		
			AC _ CC A		
GAM2002	PTGS2	3'	TAAACCTCAGCTCAGGACTGCT 6685	C	T
			AGC AGTCTTGA CTGAGGTTTA		
			TCG TCAGGACT GACTCCAAAT		
			_ C		
GAM2002	XRCC2	3'	TAAAAAGGAACAAGACTGACTG 11904	C	A GAGG
			CAG CAGTCTTG TCT TTTA		
			GTC GTCAGAAC AGG AAAT		
			A A AA_		
GAM2002	FLJ20445	3'	AAACTATCTCAATACTGGCTG 19475	C	TCT _
			CAGCCAGT TTGA GA GGTTT		
			GTCGGTCA AACT CT TCAAA		
			T _ A		
GAM2002	KIAA1328	3'	TAAATATAAAGTCAAGACTAAC 30888	CC	CTGAG
	T		AG AGTCTTGAT GTTTA		
			TC TCAGAACTG TAAAT		
			AA AAATA		
GAM2002	KIAA1361	5'	TAAAATTAGAATCAAGACAGCT 31170	CA	_ GG
	G		CAGC GTCTTGAT CTGA TTTA		
			GTCG CAGAACTA GATT AAAT		
			A_ A A_		
GAM2002	Rab11-FIP2	3'	AAACCTCAAAGTCTGGT 17094	T	GATC
			GCCAG CTT TGAGGTTT		
			TGGTC GAA ACTCCAAA		
			T _		
GAM2002	LOC146136	5'	AAACTTGTCAGGACTGGCT 36110	CTG	
			AGCCAGTCTTGAT AGGTTT		

GAM2002	LOC150577	5'	TAAACCTCAGACTCTTCCAGC	41223	CAGTCTT	_
			GC GA TCTGAGGTTTA			
			CG CT AGACTCCAAAT			
			ACCTT__ C			
GAM2002	LOC220565	3'	AAACTTGT CAGGACTGGCT	43629	CTG	
			AGCCAGTCTTGAT AGGTTT			
			TCGGTCAGGACTG TTCAA			
GAM2003	ANK3	3'	TGTTGATAAGGCACTGCCTCTT	21983	C__	C
	A		TGAGAGGCA TCTTA CAACA			
			ATTCTCCGT GGAAT GTTGT			
			CAC A			
GAM2003	AP2B1	3'	TGTTGCCCTAAGAATGCTTCTC	6956	C	C__
	A		TGAGAGGCA TCTTA CAACA			
			ACTCTTCGT AGAAT GTTGT			
			A CCC			
GAM2003	B3GAT1	5'	GTGCTGGTAAGACCTGCT	27632	C_	A
			GGCA TCTTACCA CAC			
			TCGT AGAATGGT GTG			
			CC C			
GAM2003	DRG2	3'	GGGTGTCCTAAAGTGCCTC	7076	C	CCA
			GAGGCACT TTA ACACCC			
			CTCCGTGA AAT TGTGGG			
			_ CC_			
GAM2003	GM2A	3'	GGTATGAGCAGCCTCTCA	33661	A_	T
			TGAGAGGC CTC TACC			
			ACTCTCCG GAG ATGG			
			AC T			
GAM2003	GRAF	3'	GGGTATTAAGGTCAGCCTCTCA	17443	AC_	CCAAC
			TGAGAGGC TCTTA ACCC			
			ACTCTCCG GGAAT TGGG			
			ACT TA__			
GAM2003	MGA	3'	GGTAAAGAGTGCTCCTCA	31454	AG	_
			TGAG GCACTCTT ACC			
			ACTC CGTGAGAA TGG			
			CT A			
GAM2003	NLGN2	3'	GGGCACCGGACGATGTGCCTCT	42550	_	TTA AACA
	C		GAGAGGCAC TC CC CCC			

CTCTCCGTG AG GG GGG
 T CA_ CCAC
 GAM2003 NRAP 3' GGTGTTGGCTGGACCCCTC 12834 CAC TA
 GAGG TCT CCAACACC
 |||| ||| |||||
 CTCC AGG GGTGTGG
 CC_ TC
 GAM2003 RET 3' GGCAGGCAGGTGCCTCTCA 21785 CTTA AACA
 TGAGAGGCACT CC CC
 ||||| || ||
 ACTCTCCGTGG GG GG
 AC__ AC__
 GAM2003 TNFSF11 3' GGATGTTGGCCACCAGGTGCCT 26898 CTTA__ _
 TTCA TGAGAGGCACT CCAACA CC
 ||||| |||| ||
 ACTTTCCGTGG GGTGT GG
 ACCACC A
 GAM2003 TNFSF11 3' GGATGTTGGCCACCAGGTGCCT 9801 CTTA__ _
 TTCA TGAGAGGCACT CCAACA CC
 ||||| |||| ||
 ACTTTCCGTGG GGTGT GG
 ACCACC A
 GAM2003 C12orf22 3' GGCGCTAGAGGTCTGCCTCTT 25129 ____ TA__
 A TGAGAGGCA CTCT CC
 ||||| ||| ||
 ATTCTCCGT GAGA GG
 CCTG TCGC
 GAM2003 C20orf142 3' GGCGTTGGTAAGATGTGACCCT 36931 A _ _ A
 C GAG GG CAC TCTTACCAAC CC
 ||| ||| ||||| ||
 CTC CC GTG AGAATGGTTG GG
 _ A T C
 GAM2003 DKFZP564O0423 3' GGATAGAGAAAGTGTCTCCCA 44068 A _ A__
 TGAGGCAC TCTT CC
 || ||||| ||| ||
 AC CTCTGTG AGAG GG
 C AA ATA
 GAM2003 FLJ20232 3' TGCTGAGAATGTCTCTCA 21088 C C
 TGAGAGGCA TCTTA CA
 ||||| |||| ||
 ACTCTCTGT AGAGT GT
 A C
 GAM2003 FLJ20686 3' GTGTTTTGGAGCGCCTCTCA 19594 A TACC
 TGAGAGGC CTCT AACAC
 ||||| ||| ||||
 ACTCTCCG GAGG TTGTG
 C TT__
 GAM2003 FLJ22501 5' GGTGTTGAGTTGCCTTCA 24082 G CTCTT _
 TGA AGGCA AC CAACACC
 ||| |||| || |||||

ACT TCCGT TG GTTGTGG
 _ _ _ _ _ A
 GAM2003 FLJ23120 3' GGCATTGCCAGGCCTCTCA 41265 A CTTAC CA
 TGAGAGGC CT CAA CC
 ||||| || ||
 ACTCTCCG GA GTT GG
 _ CC_ AC
 GAM2003 FLJ23309 3' GGTGTATCACAGCAGTACCTCT 24379 C _ TACCA
 CA TGAGAGG ACT CT ACACC
 ||||| || ||
 ACTCTCC TGA GA TGTGG
 A C CACTA
 GAM2003 FLJ25438 3' TGTCAGTGGGAGCCTCCA 29521 A AC CA
 TG GAGGC TCTTAC ACA
 || |||| |||| ||
 AC CTCCG AGGGTG TGT
 _ _ _ AC
 GAM2003 KLF5 3' TGTGGTAAGGTACCTCTCA 7464 C T A
 TGAGAGG AC CTTACCA CA
 ||||| || ||||| ||
 ACTCTCC TG GAATGGT GT
 A _ _
 GAM2003 PRO0659 3' GGACACGTGGGAGTCCTCCCA 15407 A C CAACA
 TG GAGG ACTCTTAC CC
 || |||| ||||| ||
 AC CTCC TGAGGGTG GG
 C _ CACA_
 GAM2003 LOC144453 3' GGATGTTGGTACTCCTCCCA 37748 A CACTCT _
 TG GAGG TACCAACA CC
 || |||| ||||| ||
 AC CTCC ATGGTTGT GG
 C TC_ A
 GAM2003 LOC148223 3' GGGTGTGACACAGGCGCCCT 38495 A A CTTAC
 C GAG GGC CT CAACACCC
 || |||| || ||||| ||
 CTC CCG GG GTTGTGGG
 C C ACACA
 GAM2003 LOC158819 5' GGATGTTGGCAAGTGCCTCTTA 42027 CTTA _
 TGAGAGGCACT CCAACA CC
 ||||| || |||| ||
 ATTCTCCGTGA GGTGT GG
 AC_ A
 GAM2003 LOC202934 3' GGCGTTTCCTCAGGCCTCTCA 43462 A CTTACC A
 TGAGAGGC CT AAC CC
 ||||| || || ||
 ACTCTCCG GA TTG GG
 _ CTCCT_ C
 GAM2003 LOC206426 3' GGTGTTTAACCACCTCCCA 43118 A CACTC CC
 TG GAGG TTA AACACC
 || |||| || ||||| ||

		AC CTCC AAT TTGTGG			
		C ACC__ _			
GAM2003	LOC255465	3'	GGCGTTTCCTCAGGCCTCTCA	46454	A CTTACC A
		TGAGAGGC CT AAC CC			
		ACTCTCCG GA TTG GG			
		_ CTCCT_ C			
GAM2004	GPR61	3'	CCAACAGGATGAACGTGTGCAA	38564	C GTC GGC_
		TTGCACACGT CA TCC GG			
		AACGTGTGCA GT AGG CC			
		A ____ ACAA			
GAM2005	AKT2	5'	GCTAGGTGACAGCGTACC	7338	C__ G
		GGTACGCTG CC TGGC			
		CCATGCGAC GG ATCG			
		AGT _			
GAM2005	TEC	3'	GCGCCACGAAAGAACTGTA	9218	ACG GCC
		TACGGT CT CGTGGCGC			
		ATGTCA GA GCACCGCG			
		AA_ AA_			
GAM2005	KIAA0429	3'	GGATGTGAGAGTAACGTACCGT	16473	C CCGTG _
A			TACGGTACG TGC GCG CC		
		ATGCCATGC ATG TGT GG			
		A AGAG_ A			
GAM2005	LOC147841	5'	GGGCGCCACGAGCAGGTGGTG	38399	G G C
		CG TAC CTGC CGTGGCGCCC			
		GT GTG GACG GCACCGCGGG			
		G _ A			
GAM2005	LOC152048	3'	CATGGCGCAGCGTACGTA	41425	G _
		TACG TACGCTGC CCGTG			
		ATGC ATGCGACG GGTAC			
		_ C			
GAM2005	LOC152271	3'	GCGCCACGGCAGACACACC	39240	ACG_ C
		GGT CTGCC GTGGCGC			
		CCA GACGG CACCGCG			
		CACA _			
GAM2005	LOC199796	5'	GCGCCACGAGGTGCCACC	36811	AC T _
		GGT GC GCC CGTGGCGC			
		CCA CG TGG GCACCGCG			
		C_ _ A			
GAM2005	LOC56270	3'	GGGCGCCACAGCACCCACC	21232	ACGC CC
		GGT TGC GTGGCGCCC			

		CCA ACG CACCGCGGG	
		CCC_ A_	
GAM2006 FMN2	3'	CTACTGACAACCGTCCTCCA 38741	CA C__ _
		TGGAGGAC GG TCA TGG	
		ACCTCCTG CC AGT ATC	
		A_ AAC C	
GAM2006 HOXC13	3'	CTATCCCATCCCCAGCCTCCA 30015	ACCA CTC
		TGGAGG GG ATGGGATAG	
		ACCTCC CC TACCCTATC	
		GA__ CC_	
GAM2006 HYOU1	3'	CTAGGGAGCCCGTCCTCCA 30003	CA A_
		TGGAGGAC GGCTC TGG	
		ACCTCCTG CCGAG ATC	
		C_ GG	
GAM2006 RAP1GA1	3'	ATCCCATGCTGGGCCCTCCA 8796	A_ GCT
		TGGAGG CCAG CATGGGAT	
		ACCTCC GGTC GTACCCTA	
		CG _	
GAM2006 DKFZP434E2318	5'	CCAGAGCCTGGTCCTGCA 25816	G A
		TG AGGACCAGGCTC TGG	
		AC TCCTGGTCCGAG ACC	
		G _	
GAM2006 FAM3A	3'	CCATCTAGCCCTGTCCTCCA 22357	CA C_
		TGGAGGAC GGCT ATGG	
		ACCTCCTG CCGA TACC	
		TC TC	
GAM2006 FGD3	3'	CTAAGAGCCTGGCCTCCA 36090	A A
		TGGAGG CCAGGCTC TGG	
		ACCTCC GGTCCGAG ATC	
		_ A	
GAM2006 KIAA0014	3'	CTAGAGCCTGGTCCTCCA 16114	A
		TGGAGGACCAGGCTC TGG	
		ACCTCCTGGTCCGAG ATC	
		_	
GAM2006 KIAA0152	3'	CTATCCCATCGAAATTCCCCA 16335	A CCAGGC _
		TGG GGA TC ATGGGATAG	
		ACC CCT AG TACCCTATC	
		_ TAA__ C	
GAM2006 KIAA0753	3'	CCATCATAGCCTGGTCCTCCA 16735	C_
		TGGAGGACCAGGCT ATGG	

		ACCTCCTGGTCCGA TACC	
		TAC	
GAM2006 KIAA1404	3'	CTATCCCAAGTGTGATCCTTCA 31051	C G CA
		TGGAGGA CA GCT TGGGATAG	
		ACTTCCT GT TGA ACCCTATC	
		A G _	
GAM2006 KIAA1987	5'	CCCCCGCCTCGTCCTCCA 42495	C TCAT
		TGGAGGAC AGGC GGG	
		ACCTCCTG TCCG CCC	
		C CC_	
GAM2006 NAV3	3'	CCAAGAGGCCAGTCCTCCA 17090	CA _ A
		TGGAGGAC GGC TC TGG	
		ACCTCCTG CCG AG ACC	
		A_ G A	
GAM2006 PDEF	5'	CCACAGACCCAGTCCTCCA 14746	CA C A _
		TGGAGGAC GG TC TG GG	
		ACCTCCTG CC AG AC CC	
		AC _ _ A	
GAM2006 RoXaN	3'	CTAGTGGTGGAGTCTGGTCCTC 24603	ATGGGA
CA		TGGAGGACCAGGCTC TAG	
		ACCTCCTGGTCTGAG ATC	
		GTGGTG	
GAM2006 LOC145813	5'	CCACTGCACCTGGTCCCCCA 40598	A CT _
		TGG GGACCAGG CA TGG	
		ACC CCTGGTCC GT ACC	
		C AC C	
GAM2006 LOC152426	5'	CTGGCCAAACCCAGTCTTCCA 41498	CA CTCA GA
		TGGAGGAC GG TGG TAG	
		ACCTTCTG CC ACC GTC	
		AC AA_ G_	
GAM2006 LOC157254	5'	TCAGGAGTGAGCCTGGCACTCC 39579	GA GG_
A		TGGAG CCAGGCTCAT GA	
		ACCTC GGTCCGAGTG CT	
		AC AGGA	
GAM2006 LOC158382	3'	CCTGAGCCTGTCCTCCA 41964	C T
		TGGAGGAC AGGCTCA GG	
		ACCTCCTG TCCGAGT CC	
		_ _	
GAM2006 LOC221393	3'	CCATAGCTCAGTCCTCCA 44337	CA C
		TGGAGGAC GGCT ATGG	

			ACCTCCTG TCGA TACC		
			AC _		
GAM2006	LOC51285	3'	CCAGAGCCTGGCCCTCC 18638	A	A
			GGAGG CCAGGCTC TGG		
			CCTCC GGTCCGAG ACC		
			C _		
GAM2006	LOC90342	5'	CTGTGAGCTGATCCTCCA 31253		CCA
			TGGAGGA GGCTCATGG		
			ACCTCCT TCGAGTGTC		
			AG _		
GAM2007	ADCY8	5'	CTTCCTCCAAATTAATA 6787	G	_
			TAG TAATTTGG GGAGG		
			ATC ATTAAACC CCTTC		
			A T		
GAM2007	ALDH3B1	3'	TTCTCACCTCCCAAGTCCC 44002	TA	G A
			GG ATTTGGG AGGT AGAA		
			CC TGAACCC TCCA TCTT		
			C_ _ C		
GAM2007	APTX	3'	CTTCTATCCCAGATTACCTA 19249		A T
			TAGGTAATTTGGGG GG AAG		
			ATCCATTAGACCCT TC TTC		
			A _		
GAM2007	B4GALT6	3'	CTTCCTACCGGGATTACCTA 30093		G G T
			TAGGTAATTT GG AGG AAG		
			ATCCATTAGG CC TCC TTC		
			G A _		
GAM2007	COL5A3	3'	CTCACCTCCCCAGGCTCACCT 17932	AA_	A
			AGGT TTTGGGGAGGT AG		
			TCCA GGACCCCTCCA TC		
			CTC C		
GAM2007	ENAM	3'	TTCTTACATATTAATTAAGCTA 25634	G	GGAG
			TAG TAATTTGG GTAAGAA		
			ATC ATTAAATT CATTCTT		
			G ATA_		
GAM2007	FOSB	3'	TTTGGTACCCCCAAACCCCC 13584	TAA	AG AG
			GG TTTGGGG GTA AAA		
			CC AAACCCC CAT TTT		
			CCC _ GG		
GAM2007	IL1B	3'	TCTCACCTCTCCTACT 6176	ATTT	A
			GGTA GGGGAGGT AGA		

			TCAT CCTCTCCA TCT			
			_____ C			
GAM2007	MPP2	3'	TCCTACCTCCCCTGCCTG 30085	ATTT	A	
			TAGGTA GGGGAGGT GA			
			GTCCGT CCCCTCCAT CT			
			_____ C			
GAM2007	MSL3L1	3'	TTCTCACCTCCTCTTAGCC 27812	AATTT	A	
			GGT GGGGAGGT AGAA			
			CCG CTCCTCCA TCTT			
			ATT_____ C			
GAM2007	MTCP1	5'	TTCTTACCTCCCAGCTACCT 15491	ATTTG		
			AGGTA GGGAGGTAAGAA			
			TCCAT CCCTCCATTCTT			
			CGA_____			
GAM2007	SRGAP1	3'	TCTCTTTTGAATAACACCTA 35760	A	GG TA	
			TAGGT ATTTGG AGG AGA			
			ATCCA TAAATC TTT TCT			
			C AG TC			
GAM2007	C(27)-3BETA-HSD	3'	TTCCACCTCTCTACCTA 24850	AATTT	AA	
			TAGGT GGGGAGGT GAA			
			ATCCA TCTCTCCA CTT			
			_____ CC			
GAM2007	DKFZp547M072	3'	TTCCTACCTCCTTCACC 30619	AATTT	A	
			GGT GGGGAGGT GAA			
			CCA TTCCTCCAT CTT			
			C_____ C			
GAM2007	FLJ14594	3'	TTCCACCTCCTCCCTACC 26568	ATTT	AA	
			GGTA GGGGAGGT GAA			
			CCAT CTCCTCCA CTT			
			CC_____ CC			
GAM2007	FUSIP1	3'	TCTCACCTCTTTCCTA 13411	TAATTT	A	
			TAGG GGGGAGGT AGA			
			ATCC TTTCTCCA TCT			
			_____ C			
GAM2007	KIAA0193	3'	TTCCACCTTACTAAATTACC 16548	GG	AA	
			GGTAATTTGG AGGT GAA			
			CCATTAAATC TCCA CTT			
			AT CC			
GAM2007	KIAA0435	3'	TCGTGCTCCCCAAATCACC 16724	A	G A	
			GGT ATTTGGGGAG TA GA			

CCA TAAACCCCTC GT CT
 C _ G
 GAM2007 KIAA1755 3' TCTCACCTCCCCACCAAGCCT 30753 AATT A
 AGGT TGGGGAGGT AGA
 ||| ||||| |||
 TCCG ACCCCTCCA TCT
 AACC C
 GAM2007 LAMP3 3' CCTACACCAAGTTACCTA 29917 GG_
 TAGGTAATTTGG AGG
 ||||| |||
 ATCCATTGAACC TCC
 ACA
 GAM2007 MacGAP 3' TCTCACCTCTATTACCT 27290 TTGG A
 AGGTAAT GGAGGT AGA
 ||||| ||||| |||
 TCCATTA TCTCCA TCT
 C
 GAM2007 MGC12217 3' TTTCCACCTCCTTCCCCCCAC 26518 AATTT_ AA
 C GGT GGGGAGGT GAAA
 ||| ||||| |||
 CCA TTCCTCCA CTTT
 CCCCC CC
 GAM2007 PPFA4 3' TCTTGCTTGTCCTCCCAAATCACC 34822 A _
 TA TAGGT ATTTGGGGA GGTAAGA
 |||| ||||| |||||
 ATCCA TAAACCCCT TCGTTCT
 C GT
 GAM2007 RAB6C 3' TTCTCACCTCTCCCTTACC 25837 TTT A
 GGTAAGGGGAGGT AGAA
 |||| ||||| |||
 CCATT CCTCTCCA TCTT
 C_ C
 GAM2007 SARM 3' TCTTACCTCCCTCCCTCCT 17463 TAATTT
 AGG GGGGAGGTAAGA
 ||| ||||| |||||
 TCC TCCCTCCATTCT
 TCCC_
 GAM2007 LOC148823 3' CTCCCCATCCAATTACCTA 29791 _
 TAGGTAATT TGGGGAG
 ||||| |||||
 ATCCATTAA ACCCCTC
 CCT
 GAM2007 LOC159121 5' TCTCACCTCCTTCATCCCCTA 42065 TA TT A
 TAGG AT GGGGAGGT AGA
 ||| || ||||| |||
 ATCC TA TTCCTCCA TCT
 CC C_ C
 GAM2007 LOC164955 3' TTCTTACTAAAAATCACC 40114 A GGGGA
 GGT ATTT GGTAAGAA
 ||| ||| |||||

CCA TAAA TCATTCTT
 C AA____
 GAM2007 LOC200269 5' CCGTCCCCAGATCACCTA 42758 A _
 TAGGT ATTTGGGGA GG
 |||| ||||| ||
 ATCCA TAGACCCCT CC
 C G
 GAM2007 LOC200830 3' TCTTTCCCCAAACACCTA 43348 AA GGT
 TAGGT TTTGGGGA AAGA
 |||| ||||| |||
 ATCCA AAACCCCT TTCT
 C_ ____
 GAM2007 LOC256946 3' TCTCACCTCTTTTCCTA 45361 TAATTT A
 TAGG GGGGAGGT AGA
 ||| ||||| |||
 ATCC TTTCTCCA TCT
 _____ C
 GAM2007 LOC85414 3' CCTACCCCCAACTTTCCCTA 26949 T__ T _
 TAGG AA TTGGGG AGG
 ||| ||||| |||
 ATCC TT AACCCC TCC
 CCT C CA
 GAM2007 LOC90110 5' CTCACCCTACTTCCAAATTAC 30841 A__ A
 GTAATTTGGGG GGT AG
 ||||| ||| ||
 CATTAAACCTT CCA TC
 CATC C
 GAM2007 LOC92659 5' CTCACCTCCCCAGCGGCTCCT 34716 TAAT_ A
 AGG TTGGGGAGGT AG
 ||| ||||| ||
 TCC GACCCCTCCA TC
 TCGGC C
 GAM2008 C8orf1 3' ACAAATAGAAACACTGCC 10530 G CAGG
 GGCAGTGTT CTA TGT
 ||||| ||| |||
 CCGTCACAA GAT ACA
 A AA____
 GAM2008 SYT1 3' GATATTGTAACAATACTGCC 12169 C GGT
 GGCAGTGTTG TACA GTATC
 ||||| ||| |||||
 CCGTCATAAC ATGT TATAG
 A ____
 GAM2008 CHST3 3' ACACCCCTTCACAGCATACACT 10474 _ ACA____
 GCC GGCAGTGT TGCT GGTGT
 ||||| ||| |||||
 CCGTCACA ACGA CCACA
 T CACTTCC
 GAM2008 KIAA1055 3' ATGCCAGCACACACTGCC 32849 _ ACA
 GGCAGTGT TGCT GGTGT
 ||||| ||| |||||

		CCGTCACA ACGA CCGTA	
		C ____	
GAM2008	SDC3	3' ATACACCCACACTCTGGCACCA 16077	T CA_____
	C	GTG TGCTA GGTGTAT	
		CAC ACGGT CCACATA	
		C CTCACAC	
GAM2008	ZNF387	5' ACACCTGTAGACGTTGCGC 16171	_ TG
		GGC AGTGT CTACAGGTGT	
		CCG TTGCA GATGTCCACA	
		C ____	
GAM2008	LOC151234	3' ATACACCTGTCAATGCC 39078	G TTGCT
		GGCA TG ACAGGTGTAT	
		CCGT AC TGTCCACATA	
		A ____	
GAM2008	LOC96597	5' ACCTGAGCCGCAACACTGCCG 33225	TA__
		CGGCAGTGTTGC CAGGT	
		GCCGTCACAACG GTCCA	
		CCGA	
GAM2009	PIK3R1	3' TAGAGCTTTCTTTCACAAAA 34039	AT__
		TTTTGTGAAA CTCTA	
		AAAACACTTT GAGAT	
		CTTTC	
GAM2009	ST7	3' TGGTTTGTTTTTACAAAATA 15099	CT_
		TATTTTGTGAAAAT CTA	
		ATAAAACATTTTTG GGT	
		TTT	
GAM2009	SVIL	3' TGGTGTTTTTTCACAAAGTA 9151	TCT
		TATTTTGTGAAAA CTA	
		ATGAAACACTTTT GGT	
		TGT	
GAM2009	SVIL	3' TGGTGTTTTTTCACAAAGTA 22348	TCT
		TATTTTGTGAAAA CTA	
		ATGAAACACTTTT GGT	
		TGT	
GAM2009	CDW92	3' GATTTTGGACTTTCACAAA 27867	A CT
		TTTGTGAAA TCT AATC	
		AAACACTTT AGG TTAG	
		C TT	
GAM2009	GNB4	3' GATTAGAGATTTCACTGATA 22269	TT A
		TATT GTGAAA TCTCTAATC	

		ATAG CACTTT AGAGATTAG		
		T_ _		
GAM2009	KIAA0530	3' GATTACTTTTCACAAAATA	35099	TCTC
		TATTTTGTGAAAA TAATC		
		ATAAAACACTTTT ATTAG		
		C_		
GAM2009	KIAA1265	3' GATTAAGACTTTTCACAAAATA	35032	_ C
		TATTTTGTGAAAA TCT TAATC		
		ATAAAACACTTTT AGA ATTAG		
		C _		
GAM2009	TTY9	3' ATTAGAGACCTTATAAAA	25677	AAA
		TTTTGTGA TCTCTAAT		
		AAAATATT AGAGATTA		
		CC_		
GAM2009	LOC120856	3' ATTAAGGTATCACAAAATA	36634	AA C
		TATTTTGTGA ATCT TAAT		
		ATAAAACACT TGGA ATTA		
		A_ A		
GAM2009	LOC157278	3' AGAGATTGAGACAAAATG	41777	GAA
		TATTTTGT AATCTCT		
		GTAAAACA TTAGAGA		
		GAG		
GAM2009	LOC221962	3' AGAGATTGAGACAAAATG	44528	GAA
		TATTTTGT AATCTCT		
		GTAAAACA TTAGAGA		
		GAG		
GAM2009	LOC255461	3' AGAGATTGAGACAAAATG	46463	GAA
		TATTTTGT AATCTCT		
		GTAAAACA TTAGAGA		
		GAG		
GAM2009	LOC255516	3' AGAGATTGAGACAAAATG	46469	GAA
		TATTTTGT AATCTCT		
		GTAAAACA TTAGAGA		
		GAG		
GAM2010	CR1	3' CGCACACAGTATCTA	6173	C CGA
		TAG ATACTGTG TGTG		
		ATC TATGACAC ACGC		
		_ _		
GAM2010	IRAK1	3' GAGTCACACTACATGC	7299	TAC CGA
		GCA TGTG TGTGACTC		

CGT ACAT ACACTGAG
 ____ C____
 GAM2010 DKFZp547l014 5' TGAGTCTTTAGGCCAGTATGCT 21470 T GATGT
 A TAGCATACTG GC GACTCA
 ||||| || |||||
 ATCGTATGAC CG CTGAGT
 _ GATTT

GAM2010 ERMAP 3' AGTCACATCATATATGC 20605 C GC
 GCATA TGT GATGTGACT
 |||| ||| |||||
 CGTAT ATA CTACACTGA

GAM2010 KIAA0527 3' TGAGCCACATCACAGTAT 45849 GC A
 ATACTGT GATGTG CTCA
 ||||| ||||| |||||
 TATGACA CTACAC GAGT
 _ C

GAM2010 Rab11-FIP2 3' ATAATGCACAGTACACTA 17096 CA A
 TAG TACTGTGCG TGT
 ||| ||||| |||||
 ATC ATGACACGT ATA
 AC A

GAM2010 RYBP 5' AGTGGCACAACAGTATGC 29908 GCGA G
 GCATACTGT TGT ACT
 ||||| |||||
 CGTATGACA ACG TGA
 AC_ G

GAM2010 LOC221035 3' CAAATCCACAGTATACT 44744 C C G
 AG ATACTGTG GAT TG
 || ||||| |||||
 TC TATGACAC CTA AC
 A _ A

GAM2011 CSDA 3' GCCACAACCTTAACCAACACC 9728 TCCATC
 GGT TAAGGTTGTGGC
 ||| |||||
 CCA ATTCCAACACCG
 CAACCA

GAM2011 LZTR1 3' CCATGGCTTAGCAGAACCCCA 13636 A CAT G TG
 TG GGTTCT CTAAG T TGG
 || |||| ||||| |||||
 AC CCAAG GATTC G ACC
 C AC_ _GT

GAM2011 SORCS2 3' CCACCCATGGAGACTGGAACCT 21872 _ A TT
 CA TGAGGTTCCA TCTA GG GTGG
 ||||| ||||| |||||
 ACTCCAAGGT AGGT CC CACC
 CAG A _

GAM2011 KIAA1922 5' GCTGGGTCTCAGATGCAACCTC 36456 C A GT G
 A TGAGGTT CATCT AG T TGGC
 ||||| ||||| |||||

ACTCCAA GTAGA TC G GTCG
 C C TG_
 GAM2011 MGC19556 3' CCCTCCTGAATGGAACCCCA 27315 A CTA TTGT
 TG GGTTCAT AGG GG
 || ||||| || ||
 AC CCAAGGTA TCC CC
 C AG_ TC_
 GAM2011 NY-REN-25 3' CAGCTTTAGACAAAACCCCA 30415 A CCA
 TG GGTT TCTAAGGTTG
 || ||| |||||
 AC CCAA AGATTTTCGAC
 C AAC
 GAM2011 PF1 5' CCACAACCTCACGTAACCTC 45603 CCATCTA
 GAGGTT AGGTTGTGG
 ||||| |||||
 CTCCAA TCCAACACC
 TGCAC_
 GAM2011 SARM 3' GCAGCCTAGACAGAACCTGCA 17459 _ CA A
 TG AGGTTT TCTA GGTTGT
 || ||||| ||| |||||
 AC TCCAAG AGAT CCGACG
 G AC _
 GAM2011 SCAMP-4 3' CCACAACCTTTGGACACCCCA 27820 A TCCA
 TG GGT TCTAAGGTTGTGG
 || ||| |||||
 AC CCA AGGTTTCAACACC
 C C_
 GAM2011 WIT-1 5' GCCCCAGAATGGAACCTCA 17989 _ AA
 TGAGGTTCCAT CT GGT
 ||||| || |||
 ACTCCAAGGTA GA CCG
 A CC
 GAM2011 LOC149271 5' ACACCTAAATGGAACCCCA 38673 A CTA T
 TG GGTTCAT AGGT GT
 || ||||| ||| ||
 AC CCAAGGTA TCCA CA
 _ AA_ _
 GAM2011 LOC221288 3' ACCTTTAAATGGAATCCCA 44967 A CT_
 TG GGTTCAT AAGGT
 || ||||| ||||
 AC CTAAGGTA TTCCA
 C AAT
 GAM2011 LOC255299 5' GCCAAAGCCAAACAGAACTTCA 46548 CATCTAA G
 TGAGGTTT GGTG TGGC
 ||||| ||| ||||
 ACTTCAAG CCGA ACCG
 ACAA_ A
 GAM2011 LOC90092 5' GCCCAAGTGAGACAGAACCTCA 30788 CA AAGG T
 TGAGGTTT TCT TTG GGC
 ||||| || ||| |||

		ACTCCAAG AGA AAC CCG	
		AC GTG_ _	
GAM2012 BECN1	3'	TCGGGTAATATTAAACAGTA 9844	—
		TACTGTTTAATATT TTGA	
		ATGACAAATTATAA GGCT	
		TG	
GAM2012 DMXL1	3'	AATCAAGATTCAAACAG 12023	AAT
		CTGTTT ATTTTGATT	
		GACAAA TAGAACTAA	
		CT_	
GAM2012 NFYC	3'	ATGAAATTAAAATATTAAATA 15493	—
		TGTTTAATATTTTGATT CAT	
		ATAAATTATAAAATTAA GTA	
		A	
GAM2012 PLS3	3'	ATGAATATTATTAGACAGTA 11471	TTTTG
		TACTGTTTAATA ATTCAT	
		ATGACAGATTAT TAAGTA	
		TA_	
GAM2012 PTPRJ	3'	CGGAATATTTAAACAGTA 8730	—
		TACTGTTTAA TATTTTG	
		ATGACAAATT ATAAGGC	
		T	
GAM2012 JDD1	3'	AATCAAAGATTTAAACAGT 31666	TA
		ACTGTTTAA TTTTGATT	
		TGACAAATT GAAACTAA	
		TA	
GAM2012 KIAA1878	3'	TGAAGAAATATTAAACA 44077	GA
		TGTTTAATATTTT TTCA	
		ACAAATTATAAAG AAGT	
		—	
GAM2012 LOC157867	5'	AATCAACTATTAAACAGTG 41854	TT
		TACTGTTTAATA TTGATT	
		GTGACAAATTAT AACTAA	
		C_	
GAM2013 COL19A1	3'	AGTACAATTAGAAACACTGTT 7593	C GGCAAT
		AATAGTG TT ATTGTACT	
		TTGTCAC AA TAACATGA	
		_ AGAT_	
GAM2013 FLNB	3'	GTACAATGACAAGCAC 31145	GCAA
		GTGCTTG TATTGTAC	

CACGAAC GTAACATG
A____
GAM2013 FLJ23322 3' TGC GTGATTGCCAAAGACCACT 42799 C____ AT
AGTG TTGGCAAT TGTA
|||| |||||| ||||
TCAC AACCGTTA GCGT
CAGA GT
GAM2013 KIAA1317 3' ATAGTTGTGTGCCAAGCACT 41622 AT____
AGTGCTTGGCA ATTGT
||||||| ||||
TCACGAACCGT TGATA
GTGT
GAM2013 TTTY9 3' AGTACAATATTGCCTGT 25676 TT
GC GGCAATATTGTACT
|| |||||||||
TG CCGTTATAACATGA
T_
GAM2013 LOC146287 5' AGTCTATACTGCCAGGCACTAT 40688 A TGT
ATAGTGCTTGGCA TAT ACT
||||||| ||| |||
TATCACGGACCGT ATA TGA
C TC_
GAM2013 LOC253039 3' AGTACAATATTGCCGATGC 45992 _
GC TTGGCAATATTGTACT
|| |||||||||
CG AGCCGTTATAACATGA
T
GAM2013 LOC257235 5' ACAACATACTAGGCACT 46371 CA A
AGTGCTTGG AT TTGT
|||||| || ||||
TCACGGATC TA AACA
A_ C
GAM2014 ATP2B2 3' TGGTCTGTGAGTTTTTGAA 7405 _ TC
TTCAAAGACT GCA CCA
||||||| ||| |||
AAGTTTTTGA TGT GGT
G CT
GAM2014 CLN5 5' TTGGGCAGGTCTTTGAA 13232 GCAT
TTCAAAGACT CCCAA
||||||| ||||
AAGTTTCTGG GGGTT
AC____
GAM2014 CTSB 3' TGTTGGGAGCCCTTTGGA 32329 ACT A
TTCAAAG GC TCCCAACA
|||||| || |||||||
AGGTTTC CG AGGGTTGT
C_ _
GAM2014 EN1 3' GTTGAAACGCAGCATTTTTTGAA 7142 _ ATCC
TTCAAAGA CTGC CAAC
|||||| ||| ||||

			AAGTTTTT GACG GTTG		
			AC CAAA		
GAM2014 KCNA6	3'	TGGGTGCAGTTCTGAA	8019	AA	T
		TTCA GACTGCA CCCA			
		AAGT TTGACGT GGGT			
		C_ _			
GAM2014 RYR3	3'	TGTTGGGATGGAAGCATGAA	6701	AAGA	G_
		TTCA CT CATCCCAACA			
		AAGT GA GTAGGGTTGT			
		AC_ AG			
GAM2014 TMEM2	3'	TGTTGGGACCATTTTTG	15043	C	CA
		CAAAGA TG TCCCAACA			
		GTTTTT AC AGGGTTGT			
		_ C_			
GAM2014 TNFRSF9	3'	TGTTGGGACTTTCTTGAA	7290	A	CTGCA
		TTCAA GA TCCCAACA			
		AAGTT CT AGGGTTGT			
		_ TTC_			
GAM2014 C20orf29	3'	GTTGGGATGGTGCTTCTGAG	20359	_	ACTG
		TTCA AAG CATCCCAAC			
		GAGT TTC GTAGGGTTG			
		C GTG_			
GAM2014 DJ971N18.2	3'	TGTTGGGATCTGTTTGGA	22137	AA	TGC
		TTCA GAC ATCCCAACA			
		AGGT TTG TAGGGTTGT			
		_ TC_			
GAM2014 DKFZP434A0131	3'	TGTTGGGAAAGTCGTTGAA	21064	A	GCA
		TTCAA GACT TCCCAACA			
		AAGTT CTGA AGGGTTGT			
		G A_			
GAM2014 ESM1	3'	TGTTGGGATATGGAATGAA	13915	AAGA	GC
		TTCA CT ATCCCAACA			
		AAGT GG TAGGGTTGT			
		AA_ TA			
GAM2014 FLJ13910	3'	TGTTGGAATCCTCTTTGAA	23058	CTGC	C
		TTCAAAGA ATCCAACA			
		AAGTTTCT TA GGTTGT			
		CC_ A			
GAM2014 GGA2	3'	GTTGCGTAGTCTTGAA	17403	A	ATCC
		TTCAA GACTGC CAAC			

			AAGTT CTGATG GTTG		
			— C—		
GAM2014	GGA2	3'	GTTGCGTAGTCTTGAA 28925	A	ATCC
			TTCAA GACTGC CAAC		
			AAGTT CTGATG GTTG		
			— C—		
GAM2014	gm117	3'	TGTTGAAATGTTTCTTTGGA 38537	CT	CC
			TTCAAAGA GCAT CAACA		
			AGGTTTCT TGTA GTTGT		
			T— AA		
GAM2014	HSU24186	5'	TGTTGGGAAAGGCTTCTTGAA 14992	A CT	A—
			TTCAA GA GC TCCCAACA		
			AAGTT CT CG AGGGTTGT		
			— T— GAA		
GAM2014	KIAA0057	3'	TGTTGAGTGTCTTTGGA 14629	CT	CC
			TTCAAAGA GCAT CAACA		
			AGGTTTCT TGTG GTTGT		
			— A—		
GAM2014	KIAA0483	3'	TGTTGGGAAGGTAATTTT 17531	C	A—
			AAGA TGC TCCCAACA		
			TTTT ATG AGGGTTGT		
			A GA		
GAM2014	MGC10960	3'	TGAGATCAGGCTCTTTGAG 26385	— C	C
			TTCAAAGA CTG ATC CA		
			GAGTTTCT GAC TAG GT		
			CG — A		
GAM2014	MGC13159	3'	TGTTGCCCAGGCTGTCTTTGAA 26753	T	ATCC—
			TTCAAAGAC GC CAACA		
			AAGTTTCTG CG GTTGT		
			T GACCC		
GAM2014	MGC2721	3'	TTGAGAATTGAGTCTTTGGA 26464	G —	C
			TTCAAAGACT CA TC CAA		
			AGGTTTCTGA GT AG GTT		
			— TA A		
GAM2014	MGC29937	3'	TGTTGGGGGGCCTTTGA 29411	ACT	AT
			TCAAAG GC CCCAACA		
			AGTTTC CG GGGTTGT		
			— GG		
GAM2014	PDE8A	3'	TGGGACTTTGATATTTTGA 31381	CTG	—
			TTCAAAGA CA TCCCA		

		AAGTTTTT GT AGGGT		
		ATA TTC		
GAM2014	RASSF2	3' TGGTCTTGCAGTTTTGAA	16399	A TC_
		TTCAA GACTGCA CCA		
		AAGTT TTGACGT GGT		
		_ TCT		
GAM2014	RYK	3' TGTCTGGTAAGTCTTTGAA	40207	GCAT CA
		TTCAAAGACT CC ACA		
		AAGTTTCTGA GG TGT		
		AT__ TC		
GAM2014	VMP1	3' TTGGGATGTTTTTTGA	25207	ACT
		TCAAAG GCATCCCAA		
		AGTTTT TGTAGGGTT		

GAM2014	LOC151647	3' TGTTGGCGTAATTTTTGAA	39159	C ATC
		TTCAAAGA TGC CCAACA		
		AAGTTTTT ATG GGTTGT		
		A C__		
GAM2014	LOC158263	3' TGTTTGATGCATCTTTGAA	39800	C CC
		TTCAAAGA TGCATC AACA		
		AAGTTTCT ACGTAG TTGT		
		_ T_		
GAM2014	LOC158714	5' TTGAGGATGGAATCTTTGAG	39887	CTG _
		TTCAAAGA CATCC CAA		
		GAGTTTCT GTAGG GTT		
		AAG A		
GAM2014	LOC168667	3' TGTTGGTTCTCATCTTTGAA	44570	C CATC
		TTCAAAGA TG CCAACA		
		AAGTTTCT AC GGTTGT		
		_ TCTT		
GAM2014	LOC201229	5' TGTTAAAATGCAGGTTTGA	42545	GA CCC
		TCAA CTGCAT AACA		
		AGTTT GACGTA TTGT		
		G_ AAA		
GAM2014	LOC256821	5' GGATGGAACCAATCTTTGAG	46639	C ____
		TTCAAAGA TG CATCC		
		GAGTTTCT AC GTAGG		
		A CAAG		
GAM2014	LOC51141	5' GTTGAAGCGTCAGTCTTTGA	34049	_ ATCC
		TCAAAGACTG C CAAC		

AGTTTCTGAC G GTTG
 T CGAA
 GAM2015 VPS26 3' ACTTTGGCTAGTTAACTCATA 11325 TCAAGC _
 TATGA GAC AGCCAAAGT
 ||||| ||| |||||
 ATACT TTG TCGGTTTCA
 CAAA_ A
 GAM2015 C20orf42 3' GACTTTGGCTTTTGTAAATCA 19214 CAA C
 TGAT GCGA AGCCAAAGTC
 ||||| ||||| |||||
 ACTA TGTT TCGGTTTCAG
 AA_ T
 GAM2015 HCGIV.9 3' ACTTTGGTCCCTTGACATA 21055 A C ACA
 TATG TCAAG G GCCAAAGT
 ||||| ||||| | |||||
 ATAC AGTTC C TGGTTTCA
 _ C _
 GAM2015 MAFB 3' ACTTTAGCATGTTGTTGATCAT 11942 G _ C
 G
 TATGATCAA CGACA GC AAAGT
 ||||| ||||| || |||||
 GTACTAGTT GTTGT CG TTTCA
 _ A A
 GAM2015 PSTPIP2 3' GACTTAGAAGCCGCCTGATCAT 23681 A ACA CA_
 A
 TATGATCA GCG GC AAGTC
 ||||| ||||| || |||||
 ATACTAGT CGC CG TTCAG
 C _ AAGA
 GAM2015 LOC148195 5' GACTTTGGCTGTTTAATCA 40876 CAAGC
 TGAT GACAGCCAAAGTC
 ||||| ||||| |||||
 ACTA TTGTCGGTTTCAG
 AT_
 GAM2015 LOC253981 3' GACTTTGGATTCCCTTGACCA 45864 A C CAG
 TG TCAAG GA CCAAAGTC
 || ||||| || |||||
 AC AGTTC CT GGTTCAG
 C _ TA_
 GAM2015 LOC90183 3' ACTTTAGCATGTTGTTGATCAT 30925 G _ C
 G
 TATGATCAA CGACA GC AAAGT
 ||||| ||||| || |||||
 GTACTAGTT GTTGT CG TTTCA
 _ A A
 GAM2016 FGFR1 3' CATTGTCCCTGAATGCTCCA 23360 A GA AT
 TG AGCATTC AGG GCAATG
 || ||||| || |||||
 AC TCGTAAG TCC TGTTAC
 C _ C_
 GAM2016 FGFR1 3' CATTGTCCCTGAATGCTCCA 23365 A GA AT
 TG AGCATTC AGG GCAATG
 || ||||| || |||||

AC TCGTAAG TCC TGTTAC
 C _ C_
 GAM2016 LASS2 3' GCATTGCACCCTGGTGT 33625 CGA A
 GCATT AGG TGCAATGC
 |||| || |||||
 TGTGG TCC ACGTTACG
 _ C
 GAM2016 PRSS8 5' CACTGCTCGCTTCGGATACTCC 8663 A C _ T A
 A TG AG ATT CGAAG GA GCA TG
 || || ||||| || || ||
 AC TC TAGGCTTC CT CGT AC
 C A G _ C
 GAM2016 DKFZP564K0322 5' GCCGTCCCCCGACTGCCTCA 25740 A T AA _
 TGA GCA TCG GGATG C
 || || || |||| |
 ACT CGT AGC CCTGC G
 C C CC C
 GAM2016 FLJ23511 5' GCACTTCAAATGCTTCA 25966 C GA
 TGAAGCATT GAAG TGC
 ||||| || ||
 ACTTCGTAA CTTC ACG
 A _
 GAM2016 MGC12904 5' CATTTCCCAAGTGCTTCA 25267 CGAA TGC
 TGAAGCATT GGA AATG
 ||||| || ||
 ACTTCGTGA CCT TTAC
 AC _ _
 GAM2016 SLC5A7 3' CATTGCATTCAAAATCTTCA 22391 C CGAA
 TGAAG ATT GGATGCAATG
 |||| || |||||
 ACTTC TAA CTTACGTTAC
 _ AA _
 GAM2016 Spir-1 3' GCATTGTATGCCTCAAATGTCT 32307 AG C A _
 CA TGA CATT GA GG ATGCAATGC
 || || || || |||||
 ACT GTAA CT CC TATGTTACG
 CT A _ G
 GAM2016 LOC163682 3' GCACCAGAGGCCTTCGAAGCCC 42092 AA A ATGCAA_
 CA TG GC TTCGAAGG TGC
 || || ||||| ||
 AC CG AAGCTTCC ACG
 CC _ GGAGACC
 GAM2016 LOC93589 3' GCACCACTTTCAAGATGCTTCA 35979 C_ A_
 TGAAGCATT GAAGG TGC
 ||||| || ||
 ACTTCGTAG CTTTC ACG
 AA ACC
 GAM2017 FGF2 3' CCATAATCGTGCCAC 7734 A TAT
 GTG GCACGATTA TGG
 || ||||| ||

CAC CGTGCTAAT ACC

GAM2017 PPP1R3A 3' ATCCAATATGTTTCCATCAC 8565 GCAC T_
GTGA GA TATATTGGAT
|||| || ||||||||
CACT CT GTATAACCTA
AC__ TT

GAM2017 UBL3 3' ATCCAGTGTGTCATGCTTAC 13964 C TAT
GTGAGCA GAT ATTGGAT
|||||| || ||||||
CATTCGT CTG TGACCTA
A ____

GAM2017 Nup43 3' CCAAGATCGTGCCAC 23933 A ATA
GTG GCACGATT TTGG
|| |||||| ||||
CAC CGTGCTAG AACC

GAM2017 PPP1R13B 3' GTCTTAATGGTGCTCAC 17632 G TATT
GTGAGCAC ATTA GGAT
|||||| |||| ||||
CACTCGTG TAAT TCTG
G ____

GAM2017 LOC148932 3' ATCCAATATCATGCCCCAC 38623 A_ C TTA
GTG GCA GA TATTGGAT
|| |||| || ||||||
CAC CGT CT ATAACCTA
CC A ____

GAM2017 LOC158376 5' CCAGGGAATCTGTGCTCAC 41972 _ ATA
GTGAGCAC GATT TTGG
|||||| |||| ||||
CACTCGTG CTAA GACC
T GG_

GAM2017 LOC221042 5' ATCCAATGCCTCGAGCCCAC 44751 A A TTA
GTG GC CGA TATTGGAT
|| || || ||||||
CAC CG GCT GTAACCTA
C A CC_

GAM2018 EGR3 3' TCCTTCTGGTATATGCATGTCA 29957 A CTGT
TGACATGCATATA CA GGA
|||||||||| || ||||
ACTGTACGTATAT GT TCCT
G CT__

GAM2018 IHPK3 5' CCCACAGTACAAAGGTACCGTC 27657 A_ ATATAAC
A TGAC TGC ACTGTGGG
|||| || ||||||
ACTG ATG TGACACCC
CC GAAACA_

GAM2018 MEIS2 3' CCCACAATGTAAATTCTGT 21347 TGC A C
ACA AT TAACA TGTGGG
|| || |||| ||||||

TGT TA ATTGT ACACCC
 CT_ A A
 GAM2018 PCSK2 3' CCACAGTTTGATGTCA 8456 G TATAAC
 TGACAT CA ACTGTGG
 ||||| || |||||
 ACTGTA GT TGACACC
 _ T____
 GAM2018 TAPBP 3' CCATGGTGTCAATACATATCA 9178 C C ATA
 TGA ATG AT ACACTGTGG
 ||| ||| || |||||
 ACT TAC TA TGTGGTACC
 A A AC_
 GAM2018 KIAA0934 3' CCTTTGCTATATGCAGTCA 32119 A A CTGT
 TGAC TGCATATA CA GGG
 ||| ||||| || |||
 ACTG ACGTATAT GT TCC
 _ C T____
 GAM2018 KIAA1184 3' CCCACAGTCTTGCAAGGTCA 22895 A TATAAC
 TGAC TGCA ACTGTGGG
 ||| ||| |||||
 ACTG ACGT TGACACCC
 G TC____
 GAM2018 PPP1R16B 3' TCCGGATCAGTACATGCATGTC 30777 ATAAC TG____
 A TGACATGCAT ACTG GGA
 ||||| ||| |||
 ACTGTACGTA TGAC CCT
 CA____ TAGG
 GAM2018 RPS6KC1 3' CCAGGGGCTGTTATATACAT 14799 C ____ G
 ATG ATATAACA CT TGG
 ||| ||||| || |||
 TAC TATATTGT GG ACC
 A CG G
 GAM2018 LOC157421 5' CCCACCAAGCTTATATGCTGCC 41794 A T CACT_
 A TG CA GCATATAA GTGGG
 || || ||||| |||||
 AC GT CGTATATT CACCC
 C _ CGAAC
 GAM2018 LOC158267 3' TCCCACAGCACTCGGTGCCTGT 39795 T ATAACA
 CA TGACA GCAT CTGTGGGA
 ||||| ||| |||||
 ACTGT CGTG GACACCCT
 C GCTCAC
 GAM2019 SEPX1 3' CAGGCCTGGGCTGTGCAGC 18457 A A G A_
 GCTG CA C AGTTTA CCTG
 ||| || ||||| |||
 CGAC GT G TCGGGT GGAC
 _ _ _ CC
 GAM2019 SLC1A3 3' GCAGGTTATGCAAGTCGCCAGG 10383 GACA_ GA T
 C GCT AC GT TAACCTGC
 ||| || || |||||

		CGG TG CG ATTGGACG	
		ACCGC AA T	
GAM2019	TARBP2	3' GCAGGCCTTTACGTCAGCTA 28628	AAC TTAA
		TAGCTGAC GAG CCTGC	
		ATCGACTG CTT GGACG	
		CA_ TCC__	
GAM2019	CEP3	3' AAATTTTGACTGTCAGCTA 13155	AC__
		TAGCTGACA GAGTTT	
		ATCGACTGT TTAAA	
		CAGT	
GAM2019	FLJ20300	3' CAGGTGCCACTGTCAGCT 19365	ACGA TTA
		AGCTGACA GT ACCTG	
		TCGACTGT CA TGGAC	
		____ CCG	
GAM2019	KIAA0433	5' AGACCTGTGCGTCAGCTA 17546	A_ A
		TAGCTGAC ACG GTTT	
		ATCGACTG TGT CAGA	
		CG C	
GAM2019	SNTG1	5' CAGATTAAACTCTCAGC 21038	CAAC C
		GCTGA GAGTTTAA CTG	
		CGACT CTCAAATT GAC	
		____ A	
GAM2019	LOC150225	3' CAGAAGCCAGTTGTCAGCTA 41187	GA AAC
		TAGCTGACAAC GTTT CTG	
		ATCGACTGTTG CGAA GAC	
		AC ____	
GAM2019	LOC91526	5' CAGATTAATGTTGTCAAGC 32971	_ AGT C
		GCT GACAACG TTAA CTG	
		CGA CTGTTGT AATT GAC	
		A ____ A	
GAM2020	PROS1	3' ATAATACACCTGGAAGTT 42254	- -
		AGCT CCAG TGTATTAT	
		TTGA GGTC ACATAATA	
		A C	
GAM2020	STK24	3' TGATAACTCCCTCTGGAGCTT 9628	TGTATTATA
		AAGCTCCAG TTATCA	
		TTCGAGGTC AATAGT	
		TCCCTC__	
GAM2020	SWAP70	3' TGATAACATGACCTGGGGCTT 35351	T AT A
		AAGCTCCAG GT TAT TTATCA	

TTCGGGGTC CA GTA AATAGT
 — — C
 GAM2020 DKFZP564I122 3' GATAATATAGTAGAG 31646 CAGTG
 CTC TATTATATTATC
 ||| |||||
 GAG ATGATATAATAG

 GAM2020 FLJ22724 3' TGATATATGTAATATACCAGAG 23737 CA —
 C GCTC GTGTATTATAT TATCA
 ||| |||||
 CGAG CATATAATGTA ATAGT
 AC T
 GAM2020 HHLA2 5' TGATGTGGAATATACTAAAGC 13938 CC ATAT
 GCT AGTGTATT TATCA
 ||| |||||
 CGA TCATATAA GTAGT
 AA GGT_
 GAM2020 KIAA0871 3' TGATAACATAATAATGTGGACG 17335 — GTG A
 C GC TCCA TATTAT TTATCA
 || ||| |||||
 CG AGGT ATAATA AATAGT
 C GTA C
 GAM2020 KIAA0931 3' ATAATATGAGCCAGAGC 33482 CAG TA
 GCTC TG TTATATTAT
 ||| || |||||
 CGAG AC AGTATAATA
 — CG
 GAM2020 PTD012 3' TGAGGCAGGAAGCACACTGGAG 15270 A_ ATATTA
 C GCTCCAGTGT TT TCA
 ||||| || |||
 CGAGGTCACA AA AGT
 CG GGACGG
 GAM2020 TAF9L 3' TGATAAGTAATTACACTGGACC 18074 C TTATA
 T AG TCCAGTGTA TTATCA
 || ||||| |||||
 TC AGGTCACAT AATAGT
 C TAATG
 GAM2020 LOC152765 3' AATAACTGTGCACTGAGCT 39311 C TA_
 AGCTC AGTGTAT TATT
 |||| ||||| |||
 TCGAG TCACGTG ATAA
 — TCA
 GAM2020 LOC203286 5' AATATACTGGTATAGCTT 43493 —
 AAGCT CCAGTGTATT
 |||| |||||
 TTCGA GGTCATATAA
 TAT
 GAM2021 DNMT3B 3' CCACAGTGCCGACAGCTCT 13763 A CGC
 AGA CTGTTGGCAC GG
 ||| ||||| ||

			TCT GACAGCCGTG CC		
			C ACA		
GAM2021	PDE4D	5'	GAGCCACGGTGCCAGGACCATC 36432	ACTG_	C
		T	AGA TTGGCACCG GGCTC		
			TCT GACCGTGGC CCGAG		
			ACCA G A		
GAM2021	IRF7	3'	GTCCAGCGCCAACAGCCTCT 10251	A_	ACC _ _
			AGA CTGTTGGC GC GG C		
			TCT GACAACCG CG CC G		
			CC _ _ A T		
GAM2021	KIAA0226	3'	AGCCGAACCTCAACAGTCTC 31786	_	CACCG
			GA ACTGTTGG CGGCT		
			CT TGACAACT GCCGA		
			C CAA_		
GAM2021	KIAA0433	5'	GAGTATTTGCCAACAGTC 17548	A	CCGCG
			GA CTGTTGGCA GCTC		
			CT GACAACCGT TGAG		
			_ TTA_		
GAM2021	VPS39	3'	GCCCAGCACCAACAGTTTT 31470	CACC _	
			AGAACTGTTGG GC GGC		
			TTTTGACAACC CG CCG		
			A_ AC		
GAM2021	ZDHHC3	5'	GAGCCGCGGCGCCTCGTTC 18688	TGTT A	
			GAAC GGC CCGCGGCTC		
			CTTG CCG GGC GCGAG		
			CT_ C		
GAM2021	LOC200213	5'	GAACCGTGGCCAACAGTTC 42740	AC C	
			GAAC TGTGGC CGCGG TC		
			CTTGACAACCG GTGCC AG		
			_ A		
GAM2021	LOC222161	5'	AGCCACAAGGAACAGTTCT 44580	GGCA GC_	
			AGAACTGTT CC GGCT		
			TCTTGACAA GG CCGA		
			_ AACAA		
GAM2022	NELL2	3'	AGAATGTTCTTTTCATTAA 12812	A C	
			TTAATGAAA AACAA TCT		
			AATTACTTT TTGT AGA		
			C A		
GAM2022	AWP1	3'	GCTGCTTCTGTTTTTTCATTAA 21080	CTCTCT	
			TTAATGAAAAAACA CAGC		

			AATTACTTTTTTGT	GTCG		
			CTTC__			
GAM2022	FLJ10520	3'	CTTAGAGAGTGTCTCTCAT	19904	AAAA	C
			ATGA ACACTCTCT AG			
			TACT TGTGAGAGA TC			
			CTCC T			
GAM2022	FLJ13657	3'	CTGAGAAAACTTTTTTATTAA	24219	ACACTC	
			TTAATGAAAAA TCTCAG			
			AATTATTTTTT AGAGTC			
			CAAAA_			
GAM2022	OSBPL8	3'	GCTGATAATTTATGTTTTTTCA	21908	CTCTC__	
	TTA		TAATGAAAAACA TCAGC			
			ATTACTTTTTTGT AGTCG			
			ATTTAAT			
GAM2022	PRO2964	3'	GCTGATCTGTATTTTCATTAA	20631	A CTCTC	
			TTAATGAAAA ACA TCAGC			
			AATTACTTTT TGT AGTCG			
			A CT__			
GAM2022	LOC146237	3'	GCTGAGAGAAGTTCCTCAT	40668	AAA AC	
			ATGA AAC TCTCTCAGC			
			TACT TTG AGAGAGTCG			
			CC_ A_			
GAM2022	LOC158381	3'	GCTGCTTCTGTTTTTTCATTAA	35176	CTCTCT	
			TTAATGAAAAAACA CAGC			
			AATTACTTTTTTGT GTCG			
			CTTC__			
GAM2022	LOC89231	3'	GCTGAGAGAGATGGGGTCTCA	44551	AAAAA _	
			TGA CA CTCTCTCAGC			
			ACT GT GAGAGAGTCG			
			CTGGG A			
GAM2023	CCR5	3'	AGAAGCCTCACTGCAAGC	6182	A ATTTA	
			GCTT CAGTGAGG TCT			
			CGAA GTCACTCC AGA			
			C GA__			
GAM2023	KIAA0310	5'	CAGACGAGACCACTGTGAGCCA	39708	GA A TA	
			TGGCTTACAGT GG TT TCTG			
			ACCGAGTGTCA CC GA AGAC			
			_ A GC			
GAM2023	POLD3	3'	GAATTCTCACTGAAGCCA	44053	A	
			TGGCTT CAGTGAGGATTT			

ACCGAA GTCACTCTTAAG

GAM2023 LOC161357 3' AAAACCTCACTGTAAACA 40016 GC A
TG TTACAGTGAGG TTT
|| ||||| |||
AC AATGTCACTCC AAA
A_ A

GAM2024 APM1 3' GGTTTCCCTCCCGATATCA 11213 A__
TGATATCGG GGAAACT
||||| |||||
ACTATAGCC CCTTTGG
CTC

GAM2024 ARHGAP6 3' GGGATAACCCTTCCTTCGATAC 15085 A ACTAT_
CA TG TATCGGAGGAA TCCC
|| ||||| |||
AC ATAGCTTCCTT AGGG
C CCAAT

GAM2024 ARHGAP6 3' GGGATAACCCTTCCTTCGATAC 6847 A ACTAT_
CA TG TATCGGAGGAA TCCC
|| ||||| |||
AC ATAGCTTCCTT AGGG
C CCAAT

GAM2024 LIMD1 3' GGAATAGATCCGATTCA 15500 T GGAAA
TGA ATCGGA CTATTCC
|| ||||| |||||
ACT TAGCCT GATAAGG
_ A__

GAM2024 VCL 3' GGATGTGCTTTTCTCCAATATC 15193 C C _
A TGATAT GGAGGAAA TAT TCC
||||| ||||| ||| |||
ACTATA CCTCTTTT GTG AGG
A C T

GAM2024 VCL 3' GGATGTGCTTTTCTCCAATATC 9404 C C _
A TGATAT GGAGGAAA TAT TCC
||||| ||||| ||| |||
ACTATA CCTCTTTT GTG AGG
A C T

GAM2024 BHLHB2 3' GAATAGCCCCCTTCGATACA 9754 A AAA
TG TATCGGAGG CTATTC
|| ||||| |||||
AC ATAGCTTCC GATAAG
_ CCC

GAM2024 BPES 3' GGCTGCGTTTCCTCCGCTATCA 23325 T TATT
TGATA CGGAGGAAAC CC
||||| ||||| |||
ACTAT GCCTCCTTTG GG
C CGTC

GAM2024 FLJ11722 3' AATAGTTTCCCAGTATTA 24518 CGGA
TGATAT GGAAACTATT
||||| |||||

		ATTATG CCTTTGATAA		
		AC__		
GAM2024	pcnp	3' GGAACAGTTTCCTTTTTTA	21629 TC	A
		TA GGAGGAAACT TTCC		
		AT TTTCCTTTGA AAGG		
		TT C		
GAM2024	ZNF297B	3' GGAATAGTCTCTTCTCTTCA	15221 TATC	A
		TGA GGAGGA ACTATTCC		
		ACT TCTTCT TGATAAGG		
		TC__ C		
GAM2024	LOC150139	5' GGAATAGTTTCCAGATA	38859 GGA	
		TATC GGAAACTATTCC		
		ATAG CCTTTGATAAGG		
		A__		
GAM2024	LOC92597	3' GAATAGTTTCCTGATGTCA	34675 GG	
		TGATATC AGGAAACTATTC		
		ACTGTAG TCCTTTGATAAG		
		—		
GAM2025	UMP-CMPK	3' AATCTTTCATAACTACATCTCA	18426 TAATCTGG	
		TGAGATGT GAAAGATT		
		ACTCTACA CTTTCTAA		
		TCAATA__		
GAM2025	LOC151959	5' TCTGACCGACTAACATCT	41409 A T GAA	
		AGATGTTA TC GG AGA		
		TCTACAAT AG CC TCT		
		C _ AG_		
GAM2025	LOC203197	3' TCCTTGTTTGACATCTCA	43011 TCT	
		TGAGATGTAA GGGA		
		ACTCTACAGTT TCCT		
		TGT		
GAM2025	LOC221431	3' AATCTTCCCCAGATTCATCT	44220 TT A	
		AGATG AATCTGGG AAGATT		
		TCTAC TTAGACCC TTCTAA		
		— C		
GAM2025	LOC93589	3' AATCTTTCATTTAACA	35975 TCTG	
		TGTTAA GGAAAGATT		
		ACAATT CCTTTCTAA		
		TA__		
GAM2026	LYPLA1	3' GTAGTTACCATACAGATTA	13029 T A	
		TAATCTGTATG TAAT AC		

		ATTAGACATAC ATTG TG		
		C A		
GAM2026	BM-002	3' TGGCCTTGTCAACATACAGA 18727	A	___
		TCTGTATGTT ATAA CCA		
		AGACATACAA TGTT GGT		
		C CC		
GAM2026	DKFZP564I052	3' GTTTTGGCATACAGTTTA 33139	T	T
		TAA CTGTATGTTAA AAC		
		ATT GACATACGGTT TTG		
		T _		
GAM2026	ERMAP	3' TTGGTTATCAGTTTGCAGAT 20610	TG	A
		ATCTGTA TT ATAACCAA		
		TAGACGT GA TATTGGTT		
		TT C		
GAM2026	FLJ13441	5' TGGTTATTACAAGAGATT 23400	GTA	T
		AATCT TGT AATAACCA		
		TTAGA ACA TTATTGGT		
		GA_ _		
GAM2026	FLJ14751	3' GTTGGTTATTGTTTACA 26610	TGT	
		TGTA TAATAACCAAC		
		ACAT GTTATTGGTTG		
		TT_		
GAM2026	NAG14	3' TGGTTAAAAAAACAGATTA 22707	ATG	AA
		TAATCTGT TT TAACCA		
		ATTAGACA AA ATTGGT		
		AA_ AA		
GAM2026	NAPG	3' GTTATGGAAATACAGATTA 46252	GTTA	
		TAATCTGTAT ATAAC		
		ATTAGACATA TATTG		
		AAGG		
GAM2026	LOC91115	3' GGTTATGTTATCTACAGATTA 32398	T	TA_
		TAATCTGTA GT ATAACC		
		ATTAGACAT TA TATTGG		
		C TTG		
GAM2027	FLJ13769	3' CCAAAAACCATGTACTAACTTA 24589	TA	GC C
		TAAGTTAGT AT GGTTTT GG		
		ATTCAATCA TG CCAAAA CC		
		_ TA A		
GAM2028	HIC2	3' CGCCCCATCAGCACTTAAGCCA 32527	ATTC	A_ A_
		TGGCTTAAGT GC ATG GCG		

ACCGAATTCA CG TAC CGC
 _____ AC CC
 GAM2029 HPSE 3' GCTGTATATTTATCTTTCA 13479 T CAATTT
 TG AAGAT ATATACAGC
 || |||| |||||
 AC TTCTA TATATGTCG
 T TT____
 GAM2029 DAMS 5' AGCTGTATAGGAACAATCACAC 22542 AA CAA A
 A TGT GAT TTT TATACAGCT
 ||| ||| ||| |||||
 ACA CTA AAG ATATGTCGA
 CA AC_ G
 GAM2029 FLJ13262 3' GCTGCATAAAATCTTGCA 24434 CAA ATA
 TGTAAGAT TTTAT CAGC
 ||||| |||| |||
 ACGTTCTA AAATA GTCG
 _____ C____
 GAM2029 SRPK1 3' AGCTGTAGATCTTGATCTTCCA 9108 T TTTATA
 TG AAGATCAA TACAGCT
 || ||||| |||||
 AC TTCTAGTT ATGTCGA
 C CTAG____
 GAM2030 PLAG1 3' GCACTCATTAGCCCTATA 8524 G CTTTTA
 TATAGGGC TAATG GC
 ||||| |||| ||
 ATATCCCG ATTAC CG
 _____ TCA____
 GAM2030 OSBPL8 3' CTAAAAGCATGCATCTA 21907 GC A
 TAGG GTA TGCTTTTAG
 |||| ||| |||||
 ATCT CGT ACGAAAATC
 A_ _
 GAM2031 CEACAM1 3' TTAGGCCTAAGAGGCTTTCTCC 7442 A T G
 A TG AGAA GCCTCTTGGG CCTAA
 || |||| ||||| |||||
 AC TCTT CGGAGAATCC GGATT
 C T _
 GAM2031 EPHB2 3' CCAAGTTGGAAAACACTCTTCA 10734 A ____ T_
 TGAAGA TG CC CTTGG
 ||||| || || |||||
 ACTTCT AC GG GAACC
 C AAAA TT
 GAM2031 LETM1 3' AGGCCCTGGGCTCCTTCA 14695 AAT CTT
 TGAAG GCCT GGGGCCT
 |||| ||| |||||
 ACTTC CGGG CCCC GGA
 CT_ T____
 GAM2031 LYZ 3' TTAAGCCTACAACATTTTCA 5759 CCTC _ C
 TGAAGAATG TTG GGGC TAA
 ||||| ||| ||||| |||

ACTTTTAC AAC TCCG ATT
 _____ A A
 GAM2031 MAP1B 3' AGGCAGTAGGCATTCTTTA 12533 _ TGGG
 TGAAGAATGCCT CT GCCT
 ||||| || ||||
 ATTTCTTACGGA GA CGGA
 T _____
 GAM2031 MAP1B 3' AGGCAGTAGGCATTCTTTA 25711 _ TGGG
 TGAAGAATGCCT CT GCCT
 ||||| || ||||
 ATTTCTTACGGA GA CGGA
 T _____
 GAM2031 PCDH1 5' TTAGGCCCCACCTAACTCTTC 26201 ATGCCTCT
 GAAGA TGGGGCCTAA
 |||| |||||
 CTTCT ACCCCGGATT
 CAATCC____
 GAM2031 PIP5K1A 3' AGACCCCCATTCTTCA 9602 CCTCTT C
 TGAAGAATG GGGG CT
 ||||| ||| ||
 ACTTCTTAC CCCC GA
 _____ A
 GAM2031 TGFBR2 3' TCCAAGAAGCTTTCCTCA 9245 A T C
 TGA GAA GC TCTTGGG
 ||| ||| |||||
 ACT CTT CG AGAACCT
 C T A
 GAM2031 USP6 5' AGGCCCTGTGCACGTCCTCA 43808 A A_ CTCT
 TGA GA TGC TGGGGCCT
 ||| ||| |||||
 ACT CT ACG GTCCCGGA
 C GC T____
 GAM2031 BTBD2 3' AGGCCCTGTGGAGACAATCCCT 19439 A_ A C _
 CA TGA GA TG CTCT TGGGGCCT
 ||| ||| ||| |||||
 ACT CT AC GAGG GTCCCGGA
 CC A A T
 GAM2031 C20orf140 3' TTAGGGAACAAGAGGCATCACT 29445 AGA GGG
 CA TGA ATGCCTCTTG CCTAA
 ||| ||||| ||||
 ACT TACGGAGAAC GGATT
 CAC AAG
 GAM2031 C20orf183 3' AGGCCCAGGGGACTCTCTCCA 25061 A ATG_ TG
 TG AGA CCTCT GGGCCT
 || ||| |||| |||||
 AC TCT GGGGA CCCGGA
 C CTCA ____
 GAM2031 DKFZp434F142 3' TTAGGCCCCGCTCATTCTTA 25997 A CCTCT
 TGA GAATG TGGGGCCTAA
 ||| |||| |||||

ATT CTTAC GCCCCGGATT
 C TC___
 GAM2031 DKFZP434J193 5' CCAAGGGGAGACATTGCTCCA 35163 A _ _
 TG AG AATG CCTCTTGG
 || || ||| |||||
 AC TC TTAC GGGGAACC
 C G AGA
 GAM2031 DKFZP434L187 5' CCAGTGGGAAAAACATTCTTC 34119 _____ C
 GAAGAATG CCT TTGG
 ||||| ||| |||
 CTTCTTAC GGG GACC
 AAAAA T
 GAM2031 DKFZP564C196 3' AGGTGAAGAGGCACTTTCA 34709 AA GGG
 TGAAG TGCCTCTT GCCT
 |||| ||||| |||
 ACTTT ACGGAGAA TGGA
 C_ G_
 GAM2031 KCND1 5' TAGGCAGTCCCAAGACACCTTT 11426 AA CC _
 CA TGAAG TG TCTTGGG GCCTA
 |||| || ||||| ||||
 ACTTT AC AGAACCC CGGAT
 CC _ TGA
 GAM2031 KIAA0155 3' TAAGCCCCAAGAGACATTT 16003 C C
 GAATG CTCTTGGGGC TA
 |||| ||||| ||
 TTTAC GAGAACCCCG AT
 A A
 GAM2031 KIAA0169 5' GCAGAGGGAGGCACTTTCA 36052 AA GGG
 TGAAG TGCCTCTT GC
 |||| ||||| ||
 ACTTT ACGGAGGG CG
 C_ AGA
 GAM2031 KIAA0441 3' TTAGAGTAATAGAGAATTCTTC 16715 GC TGGG _
 A TGAAGAAT CTCT GC CTAA
 ||||| ||| || |||
 ACTTCTTA GAGA TG GATT
 A_ TAA_ A
 GAM2031 KIAA0553 3' CCAGAAGAGGCATCTCCA 34635 A A GG
 TG AGA TGCCTCTT GG
 || ||| ||||| ||
 AC TCT ACGGAGAA CC
 C _ GA
 GAM2031 KIAA1075 5' AGGCCCCAGCATTGTTCA 30917 G CTCT
 TGAA AATGC TGGGGCCT
 ||| |||| |||||
 ACTT TTACG ACCCCGGA
 G _
 GAM2031 KIAA1143 3' CCAATCAGAGGCACTTTCA 34073 AA _
 TGAAG TGCCTCT TGG
 |||| ||||| |||

ACTTT ACGGAGA ACC
 C_ CTA
 GAM2031 KIAA1280 5' TTAGGGAGAAGATAGCATTCTT 34557 C_ GGGG
 CA TGAAGAATGC TCTT CCTAA
 ||||| ||| ||||
 ACTTCTTACG AGAA GGATT
 AT GAG_
 GAM2031 KIAA1432 3' TTAGTGTGTAAAGAATGCATTTC 33159 C_ GGG _
 TTCA TGAAGAATGC TCTT GC CTAA
 ||||| ||| ||||
 ACTTCTTACG AGAA TG GATT
 TA ATG T
 GAM2031 KIAA1856 3' AGGCCCCAAGCCTTCA 44523 AATGCCT
 TGAAG CTTGGGGCCT
 |||| |||||
 ACTTC GAACCCCGGA
 C_____
 GAM2031 MGC15631 3' AGGCCCTGTGCATGTCCCCA 26490 AA _ CTCT
 TG GA ATGC TGGGGCCT
 || || ||| |||||
 AC CT TACG GTCCCGGA
 CC G T____
 GAM2031 NLI-IF 3' AGGCCCCACAGTGCAGCTTC 22172 AA CT _
 GAAG TGC CT TGGGGCCT
 ||| ||| || |||||
 CTTC ACG GA ACCCCGGA
 G_ T_ C
 GAM2031 OAZ2 3' AGGCCCCAAGGTCTCCTTC 8375 AAT CT
 GAAG GCCT TGGGGCCT
 ||| ||| |||||
 CTTC TGGA ACCCCGGA
 CTC _
 GAM2031 PGR1 3' CTAGAAGAGGCATCTTCA 27123 A GG
 TGAAGA TGCCTCTT GG
 |||| ||||| ||
 ACTTCT ACGGAGAA TC
 _ GA
 GAM2031 PRAX-1 3' CCAAGGGGAAGCAGCTCCTCA 11146 A A_ _
 TGA GA TGC CTCTTG
 ||| || ||| |||||
 ACT CT ACG GGGAACC
 C CG AAG
 GAM2031 PTRF 5' TCAAGAAGGCCTTCTCCA 31785 A T _
 TG AGAA GCCT CTTGG
 || ||| ||| |||||
 AC TCTT CGGA GAACT
 C C A
 GAM2031 SCYD1 3' GCTCCCAGGCATTCCCCA 43712 AA CTT
 TG GAATGCCT GGGGC
 || ||||| |||||

			AC CTTACGGA CCTCG		
			CC C__		
GAM2031	LOC147093	5'	AGGCTCTGAAGCACTCCCCA	40798	AA A C TT
			TG GA TGC TC GGGGCCT		
			AC CT ACG AG TCTCGGA		
			CC C A __		
GAM2031	LOC149132	5'	AGGCCCTGAACATTCTCA	38644	A CCTC TG
			TGA GAATG T GGGCCT		
			ACT CTTAC A CCCGGA		
			_ A__ GT		
GAM2031	LOC201229	5'	AGGCCTGTAGGCATTCT	42539	CTTG
			AGAATGCCT GGGCCT		
			TCTTACGGA TCCGGA		
			TG__		
GAM2031	LOC203257	5'	AGGCCTGCGCCGGCATCCTCCG	42286	A A TCTTG
			TG AG ATGCC GGGCCT		
			GC TC TACGG TCCGGA		
			C C CCGCG		
GAM2031	LOC206426	3'	AGACCCCCATTCTTCA	43115	CCTCTT C
			TGAAGAATG GGGG CT		
			ACTTCTTAC CCCC GA		
			_____ A		
GAM2031	LOC91040	3'	AGGCCCCACACAGTCTTCA	32311	A CCTCT
			TGAAGA TG TGGGGCCT		
			ACTTCT AC ACCCCGGA		
			G AC__		
GAM2031	LOC91409	3'	AGGCCCCAGCCCGGCTCCTTCA	32803	AAT TC_
			TGAAG GCC TTGGGGCCT		
			ACTTC CGG GACCCCGGA		
			CT_ CCC		
GAM2032	FLJ20298	3'	ATCCCTAGGAATTGCCTATC	19362	CT G C
			GATAGGTAAT C AG GGAT		
			CTATCCGTTA G TC CCTA		
			AG A _		
GAM2032	LOC201695	5'	ATCCTTCCAGAAATTACCTATC	43609	_ C C
			GATAGGTAA TCT GAG GGAT		
			CTATCCATT AGA CTT CCTA		
			AA C _		
GAM2033	KIAA1219	3'	GTTACCTTCTCCATACACTA	30759	A C CA
			TAGTGTATG AG AAG TGAT		

			ATCACATAC TC TTC ATTG		
			C _ C_		
GAM2033	KIAA1822	3'	ATGCTTGCTCCCCACACTA	33549	ATGA
			TAGTGT AGCAAGCAT		
			ATCACA TCGTTCGTA		
			CCCC		
GAM2033	MKP-7	5'	CCACCAGCCTGACCTCATACAC	33004	AG_ A A A
	T		AGTGTATGA CA GC TG TGG		
			TCACATACT GT CG AC ACC		
			CCA C _ C		
GAM2033	LOC199858	5'	CCATCATGGTATTCCACAC	42634	AT GCAAG
			GTGT GAA CATGATGG		
			CACA CTT GTACTACC		
			C_ ATG_		
GAM2034	CRP	3'	GTTTGCTTGCAGTGCTTTCTT	35464	GC A_
			GAGAA GGTAC CAAGCAAAC		
			TTCTT TCGTG GTTCGTTTG		
			_ AC		
GAM2034	HD	3'	TGCCTGTGTGCTCCGG	7898	A AGCG A
			TCG GA GTACACA GCA		
			GGC CT CGTGTGT CGT		
			_ _ _ C		
GAM2034	LAPTM5	3'	TGCTTGTGTCTCCCTCG	13618	AAGC T_
			CGAG GG ACACAAGCA		
			GCTC CC TGTGTTCTG		
			_ _ _ TC		
GAM2034	NONO	3'	TTTGCTTGCCCCGCCCCCGA	39901	AGAA TACA
			TCG GCGG CAAGCAAA		
			AGC CGCC GTTCGTTT		
			CCC_ CC_		
GAM2034	PCSK1	3'	GTTTGCTTATGTAATCTCACCT	6024	AAGCGG_ C
	C		GAG TACA AAGCAAAC		
			CTC ATGT TTCGTTTG		
			CACTCTA A		
GAM2034	APELIN	5'	GTCCCTGATGCCGCTTCCCGA	18872	A _ CAA
			TCG GAAGCGGTA CA GC		
			AGC CTTGCGCGT GT TG		
			C A CCC		
GAM2034	API5	3'	GTTTGCTTTTGCCACTTTC	13363	A C CAC
			GAGA G GGTA AAGCAAAC		

		CTTT C CCGT TTCGTTTG	
		_ A T _	
GAM2034	FLJ20979	5' TGCCTGCTGCTCTTCTCGG 23575	C CA A
		TCGAGAAG GGTA CA GCA	
		GGCTCTTC TCGT GT CGT	
		_ C _ C	
GAM2034	KIAA0441	3' GCTTGCCCAAGTGCTTCTTGA 16711	GTACA
		TCGAGAAGCG CAAGC	
		AGTTCTTCGT GTTCG	
		GACCC	
GAM2034	MGC15437	3' TTTGCTTGTCTTTGCCCT 26691	C C _
		AG GGTA ACAAGCAAA	
		TC CCGT TGTTGTTTT	
		C TTC	
GAM2034	LOC144079	5' CTTGCCTGCACTTCTTGA 37673	CG CA
		TCGAGAAG GTA CAAG	
		AGTTCTTC CGT GTTC	
		A _ CC	
GAM2034	LOC146455	3' TTTGCTTGCCCTGCCCCCGA 38160	AGAA TACA
		TCG GCGG CAAGCAAA	
		AGC CGTC GTTCGTTT	
		CCC _ CC _	
GAM2034	LOC152762	3' GCTCTCTGCACTGCTTCTCGA 39307	A CA _
		TCGAGAAGCGGT CA AGC	
		AGCTCTTCGTCA GT TCG	
		C CTC	
GAM2034	LOC153196	3' GTTCGCCTGATGAGGGCTCTCG 41591	A GGTA _ A A
	A	TCGAGA GC CA CA GC AAC	
		AGCTCT CG GT GT CG TTG	
		_ GGA _ A C C	
GAM2034	LOC153505	3' TGCTCATGTTGGCCTTTCTCGA 39384	C _ CA
		TCGAGAAG GGT ACA AGCA	
		AGCTCTTT CCG TGT TCGT	
		_ GT AC	
GAM2035	ATF5	5' AGTCTCTTCTCACTACAGTGT 14319	CCA TCCTT
		ACACTGTA AGA GACT	
		TGTGACAT TCT CTGA	
		CAC TCT _	
GAM2035	IL8RA	3' AGTCAAGGGTGTGTGCAG 6265	CAAG
		CTGTAC ATCCTTGACT	

		GACGTG TGGGAACTGA		
		TG__		
GAM2035	PON1	3' AGTCTCTATGATCTTGGCACA 6032	A	CTT__
		TGT CCAAGATC GACT		
		ACA GGTTCCTAG CTGA		
		C TATCT		
GAM2035	SH3BP4	3' TCAGGAACTTGACACAGTGTT 15853	AC	A T
		AACACTGT CAAG TCCT GA		
		TTGTGACA GTTC AGGA CT		
		CA A _		
GAM2035	FLJ10540	3' CAAGGATCTTAACTGTGTT 19926	T	ACC
		AACAC GT AAGATCCTTG		
		TTGTG CA TTCTAGGAAC		
		T A__		
GAM2035	FLJ11370	3' AGTCAAGGCAGGGCACAGTG 24516	A	AAGAT
		CACTGT CC CCTTGACT		
		GTGACA GG GGAAGTGA		
		C GAC__		
GAM2035	FLJ21272	3' AGGTCTTAATGCAGTGTT 24630	CC	T
		AACACTGTA AAGA CCT		
		TTGTGACGT TTCT GGA		
		AA _		
GAM2035	HSMPP8	3' GGAATCTCAGTGCAGTGT 44903	CA	_
		ACACTGTAC AGAT CC		
		TGTGACGTG TCTA GG		
		AC A		
GAM2035	KIAA0431	3' AGCCATGGTCTTGGCACTGT 17578	T A	CT A
		AC GT CCAAGATC TG CT		
		TG CA GGTTCCTGG AC GA		
		T C T_ C		
GAM2035	KIAA0562	3' CAAAGATCCTGCGTGACAGTG 16241	_	A C
		CACTGTAC CA GATC TTG		
		GTGACGTG GT CTAG AAC		
		C C A		
GAM2035	KIAA1789	5' AGCCAAGATTGAAAACAGTGTT 33308	ACCAA	C A
		AACACTGT GATC TTG CT		
		TTGTGACA TTAG AAC GA		
		AAAG_ _ C		
GAM2035	LIN-7-C	3' TCATGACTCAGTACAGTG 20371	CA	A CT
		CACTGTAC AG TC TGA		

GTGACATG TC AG ACT
 AC _ T_
 GAM2035 LOC119504 3' AGTCAAGGTC AAGGTCAG 36615 T AA T
 CTG ACC GA CCTTGACT
 ||| ||| || |||||
 GAC TGG CT GGAAGTGA
 _ AA _
 GAM2035 LOC145547 3' TCAAGGATCTTGATGCCAAGTG 37895 _ C
 CACT GTA CAAGATCCTTGA
 |||| ||| |||||
 GTGA CGT GTTCTAGGAACT
 AC A
 GAM2035 LOC203339 3' GTCAAGGAGGGTAAGT 43525 G AAGA
 ACT TACC TCCTTGAC
 ||| |||| |||||
 TGA ATGG AGGAACTG
 _ G_
 GAM2035 LOC253128 3' TCAAGGATAGGAAGTGTT 45487 GTA AAG
 AACACT CC ATCCTTGA
 ||||| || |||||
 TTGTGA GG TAGGAACT
 A_ A_
 GAM2035 LOC254065 5' GTCAAGGATCTATAG 46523 ACCA
 CTGT AGATCCTTGAC
 |||| |||||
 GATA TCTAGGAACTG

 GAM2036 DAP 3' ACCTTAGAGGCAGGGAACAGCA 35915 CAATTA A
 TGT TTGCCTCTAA GT
 ||| ||||| |||
 ACG GACGGAGATT CA
 ACAAGG C
 GAM2036 ZNF256 5' ACTTCAGAAGCAATGGGGGCA 12346 AAT C A
 TGTC TATTGC TCT AAGT
 |||| ||||| ||| ||||
 ACGG GTAACG AGA TTCA
 GG_ A C
 GAM2036 KIAA1843 3' ACTTCAGAGGCAGCCAATCATA 31161 TCAATTA A
 TATG TTGCCTCT AAGT
 |||| ||||| ||||
 ATAC GACGGAGA TTCA
 TAACC_ C
 GAM2036 PRO0456 3' ACTTTAGAAAATTGTTGACAT 15393 T GCC
 ATGTCAAT ATT TCTAAAGT
 ||||| ||| |||||
 TACAGTTG TAA AGATTTCA
 T A_
 GAM2037 FLJ20449 3' CTGAGTACAGATATTACA 19486 A TG
 TGTAATATCTGTA TT G
 ||||| ||||| ||| |

		ACATTATAGACAT GA C	
		_ GT	
GAM2037	FLJ21044 5'	CCGGACGACAGATATTACA 22759	AA
		TGTAATATCTGT TTTGG	
		ACATTATAGACA AGGCC	
		GC	
GAM2037	KIAA0354 3'	CTTGTATTACAGATGTTACA 16996	TT_
		TGTAATATCTGTAAT GG	
		ACATTGTAGACATTA TC	
		TGT	
GAM2037	KIAA0534 3'	ACTACCTTTTACAAATGTTACA 35378	C TTT A
		TGTAATAT TGTAAGG TAGT	
		ACATTGTA ACATT CC ATCA	
		A TT_ _	
GAM2037	KIAA0825 3'	CTATCCTCCAGATATTAC 30591	TAATTT
		GTAATATCTG GGATAG	
		CATTATAGAC CCTATC	
		CT_____	
GAM2037	LOC115207 3'	TGTCCATACAGATGTTACA 28808	ATT
		TGTAATATCTGTA TGGATA	
		ACATTGTAGACAT ACCTGT	

GAM2038	FLJ20298 3'	ATCCCTAGGAATTGCCTATC 19362	CT G C
		GATAGGTAAT C AG GGAT	
		CTATCCGTTA G TC CCTA	
		AG A _	
GAM2038	LOC201695 5'	ATCCTTCCAGAAATTACCTATC 43609	_ C C
		GATAGGTAA TCT GAG GGAT	
		CTATCCATT AGA CTT CCTA	
		AA C _	
GAM2039	ABH 3'	CTCCCTCCACTCCATCTGGT 30055	CT A A
		ATCAGATGG TG AGG GAG	
		TGGTCTACC AC TCC CTC	
		TC C _	
GAM2039	ATRN 3'	CTCTCCTTCTCCATCT 29299	CTT
		AGATGG GAAGGAGAG	
		TCTACC CTTCTCTC	
		T_	
GAM2039	CTF1 3'	CTCTCCTTGTCCCCATCTGG 7011	CTTG
		TCAGATGG AAGGAGAG	

		GGTCTACC TTCCTCTC	
		CCTG	
GAM2039 DTNA	5'	CTCTCCTTCAGAACCCCGCT 7078	A C__
		AG TGG TTGAAGGAGAG	
		TC GCC GACTTCCTCTC	
		_ CCAA	
GAM2039 DTNA	5'	CTCTCCTTCAGAACCCCGCT 7081	A C__
		AG TGG TTGAAGGAGAG	
		TC GCC GACTTCCTCTC	
		_ CCAA	
GAM2039 EVC	3'	CTCTCCTTCGCCTTCTG 15883	T TT
		CAGA GGC GAAGGAGAG	
		GTCT CCG CTTCTCTC	
		T _	
GAM2039 GNPI	3'	CTCTCCTTACACGCACTGAT 11966	ATG T _
		ATCAG GC TG AAGGAGAG	
		TAGTC CG AC TTCCTCTC	
		A__ C A	
GAM2039 ICOS	3'	CTCTCCTTCAATTGCTGA 14388	ATGGC
		TCAG TTGAAGGAGAG	
		AGTC AACTTCCTCTC	
		GTT__	
GAM2039 INSR	3'	CTCTCCTTCCTTCTTATTGA 35155	AT CTT
		TCAG GG GAAGGAGAG	
		AGTT TC CTTCTCTC	
		AT TTC	
GAM2039 ITGA4	5'	CTCTCCTTCCTTTAGCCCGCT 6582	AT T__
		AG GGCT GAAGGAGAG	
		TC CCGA CTTCTCTC	
		GC TTTC	
GAM2039 LNK	3'	CTCTCCTTCCAGTCCTGA 11973	AT T
		TCAG GGCT GAAGGAGAG	
		AGTC CTGA CTTCTCTC	
		_ C	
GAM2039 MAF	5'	CTCTCCTGCAGCCCATCTGG 11835	C A
		TCAGATGG TTG AGGAGAG	
		GGTCTACC GAC TCCTCTC	
		C G	
GAM2039 MAML1	3'	CTCTCCTGACCCCATCTGG 16498	CTTGA
		TCAGATGG AGGAGAG	

			GGTCTACC TCCTCTC		
			CCAG_		
GAM2039	MMP13	3'	CTCTAAAGAGCATCTGAT 8260	G	GAA
			ATCAGATG CTT GGAG		
			TAGTCTAC GAG TCTC		
			_ AAA		
GAM2039	NTRK2	3'	CTCTCCTTCACTCTGA 12842	TGGCT	
			TCAGA TGAAGGAGAG		
			AGTCT ACTTCCTCTC		
			C_		
GAM2039	OAS3	3'	CTCTCCTTGCCAAATCT 12861	_	TTG
			AGA TGGC AAGGAGAG		
			TCT ACCG TTCCTCTC		
			AA _		
GAM2039	PTGFRN	3'	CTCACCTCACCATCTGA 33364	CT	A A
			TCAGATGG TGA GG GAG		
			AGTCTACC ACT CC CTC		
			_ C A		
GAM2039	RGS16	3'	CTCTCCTTCAGATACTG 8832	A	GC
			CAG TG TTGAAGGAGAG		
			GTC AT GACTTCCTCTC		
			_ A_		
GAM2039	RGS19IP1	3'	CTCTCCTTCCAGGCCCATC 31325	_	_
			GATGG CTTG AAGGAGAG		
			CTACC GGAC TTCCTCTC		
			C C		
GAM2039	SOX12	3'	CTCCTTTGTCCCTCTGA 13830	T	CT
			TCAGA GG TGAAGGAG		
			AGTCT CC GTTTCCTC		
			_ CT		
GAM2039	TGM2	3'	CCTTTGGAAAGCCATTGA 10954	A	_
			TCAG TGGCTT GAAGG		
			AGTT ACCGAA TTTCC		
			_ AGG		
GAM2039	TP63	3'	CTCCCCTTCCTTTGTCTGAT 9815	TG CTT	A
			ATCAGA G GAAGG GAG		
			TAGTCT T CTTCC CTC		
			GT CTC C		
GAM2039	VDR	3'	CTCTCCCTCTGGCCCTG 5947	AT	T A
			CAG GGCT GA GGAGAG		

			GTC CCGG CT CCTCTC			
			__ T C			
GAM2039	WBSCR1	3'	CTCTCCTTCCTTCCACCTG	22722	A CTT	
			CAG TGG GAAGGAGAG			
			GTC ACC CTTCCTCTC			
			C TTC			
GAM2039	WBSCR1	3'	CTCTCCTTCCTTCCACCTG	25705	A CTT	
			CAG TGG GAAGGAGAG			
			GTC ACC CTTCCTCTC			
			C TTC			
GAM2039	BIA2	3'	CTCTCCTTCCCCGCTCTG	35317	_ CTT	
			CAGA TGG GAAGGAGAG			
			GTCT GCC CTTCCTCTC			
			C C__			
GAM2039	BIVM	5'	CTCTCCTTGCTCCCTGAT	19252	AT_ TTG	
			ATCAG GGC AAGGAGAG			
			TAGTC CCG TTCCTCTC			
			CCT __			
GAM2039	CHST3	3'	CTCCCATCTCTGCCATCTG	10480	TT_ A A	
			CAGATGGC GA GG GAG			
			GTCTACCG CT CC CTC			
			TCT A _			
GAM2039	CPR2	3'	CTCTCCTTAGAGACACCT	25175	A G G	
			AG TG CTT AAGGAGAG			
			TC AC GAG TTCCTCTC			
			C A A			
GAM2039	DCOHM	3'	CTCTCCCCGGCTATCTG	25845	TGAA	
			CAGATGGCT GGAGAG			
			GTCTATCGG CCTCTC			
			CC__			
GAM2039	FKSG44	3'	CTCTCAGGACCATCCGAT	25648	A _ AG	
			ATC GATGG CTTGA GAG			
			TAG CTACC GGA CTCTC			
			C A _			
GAM2039	FLJ10932	3'	CTCCCCTTCAGGCCCGGA	20263	AGAT A	
			TC GGCTTGAAGG GAG			
			AG CCGGACTTCC CTC			
			GCCC C			
GAM2039	FLJ20729	3'	CTCTCCTTTGCACTTGAT	19656	ATG TT	
			ATCAG GC GAAGGAGAG			

			TAGTT CG TTTCTCTC			
			CA_ _			
GAM2039	FLJ21916	3'	CTCCTTCAGCCACCTGG	23380	A	T
			TCAG TGGCT GAAGGAG			
			GGTC ACCGA CTTCCTC			
			C _			
GAM2039	FLJ22202	3'	CTCTCCTTTTTTTCATTCCGAT	24337	A_	CTT
			ATC GATGG GAAGGAGAG			
			TAG TTACT TTTCTCTC			
			CC TT_			
GAM2039	FLJ23462	3'	CTCCTATTAGCCATATGAT	24266	G	TGA
			ATCA ATGGCT AGGAG			
			TAGT TACCGA TCCTC			
			A TTA			
GAM2039	GRID1	3'	CTCCCCACTCAGGCATCTGAT	33980	G	A_____
			ATCAGATG CTTGA GGAG			
			TAGTCTAC GGA CTCTC			
			_ CACC			
GAM2039	HABP2	3'	CTCTCCTTGGCACCTGA	10344	ATG	TG
			TCAG GCT AAGGAGAG			
			AGTC CGG TTCCTCTC			
			CCA _			
GAM2039	HEMK	3'	CCCTCAGGCGTCCATCTGAT	18265	__	A
			ATCAGATG GCTTGA GG			
			TAGTCTAC CGGA CTCTC			
			CTG C			
GAM2039	IL1RAPL1	5'	CTCTCCTTTTCTATCTG	15552	CTT	
			CAGATGG GAAGGAGAG			
			GTCTATC TTTCTCTC			
			T_			
GAM2039	KIAA0459	3'	CTCTCCTTCCTGATTCTGAT	30575		TGGCTT
			ATCAGA GAAGGAGAG			
			TAGTCT CTTCCTCTC			
			TAGTC_			
GAM2039	KIAA0731	3'	CTCCCCCTCAAGCCA ACT	33241	A	A A
			AG TGGCTTGA GG GAG			
			TC ACCGA ACT CC CTC			
			A C C			
GAM2039	KIAA0960	5'	CTCCTTCTCATCTGA	44517	CTT	
			TCAGATGG GAAGGAG			

AGTCTACT CTTCTC

GAM2039 KIAA1045 3' CTCTTTCAGCCATCCTGA 35196 _ T
TCAG ATGGCT GAAGGAG
||||| |||||
AGTC TACCGA CTTTCTC
C _

GAM2039 KIAA1184 3' CTCTCCTTGACATCTGG 22897 _ TTG
TCAGATG GC AAGGAGAG
||||| || |||||
GGTCTAC CG TTCCTCTC
A _

GAM2039 KIAA1323 3' CTCCTTTAAATCTGG 31561 GGC
TCAGAT TTGAAGGAG
||||| |||||
GGTCTA AATTTCCTC

GAM2039 KIAA1908 3' CTCTCCCTTCCCAGCCATCTG 36334 _ _
CAGATGGCTT GAAGG AGAG
||||||| |||||
GTCTACCGAG CTTCC TCTC
CC C

GAM2039 MACMARCKS 3' CTCCCATCAGCCATCTGGT 23272 T A A
ATCAGATGGCT GA GG GAG
||||||| || |||
TGGTCTACCGA CT CC CTC
_ A _

GAM2039 MOST2 5' CTCTCCCTCTTCAGGTCTC 21551 T _
GA GGCTTGAA GGAGAG
|| ||||| |||||
CT CTGGACTT CCTCTC
_ CTC

GAM2039 MSTP028 3' CTCCAGGAAGGCCATCTGA 25694 GAA_
TCAGATGGCTT GGAG
||||||| |||
AGTCTACCGGA CCTC
AGGA

GAM2039 NUDT4 3' CTCGTCAAACATCTGAT 21169 GC AG
ATCAGATG TTGA GAG
||||| |||||
TAGTCTAC AACT CTC
A_ G_

GAM2039 TACTILE 3' CTCTCTTTGACCATACTGA 12411 _ C G
TCAG ATGG TT AAGGAGAG
||||| ||||| |||||
AGTC TACC AG TTTCTCTC
A _ _

GAM2039 U5-116KD 3' CTCCCCTGCCCATCTGGT 10438 CTTGA A
ATCAGATGG AGG GAG
||||||| ||| |||

			TGGTCTACC	TCC CTC	
			CCG__ C		
GAM2039	UBE3B	3'	CTCTCCTTCCGTTTCTGA	37773	T TT
			TCAGA GGC GAAGGAGAG		
			AGTCT TTG CTTCCTCTC		
			_ C_		
GAM2039	USP10	3'	CTCTCCTTCAGTCTGCTCTG	31984	_ C
			CAGA TGG TTGAAGGAGAG		
			GTCT GTC GACTTCCTCTC		
			C T		
GAM2039	ZDHHC2	3'	CTCCATTAATCATCTGAT	18488	C A
			ATCAGATGG TTGA GGAG		
			TAGTCTACT AATT CCTC		
			_ A		
GAM2039	LOC138389	5'	CTCTCCTTCAAGCTGTCTG	37506	
			CAGATGGCTTGAAGGAGAG		
			GTCTGTGCGAACTTCCTCTC		
GAM2039	LOC144110	3'	CTCCCCTTTTTTCATCTG	37679	CTT A
			CAGATGG GAAGG GAG		
			GTCTACT TTTCC CTC		
			T__ C		
GAM2039	LOC144558	5'	CTCTCCTTTGGCTAATCTG	40438	_ T
			CAGAT GGCT GAAGGAGAG		
			GTCTA TCGG TTTCTCTC		
			A _		
GAM2039	LOC144893	5'	CTCTCCCTCAGAAACCGCT	40459	A C__ A
			AG TGG TTGA GGAGAG		
			TC GCC GACT CCTCTC		
			_ AAA C		
GAM2039	LOC145368	3'	CTCTCCTTCAGTCTGCTCTG	37828	_ C
			CAGA TGG TTGAAGGAGAG		
			GTCT GTC GACTTCCTCTC		
			C T		
GAM2039	LOC145719	5'	CTCTCCAAGTGCCAGCTGAT	40576	A TTGAA
			ATCAG TGGC GGAGAG		
			TAGTC ACCG CCTCTC		
			G TCAA_		
GAM2039	LOC145720	5'	CTCTCCAAGTGCCAGCTGAT	40565	A TTGAA
			ATCAG TGGC GGAGAG		

				TAGTC ACCG CCTCTC G TCAA_	
GAM2039	LOC146346	5'	CTCCCCAAAGCCATCTGGT	38135	GAA
			ATCAGATGGCTT GGAG		
			TGGTCTACCGAA CCTC		
			ACC		
GAM2039	LOC148029	5'	CTCCTTCGGCCTGGT	38445	GAT T
			ATCA GGCT GAAGGAG		
			TGGT CCGG CTTCTC		
			— —		
GAM2039	LOC150423	3'	CTCTCCTTCAGTCTGCTCTG	38968	_ C
			CAGA TGG TTGAAGGAGAG		
			GTCT GTC GACTTCCTCTC		
			C T		
GAM2039	LOC155072	3'	CTCTCCTTTGGATATCTG	41760	GC TG
			CAGATG T AAGGAGAG		
			GTCTAT G TTCCTCTC		
			A_ GT		
GAM2039	LOC158156	3'	CTCTATTGAAGACATCTGAT	39741	G G GG
			ATCAGATG CTT AA AGAG		
			TAGTCTAC GAA TT TCTC		
			A G A_		
GAM2039	LOC169270	3'	CTCTAAAAAGCCATTGAT	40274	A GAA
			ATCAG TGGCTT GGAG		
			TAGTT ACCGAA TCTC		
			— AAA		
GAM2039	LOC197114	5'	CTCTCCAAGTCCAGCTGAT	43188	A TTGAA
			ATCAG TGGC GGAGAG		
			TAGTC ACCG CCTCTC		
			G TCAA_		
GAM2039	LOC201799	3'	CTCTCCTTGGATACCTGAT	42916	A GC G
			ATCAG TG TT AAGGAGAG		
			TAGTC AT AG TTCCTCTC		
			C _ G		
GAM2039	LOC202868	3'	CTCTCCTTTGGATATCTG	43447	GC TG
			CAGATG T AAGGAGAG		
			GTCTAT G TTCCTCTC		
			A_ GT		
GAM2039	LOC220758	3'	CTCTCCCAGAGCATTGAT	43642	G GAA
			ATCAGATG CTT GGAGAG		

			TAGTTTAC GAG CCTCTC	
			_ ACC	
GAM2039	LOC221528 5'	CTCCCCATCCCCATCTGGT	44211	CT_ AA
		ATCAGATGG TG GGAG		
		TGGTCTACC AC CCTC		
		CCT C_		
GAM2039	LOC221687 3'	CTCTCCTCAGTCTTATCTGA	44307	_ T A
		TCAGAT GGCT GA GGAGAG		
		AGTCTA CTGA CT CCTCTC		
		TT _ _		
GAM2039	LOC221882 5'	CTCTCCTTCTCTCTCTG	44433	T CTT
		CAGA GG GAAGGAGAG		
		GTCT TC CTTCTCTC		
		C T_		
GAM2039	LOC255461 5'	CTCTCCTTTGGCTAATCTG	46465	_ T
		CAGAT GGCT GAAGGAGAG		
		GTCTA TCGG TTTCTCTC		
		A _		
GAM2039	LOC255516 5'	CTCTCCTTTGGCTAATCTG	46471	_ T
		CAGAT GGCT GAAGGAGAG		
		GTCTA TCGG TTTCTCTC		
		A _		
GAM2039	LOC256789 5'	CTCTCCTTCCAACCTGGT	46536	A_ CTTG
		ATCAG TGG AAGGAGAG		
		TGGTC ACC TTCCTCTC		
		CA _		
GAM2039	LOC257552 5'	CTCCCCATCCCCATCTGGT	46670	CT_ AA
		ATCAGATGG TG GGAG		
		TGGTCTACC AC CCTC		
		CCT C_		
GAM2039	LOC257602 5'	CTCCCCATCCCCATCTGGT	46700	CT_ AA
		ATCAGATGG TG GGAG		
		TGGTCTACC AC CCTC		
		CCT C_		
GAM2039	LOC90342 5'	CTCCTTCTTTGTTCTGGT	31251	TG TT_
		ATCAGA GC GAAGGAG		
		TGGTCT TG CTTCTC		
		_ TTT		
GAM2040	ADAMTS1 3'	GTTTTACTTTACCTTCACTAAC	13852	A TC_
	A	TGTTAGT AA AAAGTAAAC		

		ACAATCA TT TTTCATTTTG	
		C CCA	
GAM2040 EFEMP1	3'	TTTACTTTGATGTATCATA 10319	TTA A
		TATG GTA ATCAAAGTAAA	
		ATAC TAT TAGTTTCATTT	
		___ G	
GAM2040 EFEMP1	3'	TTTACTTTGATGTATCATA 20839	TTA A
		TATG GTA ATCAAAGTAAA	
		ATAC TAT TAGTTTCATTT	
		___ G	
GAM2040 ENTPD3	3'	TACTCTATGATTTACTAAC 6921	A__
		GTTAGTAAATCA AGTA	
		CAATCATTTAGT TCAT	
		ATC	
GAM2040 PPAT	3'	TTACTTTGATTTTTTAAACA 8552	AGT_
		TGTT AAATCAAAGTAA	
		ACAA TTTAGTTTCATT	
		AATT	
GAM2040 SCG3	3'	TTTGCTGGATTTACTAACA 14905	AA
		TGTTAGTAAATC AGTAAA	
		ACAATCATTTAG TCGTTT	
		G_	
GAM2040 SH3BP2	3'	GCTTTGGGAGGACTCACTGACA 8950	AAA_____
	TA	TATGTTAGT TCAAAGT	
		ATACAGTCA GGTTTCG	
		CTCAGGAG	
GAM2040 KIAA1795	3'	TGATCATTTTACTAACATA 35703	_____
		TATGTTAGTAA ATCA	
		ATACAATCATT TAGT	
		TTAC	
GAM2040 UBE3B	3'	TACTTTGATGGAAACATG 37776	AGTAA
		TATGTT ATCAAAGTA	
		GTACAA TAGTTTCAT	
		AGG_	
GAM2040 LOC129446	3'	GTTTTACAGGTTACTAACA 37467	ATCAAA
		TGTTAGTAA GTAAAAC	
		ACAATCATT CATTTTG	
		GGA_	
GAM2040 LOC158549	3'	GTTTTACTTTAGATTAATAA 42010	A _
		TTAGT AATC AAAGTAAAAC	

			AATCA TTAG TTTCATTTTG		
			A A		
GAM2041	CLASP1	3'	TGAGTAAAATTCTTAAGC 32541	AT	A
			GCTTAAGAAT TTTA TCG		
			CGAATTCTTA AAAT AGT		
			— G		
GAM2041	HRH1	5'	CTCGATTAAAAAGGGAGTGAGC 6523	AGAATA	
			GCTTA TTTTAATCGAG		
			CGAGT AAAATTAGCTC		
			GAGGGA		
GAM2041	PRKAB1	3'	TCGATTTTTCTTAAGC 12933	TATTTT	
			GCTTAAGAA AATCGA		
			CGAATTCTT TTAGCT		
			T_____		
GAM2041	TERA	3'	CTCGATTAAAAATGTTAAGCTA 22204	GA	A
			TAGCTTAA AT TTTTAATCGAG		
			ATCGAATT TA AAAATTAGCTC		
			G_ _		
GAM2042	FLNB	3'	TCACCATCGAAGGCCCATCCA 31148	C	A GGCA
			TG GATGG GC CGATGGTGA		
			AC CTACC CG GCTACCACT		
			_ _ GAA_		
GAM2042	JPH3	3'	CACCAGGGTCGCTCCATC 21826	ACGA	
			GATGGAGCGGC TGGTG		
			CTACCTCGCTG ACCAC		
			GG_		
GAM2042	FLJ23598	5'	TCACCATCACCAACCCATCCCA 24157	C	AGC CAC
			TG GATGG GG GATGGTGA		
			AC CTACC CC CTACCACT		
			C CAA A_		
GAM2042	KIAA0295	3'	TCACCATCATTACCACCATC 33785	AGC	CAC_
			GATGG GG GATGGTGA		
			CTACC CC CTACCACT		
			A_ ATTA		
GAM2042	LOC149372	5'	CACCATCGAATTCCATAACA 38725	CG	CGGCA
			TG ATGGAG CGATGGTG		
			AC TACCTT GCTACCAC		
			AA AA_		
GAM2042	LOC150577	3'	CACCATCGTACCACTGCACTCC 41217	C _	G C C
			TG GA TG AG GG ACGATGGTG		

			AC CT AC TC CC TGCTACCAC		
			_ C G A A		
GAM2042	LOC157627	3'	CACCACTGCCATCACA 39619	C	GA CACGA
			TG GATG GCGG TGGTG		
			AC CTAC CGTC ACCAC		
			A _ _ _ _		
GAM2043	ACTN2	3'	TGACACAGGATGCTACATGC 6760	_	CAC
			GCATGTAGT CTTG GTCA		
			CGTACATCG GGAC CAGT		
			TA A _		
GAM2043	PTPRG	3'	TGACGACATACATGCTA 8728	_	TTGCAC
			TAGCATGTA GTC GTCA		
			ATCGTACAT CAG CAGT		
			A _ _ _ _		
GAM2043	MIC2L1	3'	ACGGGACAGAACCACATGCTA 25489	A	CT CA _
			TAGCATGT GT TG CGT		
			ATCGTACA CA AC GCA		
			C AG AGG		
GAM2044	C8orf1	5'	GCGTCTGCACCCCGGCAGCGCG 10531	AACA _	TAAA
	A		TCG TGG GTGCAGACGC		
			AGC GCC CACGTCTGCG		
			GCGACG C _		
GAM2044	CUL3	3'	CACTTTTACCATACTTGA 9644	AC	_
			TCGA ATGGTAAA GTG		
			AGTT TACCATT CAC		
			CA T		
GAM2044	HTR4	3'	CGTCCGTCACAGCCATGTTC 6542	AAA _	A
			GAACATGGT GTG C GACG		
			CTTGTACCG CAC G CTGC		
			A _ T C		
GAM2044	RABIF	3'	GCATCTCTAATACCATGTTTGA 8781	A _ _	
			TCGAACATGGTA AG TGC		
			AGTTTGTACCAT TC ACG		
			AATC T		
GAM2044	TRPC6	5'	GCGTCTGCACCCCTGCTTC 10976	_	T TAAA
			GAA CA GG GTGCAGACGC		
			CTTGTCC CACGTCTGCG		
			C C C _		
GAM2044	WHSC1	3'	GCGTCTGCACTGATGACCGT 17183	AA _	
			ATGGT AGTGCAGACGC		

			TGCCA TCACGTCTGCG		
			GTAG		
GAM2044 WHSC1	3'	GCGTCTGCACTGATGACCGT	28447	AA__	
		ATGGT AGTGCAGACGC			
		TGCCA TCACGTCTGCG			
		GTAG			
GAM2044 WHSC1	3'	GCGTCTGCACTGATGACCGT	28464	AA__	
		ATGGT AGTGCAGACGC			
		TGCCA TCACGTCTGCG			
		GTAG			
GAM2044 WHSC1	3'	GCGTCTGCACTGATGACCGT	28475	AA__	
		ATGGT AGTGCAGACGC			
		TGCCA TCACGTCTGCG			
		GTAG			
GAM2044 COTL1	3'	GCGTCTGCACCACACATTC	42467	CA GTAAA	
		GAA TG GTGCAGACGC			
		CTT AC CACGTCTGCG			
		AC AC__			
GAM2044 DKFZp434J1015	3'	GCAATGCTCTTTACCACGTTC	44506	A T GAC	
		GAAC TGGTAAAG GCA GC			
		CTTG ACCATTTC CGT CG			
		C T AA_			
GAM2044 IMAGE:4907098	5'	CCCTGCACTTGCTCGA	44060	ACATG A AC	
		TCGA GTAA GTGCAG G			
		AGCT CGTT CACGTC C			
		____ CA			
GAM2044 LOC123876	3'	GCAGACGCACAAAACCTTTACCA	36733	T_____ AGAC	
		TGTTAGA CATGGTAAAG GC GC			
		GTACCATTTC CG CG			
		AAAACA CAGA			
GAM2044 LOC146316	5'	GCGTCTGCACCTGTGTCTGCTC	30526	A T GT AA_	
		GG TCGA CA G A GTGCAGACGC			
		GGCT GT C T CACGTCTGCG			
		C _ TG GTC			
GAM2044 LOC200470	5'	GCGTCTGCAGAGCGGCCTGCTC	43309	A T AAAG_	
		GA CA GGT TGCAGACGC			
		CT GT CCG ACGTCTGCG			
		C _ GCGAG			
GAM2045 IL1R1	3'	CCAAATTCATGTACAGCA	6564	C GA	
		TGT GTACATGAAT GG			

ACG CATGTA CTTA CC
 A AA
 GAM2045 WRB 3' ACCGTCCTCGATCTGTACGA 10997 T A
 TCGTACA GA TGAGGACGGT
 ||||| || |||||
 AGCATGT CT GCTCCTGCCA
 _ A
 GAM2045 C6orf5 3' ACCAAACTGATTCATGTAC 17777 G GAC
 GTACATGAAT AG GGT
 ||||| || |||
 CATGTA CTTA TC CCA
 G AAA
 GAM2045 LOC203595 5' CCGTCCTCACACACGACA 43606 ACA AA
 TGTCGT TG TGAGGACGG
 |||| || |||||
 ACAGCA AC ACTCCTGCC
 C _ _
 GAM2045 LOC51667 3' ACCGTCCTCACTGCGCCAC 18196 C TA TGAA
 GT G CA TGAGGACGGT
 || || |||||
 CA C GT ACTCCTGCCA
 C GC C _ _
 GAM2046 G2A 5' CACGGAAGGACACACGCTGAAG 14988 GCGGG
 TTTCAGCGTGTGTCC CGTG
 ||||| |||||
 GAAGTCGCACACAGG GCAC
 AAG _ _
 GAM2047 CXX1 5' CATCACCCGCCTCACAGG 10023 A _
 CC TGAGGCGGGTGATG
 || |||||
 GG ACTCCGCCCACTAC
 AC
 GAM2047 DEDD 3' CATCACCCACCTCTGGA 26878 T C
 TCCA GAGG GGGTGATG
 ||| ||| |||||
 AGGT CTCC CCCACTAC
 _ A
 GAM2047 GDI1 3' CATCACCCACCTCATTGA 30131 C C
 TC ATGAGG GGGTGATG
 || ||||| |||||
 AG TACTCC CCCACTAC
 T A
 GAM2047 HOXC11 3' GCAGTGCCCCACTTCATGGA 30210 C _ GA
 TCCATGAGG GGGT TGC
 ||||| ||| |||
 AGGTACTTC CCCG ACG
 AC TG
 GAM2047 PCTK3 5' CGGGCGCACCGCGGCCCCAGG 36124 A A C _ A
 A
 TCC TG GG GG GTG TGCGCCCG
 ||| || || ||| |||||

AGG AC CC CC CGC ACGCGGGC
 _ _ _ GG C
 GAM2047 TCF19 3' GGACACACCTGCCCATG 46659 A A CGC
 CATG GCGGGGTG TG CC
 ||| ||||| || ||
 GTAC CCGTCCAC AC GG
 _ _ A_
 GAM2047 TCF19 3' GGACACACCTGCCCATG 46708 A A CGC
 CATG GCGGGGTG TG CC
 ||| ||||| || ||
 GTAC CCGTCCAC AC GG
 _ _ A_
 GAM2047 TFAP2C 3' CATCACCCGCCCCTGGA 9221 TGA
 TCCA GCGGGGTGATG
 ||| |||||
 AGGT CCGCCCACTAC
 CC_
 GAM2047 UBE2L6 3' CGGACGGACACACCTCATGGA 10419 CGG ATG C
 TCCATGAGG GTG CG CCG
 ||||| || |||||
 AGGTACTCC CAC GC GGC
 A_ AG_ A
 GAM2047 ZNF236 3' GGGCGCACCAAGTGCCTGGA 14274 TGA GG A
 TCCA GCGG TG TGCGCCC
 ||| ||| || |||||
 AGGT CCGT AC ACGCGGG
 _ G_ C
 GAM2047 DKFZP564B147 5' CATCACCCGCCTCACGGG 39934 A
 TCC TGAGGCGGGTATG
 ||| |||||
 GGG ACTCCGCCCCACTAC
 C
 GAM2047 FLJ10352 3' GGCGGCTCGCCCGCCTCCGGA 25827 AT T _
 TCC GAGGCGGGTGA GC GCC
 ||| ||||| || |||
 AGG CTCCGCCCCGCT CG CGG
 C_ _ G
 GAM2047 KIAA0140 3' GGGCACATCACCCACCTCA 16109 C C
 TGAGG GGGTGATG GCCC
 |||| ||||| |||
 ACTCC CCCACTAC CGGG
 A A
 GAM2047 KIAA0329 3' GGCTGCCCGCCTCCTGGA 16879 T ATGC
 TCCA GAGGCGGGTG GCC
 ||| ||||| |||
 AGGT CTCCGCCCCGT CGG
 C _
 GAM2047 KIAA0863 5' CGGGCGCAGGCGGCCCCACGGG 17154 A A C G A_
 A TCC TG GG GG TG TGCGCCCG
 ||| || || || || |||||

AGG GC CC CC GC ACGCGGGC
 _ A _ G GG
 GAM2047 RIN3 3' GCCCAGCCCCGCCTCAGGGA 24233 A TGA C
 TCC TGAGGCGGG TG GC
 ||| ||||| ||
 AGG ACTCCGCCC AC CG
 G CG_ C
 GAM2047 LOC144305 3' GGCTGACTGCCACCCGCCCAT 40401 A AT _____
 GGG TCCATG GGCGGGTG GC GCC
 ||||| ||||| || |||
 GGGTAC CCGCCCAC CG CGG
 C _ TCAGT
 GAM2047 LOC154877 3' CAGCACCCGCCTCACAGG 41740 A_ A
 CC TGAGGCGGGTG TG
 || ||||| ||
 GG ACTCCGCCCAC AC
 AC G
 GAM2047 LOC157983 3' CGGGCGCATCACGAGGTCAGGA 39686 A GGCGG
 TCC TGA GTGATGCGCCCG
 ||| ||| |||||
 AGG ACT CACTACGCGGGC
 _ GGAG_
 GAM2047 LOC203289 3' CGGGCGCATCACGAGGTCAGGA 43028 A GGCGG
 TCC TGA GTGATGCGCCCG
 ||| ||| |||||
 AGG ACT CACTACGCGGGC
 _ GGAG_
 GAM2047 LOC256544 3' CGGGCGCATCACGAGGTCAGGA 46015 A GGCGG
 TCC TGA GTGATGCGCCCG
 ||| ||| |||||
 AGG ACT CACTACGCGGGC
 _ GGAG_
 GAM2048 F2RL3 3' ACCCACCGCAACCTCATC 10079 AAAGCG
 GATGAG GCGGTGGGT
 ||||| |||||
 CTACTC CGCCACCCA
 CAA_
 GAM2048 M6PR 3' CTCCAGTCCCTCATCTCA 8163 AAAGC GGT
 TGAGATGAG GGC GGG
 ||||| ||| |||
 ACTCTACTC CTG CTC
 C_ AC_
 GAM2048 NHLH1 3' ACTTCTGCTTCCTCATCTCA 12123 A C
 TGAGATGAG AAGCGG GGT
 ||||| ||||| |||
 ACTCTACTC TTCGTC TCA
 C T
 GAM2048 CNOT4 3' ACCCACAGCTCCCTTCTCATCT 14964 AGC G
 C GAGATGAGAA GGC GTGGGT
 ||||| ||| |||||

			CTCTACTCTT TCG CACCCA		
			CCC A		
GAM2048	EFA6R	3'	ACCCACCTCCGTCGCCACCTC 17621	A AGAAA C	
	A		TGAG TG GCGG GGTGGGT		
			ACTC AC TGCC CCACCCA		
			C CCGC_ T		
GAM2048	FLJ20220	3'	CCCACGGTCTCCATCTCA 19303	A AAGC G	
			TGAGATG GA GGC GTGGG		
			ACTCTAC CT CTG CACCC		
			_ _ _ _ G		
GAM2048	FLJ20392	5'	CCACCTTCCCATCTCA 19444	A AGCGGC	
			TGAGATG GAA GGTGG		
			ACTCTAC CTT CCACC		
			C _ _ _ _		
GAM2048	FLJ20445	5'	ATCGCCGCTCCCCGCTCA 19477	A A_ AA	
			TGAG TG GA GCGGCGGT		
			ACTC GC CT CGCCGCTA		
			C CC C_		
GAM2048	FLJ22596	5'	ACCCATCCCCATCTCATCTCA 24701	AAGC C	
			TGAGATGAGA GG GGTGGGT		
			ACTCTACTCT CC CTACCCA		
			AC_ _ _		
GAM2048	KIAA1046	3'	ACCCAAAGGCCTTTTCATCTCA 17216	AAGC GG_	
			TGAGATGAGA GGC TGGGT		
			ACTCTACTTT CCG ACCCA		
			_ _ _ GAA		
GAM2048	MSC	5'	ACCCACCTCGCTTTCTCA 37532	C	
			TGAGAAAGCGG GGTGGGT		
			ACTCTTTCGCT CCACCCA		
			_		
GAM2048	PRPF8	3'	CCCAGACTTTCTCATCCA 30678	A CGGCGG	
			TG GATGAGAAAG TGGG		
			AC CTACTCTTTC ACCC		
			_ AG_ _ _		
GAM2048	TBPL1	5'	GCCACCGCTCCCTCTTCCCA 11289	A T AA C	
			TG GA GAG AGCGG GGT		
			AC CT CTC TCGCC CCG		
			C T CC A		
GAM2048	VPS39	3'	CCCAGGCTTTCTCTCCCA 31468	A T GGCGG	
			TG GA GAGAAAGC TGGG		

		AC CT CTCTTTTCG ACCC	
		C _ G _	
GAM2048	ZTL1	3' ACCCACCACCACACCCAGCTCA 23490	A AGAAAGC C
		TGAG TG GG GGTGGGT	
		ACTC AC CC CCACCCA	
		G CCACA_ A	
GAM2048	LOC150067	5' CCGCCGCCTCCTCATTCA 30258	A AAAGC
		TGAG TGAG GGCGGTGG	
		ACTT ACTC CCGCCGCC	
		_ CT _	
GAM2048	LOC151057	3' ACCTCCACTTCCTCATTTC 41292	A C C
		TGAGATGAG AAG GG GGT	
		ACTTTACTC TTC CC CCA	
		C A T	
GAM2048	LOC153443	3' CCATGCCCAGCTTTTCTCA 39373	_ G
		TGAGAAAGC GGCG TGG	
		ACTCTTTTCG CCGT ACC	
		AC _	
GAM2048	LOC197003	3' ACCCACCGCCCAGGCTCATCT 42442	AAAGC
		AGATGAG GGCGGTGGGT	
		TCTACTC CCGCCACCCA	
		GGAC_	
GAM2048	LOC200205	3' ACCCACTGGCTTCCCCCTTCCC 42734	A TGAGA_ GG
	A	TG GA AAGC CGGTGGGT	
		AC CT TTCG GTCACCCA	
		C TCCCCC _	
GAM2048	LOC219401	3' CTACAGCCTCCTCATCTCA 44592	AAAGC G
		TGAGATGAG GGC GTGG	
		ACTCTACTC CCG CATC	
		CT_ A	
GAM2048	LOC255126	5' ACCCCTAACTTTCTCACCTC 46550	A CGGC T
		GAG TGAGAAAG GG GGT	
		CTC ACTCTTTC TC CCCA	
		C AA_ _	
GAM2048	LOC51072	5' CCGCCGCCTCCTCATTCA 18067	A AAAGC
		TGAG TGAG GGCGGTGG	
		ACTT ACTC CCGCCGCC	
		_ CT _	
GAM2048	LOC90139	3' ACCCTGGGCCCTCTCTCCTCA 28273	AT A C GGT
		TGAG GAGA AG GGC GGGT	

ACTC CTCT TC CCG CCCA
 — C — GGT
 GAM2048 LOC91373 3' ATTCTCGCCTGCTTTCTCATCT 32750 — T
 CA TGAGATGAGAAAGC GGCGG GGGT
 ||||| |||| ||||
 ACTCTACTCTTTTCG CCGCT CTTA
 T —
 GAM2049 C7 3' TGAATGCTCCATTTCAGGCCTAT 6192 CAA CGA
 CA TGA GCCTGA GAGCGTTCA
 || |||| |||||
 ACT CGGACT CTCGTAAGT
 ATC TAC
 GAM2049 DUSP5 3' TGAGTGGTCACCAGGCTTGCA 10686 A ACGA G
 TG CAAGCCTG GA CGTTCA
 || ||||| || |||||
 AC GTTCGGAC CT GTGAGT
 — CA — G
 GAM2049 DKFZP564C103 3' TGAAGAGAGCGTCAGGCCATCA 17901 CAA AGAGCG
 TGA GCCTGACG TTCA
 || ||||| ||||
 ACT CGGACTGC AAGT
 AC_ GAGAG_
 GAM2049 KIAA0561 5' ACCCTCTCGTCAAGCTCATC 32762 CA C C
 GA AGC TGACGAGAG GT
 || || ||||| ||
 CT TCG ACTGCTCTC CA
 AC A C
 GAM2049 KIAA0935 3' GCCCTGCCAGGCTTGCCA 36012 A A G A
 TG CAAGCCTG C AG GC
 || ||||| | || ||
 AC GTTCGGAC G TC CG
 C C_ C
 GAM2049 PPP4R1L 5' CGCTCTTCATCAGACTTGTCA 38816 C C_
 TGACAAG CTGA GAGAGCG
 ||||| |||| |||||
 ACTGTTC GACT TTCTCGC
 A AC
 GAM2049 ZAK 3' GAACTGATCTGGCTTGTCA 18778 TGACG GC_
 TGACAAGCC AGA GTTC
 ||||| || ||||
 ACTGTTCGG TCT CAAG
 — AGT
 GAM2049 LOC149566 3' AACGTTACCCAACTTGTCA 41012 CC ACGA
 TGACAAG TG GAGCGTT
 ||||| || |||||
 ACTGTTC AC CTTGCAA
 A_ CCA_
 GAM2049 LOC150368 3' GAGACTGTCACAGGCTTGCCA 38911 A AC G CG
 TG CAAGCCTG GA AG TTC
 || ||||| || || ||

		AC GTTCGGAC CT TC GAG		
		C A_ G A_		
GAM2049	LOC255718 5'	GGACCCTCAGGCCTGTCA 46582	A	CGAGA C
		TGACA GCCTGA G GTTC		
		ACTGT CGGACT C CAGG		
		C ____ C		
GAM2050	KIAA0820 3'	AATTATGACAAAAATTACTCT 34215	C	C
		GGGGT ATTTT GTCATAATT		
		TCTCA TAAAA CAGTATTAA		
		T A		
GAM2050	LOC205327 3'	AGAATTATATTTTAATGACTCC 43103		TTC C
	A	TGGGGTCATT GT ATAATTCT		
		ACCTCAGTAA TA TATTAAGA		
		TTT _		
GAM2050	LOC222681 3'	AGAACATGAAGAAATGACCCCA 44607		CG AA
		TGGGGTCATTTT TCAT TTCT		
		ACCCAGTAAAG AGTA AAGA		
		A_ C_		
GAM2050	LOC257507 3'	AGAACATGAAGAAATGACCCCA 46673		CG AA
		TGGGGTCATTTT TCAT TTCT		
		ACCCAGTAAAG AGTA AAGA		
		A_ C_		
GAM2050	LOC257625 3'	AGAACATGAAGAAATGACCCCA 46729		CG AA
		TGGGGTCATTTT TCAT TTCT		
		ACCCAGTAAAG AGTA AAGA		
		A_ C_		
GAM2051	MAP3K14 3'	CAGCATCACACTGACACTC 10089		TAG A TTA
		GAGT CAG GTG ATGCTG		
		CTCA GTC CAC TACGAC		
		CA_ A _		
GAM2051	MAT2A 3'	CAGCACTAGCCAAACCTCACCA 12543		AGCA T____ A
	ACTC	GAGTT GAG GTTA TGCTG		
		CTCAA CTC CGAT ACGAC		
		CCA_ CAAAC C		
GAM2051	NSF 3'	CAGCACTAATTAGTGTCCTCAACT 31587	A_	GAGT A
	C	GAGTT GCA GTTA TGCTG		
		CTCAA TGT TAAT ACGAC		
		CC GAT_ C		
GAM2051	P2RY6 5'	AGCGAGGCACTTGCTAACTCT 10353	G	AA
		AGAGTTAGCA AGTGTT TGCT		

			TCTCAATCGT TCACGG GCGA		
			— A—		
GAM2051	RNF26	3'	CAGCATTAACACCTCATCTC 25727	TTAGC A	
			GAG AG GTGTTAATGCTG		
			CTC TC CACAATTACGAC		
			TAC__ _		
GAM2051	CES2	5'	AGCGCACCCCGCTGACTC 9956	AGA TAAT	
			GAGTTAGC GTGT GCT		
			CTCAGTCG CACG CGA		
			CCC ____		
GAM2051	FLJ14642	3'	CAGCACAGACTTCTGCTAA 26594	T AA	
			TTAGCAGAG GTT TGCTG		
			AATCGTCTT CAG ACGAC		
			— AC		
GAM2051	HSNOV1	3'	CAGAATGGACACTCTACAACCC 18964	A AGC AATG	
	T		AG GTT AGAGTGTT CTG		
			TC CAA TCTCACAG GAC		
			C CA_ GTAA		
GAM2051	KIAA0757	3'	CAGCATTACAGTAACTA ACTCT 12670	CAGAG T	
			AGAGTTAG TGT AATGCTG		
			TCTCAATC ACA TTACGAC		
			AATG_ _		
GAM2051	NDRG4	3'	CAGCCCACACTCTGCCACCTC 21696	TTA TAAT	
			GAG GCAGAGTGT GCTG		
			CTC CGTCTCACA CGAC		
			CAC CC_		
GAM2051	NDRG4	3'	CAGCCCACACTCTGCCACCTC 23211	TTA TAAT	
			GAG GCAGAGTGT GCTG		
			CTC CGTCTCACA CGAC		
			CAC CC_		
GAM2051	PRDM7	3'	CAGCGAAAGTCTGCTAAC 27567	GTG AA	
			GTTAGCAGA TT TGCTG		
			CAATCGTCT AA GCGAC		
			GA_ _		
GAM2051	LOC145497	5'	CAGCACTGCTCTGCCAAGC 37872	A_ TTAA	
			GTT GCAGAGTG TGCTG		
			CGA CGTCTCGT ACGAC		
			AC C_		
GAM2052	AP2B1	5'	CACCATCTTTGTCCCTGGCAAA 6951	AA_ TG	
			TTTGC GG GAGATGGTG		

		AAACG CT TTCTACCAC		
		GTCC GT		
GAM2052	CDH1	3' TCACCCAGCACCTTGCAGA 10565	GAGAT	
		TTTGCAAGGTG GGTGA		
		AGACGTTCCAC CCACT		
		GAC__		
GAM2052	DCN	5' CCTTTCCACACCTGCAAA 7635	AG_ T	
		TTTGCA GTGGAGA GG		
		AAACGT CACCTTT CC		
		CCA _		
GAM2052	HMGA2	3' TCACCATCTCTTCATTCAAA 9571	C GGT	
		TTTG AA GGAGATGGTGA		
		AAAC TT TCTCTACCACT		
		_ ACT		
GAM2052	IFNAR2	3' CACCATGCCTAGCAAA 6553	A GGAG	
		TTTGC AGGT ATGGTG		
		AAACG TCCG TACCAC		
		A _		
GAM2052	ITGBL1	5' ACCCCACCTTGCAGA 11200	AGAT	
		TTTGCAAGGTGG GGT		
		AGACGTTCCACC CCA		

GAM2052	MSF	3' TCACCACCCCCACTGGCGAG 42524	AA AGA	
		TTTGC GGTGG TGGTGA		
		GAGCG TCACC ACCACT		
		G_ CCC		
GAM2052	PCDHA9	3' TCAAGGCTCCACCTCAGA 15212	CA ATGG	
		TTTG AGGTGGAG TGA		
		AGAC TCCACCTC ACT		
		_ GGA_		
GAM2052	PRSS16	3' TCACCATCTTTTCCCACAA 12481	CAA TG	
		TTG GG GAGATGGTGA		
		AAC CC TTCTACCACT		
		AC_ TT		
GAM2052	PTPRF	3' TCACCATCGTGTGTTTGCAAA 28197	GTGGA	
		TTTGCAAG GATGGTGA		
		AAACGTTT CTACCACT		
		GTG__		
GAM2052	PTPRF	3' TCACCATCGTGTGTTTGCAAA 8723	GTGGA	
		TTTGCAAG GATGGTGA		

			AAACGTTT CTACCACT	
			GTG__	
GAM2052 SMP1	3'	CCAGCCACCTTGTA	15610	AGA
		TTTGCAAGGTGG	TGG	
		AAATGTTCCACC	ACC	
		G__		
GAM2052 SON	3'	CACCATCTCCCCTCAA	29042	CA T
		TTTG AGG GGAGATGGTG		
		AAAC TCC CCTCTACCAC		
		— —		
GAM2052 SON	3'	CACCATCTCCCCTCAA	29046	CA T
		TTTG AGG GGAGATGGTG		
		AAAC TCC CCTCTACCAC		
		— —		
GAM2052 SON	3'	CACCATCTCCCCTCAA	27746	CA T
		TTTG AGG GGAGATGGTG		
		AAAC TCC CCTCTACCAC		
		— —		
GAM2052 STS	3'	TCACCATCTTCACTACAA	5910	CAA
		TTTG GGTGGAGATGGTGA		
		AAAC TCACTTCTACCACT		
		A__		
GAM2052 TAF7L	3'	TCACCATCCAGACTGCAGA	24338	A G_ GA
		TTTGCA G TGGA TGGTGA		
		AGACGT C ACCT ACCACT		
		_AG _		
GAM2052 TFAP4	3'	TCATCTTCCACCCCAA	9226	CAA _
		TTTG GGTGGA GATGG		
		AAAC CCACCT CTA	CTACT	
		C__ T		
GAM2052 WWP2	3'	GCCCCACCTTTGCAA	30624	_ AGAT
		TTTGCAA GGTGG	GGT	
		AAACGTT CCACC	CCG	
		T ____		
GAM2052 APOA5	3'	CACCAGGCTTTGCAA	27538	GGAGA
		TTTGCAAGGT	TGGTG	
		AAACGTTTCG	ACCAC	
		G____		
GAM2052 DSTN	3'	CCACGCTCATCTTGCAA	13741	G A_
		TTTGCAAGGTG	AG TGG	

			AAACGTTCTAC TC ACC		
			_ GC		
GAM2052	FLJ10081	3'	CATGCAACTCCACCTTAGAA 19722	GC	A _
			TTT AAGGTGGAG TG GTG		
			AAG TTCCACCTC AC TAC		
			A_ A G		
GAM2052	FLJ11726	3'	CCGTCCCGCCTCACAAA 24525	CA	A
			TTTG AGGTGG GATGG		
			AAAC TCCGCC CTGCC		
			AC _		
GAM2052	FLJ14327	3'	CCACCACCTTGCAGA 24423	AGA	
			TTTGCAAGGTGG TGG		
			AGACGTTCCACC ACC		

GAM2052	ICK	3'	CACCCTCCTCCACCTCCCAA 17194	CA	AT_
			TTTG AGGTGGAG GGTG		
			AAAC TCCACCTC CCAC		
			CC CTC		
GAM2052	KIAA0532	3'	CCACCTCCACCTCCCAA 35022	CA	A
			TTTG AGGTGGAG TGG		
			AAAC TCCACCTC ACC		
			CC C		
GAM2052	KIAA0682	3'	CCTTTGGTACACCTTGCAA 16901	GA__ T	
			TTTGCAAGGTG GA GG		
			AAACGTTCCAC TT CC		
			ATGG T		
GAM2052	KIAA0766	3'	TCACCATAGCACTTGTA 16744	G GAG	
			TTTGCAAG TG ATGGTGA		
			AAATGTTC AC TACCACT		
			_ GA_		
GAM2052	KIAA1045	3'	TCACCATTCCTCACA 35199	CA T A	
			TTG AGG GGAG TGGTGA		
			AAC TCC CCTT ACCACT		
			AC _ _		
GAM2052	KIAA1184	3'	CACCCATCCCTGCAA 22894	AGGT A _	
			TTTGCA GG GATGG TG		
			AAACGT CC CTACC AC		
			_____ C		
GAM2052	KIAA1579	3'	CACCACCTGGTTTTGTAA 20119	TGG A	
			TTTGCAAGG AG TGGTG		

		AAATGTTTT TC ACCAC	
		GG_ C	
GAM2052 KIAA1908	3'	CACCATCTGTGTTGCAAG 36328	G TG GA
		TTTGCAA G GA TGGTG	
		I II	
		GAACGTT T CT ACCAC	
		G GT _	
GAM2052 KIAA1908	3'	TCATTATCCACACTGCAAA 36338	AG GA
		TTTGCA GTGGA TGGTGA	
		AAACGT CACCT ATTACT	
		CA _	
GAM2052 LAMP3	3'	CACCATCTTCTATTCAAA 29916	C GGT
		TTTG AA GGAGATGGTG	
		II	
		AAAC TT CTTCTACCAC	
		_ AT_	
GAM2052 PPP1R16B	3'	TCACCATCATATGCCCAAA 30776	CAA GA_
		TTTG GGTG GATGGTGA	
		AAAC CCGT CTACCACT	
		C_ ATA	
GAM2052 SDCBP	3'	CCTGACTCCTCCTTGCAAA 12135	T AT_
		TTTGCAAGG GGAG GG	
		II	
		AAACGTTCC CCTC CC	
		T AGT	
GAM2052 SE70-2	5'	CACCACCTCCACTTCCAGA 22663	CA A
		TTTG AGGTGGAG TGGTG	
		AGAC TTCACCTC ACCAC	
		C_ C	
GAM2052 LOC112476	3'	TCACCGTTTACTCTGCAAA 29752	AG GA
		TTTGCA GTG GATGGTGA	
		AAACGT CAT TTGCCACT	
		CT _	
GAM2052 LOC115399	5'	CACCACCCCTGGCCTTGCAA 36345	_ AGA
		TTGCAAGGT GG TGGTG	
		II	
		AACGTTCCG CC ACCAC	
		GT CCC	
GAM2052 LOC130595	5'	CTATTTTCCACCCTGCAGA 37299	A _
		TTTGCA GGTGGAGA TGG	
		AGACGT CCACCTTT ATC	
		C T	
GAM2052 LOC134266	3'	TCACCACTGCGCCCGCAAA 37071	AA G A
		TTTGC GGTG AG TGGTGA	
		II	

	AAACG CCGC TC ACCACT		
	C_ G _		
GAM2052 LOC149103 3'	TCACCATCTCAGTCTTCAAA 38653	C	TG
	TTTG AAGG GAGATGGTGA		
	AAAC TTCT CTCTACCACT		
	_ GA		
GAM2052 LOC150577 3'	TCATTTCCACCTGCAAA 41226	A	
	TTTGCA GGTGGAGATGG		
	AAACGT CCACCTTTACT		
	-		
GAM2052 LOC158572 3'	TCACCATTCACTCAACAAA 39872	CAA	GA
	TTTG GGTG GATGGTGA		
	AAAC TCAC TTACCACT		
	AAC _		
GAM2052 LOC199704 3'	TCACCATCCCCAGTAAA 42603	AAGG	A
	TTTGC TGG GATGGTGA		
	AAATG ACC CTACCACT		
	_ C		
GAM2052 LOC220573 3'	CCACATTACCTTGTAAG 34483		GA
	TTTGCAAGGTGGA TGG		
	AAATGTTCCACTT ACC		
	AC		
GAM2052 LOC255098 5'	TCACCATCATTAACAGCAAA 45690	AAGG	A
	TTTGC TGG GATGGTGA		
	AAACG ATT CTACCACT		
	ACA_ A		
GAM2052 LOC257000 3'	CCATTTCCACCCCCAAA 46272	CAA	
	TTTG GGTGGAGATGG		
	AAAC CCACCTTTACC		
	CC_		
GAM2052 LOC257465 3'	CACCGTGTCCAGCCTTGCAAA 39665	_	G
	TTTGCAAGG TGGA ATGGTG		
	AAACGTTCC ACCT TGCCAC		
	G G		
GAM2052 LOC57105 3'	CACCACTACCCTTGTAAG 21636	TGG	A
	TTTGCAAGG AG TGGTG		
	AAATGTTCC TC ACCAC		
	CA_ _		
GAM2052 LOC90333 3'	CACCCGACTCCACCTCCCAAA 31222	CA	AT_
	TTTG AGGTGGAG GGTG		

		AAAC TCCACCTC CCAC		
		CC AGC		
GAM2052	LOC90494 5'	CCAGTTTTCCACCTCGCA	31576	A _
		TGC AGGTGGAGA TGG		
		ACG TCCACCTTT ACC		
		C TG		
GAM2052	LOC92299 5'	TCGTTTCCCCTCGCAA	34132	A T
		TTTGC AGG GGAGATGG		
		AAACG TCC CCTTTGCT		
		C _		
GAM2053	FABP2 3'	AATTAAATTATTGTATTACA	5620	TGC
		TGTAATGC AATTTAATT		
		ACATTATG TTAAATTAA		
		TTA		
GAM2053	HMGB3 3'	GTAAATAAACAGTATTACA	11818	CA_
		TGTAATGCTG ATTTAAT		
		ACATTATGAC TAAATTG		
		AAA		
GAM2053	HN1L 3'	GTTGAATTAAACTAGCA	29378	CAA
		TGCTG TTTAATTCAAC		
		ACGAT AAATTAAGTTG		
		C_		
GAM2053	PAPOLG 3'	AAATTGCCATCTACAGTATTAC	23153	_____
	A	TGTAATGCT GCAATTT		
		ACATTATGA CGTTAAA		
		CATCTAC		
GAM2053	LOC145790 3'	ATTGAATGCAGCATTAC	37977	A
		GTAATGCTGCA TTTAAT		
		CATTACGACGT AAGTTA		
		-		
GAM2053	LOC219654 3'	GTAAATGACAGCATAACA	43876	A CA
		TGT ATGCTG ATTTAAT		
		ACA TACGAC TAAATTG		
		A AG		
GAM2054	CDKN2C 5'	ACTCAAAAAGCGCTCAA	6927	GTCTAC
		TTGAGTGCTTT GAGT		
		AACTCGCGAAA CTCA		
		AA_		
GAM2054	DKFZp761N0624 3'	AACTCACAGCCGAAGCACTC	26071	T AC
		GAGTGCTTTG CT GAGTT		

CTCACGAAGC GA CTCAA
C CA

GAM2054 NR4A3 5' ACCGCCACAGCACTCAA 13843 T TCTA A
TTGAGTGCT TG CG GT
||||||| || ||
AACTCACGA AC GC CA
C C__ _

GAM2054 LOC149073 5' AACTCATTGCGCAAACTCAA 40943 GC C__
TTGAGT TTTGTCTA GAGTT
||||| ||||| ||||
AACTCA AAACGGGT CTCAA
__ TTA

GAM2055 BIG1 3' TTGATGTAGATTTTACT 13140 CAT
AGTGAAGTC TACATCAA
||||||| |||||
TCATTTTAG ATGTAGTT

GAM2055 FCMD 3' TGATGTAATTCTCTCACTT 13578 A TCC
AAGTGA G ATTACATCA
||||| | |||||
TTCAC T C TAATGTAGT
_ TCT

GAM2055 FTSJ2 3' TTGACGGGACTTCATCTT 15045 _ ATTACA
AAG TGAAGTCC TCAA
||| ||||| |||
TTC ACTTCAGG AGTT
T GC__

GAM2055 PBP 3' TTTGATCAAATTTGAAC TTCAT 8417 C TTAC__
TTTG CAAAGTGAAGT CA ATCAAA
||||||| || |||||
GTTTTACTTCA GT TAGTTT
A TTAAAC

GAM2055 STK10 3' TGTTGGACTTCTCTTCA 12615 A T TT
C AAG GAAGTCCA ACA
| ||| ||||| |||
A TTC CTTCAGGT TGT
C T _

GAM2055 ARHGAP5 5' TTTGAGACGGAATTTCACTTCA 37824 A _ ATTACA
C AAGTGAAGT CC TCAAA
| ||||| || |||||
A TTCAC TTTA GG AGTTT
C A CAG__

GAM2055 C1orf22 3' TGATGGAGAATTCAC TTTG 24842 G__
CAAAGTGAA TCCATTA
||||||| |||||
GTTTCACTT AGGTAGT
AAG

GAM2055 CBX6 3' TGTCGGACCTTCACTTCA 15580 A _ ATT
C AAGTGAAG TCC ACA
| ||||| ||| |||

A TTCACTTC AGG TGT
 C C C__
 GAM2055 DKFZP434A043 5' TGATGTAGTTCACCTT 17704 AGTCC
 AAGTGA ATTACATCA
 ||||| |||||
 TTCACT TGATGTAGT

 GAM2055 DKFZP434C212 3' TTTGATGTAATATGGACATC 34172 A ____
 GA GTCCAT TACATCAAA
 || ||||| |||||
 CT CAGGTA ATGTAGTTT
 A TA
 GAM2055 DKFZP434J037 3' TGCTGTGTGGACTTCAT 25221 T T
 GTGAAGTCCAT ACA CA
 ||||| |||||
 TACTTCAGGTG TGT GT
 _ C
 GAM2055 FLJ23129 3' TTTGATGTATAACTTCCCCTT 24122 T_ CCAT
 AAG GAAGT TACATCAAA
 || ||||| |||||
 TTC CTTCA ATGTAGTTT
 CC AT__
 GAM2055 HEMK 3' TTGGGCAGATGACTTCAC 18275 C ACA
 GTGAAGTC ATT TCAA
 ||||| |||||
 CACTTCAG TAG GGT
 _ ACG
 GAM2055 KIAA0781 3' GATGTAATAACTACTTTG 33500 GA CC
 CAAAGT AGT ATTACATC
 ||||| |||||
 GTTTCA TCA TAATGTAG
 _ A_
 GAM2055 KIAA1034 3' TGATTTCTGCTTCACCTTTG 31313 CCATTAC
 CAAAGTGAAGT ATCA
 ||||| |||||
 GTTTCACCTTCG TAGT
 TCTT____
 GAM2055 KIAA1508 5' TTTGATGTAACCTTCTCAC 30997 A TCCA
 GTGA G TTACATCAAA
 ||||| |||||
 CACT C AATGTAGTTT
 _ TTC_
 GAM2055 KIAA1804 3' TGATTCGGCTTCACTTTG 34589 CATTAC
 CAAAGTGAAGTC ATCA
 ||||| |||||
 GTTTCACCTTCGG TAGT
 CT____
 GAM2055 OAZ3 5' TGTGAACCTTCACTTTG 18281 CCA
 CAAAGTGAAGT TTACA
 ||||| |||||

GTTTCACTTCA AGTGT

GAM2055 PI4KII 3' TTTGATGTAAGAGTTCAGTTTG 20485 G G CA
CAAA TGAA TC TTACATCAAA
||||| || |||||
GTTT ACTT AG AATGTAGTTT
G G _

GAM2055 RHOBTB1 3' GTGGCCAACCTTCACTTTG 43953 _
CAAAGTGAAGT CCAT
||||| |||
GTTTCACTTCA GGTG
ACC

GAM2055 VEZATIN 3' TGAATGCAGACTTCATTT 19071 _ A
AAGTGAAGTC CATT CA
||||| ||| ||
TTTACTTCAG GTAA GT
AC _

GAM2055 ZFP106 3' TGATTTGGACTTCGCTTTG 22836 TTAC
CAAAGTGAAGTCCA ATCA
||||| |||
GTTTCGCTTCAGGT TAGT
T_

GAM2055 ZNF363 3' TTGATGTAATAACTGCT 36357 GA CC
AGT AGT ATTACATCAA
||| ||| |||||
TCG TCA TAATGTAGTT
_ A_

GAM2055 LOC149821 5' TTGTGTAGTAAACCTTACTTTG 41110 A CC T
CAAAGTGA GT ATTACA CAA
||||| || ||||| |||
GTTTCATT CA TGATGT GTT
C AA _

GAM2055 LOC150271 3' TGGCCTGGACTTCTCTTTG 41176 T TTA
CAAAG GAAGTCCA CA
||||| ||||| ||
GTTTC CTTCAGGT GT
T CCG

GAM2055 LOC150445 3' TTTGATCAAATTTGAACTTCAT 38972 C TTAC_
TTTG CAAAGTGAAGT CA ATCAAA
||||| || |||||
GTTTTACTTCA GT TAGTTT
A TTAAAC

GAM2055 LOC90736 3' TGCATGCGGACTTACTTTG 31958 A ATTA _
CAAAGTGA GTCC CAT CA
||||| ||| ||| ||
GTTTCATT CAGG GTA GT
_ C_ C

GAM2056 ALS2 3' GATTTGTGTTAAGTGAAGTGA 21930 _ T GA
A TTC CAGTC AT TAACACAAATC
||| ||||| || |||||

AAG GTCAG TG ATTGTGTTTAG
 A _ A_
 GAM2056 B3GALT2 5' GATTTCATATTATAGACT 9873 ACAC
 AGTCTATGATA AAATC
 ||||| ||||
 TCAGATATTAT TTTAG
 AC__
 GAM2056 NXF2 5' ATTTGTGGATAGACTG 19456 GATAA
 CAGTCTAT CACAAAT
 ||||| |||||
 GTCAGATA GTGTTTA
 G____
 GAM2056 DKFZP434C1715 3' TGTGTTGTGATACTGGAA 41678 CT G
 TTCCAGT AT ATAACACA
 ||||| || |||||
 AAGGTCA TA TGTTGTGT
 _ G
 GAM2056 KIAA1831 5' ATTTGTGCTGGGATGGAA 31900 GT TGATAA
 TTCCA CTA CACAAAT
 |||| || |||||
 AAGGT GGT GTGTTTA
 AG C____
 GAM2056 MGC16824 5' ATTTGCATCATGCCGACTGGAG 21571 _ AACAA
 TTCCAGTC TATGAT CAAAT
 ||||| ||||| ||||
 GAGGTCAG GTACTA GTTTA
 CC C____
 GAM2056 MGC4562 5' GTGATCCCAGACTGGAA 28498 AT AA
 TTCCAGTCT GAT CAC
 ||||| || ||||
 AAGGTCAGA CTA GTG
 CC _
 GAM2056 RAB10 3' TTGTATTACCATGGGTTTGGA 41284 _GT A C
 TCC A CTATG TAA ACAA
 || | |||| || ||||
 AGG T GGTAC ATT TGTT
 T TG C A
 GAM2056 LOC221362 3' TTGCATTATTATAGACTGGGA 45024 CA
 TTCCAGTCTATGATAA CAA
 ||||| ||||| ||||
 AGGGTCAGATATTATT GTT
 AC
 GAM2057 FYCO1 3' TAACAAAAGTCTTTGATA 23712 C_
 TATCAAAGAT TTGTTA
 ||||| |||||
 ATAGTTTCTG AACAAAT
 AA
 GAM2058 ADAR 3' CAGCACCCCTCAGATGATTTCCC 6770 C_ ATAT
 TC
 GAGGGAAATC CT GTGCTG
 ||||| || |||||

			CTCCCTTTAG GA CACGAC		
			TA CTCC		
GAM2058	ADAR	3'	CAGCACCCCTCAGATGATTTCCC 17956	C_	ATAT
	TC		GAGGGAAATC CT GTGCTG		
			CTCCCTTTAG GA CACGAC		
			TA CTCC		
GAM2058	ADAR	3'	CAGCACCCCTCAGATGATTTCCC 17963	C_	ATAT
	TC		GAGGGAAATC CT GTGCTG		
			CTCCCTTTAG GA CACGAC		
			TA CTCC		
GAM2058	COL4A3	3'	AGCATATAAAATTTTCCCCCT 25359	A	TCCCTA
			AG GGGAAA TATGTGCT		
			TC CCCTTT ATATACGA		
			C TAAA__		
GAM2058	COL4A3	3'	AGCATATAAAATTTTCCCCCT 25353	A	TCCCTA
			AG GGGAAA TATGTGCT		
			TC CCCTTT ATATACGA		
			C TAAA__		
GAM2058	COL4A3	3'	AGCATATAAAATTTTCCCCCT 5546	A	TCCCTA
			AG GGGAAA TATGTGCT		
			TC CCCTTT ATATACGA		
			C TAAA__		
GAM2058	DAP	3'	CAGCAATGCCAAATTTCCCTCT 35916		CCCTATATG
			AGAGGGAAAT TGCTG		
			TCTCCCTTTA ACGAC		
			AACCGTA__		
GAM2058	MSN	3'	CAGCCTCTAGGGACCCCTC 30228	AAA	TATGT
			GAGGG TCCCTA GCTG		
			CTCCC AGGGAT CGAC		
			C__ CTC__		
GAM2058	NR1I2	3'	CAGCACAAGGAATTTCCCT 22545	C	ATA
			AGGGAAAT CCT TGTGCTG		
			TCCCTTTA GGA ACACGAC		
			A __		
GAM2058	NR1I2	3'	CAGCACAAGGAATTTCCCT 9972	C	ATA
			AGGGAAAT CCT TGTGCTG		
			TCCCTTTA GGA ACACGAC		
			A __		
GAM2058	PRKRA	3'	CACATAAAAAGTTCCCCTCT 9800	A	CCCTA
			AGAGGG AAT TATGTG		

			TCTCCC TTG ATACAC	
			C AAAA_	
GAM2058	SLC9A6	3'	CAGCATCTGGAAGACTTTCCTC 13053	A CCTA T
		T	AGAGGGAA TC TA GTGCTG	
			TCTCCTTT AG GT TACGAC	
			C AAG_ C	
GAM2058	TNFSF4	3'	TAGTTAATAGAAATTTCCCTT 9334	CC ATGT
			GAGGGAAAT CTAT GCTG	
			TTCCCTTTA GATA TGAT	
			AA AT__	
GAM2058	AGMAT	3'	CACAGTAAGATTCCCTCT 24105	A CC A
			AGAGGGAA TC TAT TGTG	
			TCTCCCTT AG ATG ACAC	
			_ A_ _	
GAM2058	ATP6V0A1	3'	CAGTGCACAGGGCTTCCCTCT 11675	AT ATA TG
			AGAGGGAA CCCT TG CTG	
			TCTCCCTT GGGA AC GAC	
			C_ C__ GT	
GAM2058	CECR6	3'	GGCTGCAGAACTTTCCTCT 25638	TCCCTATA _
			AGAGGGAAA TGT GCT	
			TCTCCCTTT ACG CGG	
			CAAG____ T	
GAM2058	DIO2	3'	CAGCACAGCCTTGATTTCCT 15166	CCTATA
			GGGAAATC TGTGCTG	
			TCCTTTAG ACACGAC	
			TTCCG_	
GAM2058	DIO2	3'	CAGCACAGCCTTGATTTCCT 6456	CCTATA
			GGGAAATC TGTGCTG	
			TCCTTTAG ACACGAC	
			TTCCG_	
GAM2058	DKFZP564P1916	3'	AGCAGTGAACCTTCCCTCT 17898	ATCCC ATG
			AGAGGGAA TAT TGCT	
			TCTCCCTT GTG ACGA	
			CAA_ _	
GAM2058	ERG-1	5'	GTATAAAGATTCCCTCT 22556	A CC
			AGAGGGAA TC TATAT	
			TCTCCCTT AG ATATG	
			_ AA	
GAM2058	FLJ14437	5'	AGGGCGTGAAGAATTTCCCTCT 26307	CC A G
			AGAGGGAAAT CT TATGT CT	

			TCTCCCTTTA GA GTGCG GA		
			A_ A G		
GAM2058	HCAP-G	5'	CAGTCTCGCGGGATTTCCT 22746	A	TATATGT
			AG GGGAAATCCC GCTG		
			TC CCCTTTAGGG TGAC		
			C CGCTC__		
GAM2058	KIAA0205	3'	CAGCACATAAGGCTCCC 17003	AATC	A
			GGGA CCT TATGTGCTG		
			CCCT GGA ATACACGAC		
			C__ _		
GAM2058	MGC4737	3'	CAGCAGAGGGACCTCCCTC 25504	AA	ATATG
			GAGGGA TCCCT TGCTG		
			CTCCCT AGGGA ACGAC		
			CC G__		
GAM2058	STARD7	3'	TACAAAGAAATTTCCCTC 29263	CC	ATA
			GAGGGAAAT CT TGTG		
			CTCCCTTTA GA ACAT		
			AA A__		
GAM2058	STARD7	3'	TACAAAGAAATTTCCCTC 21361	CC	ATA
			GAGGGAAAT CT TGTG		
			CTCCCTTTA GA ACAT		
			AA A__		
GAM2058	TIAF1	3'	AGCACGTTGACCTCCCTCT 27796	AA	CCTAT
			AGAGGGA TC ATGTGCT		
			TCTCCCT AG TGCACGA		
			CC T__		
GAM2058	LOC131368	3'	CAGCACATGTTAACCTCTCCTC 37354	_	AATCCCT
			GAGG GA ATATGTGCTG		
			CTCC CT TGTACACGAC		
			T CAAT__		
GAM2058	LOC148930	3'	AGCCCCAGGGTTTCCCTC 38617	T	ATATGT
			GAGGGAAA CCCT GCT		
			CTCCCTTT GGA CGA		
			_ CCC__		
GAM2058	LOC149506	5'	AGACAGAGGTTTCCCCCT 41001	A	CCTATA G
			AG GGGAAATC TGT CT		
			TC CCCTTTGG ACA GA		
			C AG__ _		
GAM2058	LOC158434	5'	CAGCACGGTGGCAATTTCCCTC 41983	CC	A
			GAGGGAAAT CTAT TGTGCTG		

		CTCCCTTTA GGTG GCACGAC		
		AC _		
GAM2058	LOC196955 3'	CAGCACTTGCATGGCACTTCCC 37930		ATC TATAT_
	TCT	AGAGGGAA CC GTGCTG		
		TCTCCCTT GG CACGAC		
		CAC TACGTT		
GAM2058	LOC256789 3'	GTCATAATAGACTTCCCTCT 46538		A CCTA T
		AGAGGGAA TC TATG GC		
		TCTCCCTT AG ATAC TG		
		C ATA_ _		
GAM2059	DAZ 3'	GACATACATCATTCTGTGATTA 10282		C A C
		TAATCGCA AATGAT TA GTC		
		ATTAGTGT TTAATA AT CAG		
		C C A		
GAM2059	DAZL 3'	GACACATATCATTCTGTGATTA 33801		C AC
		TAATCGCA AATGATAT GTC		
		ATTAGTGT TTAATA CAG		
		C CA		
GAM2059	FLJ20330 5'	GACGTTTGTCTGTGCGATT 21060		AT T
		AATCGCACA GATA ACGTC		
		TTAGCGTGT CTGT TGCAG		
		_ T		
GAM2059	KIAA1908 3'	GATGGGTTTCATTGTGGAT 36336	G	TATA
		ATC CACAATGA CGTC		
		TAG GTGTTACT GTAG		
		_ TGG_		
GAM2060	C1orf24 3'	CCTGGGTAAGACTGAAAGCATT 27531	A	GTGGT_
		GAT CTTTCAGTCT GG		
		TTA GAAAGTCAGA CC		
		C ATGGGT		
GAM2060	FLJ12761 3'	CCTGGACTGAAAGTATC 23757		T
		GATACTTTCAGTCTG GG		
		CTATGAAAGTCAGGT CC		
		_		
GAM2060	KIAA0574 3'	CCTAAAGACTCAAAGTATCTC 34343	C	GT_
		GAGATACTTT AGTCT GG		
		CTCTATGAAA TCAGA CC		
		C AAT		
GAM2060	KIAA1766 3'	CCTTACTGAAAGTACCTCT 35352	A	CTGT
		AGAG TACTTTCAGT GG		

TCTC ATGAAAGTCA CC
 C TT__
 GAM2060 NIBAN 3' CCTGGGTAAGACTGAAAGCATT 22628 A GTGGT_
 GAT CTTTCAGTCT GG
 ||| ||||| ||
 TTA GAAAGTCAGA CC
 C ATGGGT
 GAM2060 LOC90381 3' GCCACCACTGTGACAACCAAAA 31344 CA__ T__ |||
 GTATCTC ACTTT GTC GTGGTGG C
 |||| ||| ||||| |
 TGAAA CAG CACCACC G
 ACCAA TGT |||
 GAM2060 LOC91960 3' CCACCTCTTCCTGAAAGTCCTC 33609 AT TCTGT
 GAG ACTTTCAG GGTGG
 ||| ||||| |||||
 CTC TGAAAGTC CCACC
 C_ CTTCT
 GAM2061 ABCD2 3' GTACAAAATAGCTGACAGTTTT 11660 GTGAA
 AAAACTGT ATTTTGTAC
 ||||| |||||
 TTTTGACA TAAACATG
 GTCGA
 GAM2061 DNA2L 3' TACAAAATTTAATGCAGTATTT 43881 A G
 A TAAA ACTGTGT AAATTTTGTA
 ||| ||||| |||||
 ATTT TGACGTA TTAAAACAT
 A A
 GAM2061 RPL10 3' ACCTGGGGTTCACACAGCTTTTT 12622 _ ATTTT
 AAAAA CTGTGTGAA GT
 ||||| ||||| ||
 TTTTT GACACACTT CA
 C GGGTC
 GAM2061 DKFZP566M114 3' ACACAGTGCTACACAGCTTTTA 25813 A AA T
 TAAAA CTGTGTG ATT TGT
 ||||| ||||| ||| |||
 ATTTT GACACAT TGA ACA
 C CG C
 GAM2061 FLJ20519 3' TACAAAATTCCATCTCAG 19539 T_ A
 CTG GTG AATTTTGTA
 ||| ||| |||||
 GAC TAC TAAAACAT
 TC C
 GAM2061 FLJ21369 3' ACAAATTTACAGTTTT 24182 TGA
 AAAACTGTG AATTTTGT
 ||||| |||||
 TTTTGACAT TAAAACA
 —
 GAM2061 FLJ23462 3' ACAAATTTCCAGGGTTTTTG 24259 G T A
 TAAAACT TG GAA TTTTGT
 ||||| ||| |||||

		GTTTTTGG AC CTT AAAACA	
		G _ _	
GAM2061	KIAA1237	3' ACACAGTCTCCACAGTTT 39214	T A T
		AAACTGTG GA ATT TGT	
		TTTGACAC CT TGA ACA	
		_ C C	
GAM2061	KIAA1554	3' GTAAGTGAAGTTCACACAGT 45613	A TTG
		ACTGTGTGAA TT TAC	
		TGACACACTT AG ATG	
		C TCA	
GAM2061	OAZIN	3' TACAAGAACACAGTTTTTA 18022	GAAA
		TAAAAACTGTGT TTTTGTA	
		ATTTTTGACACA AGAACAT	

GAM2061	LOC147072	3' TACAAAATTCATAGTT 30300	TGA
		AACTGTG AATTTTGTA	
		TTGATAC TTAAAACAT	

GAM2061	LOC147093	3' GCACAAGGTCACATAGCTTTTA 40803	A AA T
		TAAAA CTGTGTGA TT TGT	
		ATTTT GATACACT AA ACG	
		C GG C	
GAM2061	LOC201626	3' GTACAAATGAACACAGTTT 42889	GAAAT
		AAACTGTGT TTTGTAC	
		TTTGACACA AAACATG	
		AGT_	
GAM2061	LOC93097	5' TACAAAATAGCACCACAGT 35356	_ AA
		ACTGTG TG ATTTTGTA	
		TGACAC AC TAAAACAT	
		C GA	
GAM2062	BSN	3' CCTCTGGGTGACATCGGA 9516	TT A
		TCCGATGTT CTTA AGG	
		AGGCTACAG GGGT TCC	
		T_ C	
GAM2062	DXS1283E	3' GTCCTTTAAAAAATGGAGGA 35067	GA C
		TCC TGTTTT TTAAAGGAC	
		AGG GTAAAA AATTCCTG	
		AG _	
GAM2062	ITK	3' GTCTAGAAAGAAAACATTGGA 12078	AAA
		TCCGATGTTTTCTT GGAC	

			AGGTTACAAAAGAA	TCTG		
			AGA			
GAM2062	PCDH11X	3'	CCGGGAAAACATGGGA	26805	G	AAA
			TCC ATGTTTTCTT	GG		
			AGG TACAAAAGGG	CC		
			G			
GAM2062	PCDH11X	3'	CCGGGAAAACATGGGA	26790	G	AAA
			TCC ATGTTTTCTT	GG		
			AGG TACAAAAGGG	CC		
			G			
GAM2062	RAP1B	3'	CCTTTAAGAGGCGGA	17896	ATGT	
			TCCG TTTCTTAAAG			
			AGGC	GGAGAATTTCC		
GAM2062	RPA1	3'	GTCCCCTAAGGAAATCCG	8855	AT	AA
			CG GTTTTCTTA	GGAC		
			GC TAAAGGAAT	CCTG		
			C_	CC		
GAM2062	SERPINA5	3'	TCCTTTAAGAAAAACATCTGG	6241	-	-
			CC GATGTTTT	CTTAAAGGA		
			GG CTACAAA	GAATTCCT		
			T	A		
GAM2062	ARL8	3'	TCCTTTAAAAAATATTTGG	44766	-	C
			CCGA TGTTTT	TTAAAGGA		
			GGTT ATAAAA	AATTCCT		
			T			
GAM2062	C1orf22	3'	TCCTTTAAGAGATATTAGA	24841	CG	T
			TC ATGTTT	CTTAAAGGA		
			AG TATAGA	GAATTCCT		
			AT			
GAM2062	C20orf20	3'	CCAGGAAAACCTCGGA	20244	T	AAA
			TCCGA GTTTTCTT	GG		
			AGGCT CAAAAGGG	CC		
			C	A_		
GAM2062	C9orf12	3'	CTTTTAAGAAAACATGGA	22992	G	
			TCC ATGTTTTCTTAAAG			
			AGG TACAAAAGAATTTTC			
GAM2062	CDC14B	3'	GTCCTTCCCTGTAACATTGGA	9762		TTCTTA
			TCCGATGTT	AAGGAC		

AGGTTACAA TTCCTG
 TGTCCC
 GAM2062 CDC14B 3' GTCCTTCCCTGTAACATTGGA 27165 TTCTTA
 TCCGATGTT AAGGAC
 ||||| |||||
 AGGTTACAA TTCCTG
 TGTCCC
 GAM2062 DKFZP564C196 3' GTTAGAGAGGAAAACATCGGA 34713 AAAG
 TCCGATGTTTTCTT GAC
 ||||| |||||
 AGGCTACAAAAGGA TTG
 GAGA
 GAM2062 EFNA5 3' GTCACAGAAAACATCAGG 7686 _ TAAAG
 CC GATGTTTTCT GAC
 || ||||| |||||
 GG CTACAAAAGA CTG
 A CA__
 GAM2062 FLJ12409 3' CCTTTAAGAATTCGTGGA 24753 G TT
 TCC ATG TTCTTAAAGG
 ||| ||| |||||
 AGG TGC AAGAATTTC
 _ TT
 GAM2062 FLJ12604 3' GTCCTTTAAGAAGAAGGG 32191 GATG
 CC TTTTCTTAAAGGAC
 || |||||
 GG AGAAGAATTCCTG
 GA__
 GAM2062 FLJ14640 5' TCCTTTGAAACACTGGA 26586 A TTC
 TCCG TGTT TTAAAGGA
 ||| ||| |||||
 AGGT ACAA AGTTTCCT
 C _
 GAM2062 FLJ20413 3' TCCTTTAAAAACCGATCGG 19453 _ CT
 CCGAT GTTTT TAAAGGA
 |||| |||| |||||
 GGCTA CAAAA ATTCCT
 GC _
 GAM2062 H_GS165L15.1 3' CCTTTGCCTGAAACATTG 11339 CT_
 CGATGTTTT TAAAGG
 ||||| |||||
 GTTACAAAG GTTTCC
 TCC
 GAM2062 HN1L 3' CCTCTAAGCTGCATTGAGA 29375 _ TTT A
 TC CGATGT CTTA AGG
 || |||| |||||
 AG GTTACG GAAT TCC
 A TC_ C
 GAM2062 KIAA0379 3' GTCCTCCAAGAGAACCCTG 33813 AT AA
 CG GTTTTCTT AGGAC
 || ||||| |||||

			GT CAAGAGAA TCCTG		
			CC CC		
GAM2062	KIAA0560	5'	GTCCTTTAGTTTCCACTGGA	30838	A TTTTC
			TCCG TG TTAAAGGAC		
			AGGT AC GATTCCTG		
			C CTTT_		
GAM2062	KIAA0916	3'	TCCCCCAAGAGGATGCGG	17417	A AAA
			CCG TGTTTTCTT GGA		
			GGC GTAGGAGAA CCT		
			_ CCC		
GAM2062	KIAA1211	3'	CCTTTAAAAACATCTGA	34163	C C
			TC GATGTTTT TTAAAGG		
			AG CTACAAAA AATTTC		
			T _		
GAM2062	KIAA1376	3'	CCTTTAAGAAAACATGGA	31823	G
			TCC ATGTTTTCTTAAAGG		
			AGG TACAAAAGAATTTC		
			_		
GAM2062	MBLL39	3'	CCTTTAATAATGGAGCATC	29570	C__
			GATGTTTT TTAAAGG		
			CTACGAGG AATTTC		
			TAAT		
GAM2062	NAPG	3'	TCCTTTAGATCCAATCGGA	46254	GTTT T
			TCCGAT TCT AAAGGA		
			AGGCTA AGA TTTCT		
			ACCT _		
GAM2062	PELI2	3'	TCCTTTAGGACATGAGA	22231	CG TTT
			TC ATG TCTTAAAGGA		
			AG TAC AGGATTTCT		
			AG _		
GAM2062	PSKH1	3'	GTCCTCCATGAGGACATGGGA	33868	G TTAA
			TCC ATGTTTTC AGGAC		
			AGG TACAGGAG TCCTG		
			G TACC		
GAM2062	SEC14L2	5'	TCCTTTAAGAGGCGGG	14806	ATGT
			TCCG TTTCTTAAAGGA		
			GGGC GGAGAATTCCT		
			_		
GAM2062	ZNF339	3'	GTCCTTTTGAAACATC	22200	CTT
			GATGTTTT AAAGGAC		

		CTACAAAG TTTCTG		
		T__		
GAM2062	LOC138654 5'	CCTCTCAAGAAAACACTGGA	37397	A AA_
		TCCG TGTTTTCTT AGG		
		AGGT ACAAAGAA TCC		
		C CTC		
GAM2062	LOC142948 3'	GTCCTGGGGAAAACATGGA	40326	G TAA
		TCC ATGTTTTCT AGGAC		
		AGG TACAAAAGG TCCTG		
		_ GG_		
GAM2062	LOC143916 3'	TCCTTTCTGAACACTGGA	37654	A TCTT
		TCCG TGTTT AAAGGA		
		AGGT ACAAG TTTCT		
		C TC_		
GAM2062	LOC145439 5'	GTCCTTTAAAAGCATT	37866	CT
		GATGTTTT TAAAGGAC		
		TTACGAAA ATTCCTG		
		_		
GAM2062	LOC147178 3'	TCCTTTAAGGTCTTTGGA	30744	TGTTT
		TCCGA TCTTAAAGGA		
		AGGTT GGAATTCCT		
		TCT_		
GAM2062	LOC151194 3'	TCCATAGAAAACACTGGA	29798	A TAAA
		TCCG TGTTTTCT GGA		
		AGGT ACAAAGA CCT		
		C TA_		
GAM2062	LOC153416 3'	CCTTTAAGAGGCGGA	30361	ATGT
		TCCG TTTCTTAAAGG		
		AGGC GGAGAATTTC		
		_		
GAM2062	LOC157450 3'	CCTCTAATAAGACATCGG	35146	C A
		CCGATGTTTT TTA AGG		
		GGCTACAGAA AAT TCC		
		T C		
GAM2062	LOC157556 5'	GTCCTTCAAGAGGACCTC	41823	T A
		GA GTTTTCTT AAGGAC		
		CT CAGGAGAA TTCCTG		
		C C		
GAM2062	LOC158629 5'	CCAGGAAAACATGGA	42020	G AAA
		TCC ATGTTTTCTT GG		

AGG TACAAAAGGA CC

GAM2062 LOC200301 3' GTTTAGAAGAAAACATTAGA 42784 CG AAA
TC ATGTTTTCTT GGAC
|| ||||| |||
AG TACAAAAGAA TTTG
AT GA_

GAM2062 LOC220790 3' CCTTTAAGAGGCGGA 43838 ATGT
TCCG TTTCTTAAAGG
||| |||||
AGGC GGAGAATTTC

GAM2062 LOC221795 5' TCCTTTGAACATGGGA 44424 G TTTC
TCC ATGT TTAAAGGA
||| ||| |||||
AGG TACA AGTTTCCT
G _

GAM2062 LOC257019 5' GTCCTTTAAACAGAATGGA 45995 GA__ TCT
TCC TGTTT TAAAGGAC
||| ||| |||||
AGG ACAA ATTCCTG
TAAG _

GAM2062 LOC91664 3' CCCTTAAGGAACATCAGA 33213 C T A
TC GATGTTT CTAA GG
|| ||||| ||||| ||
AG CTACAAG GAATT CC
A _ C

GAM2062 LOC93320 3' CCTCTAATAAGACATCGG 35655 C A
CCGATGTTTT TTA AGG
||||||| ||| |||
GGCTACAGAA AAT TCC
T C

GAM2063 DGKB 3' CACAGACAGACAATAAGC 44447 A
GCTTATT TCTGTTTGTG
||||| |||||
CGAATAA AGACAGACAC
C

GAM2063 MOG 3' AGACACAAACAAACAAGCTA 8278 A ATC _
TAGCTT TT TGTTTGTG CT
||||| || ||||| ||
ATCGAA AA ACAAACAC GA
C _ A

GAM2063 SACM1L 3' AGTTCAGTAATAAGCTA 15236 T TTTGT
TAGCTTATTA CTG GCT
||||||| ||| |||
ATCGAATAAT GAC TGA
_ T_

GAM2063 VCAM1 3' TATAGACAAATAATAAGC 27985 C
GCTTATTAT TGTTTGTG
||||||| |||||

			CGAATAATA ACAGATAT		
			A		
GAM2063	VCAM1	3'	TATAGACAAATAATAAGC 6739	C	
			GCTTATTAT TGTTTGTG		
			CGAATAATA ACAGATAT		
			A		
GAM2063	CDC14B	3'	TTAGTACTCAGATAATAA 27177	TTT	
			TTATTATCTG GTGCTAA		
			AATAATAGAC CATGATT		
			T__		
GAM2063	FLJ00060	3'	AGCACTGCTGAACAGACAAC TA 30626	A	_____
			GC GCT TT TCTGTTT GTGCT		
			CGA AA AGACAAG CACGA		
			TC C TCGT		
GAM2063	KIAA0419	3'	TATAGACAGAAATAATAAGC 16259	__	
			GCTTATTA TCTGTTTGTG		
			CGAATAAT AGACAGATAT		
			AA		
GAM2063	LHFPL2	3'	AGCAGCACAGAAACAAGCTA 34659	A A	TTG
			TAGCTT TT TCTGT TGCT		
			ATCGAA AA AGACA ACGA		
			C _ CG_		
GAM2063	LOC256683	5'	AGACAACAGATTATAAGCTA 46069	T	T G
			TAGCTTAT ATCTGTT GT CT		
			ATCGAATA TAGACAA CA GA		
			T _ _		
GAM2064	CD44	5'	GACCCAAGCTTCTAGAGATCCC 6212	A	AAA A
			GG ATCTCTAGAA TT GGTC		
			CC TAGAGATCTT AA CCAG		
			C CG_ C		
GAM2064	MRPL49	3'	ACCCTCACTCCTGGAGATTCCA 34476		AAAAATTA
			TGGAATCTCTAG GGT		
			ACCTTAGAGGTC CCA		
			CTCACTC_		
GAM2064	NPTX1	3'	GACAAGTCTTTCTAGAAATTCT 8354	C	A AG
			A TGG AAT TCTAGAAA ATT GTC		
			ATCTTA AGATCTTT TGA CAG		
			A C A_		
GAM2064	STAU	3'	GACCCAAC TTTTCTAGTGTGCC 10943	AATCT	A A
			A TGG CTAGAAAA TT GGTC		

			ACC GATCTTTT AA CCAG		
			GTGT_ C C		
GAM2064	STAU	3'	GACCCAACTTTTCTAGTGTGCC 18915	AATCT	A A
	A		TGG CTAGAAAA TT GGTC		
			ACC GATCTTTT AA CCAG		
			GTGT_ C C		
GAM2064	STAU	3'	GACCCAACTTTTCTAGTGTGCC 18921	AATCT	A A
	A		TGG CTAGAAAA TT GGTC		
			ACC GATCTTTT AA CCAG		
			GTGT_ C C		
GAM2064	STAU	3'	GACCCAACTTTTCTAGTGTGCC 18927	AATCT	A A
	A		TGG CTAGAAAA TT GGTC		
			ACC GATCTTTT AA CCAG		
			GTGT_ C C		
GAM2064	C5orf6	3'	GCCCTCTAGAGAATCCA 18704	A	AAAATTA
			TGGA TCTCTAGA GGT		
			ACCT AGAGATCT CCG		
			A C_____		
GAM2064	HEY1	3'	ACCTAATTTTCCTGGGACTGCC 43847	AA_ T	A
	A		TGG TC CTAG AAAATTAGGT		
			ACC AG GGTC TTTTAATCCA		
			GTC _ C		
GAM2064	KIAA0335	3'	GACCTAGGCTTTCAAAAGATTC 16731	CTA	AA
	CA		TGGAATCT GAAA TTAGGTC		
			ACCTTAGA CTTT GATCCAG		
			AAA CG		
GAM2064	KIAA0763	3'	GACTGTCCCCTTTAGAGATCCC 16967	A	AAAATTA
	A		TGG ATCTCTAGA GGTC		
			ACC TAGAGATTT TCAG		
			C CCCCTG_		
GAM2064	LOC221683	5'	GACCTAATTTGCAGACGAGCCC 45002	AA _	AGAA
			GG TC TCT AAATTAGGTC		
			CC AG AGA TTTAATCCAG		
			CG C CG_		
GAM2064	LOC91445	3'	GCCTCTTTCTGGAGACCCCA 30370	AA	AATT
			TGG TCTCTAGAAA AGGT		
			ACC AGAGGTCTTT TCCG		
			CC C_____		
GAM2065	APM1	3'	CCCATGGAGGAATTCTGA 11208	TG	A
			TCAGAAT TCTTCAT GG		

			AGTCTTA AGGAGGTA CC		
			— C		
GAM2065	PRKCB1	3'	CCTATGGAAAATGCAGCTG 34903	AA	C__
			CAG TTGT TTCCATAGG		
			GTC GACG AAGGTATCC		
			— TAA		
GAM2065	CAMK2G	5'	CCTATGGAAAACCTGTGGATA 34191	AGAATT	C
			TATC GT TTCCATAGG		
			ATAG CA AAGGTATCC		
			GTGTC_ A		
GAM2065	FLJ13769	3'	CCCATGGAAGACCCTGA 24591	AATT	A
			TCAG GTCTTCCAT GG		
			AGTC CAGAAGGTA CC		
			C__ C		
GAM2065	FLJ13955	3'	CCTATGGAACCTTGCCTGATG 24109	AATTGTC	
			TATCAG TTCCATAGG		
			GTAGTC AAGGTATCC		
			CGTTTC_		
GAM2065	FLJ13964	3'	CCTATGGTCACTTCTGATA 25902	T	TCTT
			TATCAGAA TG CCATAGG		
			ATAGTCTT AC GGTATCC		
			C T__		
GAM2065	HEMK	3'	CCTATGGAATCCAGTTCTGA 18266	TC	
			TCAGAATTG TTCCATAGG		
			AGTCTTGAC AAGGTATCC		
			CT		
GAM2065	HSPCAL3	3'	CCTATAGTTGACAATTCTG 37618	TTCC	
			CAGAATTGTC ATAGG		
			GTCTTAACAG TATCC		
			TTGA		
GAM2065	KIAA0217	3'	CCTACAGAGAAAATTCTGATA 33279	G	CCA
			TATCAGAATT TCTT TAGG		
			ATAGTCTTAA AGAG ATCC		
			A AC_		
GAM2065	Rpo1-2	3'	ATGGAGGACAATCCTGATA 21097	A	
			TATCAG ATTGTCTTCCAT		
			ATAGTC TAACAGGAGGTA		
			C		
GAM2065	TGOLN2	3'	CCTACAGAAGACATAGAAGATG 32023	AGAAT	CA
			TATC TGTCTTC TAGG		

		GTAG ACAGAAG ATCC	
		AAGAT AC	
GAM2065	LOC149844 3'	CCTATGGAAGATCCTGAT 38821	AATT
		ATCAG GTCTTCCATAGG	
		TAGTC TAGAAGGTATCC	
		C__	
GAM2065	LOC157567 3'	GGAAAAATAATTCTGATA 39612	C_
		TATCAGAATTGT TTCC	
		ATAGTCTTAATA AAGG	
		AA	
GAM2065	LOC158219 3'	CCTATGGAATGGCATTCT 39762	T _
		AGAAT GTC TTCCATAGG	
		TCTTA CGG AAGGTATCC	
		_ T	
GAM2065	LOC170132 5'	CCTATGGAAGTATTTCCGA 40177	A T T
		TC GAA TG CTTCCATAGG	
		AG CTT AT GAAGGTATCC	
		C T _	
GAM2065	LOC203350 3'	CCTACAGAACGGCAGTTTGA 43533	A _ CA
		TCAGA TTGTC TTC TAGG	
		AGTTT GACGG AAG ATCC	
		_ C AC	
GAM2065	LOC51313 3'	CCTATGGAAATCATTACATCT 18719	AT____ TC
	GA	TCAGA TG TTCCATAGG	
		AGTCT AC AAGGTATCC	
		ACACTT TA	
GAM2066	BAALC 3'	TCAATAAATTCCATGTTTAG 24198	CA
		TTAAACATGGAAT GTTGA	
		GATTGTACCTTA TAACT	
		AA	
GAM2066	cerk 3'	TTAGTGATTTACGTTTAA 23014	A G
		TTAAAC TGGAATCA TTGA	
		AATTTG ACTTTAGT GATT	
		C _	
GAM2066	DNCLI1 3'	TTTCAACTGTAATCAGTTAATA 29929	A A AAT
		TATTAA C TGG CAGTTGAAA	
		ATAATT G ACT GTCAACTTT	
		_ _ AAT	
GAM2066	HRH4 3'	TTTCTATGTTCCATGCATAATA 22265	AA T GTT
		TATTA CATGGAA CA GAAA	

ATAAT GTACCTT GT CTTT
 AC _ AT_
 GAM2066 KIAA0368 3' TTTCGTGGAAACTCCATGTTTA 32491 A__ AGT
 TAAACATGGA TC TGAAA
 ||||| || ||||
 ATTTGTACCT AG GCTTT
 CAA GT_
 GAM2066 SEMA3E 3' TTTCGTGATTCCACGTCTA 14811 A A GT
 TA AC TGGAATCA TGAA
 || || ||||| ||||
 AT TG ACCTTAGT GCTT
 C C _
 GAM2066 LOC153139 5' TTTCTTTATTCCATGTTCTATA 41575 TA CAGTT
 TAT AACATGGAAT GAAA
 || ||||| ||||
 ATA TTGTACCTTA CTTT
 TC TTT_
 GAM2066 LOC154184 5' TTTCTTTATTCCATGTTCTATA 41687 TA CAGTT
 TAT AACATGGAAT GAAA
 || ||||| ||||
 ATA TTGTACCTTA CTTT
 TC TTT_
 GAM2066 LOC221601 5' TTTCTTTATTCCATGTTCTATA 44984 TA CAGTT
 TAT AACATGGAAT GAAA
 || ||||| ||||
 ATA TTGTACCTTA CTTT
 TC TTT_
 GAM2067 KIAA1323 3' TCTTATTATATGTCCCTTA 31571 T ACGC
 TAAG GGACATATAG AGA
 |||| ||||| ||||
 ATTTCCTGTATATT TCT
 _ AT_
 GAM2067 MAP 3' TGCCTGTGTCCACTTG 23098 TATA
 TAAGTGGACA GACGCA
 ||||| ||||
 GTTCACCTGT CTGCGT
 _
 GAM2067 PP1044 5' CTGCATCTTTACCTATATCCAT 22327 C T__ C
 TTA TAAGTGGA ATA AGA GCAG
 ||||| || ||||
 ATTTACCT TAT TCT CGTC
 A CCATT A
 GAM2067 SIRPB1 3' TGCATGTGTCCACTTA 12712 AGAC
 TAAGTGGACATAT GCA
 ||||| ||||
 ATTCACCTGTGTA CGT
 _
 GAM2067 LOC93496 3' TCTATTGTATGTCACTTA 35867 G ACGC
 TAAGTG ACATATAG AGA
 |||| ||||| ||||

ATTCAC TGTATGTT TCT
 — A—
 GAM2068 ABCB10 3' ATGAGACTTTAATGCAA 14373 C A
 TTGCA TTAAAGTCT CAT
 |||| ||||| ||
 AACGT AATTCAGA GTA

— —
 GAM2068 PCDHA9 3' ACACTCTACCTTTAGTGCAAG 15207 T TCTACAT
 CTTGCACT AAAG TGT
 ||||| ||| ||
 GAACGTGA TTTC ACA
 — CATCTC—

GAM2068 PTGS1 3' TACAATCAGTTGACTTTAAGTG 27898 G T —
 AAAG CTT CACTTAAAGTC AC ATTGTA
 || ||||| || |||||
 GAA GTGAATTCAG TG TAACAT
 A T AC

GAM2068 PTGS1 3' TACAATCAGTTGACTTTAAGTG 6677 G T —
 AAAG CTT CACTTAAAGTC AC ATTGTA
 || ||||| || |||||
 GAA GTGAATTCAG TG TAACAT
 A T AC

GAM2068 KIAA1323 3' TGTAGACTTTAAAAACAA 31573 CAC
 TTG TTAAAGTCTACA
 || ||||| ||
 AAC AATTCAGATGT
 AAA

GAM2069 ABCB10 3' GAAGAAACCACTATTT 14375 CAG A
 AGATAGTGGT TTC TC
 ||||| ||| ||
 TTTATCACCA AAG AG
 — A

GAM2069 COG3 3' AAGGATGACAAACACTATC 25425 GTCAGT
 GATAGTG TCATCCTT
 ||||| |||||
 CTATCAC AGTAGGAA
 AAAC—

GAM2069 DMXL1 3' AAGGATGAACTAAATATTTTA 12022 GTGGTC
 TAAGATA AGTTCATCCTT
 ||||| |||||
 ATTTTAT TCAAGTAGGAA
 AAA—

GAM2069 GDF8 3' AAGAATAAACTGATGCTATCT 11763 G C C
 AGATAGTG TCAGTT AT CTT
 ||||| ||||| |||
 TCTATCGT AGTCAA TA GAA
 — A A

GAM2069 A4GALT 3' AAGGATGAACCTCAGGGCAC 18893 G A —
 GTG TC GTTCATCCTT
 ||| || |||||

			CAC GG CAAGTAGGAA		
			G ACTC		
GAM2069	KIAA1317	3'	ATGAACTGATCTGCATTC	41623	TA _
			GA GT GGTCAGTTCAT		
			CT CG CTAGTCAAGTA		
			TA T		
GAM2069	LOC114932	3'	AAGGATGAACTGACACCT	36003	TG
			AG GTCAGTTCATCCTT		
			TC CAGTCAAGTAGGAA		
			CA		
GAM2070	LPL	3'	TAGAACCTCCTATTTTAATTGG	5751	C AAAA
			CC GTTGAAATAG TTCTA		
			GG TAATTTTATC AAGAT		
			T CTCC		
GAM2070	FLJ14624	3'	AATTTTCTATCAAATGG	35336	GAA
			CCGTT ATAGAAAATT		
			GGTAA TATCTTTTAA		
			AC_		
GAM2070	GRID1	3'	TAGAATTTTCTACCCTTGGC	33981	TG AA_
			GT A TAGAAAATTCTA		
			CG T ATCTTTTAAGAT		
			GT CCC		
GAM2070	KIAA1336	3'	TAGAATTTTCCCACCAACG	35803	AAATA
			CGTTG GAAAATTCTA		
			GCAAC CTTTAAAGAT		
			CACC_		
GAM2070	STRIN	3'	TAGGAAAGCTATTTCAAC	18397	AAAA
			GTTGAAATAG TTCTA		
			CAACTTTATC AGGAT		
			GAA_		
GAM2070	LOC158314	3'	TAGAGGTAATTTCAAT	41953	AAAA
			GTTGAAATAG TTCTA		
			TAACTTTATC GAGAT		
			ATG_		
GAM2071	ADAR	3'	CAGCCATCCTCCCATCC	6771	A CAGCAT
			GGA TGGGAGGAT CTG		
			CCT ACCCTCCTA GAC		
			_ CC_		
GAM2071	ADAR	3'	CAGCCATCCTCCCATCC	17957	A CAGCAT
			GGA TGGGAGGAT CTG		

			CCT ACCCTCCTA	GAC		
			— CC—			
GAM2071	ADAR	3'	CAGCCATCCTCCCATCC	17964	A	CAGCAT
			GGA TGGGAGGAT	CTG		
			CCT ACCCTCCTA	GAC		
			— CC—			
GAM2071	COL6A1	3'	CCAAACCCTGTCCTCCCACCCC	7585	AA	T CATC
			GG TGGGAGGA CAG	TGG		
			CC ACCCTCCT GTC	ACC		
			CC — CCAA			
GAM2071	EBAF	3'	CAAATACTGACCCATTCTG	32606		AGGA C C
			CGGAATGGG TCAG AT TG			
			GTCTTACCC AGTC TA AC			
			— A A			
GAM2071	GJB1	3'	CAGGCAACCTCCCATCCC	30129	A	ATCA AT
			GG ATGGGAGG GC	CTG		
			CC TACCCTCC CG	GAC		
			C AA—			
GAM2071	HPCAL1	3'	GTGATGATCCTCCCATCCG	28637	A	G
			CGGA TGGGAGGATCA	CAT		
			GCCT ACCCTCCTAGT	GTG		
			— A			
GAM2071	HPCAL1	3'	GTGATGATCCTCCCATCCG	7930	A	G
			CGGA TGGGAGGATCA	CAT		
			GCCT ACCCTCCTAGT	GTG		
			— A			
GAM2071	HUNK	3'	CCAGATTCAAGTGATCCTCCCA	15947	GA	GC—
	TCTC		G ATGGGAGGATCA	ATCTGG		
			C TACCCTCCTAGT	TAGACC		
			TC GAACT			
GAM2071	IL2RA	5'	CCAGGCGGACCGATCTTCCCAT	5999	A	AGCA—
	CCC		GG ATGGGAGGATC	TCTGG		
			CC TACCCTTCTAG	GGACC		
			C CCAGGC			
GAM2071	MEIS1	3'	CAGATGCCCCCCCATCC	8217	A	A ATCA
			GGA TGGG GG GCATCTG			
			CCT ACCC CC CGTAGAC			
			— — C—			
GAM2071	NPR2L	3'	CCAAGAGTAACCCTCCCATCCC	13299	A	ATCA A —
			GG ATGGGAGG GC TCT GG			

CC TACCCTCC TG AGA CC
 C CAA_ _ A
 GAM2071 PVR 3' CCAAGTCATCCTCCCACC 13254 AA CA ATC
 GG TGGGAGGAT GC TGG
 || ||||| || |||
 CC ACCCTCCTA TG ACC
 _ C_ A_
 GAM2071 TJP1 5' CCAGAAGGGGATCCTCCCGCTC 9262 A AGCA
 CG CGGA TGGGAGGATC TCTGG
 ||| ||||| |||
 GCCT GCCCTCCTAG AGACC
 C GGGA
 GAM2071 CXorf1 3' CCAGACAATTCTCCCAGTCC 11054 A CAGCA
 GGA TGGGAGGAT TCTGG
 || ||||| |||
 CCT ACCCTCTTA AGACC
 G AC_
 GAM2071 DKFZP434K1772 5' CCAGATGCCCGCCCCGCCCC 33629 AA A_ ATCA
 GG TGGG GG GCATCTGG
 || ||| || |||||
 CC GCCC CC CGTAGACC
 CC CG ____
 GAM2071 DKFZp547D155 3' CCAAACATGGACGTCCTCCCCT 34867 AT CAG C_
 CC GGA GGGAGGAT CAT TGG
 ||| ||||| || |||
 CCT CCCTCCTG GTA ACC
 C_ CAG CAA
 GAM2071 FLJ12242 3' CCAGGGGGTCACTCCTCCCACC 23994 AA TCA A_
 CC GG TGGGAGGA GC TCTGG
 || ||||| || |||
 CC ACCCTCCT TG GGACC
 CC CAC GG
 GAM2071 FLJ12387 3' CCAGGCCTTAATCACCCCCATT 23100 AG_ C CA
 CCG CGGAATGGG GAT AG TCTGG
 ||||| ||| || |||
 GCCTTACCC CTA TT GGACC
 CCA A CC
 GAM2071 FLJ12975 3' CCAAGCAATCCTCCCACC 34479 AA CA ATC
 GG TGGGAGGAT GC TGG
 || ||||| || |||
 CC ACCCTCCTA CG ACC
 _ A_ A_
 GAM2071 KIAA0155 3' CCAGATGCTAAATCATTCC 16002 GAGGATC
 GGAATGG AGCATCTGG
 ||||| |||||
 CCTTACT TCGTAGACC
 AAA____
 GAM2071 KIAA1649 3' CCAGACTCAAGTGATCCTCCCA 26104 AA GCA____
 CC GG TGGGAGGATCA TCTGG
 || ||||| |||

CC ACCCTCCTAGT AGACC
 — GAACTC
 GAM2071 PRO0899 5' CCAAGAGATCCTCCCACCTCG 20648 AA AGCA _
 CGG TGGGAGGATC TCT GG
 ||| ||||| ||| ||
 GCT ACCCTCCTAG AGA CC
 CC — A
 GAM2071 TLOC1 5' CCAGGCGGCCGACCTCCCCATT 9272 _ A A A_
 CC GGAATGGG AGG TC GC TCTGG
 ||||| ||| || |||||
 CCTTACCC TCC AG CG GGACC
 C _ C GC
 GAM2071 LOC151877 3' CCAAATGATCTTCCCACCCC 41394 AA GCATC
 GG TGGGAGGATCA TGG
 || ||||| |||
 CC ACCCTTCTAGT ACC
 CC AA_
 GAM2071 LOC152179 5' CCAGATGCCAACAGCCACCATT 41432 GA ATCA_
 C GAATGG GG GCATCTGG
 ||||| || |||||
 CTTACC CC CGTAGACC
 A_ GACAAC
 GAM2071 LOC164714 5' CAGATGCTGAACCACTA 42176 GA A
 TGG GG TCAGCATCTG
 ||| || |||||
 ATC CC AGTCGTAGAC
 A_ A
 GAM2071 LOC253783 5' CCAAGTCATCCTCCCACC 45641 AA CA ATC
 GG TGGGAGGAT GC TGG
 || ||||| || |||
 CC ACCCTCCTA TG ACC
 — C_ A_
 GAM2071 LOC93166 3' CAGACGCATCCCATTTC 35460 GGATCA A
 GGAATGGGA GC TCTG
 ||||| || |||||
 CTTTACCCT CG AGAC
 A_ C
 GAM2072 COL17A1 3' ATACTAGAGTTCATGGATA 6106 _
 TATTCGT CTCTAGTAT
 ||||| |||||
 ATAGGTA GAGATCATA
 CTT
 GAM2073 C20orf98 3' CTGATAATAAATGGGCTCT 35415 CTC C
 AGAGCTCGTT AT ATCAG
 ||||| || |||||
 TCTCGGGTAA TA TAGTC
 A_ A
 GAM2073 KCNV1 3' ATTCTGATGATGAGTCTCT 15710 CTCGTT
 AGAG CTCATCATCAGAAT
 ||| |||||

TCTC GAGTAGTAGTCTTA
 T____
 GAM2073 KIAA0087 3' TTTGACAAAAATGAGCTCT 16562 CTCATCA
 AGAGCTCGTT TCAGA
 ||||| ||||
 TCTCGAGTAA AGTTT
 AAAC____
 GAM2073 KIAA1877 3' ATTCTGATAGTTTAGAAC 32879 C_ C
 GTTCT AT ATCAGAAAT
 |||| |||||
 CAAGA TG TAGTCTTA
 TT A
 GAM2073 MGC4643 3' TCCAATGATGGGACAGGCCT 26441 A TC T CA
 AG GC GTTC CATCAT GA
 || || |||| ||
 TC CG CAGG GTAGTA CT
 _ GA _ AC
 GAM2073 LOC219818 3' ATTCTGATGATGACTCCTACTC 43698 CTCGTTC
 GAG TCATCATCAGAAT
 || |||||
 CTC AGTAGTAGTCTTA
 ATCCTC_
 GAM2073 LOC254219 3' ATTCTGATGATTACTCAGAACT 46173 C GTTCTC
 CT AGAG TC ATCATCAGAAT
 |||| || |||||
 TCTC AG TAGTAGTCTTA
 A ACTCAT
 GAM2074 FLJ22405 5' CAAACACGAATGGGGATATCTG 22864 AATG_ A
 T ATAGATATT TCGT TTTG
 ||||| ||||
 TGTCTATAG AGCA AAAC
 GGGTA C
 GAM2074 KIAA1143 3' TTCAAAAACCTGACATTAATAG 34078 A _ A
 CTA TAG TATTAATGTC GT TTTGAA
 || ||||| |||||
 ATC ATAATTACAG CA AAACCTT
 G TC A
 GAM2075 ESRRG 3' TGATAATTTAGCAGCAA 32999 CCACA
 TTGCTGCTAAA TGTCA
 ||||| ||||
 AACGACGATTT ATAGT
 A____
 GAM2075 ITGAL 3' GATTGACGTACTTAGCAGC 7972 ACCAC
 GCTGCTAA ATGTCAATC
 ||||| |||||
 CGACGATT TGCAGTTAG
 CA____
 GAM2075 NUFIP1 3' ATTGAAGATAGGTTTAGCAGTA 14737 ACATG
 A TTGCTGCTAAACC TCAAT
 ||||| ||||

		AATGACGATTTGG AGTTA	
		ATAGA	
GAM2075	POU2AF1 3'	GATTTACAGTCCAGGCAGCAA 12892	AAACC A C
		TTGCTGCT AC TGT AATC	
		AACGACGG TG ACA TTAG	
		ACC__ _ T	
GAM2075	RAG2 5'	ATTAATACCTGGTTTAGCGGCA 39985	CA C
	A	TTGCTGCTAAACCA TGT AAT	
		AACGGCGATTTGGT ATA TTA	
		CC A	
GAM2075	TNS 3'	GGCATGTGGCTCAGCAGCAA 22903	AAA
		TTGCTGCT CCACATGTC	
		AACGACGA GGTGTACGG	
		CTC	
GAM2075	DKFZP434I092 3'	ATTGACATTCCAGTAGAGCAA 33673	G AACCAC
		TTGCT CTA ATGTCAAT	
		AACGA GAT TACAGTTA	
		_ GACCT_	
GAM2075	FLJ10656 3'	ATTAACATGGTAAGCCTTAGCA 19988	ACCA__ C
	GCAA	TTGCTGCTAA CATGT AAT	
		AACGACGATT GTACA TTA	
		CCGAATG A	
GAM2075	GABARAPL1 3'	TGGCAGTCCAGCAGCAA 25392	AA CACA
		TTGCTGCT AC TGTCA	
		AACGACGA TG ACGGT	
		CC ____	
GAM2075	GABARAPL3 3'	TGGCAGTCCAGCAGCAA 26300	AA CACA
		TTGCTGCT AC TGTCA	
		AACGACGA TG ACGGT	
		CC ____	
GAM2075	HT002 3'	GACGGTGATGACCCAGCAGCAA 15281	AAAC__ A
		TTGCTGCT CAC TGTC	
		AACGACGA GTG GCAG	
		CCCAGTA _	
GAM2075	KIAA0475 3'	GATTGGAAGTGGCCAGCAGCAA 16949	AAA ATG
		TTGCTGCT CCAC TCAATC	
		AACGACGA GGTG GGTTAG	
		CC_ AA_	
GAM2075	KIAA0712 5'	ATGCAGTTTCAGCAGCAA 16262	_ CA
		TTGCTGCT AAAC CAT	

		AACGACGA TTTG GTA		
		C AC		
GAM2075 KIAA1301	3'	GATTGACATATGGTTTGCCAG 32978	C	C
		CTG TAAACCA ATGTCAATC		
		GAC GTTTGGT TACAGTTAG		
		C A		
GAM2075 SEZ6	3'	GACTTGCACCACAGTCCAGCAG 36774	AA	CA_____ T
	CAA	TTGCTGCT AC CA GTC		
		AACGACGA TG GT CAG		
		CC ACACCAC T		
GAM2075 VMP1	3'	ATGTGATGTTTCAGCAGCAA 25204	A	__
		TTGCTGCT AAC CACAT		
		AACGACGA TTG GTGTA		
		C TA		
GAM2075 LOC115110	3'	ACGTGAGTCAGCAGCAA 35503	AA	CA
		TTGCTGCT AC CATGT		
		AACGACGA TG GTGCA		
		C_ A_		
GAM2075 LOC132235	5'	TGACACGGGAGCTAGCAGCA 37483	AA_	ACA
		TGCTGCTA CC TGTCA		
		ACGACGAT GG ACAGT		
		CGA GC_		
GAM2075 LOC142941	3'	CATGTGGTTTGCAGCAA 40322	T	
		TTGCTGC AAACCACATG		
		AACGACG TTTGGTGTAC		
		—		
GAM2075 LOC158549	5'	GACGTGTTTAAACAGCAA 42007	C	CC
		TTGCTG TAAA ACATGTC		
		AACGAC ATTT TGTGCAG		
		A _		
GAM2075 LOC221882	5'	GATTGGTATGGTAATTTAAAGC 44434	GC	CCA_ GT
	AA	TTGCT TAAA CAT CAATC		
		AACGA ATTT GTA GTTAG		
		A_ AATG TG		
GAM2076 DKFZP434F2021	3'	TTAACAAGGCTAGTTCA 33235	T	C
		TGAACTAG CC TGTTAG		
		ACTTGATC GG ACAATT		
		_ A		
GAM2076 PRO2435	5'	ATGTCACAGAGACTAGTTCA 20601	C	TA
		TGAACTAGTC CTGT GCAT		

ACTTGATCAG GACA TGTA
 A C_
 GAM2076 LOC220980 5' TGCAAATGACTAGTTCA 44740 CCT A
 TGAAGTAGTC GTT GCA
 ||||| ||||
 ACTTGATCAG TAA CGT
 _ A
 GAM2077 KIAA1582 5' CAACTATAACAATAAACTGTA 32583 A AATG
 AA TTTACAG TTTA TATAGTTG
 ||||| ||| |||||
 AAATGTC AAAT ATATCAAC
 A AACA
 GAM2077 LOC148709 3' TACATTTACACCTGTAAA 38584 ATT
 TTTACAG TAAATGTA
 ||||| |||||
 AAATGTC ATTTACAT
 CAC
 GAM2077 LOC57795 3' CAACTAAGCAGCCTCAGATCTG 34359 AAA_ A
 TAAA TTTACAGATTT TGT TAGTTG
 ||||| ||| |||||
 AAATGTCTAGA ACG ATCAAC
 CTCCG A
 GAM2078 CAPZA1 3' ATTAACAGCTATGTAAA 35947 CAA
 TTTACA CTGTTTAAT
 ||||| |||||
 AAATGT GACAAATTA
 ATC
 GAM2078 DKFZP586M1120 5' TCCGTTGACAGTTGTGTAAAA 25325 T TA
 TTTTACACAAGTGT AA GA
 ||||| || ||
 AAAATGTGTTGACAG TT CT
 _ GC
 GAM2078 KIAA0555 3' GAACAGTTCTGCAAAATA 30188 A C
 TATTTT CA AACTGTTT
 ||||| || |||||
 ATAAAA GT TTGACAAG
 C C
 GAM2078 PELI1 5' TTAAACAGTTTTGTAAAATA 21819 C
 TATTTTACA AACTGTTTAA
 ||||| |||||
 ATAAAATGT TTGACAAATT
 T
 GAM2078 RIN3 3' GGACAGTTGTGAAAATA 24234 A
 TATTTT CACAAGTGT
 ||||| |||||
 ATAAAA GTGTTGACAGG
 _
 GAM2078 LOC133686 3' TCTATTAGGAGTTTGGTAAAAT 37055 AC G
 A TATTTTAC AACT TTAAATAGA
 ||||| ||| |||||

ATAAAATG TTGA GGATTATCT
 GT _
 GAM2078 LOC153205 3' TCTATGATTCAAGTTTATGTAAA 41582 C_ TTTA
 ATA TATTTTACA AACTG ATAGA
 ||||| ||| |||
 ATAAAATGT TTGAC TATCT
 AT TTAG
 GAM2078 LOC221810 3' GAACAATGTGTAAAATA 45084 AC
 TATTTTACACA TGTTT
 ||||| |||
 ATAAAATGTGT ACAAG
 A_
 GAM2079 DXF68S1E 3' CATATGTATGTAGATATG 30151 G_
 TATG TACATACATATG
 ||| |||||
 GTAT ATGTATGTATAC
 AG
 GAM2079 PLAG1 3' ATGTATGTACAAGTTAGGT 8517 TG__
 ACCTA GTACATACAT
 ||| |||||
 TGGAT CATGTATGTA
 TGAA
 GAM2079 ELL2 3' CATATGTATATACAGGCTGA 14366 A ATG C
 TTA CCT GTA ATACATATG
 ||| ||| ||| |||||
 AGT GGA CAT TATGTATAC
 C _ A
 GAM2079 KIAA0090 3' CATAACATATGTGCAAGGTTAG 42652 ATG CA
 TTAACCT GTACATA TATG
 ||||| ||||| |||
 GATTGGA CGTGTAT ATAC
 A_ AC
 GAM2079 KIAA1622 3' ATATGTATGTGTGGTTA 27764 TATGG
 TAACC TACATACATAT
 ||||| |||||
 ATTGG GTGTATGTATA
 T____
 GAM2079 RERG 3' CATATGTATGTATTTATA 26738 _
 TATGG TACATACATATG
 ||||| |||||
 ATATT ATGTATGTATAC
 T
 GAM2079 LOC221288 3' TATGTACTATAGACATGTTAAT 44970 ____
 ATTAAC CTATGGTACATA
 ||||| |||||
 TAATTG GATATCATGTAT
 TACA
 GAM2079 LOC90488 3' CATATGTATAATGTGCCAGGT 31557 AT ____
 ACCT GGTACA TACATATG
 ||| ||||| |||||

			TGGA CCGTGT ATGTATAC		
			___ AAT		
GAM2080	CX3CR1	3'	TTGAAGTCAGATGTGGTA 34983	AC	C
			TACCACAT GACT CAG		
			ATGGTGTA CTGA GTT		
			GA A		
GAM2080	KIAA0720	5'	CAACCTCTGCGAGGCCTGTG 31231	TACGA	_
			CACA CTC CAGAGGTTG		
			GTGT GAG GTCTCCAAC		
			CCG_ C		
GAM2080	KIAA1102	3'	CTTAATAGAATCTATGTGGTA 34213	C C	CA_
			TACCACATA GA TC GAG		
			ATGGTGTAT CT AG TTC		
			_ A ATAA		
GAM2080	KIAA1257	3'	CAACCTCTAGAGTAGCTGGG 31430	A TACG	C
			CC CA ACTC AGAGGTTG		
			GG GT TGAG TCTCCAAC		
			_ CGA_ A		
GAM2080	PFTK1	3'	CAACCTCTAGAGATTGAGGTA 14751	A TACGA	C
			TACC CA CTC AGAGGTTG		
			ATGG GT GAG TCTCCAAC		
			A TA_ A		
GAM2081	CLN5	5'	CTTCAAATCAGACATTACA 13226	TTCC	A
			TGTGATGTCTG ATTT AAG		
			ACATTACAGAC TAAA TTC		
			___ C		
GAM2081	ARFGAP3	3'	TCTTTAAATGAACAAGTAACCA 15925	A_ TC	C
	CA		TGTG TG TGTTTCAATTAAGA		
			ACAC AT ACAAG TAAATTTCT		
			CA GA _		
GAM2081	FLJ30532	3'	AAATGGAACAACCTTCAC 29546	T C	
			GTGA GT TGTTCATTT		
			CACT CA ACAAGGTAAA		
			T _		
GAM2081	KIAA0319	3'	TGGGAAATCAAACATCACA 16764	C	___
			TGTGATGT TG TTCCA		
			AACTACA AC AGGGT		
			A TAA		
GAM2081	KIAA0416	3'	GAACGGAACAGCATCACA 17834	T	A
			TGTGATG CTGTTCC TTT		

			ACACTAC GACAAGG AAG			
			— C			
GAM2081	KIAA0555	3'	AGATAAAACAGACATCCA 30186	T	CC	
			TG GATGTCTGTT ATTT			
			AC CTACAGACAA TAGA			
			— AA			
GAM2081	MGC30052	3'	CTCTAAATGGGATTTAACCCAC 29542	ATGTCT	A	
	A		TGTG GTTCCATTTA AG			
			ACAC TAGGGTAAAT TC			
			CCAATT C			
GAM2081	MGC5139	5'	CTTAGTGGACAGACTCCACA 36677	AT T TA		
			TGTG GTCTGT CCATT AAG			
			ACAC CAGACA GGTGA TTC			
			CT — —			
GAM2081	NSG-X	3'	TAAATGAAAGTGGCATCACA 15754	TG C		
			TGTGATGTC TT CATTTA			
			ACACTACGG AA GTAAAT			
			TG A			
GAM2081	SLC12A5	3'	GATGAAACAGACATCCCA 21856	T C		
			TG GATGTCTGTT CATT			
			AC CTACAGACAA GTAG			
			C A			
GAM2081	TRIP-Br2	3'	CTTTATGAAAGACATCACA 16489	G CATT		
			TGTGATGTCT TTC TAAAG			
			ACACTACAGA AAG ATTTC			
			— T —			
GAM2081	LOC128954	5'	CTTTAAATGGACCATCCA 37320	T TCTGT		
			TG GATG TCCATTAAAG			
			AC CTAC AGGTAAATTTC			
			— C —			
GAM2081	LOC91948	3'	CTTTCTGGGAATAAACATCACA 33574	C ATTT		
			TGTGATGT TGTTCC AAAG			
			ACACTACA ATAAGG TTTC			
			A GTC_			
GAM2082	CAPZA1	3'	GAAAAACTAAAAATGAACCA 35952	AG C C		
			TGG TCA TTTAGTT TTC			
			ACC AGT AAAATCAA AAG			
			A_ A A			
GAM2082	FZD4	3'	GAAGAACCATTTTAACATC 14485	CACTTTTA		
			GATGGAGT GTTCTTC			

		CTACCTCA	CAAGAAG		
		ATTTTAC_			
GAM2082	SLC17A4	3'	AAGAACAATAATGATTCCATCA	11997	CTT A
			TGATGGAGTCA	TT GTTCTT	
			ACTACCTTAGT	AA CAAGAA	
			AAT _		
GAM2082	C6orf5	5'	GAAATAAAGTGACTCCTCA	17781	T TAG
			TGA GGAGTCACTTT	TTC	
			ACT CCTCAGTGAAA	AAG	
			_ TA_		
GAM2082	DKFZp434G179	3'	GAGAGAGGAAAGTAGACTCCAT	39041	_ AG
	CA		TGATGGAGTC ACTTTT	TTCTT	
			ACTACCTCAG TGAAAG	GAGAG	
			A GA		
GAM2082	FLJ20712	5'	GAAAAACTAAAAGAGTGCCCCA	19629	A T _ C
			TGG G CACTT	TTAGTT TTC	
			ACC C GTGAG	AATCAA AAG	
			C _ AA A		
GAM2082	KIAA1301	3'	GACTAACAGCAACTCCATCA	32977	CA T
			TGATGGAGT	CT TTAGTT	
			ACTACCTCA	GA AATCAG	
			AC C		
GAM2082	RAI17	3'	AGCTTGGAAGTCCATCA	43857	CAC TT
			TGATGGAGT	TT AGTT	
			ACTACCTCA	AG TCGA	
			_ GT		
GAM2082	LOC150630	5'	AACTAAAACAAGTCCAT	41236	CAC
			ATGGAGT	TTTTAGTT	
			TACCTCA	AAAATCAA	
			AC_		
GAM2082	LOC153259	5'	GAAAAATGGTGACTCCACA	41601	A TTTAG
			TG TGGAGTCACT	TTC	
			AC ACCTCAGTGG	AAG	
			_ TAAA_		
GAM2082	LOC201799	3'	AAGAATAATGTTCTCCTCA	42911	T TC TT
			TGA GGAG	AC TTAGTTCTT	
			ACT CCTC	TG AATCAAGAA	
			_ T_ T_		
GAM2082	LOC219578	5'	AAGCACTTAAACGACTTCATCA	45308	AC T T
			TGATGGAGTC	TTT AGT CTT	

			ACTACTTCAG AAA TCA GAA	
			C_ T C	
GAM2083	CDK2AP1	3'	TTTAAAAGATGCACGGAAAGTT 11017	A ACAC
	A		TAAC TT CC CATT TTTTAAA	
			ATTGAA GG GTAGAAAATTT	
			A CAC_	
GAM2083	GALNT7	3'	AGAATGGCAAGTAAGTTA 18876	CACA
			TAAC TTAC CCATTTT	
			ATTGAATG GGTAAGA	
			AAC_	
GAM2083	RAP1	3'	TAAAAAATAGTGGTGAG 21046	ACC
			CTTACCAC ATTTTTTA	
			GAGTGGTG TAAAAAAT	
			A_	
GAM2083	KIAA1096	3'	TTTAAAAAACGGTGCCAGGTA 33998	A_ A
			TACC CACC TTTTTTAAA	
			ATGG GTGG AAAAAATTT	
			ACC C	
GAM2083	PRO0097	5'	TTTAAATTGTTAATGTGGTAAG 15367	CC_ TT
	T		ACTTACCACA AT TTAAA	
			TGAATGGTGT TG AAATTT	
			AAT TT	
GAM2083	LOC255196	5'	TTTAGGAGACGTGGTAGGT 46416	ACCA
			ACTTACCAC TTTTTTAAA	
			TGGATGGTG AGAGGATTT	
			C_	
GAM2084	CYP1B1	3'	TAATTAATATATTTAAATTCCA 5566	AC_
	A		TTGGAATTT TGTATTAATTA	
			AACCTTAAA ATATAATTAAT	
			ATT	
GAM2084	FLJ14803	3'	TAATTAGTAAATTCCAA 26628	T
			TTGGAATTTACTG ATTA	
			AACCTTAAATGAT TAAT	
			-	
GAM2084	PTK9	3'	AATTATACTCTAAATTCCA 8690	CT T
			TGGAATTTA GTAT AATT	
			ACCTTAAAT CATA TTAA	
			CT _	
GAM2084	LOC122773	3'	TAATACAGTGGGTCAAATA 36711	G A
			TATT GA TTTACTGTATTA	

		ATAA CT GGGTGACATAAT		
		A _		
GAM2085	TSPY	3' ACTCCTGTCTCTGTAGAATA	39944	___ T
		TATTCTACAG CGGG GT		
		ATAAGATGTC GTCC CA		
		TCT T		
GAM2085	DAPK2	3' AAAAATTACACCAGAGAG	15631	ACAGCG
		TTCT GGTGTAATTTTT		
		GAGA CCACATTAAAAA		
		GA___		
GAM2085	LOC120856	3' AAAAATTACACAAAAGTAGAAT	36630	CAGCGG
	A	TATTCTA GTGTAATTTTT		
		ATAAGAT CACATTAAAAA		
		CAAAA_		
GAM2086	BAALC	3' AGGTCAGTTTATGAAACA	24194	A TT A
		TGTT TCATAAG CTGA CCT		
		ACAA AGTATTT GACT GGA		
		- - -		
GAM2086	NPTX1	3' TTCTTGCTTTTGATAACA	8358	T TCT
		TGTTATCA AAGT GAA		
		ACAATAGT TTCG CTT		
		T TT_		
GAM2086	BART1	3' TAGGCTCAGCTCATGATGACA	14425	A TT A
		TGTTATCAT AG CTGA CCTA		
		ACAGTAGTA TC GACT GGAT		
		C _ C		
GAM2086	KIAA0871	3' TAGGTAACCTATGATAACA	17334	A CTGA
		TGTTATCATA GTT ACCTA		
		ACAATAGTAT CAA TGGAT		
		C _ _		
GAM2086	KIAA0984	3' TAGGTTTCAGGGATGAGCAACA	32645	A_ AAG
		TGTT TCAT TTCTGAACCTA		
		ACAA AGTA GGGACTTGGAT		
		CG _		
GAM2086	MGC11242	3' GTAGGTTTCTCTCTGTAATAAC	23609	C _ TTCT
	A	TGTTAT ATA AG GAACCTAC		
		ACAATA TGT TC TTTGGATG		
		A C TC_		
GAM2086	SS18L1	3' TCAGAACTCATGCCAACA	32564	AT A
		TGTT CAT AGTTCTGA		

ACAA GTA TCAAGACT
 CC C
 GAM2086 LOC134553 3' AGGTTCAAGTGTAAACA 37076 T AAGTTC
 TGTTA CAT TGAACCT
 ||||| ||| |||||
 ACAAT GTG ACTTGGA
 _ A _
 GAM2086 LOC165552 3' TAGGCTCAGAACTTTTACA 40133 TATCAT A
 TGT AAGTTCTGA CCTA
 ||| ||||| |||||
 ACA TTCAAGACT GGAT
 TT _ C
 GAM2087 AF3P21 3' AGGCTGGACCAGACCCCC 18567 AA A TTT
 GG GT CTGGTTTA CCT
 || || ||||| |||
 CC CA GACCAGGT GGA
 CC _ C _
 GAM2087 GLP1R 3' TTAGGGAAACCAATAGTCC 7827 AG C TAT
 GGA TA TGGTT TTCCTAA
 ||| || ||||| |||||
 CCT AT ACCAA AGGGATT
 G _ A _
 GAM2087 GPR4 5' TAGGAAATGCCAGCACTCCC 30100 A A TT
 GG AGT CTGGT ATTCCTA
 || || ||||| |||||
 CC TCA GACCG TAAAGGAT
 C C _
 GAM2087 HOXD4 3' GATGAAACCAGTCTTCC 15979 T ATT
 GGAAG ACTGGTTT TC
 ||||| ||||| ||
 CCTTC TGACCAA AG
 _ GT _
 GAM2087 BIRC3 5' TAAGAAATAAAAGTGCTTCT 33369 GG C
 GGAAGTACT TTTATTTC TA
 ||||| ||||| ||
 TCTTCGTGA AAATAAAG AT
 _ A
 GAM2087 DCAMKL1 3' AGGAAATAGATGGTGCCCCC 11111 AA G
 GG GTACTG TTTATTTCCT
 || ||||| |||||
 CC CGTGGT AGATAAAGGA
 CC _
 GAM2087 DKFZP434C212 3' TTAGGAAATGTCTAGACCTCC 34171 A A TT
 GGA GT CTGG TATTTCCTAA
 ||| || ||||| |||||
 CCT CA GATC GTAAAGGATT
 C _ T _
 GAM2087 FLJ14641 5' TTAGGAAATCTAGGACTTCC 26592 A TTT
 GGAAGT CTGG ATTCCTAA
 ||||| ||||| |||||

CCTTCA GATC TAAAGGATT
 G ____
 GAM2087 GFRA4 3' TAGGAAATTGTATCAGCCTCC 22702 AGTA TT_
 GGA CTGGT ATTCCTA
 ||| |||| |||||
 CCT GACTA TAAAGGAT
 CC__ TGT
 GAM2087 KIAA0939 3' AGGAGGTACCAGCACCTGCC 31057 AA_ A TT
 GG GT CTGGT ATTCCT
 || ||||| |||||
 CC CA GACCA TGGAGGA
 GTC C ____
 GAM2087 KIAA0961 3' TTTAAGAAATAAGGTGGAAGCTC 17076 A A G C
 C GGA GT CTG TTTATTTC TAAA
 ||| || ||||| |||||
 CCT CA GGT GAATAAAG ATTT
 _ A G A
 GAM2087 KIAA1054 3' TAGGAAATAGTCCACTTGC 33956 G ACT T
 G AAGT GG TTATTCCTA
 | ||| || |||||
 C TTCA CC GATAAAGGAT
 G ____ T
 GAM2087 KIAA1297 5' AGGAGAGCCCCAGTACTGCC 35706 A TTTA
 GG AGTACTGG TTCCT
 || ||||| |||||
 CC TCATGACC AGAGGA
 G CCG_
 GAM2087 KIAA1854 3' AGGAGCCAGTCTTCC 35522 T TTATT
 GGAAG ACTGGT TCCT
 |||| ||||| |||||
 CCTTC TGACCG AGGA
 _ _
 GAM2087 MGC10715 3' AGGAAATGTCTTGACTCCC 23612 A ACT TT
 GG AGT GG TATTCCT
 || ||| || |||||
 CC TCA TC GTAAAGGA
 C GT_ T_
 GAM2087 My015 3' AAATACCTAACCAGTACTTCT 33104 ____
 GGAAGTACTGGTT TATTT
 ||||| |||||
 TCTTCATGACCAA ATAAA
 TCC
 GAM2087 PRO2893 3' TTTAGGAAATTGCACATACCTT 20706 TAC _ TT
 C GAAG TG GT ATTCCTAAA
 ||| || || |||||
 CTTC AC CG TAAAGGATTT
 CAT A T_
 GAM2087 RNP24 3' AGGATAAACCATACTTCC 13693 C TT
 GGAAGTA TGGTTTA TCCT
 ||||| ||||| |||||

CCTTCAT ACCAAAT AGGA

GAM2087 TNRC9 3' AGTGAGTAAACCACACTTCC 35319 AC TC
GGAAGT TGGTTTATT CT
||||| ||||| ||
CCTTCA ACCAAATGA GA
C_ GT

GAM2087 LOC121838 5' TTTAGGAAACAAAGATGGACTT 37419 A G_ A
CT GGAAGT CTG TTT TTTCCTAAA
||||| ||| ||| |||||
TCTTCA GGT AAA AAAGGATTT

GAM2087 LOC130814 3' TTTAGGAAATAAATCCTCTCC 37008 A TACT
GGA G GGTATTTCCTAAA
||| |||||
CCT C CTAAATAAAGGATTT
_ TC_

GAM2087 LOC144845 3' TTAGGAGTGCACCAGTACTCTC 28824 GA T T
G AGTACTGGT TATT CCTAA
| ||||| ||| |||||
C TCATGACCA GTGA GGATT
TC C _

GAM2087 LOC93550 3' TTTAGGAAACGAAATATTTCC 35934 CTGG TA
GGAAGTA TT TTTCCTAAA
||||| || |||||
CCTTTAT AA AAAGGATTT
A_ GC

GAM2088 IQGAP2 3' ATTTGATACTATAATAGAATGA 13428 _ TA_ |||
GACATA TCTC TTCT TATCAAA T
||| ||| ||||| |
AGAG AAGA ATAGTTT A
T TAATATC |||

GAM2088 NCSTN 3' TGA CTGGGAAGGACATA 36509 T TA
TATGTC CTTCTTA TCA
||||| ||||| |||
ATACAG GAAGGGT AGT
_ C_

GAM2088 CHST3 3' TTTGAAAAGAAGAGACA 10487 ATA
TGTCTCTTCTT TCAAA
||||||| |||||
ACAGAGAAGAA AGTTT
A_

GAM2088 FLJ11577 3' ATTTGAAGAAACATAGGA 24799 C TT
TTCTATGT TCTTC AT
||||| ||||| ||
AGGATACA AGAAG TA
A TT

GAM2088 FTS 3' GTGAGAAGAAACCAGAA 22844 AT C
TTCT GT TCTTCTTAT
||| || |||||

		AAGA CA AGAAGAGTG			
		C_ A			
GAM2088	GIT2	3' TTTGATTTTTC	AAGAGACAAGA 16607	A	CTTAT
	A	TTCT TGTCTCTT ATCAAA			
		AAGA ACAGAGAA TAGTTT			
		_ CTTT			
GAM2088	GIT2	3' TTTGATTTTTC	AAGAGACAAGA 27689	A	CTTAT
	A	TTCT TGTCTCTT ATCAAA			
		AAGA ACAGAGAA TAGTTT			
		_ CTTT			
GAM2088	GIT2	3' TTTGATTTTTC	AAGAGACAAGA 27702	A	CTTAT
	A	TTCT TGTCTCTT ATCAAA			
		AAGA ACAGAGAA TAGTTT			
		_ CTTT			
GAM2088	IDN3	3' TTTGATATAAAA	AGAACTATA 28514	_ C	C
	G	CTAT GT TCTT TTATATCAAA			
		GATA CA AGAA AATATAGTTT			
		T A A			
GAM2088	KIAA0478	3' TATGGGTAAAG	AGACATGAA 16985	T	_
		TTC ATGTCTCTT CTTATA			
		AAG TACAGAGAA GGGTAT			
		_ AT			
GAM2088	KIAA1681	3' TTTGGGTGGAAG	AGGCATAGAA 30612		TATA
		TTCTATGTCTCTTCT TCAAA			
		AAGATACGGAGAAGG GGTTT			
		TG_			
GAM2088	LOC153688	3' TTTGACAGGGGG	GAGAAACAGAA 41664	ATG	ATA
		TTCT TCTCTTCTT TCAAA			
		AAGA AGAGGGGGA AGTTT			
		CAA C_			
GAM2088	LOC200301	3' ATGAGAGAGAC	ACAGAA 42780	A	T
		TTCT TGTCTCT CTTAT			
		AAGA ACAGAGA GAGTA			
		C _			
GAM2088	LOC255458	5' TATAAAAAG	AGACACAAGA 46408	A_	C
		TCT TGTCTCTT TTATA			
		AGA ACAGAGAA AATAT			
		AC A			
GAM2089	PRKG1	3' AGTAACTACAG	TGGCATTAA 12936	A	_
		TAAT CTACTGTAGT ACT			

		ATTA GGTGACATCA TGA		
		C A		
GAM2089	ASPN	3' TCTATTAATAATGGTAGTATTA 19225	A	AC
		TAATACTACTGT GT TAATAGA		
		ATTATGATGGTA TA ATTATCT		
		A ____		
GAM2089	DKFZp434A2417	3' TCTACTAGGTTATAAGTAGTAT 32863	GTAGTA	A
		ATACTACT CTA TAGA		
		TATGATGA GAT ATCT		
		ATATTG C		
GAM2089	LOC257017	5' CTATTTGAGACTAAAGTAGTAT 46495	G	ACT_
		ATACTACT TAGT AATAG		
		TATGATGA ATCA TTATC		
		A GAGT		
GAM2090	M11S1	3' AGCTTTTCCAGTTAAATTG 12515	A	
		TAATTTAACT GAAAAGCT		
		GTAAATTGA CTTTTCGA		
		C		
GAM2090	MEIS2	3' AGCCCCACAATGTAAATTCTG 21346	T	TAGAAAA_
	TA	TACAG AATTTAAC GCT		
		ATGTC TTAAATTG CGA		
		____ TAACACCC		
GAM2090	RRM2	3' AGCTTCTTAAGTTAAATCACT 6697	A	A A
		AGT ATTTAACT GA AAGCT		
		TCA TAAATTGA TT TTCGA		
		C A C		
GAM2090	SLC4A4	3' CTTTTTTTTTAATTACTGTA 9836	TA	ACT
		TACAGTAATT AGAAAAG		
		ATGTCATTAA TTTTTTC		
		TT____		
GAM2090	C1orf22	3' AGCTTTTAAAATTTAAATTAC 24835	CTAG_	
		GTAATTTAA AAAAGCT		
		CATTAAATT TTTTCGA		
		TAAAA		
GAM2090	INSM2	5' AGCTCTTCTAGTTCATCTGCT 26325	ATTT	A
		AGTA AACTAGAA AGCT		
		TCGT TTGATCTT TCGA		
		CTAC C		
GAM2090	KIAA0352	3' AGCCTCTCTAGTTTTAGTTTAC 16821	TTT_	AAA
	TG	CAGTAA AACTAGA GCT		

		GTCATT TTGATCT CGA	
		TGATT CTC	
GAM2090	PRO2730	5' AGCTTTTCTAACTGTCACTG 24897	A TTAAC
		CAGT AT TAGAAAAGCT	
		GTCA TG ATCTTTTCGA	
		C TCA__	
GAM2090	Spir-1	3' TTTTCTAACTATATTACTGTA 32310	T AC
		TACAGTAAT TA TAGAAAAG	
		ATGTCATTA AT ATCTTTT	
		T CA	
GAM2090	LOC253649	5' AGCTTTTCTACCTGTCCCTGTA 45998	TA TTAAC
		TACAG AT TAGAAAAGCT	
		ATGTC TG ATCTTTTCGA	
		CC TCC__	
GAM2090	LOC253650	5' AGCTTTTCTACCTGTCCCTGTA 45996	TA TTAAC
		TACAG AT TAGAAAAGCT	
		ATGTC TG ATCTTTTCGA	
		CC TCC__	
GAM2091	FGF7	5' AAACAAAAGTCAAATAGCA 7746	GG_
		TGCTATTTGGT TGTT	
		ACGATAAACTG ACAA	
		AAA	
GAM2091	GAD1	3' AAACACCACCAAATGACA 6477	C
		TG TATTTGGTGGTGTTT	
		AC GTAAACCACCACAAA	
		A	
GAM2091	SURF4	3' GAAACACATCAAAATAAATAAT 27013	GCTA G
	G	CATTAT TTTGGTG TGTTTC	
		GTAATA AAACCTAC ACAAAG	
		AATA _	
GAM2091	KIAA1866	3' AAACACCACCAAAGAAAATAA 30551	GCTA
		TTAT TTTGGTGGTGTTT	
		AATA AAACCACCACAAA	
		AAAG	
GAM2091	RGS18	3' TTACCAAAGCAGCATAAT 28271	A_
		ATTATGCT TTTGGTGG	
		TAATACGA AAACCATT	
		CG	
GAM2091	ZNF237	3' AAACACACGAAGCATAAT 15503	ATT G G
		ATTATGCT T GTG TGTTT	

TAATACGA A CAC ACAA
 ____ G ____
 GAM2091 LOC144874 5' GAAACACAAATTATAGCATAA 40467 TTGGTG
 TTATGCTAT GTGTTTC
 ||||| |||||
 AATACGATA CACAAAG
 TTAAA_
 GAM2092 TEM8 3' TCCTAAAATTCCTGTCC 25920 CTTAT C
 GGAT AGGAATT TAGGA
 ||| ||||| |||||
 CCTG TCCTTAA ATCCT
 ____ A
 GAM2092 FLJ10458 3' TCCTAGAATCCCCATGACTC 19867 TC A A
 GA TTAT GG ATTCTAGGA
 || ||| || |||||
 CT AGTA CC TAAGATCCT
 C_ C C
 GAM2092 KIAA0478 5' TCCTAGAATTTGGATAAACC 16987 ATC AG
 GG TTAT GAATTCTAGGA
 || ||| |||||
 CC AATA TTTAAGATCCT
 A_ GG
 GAM2092 ZWINT 3' TCCTAGAAAAGGTCAGACCC 26877 A T AGGAA
 GG TCT AT TTCTAGGA
 || ||| || |||||
 CC AGA TG AAGATCCT
 C C GAA_
 GAM2092 LOC144231 5' TCCTGGGAGCCCACAAGATCC 40395 ATA AA
 GGATCTT GG TTCTAGGA
 ||||| || |||||
 CCTAGAA CC AGGGTCCT
 CA_ CG
 GAM2093 AP1S2 3' AACGTTCAACGTACAAACA 9999 T TTACG
 TGTTT GTAT TGAACGTT
 ||||| ||| |||||
 ACAAA CATG ACTTGCAA
 _ CA_
 GAM2094 GM2A 3' CAGAAAGTCACAGCACATGTG 33658 AAA A
 CACATGT TGT ACTTTCTG
 ||||| ||| |||||
 GTGTACA ACA TGAAAGAC
 CG_ C
 GAM2094 LCP1 3' AGAAAGCCAACATGTGG 8081 AAA TAA
 TCACATGT TG CTTTCT
 ||||| || |||||
 GGTGTACA AC GAAAGA
 ____ C_
 GAM2094 RPS6KA5 3' CAGAAAACAAGTACTATGTGAT 11142 _ AA AAC
 ATCACAT GTA TGT TTTCTG
 ||||| ||| ||| |||||

			TAGTGTA CAT ACA AAAGAC		
			T GA ____		
GAM2094	TP63	3'	AAAGGTATTATACATGTGAT 9814	AAT	A
			ATCACATGTA GTA CTTT		
			TAGTGACAT TAT GAAA		
			AT_ G		
GAM2094	VPS41	3'	CAGTTTATTACATTTACAT 15737	CTTT	
			ATGTAAATGTAA CTG		
			TACATTTACATT GAC		
			ATTT		
GAM2094	KIAA0766	3'	CAGAAAAAAGTTACATGTCTGA 16740	_	ATGTAAC
			T ATC ACATGTAA TTTCTG		
			TAG TGTACATT AAAGAC		
			C GAAAA_		
GAM2094	PEG10	3'	AGAAAGTTTACATACAT 17422	AA	_
			ATGTA TGTA CTTTCT		
			TACAT ACATT GAAAGA		
			_ T		
GAM2094	LOC146506	3'	AGAAATACTCCATGTGAT 38177	TAAAT	AC
			ATCACATG GTA TTTCT		
			TAGTGAC CAT AAAGA		
			CT_ _		
GAM2094	LOC149301	3'	CAGGCTTCACTTTACATGTGAT 38689	T	AACTT
			ATCACATGTAAA GT TCTG		
			TAGTGACATTT CA GGAC		
			_ CTTC_		
GAM2094	LOC153525	3'	CAGAAAGTTACATTGCTTTGT 41637	TGTA	
			ACA AATGTA AACTTTCTG		
			TGT TTACATTGAAAGAC		
			TTCG		
GAM2094	LOC255520	3'	CAGAAAAGGTTACACATG 45878	AAAT	_
			CATGT GTA AACT TTCTG		
			GTACA CATTGG AAGAC		
			_ AA		
GAM2095	KIT	3'	GAACCATCCATAGTAGTATGAT 5732	GCAG	AA
			G CATCATAT GTGGAT TTC		
			GTAGTATG TACCTA AAG		
			ATGA CC		
GAM2095	PUM2	3'	GATAATTCCAGAATGCCTGTAT 17634	T_	TAAT
			ATGATG ATATGCAGG GGA TC		

TATATGTCC CCT AG
 GTAAGAIII TAAT
 GAM2095 SLC25A13 3' AAATTCCAAAAGTCTCATATG 15523 CA_ T_____ TAAT
 ATG TCATATG GG GGA T
 ||||| || || |
 AGTATAC TC CCT A
 TCG AAAAIII TAAT
 GAM2095 STARD5 5' AATTATCCAAAGCATCACTGA 24947 T__ AGG
 TCA ATGC TGGATAATT
 || ||| |||||
 AGT TACG ACCTATTAA
 CAC AA_
 GAM2095 TMEM1 3' AATTATCCAACTACATAT 9287 C G
 ATATG AG TGGATAATT
 |||| || |||||
 TATAC TC ACCTATTAA
 A A
 GAM2095 BC022889 3' AATTATCTCCTGTGCACATGA 40682 A _ TG
 TCAT TGCA GG GATAATT
 ||| ||| || |||||
 AGTA ACGT TC CTATTAA
 C G CT
 GAM2095 C22orf19 3' AAATTCCAGAAATCTGCATATA 9771 C T_____ TAAT
 AT TATATGCAGG GGA T
 | ||||| || |
 A TATACGTCT CCT A
 A AAAGAIII TAAT
 GAM2095 DKFZp761D221 3' GAATTATCCAGCATATGA 26055 AGG
 TCATATGC TGGATAATTC
 ||||| |||||
 AGTATACG ACCTATTAAG

 GAM2095 DKFZP761G1913 3' GAACTATCCACCTCATTA 25544 T C A
 A ATG AGGTGGATA TTC
 | || ||||| |||
 A TAC TCCACCTAT AAG
 T _ C
 GAM2095 FLJ10706 5' AATTATTCGATGACATGATG 20037 ATG GG
 CATCAT CA TGGATAATT
 |||| || |||||
 GTAGTA GT GCTTATTAA
 CA_ A_
 GAM2095 HSD17B12 3' GGAATTATTTCTGACACATGA 18226 A _ TG
 TCAT TG CAGG GATAATTCC
 ||| || ||| |||||
 AGTA AC GTCT TTATTAAGG
 C A _
 GAM2095 KIAA1078 3' GAACTAATGTCTCATATGATG 32470 C GT GA A
 CATCATATG AG G TA TTC
 ||||| || | |||

GTAGTATAC TC T AT AAG
 _ TG A_ C
 GAM2095 SEC24D 5' GAATTATCCTATGGAATGAT 16800 ATG GGT
 ATCAT CA GGATAATTC
 |||| || |||||
 TAGTA GT CCTATTAAG
 AG_ AT_
 GAM2095 LOC158428 5' GAATTAACATATATGATG 34921 GCAG GA
 CATCATAT GTG TAATTC
 ||||| || |||||
 GTAGTATA TAC ATTAAG
 ____ A_
 GAM2095 LOC257428 5' GATAATTCCGAAACGCCTGCAC 45262 A T_____ TAAT
 ATGA AT TGCAGG GGA TC
 || ||||| || ||
 TA ACGTCC CCT AG
 C GCAAAG||| TAAT
 GAM2095 LOC91549 3' GAATCATAGTTGCCTGCATATA 33014 C TG ATA_
 TG CAT ATATGCAGG G ATTC
 ||| ||||| | |||
 GTA TATACGTCC T TAAG
 _ GT GATAC
 GAM2096 LEC3 3' TGATAAACTAATGGCA 17574 A GTATC
 TGCCATTA GT TATCA
 ||||| || ||||
 ACGGTAAT CA ATAGT
 _ AA_
 GAM2097 PDE4D 3' TTCATCTGCCACTGGTTA 36438 A TATC
 TAACCGGT GTA TGAA
 ||||| || |||
 ATTGGTCA CGT ACTT
 C CT_
 GAM2097 TRO 5' ATTCAGATATACAGACTG 18247 A_
 CGGT GTATATCTGAAAT
 ||| |||||
 GTCA CATATAGACTTTA
 GA
 GAM2097 SFRS12 5' ATTCAGATGATGCAGCC 29175 A _
 GGT GTAT ATCTGAAAT
 ||| ||| |||||
 CCG CGTA TAGACTTTA
 A G
 GAM2097 TM4SF11 3' ATTCAGACATACCAGTTA 18083 C GTATA
 TAAC GGTA TCTGAAAT
 ||| ||| |||||
 ATTG CCAT AGACTTTA
 A AC_
 GAM2097 ZNF11B 5' ATTCAGGGGTCTACCGG 36614 T AT
 CCGGTAG AT CTGAAAT
 ||||| || |||||

GGCCATC TG GACTTTA
 _ GG
 GAM2097 LOC158476 3' ATTTCAGATGACTGCAGTTA 41997 CG A
 TAAC GTAGT TATCTGAAAT
 |||| |||| ||||
 ATTG CGTCA GTAGACTTTA
 A_ _
 GAM2098 ABCB4 5' ATGGTCATGGTAGACTGAT 6030 A _ T
 ATCA TCTATCAT AC CGT
 |||| |||| || ||
 TAGT AGATGGTA TG GTA
 C C _
 GAM2098 ABCB4 5' ATGGTCATGGTAGACTGAT 20835 A _ T
 ATCA TCTATCAT AC CGT
 |||| |||| || ||
 TAGT AGATGGTA TG GTA
 C C _
 GAM2098 GEMIN5 3' ATAACAAATGGATTGATG 42972 CATACTC
 CATCAATCTAT GTTAT
 |||| ||||
 GTAGTTAGGTA CAATA
 AA_____
 GAM2098 FLJ20152 3' AGCTGACACTGATAGATTGAT 21071 TAC _
 ATCAATCTATCA TC GTT
 |||| || ||
 TAGTTAGATAGT AG CGA
 CAC T
 GAM2098 KIAA0923 3' TAGCCATGATAGATGATG 15244 A ACTC
 CATCA TCTATCAT GTTA
 |||| |||| ||
 GTAGT AGATAGTA CGAT
 _ C____
 GAM2098 LOC144920 3' ATAACGAGTATGCAATTTG 40465 TCTAT
 CAA CATACTCGTTAT
 || ||||
 GTT GTATGAGCAATA
 TAAC_
 GAM2099 NEBL 3' AATACAGATATATACAAATAT 13095 C A
 ATATTTGTATA ATCT GTATT
 |||| || ||||
 TATAAACATAT TAGA CATAA
 A _
 GAM2099 DKFZp761K1423 3' TAGTTGTATATAAATATTA 20473 T
 TAATATTTGTATACA CTA
 |||| || ||
 ATTATAAATATATGT GAT
 T
 GAM2099 NESHBP 3' AATACTAGATGTTTATTATTA 17726 TTT T
 TAATA GTA ACATCTAGTATT
 |||| || ||||

		ATTAT TAT TGTAGATCATAA		
		____ T		
GAM2099	LOC145786 5'	ACAGTCTGTATACAAATA 40589		T_ A
		TATTTGTATACA CT GT		
		ATAAACATATGT GA CA		
		CT _		
GAM2099	LOC157292 3'	AGAAGATATACAAATATTA 41773		CA_
		TAATATTTGTATA TCT		
		ATTATAAACATAT AGA		
		AGA		
GAM2100	ARHGEF12 3'	TCCAGATTTCTGTTTCTGTCCT 17630		_ AAT TA
	AA	TTAGG CA ATA AAATCTGGA		
		AATCC GT TGT TTAGACCT		
		T CTT C_		
GAM2100	PTGS1 3'	CCAAATATGTATTTTCCTAA 27893	C	AAATC
		TTAGG AAATATATA TGG		
		AATCC TTTATGTAT ACC		
		T AA_		
GAM2100	PTGS1 3'	CCAAATATGTATTTTCCTAA 6672	C	AAATC
		TTAGG AAATATATA TGG		
		AATCC TTTATGTAT ACC		
		T AA_		
GAM2100	SQSTM1 3'	CCAGCACATAGCTTGCCTAA 9988		ATA AAAAT
		TTAGGCAA TAT CTGG		
		AATCCGTT ATA GACC		
		CG_ CAC_		
GAM2100	BCMP1 3'	CCACATACATTTGCCTA 25455	A	AAAATC
		TAGGCAAAT TAT TGG		
		ATCCGTTTA ATA ACC		
		C C_		
GAM2100	C20orf45 3'	ATTTTACATTTGCCTAA 18121		ATA
		TTAGGCAAAT TAAAT		
		AATCCGTTTA ATTTA		
		C_		
GAM2100	FLJ10726 3'	TCCATTGCTGTATATTTGCCTA 20059		AAATC
	A	TTAGGCAAATATATA TGGA		
		AATCCGTTTATATGT ACCT		
		CGTT_		
GAM2100	FLJ20079 3'	CCAGATTTTCATATTGCT 19171	AAT	A
		GGCA ATAT AAATCTGG		

		TCGT TATA TTTAGACC		
		___ C		
GAM2100	FLJ20508	3' CCAAATCTTTGTGTTTGCCTA	19516	TAAA C
		TAGGCAAATATA AT TGG		
		ATCCGTTTGTGT TA ACC		
		TTC_ A		
GAM2100	FLJ22794	3' TTTCATATCTTTGCCTAA	44039	T A
		TTAGGCAAA ATAT AAA		
		AATCCGTTT TATA TTT		
		C C		
GAM2100	HRH4	3' TCCAGATTTTATATTCCTAA	22263	CAAAT
		TTAGG ATATAAAATCTGGA		
		AATCC TATATTTTAGACCT		
		T___		
GAM2100	KIAA0565	3' CCAGATTAAGGTATTTGTCTAA	33218	ATAA
		TTAGGCAAATAT AATCTGG		
		AATCTGTTTATG TTAGACC		
		GAA_		
GAM2100	PDE3A	3' CCAGGTCTACTTGCCTAA	6631	A TATAAA
		TTAGGCAA TA ATCTGG		
		AATCCGTT AT TGGACC		
		C C___		
GAM2100	LOC148254	3' TCCAGATTCTTATTCCTGCC	38505	AAT TAA
		GGCA ATA AATCTGGA		
		CCGT TAT TTAGACCT		
		CCT TC_		
GAM2100	LOC256207	3' CCAGATTAAGGTATTTGTCTAA	45619	ATAA
		TTAGGCAAATAT AATCTGG		
		AATCTGTTTATG TTAGACC		
		GAA_		
GAM2101	BARHL1	3' AAACCTTCTTACAAATGACCAG	21299	A TACATT
		CTGGT CATTTGTA GTTT		
		GACCA GTAAACAT CAAA		
		_ TCTT_		
GAM2101	COL1A1	3' AAACAATGTATTGTCTGCCCAG	5537	TA TTTGT
		CTGG CA ATACATTGTTT		
		GACC GT TATGTAACAAA		
		C_ CTGT_		
GAM2101	SMARCA3	3' AAACAATATATACAGACTATAC	9036	CA_ C
		GTA TTTGTATA ATTGTTT		

			CAT	AGACATAT	TAACAAA	
			ATC	A		
GAM2101	ABLM	3'	AAACAATGTATAGGTACACAG	8109	_	ATTG
			CTG GTAC	TATACATTGTTT		
			GAC CATG	ATATGTAACAAA		
			A	G__		
GAM2101	ABLM	3'	AAACAATGTATAGGTACACAG	13542	_	ATTG
			CTG GTAC	TATACATTGTTT		
			GAC CATG	ATATGTAACAAA		
			A	G__		
GAM2101	LOC202451	3'	AAACAATGTGATAGAATATCCA	43434		TACA A
	G		CTGG	TTTGT TACATTGTTT		
			GACC	AGATA GTGTAACAAA		
			TATA	_		
GAM2102	HS2ST1	3'	TATATGATATTGGGTTGATA	14578		TAGA
			TATCA	CAGTATCATATA		
			ATAGT	GTTATAGTATAT		
			TGG_			
GAM2102	PLAGL1	3'	TATATGATATACTATGA	8529		ACA
			TCATAG	GTATCATATA		
			AGTATC	TATAGTATAT		
			A__			
GAM2102	PPP1CB	3'	ATATGATACTGTATAGA	8555		A G
			TC TA	ACAGTATCATAT		
			AG AT	TGTCATAGTATA		
			_ A			
GAM2102	PTPRJ	3'	ATGAAGCTGCATATGATA	8729		GA A
			TATCATA	CAGT TCAT		
			ATAGTAT	GTCG AGTA		
			AC	A		
GAM2102	TACSTD2	3'	ATATGTTGTCTTTGATA	8159		T TAT
			TATCA	AGACAG CATAT		
			ATAGT	TCTGTT GTATA		
			T	__		
GAM2102	CAT56	3'	TATGGTCTATCTATGAT	24933		C T
			ATCATAGA	AG ATCATA		
			TAGTATCT	TC TGGTAT		
			A	_		
GAM2102	DKFZp761K1423	3'	TATATGATACATGTAAATG	20474		AG _
			CAT	ACA GTATCATATA		

		GTA TGT CATAGTATAT		
		AA A		
GAM2102	KIAA0155	3' TATATGAAAGCTGTGATA	16004	ACAGTA
		TATCATAG TCATATA		
		ATAGTGTC AGTATAT		
		GAA__		
GAM2102	KIAA1198	3' TATATGTGGGTCTATGATG	31714	AGTAT
		TATCATAGAC CATATA		
		GTAGTATCTG GTATAT		
		GGT__		
GAM2102	KIAA1915	3' ATATGATGTCTATGA	36267	GTA
		TCATAGACA TCATAT		
		AGTATCTGT AGTATA		

GAM2102	ZNF387	3' ATATGTGCTGTCTATTATA	16173	C T
		TAT ATAGACAGTA CATAT		
		ATA TATCTGTCGT GTATA		
		T _		
GAM2102	LOC147343	5' TATATGCATTTGTCTATG	40832	TAT
		CATAGACAG CATATA		
		GTATCTGTT GTATAT		
		TAC		
GAM2102	LOC164684	3' TATATGAATAGGCTATGGTA	40161	ACAGTA
		TATCATAG TCATATA		
		ATGGTATC AGTATAT		
		GGATA_		
GAM2103	PCDH10	3' TAGTTTTGTGACTTAATTAC	26771	AG A
		GTAATTAA CA TAAACTA		
		CATTAATT GT GTTTTGAT		
		CA _		
GAM2103	LOC150848	5' TAGTTCTACTGCTTGATTACTT	41257	A A A
		AAGTAATTAA GCA TA AACTA		
		TTCATTAGTT CGT AT TTGAT		
		_ C C		
GAM2103	LOC160414	3' TAGTTTTGGTGTCCCACAATTA	42105	AAA__ A
	CTTA	TAAGTAATT GCA TAAACTA		
		ATTCATTAA TGT GTTTTGAT		
		CACCC G		
GAM2104	CTNNBIP1	3' ATCGTTTGTTTATGAAATGCCA	21542	CC TAAT
		TGGTAT CATAAATG CGAT		

ACCGTA GTATTTGT GCTA
 AA TT__
 GAM2105 KIAA0459 3' CACACATGAGCTCACACA 30571 C TT CA
 TG GT GC TCATGTGTG
 || || || |||||
 AC CA CG AGTACACAC
 A CT __
 GAM2106 CBS 5' CCGAAGCAAGAAGTTAACCAA 5517 C CTAA_
 TTGGTTAAC TCT CGG
 ||||| || ||
 AACCAATTG AGA GCC
 A ACGAA
 GAM2106 RAB6A 3' CTGGGAGAGAAAATTAACCAA 8776 CC_ AA
 TTGGTTAA TCTCT CGG
 ||||| |||| ||
 AACCAATT AGAGA GTC
 AAA GG
 GAM2106 SCN1A 3' TCCACCGCCAGAAGACTGAATT 42835 CC___ _ AA A
 GACCAA TGGTTAA TCT CT CGGT GA
 ||||| || || |||||
 ACCAGTT AGA GA GCCA CT
 AAGTC A CC C
 GAM2106 SEC14L2 3' TGTTAGGAAAATTAACCAA 14807 CC_ T
 TTGGTTAA TC CTAACG
 ||||| || |||||
 AACCAATT AG GATTGT
 AAA _
 GAM2106 SEP15 3' TCTAAATTAGAGAGGTTAAC 10454 CGG
 GTTAACCTCTCTAA TAGA
 ||||| ||||| |||||
 CAATTGGAGAGATT ATCT
 AA_
 GAM2106 LOC147514 3' ACCATTAGCAAGATTAACCAA 33547 C CT C
 TTGGTTAA CT CTAA GGT
 ||||| || |||||
 AACCAATT GA GATT CCA
 A AC A
 GAM2106 LOC90625 5' CTACCAAGTTTAAATTAACCAA 31818 CCTCT_ AAC
 TTGGTTAA CT GGTAG
 ||||| || |||||
 AACCAATT GA CCATC
 AAATTT A__
 GAM2107 ATP11B 3' CAGAAATTAAGACTTT 39146 TT
 AAAGTCTTAATT TCTG
 ||||| |||||
 TTTCAGAATTAA AGAC
 _
 GAM2107 ZNF76 5' CCCAGAAGGAAATCTCTGAC 9477 A TCTTAA
 GTCA AG TTTTCTGGG
 |||| || |||||

CAGT TC AGGAAGACCC
 C TAA____
 GAM2107 ZNF83 5' CCCAGAAAAATGTACATGAC 20292 AA CTTA
 GTCA GT ATTTTCTGGG
 ||| || |||||
 CAGT CA TAAAAAGACCC
 A_ TG_
 GAM2107 FLJ11608 3' GCCCAGAGGAGGGTAAGACTCT 23778 A A_
 G CA AGTCTTA TTTTCTGGGC
 || ||||| |||||
 GT TCAGAAT GAGGAGACCCG
 C GG
 GAM2107 HEMK 3' GCCCAGAAAAATGTGCAGCTTG 18270 A CTTA_
 AC GTCAA GT ATTTTCTGGGC
 ||| || |||||
 CAGTT CG TAAAAAGACCCG
 _ ACGTG
 GAM2107 KIAA0798 3' GCCCAGAAATAAACCTTAAC 16069 C A C ATT
 GT AA GT TTA TTTCTGGGC
 || || || || |||||
 CA TT CA AAT AAAGACCCG
 A C A ____
 GAM2107 KIAA1373 3' CCCAGAAATATACCCTGAC 35125 AA CTTA T
 GTCA GT AT TTTCTGGG
 ||| || || |||||
 CAGT CA TA AAAGACCC
 CC ____ T
 GAM2107 MDS024 3' CCCAGGAATGAAAATTAAGATT 22398 ____
 TTGAC GTCAAAGTCTTAATT TTCTGGG
 ||||| |||||
 CAGTTTTAGAATTAAA AGGACCC
 AGTA
 GAM2107 LOC147976 3' CCCAGAAATCTGAACGTTTCGAC 38425 AAA_ C ATT
 GTC GT TTA TTTCTGGG
 || || || |||||
 CAG CA AGT AAAGACCC
 CTTG _ CT_
 GAM2107 LOC254170 3' CAGAAAAGCCAAGACTTTAAC 45503 C AA
 GT AAAGTCTT TTTTCTG
 || ||||| |||||
 CA TTTCAGAA GAAAAGAC
 A CC
 GAM2108 XPNPEP2 3' GCAGAGGGAGTTAAGCCA 9434 C AAATT A
 TGGCT AAT TTCC CTGT
 |||| || |||||
 ACCGA TTG AGGG GACG
 A ____ A
 GAM2108 KIAA0429 5' ACAGTGAAAAAATTTAAAGC 16463 CAA C_
 GCT TAAATTTT CACTGT
 || ||||| |||||

		CGA	ATTTAAAA	GTGACA		
		A__	AA			
GAM2108	KIAA1553	3'	GGAAAATTTATTGAATCA	44145	GC	
			TG TCAATAAATTTTCC			
			AC AGTTATTTAAAAGG			
			TA			
GAM2108	SDC3	3'	GACAGTGGAAAAAAGAGACCA	16085	_ AATAAA	
			TGG CTC TTTTCCACTGTC			
			ACC GAG AAAAGGTGACAG			
			A AA__			
GAM2108	ZNF33A	3'	GGCAAAACTATTGAGCCA	43898	AA T	
			TGGCTCAATA TTT CC			
			ACCGAGTTAT AAA GG			
			CA C			
GAM2108	LOC149401	5'	ACAGCACTTGTTATTTATTGAG	38734	TTTCCA__	
		C	GCTCAATAAAT CTGT			
			CGAGTTATTTA GACA			
			TTGTTTCCAC			
GAM2108	LOC150622	5'	ACAGTGGGCACTATAAGCCA	38995	CA AATTT	
			TGGCT ATA TCCACTGT			
			ACCGA TAT GGGTGACA			
			A_ CAC__			
GAM2108	LOC219621	3'	ACAGCCTCTGAATTTATTGCAC	43968	CT TCCA_	
		CA	TGG CAATAAATTT CTGT			
			ACC GTTATTTAAG GACA			
			AC TCTCC			
GAM2108	LOC221477	3'	GCAGTGGGGACCATTGAGC	44255	AAAT TT	
			GCTCAAT T CCACTGT			
			CGAGTTA A GGTGACG			
			CC_ GG			
GAM2108	LOC255995	5'	GACAATCTATTTCTTGAGCCA	46325	T TTTCCAC	
			TGGCTCAA AAAT TGTC			
			ACCGAGTT TTTA ACAG			
			C TCTA__			
GAM2109	LOC91408	3'	CAAGCTAGATATCTTTATTTGA	32790	C AAA	
		TA	TATCAAATAA GATATT CTTG			
			ATAGTTTATT CTATAG GAAC			
			T ATC			
GAM2110	GPC1	3'	CCCATGGCTTGTTCTCTGGAAC	7869	C CCTTGG	
		C	GG TCCA AAGCCATGGG			

			CC AGGT	TTCGGTACCC		
			A	CTCTTG		
GAM2110	GPR44	3'	CCCAAAGTGCTTCCAAGGCAGA	11174	_ CA	CA__
		AGC	GCT C	CCTTGGAAGC	TGGG	
			CGA G	GGAACCTTCG	ACCC	
			A AC	TGAA		
GAM2110	ICA1	3'	CCCAAGGTTTCCAAGATAAAAC	22737	CTCCAC	A
		CA	TGG	CTTGGAAGCC	TGGG	
			ACC	GAACCTTTGG	ACCC	
			AAAATA	A		
GAM2110	LENG4	3'	CCCATGGCTTCCATCTGAGCCA	23583	CACCT	
			TGGCTC	TGGAAGCCATGGG		
			ACCGAG	ACCTTCGGTACCC		
			TCT__			
GAM2110	PAIP2	3'	CCCATGGCTTGATGTGAAGACA	18579	G C C GG	
			TG CT CAC TT	AAGCCATGGG		
			AC GA GTG AG	TTCGGTACCC		
			A A T			
GAM2110	SECTM1	3'	CCTCAGTTTCCAAAATGGAACC	8910	C CC	CAT
		A	TGG TCCA	TTGGAAGC	GG	
			ACC AGGT	AACCTTTG	CC	
			A AA	ACT		
GAM2110	SLC30A3	3'	CCCATGGTTCATGTGGAGCCA	9523	CT AA	
			TGGCTCCAC	TGG GCCATGGG		
			ACCGAGGTG	ACT TGGTACCC		
			T_			
GAM2110	SLC7A5	3'	CCAGCCAGAGGTGGAGCCA	9575	GGAA CA	
			TGGCTCCACCTT	GC TGG		
			ACCGAGGTGGAG	CG ACC		
			AC_			
GAM2110	STARD4	3'	CCCATTTTGACAAAGTGGAACA	29171	GC C GA CC	
			TG TCCAC TTG	AG ATGGG		
			AC AGGTG AAC TT	TACCC		
			A_ A AG T_			
GAM2110	CHK	3'	CCATGGCTGAAGCGGAGC	6943	AC GGA	
			GCTCC CTT	AGCCATGG		
			CGAGG GAA	TCGGTACC		
			C_ G_			
GAM2110	DKFZP434N1817	5'	CCCTTGCTTCCAAAGCGAACCA	33814	C CACC	CAT
			TGG TC	TTGGAAGC	GGG	

		ACC AG AACCTTCG CCC		
		A CGA_ TT_		
GAM2110 H11	3'	CCCATGGCTCCCAAACCATGCC 15692	TCCACC	A
		GGC TTGG AGCCATGGG		
		CCG AACC TCGGTACCC		
		TACCA_ C		
GAM2110 KIAA0329	3'	CCAGGGCCAGATGGAGCCA 16877	C TGGAA	A
		TGGCTCCA CT GCC TGG		
		ACCGAGGT GA CGG ACC		
		A C_ G		
GAM2110 KIAA0557	3'	CCCATGGCCCAGTATGAGGCCA 38204	TC CC	AA
		TGGC CA TTGG GCCATGGG		
		ACCG GT GACC CGGTACCC		
		GA AT _		
GAM2110 MGC4415	3'	GGCTCCCAAATTGGAACCA 25571	C CC	A
		TGG TCCA TTGG AGCC		
		ACC AGGT AACC TCGG		
		A TA C		
GAM2110 SNPH	3'	CCCAGCCTTCCAAGGTGAGGCC 16291	TC	CCA
A		TGGC CACCTTGGAAG TGGG		
		ACCG GTGGAACCTTC ACCC		
		GA CG_		
GAM2110 LOC150504	5'	CCCATGGCTTCAGAAGAGCTA 29849	CACCTTG	
		TGGCTC GAAGCCATGGG		
		ATCGAG CTTCGGTACCC		
		AAGA_		
GAM2110 LOC151443	5'	CCCACGGCTTCTAATAGAGCTA 39114	CACC	A
		TGGCTC TTGGAAGCC TGGG		
		ATCGAG AATCTTCGG ACCC		
		AT_ C		
GAM2110 LOC158236	5'	CATCTTCCAGGGCAAAACCA 41926	CTCCA	CC
		TGG CCTTGAAG ATG		
		ACC GGGACCTTC TAC		
		AAAAC _		
GAM2110 LOC158376	3'	CCCATGGCCATGGAATAAATGC 41973	TCCA_ T	GAA
C		GGC CC TG GCCATGGG		
		CCG GG AC CGGTACCC		
		TAAATAA T _		
GAM2110 LOC158402	5'	CCATGACCCTTCCAAGCCA 41974	CCACCT	C_
		TGGCT TGGAAG CATGG		

		ACCGA ACCTTC GTACC	
		_____ CCA	
GAM2110	LOC199676	3' CCCATGGCTTGGCTGAAGCC 43224	C _ TTGG
		GGCT CA CC AAGCCATGGG	
		CCGA GT GG TTCGGTACCC	
		A C _____	
GAM2110	LOC254065	5' CCATGGGATATGGAGCCA 46522	CC GGAAG
		TGGCTCCA TT CCATGG	
		ACCGAGGT AG GGTACC	
		AT _____	
GAM2111	AR	5' AAAAACAAAACAAACAA 5485	GA
		TTTGT TTGT TGTTTTT	
		AAACAAACA ACAAAAA	
		AA	
GAM2111	CCND1	3' TAAAAACATTTTAAAAACATAG 27602	T GT__
	AA	TTCT TGTTT GATGTTTTTA	
		AAGA ACAA TTACAAAAAT	
		T AATT	
GAM2111	CD83	3' AAAAACATATACAAATAAA 10425	_
		TTTGT TTGTG ATGTTTTT	
		AAATAAACAT TACAAAAA	
		A	
GAM2111	CHAC	3' AAAAACAAAAACAAACAAA 27137	GA_
		TTTGT TTGT TGTTTTT	
		AAACAAACA ACAAAAA	
		AAA	
GAM2111	CYP1A2	3' AAAAACAAACAAACAAA 6410	GA
		TTTGT TTGT TGTTTTT	
		AAACAAACA ACAAAAA	
		A_	
GAM2111	CYP1A2	3' AAAAACAAACAAACAAA 34253	GA
		TTTGT TTGT TGTTTTT	
		AAACAAACA ACAAAAA	
		A_	
GAM2111	DAPP1	3' AAAAACAAACAAACAAA 15728	GA
		TTTGT TTGT TGTTTTT	
		AAACAAACA ACAAAAA	
		A_	
GAM2111	DSC2	3' AAAAAAATTACAAACCAAGAA 11391	T G
		TTCTT GTTTGTGAT TTTT	

			AAGAA CAAACATTA AAAAA	
			C A	
GAM2111	DTNB	3'	AAAAACAAACAAACAAA 27005	GA
			TTTGTTTGT TGTTTTT	
			AAACAAACA ACAAAAA	
			A_	
GAM2111	DVL3	3'	AAAAGCAAACCTAACAAAGAA 10687	T GA
			TTCTTTGTT GT TGTTTTT	
			AAGAAACAA CA ACGAAAA	
			T A_	
GAM2111	EXTL2	3'	AAAAACAAAAACAAAGAA 7159	GTGA
			TTCTTTGTTT TGTTTTT	
			AAGAAACAAA ACAAAAA	
			A_	
GAM2111	HLCS	3'	AAAAACAAACAAACAAA 5986	GA
			TTTGTTTGT TGTTTTT	
			AAACAAACA ACAAAAA	
			A_	
GAM2111	HRV	5'	TAAAAGAGACACAAACAAA 12048	ATG
			TTTGTTTGTG TTTTAA	
			AAACAAACAC GAAAAT	
			AGA	
GAM2111	NR1I2	5'	TAAAAACAAAACAAACAAA 9973	GA
			TTTGTTTGT TGTTTTTA	
			AAACAAACA ACAAAAAT	
			AA	
GAM2111	NR4A2	3'	GAAAACAAACAAACAAA 12856	GA
			TTTGTTTGT TGTTTTT	
			AAACAAACA ACAAAAG	
			A_	
GAM2111	P53AIP1	3'	AAAAACAAACAAACAAA 22657	GA
			TTTGTTTGT TGTTTTT	
			AAACAAACA ACAAAAA	
			A_	
GAM2111	PRKG1	3'	AAAAACAACAACAAACAAA 12935	GA__
			TTTGTTTGT TGTTTTT	
			AAACAAACA ACAAAAA	
			AACA	
GAM2111	PTPN2	3'	AAAGAAAAGCAAACAAAGAA 8704	GATG
			TTCTTTGTTTGT TTTT	

			AAGAAACAAACG	AGAAA	
			AAA_		
GAM2111	SYT4	3'	AAATTAGCACAAACAAAGAA	31291	T AT_
			TTCTTTGTG GTG GTTT		
			AAGAAACAA CAC TAAA		
			_ GAT		
GAM2111	XKRY	5'	TAAGTACACACAAACAAA	11044	A T
			TTTGTTTGTG TGT TTTA		
			AAACAAACAC ACA GAAT		
			_ T		
GAM2111	XKRY	5'	TAAGTACACACAAACAAA	30153	A T
			TTTGTTTGTG TGT TTTA		
			AAACAAACAC ACA GAAT		
			_ T		
GAM2111	ARSDR1	3'	TAAAAACAAACAAACAAA	18110	GA
			TTTGTTTGT TGTTTTTA		
			AAACAAACA ACAAAAAT		
			A_		
GAM2111	C6orf37	3'	AAAAACAGCTGTAACAAAGAA	33506	TGTGA
			TTCTTTGTG TGTTTTT		
			AAGAAACAA ACAAAAA		
			TGTGC		
GAM2111	C6orf5	3'	AAAAACAAACAAACAAA	17776	GA
			TTTGTTTGT TGTTTTT		
			AAACAAACA ACAAAAA		
			A_		
GAM2111	CAMKK2	5'	AAACAAACAAAACAAAGAA	13307	_ GA
			TTCTTTGTTT GT TGTTT		
			AAGAAACAAA CA ACAA		
			A A_		
GAM2111	COL21A1	3'	TAAAAACATTTTAGACAAA	25149	T
			TTTGTTTG GATGTTTTTA		
			AAACAGAT TTACAAAAAT		
			T		
GAM2111	CSAD	3'	AAAAACAAACAAACAAA	18081	GA
			TTTGTTTGT TGTTTTT		
			AAACAAACA ACAAAAA		
			A_		
GAM2111	DKFZP547L112	3'	ATTACACAAGACAAAGAA	33057	___
			TTCTTTGTG TGTGAT		

	AAGAAACAG ACATTA	
	AAC	
GAM2111 FLJ12568	3' TAAAAACACACATACAAA 24554	T A
	TTTGT TGTG TGTTTTTA	
	AAACA ACAC ACAAAAAT	
	T _	
GAM2111 FLJ13409	3' TAAAAACATTTTCAAAGGA 23879	TTTGT
	TTCTTTG GATGTTTTTA	
	AGGAAAC TTACAAAAAT	
	TT__	
GAM2111 FLJ13841	3' AAAAACAAACAAACAAA 24015	GA
	TTTGTTTGT TGTTTTT	
	AAACAAACA ACAAAAA	
	A_	
GAM2111 FLJ20340	3' AAAAACAAACAAACAAA 19395	GA
	TTTGTTTGT TGTTTTT	
	AAACAAACA ACAAAAA	
	AA	
GAM2111 FLJ23058	3' TAAAAACAAAATGGACAAA 24005	TG GA
	TTTGTT T TGTTTTTA	
	AAACAG A ACAAAAAT	
	GT AA	
GAM2111 FLJ23548	3' TAAAAACATCATTCAGA 23826	TTT
	TTTG GTGATGTTTTTA	
	AGAC TACTACAAAAAT	
	T__	
GAM2111 GTPBP5	3' AAAAACAAACAAACAAA 32573	GA
	TTTGTTTGT TGTTTTT	
	AAACAAACA ACAAAAA	
	A_	
GAM2111 ICAP-1A	3' TAAAAACATTAAAAATAAA 11156	G
	TTTGTTT TGATGTTTTTA	
	AAATAAA ATTACAAAAAT	
	A	
GAM2111 KIAA0455	3' AAAACAAGCAAACAAA 35880	GA
	TTTGTTTGT TGTTTTT	
	AAACAAACG ACAAAAA	
	A_	
GAM2111 KIAA0471	3' TAAAGACTAGAAACAAAGAA 16913	G AT
	TTCTTTGTTT TG GTTTTTA	

			AAGAAACAAA AT CAGAAAT		
			G _		
GAM2111	KIAA1086	3'	AGAAACAAACAAACAAA 35011	GA	
			TTTGTTTGT TGTTTTT		
			AAACAAACA ACAAAGA		
			A_		
GAM2111	KIAA1260	3'	AAACAGACAAACAAGAA 30154	T GA	
			TTCTT GTTTGT TGTTT		
			AAGAA CAAACA ACAA		
			_ G_		
GAM2111	KIAA1677	3'	AAAAAAGAGGCAAACAAAG 33289	GATG	
			CTTTGTTTGT TTTT		
			GAAACAAACG AAAAA		
			GAGA		
GAM2111	KIAA1829	3'	TAAAAACATATCAGAACAAATG 31033	_ GTG_	
	AA		TTC TTTGTTT ATGTTTTTA		
			AAG AAACAAG TACAAAAAT		
			T ACTA		
GAM2111	KIAA1866	3'	TAAAAACACCACCAAGAA 30556	TTT A	
			TTCTTTG GTG TGTTTTTA		
			AAGAAAC CAC ACAAAAAT		
			_ C		
GAM2111	MBLL39	3'	TAAAAACCTAGTCAAACAAGGA 29574	TGAT_	
	A		TTCTTTGTTTG GTTTTTA		
			AAGGAACAAAC CAAAAAT		
			TGATC		
GAM2111	MGC29891	3'	AAAAACAAAACAAACAAA 29436	GA	
			TTTGTTTGT TGTTTTT		
			AAACAAACA ACAAAAA		
			AA		
GAM2111	MOT8	3'	TAAAAACAAAACAAACAAA 20826	GA	
			TTTGTTTGT TGTTTTTA		
			AAACAAACA ACAAAAAT		
			AA		
GAM2111	ODZ2	3'	AAAAACGAATAAGCAAAGAA 35095	GA	
			TTCTTTGTTTGT TGTTTTT		
			AAGAAACGAATA GCAAAAA		
			A_		
GAM2111	PCSK7	3'	TAAAAACCTTCCAAACAAA 11077	T T_	
			TTTGTTTG GA GTTTTTA		

		AAACAAAC CT CAAAAAT		
		_ TC		
GAM2111	PLEKHA3	3' AAAACAGACAAACAAGAA 21166	T	GA
		TTCTT GTTTGT TGTTTT		
		AAGAA CAAACA ACAAAA		
		_ G_		
GAM2111	PRO0478	3' AAAAACAAACAAACAAA 15396	GA	
		TTTGTTTGT TGTTTTT		
		AAACAAACA ACAAAAA		
		A_		
GAM2111	RAB14	3' AAAAACAAACAAACAAA 18445	GA	
		TTTGTTTGT TGTTTTT		
		AAACAAACA ACAAAAA		
		AA		
GAM2111	RICH1	3' AAAAAAATCCAAACAAAGAA 19814	GT	G
		TTCTTTGTTT GAT TTTTT		
		AAGAAACAAA CTA AAAAA		
		AC A		
GAM2111	SLC11A1	3' AAAAACAAACAAACGAA 29901	GA	
		TTTGTTTGT TGTTTTT		
		AAGCAAACA ACAAAAA		
		A_		
GAM2111	LOC125434	3' AAAAACAAACAAACAAA 36795	GA	
		TTTGTTTGT TGTTTTT		
		AAACAAACA ACAAAAA		
		AA		
GAM2111	LOC145945	5' AAAACAAACAAACAAA 40627	GA	
		TTTGTTTGT TGTTTTT		
		AAACAAACA ACAAAAA		
		A_		
GAM2111	LOC146520	5' AACACAAACAAAGAA 38183	GA	
		TTCTTTGTTTGT TGTT		
		AAGAAACAAACA ACAA		
		—		
GAM2111	LOC149127	5' TAAAAACATCGTGAATGAA 40951	TG	TG
		TT TT TGATGTTTTTA		
		AA AA GCTACAAAAAT		
		GT GT		
GAM2111	LOC158427	3' AAAAGCAACAAACAAA 29244	GA	
		TTTGTTTGT TGTTTTT		

AAACAAACA ACGAAAA

GAM2111 LOC199858 3' AAAAACAACAAACAAA 42628 GA
TTTGTTTGT TGTTTTT
||||||| |||||
AAACAAACA ACAAAAA

A_

GAM2111 LOC199923 3' AAAAACAACAAACAAA 42663 GA_
TTTGTTTGT TGTTTTT
||||||| |||||
AAACAAACA ACAAAAA

AAA

GAM2111 LOC199923 3' AAAAACAACAAACAAA 42664 GA
TTTGTTTGT TGTTTTT
||||||| |||||
AAACAAACA ACAAAAA

A_

GAM2111 LOC206338 5' AATACAACAACAAAGAA 43111 GA
TTCTTTGTTTGT TGTT
||||||| |||
AAGAAACAACA ATAA

AC

GAM2111 LOC219672 5' AAAAACAACAAGCAAA 43887 GA
TTTGTTTGT TGTTTTT
||||||| |||||
AAACGAACA ACAAAAA

A_

GAM2111 LOC221814 3' TAAAAACAACCTTTAACAAAGA 45095 T__ GA
G TTCTTTGTT GT TGTTTTTA
||||||| || |||||
GAGAAACAA CA ACAAAAAT

TTT A_

GAM2111 LOC221943 5' AAAAACAACAAACAAA 45115 GA
TTTGTTTGT TGTTTTT
||||||| |||||
AAACAAACA ACAAAAA

A_

GAM2111 LOC253639 3' AAAAACAACAAACAAA 45853 GA
TTTGTTTGT TGTTTTT
||||||| |||||
AAACAAACA ACAAAAA

A_

GAM2111 LOC254659 5' AAAAACAACAAACAAA 45598 GA
TTTGTTTGT TGTTTTT
||||||| |||||
AAACAAACA ACAAAAA

A_

GAM2111 LOC51141 3' AAAAACAACAAACAAA 34045 GA
TTTGTTTGT TGTTTTT
||||||| |||||

		AAACAAACA ACAAAAA		
		A_		
GAM2111	LOC56920	3' AAAACAACCAAGACAAAGAA	21379	GTGA
		TTCTTTGTTT TGTTTT		
		AAGAAACAGA ACAAAA		
		ACCA		
GAM2111	LOC90155	5' AAAAACAAAAACAAACAAA	30898	GA__
		TTTGTTTGT TGTTTTT		
		AAACAAACA ACAAAAA		
		AAAA		
GAM2111	LOC91496	5' TAAAAACATCATGGGAAAA	32919	G TG
		TTT TT TGATGTTTTTA		
		AAA GG ACTACAAAAAT		
		A GT		
GAM2111	LOC92973	5' AAAAAAGCAAACGAAGAA	35180	GATG
		TTCTTTGTTTGT TTTT		
		AAGAAGCAAACG AAAA		
		AA__		
GAM2112	ESR1	3' TCCCCTAGTTGGCCAAGACT	5600	AAGTTC A
		AGTCT CCAACTAG GGA		
		TCAGA GGTTGATC CCT		
		ACC__ C		
GAM2112	PKD2L1	5' TCCTCTAGCTGAGAGTGGGC	18194	AG C A
		GTCTA TTC CA CTAGAGGA		
		CGGGT GAG GT GATCTCCT		
		_ A C		
GAM2112	CGGBP1	3' AGCTGGAAACTTGGACTA	9739	C A
		TAGTCTAAGTT CCA CT		
		ATCAGGTTCAA GGT GA		
		A C		
GAM2112	VRP	5' TCCTGGGCAAGGAAGTTAAACT	13927	C CAA AG
		AGT TAAGTTCC CT AGGA		
		TCA ATTCAAGG GG TCCT		
		A AAC G_		
GAM2112	LOC155382	3' CCCCCAGTTGGGGGGCCTAGAC	41763	A _ AGA
		GTCTA GTTCCC AACT GG		
		CAGAT CGGGGG TTGA CC		
		C G CCC		
GAM2113	ABCD4	3' AACGGGGAGTAGCAGTAG	21586	AA
		TTACTGCTACT CTGTT		

			GATGACGATGA GGCAA		
			GG		
GAM2113	EIF2C1	3'	CTTGGTGTAGTAGCAATAA 14503	C	ACTGTT
			TTA TGCTACTA CTAAG		
			AAT ACGATGAT GGTTT		
			A GT____		
GAM2113	OCRL	3'	TCTTAGATCACATTTAGTAGCA 7308	C	__
			TGCTACTAA TGT TCTAAGA		
			ACGATGATT ACA AGATTCT		
			T CT		
GAM2113	OCRL	3'	TCTTAGATCACATTTAGTAGCA 5821	C	__
			TGCTACTAA TGT TCTAAGA		
			ACGATGATT ACA AGATTCT		
			T CT		
GAM2113	RAG2	3'	CTTAAACACCCAGAAGCAGTAA 39986	A AAC	C
			TTACTGCT CT TGTT TAAG		
			AATGACGA GA ACAA ATTC		
			A CCC _		
GAM2113	SOX9	3'	TCTCAGAACACCAGCAGT 5902	ACTAAC	A
			ACTGCT TGTTCT AGA		
			TGACGA ACAAGA TCT		
			CC____ C		
GAM2113	FLJ20211	3'	AGAGCATTGTAGTCAGCAGTAA 19295	_ AC_	
			TTACTGCT ACTA TGTTCT		
			AATGACGA TGAT ACGAGA		
			C GTT		
GAM2113	FLJ20574	3'	CTTAGGATAACAGCAGTA 19554	ACTAAC	
			TACTGCT TGTTCTAAG		
			ATGACGA ATAGGATTC		
			CA____		
GAM2113	JM11	3'	TCTTGGGCACTGGTAGCAG 27332	AC	T
			CTGCTACTA TGT CTAAGA		
			GACGATGGT ACG GGTTCT		
			C_ _		
GAM2113	KIAA0247	3'	TCTTAGAAGATAGATGCAGCAG 16380	ACTAA	__
	TAA		TTACTGCT CTGT TCTAAGA		
			AATGACGA GATA AGATTCT		
			CGTA_ GA		
GAM2113	KIAA1024	3'	TCTTAGAATCTTGCAGCAGTGA 34237	ACTAACT	
			TTACTGCT GTTCTAAGA		

			AGTGACGA	TAAGATTCT		
			CGTTC__			
GAM2113	KIAA1819	5'	CTGCTGAACAGTAGCAATAA	34534	C	ACTA TA_
			TTA TGCT ACTGTTC AG			
			AAT ACGA TGACAAG TC			
			A ____ TCG			
GAM2113	MEGF10	3'	ATGGTGGTCAAAGCAGTAA	26211	__	A
			TTACTGCT ACTA CTGT			
			AATGACGA TGGT GGTA			
			AAC _			
GAM2114	MAPK9	3'	AGCATTGAAGGAACTCTC	8631	AC	CTC
			GAGA TCCTTCAA GCT			
			CTCT AGGAAGTT CGA			
			CA A__			
GAM2114	MAPK9	3'	AGCATTGAAGGAACTCTC	29136	AC	CTC
			GAGA TCCTTCAA GCT			
			CTCT AGGAAGTT CGA			
			CA A__			
GAM2114	MAPK9	3'	AGCATTGAAGGAACTCTC	29138	AC	CTC
			GAGA TCCTTCAA GCT			
			CTCT AGGAAGTT CGA			
			CA A__			
GAM2114	MAPK9	3'	AGCATTGAAGGAACTCTC	29140	AC	CTC
			GAGA TCCTTCAA GCT			
			CTCT AGGAAGTT CGA			
			CA A__			
GAM2114	PARK2	3'	GTAGCTGGAGAGAGAGTTCTC	10906	_	CAA C
			GAGAACTC CTT CT GCTAC			
			CTCTTGAG GAG GG CGATG			
			A A__ T			
GAM2114	PARK2	3'	GTAGCTGGAGAGAGAGTTCTC	15153	_	CAA C
			GAGAACTC CTT CT GCTAC			
			CTCTTGAG GAG GG CGATG			
			A A__ T			
GAM2114	PARK2	3'	GTAGCTGGAGAGAGAGTTCTC	15160	_	CAA C
			GAGAACTC CTT CT GCTAC			
			CTCTTGAG GAG GG CGATG			
			A A__ T			
GAM2114	PMP2	3'	AGCTTGAAGGGGCTC	8543	AA	CTC
			GAG CTCCTTCAA GCT			

CTC GGGGAAGTT CGA

GAM2114	PTK7	3'	GGCAGATGAAGGAGTTTTTC	8689	A	C
			GAGAACTCCTTCA CT GCT			
			CTTTTGAGGAAGT GA CGG			
			A _			
GAM2114	RAD52	3'	AGACGGGCTGAAGCGAGCCCTC	28643	AA	_ A _
			GAG CTC CTTCA CTCG CT			
			CTC GAG GAAGT GGGC GA			
			CC C C A			
GAM2114	SVIL	5'	AGCTTTCAGAAGGAGTTCTC	22345	AACTC	
			GAGAACTCCTTC GCT			
			CTCTTGAGGAAG CGA			
			ACTTT			
GAM2114	SVIL	5'	AGCTTTCAGAAGGAGTTCTC	9148	AACTC	
			GAGAACTCCTTC GCT			
			CTCTTGAGGAAG CGA			
			ACTTT			
GAM2114	AF9Q34	5'	GGCTGAAGGAGTCTCG	26276	A	ACTC
			CGAGA CTCCTTCA GCT			
			GCTCT GAGGAAGT CGG			
GAM2114	C16orf5	5'	AGCAGCTGAAGGAGCCTC	15051	AA	A C
			GAG CTCCTTCA CT GCT			
			CTC GAGGAAGT GA CGA			
			C_ C _			
GAM2114	DKFZp547M236	3'	AGTGTTCAAAGAAGTTCTTG	20791	C	CAACT
			CGAGAACT CTT CGCT			
			GTTCTTGA GAA GTGA			
			A ACTT_			
GAM2114	ELF4	3'	GGCAGCCAGGAGTTCCCG	7124	A	TCAA C
			CG GAACTCCT CT GCT			
			GC CTTGAGGA GA CGG			
			C CC_ _			
GAM2114	NPAS3	3'	GTGGTCAAGAGAGTTCTC	22667	_	CA T
			GAGAACTC CTT AC CGC			
			CTCTTGAG GAA TG GTG			
			A C_ _			
GAM2114	SLC11A2	3'	GGTGTTGAAGGACTTCTC	6226	C	_
			GAGAA TCCTTCAAC TC			

		CTCTT AGGAAGTTG GG	
		C T	
GAM2114	TIX1	3' AGCAAGCAAGATGGGGTTCTC 30927	T AA_ C
		GAGAACTCC TC CT GCT	
		CTCTTGGGG AG GA CGA	
		T AAC A	
GAM2114	LOC143173	5' GGCGAGTTGAAGAATTTCTC 30271	CTC
		GAGAA CTTCAACTCGCT	
		CTCTT GAAGTTGAGCGG	
		TAA	
GAM2114	LOC143915	3' GGCAAATGATGAAGGAGTTCT 40379	ACTC__
	C	GAGAACTCCTTCA GCT	
		CTCTTGAGGAAGT CGG	
		AGTAAAA	
GAM2114	LOC149302	5' AGCCTGAAGGAGTTCT 38702	ACTC
		AGAACTCCTTCA GCT	
		TCTTGAGGAAGT CGA	
		C__	
GAM2114	LOC170082	3' GCTTAGTTGAAGGAGTTTCG 40170	A C_
		CGAGA CTCCTTCAACT GC	
		GCTTT GAGGAAGTTGA CG	
		TT	
GAM2114	LOC221477	3' GGCTGATTAAAGAAGTTCTTG 44257	C C C _
		CGAGAACT CTT AA TC GCT	
		GTTCTTGA GAA TT AG CGG	
		A A _ T	
GAM2114	LOC221760	5' AGCTCTGGAGGAGCCCTCG 45031	AA ACTC
		CGAG CTCCTTCA GCT	
		GCTC GAGGAGGT CGA	
		CC CT__	
GAM2114	LOC245806	5' GGTAGCGAGCCAGCTGGATTCC 44131	A C TTCAA_
	G	CG GAA TCC CTCGCTACC	
		GC CTT AGG GAGCGATGG	
		_ _ TCGACC	
GAM2115	YWHAZ	3' GTTAAGAACACGTGTATTA 9445	ATCA
		TAATACACGT TTGAT	
		ATTATGTGCA AATTG	
		CAAG	
GAM2115	PARVA	3' ATAATCAATTGTGCTGATATTA 20145	_ C C
		TAATA CA GTAT ATTGATTAT	

		ATTAT GT CGTG TAACTAATA	
		A _ T	
GAM2115	LOC254251	3' ATAATCATATATACGTGTA 45894	CAT
		TACACGTAT TGATTAT	
		ATGTGCATA ACTAATA	
		TAT	
GAM2116	ASPH	3' ATATTGGTGATGTAGCAGCAA 26222	G__ C
		TTGCTGCTA ACCA ATGT	
		AACGACGAT TGGT TATA	
		GTAG _	
GAM2116	ASPH	3' ATATTGGTGATGTAGCAGCAA 26227	G__ C
		TTGCTGCTA ACCA ATGT	
		AACGACGAT TGGT TATA	
		GTAG _	
GAM2116	ESRRG	3' TGATAATTTAGCAGCAA 32999	CCACA
		TTGCTGCTAGA TGTCA	
		AACGACGATTT ATAGT	
		A__	
GAM2116	TNS	3' GGCATGTGGCTCAGCAGCAA 22903	_ A
		TTGCTGCT AG CCACATGTC	
		AACGACGA TC GGTGTACGG	
		C _	
GAM2116	FLJ10656	3' ATTAACATGGTAAGCCTTAGCA 19988	ACCA__ C
	GCAA	TTGCTGCTAG CATGT AAT	
		AACGACGATT GTACA TTA	
		CCGAATG A	
GAM2116	GABARAPL1	3' TGGCAGTCCAGCAGCAA 25392	A CACA
		TTGCTGCT GAC TGTCA	
		AACGACGA CTG ACGGT	
		C _	
GAM2116	GABARAPL3	3' TGGCAGTCCAGCAGCAA 26300	A CACA
		TTGCTGCT GAC TGTCA	
		AACGACGA CTG ACGGT	
		C _	
GAM2116	HT002	3' GACGGTGATGACCCAGCAGCAA 15281	AGAC__ A
		TTGCTGCT CAC TGTC	
		AACGACGA GTG GCAG	
		CCCAGTA _	
GAM2116	KIAA0194	3' GACATAACCTAGCAGCAG 32825	ACCAC
		TTGCTGCTAG ATGTC	

	GACGACGATC	TACAG	
	CAA__		
GAM2116 KIAA0435	3' GACACGGCCTCGCAGCAA	16721	T A ACA
	TTGCTGC AG CC TGTC		
	AACGACG TC GG ACAG		
	C C C__		
GAM2116 KIAA0475	3' GATTGGAAGTGGCCAGCAGCAA	16949	AGA ATG
	TTGCTGCT CCAC TCAATC		
	AACGACGA GGTG GGTTAG		
	CC_ AA_		
GAM2116 KIAA0542	3' ACTTGAGGAGATCCAGCAGCAA	32856	A ____ A T
	TTGCTGCT GA CC CA GT		
	AACGACGA CT GG GT CA		
	C AGA A T		
GAM2116 KIAA1301	3' ATTGACATATGGTTTGC	32974	T C
	GC AGACCA ATGTCAAT		
	CG TTTGGT TACAGTTA		
	_ A		
GAM2116 KIAA1323	5' GACATACAATCCAGCAGCAG	31563	A CCAC
	TTGCTGCT GA ATGTC		
	GACGACGA CT TACAG		
	C AACA		
GAM2116 SEZ6	3' GACTTGCACCACAGTCCAGCAG	36774	A CA_____ T
CAA	TTGCTGCT GAC CA GTC		
	AACGACGA CTG GT CAG		
	C ACACCAC T		
GAM2116 LOC132235	5' TGACACGGGAGCTAGCAGCA	37483	A_ ACA
	TGCTGCTAG CC TGTCA		
	ACGACGATC GG ACAGT		
	GA GC_		
GAM2116 LOC146895	5' TGGCTGTGGTCTCCTGCAGCAA	40761	TA T
	TTGCTGC GACCACA GTCA		
	AACGACG CTGGTGT CGGT		
	TC _		
GAM2116 LOC152024	5' ACATGCCTATCTAGCAGCA	39198	CCA_
	TGCTGCTAGA CATGT		
	ACGACGATCT GTACA		
	ATCC		
GAM2117 F8	3' ATAACACAACAAAAATGTAACA	5613	CATATT
	TGTTACATT TTGTGTTAT		

		ACAATGTAA AACACAATA		
		AAAC__		
GAM2117	MAPRE1	3' CAAAATATAAAATGTAACA 14706	C_	
		TGTTACATT ATATTTTG		
		ACAATGTAA TATAAAAC		
		AA		
GAM2117	E2F5	3' TAAAATAATGAATGTAACA 7673	_	
		TGTTACATTCAT ATTTTG		
		ACAATGTAAGTA TAAAAT		
		A		
GAM2117	ELF2	3' ATAGAATATACATGTAACA 13743	TC	
		TGTTACAT ATATTTTG		
		ACAATGTA TATAAGATA		
		CA		
GAM2117	KIAA0252	3' TGCTAAATATGACTGTAACA 31451	T T	
		TGTTACA TCATATTT GTG		
		ACAATGT AGTATAAA CGT		
		C T		
GAM2117	KIAA1855	3' GCCAAACAGAATGTAACA 44359	ATAT T	
		TGTTACATTC TTTG GT		
		ACAATGTAAG AAAC CG		
		AC__ _		
GAM2117	LOC152578	5' AACACAAATGTGACA 41526	CATATTT	
		TGTTACATT TGTGTT		
		ACAGTGTAAC ACACAA		
GAM2118	KLF8	5' CATGGGCCATTTAAAGTGTTTC 14122	A TCAC_	
	A	TGAAACAC TTA TCCATG		
		ACTTTGTG AAT GGGTAC		
		A TTACC		
GAM2118	TRIM9	3' ATCAAAGACAAGTAATGTGTCT 27548	A CAC CA	
	CA	TGA ACACATTAT TC TGAT		
		ACT TGTGTAATG AG ACTA		
		C AAC AA		
GAM2118	TRPC1	3' ATCATGGAGCGAATAATTTTCA 9304	CAC _A	
		TGAAA ATTAT C CTCCATGAT		
		ACTTT TAATA G GAGGTACTA		
		_ A C		
GAM2118	BTN3A1	3' ATCATGGGGAACAGATGTGTTC 13920	A ATCA	
	CA	TG AACACATT CTCCATGAT		

	AC TTGTGTAG GGGGTACTA		
	C ACAA		
GAM2118 DKFZp761J139	5' CATGAGTAATGTGTTACA 26034	A	ATC C
	TG AACACATT ACTC ATG		
	AC TTGTGTAA TGAG TAC		
	A _ _		
GAM2118 FLJ20147	3' ATCATAGAAGGTGAGAATGTGT 19241	A	_ C
TT	AAACACATT TCAC TC ATGAT		
	TTTGTGTAA AGTG AG TACTA		
	G GA A		
GAM2118 MGC12466	3' ATCATGGAGCTGAGAATTTCA 38608	CACATTA	_
	TGAAA TCA CTCCATGAT		
	ACTTT AGT GAGGTACTA		
	AAG_ C		
GAM2118 MGC12466	3' ATCATGGAGCTGAGAATTTCA 27066	CACATTA	_
	TGAAA TCA CTCCATGAT		
	ACTTT AGT GAGGTACTA		
	AAG_ C		
GAM2118 SPRY2	5' ATCACGGAGTTCAGATGTGTT 12453	ATC	A
	AACACATT ACTCC TGAT		
	TTGTGTAG TGAGG ACTA		
	ACT C		
GAM2118 LOC202934	5' ATCATGGAGGCAGGTATTTTC 43453	C	ATTATCA
	GAAA AC CTCCATGAT		
	CTTT TG GAGGTACTA		
	A GACG_		
GAM2118 LOC255465	5' ATCATGGAGGCAGGTATTTTC 46447	C	ATTATCA
	GAAA AC CTCCATGAT		
	CTTT TG GAGGTACTA		
	A GACG_		
GAM2119 PRO2435	5' AATGTCACAGAGACTAGTTCA 20598	C	TA
	TGAACTAGTC CTGT GCATT		
	ACTTGATCAG GACA TGTA		
	A C_		
GAM2119 LOC143425	3' CTAATGCAAGGAGGGCTAGTTC 42354	T	G A
A	TGAACTAG CCCT TT GCATTAG		
	ACTTGATC GGGA GA CGTAATC		
	_ G A		
GAM2120 ABCA1	3' ATACATAAATGCCAGC 12012	TAAGAA	C
	GCT GGCATTTA GTAT		

			CGA	CCGTAAAT CATA		
			C_____	A		
GAM2120	RET	3'	ACGTAAATGCAGAAGTTA	5866	AAGAAG	
			TAGCTT	GCATTTACGT		
			ATTGAA	CGTAAATGCA		
			GA_____			
GAM2120	RET	3'	ACGTAAATGCAGAAGTTA	21780	AAGAAG	
			TAGCTT	GCATTTACGT		
			ATTGAA	CGTAAATGCA		
			GA_____			
GAM2120	RET	3'	ACGTAAATGCAGAAGTTA	21782	AAGAAG	
			TAGCTT	GCATTTACGT		
			ATTGAA	CGTAAATGCA		
			GA_____			
GAM2120	RET	3'	ACGTAAATGCAGAAGTTA	21959	AAGAAG	
			TAGCTT	GCATTTACGT		
			ATTGAA	CGTAAATGCA		
			GA_____			
GAM2120	FLJ20360	3'	AGATGCCTTCTAAGCTA	43679	A	
			TAGCTTA	GAAGGCATTT		
			ATCGAAT	CTTCCGTAGA		

GAM2120	KIAA1023	3'	ATGGCAATGCATTCTCAAGC	19086	A G TA	
			GCTT	AGAA GCATT CGT		
			CGAA	TCTT CGTAA GTA		
			C A CG			
GAM2120	UST	3'	AAATACCTTTTAAGCTA	12269	A C	
			TAGCTTAAGA	GG ATTT		
			ATCGAATTTT	CC TAAA		
			_ A			
GAM2121	FYCO1	3'	TAACAAAAGTCTTTGATA	23712	C_	
			TATCAAAGAT	TTGTTA		
			ATAGTTTCTG	AACAAT		
			AA			
GAM2122	ECH1	5'	AAAGAACGGCGTCATTGCCTGT	30097	CACAA	
	CA		TGACAGGCGA	TCGTTCTTT		
			ACTGTCCGTT	GGCAAGAAA		
			ACTGC			
GAM2122	LOC203317	5'	CGACTGTGTGCCTGTCA	43030	G A	
			TGACAGGC	ACACA TCG		

			ACTGTCCG TGTGT AGC		
			— C		
GAM2123	DACH	3'	TCTGGAGTCACAGTATTAATGA 28042	ACCAC	—
			TCAT ATAC GACTCCAGA		
			AGTA TATG CTGAGGTCT		
			AT— ACA		
GAM2123	FMR1	3'	CTGAAATGTGTGTGATGTGA 7776	C	ACTC
			TCATA CACATACG CAG		
			AGTGT GTGTGTGT GTC		
			A AAA—		
GAM2123	MGAM	3'	CTAGAGCCCGCTGGTATGAT 35822	CATA A_	C
			ATCATACCA CG CTC AG		
			TAGTATGGT GC GAG TC		
			C— CC A		
GAM2123	MHC2TA	3'	TCTGGAATCCAGTGGTATGAT 5784	ATAC	C
			ATCATACCAC GA TCCAGA		
			TAGTATGGTG CT AGGTCT		
			AC— A		
GAM2123	C8orf13	3'	TCTGGGGTCATACGGCATGG 39657	A ACA	C
			TCAT CC TA GACTCCAGA		
			GGTA GG AT CTGGGGTCT		
			C C— A		
GAM2123	FLJ11827	3'	CTGGTTGTGACATTGTGGTATA 24723	C	— CT
	ATA		TAT ATACCACA TACGA CCAG		
			ATA TATGGTGT GTGTT GGTC		
			A TACA —		
GAM2123	KIAA0472	5'	TCTGGAGTACAATGGCATGAT 35583	A	CATACG
			ATCAT CCA ACTCCAGA		
			TAGTA GGT TGAGGTCT		
			C AACA—		
GAM2123	SOX6	3'	AGTGCGTGATGTGGTATGA 27159	—	—
			TCATACCACAT ACG ACT		
			AGTATGGTGTA TGC TGA		
			G G		
GAM2123	LOC149276	3'	TCTGAATGTTGTGTATGTGGCT 40977	TA	— TC_
	GATA		TATCA CCACATAC GAC CAGA		
			ATAGT GGTGTATG TTG GTCT		
			C_ TG TAA		
GAM2123	LOC153910	5'	TCTGGAGTGCAGTGGTACAATA 39441	CA	ATA G
			TAT TACCAC C ACTCCAGA		

			ATA ATGGTG G TGAGGTCT	
			AC AC__	
GAM2124	ELOVL4	3'	TGCTGTTAGAATATGTTGA 22928	GTCATA
			TCAATA CTAACAGCA	
			AGTTGT GATTGTCGT	
			ATAA__	
GAM2124	GLS	3'	TGCTGTTGACTGTGCTATT 17110	T C_
			AATAG CATA TAACAGCA	
			TTATC GTGT GTTGTCGT	
			_ CA	
GAM2124	HOXC5	3'	TGCTGTTGTCCAACACTATT 21022	CAT T
			AATAGT AC AACAGCA	
			TTATCA TG TTGTCGT	
			ACC _	
GAM2124	IGFBP3	3'	CTGCTTGGGGACTATTGG 6199	ATA _
			TCAATAGTC CTAA CAG	
			GGTTATCAG GGTT GTC	
			G_ C	
GAM2124	LBR	3'	CTGTGAAGAATGCTATTGA 29851	T A A_
			TCAATAG CAT CT ACAG	
			AGTTATC GTA GA TGTC	
			_ A AG	
GAM2124	PRDM2	3'	TGCTGTTAGTTATTTTATTG 18007	TCAT
			CAATAG ACTAACAGCA	
			GTTATT TGATTGTCGT	
			TTAT	
GAM2124	SLC4A7	3'	TGCTGTTTATGTGTGACTA 9673	T__
			TAGTCATAC AACAGCA	
			ATCAGTGTG TTGTCGT	
			TAT	
GAM2124	SNX6	3'	TGCTGTTTGAACGTGTTGA 22219	_ TACT
			TCAATAGT CA AACAGCA	
			AGTTGTCA GT TTGTCGT	
			A ____	
GAM2124	TK2	3'	TGCTGCCAAGTTAGCTATTGG 10960	CAT AA_
			TCAATAGT ACT CAGCA	
			GGTTATCG TGA GTCGT	
			AT_ ACC	
GAM2124	TMOD2	3'	CTGTGGTATGGCCATTGA 15860	A A
			TCAAT GTCATACTA CAG	

AGTTA CGGTATGGT GTC
 C _
 GAM2124 WASF3 5' TGCTGTAACTACTACTGA 13445 A CATAC
 TCA TAGT TAACAGCA
 ||| ||| |||||
 AGT ATCA ATTGTCGT
 C TCA__
 GAM2124 C11orf21 3' TGCTGTTCCAGATATGACTACT 15428 A _ _
 GA TCA TAGTCATA CT AACAGCA
 ||| ||||| || |||||
 AGT ATCAGTAT GA TTGTCGT
 C A CC
 GAM2124 DNAJA3 3' GCCTGTCCCTGACTATTGA 30335 TACTA _
 TCAATAGTCA ACAG C
 ||||| ||| |
 AGTTATCAGT TGTC G
 CCC__ C
 GAM2124 FLJ12761 3' TGCTGTTAATTGTATGTAC 23758 _ _
 GT CATAC TAACAGCA
 || ||| |||||
 CA GTATG ATTGTCGT
 T TTA
 GAM2124 FLJ12788 3' TGCTATGTATGACTCTGA 22874 AT TAAC
 TCA AGTCATAC AGCA
 ||| ||||| |||
 AGT TCAGTATG TCGT
 C_ TA__
 GAM2124 FLJ20783 3' TGTTGTATGCCTATTGA 19672 T T
 TCAATAG CATAC AACA
 ||||| |||| |||
 AGTTATC GTATG TTGT
 C _
 GAM2124 KIAA0179 3' TGCTGTTAATCGTCACTGT 32368 C AC_
 ATAGT AT TAACAGCA
 |||| || |||||
 TGTCA TG ATTGTCGT
 C CTA
 GAM2124 KIAA1209 3' TGCTGTTAGTTTCTATT 30474 TCAT
 AATAG ACTAACAGCA
 |||| |||||
 TTATC TGATTGTCGT
 TT__
 GAM2124 KIAA1432 3' TGCTGTTAGATACCACTA 33156 CA _
 TAGT TA CTAACAGCA
 |||| || |||||
 ATCA AT GATTGTCGT
 CC A
 GAM2124 KIAA1582 5' TGCTGTTAGTACTGCTGCTG 32592 A CA
 CA TAGT TACTAACAGCA
 || ||| |||||

		GT GTCG ATGATTGTCGT	
		C TC	
GAM2124 KIAA1804	3'	TGCTGTTAGCCATGTCTATTG 34590	T A_
		CAATAG CAT CTAACAGCA	
		GTTATC GTA GATTGTCGT	
		T CC	
GAM2124 MGC21636	5'	CTGTGGAATGCTATTGA 29648	T A A
		TCAATAG CAT CTA CAG	
		AGTTATC GTA GGT GTC	
		_ A _	
GAM2124 MGC5149	3'	TGTGTGTGACTATTGA 35785	TA
		TCAATAGTCATAC ACA	
		AGTTATCAGTGTG TGT	
		—	
GAM2124 RNF8	3'	TGCTGTTAGTAACTGTGTGA 10098	_ CA
		TCA ATAGT TACTAACAGCA	
		AGT TGTCA ATGATTGTCGT	
		G _	
GAM2124 SEMA3C	3'	TGCTGTTAATGTATACTACTG 13075	A C _
		CA TAGT ATAC TAACAGCA	
		GT ATCA TATG ATTGTCGT	
		C _ TA	
GAM2124 SHAPY	3'	TGCTGTCAGCATAATGATTGT 29017	A__ A
		ATAGTCAT CT ACAGCA	
		TGTTAGTA GA TGTCGT	
		ATAC C	
GAM2124 STAG2	3'	GCTGTTAGTTGGCTTTTGA 34930	T T
		TCAA AGTCA ACTAACAGC	
		AGTT TCGGT TGATTGTCG	
		T _	
GAM2124 YAP1	3'	TGCTGTTAATGTATTGCTG 12755	C _
		TAGT ATAC TAACAGCA	
		GTCG TATG ATTGTCGT	
		T TA	
GAM2124 ZFR	3'	TGCTGTTAGTTGTGCATTA 18189	_ _
		TAGT CATA CTAACAGCA	
		ATTA GTGT GATTGTCGT	
		C T	
GAM2124 ZNF294	3'	CTGGGTAAAATGACTATTGA 35057	AC A_
		TCAATAGTCAT TA CAG	

	AGTTATCAGTA AT GTC	
	AA GG	
GAM2124 LOC118706 5'	TGCTGAGGTGACTGTTGA 36597	ACTAA
	TCAATAGTCAT CAGCA	
	AGTTGTCAGTG GTCGT	
	GA__	
GAM2124 LOC127428 3'	CTGCTAGTAACTATTGG 36898	CA A
	TCAATAGT TACTA CAG	
	GGTTATCA ATGAT GTC	
	__ C	
GAM2124 LOC133686 3'	TGATGTTATGACTATTGA 37057	CTA G
	TCAATAGTCATA ACA CA	
	AGTTATCAGTAT TGT GT	
	__ A	
GAM2124 LOC143158 5'	TGCTGAGGTGACTGTTGA 37592	ACTAA
	TCAATAGTCAT CAGCA	
	AGTTGTCAGTG GTCGT	
	GA__	
GAM2124 LOC144438 3'	TGCTGTTAGCTGAACTGT 37739	_ TA
	ATAGT CA CTAACAGCA	
	TGTCA GT GATTGTCGT	
	A C_	
GAM2124 LOC145820 3'	TGCTGTTAAGTGTCTTCTGA 37993	AT T AC
	TCA AG CAT TAACAGCA	
	AGT TC GTG ATTGTCGT	
	CT T A_	
GAM2124 LOC147160 5'	CTGGGGTGTGACTTTGA 40809	T AA
	TCAA AGTCATACT CAG	
	AGTT TCAGTGTGG GTC	
	_ G_	
GAM2124 LOC147463 3'	TGCTATTCAAAGATGGACTATT 38342	ATA __ C
GA	TCAATAGTC CT AA AGCA	
	AGTTATCAG GA TT TCGT	
	GTA AAC A	
GAM2124 LOC159053 3'	CTGTTTCATTGTCACTATTGA 42060	C CT__
	TCAATAGT ATA AACAG	
	AGTTATCA TGT TTGTC	
	C TACT	
GAM2124 LOC201931 3'	TGCTGTTAGCACTGTT 42930	CATA
	AATAGT CTAACAGCA	

		TTGTCA GATTGTCGT	
		C__	
GAM2124	LOC220466	5' TGCTGAGGTGACTGTTGA 36611	ACTAA
		TCAATAGTCAT CAGCA	
		AGTTGTCAGTG GTCGT	
		GA__	
GAM2125	ACE2	3' AAATGTCTGTTGAATTTCTGAA 22356	T T TG
		TTCAGAAATT CAACA G TTT	
		AAGTCTTTAA GTTGT T AAA	
		_ C GT	
GAM2125	MAP3K5	3' AAACACACTGAAATTTT 12546	ACA
		GAAATTTCA TGTGTTT	
		CTTTAAAGT ACACAAA	
		C__	
GAM2125	NPEPPS	3' ACTGTGAAACTTTTCTGAA 12996	_ A T
		TTCAGAAA TTTCA CA GT	
		AAGTCTTT AAAGT GT CA	
		C _ _	
GAM2125	PRKAA2	3' AATGCTATTGAAATTACTGAA 12927	A CAT
		TTCAG AATTTCAA GTGTT	
		AAGTC TTAAAGTT CGTAA	
		A AT_	
GAM2125	PTGS2	3' AAACAATAATTTGAAATTTCT 6681	CATG_
		AGAAATTTCAA TGTTT	
		TCTTTAAAGTT ACAAA	
		TAATA	
GAM2125	C6orf35	3' AAGGACATTTTGAATTTT 20526	C G
		GAAATTTCAA ATGT TTT	
		CTTTAAAGTT TACA GAA	
		_ G	
GAM2125	FLJ20730	3' AAACACATGTTGACTTTT 19639	TT
		AAA TCAACATGTGTTT	
		TTT AGTTGTACACAAA	
		TC	
GAM2125	FLJ22833	3' ATGTTGTCAAAGTTTCTGAA 23119	__
		TTCAGAAATTT CAACAT	
		AAGTCTTTGAA GTTGTA	
		ACT	
GAM2125	FLJ23462	3' AAACAGTGATTGAAATTTT 24258	_ G
		GAAATTTCAA CAT TGTTT	

		CTTTAAAGTT GTG ACAA	
		A _	
GAM2125	MADP-1	3' AAAGATATTTGAAATTC 26961	C G
		GAAATTTCAA ATGT TTT	
		CTTTAAAGTT TATA AAA	
		_ G	
GAM2125	MCM10	3' ACATGCTAAATTTCTGAA 20591	CAA
		TTCAGAAATTT CATGT	
		AAGTCTTTAAA GTACA	
		TC_	
GAM2125	PLCL1	3' AAACAGATGATGAGAATTTCT 12888	_ A G
		AGAAAT TTCA CAT TGTTT	
		TCTTTA GAGT GTA ACAA	
		A A G	
GAM2125	LOC151473	3' AAACACATGTTGTATGTTTT 39117	TT_
		GAAAT CAACATGTGTTT	
		TTTTG GTTGACACAAA	
		TAT	
GAM2125	LOC162461	3' AAACACATGTCCTCACTGAA 40056	AAATTTCA
		TTCAG ACATGTGTTT	
		AAGTC TGTACACAAA	
		ACTCC__	
GAM2125	LOC220776	3' AAACACATGTTTTTTTCTGA 33926	TTTC
		TCAGAAA AACATGTGTTT	
		AGTCTTT TTGTACACAAA	
		TT_	
GAM2125	LOC253019	5' AAACACATGCTGTGTTTGAA 45665	AATTT A
		TTCAGA CA CATGTGTTT	
		AAGTTT GT GTACACAAA	
		GT_ C	
GAM2125	LOC253975	5' AAACACATGCTGTGTTTGAA 45932	AATTT A
		TTCAGA CA CATGTGTTT	
		AAGTTT GT GTACACAAA	
		GT_ C	
GAM2125	LOC85479	5' AAACATTATAATTAAATTTCTG 26955	CAACAT_
	AA	TTCAGAAATTT GTGTTT	
		AAGTCTTTAAA TACAAA	
		TTAATAT	
GAM2126	APPBP2	3' GTGATAAAACAACATGGTA 13083	CTA G
		TACC TTGTTTTAT AT	

			ATGG AACAAAATA TG		
			TAC G		
GAM2126	AQP6	3'	GTTTCATCATATTGGTCAGGGT 7360	ATTGTTT	A
	G		TACCCT TATGAT AAAC		
			GTGGGA ATACTA TTTG		
			CTGGTT_ C		
GAM2126	AQP6	3'	GTTTCATCATATTGGTCAGGGT 27617	ATTGTTT	A
	G		TACCCT TATGAT AAAC		
			GTGGGA ATACTA TTTG		
			CTGGTT_ C		
GAM2126	HS2ST1	3'	TTTTATCATATTTTAGGGTG 14581	TTGTTT	
			TACCCTA TATGATAAAA		
			GTGGGAT ATACTATTTT		
			TTT_		
GAM2126	RPP30	3'	TCTAAAACAATGGAGTA 13122	C	T
			TAC CTATTGTTTTA GA		
			ATG GGTAACAAAAT CT		
			A _		
GAM2126	XK	3'	TTTTACCATATGGAATAGGG 22064	G TT	A
			CCCTATT T TATG TAAAA		
			GGGATAA G ATAC ATTTT		
			_GT C		
GAM2126	HCA4	3'	TTATAAAACAATAGCGTA 38029	C	
			TAC CTATTGTTTTATGA		
			ATG GATAACAAAATATT		
			C		
GAM2126	KIAA0635	3'	GTTTTGTATAAAACAATAG 16058	G	
			CTATTGTTTTAT ATAAAC		
			GATAACAAAATA TGTTTTG		
			_		
GAM2126	LOC158219	5'	GTTTTATCATGCCCCGAATAGAG 39763	C	GTTT
	T		AC CTATT TATGATAAAAC		
			TG GATAA GTACTATTTTG		
			A GCCC		
GAM2126	LOC158434	3'	TTGTTGAAAACAATAGGG 41989	A	
			CCCTATTGTTTT TGATAA		
			GGGATAACAAAA GTTGTT		
			_		
GAM2126	LOC221337	5'	TTTGTATAAAACAATAGG 44237	G	
			CCTATTGTTTTAT ATAAA		

GGATAACAAAATA TGTTT

GAM2126 LOC256021 3' TCATGAAATGCAAAACAATAGG 46165

CCTATTGTT TTATGA

||||||| |||||

GGATAACAA AGTACT

AACGTAA

GAM2127 FLJ21615 3' ATCTACACATATTTATATCACA 25909

T C A

TGTGATGT AG AT TG TAGAT

||||||| || || |||||

ACACTATA TT TA ACATCTA

T A C

GAM2127 GABARAPL3 3' ATCTCACTCACAAACATCACA 26296

AGCATA T

TGTGATGTT TG AGAT

||||||| || |||||

ACACTACAA AC TCTA

ACACTC _

GAM2127 KIAA0077 3' TCTCAATGCTAACACCACA 33267

A A T

TGTG TGTTAGCAT TG AGA

||| ||||| || |||

ACAC ACAATCGTA AC TCT

C _ _

GAM2127 KIAA0923 3' ATCAACACTACTAACATTACA 15240

CATA A

TGTGATGTTAG TGT GAT

||||||| || |||

ACATTACAATC ACA CTA

ATC_ A

GAM2127 LAT1-3TM 5' ACTTGATGCACAACATCACA 34053

A_ AT_

TGTGATGTT GCAT GT

||||||| ||| ||

ACACTACAA CGTA CA

CA GTT

GAM2127 MGC13071 3' ACAGAATGTCAACATCACA 26407

AG A_

TGTGATGTT CAT TGT

||||||| ||| |||

ACACTACAA GTA ACA

CT AG

GAM2127 VEZATIN 3' CTGCCTACTAACATCA 19070

CA T

TGATGTTAG TA GTAG

||||||| || |||||

ACTACAATC AT CGTC

_ C

GAM2127 LOC116236 3' CTGTCCTGACATCACA 36541

CATA _

TGTGATGTTAG TG TAG

||||||| || |||

ACACTACAGTC AC GTC

_ T

GAM2127 LOC122786 3' ACATGTAACATCACA 36696

AGC

TGTGATGTT ATATGT

||||||| |||||

ACACTACAA TGTACA

GAM2127 LOC145371 3' ACCTATGCCACATCACA 37842 TA T
TGTGATGT GCATA GT
||||||| |||||
ACACTACA CGTAT CA
C_ C

GAM2127 LOC162239 3' TTTCCATACTAAACATCACA 40055 _ CA T
TGTGATGTT AG TATG AGA
||||||| || |||||
ACACTACAA TC ATAC TTT
A _ C

GAM2127 LOC169026 3' TCTGTATGCTAACGCCACA 40268 A GT
TGTG TGTTAGCATAT AGA
||| ||||||||| |||
ACAC GCAATCGTATG TCT
C _

GAM2127 LOC222070 5' ATCTACAGCCAAGCATCACA 45176 A_ ATA
TGTGATGTT GC TG TAGAT
||||||| || |||||||
ACACTACGA CG ACATCTA
AC _

GAM2127 LOC93333 5' ATCAACACCATAACATCACA 35664 GCATA A
TGTGATGTTA TGT GAT
||||||| || |||||
ACACTACAAT ACA CTA
ACC_ A

GAM2128 DLG5 3' GCTTTAGTACAACAAATAAAGG 40339 G CA GTT
TC GA CTTTATTTGT TA AAGC
|| ||||||||| || |||||
CT GAAATAAACA AT TTCG
G AC GAT

GAM2128 MGC23937 3' GCTTGAAGCCACAAATAAAACT 29682 C CATAG
C GAG TTTATTTGT TTAAGC
||| ||||||||| |||||||
CTC AAATAAACA AGTTTCG
A CCGA_

GAM2128 LOC158969 3' GCCATGACAAATAAAGCT 39922 A
AGCTTTATTTGTCAT GT
||||||||||| ||
TCGAAATAAACAGTA CG
C

GAM2129 CRIM1 3' CCTGGTAACATAAAAGCAGTTC 18558 CA A_
A TGGACTGCTTTTA TTA AGG
||||||||||| ||| |||
ACTTGACGAAAAT AAT TCC
AC GG

GAM2129 MASP1 3' CCTCCGATGAAAGCAGCCA 7605 A TA AA
TGG CTGCTTT CATT AGG
||| ||||||| ||||| |||

		ACC GACGAAA GTAG TCC		
		— — CC		
GAM2129	ROCK2	3' CCTTCTATGAAAGCAGTC 32839	TA	TA
		GA CTGCTTT CAT AAGG		
		CTGACGAAA GTA TTCC		
		— TC		
GAM2129	CASPR3	3' GATGTGCAAAACGCAGTCCA 27386	—	—
		TGGACTGC TTT TACATT		
		ACCTGACG AAA GTGTAG		
		C AC		
GAM2129	FHR5	3' CTCTAATGTAAGTCTA 25083	GCTTT	A
		TGGACT TACATTA AG		
		ATCTGA ATGTAAT TC		
		— C		
GAM2129	FLJ11726	3' CCTTTAATGCAATCCTCAGTC 24526	CTT_	A
		GA CTG TT CATTAAAGG		
		CTGAC AA GTAATTTCC		
		TCCT C		
GAM2129	FLJ20085	5' CCTCATGAAAAGCAGTCC 19185	A	TAA
		GGACTGCTTTT CAT AGG		
		CCTGACGAAAA GTA TCC		
		— C_		
GAM2129	KIAA0475	3' CCTTTTGCCAAAAGCAGTCC 16948	ACATT	
		GGACTGCTTTT AAAGG		
		CCTGACGAAAA TTTCC		
		CCGT_		
GAM2129	RAB40A	5' CCTAGGGTTTGTAAAAGAAATC 39929	CTG	TTAA_
	CA	TGGA CTTTTACA AGG		
		ACCT GAAAATGT TCC		
		AAA TTGGGA		
GAM2129	TUSP	3' CCTAAATTTAAAAGCAGTCCA 21523	C	AA
		TGGACTGCTTTTA ATT AGG		
		ACCTGACGAAAAT TAA TCC		
		T A_		
GAM2129	USP2	5' CCTCCAAGAAGAGGCAGCCCA 10400	A	ACA AA
		TGG CTGCTTTT TT AGG		
		ACC GACGGAGA AA TCC		
		C AG_ CC		
GAM2129	LOC219920	5' CCTTAGAAAAAAGCAGTCC 44806	ACA	A
		GGACTGCTTTT TT AAGG		

CCTGACGAAAA AG TTCC
 A__ A
 GAM2129 LOC255589 5' CCTTCAGAGAAGCAGACCA 46314 A ACATTA
 TGG CTGCTTTT AAGG
 ||| ||||| |||
 ACC GACGAAGA TTCC
 A GAC__
 GAM2130 ACTN2 3' CATGCTTTTTGTTAGAGCTTAT 6755 A TT TC
 ATAA CTCT AT AAAGCATG
 |||| ||| || |||||
 TATT GAGA TG TTTCGTAC
 C T_ TT
 GAM2130 EIF2C1 3' ATGCCTGATGAGTTTATA 14500 TTTAT AA
 TATAAACTC TCA GCAT
 ||||| ||| |||
 ATATTTGAG AGT CGTA
 T__ C_
 GAM2130 PRO2000 5' CATGCTTTGGAAAAGTTTA 15337 CTTTA
 TAAACT TTCAAAGCATG
 ||||| |||||
 ATTTGA AGGTTTCGTAC
 AA__
 GAM2130 LOC150383 3' CATGAAGGAATGAATAAAGAGT 38945 AAG__
 TT AAACTCTTTATTCA CATG
 ||||| |||
 TTTGAGAAATAAGT GTAC
 AAGGAA
 GAM2131 ADRBK2 3' ACAAAAAGCAGGTCTGTTTTATG 11642 _ AT
 TC GACATAAAACA ACT CTTTTGT
 ||||| ||| |||||
 CTGTATTTTGT TGG GAAAACA
 C AC
 GAM2131 TRAM 3' ACAAAAAGACAATGTGCTTTATG 15589 A ACTA_
 TTA TGACATAAA CA TCTTTTGT
 ||||| || |||||
 ATTGTATTT GT AGAAAACA
 C GTAAC
 GAM2131 COQ7 3' ACAAAAAGATAATTGGAAACATG 18221 AAAA_ C
 CAT CAA TATCTTTTGT
 ||| ||| |||||
 GTA GTT ATAGAAAACA
 CAAAG A
 GAM2131 FLJ22965 3' AGATGTTATTTTATGTCA 22642 C T
 TGACATAAAA AAC ATCT
 ||||| ||| |||
 ACTGTATTTT TTG TAGA
 A _
 GAM2131 SMOC1 3' ACAAAGGATTTGCATTACGTCA 22697 A AA CT
 TGAC TAA CAA ATCTTTTGT
 |||| ||| ||| |||||

		ACTG ATT GTT TAGGAAACA	
		C AC _	
GAM2131	LOC155072 3'	AAAAGAAAGAAATTGCCTTATG 41758	AA _ A
	TCA	TGACATAA CAA CT TCTTTT	
		ACTGTATT GTT GA AGAAAA	
		CC AAA A	
GAM2131	LOC202868 3'	AAAAGAAAGAAATTGCCTTATG 43445	AA _ A
	TCA	TGACATAA CAA CT TCTTTT	
		ACTGTATT GTT GA AGAAAA	
		CC AAA A	
GAM2132	MEL	3' GGGCCCACGGCCACCA 11846 AAGA AT	
		TGGT GC CGTGGGCCC	
		ACCA CG GCACCCGGG	
		C _ _	
GAM2132	MEN1	3' CCCACGATTTTCTCCA 28288 TA C	
		TGG AGAG ATCGTGGG	
		ACC TCTT TAGCACCC	
		_ T	
GAM2132	MEN1	3' CCCACGATTTTCTCCA 28290 TA C	
		TGG AGAG ATCGTGGG	
		ACC TCTT TAGCACCC	
		_ T	
GAM2132	MEN1	3' CCCACGATTTTCTCCA 28292 TA C	
		TGG AGAG ATCGTGGG	
		ACC TCTT TAGCACCC	
		_ T	
GAM2132	MEN1	3' CCCACGATTTTCTCCA 28294 TA C	
		TGG AGAG ATCGTGGG	
		ACC TCTT TAGCACCC	
		_ T	
GAM2132	MEN1	3' CCCACGATTTTCTCCA 28297 TA C	
		TGG AGAG ATCGTGGG	
		ACC TCTT TAGCACCC	
		_ T	
GAM2132	MEN1	3' CCCACGATTTTCTCCA 28301 TA C	
		TGG AGAG ATCGTGGG	
		ACC TCTT TAGCACCC	
		_ T	
GAM2132	MEN1	3' CCCACGATTTTCTCCA 5774 TA C	
		TGG AGAG ATCGTGGG	

ACC TCTT TAGCACCC
 _ T
 GAM2132 KIAA0513 3' TTGGGCCCTTCCCCACCA 16366 AA_ CATCGT
 TGGT GAG GGGCCCAA
 ||| ||| |||||
 ACCA CTT CCCGGGTT
 CCC C____
 GAM2132 LOC115795 5' TGGGCCCAGGTTCCCACC 36418 AA ATCG
 GGT GAGC TGGGCCCA
 ||| ||| |||||
 CCA CTTG ACCCGGGT
 CC G____
 GAM2132 LOC130813 5' TGGGCTCAAATGCTCTCCCA 37315 TA CG
 TGG AGAGCAT TGGGCCCA
 ||| ||||| |||||
 ACC TCTCGTA ACTCGGGT
 CC A_
 GAM2133 AP2B1 3' ACCTTGAGAATCTCCAAGAGAA 6949 CAA G C_
 AAA TTTTCTCT AGAT CTT GGT
 ||||| ||| ||| |||
 AAAAAGAGA TCTA GAG CCA
 ACC A TT
 GAM2133 BCL11B 3' CTCGGTACAACCTTTGAGAAAA 23161 C AT_____ TTCG
 AGA TTT TCTCAAAG GC G
 ||| ||||| || |
 AAA AGAGTTTC TG C
 A CAACA||| GCTT
 GAM2133 CYP19 3' CCAGGCTACAAGAGAAAAA 25270 CAAAGAT C
 TTTTCTCT GCTT GG
 ||||| ||| ||
 AAAAAGAGA CGGA CC
 ACAT_____
 GAM2133 CYP19 3' CCAGGCTACAAGAGAAAAA 5560 CAAAGAT C
 TTTTCTCT GCTT GG
 ||||| ||| ||
 AAAAAGAGA CGGA CC
 ACAT_____
 GAM2133 G6PC 3' GTACATCTTTGAAAAGAAAA 5656 C_ T_____
 TTTTCT TCAAAGA GC
 ||||| ||||| ||
 AAAAGA AGTTTCT TG
 AA ACA|||
 GAM2133 VAPB 3' AGCATCTTGAAAAGAAAAA 11131 CTCA
 TTTTCT AAGATGCT
 ||||| |||||
 AAAAAGA TTCTACGA
 AAAG
 GAM2133 C21orf25 3' CTCGGTACAATCTTTGAAAGAA 31799 C T_____ TTCG
 A TTTCT TCAAAGA GC G
 ||||| ||||| || |

		AAAGA AGTTTCT	TG C	
		A AACAI GCTT		
GAM2133	FLJ14735	3' CTGACCTTTGGGAGAAAA	26608	ATGCT
		TTTTTCTCTCAAAG	TCGG	
		AAAAAGAGGGTTTC	AGTC	
		C____		
GAM2133	MBD2	3' ACCGACTTTCCCAAGAGAAAA	17944	CAAA TGCT
		TTTTCTCT	GA TCGGT	
		AAAAGAGA	CT AGCCA	
		ACCC	TTC_	
GAM2133	MGC21738	5' CTCGGTATCACCTTTGAGGAAA	29676	T AT_____ TTCG
	AA	TTTC CTCAAAG	GC G	
		AAAG GAGTTTC	TG C	
		_	CACTAI GCTT	
GAM2133	PPP1R1A	3' ACCAAGCATAAGAGAAGAA	13590	CAAAG C
		TTTTTCTCT	ATGCTT GGT	
		AAGAAGAGA	TACGAA CCA	
		A_____		
GAM2133	LOC203248	3' ACTTGGTATCCTTTAGAGAAAA	43016	C A TC
	A	TTTTTCTCT AA	GATGCT GGT	
		AAAAAGAGA TT	CTATGG TCA	
		T C	T_	
GAM2134	CTNNA1	3' GCCTGTGGTAAGCAAC	32785	GAGA C
		GTTGCTTATT	ACAGG C	
		CAACGAATGG	TGTCC G	
		_____	A	
GAM2134	LGI1	5' TGACCTGTTCTTAGAGCAA	11564	AT C
		TTGCTT	TGAGAACAGG CA	
		AACGAG	ATTCTTGTCC GT	
		_____	A	
GAM2134	RGS16	3' GCCTGTTTGGGAAGCAGCA	8834	ATTGA
		TGTTGCTT	GAACAGGC	
		ACGACGAA	TTTGTCCG	
		GGG_		
GAM2134	FHOD2	5' CCTGCCCTCACCTGTGGGCAAC	36553	_____ AA
	A	TGTTGCTTAT	TGAG CAGG	
		ACAACGGGTG	ACTC GTCC	
		TCC	CC	
GAM2134	FLJ12409	3' GGCCTGTTACAGCTACA	24754	T TATT A
		TGT GCT	G GAACAGGCC	

		ACA CGA C CTTGTCCGG	
		T ____ A	
GAM2134	FLJ20445	3' GCCTGACCATGAAGCAACA 19482	AT AGAA
		TGTTGCTT TG CAGGC	
		ACAACGAA AC GTCCG	
		GT CA__	
GAM2134	FLJ20739	5' GCCTGTTCCGCCGAGCAGCA 33705	AT_ A
		TGTTGCTT TG GAACAGGC	
		ACGACGAG GC CTTGTCCG	
		GCC _	
GAM2134	FLJ30567	3' CCTGTTCTTGCAACA 29630	TTATT
		TGTTGC GAGAACAGG	
		ACAACG TTCTTGTCC	

GAM2134	KIAA0266	3' GCCTGGGCAATAAGCAA 22311	AGAA
		TTGCTTATTG CAGGC	
		AACGAATAAC GTCCG	
		GG__	
GAM2134	KIAA1336	3' TGTGCCTAACAAGCAACA 35804	A GAGAAC _
		TGTTGCTT TT AGGC CA	
		ACAACGAA AA TCCG GT	
		C _____ T	
GAM2134	SKIP	3' TGGCCTGTCCCCACATCCAGCA 28265	CTTAT AGA
		TGTTG TG ACAGGCCA	
		ACGAC AC TGTCCGGT	
		CTAC_ CCC	
GAM2134	SKIP	3' TGGCCTGTCCCCACATCCAGCA 18601	CTTAT AGA
		TGTTG TG ACAGGCCA	
		ACGAC AC TGTCCGGT	
		CTAC_ CCC	
GAM2134	Spir-1	3' CCTGCTGACAGGCAACA 32305	A G AA
		TGTTGCTT TT AG CAGG	
		ACAACGGA AG TC GTCC	
		C _ _	
GAM2134	LOC144231	5' GCCTGCTGTATAAGTAACA 40394	TG AA
		TGTTGCTTAT AG CAGGC	
		ACAATGAATA TC GTCCG	
		TG _	
GAM2134	LOC154215	3' TGGCCCAAAAGAGACAAGTAAC 39464	A GAGAA
	A	TGTTGCTT TT GGCCA	

		ACAATGAA AG CCGGT		
		C AGAAAAC		
GAM2135	BAI3	3' AGGACCTTCATGTGCCAA 7427	AA	
		TTGGCACATGGA TCCT		
		AACCGTGTACTT AGGA		
		CC		
GAM2135	KIAA0210	3' GAGAACATTCCACATGCCAA 16424	CA	ATCCT
		TTGGCA TGGAA TTTTC		
		AACCGT ACCTT AAGAG		
		AC AC__		
GAM2135	KIAA1204	3' AAGATGATTTCCATATACCAG 34311	CAC	C
		TTGG ATGGAAATC TTTT		
		GACC TACCTTTAG AGAA		
		ATA T		
GAM2135	LOC219988	5' GAAAGGATCCATATGCCAA 44045	C	AA
		TTGGCA ATGGA TCCTTTT		
		AACCGT TACCT AGGAAAG		
		A _		
GAM2136	ADPRT	3' TGCACTTATTGTCCCCTTT 7327	AA	ATGT TG
		AAAGG ACAATA AGTG A		
		TTTCC TGTTAT TCAC T		
		CC _ GT		
GAM2136	CDH19	3' CATGAAGTATTGTTTCCTTT 22127	ATGTA	
		AAAGGAAACAATA GTG		
		TTTCCTTTGTTAT TAC		
		GAAG_		
GAM2136	CYBB	3' CATACTACTATTCCCTTT 37537	ACAATAAT	
		AAAGGAA GTAGTGTG		
		TTTCCTT CATCATAC		
		AT__		
GAM2136	DDB1	3' TCACACTCATGCATTGTCCTCT 7640	AA	A_ T
	TT	AAAGG ACAAT ATG AGTGTGA		
		TTTCT TGTTA TAC TCACACT		
		CC CG _		
GAM2136	G6PC	3' TCACATTACATCATCCTCCTT 5657	AACA	A
		AAGGA AT ATGTAGTGTGA		
		TTCCT TA TACATTACACT		
		CC_ C		
GAM2136	LYZ	3' TCACACTACCATTTTCCCCT 5758	AAAC	_
	T	AAGG AATAATG TAGTGTGA		

		TTCC TTATTAC ATCACACT	
		CCT_ C	
GAM2136 MAN2A1	5'	CACAGTGC	8177
		AAAGGA ACA TGTA TGTG	
		TTTCCT TGT GCGT ACAC	
		C C__ G	
GAM2136 MEL	3'	CATTGGCATCATCGTTTCTTTT	11843
		AAAGGAAAC AT ATGT GTG	
		TTTTCTTTG TA TACG TAC	
		C C GT_	
GAM2136 OXR1	3'	TCACACTACAACATTCTCTTT	19733
		AAGGA AAT TGTAGTGTGA	
		TTTCT TTA ACATCACACT	
		C__ CA	
GAM2136 PIK3R3	3'	TCACACCACATTACACATGTGC	30608
TTC		GGA ACA TAATGT GTGTGA	
		CTT TGT ATTACA CACACT	
		CG ACAC C	
GAM2136 PSME3	3'	TCACATGAGGTTACTGTTTCTT	12372
T		AAGGAAACA TAAT GTGTGA	
		TTTCTTTGT ATTG TACACT	
		C GAG	
GAM2136 RBM8A	3'	CACCTATGTCATACTGTCTCCT	11579
CC		A AGGA ACA TA ATGTAG GTG	
		C TCCT TGT AT TGTATC CAC	
		C C C AC _	
GAM2136 SBF1	5'	GCACTGCTGTTTCCT	32626
		AGGAAACA GTAGTGT	
		TCCTTTGT CGTCACG	

GAM2136 SERPINB9	3'	ACACTTATTATTTTCCTTT	10359
		AAAGGAAA ATAATG AGTGT	
		TTTCCTTT TATTAT TCACA	

GAM2136 TIRAP	3'	TCACACTACTCTGTTTCCT	27478
		AGGAA CA GTAGTGTGA	
		TCCTT GT CATCACACT	
		_ CT__	
GAM2136 TK1	3'	TCACGCCCTCTTGTTTCCTTT	9271
		AAAGGAAACAA GTGTGA	

		TTTCCTTTGTT	CGCACT	
		CTCC__		
GAM2136	TRPV1	3' CACACCTGGCTGTTTTCTTT	27992	ATAATGTA
		AAAGGAAACA	GTGTG	
		TTTCTTTTGT	CACAC	
		CGGTC__		
GAM2136	TRPV1	3' CACACCTGGCTGTTTTCTTT	28000	ATAATGTA
		AAAGGAAACA	GTGTG	
		TTTCTTTTGT	CACAC	
		CGGTC__		
GAM2136	TRPV1	3' CACACCTGGCTGTTTTCTTT	28008	ATAATGTA
		AAAGGAAACA	GTGTG	
		TTTCTTTTGT	CACAC	
		CGGTC__		
GAM2136	TRPV1	3' CACACCTGGCTGTTTTCTTT	20812	ATAATGTA
		AAAGGAAACA	GTGTG	
		TTTCTTTTGT	CACAC	
		CGGTC__		
GAM2136	B3GALT6	3' CACTGAACCCATTGTTTCTTT	27924	AATG_
		AAGGAAACAAT	TAGTG	
		TTTCTTTGTTA	GTCAC	
		CCCAA		
GAM2136	C1orf19	3' CACACTCAAAGTTGTCTCTTT	33839	A AA T
		AAGGA ACAAT	TG AGTGTG	
		TTTCT TGTTG	AC TCACAC	
		C AA _		
GAM2136	CNOT7	3' TCACATTGGTTTGTCTCC	15003	A TAATG
		GGA ACAA	TAGTGTGA	
		CCT TGTT	GTTACACT	
		C TG__		
GAM2136	COPS7A	3' TCACACTACAGTCATTTCTTTT	18436	CAATAA
		AAAGGAAA	TGTAGTGTGA	
		TTTTCTTT	ACATCACACT	
		ACTG__		
GAM2136	DKFZp547I014	5' CAGGCTATGTATTATCTCCTTT	21466	AAC A G
		AAAGGA	AATA TGTAGT TG	
		TTTCCT	TTAT GTATCG AC	
		CTA _ G		
GAM2136	DKFZP586D2223	3' CACATTTTATTGTTTTCTTT	20644	_ TGT
		AAAGGAAA	CAATAA AGTGTG	

TTTCTTTT GTTATT TTACAC
 T ____
 GAM2136 DKFZP727C091 3' TCACTTTGCCATGTTTCCTT 32907 ATAAT T
 AAGGAAACA GTAG GTGA
 ||||| ||| |||
 TTCCTTTGT CGTT CACT
 AC__ T
 GAM2136 FLJ10618 3' TCACACCACATTACTTGGCCTT 19966 AAA _ A
 T AAAGG CAA TAATGT GTGTGA
 |||| ||| ||||| |||||
 TTTCC GTT ATTACA CACACT
 G_ C C
 GAM2136 FLJ10687 3' CATCATTTTTGTTTCCTTT 20008 T TAGT
 AAAGGAAACAA AATG GTG
 ||||| ||| |||
 TTTCTTTGTT TTAC TAC
 T ____
 GAM2136 FLJ11184 3' CACACTAATGCTTCCTTT 20364 A ATAATG
 AAAGGAA CA TAGTGTG
 ||||| || |||||
 TTTCTT GT ATCACAC
 C A____
 GAM2136 FLJ12644 3' TACATATTGTCTCCTTT 23331 A A
 AAAGGA ACAATA TGTA
 ||||| ||||| |||
 TTTCTT TGTTAT ACAT
 C _
 GAM2136 FLJ12987 3' CACCCTATTCATTTCCTTT 24806 CAATAAT T
 AAAGGAAA GTAG GTG
 ||||| ||| |||
 TTTCTTT TATC CAC
 ACT__ C
 GAM2136 FLJ20666 3' CACAGATACTGTTTCCT 20335 ATAAT G_
 AGGAAACA GTA TGTG
 ||||| ||| |||
 TCCTTTGT CAT ACAC
 ____ AG
 GAM2136 FLJ20666 3' CACAGATACTGTTTCCT 19581 ATAAT G_
 AGGAAACA GTA TGTG
 ||||| ||| |||
 TCCTTTGT CAT ACAC
 ____ AG
 GAM2136 FLJ23189 3' TCACCATTATTTACTGTTTCCT 24659 A T _
 AGGAAACA TAA GTAGTG TGA
 ||||| ||| ||||| |||
 TCCTTTGT ATT TATTAC ACT
 C _ C
 GAM2136 GFR 3' CACACAGACCTGTTTCCTTT 14635 ATAA A
 AAAGGAAACA TGT GTG
 ||||| ||| |||

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      TTTCTTTGT  ACA CAC
      CCAG  _
GAM2136 GRID1  3' TCACACCAACTCTGTTTCCTCA 33982  A   ATAAT A_
      A AGGAAACA  GT GTGTGA
      | |||||  || |||||
      A TCCTTTGT  CA CACACT
      C   CT__ AC
GAM2136 KIAA0258 3' TCACACTAGTGTGGTCCCTT 16651  AAA  ATG
      AAGG CAATA TAGTGTGA
      ||| |||| |||||
      TTCC GTTGT ATCACACT
      CTG  G__
GAM2136 KIAA0863 3' CACATCTATTGTTTCCT 17152  ATGTA
      AGGAAACAATA GTGTG
      ||||| ||||
      TCCTTTGTTAT TACAC
      C____
GAM2136 KIAA0863 3' CACATCTATTGTTTCCT 45632  ATGTA
      AGGAAACAATA GTGTG
      ||||| ||||
      TCCTTTGTTAT TACAC
      C____
GAM2136 KIAA1443 3' TCACAAATATTAATATTCCTT 31932  CAA  AG
      T      AAAGGAAA TAATGT TGTGA
      ||||| |||| ||||
      TTTCTTT ATTATA ACACT
      ATA  A_
GAM2136 MFN2  3' CTCATTATTGTGTCCTTT 17011  A   T
      AAAGGA ACAATAATG AG
      |||| ||||| ||
      TTTCTT TGTATTAC TC
      G   _
GAM2136 NLN  3' CACACTTAAATTACGTTTCCTCC 21857  A  ACAA  GT_
      A AGGAA TAAT AGTGTG
      | ||||  ||| |||||
      C TCCTT ATTA TCACAC
      C  GC__ AAT
GAM2136 PB1  3' TCACACCATTACGTTTCTTTT 19982  AA  TA
      AAAGGAAAC TAATG GTGTGA
      ||||| |||| |||||
      TTTTCTTTG ATTAC CACACT
      C_  __
GAM2136 PCDH19 3' CTGCCACATTGTTTCCTTT 31863  AAT
      AAAGGAAACAAT GTAG
      ||||| |||
      TTTCTTTGTTA CGTC
      CAC
GAM2136 PPP1R10 3' TCACACTACATGCACTGCCTTT 8579  AAACAATA
      AAAGG  ATGTAGTGTGA
      ||||  |||||

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		TTTCC	TACATCACACT		
		GTCACG__			
GAM2136	PRRG1	3'	TCACACTTGTGTTTATTTTCTTT 6657	CAAT	T
			AAAGGAAA AATG AGTGTGA		
			TTTCTTTT TTGT TCACACT		
			ATT_ _		
GAM2136	SRF	3'	CACTTATTTATTGTTGCCTTT 9096	A	TGT
			AAAGG AACAATAA AGTG		
			TTTCC TTGTTATT TCAC		
			G TAT		
GAM2136	LOC125929	3'	TCACACTGGTTCATTTTCCTT 37270	CAAT	G
			AAGGAAA AAT TAGTGTGA		
			TTCTTTT TTG GTCACACT		
			ACC_ _		
GAM2136	LOC130162	3'	ATACTATTGCTTCCTTT 36984	A	ATAAT
			AAAGGAA CA GTAGTGT		
			TTTCCTT GT TATCATA		
			C _		
GAM2136	LOC130589	3'	TCACATTGCTTTTATTTCTCC 29023	A	C TAAT
			A AGGAAA AA GTAGTGTGA		
			C TCCTTT TT CGTTACACT		
			C A TT_		
GAM2136	LOC132228	3'	CACATCTACACTATTTCTT 37021	ACA	A _
			AAGGAA ATA TGTAG TGTG		
			TTCTT TAT ACATC ACAC		
			_ C T		
GAM2136	LOC146784	5'	TCACACCATTTCTGTTTCTTT 38239	AT_	TA
			AAGGAAACA AATG GTGTGA		
			TTTCTTTGT TTAC CACACT		
			CCT _		
GAM2136	LOC153077	3'	TCAAAAAACATTATTTTCTT 41568	C	AGTG
		T	AAAGGAAA AATAATGT TGA		
			TTTCCTTT TTATTACA ACT		
			_ AAAA		
GAM2136	LOC158581	5'	CACAGGCATTGTTTGCTTT 42014	G	ATA AG
			AAAG AAACA ATGT TGTG		
			TTTC TTTGT TACG ACAC		
			G _ G_		
GAM2136	LOC221143	3'	CTTCATTATTGTTTCCTT 44942	T	
			AAGGAAACAATAATG AG		

TTCCTTTGTTATTAC TC
 T
 GAM2136 LOC221296 3' CTGCACCCTGTTTCCTTT 44168 ATAA
 AAAGGAAACA TGTAG
 ||||| ||||
 TTTCTTTGT ACGTC
 CCC_
 GAM2137 MAPRE2 3' CATTCATCCAACTTC 15546 T ATTA
 GGA GTTG GATGAATG
 ||| ||| |||||
 CTT CAAC CTACTTAC
 — —
 GAM2137 ZNF255 5' CACCCATGTCAACATCT 12347 TAG AA
 GGATGTTGAT ATG TG
 ||||| ||| ||
 TCTACAACTG TAC AC
 — CC
 GAM2137 FLJ12488 3' CACTCATCCACATCCTG 25266 T T A
 TAGGATGT GAT AG TG
 ||||| ||| |||
 GTCCTACA CTA TC AC
 C C _
 GAM2137 FLJ12788 3' CATCCACTGAAACATCCT 22871 GA A A
 AGGATGTT TTAG TG ATG
 ||||| ||| |||
 TCCTACAA AGTC AC TAC
 — _ C
 GAM2137 HSA250839 3' TGCAGAGTGTAATCAGCACCC 20439 A G GAA
 GG TGTTGATTA AT TGCA
 || ||||| || ||||
 CC ACGACTAAT TG ACGT
 C G AG_
 GAM2137 KIAA1877 3' TGCATTCATCATTAATATCCT 32886 GATTA
 A TAGGATGTT GATGAATGCA
 ||||| |||||
 ATCCTATAA CTACTTACGT
 ATTA_
 GAM2137 MGC3771 5' TGCATTCATCCAGCTCACC 25234 AT_ ATTA
 GG GTTG GATGAATGCA
 || ||| |||||
 CC CGAC CTACTTACGT
 ACT —
 GAM2137 LOC162333 5' TGTCTAATCAACATCCTA 42140
 TAGGATGTTGATTAGATG
 |||||
 ATCCTACAACATAATCTGT
 GAM2137 LOC90410 5' TGCATTCATCTTTGTACCCCC 31400 AT TGATT
 GG GT AGATGAATGCA
 || || |||||

			CC CA TCTACTTACGT		
			CC TGTT_		
GAM2138	CYP27B1	3'	TGACTAGGTGTCACCATACA 6434	A	GA A
			TGTATGGT ACAT TA TCA		
			ACATACCA TGTG AT AGT		
			C G_ C		
GAM2138	G6PC	3'	ATTATATAGTATACCATACATT 5654	_	ATG
	A		TAATGTATGGTA AC ATAAT		
			ATTACATACCAT TG TATTA		
			A ATA		
GAM2138	KIAA0349	3'	ATTATTATGTACCACACA 44340	A	A
			TGT TGGTA CATGATAAT		
			ACA ACCAT GTATTATTA		
			C _		
GAM2138	MIG	3'	TGATTATCAATTACCACAC 8249	A	CA
			GT TGGTAA TGATAATCA		
			CA ACCATT ACTATTAGT		
			C A_		
GAM2138	LOC152925	3'	TGTTATGCTACATACATTA 39338	G	A
			TAATGTATG TA CATGATA		
			ATTACATAC AT GTATTGT		
			_ C		
GAM2138	LOC158295	5'	ATTATCATGGCATCATCAT 41937	T	AA
			ATG ATGGT CATGATAAT		
			TAC TACTA GTACTATTA		
			_ CG		
GAM2138	LOC55885	3'	ATCTGTTACCACAATTA 20710	GTA	T
			TAAT TGGTAACA GAT		
			ATTA ACCATTGT CTA		
			AC_ _		
GAM2139	NOTCH2	3'	GTCAAATAGGAAACATCAC 23649	T	G
			GTG TGTTT TTATTTGAC		
			CAC ACAA GATAAACTG		
			T G		
GAM2139	GNG4	3'	CAAATAACAAATGTGCCATG 10807	TG	T
			CATGG T GTTTGTTATTTG		
			GTACC G TAAACAATAAAC		
			GT _		
GAM2139	KIAA1495	3'	CAAATGGCAACACCA 36223	TTGT	
			TGGTGTGT TATTTG		

ACCACAACG GTAAAC

GAM2139 KIAA1582 5' CAAATAACACTAACCCCATGA 32582 T TT
TCATGG GTTG TGTTATTTG
||||| ||| |||||
AGTACC CAAT ACAATAAAC
C C_
GAM2139 LOC254826 3' TCAGTTCAAAACAACACATGA 46435 G GTTAT
TCATG TGTTGTTT TTGA
||||| ||||| |||
AGTAC ACAACAAA GACT
_ ACTT_
GAM2140 BAZ1A 3' TCAGCTTTACAGAACTGTATTA 15115 C TAT
TAATACGGT CTGTAG CTGA
||||| ||||| |||
ATTATGTCA GACATT GACT
A TC_
GAM2140 APCL 3' TCAGTGCCCAAGGACCG 12503 TA T
CGGTCCTG GTA CTGA
||||| ||| |||
GCCAGGAC CGT GACT
C_ _
GAM2140 P5-1 3' CAGATCTCTTAAGACTGTA 13497 C T_ T
TACGGTC TG AG ATCTG
||||| || ||| |||
ATGTCAG AT TC TAGAC
A TC _
GAM2140 LOC91286 5' TCAGATACCACAACTTTA 32623 C CC A
TA GGT TGT GTATCTGA
|| ||| ||| |||||
AT TCA ACA CATAGACT
T A_ C
GAM2141 ESDN 3' AGTTTTCCATAAACTGTTA 28151 T
TAGCAGTTTATGGAAA CT
||||| ||||| |||
ATTGTCAAATACCTTT GA
T
GAM2141 KIAA1317 3' TGACAAGGGCCATAAATTGCTA 41631 AAA A
TAGCAGTTTATGG TCTT TCA
||||| ||| |||
ATCGTTAAATACC GGAA AGT
G_ C
GAM2141 LOC158295 5' TGATAAGACTCCCATTTAGAC 41939 _ AAA
GTTTA TGG TCTTATCA
||||| ||| |||||
CAGAT ACC AGAATAGT
TT CTC
GAM2142 DBT 3' GTTGAAAACGTGTATGCCAAA 7634 ATC_
TTTGGTATACA TCGAC
||||| |||||

			AAACCGTATGT AGTTG		
			CAAA		
GAM2142 RFC1	3'	AGATTGTCATCTTGTACAGCAA 8817	GTA TCTC		
	A	TTTG TACAA GACAATCT			
		AAAC ATGTT CTGTTAGA			
		GAC CTA_			
GAM2142 SOCS5	3'	TGAAGATCATATACCAA 15232	CA _		
		TTTGGTATA ATCT CG			
		AAACCATAT TAGA GT			
		AC A			
GAM2142 KIAA1376	3'	AGACTGTCAAGATTGTATACC 31822	C A		
		GGTATACAATCT GACA TCT			
		CCATATGTTAGA CTGT AGA			
		A C			
GAM2142 KIAA1617	3'	TGTTGGATTATATATCAA 43945	C T		
		TTTGGTATA AATC CGACA			
		AAACTATAT TTAG GTTGT			
		A _			
GAM2142 NYD-SP20	5'	AGACTGTGCGTTGATACCAA 26328	A TCT _ A		
		TTTGGTAT CAA CG ACA TCT			
		AAACCATA GTT GC TGT AGA			
		_ _ _ G C			
GAM2142 TIEG	3'	AGATTTGAAAATTGTATACCAA 12193	C_ CA		
		TTGGTATACAAT TCGA ATCT			
		AACCATATGTTA AGTT TAGA			
		AA _			
GAM2142 LOC51339	3'	ATTGCTTTTTTGTATACCAA 18768	TCTCGA		
		TTGGTATACAA CAAT			
		AACCATATGTT GTTA			
		TTTC_			
GAM2143 ESPN	3'	AGAAACATGAAAAGTGCCT 25548	A CTGG		
		AG GTA TTTCATGTTTCT			
		TC CGT AAAGTACAAAGA			
		_ CA_			
GAM2143 GRLF1	3'	AGAAACGTTCCCAAAGTC 38407	AC TTTC		
		GAGT TGG ATGTTTCT			
		CTCA ACC TGCAAAGA			
		A_ CT_			
GAM2143 ITGA2	3'	AGAAACATGAAATGCTT 7962	ACTG		
		GAGT GTTTCATGTTTCT			

TTCG TAAAGTACAAAGA

GAM2143 WT1 3' AGAACTAACCAGTACCTC 23667 A TCATGT
GAG GTACTGGTT TTCT
||| ||||| |||
CTC CATGACCAA AAGA

TC____
GAM2143 WT1 3' AGAACTAACCAGTACCTC 23671 A TCATGT
GAG GTACTGGTT TTCT
||| ||||| |||
CTC CATGACCAA AAGA

TC____
GAM2143 WT1 3' AGAACTAACCAGTACCTC 23675 A TCATGT
GAG GTACTGGTT TTCT
||| ||||| |||
CTC CATGACCAA AAGA

TC____
GAM2143 WT1 3' AGAACTAACCAGTACCTC 5951 A TCATGT
GAG GTACTGGTT TTCT
||| ||||| |||
CTC CATGACCAA AAGA

TC____
GAM2143 A2BP1 5' AGTGCGTGAGAAACCAGCAC 20803 A _ TT
GT CTGGTT TCATGT CT
|| ||||| ||||| ||
CA GACCAA AGTGCG GA
C AG T_

GAM2143 KIAA0993 3' TAGAAGGTGGAACCAAAACCC 32083 A AC ATG
TC GAG GT TGGTTTC TTTCTA
||| || ||||| |||||
CTC CA ACCAAAG GAAGAT
C AA GTG

GAM2143 KIAA1416 5' AGAAACATGCAGCAGTCTC 41797 T G T
GAG ACTG TT CATGTTTCT
||| |||| || |||||
CTC TGAC GA GTACAAAGA
_ _ C

GAM2143 My015 3' AAATACCTAACCAGTACTT 33103 TCA
GAGTACTGGTT TGTTT
||||||| |||||
TTCATGACCAA ATAAA
TCC

GAM2143 RASSF2 3' AGAAGAGAACAGTACTCTC 16388 G ATGT
GAGAGTACTG TTTC TTCT
||||||| |||||
CTCTCATGAC AGAG AAGA
A ____

GAM2143 TP53INP1 3' AAACATGAAGGACTCC 27101 A A GGT
G GAGT CT TTCATGTTT
| |||| || |||||

C CTCA GG AAGTACAAA

GAM2143 TP53INP1 3' AAACATGAAGGACTCC 36112 A A GGT
G GAGT CT TTCATGTTT
| ||| || |||||
C CTCA GG AAGTACAAA

GAM2143 LOC149711 5' AAACATAAACCAGTACCTC 41065 A C
GAG GTACTGGTTT ATGTTT
||| ||||| |||||
CTC CATGACCAAA TACAAA

GAM2143 LOC157503 3' TAGAAACATGAAACCATGCACT 41815 A C
T GAG GTA TGGTTTCATGTTTCTA
||| ||| ||||| |||||
TTC CGT ACCAAAGTACAAAGAT
A _

GAM2144 ATP11A 3' TGCACACACATATACACACA 37808 _ A AG
TGTG GTATATGT TG GTA
||| ||||| || |||
ACAC CATATACA AC CGT
A C A _

GAM2144 CXCR6 3' TACCCACACACATACACACA 13333 _ A A A
TGTG GTAT TGT TG GGTA
||| ||| ||| || |||
ACAC CATA ACA AC CCAT
A C C _

GAM2144 DDIT3 5' CTTCATACATCACCACA 10287 AT
TGTGGT ATGTATGAGG
||| ||| |||||
ACACCA TACATACTTC
C _

GAM2144 FGFR1 3' TGCCTGGACACACACACACACA 22451 _ ATA A AGG
TGTG GT TGT TG TAGGCA
||| || ||| || |||||
ACAC CA ACA AC GTCCGT
A C _ C AG _

GAM2144 SLC4A4 3' TACACATACATACACACA 9838 GTA AG
TGTG TATGTATG GTA
||| ||||| |||
ACAC ATACATAC CAT
AC _ A _

GAM2144 TMOD 3' TGCCTTTTAATATACCACA 9294 GTAT
TGTGGTATAT GAGGTA
||| ||||| |||||
ACACCATATA TTCCGT
ATT _

GAM2144 FGD3 3' GCCTGCACACCACCACA 36091 ATA ATGAG _
TGTGGT TGT GTAGG C
||| || ||| ||| |

		ACACCA ACA CGTCC G		
		CC_ _____ C		
GAM2144	FLJ12838	3' TACCCTTCACAATACCACA 23924	A	ATGA
		TGTGGTAT TGT GGTA		
		ACACCATA ACA CCAT		
		_ CTTC		
GAM2144	HIC	3' TACACATACATACACACA 33494	GTA	AG
		TGTG TATGTATG GTA		
		ACAC ATACATAC CAT		
		AC_ A_		
GAM2144	KIAA1309	3' TACATACATACATACACACA 27264	_ A	AG_
		TGTG GTAT TGTATG GTA		
		ACAC CATA ACATAC CAT		
		A C ATA		
GAM2144	SCN12A	3' GCCTACCTCATAGCTTCACA 15410	TATATG	
		TGTGG TATGAGGTAGGC		
		ACACT ATACTCCATCCG		
		TCG_____		
GAM2144	LOC145333	3' GCCCACCTCATAACCATA 40533	ATATG	A
		TGTGGT TATGAGGT GGC		
		ATACCA ATACTCCA CCG		
		_____ C		
GAM2144	LOC162333	5' TGCCTACCCCAGTTCCTATCCA 42137	TATATGTA	A
	CA	TGTGG TG GGTAGGCA		
		ACACC AC CCATCCGT		
		TATCCTTG C		
GAM2144	LOC222662	3' ACACATACATACACACACA 44600	_ A	AG
		TGTG GT TATGTATG GT		
		ACAC CA ATACATAC CA		
		A C A_		
GAM2144	LOC255082	5' ACTTCAGACACACACCACA 46115	ATA	A
		TGTGGT TGT TGAGGT		
		ACACCA ACA ACTTCA		
		CAC G		
GAM2145	EGR2	3' TATTATGGAGAAAAAATCACT 5971	ATCCG	AG
		AGTGG TT CTCCATAATA		
		TCACT AA GAGGTATTAT		
		AAA_ AA		
GAM2145	LOC147184	5' ATTATGGAGATTAACCACT 29787	ATCCG	_
		AGTGG TTAG CTCCATAAT		

		TCACC	AATT GAGGTATTA	
		_____	A	
GAM2145	LOC90499	3'	TATTATGGAGCTGCTTCCTCT 31583	T TCCGT
			AG GGA TAGCTCCATAATA	
			TC CCT GTCGAGGTATTAT	
			T TC_____	
GAM2146	LPIN2	3'	AAGAGAACTGTCAGGAGCCCAG 16059	_ CC_____ C
	A		TCTGGGC CC GT CTCTT	
			AGACCCG GG CA GAGAA	
			A ACTGT A	
GAM2146	acmsd	5'	AGAATGGCCAGATCTAA 28728	GCCC C
			TTAGATCTGG CCGT CT	
			AATCTAGACC GGTA GA	
			_____ A	
GAM2146	C1orf34	3'	AAGAGGACAGGAAGGCTTCTGA 30431	TCTG _ C
			TTAGA GGCC CC GTCCTCTT	
			AGTCT TCGG GG CAGGAGAA	
			_____ AA A	
GAM2146	KIAA1110	3'	AAGAAAACGAGCTGAGGGTCTA 30980	G_ CCC CC
	A		TTAGATCT GGC CGT TCTT	
			AATCTGGG TCG GCA AGAA	
			AG A_ AA	
GAM2146	MGC14258	3'	GACAGGACCTAGATCTAA 26724	C CC
			TTAGATCTGGG CC GTC	
			AATCTAGATCC GG CAG	
			A A_	
GAM2146	LOC150372	3'	GGCGGGGGCCCCAGAACTAA 38942	A
			TTAG TCTGGGCCCCCGTC	
			AATC AGACCCGGGGGCGG	
			A	
GAM2146	LOC153516	3'	AAGAGGAATCACCAGGGCCCGG 28840	CCG_____
	ATCTAA		TAGATCTGGGCC TCCTCTT	
			ATCTAGGCCCGGG AGGAGAA	
			ACCACTA	
GAM2147	GAC1	3'	GCCTGTTCTCAGCAGTAGAGA 13038	C A C G
			TC CTG CTGC GAG AGCAGGC	
			AG GAT GACG CTC TTGTCCG	
			A _ A _	
GAM2147	LAPTM5	3'	GGCCTGCTCCTCCTGCAGGG 13617	ACTGCC
			CCCTG GAGGAGCAGGCC	

GGGAC CTCCTCGTCCGG
GTC____
GAM2147 SCN4A 3' CCTGAGCGGGAGTCAGGGA 5889 G AGGAG
TCCCTGACT CCG CAGG
||||||| ||| ||||
AGGGACTGA GGC GTCC
G GA____
GAM2147 SLC22A3 3' GGCCCTGTTCCAGCAATAAG 22506 GAC CGA _
CT TGC GGAGCAGG CC
|| ||| ||||||| ||
GA ACG CCTTGTCC GG
ATA A__ C
GAM2147 TCTA 3' GCCTGCTCCCTCACCCAGG 22731 AC CCGA
CCTG TG GGAGCAGGC
|||| || |||||||
GGAC AC CCTCGTCCG
CC TC____
GAM2147 WHSC1 3' GGCCTGCCCATGAGTCAGGGG 14251 GC A A
TCCCTGACT CG GG GCAGGCC
||||||| || || |||||||
GGGGACTGA GT CC CGTCCGG
__ A _
GAM2147 WWP2 3' CCCGCGGATGGCAGTCTGGA 30622 CT AGGA A
TCC GACTGCCG GC GG
||| ||||||| |||
AGG CTGACGGT CG CC
T_ AGG_ C
GAM2147 C1QR1 3' CCTGTTCTCAACAACAGGGA 14332 AC CC G
TCCCTG TG GAG AGCAGG
||||| || ||| |||||||
AGGGAC AC CTC TTGTCC
A_ AA _
GAM2147 CPR2 3' CCTGACTAAATAGCAGTCAGGG 25174 CGAGG _
A TCCCTGACTGC AG CAGG
||||||||| || ||||
AGGGACTGACG TC GTCC
ATAAA A
GAM2147 FLJ21195 3' GCCACCCAGCAGTCAGAGA 22827 C CGA AGCA
TC CTGACTGC GG GGC
|| ||||||| || |||
AG GACTGACG CC CCG
A AC_ A____
GAM2147 FLJ22795 3' GGCCCTCTCTGGGCAGTCAG 24690 G _ CA
CTGACTGCC AG GAG GGCC
||||||| || ||| ||||
GACTGACGG TC CTC CCGG
G T C_
GAM2147 GRIP1 5' CCTGCGGACAGTCAGG 34962 _ GAGGA
CCTGACTG CC GCAGG
||||||| || |||||

GGACTGAC GG CGTCC
A _____
GAM2147 KIAA0014 3' GGCCAGTCTCGGCAGTCGAG 16116 _ AGCA
CT GACTGCCGAGG GGCC
|| ||||| ||||
GA CTGACGGCTCT CCGG
G GA__
GAM2147 KIAA1157 3' GCCAGTGTCTCAGCAGTCAGAGA 35752 C C GGA A
TC CTGACTGC GA GC GGC
|| ||||| || ||||
AG GACTGACG CT TG CCG
A A G__ A
GAM2147 KIAA1274 3' GGCCTGCTCCACTTGTCTGGGA 43912 T TGCCGA
TCCC GAC GGAGCAGGCC
||||| |||||
AGGG CTG CCTCGTCCGG
T TTCA__
GAM2147 KIAA1393 3' CCTGCTCCTCCAAAGCCAG 35687 A GCC
CTG CT GAGGAGCAGG
||| || |||||
GAC GA CTCCTCGTCC
C AAC
GAM2147 KIAA1909 5' GCCTGCTCTGGACCAGGGA 36558 ACTG GA
TCCCTG CC GGAGCAGGC
||||| || |||||
AGGGAC GG TCTCGTCCG
CA__ __
GAM2147 KLK6 5' GGCCTGCTCCCCAGCCCGGG 8665 A_ CCGA
CCCTG CTG GGAGCAGGCC
||||| || |||||
GGGGC GAC CCTCGTCCGG
CC C__
GAM2147 L3MBTL2 3' GCTTGTCTCGGCAGCTAAG 42792 GA_ GA
CT CTGCCGAG GCAGGC
|| ||||| |||||
GA GACGGCTC TGTTCTG
ATC __
GAM2147 LIMK2 5' GCCTGAGGCAGTCACAGA 18786 CC GAGGAG
TC TGA CTGCC CAGGC
|| ||||| |||||
AG ACTGACGG GTCCG
AC A__
GAM2147 MGC15476 5' GGCCTGCTCCTCGGCGGAGCGG 29689 A_
CTG CTGCCGAGGAGCAGGCC
||| |||||
GGC GGCGGCTCCTCGTCCGG
GA
GAM2147 MMP24 3' CCTGCTCCACTTGTCTCAGGG 13505 TGCCGA
CCCTGAC GGAGCAGG
||||| |||||

		GGGACTG CCTCGTCC	
		TTCA__	
GAM2147 OSBPL5	3'	GCCTGCTCCATGGAGGCAGAGA 35989	C A G A
		TC CTG CT CCG GGAGCAGGC	
		AG GAC GG GGT CCTCGTCCG	
		A _ A A	
GAM2147 SHANK3	3'	GCCCCACCCAGCGCACAGTCAGG 32633	C_ A_ AGCA
		CCTGACTG CG GG GGC	
		GGA CTGAC GC CC CCG	
		AC GA CAC_	
GAM2147 USP20	3'	GGCCTGGGCCAGAGTCAGGGA 13503	GCCGA AG
		TCCCTGACT GG CAGGCC	
		AGGGACTGA CC GTCCGG	
		GA__ GG	
GAM2147 LOC145717	3'	GGCCCCTCTCTGGGCAGTCAG 33194	G _ CA
		CTGACTGCC AG GAG GGCC	
		GACTGACGG TC CTC CCGG	
		G T C_	
GAM2147 LOC157503	3'	CCTGCTCCCAAATGGCAAGG 41814	GAC A__
		CCT TGCCG GGAGCAGG	
		GGA ACGGT CCTCGTCC	
		__ AAAC	
GAM2147 LOC159199	5'	CCTGCTCCCCGAGGCCGGCGA 39981	C A GC A
		TC CTG CT CG GGAGCAGG	
		AG GGC GG GC CCTCGTCC	
		C C A_ C	
GAM2147 LOC205143	5'	GCCTGCTCCATCAGGGA 43585	CTGCCGA
		TCCCTGA GGAGCAGGC	
		AGGGACT CCTCGTCCG	
		A_____	
GAM2147 LOC220537	3'	GGCCCCTCTCTGGGCAGTCAG 43623	G _ CA
		CTGACTGCC AG GAG GGCC	
		GACTGACGG TC CTC CCGG	
		G T C_	
GAM2147 LOC256230	5'	GCCTGCTCCAGCTGCAGGGA 46541	ACT CGA
		TCCCTG GC GGAGCAGGC	
		AGGGAC CG CCTCGTCCG	
		GT_ A__	
GAM2147 LOC256231	5'	GCCTGCTCCAGCTGCAGGGA 46543	ACT CGA
		TCCCTG GC GGAGCAGGC	

AGGGAC CG CCTCGTCCG
 GT_ A_
 GAM2147 LOC256789 3' GCCTGCTCCACCCAGGGA 46537 ACTGCCGA
 TCCCTG GGAGCAGGC
 ||||| |||||
 AGGGAC CCTCGTCCG
 CCA____
 GAM2147 LOC93538 5' GGCATGCTCGGCAGCCCGGGA 35924 TGA GAG G
 TCCC CTGCC GAGCA GCC
 ||| |||| |||||
 AGGG GACGG CTCGT CGG
 CCC ____ A
 GAM2148 LDLR 3' AGTAAGACCCCATCTCTTA 6126 AATACA
 TGAGAGAT TCTTACT
 ||||| |||||
 ATTCTCTA AGAATGA
 CCCC_
 GAM2148 PAFAH1B1 3' AGTAAGATTTGTTGCTCTCA 6007 A C
 TGAGAG TAATA ATCTTACT
 ||||| ||||| |||||
 ACTCTC GTTGT TAGAATGA
 _ T
 GAM2148 RAD50 3' TAAGAACTTATTTCTCA 12296 TACA
 TGAGAGATAA TCTTA
 ||||| |||||
 ACTCTTTATT AGAAT
 CAA_
 GAM2148 RAD50 3' TAAGAACTTATTTCTCA 28554 TACA
 TGAGAGATAA TCTTA
 ||||| |||||
 ACTCTTTATT AGAAT
 CAA_
 GAM2148 C21orf51 3' AGTAAGATAATCTCATCA 27742 _ AATAC
 TGA GAGAT ATCTTACT
 || |||| |||||
 ACT CTCTA TAGAATGA
 A A____
 GAM2148 FLJ10618 3' AGTAAAATGTTGATTTCTC 19965 AAT C
 GAGAGAT ACAT TTA
 ||||| |||||
 CTCTTTA TGTA AATGA
 GT_ A
 GAM2148 KIAA0560 3' AGTAAGATACAGGTTTCTT 30836 AATAC
 GAGAGAT ATCTTACT
 ||||| |||||
 TTCTTTG TAGAATGA
 GACA_
 GAM2148 KIAA0748 3' AGTAAGATGCACGCATTTCCA 16700 A AATA_
 TG GAGAT CATCTTACT
 || |||| |||||

			AC CTTTA	GTAGAATGA		
			—	CGCAC		
GAM2148	KIAA0930	3'	AGTAAGGTGTTACTCCCA	34910	A	ATAAT
			TG GAG	ACATCTTACT		
			AC CTC	TGTGGAATGA		
			C	AT__		
GAM2148	KIAA1238	3'	AGTAAGATGTTACTTTCA	35214		ATAAT
			TGAGAG	ACATCTTACT		
			ACTTTC	TGTAGAATGA		
				AT__		
GAM2148	SEF	3'	AGGTGTGTACATCTCTCA	34425	A_	
			TGAGAGAT	ATACATCT		
			ACTCTCTA	TGTGTGGA		
				CA		
GAM2148	UHRF2	3'	AGTAAGAGGCCCATTTCTCA	36355		AATACA
			TGAGAGAT	TCTTACT		
			ACTCTTTA	AGAATGA		
				CCCGG_		
GAM2148	LOC133258	5'	AGTAAGATACCCAAGTCCTCA	37377	A	AATAC_
			TGAG GAT	ATCTTACT		
			ACTC CTG	TAGAATGA		
			—	AACCCA		
GAM2148	LOC146229	3'	AGGTGTGTATATCTCTCA	38106		—
			TGAGAGATA	ATACATCT		
			ACTCTCTAT	TGTGTGGA		
				A		
GAM2148	LOC148824	3'	AGTAAGATGCATTTTCA	40907	A	AATA
			TG GAGAT	CATCTTACT		
			AC CTTTA	GTAGAATGA		
			A	C__		
GAM2148	LOC221042	3'	AGTAAGATGTCCTCTTTC	44749		TAAT
			GAGAGA	ACATCTTACT		
			CTTTCT	TGTAGAATGA		
				CC__		
GAM2149	ABCA1	3'	CTATTATGGAACCCAATGGACA	12014	C	T__
	T		GTG CCATTGGGTTCT	GTAG		
			TAC GGTAACCCAAGG	TATC		
			A	TAT		
GAM2149	GTF2I	3'	CTACAAGAAGCTAGGCTCTGT	26884	T	CAT G
			ACAG GCC	TGG TTCTTGTAG		

TGTC CGG ATC AAGAACATC
 T _ G
 GAM2149 GTF2I 3' CTACAAGAAGCTAGGCTCTGT 26888 T CAT G
 ACAG GCC TGG TTCTTGTAG
 ||||| ||| ||| |||||
 TGTC CGG ATC AAGAACATC
 T _ G
 GAM2149 CSMD1 5' CAGGGTCCCAATGGCACT 36186 C TT
 AGTGCC ATTGGG CTTG
 ||||| ||||| |||
 TCACGG TAACCC GGAC
 _ TG
 GAM2149 FLJ21736 5' ACAAGAGTGTGTCAGCACTGT 24457 C_ TGGGT
 ACAGTGC CAT TCTTGT
 ||||| ||| |||||
 TGTCACG GTG AGAACA
 ACT _
 GAM2149 KIAA1582 5' CGGGAACCCAACAGGCACT 32588 CA
 AGTGCC TTGGGTTCTTG
 ||||| |||||
 TCACGG AACCCAAGGGC
 AC
 GAM2149 KIAA1775 3' CAAGCGCCCCAGCAGGCACTGT 26940 CA TT_
 ACAGTGCC TTGGG CTTG
 ||||| ||||| |||
 TGTCACGG GACCC GAAC
 AC CGC
 GAM2149 LAMP3 3' CTACAAGAACAATGACAC 29918 CC GG
 GTG CATT GTTCTTGTAG
 ||| ||||| |||||
 CAC GTAA CAAGAACATC
 A_ _
 GAM2149 LW-1 5' CTACAGCCTGACCCATGGGCAC 30232 A T C_
 CGT AC GTGCCCAT GGGTT TTGTAG
 || ||||| ||||| |||||
 TG CACGGGTA CCCAG GACATC
 C _ TCC
 GAM2149 LW-1 5' CTACAGCCTGACCCATGGGCAC 18241 A T C_
 CGT AC GTGCCCAT GGGTT TTGTAG
 || ||||| ||||| |||||
 TG CACGGGTA CCCAG GACATC
 C _ TCC
 GAM2149 PRO1386 3' CTACAAAAAATTAGCTGGGCAC 25290 _ G C
 TGT ACAGTGCCCA TTGG TT TTGTAG
 ||||| ||||| ||| |||||
 TGTCACGGGT GATT AA AACATC
 C A A
 GAM2149 LOC145781 3' ACAAGAAGCATGGGCAC 37981 TGGG
 GTGCCCAT TTCTTGT
 ||||| |||||

CACGGGTA AAGAACA
CG__
GAM2150 MS4A1 3' TTTCAACTTCAATGTCA 5635 T C
TGACATTG AGT TGAAG
||||| ||| ||||
ACTGTAAC TCA ACTTT
T _
GAM2150 DKFZp434F1719 3' AGATCCTGTACAACCTCA 25987 CA GTCTGA
TGA TTGTA AGGATCT
||| |||| |
ACT AACAT TCCTAGA
CC G____
GAM2150 FLJ14082 3' AGATCCTTCTAAAACAACAGTC 24607 A_ AGTCT
A TGAC TTGT GAAGGATCT
||| ||| |
ACTG AACA CTTCTCTAGA
AC AAAT_
GAM2150 KIAA0471 3' AGATCCTTTTAAGAATGC 16906 G _
GTA TCT GAAGGATCT
||| ||| |
CGT AGA TTTCCTAGA
A AT
GAM2150 KIAA0523 3' TAGATCCTTGAAAGCAATGTCA 33645 AG TG
TGACATTGT TC AAGGATCTA
||||| || |
ACTGTAACG AG TTCCTAGAT
AA _
GAM2150 KIAA1674 3' AGATCCTTTTACATCATCA 34101 CAT GTCT
TGA TGTA GAAGGATCT
||| ||| |
ACT ACAT TTTCCTAGA
ACT _
GAM2150 KIAA1775 3' ATCCTTGGCACTACTACAATG 26939 _ G
CATTGTAGT CT AAGGAT
||||| || |
GTAACATCA GG TTCCTA
TCAC _
GAM2150 LOC145135 5' AGATCCTTCAGAAATGTCA 40497 GTAG
TGACATT TCTGAAGGATCT
||||| |
ACTGTAA AGACTTCCTAGA

GAM2150 LOC92285 5' ATCCTTCATTTCCTCAAGTCA 34094 A TAGTC
TGAC TTG TGAAGGAT
||| ||| |
ACTG AAC ACTTCCTA
_ CTTT_
GAM2151 ADAM10 5' GGAGGCGGCGGCGGCGGC 6768 ACA A
GCC GCCGCCGTCGCC TCC
||| ||||| |||

CGG CGGCGGCGGCGG AGG

GAM2151 ADPRT 5' GGGAACGGCGGTGGCCGGTGCG 7325 A ____ CCA
GC GCC CA GCCGCCGTCG TCCC

||| || ||||| |||
CGG GT CGGTGGCGGC AGGG
C GGC A__

GAM2151 AGPAT2 3' GATGAGGCTTGCGGCTGTGGC 13118 C_ GC
GCCACAGCCGC GTC CATC

||||| ||| |||
CGGTGTCGGCG CGG GTAG
TT A_

GAM2151 AGPAT2 3' GATGAGGCTTGCGGCTGTGGC 32745 C_ GC
GCCACAGCCGC GTC CATC

||||| ||| |||
CGGTGTCGGCG CGG GTAG
TT A_

GAM2151 AGR2 3' GGAAACGTGAAAGGCTGTGGC 13114 GCCG CA_
GCCACAGCC TCGC TCC

||||| ||| |||
CGGTGTCGG AGTG AGG
AA__ CAA

GAM2151 ARAF1 5' GGAGACGGCGGCGGCTGTAGC 31982 C CCA
GC ACAGCCGCCGTCG TCC

|| ||||| |||
CG TGTCGGCGGCGGC AGG
A AG_

GAM2151 ASCL2 5' GGCGACGGCGGCGGC 42324 ACA
GCC GCCGCCGTCGCC

||| |||||
CGG CGGCGGCAGCGG

GAM2151 ASCL2 5' GGCGACGGCGGCGGC 11671 ACA
GCC GCCGCCGTCGCC

||| |||||
CGG CGGCGGCAGCGG

GAM2151 ATP5J 5' GATGGCGGAGGCTGTG 7407 G GTC
CACAGCC CC GCCATC

||||| || |||||
GTGTCGG GG CGGTAG
A ____

GAM2151 BCL11B 5' GGAGGTGCGGCGGCGGCGGC 28891 ACA C _
GCC GCCGCCGTCGC ATC CC

||| ||||| ||| |||
CGG CGGCGGCGGCG TGG GG

GAM2151 BCL11B 5' GGAGGTGCGGCGGCGGCGGC 23167 ACA C _
GCC GCCGCCGTCGC ATC CC

||| ||||| ||| |||

			CGG CGGCGGCGGCG TGG GG		
			— — A		
GAM2151	BCR	5'	GGAGGCGGCGGCGGCGGC 22238	ACA	A
			GCC GCCGCCGTCGCC TCC		
			CGG CGGCGGCGGCGG AGG		
			— —		
GAM2151	BCR	5'	GGAGGCGGCGGCGGCGGC 10527	ACA	A
			GCC GCCGCCGTCGCC TCC		
			CGG CGGCGGCGGCGG AGG		
			— —		
GAM2151	CAPON	3'	GGAGATGGAGGCGGCGGCGTGG 31989	A	G _
	C		GCCAC GCCGCCGTC CCATC CC		
			CGGTG CGGCGGCGG GG TAG GG		
			— A A		
GAM2151	CCNDBP1	5'	GGAAACGAGCCCTTGACGCTGT 14449	C_____	CG
	GGC		GCCACAGC GC CGT CC		
			CGGTGTCG CG GCA GG		
			CAGTTCC A AA		
GAM2151	CDH23	5'	GGACGCGTCCGACGGCGGCGCGG 27418	ACA	CCA_____
			CC GCCGCCGTCG TCC		
			GG CGGCGGCAGC AGG		
			C_____ CTGCGC		
GAM2151	CDH23	5'	GGACGCGTCCGACGGCGGCGCGG 22670	ACA	CCA_____
			CC GCCGCCGTCG TCC		
			GG CGGCGGCAGC AGG		
			C_____ CTGCGC		
GAM2151	CHS1	5'	GGGGAGTGCGCGGCGGCGCGCAG 5528	CACA	T CA
	C		GC GCCGCCG CGC TCCCC		
			CG CGGCGGC GCG AGGGG		
			ACGC _ TG		
GAM2151	DXYS155E	3'	GGAGCGGCGGCGGCTGCAGG 11541	A_	CA
			CC CAGCCGCCGTCGC TCC		
			GG GTCGGCGGCGGCG AGG		
			AC _		
GAM2151	EN2	5'	GGGGACGGCCGGGCGGCGGCGG 7146	ACA	__ A
	CGGC		GCC GCCGCCGTC GCC TCCCC		
			CGG CGGCGGCGG CGG AGGGG		
			CGG GC C		
GAM2151	FBXL5	5'	GGAGAGGCGGCGGCCGCGGC 27304	ACA C	A_
			GCC GC GCCGTCGCC TCC		

			CGG CG CGGCGGCGG AGG		
			___ C AG		
GAM2151 FBXL7	5'	GGGACCCGGCGGCGGCGGC	14672	A___	
		GCCGCCGTGCGC TCCC			
		CGGCGGCGGCGG AGGG			
		CCC			
GAM2151 FOXD2	5'	GGAGAGTGGCGGCGGCGGCGGC	10788	ACA	_ _
		GCC GCCGCCGTGCGCA TC CC			
		CGG CGGCGGCGGCGGT AG GG			
		___ G A			
GAM2151 FSTL1	3'	GGATGGCGACAAGGGCAGC	13951	C ___	
		GC GCC GTCGCCATCC			
		CG CGG CAGCGGTAGG			
		A GAA			
GAM2151 HIRA	5'	GGAAGCGGCGGCGGTGGC	9326	A	CG
		GCCAC GCCGCCGT CC			
		CGGTG CGGCGGCG GG			
		G AA			
GAM2151 HOXA3	3'	GGGGCTCCAGGCGGCTGCGGC	24994	A	GTCGCCAT
		GCC CAGCCGCC CCCC			
		CGG GTCGGCGG GGGG			
		C ACCTC___			
GAM2151 IQGAP2	5'	GCGCGCGGCGGCCGTGGC	13429	A	_
		GCCAC GCCGCCGT CGC			
		CGGTG CGGCGGCG GCG			
		C C			
GAM2151 ITGAM	3'	GGTGACGGCAGCGTAGC	6250	C A C	
		GC AC GC GCCGTCGCC			
		CG TG CG CGGCAGTGG			
		A _ A			
GAM2151 ITPR2	5'	GGGGAGCGGGCGGCGGCTGCGG	7993	A	_ CA
C		GCC CAGCCGCCGTG GC TCCCC			
		CGG GTCGGCGGCGG CG AGGGG			
		C G ___			
GAM2151 KCND2	5'	GTGGGGCAGCGGCTGTG	14609	C G	
		CACAGCCGC GTC CCAT			
		GTGTCGGCG CGG GGTG			
		A _			
GAM2151 LMO2	5'	GGCGACGGCGGCGGCGGC	12103	ACA	
		GCC GCCGCCGTGCGC			

			CGG CGGCGGCAGCGG			
			CGG			
GAM2151	MAP3K5	5'	GGAGGCGGCGGCGCGGC	12547	ACA C	A
			GCC GC GCCGTCGCC TCC			
			CGG CG CGGCGGCGG AGG			
			— — —			
GAM2151	MAP3K7IP2	5'	GGAGAGGCGGCGGCGGCGGC	17486	ACA	A_
			GCC GCCGCCGTCGCC TCC			
			CGG CGGCGGCGGCGG AGG			
			— AG			
GAM2151	MAP4K5	5'	GGGAACGTGGTGCGGCGGCGGC	13342	ACA	T —
	GGC		GCC GCCGCCG CGCCA TCCC			
			CGG CGGCGGC GTGGT AGGG			
			CGG — GCA			
GAM2151	MPDU1	3'	GGGACTGGGAGGCTGTGGC	11298	GCCG G	_
			GCCACAGCC TC CCA TCCC			
			CGGTGTCCG AG GGT AGGG			
			— — C			
GAM2151	OGG1	5'	GACGGCAGGCAGCAGCTGTGGC	18807	C C	_ A
			GCCACAGC GC GTC GCC TC			
			CGGTGTCCG CG CGG CGG AG			
			A A A C			
GAM2151	OGG1	5'	GACGGCAGGCAGCAGCTGTGGC	18812	C C	_ A
			GCCACAGC GC GTC GCC TC			
			CGGTGTCCG CG CGG CGG AG			
			A A A C			
GAM2151	OGG1	5'	GACGGCAGGCAGCAGCTGTGGC	8390	C C	_ A
			GCCACAGC GC GTC GCC TC			
			CGGTGTCCG CG CGG CGG AG			
			A A A C			
GAM2151	PEA15	5'	GAGGCGGCGGCGGCGGC	9850	ACA	A
			GCC GCCGCCGTCGCC TC			
			CGG CGGCGGCGGCGG AG			
			— —			
GAM2151	PKIA	3'	TGAGGGCAGAGGCTGTGGC	13702	—	G
			GCCACAGCC GCC TCG			
			CGGTGTCCG CGG AGT			
			AGA G			
GAM2151	POU2F2	3'	GGTCTCAGCAGCGGCTGCGGC	8549	A	C C_
			GCC CAGCCGC GT GCC			

			CGG GTCGGCG CG TGG		
			C A ACTC		
GAM2151	PPP3CC	5'	GAAGGCGGCGGCCGCGC	12127	ACA C A
			GCC GC GCCGTCGCC TC		
			CGG CG CGGCGGCGG AG		
			___ C A		
GAM2151	PTEN	5'	GGAGATGAGAGACGGCGGCGGC	5854	ACA GC_ _
			GCC GCCGCCGTC CATC CC		
			CGG CGGCGGCAG GTAG GG		
			___ AGA A		
GAM2151	PTEN	5'	GGCCGCGGCGGCTGCAGC	5855	CA C
			GC CAGCCGCCGT GCC		
			CG GTCGGCGGCG CGG		
			AC C		
GAM2151	PTEN	5'	GGCGGCGGCGGCCGCGGC	5856	ACA
			GCC GCCGCCGTCGCC		
			CGG CGGCGGCGGCGG		
			CGC		
GAM2151	PTEN	5'	GGCGGCGGCGGCGGC	5857	ACA
			GCC GCCGCCGTCGCC		
			CGG CGGCGGCGGCGG		

GAM2151	PTEN	5'	GACGGCGGCGGCCGCGGC	5853	ACA C A
			GCC GC GCCGTCGCC TC		
			CGG CG CGGCGGCGG AG		
			___ C C		
GAM2151	PTP4A2	5'	GGAGACGCAGCGGCGGCCGAG	9553	CACA C CA_
	C		GC GCCGCCGT GC TCC		
			CG CGGCGGCG CG AGG		
			ACGC A CAG		
GAM2151	PTP4A2	5'	GGAGACGCAGCGGCGGCCGAG	27830	CACA C CA_
	C		GC GCCGCCGT GC TCC		
			CG CGGCGGCG CG AGG		
			ACGC A CAG		
GAM2151	RAB1A	5'	GGAGAGTCAGGGCGGCGGCTGC	34789	A ___ CA
	GGC		GCC CAGCCGCCGTC GC TCC		
			CGG GTCGGCGGCGG TG AGG		
			C GAC AG		
GAM2151	RAB30	3'	GGAGATCTGGCGATGACTGTGG	15832	CCGC ___ _
	C		GCCACAG CGTCGCCA TC CC		

			CGGTGTC	GTAGCGGT	AG GG		
			A__	CT A			
GAM2151	RAD21	5'	GGAGGCGCCGGCTGTGGC	12946		C	G
			GCCACAGCCG	CGTC CC			
			CGGTGTCGGC	GCGG GG			
			C	A			
GAM2151	REPS2	5'	GGAGGCGGTGGCTGTGGC	11098		G	
			GCCACAGCCGCCGTC	CC			
			CGGTGTCGGTGGCGG	GG			
			A				
GAM2151	RFC4	5'	GGAACGAGCCGGCGGCGGTG	8821	A	__	CCA
			CAC GCCGCCG	TCG TCC			
			GTG CGGCGGC	AGC AGG			
			G	CG A__			
GAM2151	RGL	5'	GGGATGGGCAGCAGCGGC	17507	C	C	_
			GCCGC	GT GCC ATCCC			
			CGGCG	CG CGG TAGGG			
			A	A G			
GAM2151	ROCK2	5'	GGCGGCCGCGCGCGACCATGGC	32841	CA__		_
			GCCA	GCCGCCG TCGCC			
			CGGT	CGGCGGC GGCGG			
			ACCAG	C			
GAM2151	TAZ	5'	GGGCGGGACGGCGGCCCGCCGC	17753	CACA		G AT
			GC	GCCGCCGTC CC CCC			
			CG	CGGCGGCAG GG GGG			
			CCGC	_ C_			
GAM2151	TFG	5'	GGAGAGGCGGCGGCCGCGGC	12713	ACA	C	A_
			GCC	GC GCCGTCGCC TCC			
			CGG	CG CGGCGGCGG AGG			
			_	C AG			
GAM2151	TSN	5'	GGACCCTAGCGACGGTCGTGGC	10986	AGCC		CA__
			GCCAC	GCCGTCGC TCC			
			CGGTG	TGGCAGCG AGG			
			C__	ATCCC			
GAM2151	WHSC1L1	5'	GGAGAGGCGGCGGCGGCGGC	19410	ACA		A_
			GCC	GCCGCCGTCGCC TCC			
			CGG	CGGCGGCGGCGG AGG			
			_	AG			
GAM2151	WHSC1L1	5'	GGAGAGGCGGCGGCGGCGGC	23317	ACA		A_
			GCC	GCCGCCGTCGCC TCC			

CGG CGGCGGCGGCGG AGG
 _____ AG
 GAM2151 ZFP103 5' GGGATGGCCGGCCAGTG 12221 AGCC TC
 CAC GCCG GCCATCCC
 ||| |||| |||||
 GTG CGGC CGGTAGGG
 AC__ __
 GAM2151 ZNF6 5' GGCGGCGGCAGCTGTAGC 22536 C C
 GC ACAGC GCCGTCGCC
 || |||| |||||
 CG TGTCG CGGCGGCGG
 A A
 GAM2151 BDG-29 3' GGGGACGGCGACAGCGCGGCTC 35818 __ C__ A
 TGTG CACA GCCGC GTCGCC TCCCC
 ||| |||| |||||
 GTGT CGGCG CAGCGG AGGGG
 CT CGA C
 GAM2151 C3IP1 5' GGGACGGGCCCCGGTGC GGC 22276 ACA C TC A_
 GCC GC GCCG GCC TCCC
 ||| || |||| ||| ||||
 CGG CG TGGC CGG AGGG
 __ _ C_ GC
 GAM2151 CASPR3 3' ATGGCTATAAAGCTGTGGC 27384 CGCC C
 GCCACAGC GT GCCAT
 ||||| || ||||
 CGGTGTCG TA CGGTA
 AAA_ T
 GAM2151 CENTG2 5' GGGCTGGAAGGCGGCTGC GGC 17160 A GTCG T
 GCC CAGCCGCC CCA CCC
 ||| ||||| ||| |||
 CGG GTCGGCGG GGT GGG
 C AA_ C
 GAM2151 COASTER 5' GGGGATTCGTGGCGACGGCGGC 17823 ACA ____
 GGC CC GCCGCCGTCGCCA TCCCC
 || ||||| ||||
 GG CGGCGGCAGCGGT AGGGG
 __ GCTT
 GAM2151 COL4A3BP 5' GGGGTCACGGCGACGGCGGCGG 12267 ACA AT__
 CGGC GCC GCCGCCGTCGCC CCCC
 ||| ||||| ||||
 CGG CGGCGGCAGCGG GGGG
 CGG CACT
 GAM2151 D123 5' GGAAAGGCAGCAGCGGCGGC 12641 ACA C C A_
 GCC GCCGC GT GCC TCC
 ||| |||| || ||| |||
 CGG CGGCG CG CGG AGG
 __ A A AA
 GAM2151 DAPK2 3' GGAGACCCTGGGAGCTGTGGC 15635 CG __ G
 GCCACAGC CC GTC CC
 ||||| || ||| ||

CGGTGTCG GG CAG GG
 AG TCC A
 GAM2151 DKFZP434M154 5' GGACCTGGCGGCGGCAGC 35808 C ____
 GC GCCGTCGCCA TCC
 || ||||| ||
 CG CGGCGGCGGT AGG
 A CC
 GAM2151 DKFZp434O0320 5' GGAAACTCAAGACGGCGGCCTG 40707 CA GCCA____
 GC GCCA GCCGCCGTC TCC
 ||| ||||| ||
 CGGT CGGCGGCAG AGG
 C_ AACTCAA
 GAM2151 DKFZP566K1924 5' GGCGGACGGCGGCGACGGC 36521 ACA _
 GCC GCCGCCGTC GCC
 ||| ||||| ||
 CGG CGGCGGCAG CGG
 CAG G
 GAM2151 Dlc2 5' GGAGACCGCGGCGGCGGCGGC 27970 ACA CA _
 GCC GCCGCCGTCGC TC CC
 ||| ||||| ||
 CGG CGGCGGCGGCG AG GG
 ____ CC A
 GAM2151 EHM2 5' GGAGAGCGCGCGGCGGCGGCGG 21188 ACA _ CA
 C GCC GCCGCCGT CGC TCC
 ||| ||||| ||
 CGG CGGCGGCG GCG AGG
 CGG C AG
 GAM2151 ELKS 5' GGACGGTGAGACGGCCGCGGC 17421 ACA C _ A
 GCC GC GCCGTC GCC TCC
 ||| || ||||| ||
 CGG CG CGGCAG TGG AGG
 ____ C AG C
 GAM2151 EZFIT 5' GGGATGGCTGCTCAGCTGCTG 22196 C C__ C
 CAGC GC GT GCCATCCC
 |||| || |||||
 GTCG CG CG GGTAGGG
 T ACT T
 GAM2151 FEM1B 5' GGCGCACGGCAGCTGCAGC 17642 CA C _
 GC CAGC GCCGT CGCC
 || ||| ||||| ||
 CG GTCG CGGCA GCGG
 AC A C
 GAM2151 FLJ10101 5' GGCAAGACAGCGCTGTGGC 24049 C C ____
 GCCACAGC GC GTC GCC
 ||||| || ||| ||
 CGGTGTCG CG CAG CGG
 _ A AA
 GAM2151 FLJ10244 5' GGCGGCGGCGGCCGTGGC 19781 A
 GCCAC GCCGCCGTCGCC
 ||||| |||||

CCGTG CGGCGGCGGCGG
 C
 GAM2151 FLJ12076 5' GGAAAGCGGGGCTGTGGC 24824 G CG_
 GCCACAGCC CCGT CC
 ||||| ||| ||
 CCGTGTCGG GGCG GG
 _ AAA
 GAM2151 FLJ13204 5' GGAGCGACGGCGGCTGCAGC 24117 CA CA
 GC CAGCCGCCGTCGC TCC
 || ||||| |||
 CG GTCGGCGGCAGCG AGG
 AC _
 GAM2151 FLJ13621 5' GGCAACGGCGGCTGGAGC 24581 CA C
 GC CAGCCGCCGT GCC
 || ||||| |||
 CG GTCGGCGGCA CGG
 AG A
 GAM2151 FLJ14356 5' GGAAATGATTGTGCGGCTGT 25153 _ _ CCA
 ACAGCCGC CG TCG TCC
 ||||| || |||
 TGTCGGCG GT AGT AGG
 T T AA_
 GAM2151 FLJ20080 5' GGAGGCGGCGGCGGCGGC 19180 ACA A
 GCC GCCGCCGTCGCC TCC
 ||| ||||| |||
 CGG CGGCGGCGGCGG AGG
 _ _
 GAM2151 FLJ20435 3' GGGATGGACGGCTTCGGC 19471 CC _
 GCCG GTCG CCATCCC
 ||| ||| |||||
 CGGC CGGC GG TAGGG
 TT A
 GAM2151 FLJ20718 5' GGCCGAGGCGGCTGCGGC 19635 A G _
 GCC CAGCCGCC TCG CC
 ||| ||||| ||| ||
 CGG GTCGGCGG AGC GG
 C _ C
 GAM2151 FLJ22393 5' GGAGAGCAGCGGCGGCGGCGGC 24756 ACA CA_ _
 GCC GCCGCCGTCGC TC CC
 ||| ||||| ||| ||
 CGG CGGCGGCGGCG AG GG
 _ ACG A
 GAM2151 FLJ22405 5' GGATGGCAGCGGACCGGCGGC 22866 ACA _ C
 GCC GCCG CCGT GCCATCC
 ||| ||| ||| |||||
 CGG CGGC GGCG CGGTAGG
 _ CAG A
 GAM2151 FLJ22457 5' GACAGCGCGTGGCTTGGC 24389 C C T CA
 GCCA AGCCGC G CGC TC
 |||| ||||| | ||| ||

		CGGT TCGGTG C GCG AG		
		— — — AC		
GAM2151 FTS	5'	GGAGATGCTGTGCGGGCCGCGGC 22843	ACA C _ T C _	
		GCC GC GCC G CG CATC CC		
		CGG CG CGG C GT GTAG GG		
		— C G T C A		
GAM2151 GDBR1	5'	GGAGAGTGACGGCGGCCCGGC 18262	ACA CA	
		GCC GCCGCCGTCGC TCC		
		CGG CGGCGGCAGTG AGG		
		CC_ AG		
GAM2151 HSPC195	5'	GGGGATGTAGAGGCGGCGGC 39424	GC_	
		GCCGCCGTC CATCCCC		
		CGGCGGCGG GTAGGGG		
		AGAT		
GAM2151 HSPC195	5'	GGCGACGGCGGCGGTGGC 39423	A	
		GCCAC GCCGCCGTCGCC		
		CGGTG CGGCGGCAGCGG		
		G		
GAM2151 ICAP-1A	5'	GGGGATGGGCCCGCGGCTG 11154	CGTCG	
		CAGCCGC CCATCCCC		
		GTCGGCG GGTAGGGG		
		CCCG_		
GAM2151 IGF2AS	3'	GGGACGGCGTGGCTGTG 18541	CGTC A	
		CACAGCCGC GCC TCCC		
		GTGTCGGTG CGG AGGG		
		— C		
GAM2151 ITPK1	5'	GGAAGTGGCGGCGGCGGCGGC 15482	ACA CC	
		GCC GCCGCCGTCGCCAT CC		
		CGG CGGCGGCGGCGGTG GG		
		— AA		
GAM2151 JIK	5'	GGAAGCGGCGGCGGCGGC 18406	ACA CA	
		GCC GCCGCCGTCGC TCC		
		CGG CGGCGGCGGCG AGG		
		— A_		
GAM2151 KIAA0191	5'	GGCGACGGCGGCGGC 32788	ACA	
		GCC GCCGCCGTCGCC		
		CGG CGGCGGCAGCGG		
		—		
GAM2151 KIAA0210	3'	GGATGGCGAGGCAGCCGGGC 16426	ACA C G	
		GCC GC GCC TCGCCATCC		

		CGG CG CGG AGCGGTAGG		
		GC_ A _		
GAM2151	KIAA0227	5' GGGAAGGCGCGGCGGCGGCGGC 30454	ACA	T A
		GCC GCCGCCG CGCC TCCC		
		CGG CGGCGGC GCGG AGGG		
		CGG _ A		
GAM2151	KIAA0544	3' GGGGACAGGTCGGCTGTGG 35115	_ _	G
		CCACAGCCG CC GTC CC		
		GGTGTGGC GG CAG GG		
		T A G		
GAM2151	KIAA0607	3' GAGACGCGACTGGCGGCTCCAG 35926	CAC	_ CA_
	C	GC AGCCGCC GTCGC TC		
		CG TCGGCGG CAGCG AG		
		ACC T CAG		
GAM2151	KIAA0701	5' GGCGCCCGCGGCGGCGCTGGC 34458	A	___
		GCCAC GCCGCCGT CGCC		
		CGGTG CGGCGGCG GCGG		
		C CCC		
GAM2151	KIAA0701	5' GGGTTCTCGGCGGCGGCTGTGG 34459		CCAT
	C	GCCACAGCCGCCGTG CCC		
		CGGTGTGCGGCGGCGG GGG		
		TCTT		
GAM2151	KIAA0721	3' GGAATGAGCCTGCTGTGGC 45928	C_ _	CG
		GCCACAGC GC CGT CC		
		CGGTGTGCG CG GTA GG		
		TC A A_		
GAM2151	KIAA0721	3' GGAATGAGCCTGCTGTGGC 22321	C_ _	CG
		GCCACAGC GC CGT CC		
		CGGTGTGCG CG GTA GG		
		TC A A_		
GAM2151	KIAA0995	5' GGGGACGGCGGCGGCGGCGGCG 36066	ACA	A
	GC	GCC GCCGCCGTCGCC TCCCC		
		CGG CGGCGGCGGCGG AGGGG		
		CGG C		
GAM2151	KIAA1028	5' GGGACTGAGCGGCGGCGGC 44161	_ _	
		GCCGCCGTGCG CA TCCC		
		CGGCGGCGGCG GT AGGG		
		A C		
GAM2151	KIAA1233	5' GGCGGCGGCGACTGCGGC 31591	A	C
		GCC CAG CGCCGTCGCC		

		CGG GTC GCGGCGGCGG	
		C A	
GAM2151 KIAA1322	5'	GGGGATGGCGTCGGAGCCGC 36031	CACA CG T
		GC GC CCG CGCCATCCCC	
		CG CG GGC GCGGTAGGGG	
		C__ A_ T	
GAM2151 KIAA1822	3'	GGAACAGCAGCCGGGCTGTGG 33553	GCC C CA_
		CCACAGCC GT GC TCC	
		GGTGTCCG CG CG AGG	
		GC_ A ACA	
GAM2151 KIAA1940	5'	GGTCATCAGCAGCAGCTGTGGC 39008	C C C__
		GCCACAGC GC GT GCC	
		CGGTGTCCG CG CG TGG	
		A A ACTAC	
GAM2151 KIAA1987	3'	GGAGATGGAGCCGGGTGCGGC 42499	A G _ G
		GCC CA CCG CCGTC CC	
		CGG GT GGC GG TAG GG	
		C G CGA A	
GAM2151 KLHL4	3'	ATGGTGTTCAGGCCACTATGGC 21192	C CC GT__
		GCCA AG GCC CGCCAT	
		CGGT TC CGG GTGGTA	
		A AC ACTT	
GAM2151 LSR68	5'	GGACAGTAATGACGGCTGTG 20752	C CG CA
		CACAGCCG CGT C TCC	
		GTGTCGGC GTA G AGG	
		A AT AC	
GAM2151 MESDC1	5'	GAAGGCGGCGGCGGCGGC 22883	ACA A
		GCC GCCGCCGTCGCC TC	
		CGG CGGCGGCGGCGG AG	
		_ A	
GAM2151 MGC11296	5'	GGAAAGCGACGGCGCGGC 26141	ACA C CA
		GCC GC GCCGTCGC TCC	
		CGG CG CGGCAGCG AGG	
		_ _ AA	
GAM2151 MGC11324	5'	GGGGACAGGGACTGCTGTGGC 26445	CGCC G A_
		GCCACAGC GTC CC TCCCC	
		CGGTGTCC CAG GG AGGGG	
		T__ _ AC	
GAM2151 MGC26684	5'	GGGGACCCGGTAGCGGCGGTGG 29373	A CG CCA
C		GCCAC GCCGC TCG TCCCC	

CCGTG CGGCG GGC AGGGG
 G AT CC_
 GAM2151 MGC3265 3' GGGTCCACACGGCGGCTGCTGC 23459 CA CGCCAT
 GC CAGCCGCCGT CCC
 || ||||| |||
 CG GTCGGCGGCA GGG
 TC CACCT_
 GAM2151 MGC4368 5' GGGGATGGCTCGGCCACTG 23701 CC TC
 CAG GCCG GCCATCCCC
 ||| ||| |||||
 GTC CGGC CGGTAGGGG
 AC T_
 GAM2151 MIR 5' GGGGACGCGAGTGGCGGCCGCG 43739 ACA _ CA
 G CC GCCGCCG TCGC TCCCC
 || ||||| ||| |||||
 GG CGGCGGT AGCG AGGGG
 CGC G C_
 GAM2151 MPZL1 5' GGGACGCGGCGGCGGCGGCGGC 10088 ACA A_
 GCC GCCGCCGTCGCC TCCC
 ||| ||||| ||| |||||
 CGG CGGCGGCGGCGG AGGG
 _ CGC
 GAM2151 MY014 5' GGAGGTGGCGGCGGCGGC 25191 _
 GCCGCCGTCGCCATC CC
 ||||| ||||| ||
 CGGCGGCGGCGGTGG GG
 A
 GAM2151 NCOR1 5' GGTGGCGAAGCAGCAGCCGCGG 13002 ACA C CG_
 C GCC GC GC TCGCCATC
 ||| ||| |||||
 CGG CG CG AGCGGTGG
 CGC A ACGA
 GAM2151 NTN4 5' GGAGGCGGCGGCGGCGGC 31515 ACA A
 GCC GCCGCCGTCGCC TCC
 ||| ||||| ||| |||||
 CGG CGGCGGCGGCGG AGG
 _ _
 GAM2151 NXN 3' GGGATGGACGGCTTCGGC 22811 CC _
 GCCG GTCG CCATCCC
 |||| ||| |||||
 CGGC CGGC GG TAGGG
 TT A
 GAM2151 OR2C3 3' GGGGACCTGGTGGCAGCGGCGG 37175 ACA C _
 C GCC GCCGC GTCGCCA TCCCC
 ||| ||||| ||||| |||||
 CGG CGGCG CGGTGGT AGGGG
 _ A CC
 GAM2151 OSBPL5 3' GGAGGCGCGGCGGCTGCAGGC 35990 A_ T A
 GCC CAGCCGCCG CGCC TCC
 ||| ||||| ||| |||

				CGG	GTGGCGGC	GCGG	AGG			
				AC	_	_				
GAM2151	P5-1	3'	GGATGGT	GA	CTGC	CCCATGGC	13499	CA	C	C
				GCCA	GC	GC	GT	CG	CCATCC	
				CGGT	CG	CG	CAGTGGTAGG			
				AC	_	T				
GAM2151	PCAF GC	5'	GGAGACCCT	GG	CGGCGGCGGCG	9964	ACA			
				GCC	GCCGCCGT	CGCCA	TC	CC		
				CGG	CGGCGGCGGCGGT	AG	GG			
						CCC	A			
GAM2151	PCSK7	5'	GGGAGGCGGCGGCAGCTGCGGC	11076	A	C		A		
				GCC	CAGC	GCCGTCGCC	TCCC			
				CGG	GT	CG	CGGCGGCGG	AGGG		
				C	A	_				
GAM2151	PDCD7	3'	GATGGCAGTGGCTGTAGG	35696	_		CGTC			
				CC	ACAGCCGC	GCCATC				
				GG	TGTCGGTG	CGGTAG				
				A	A	_				
GAM2151	PEGASUS	5'	GACGGCGGCGGCGGCGCACGGC	22814	ACA		A			
				GCC	GCCGCCGT	CGCC	TC			
				CGG	CGGCGGCGGCGG	AG				
				CAG		C				
GAM2151	PEGASUS	5'	GATGGCGGCGGTGACTGTG	22815	C					
				CACAG	CGCCGT	CGCCATC				
				GTGTC	GTGGCGGCGGTAG					
				A						
GAM2151	PEPP3	3'	GGGAACAGTGCTGGCTGTGGC	17236		CC	T	CA_		
				GCCACAGCCG	G	CGC	TCCC			
				CGGTGT	CGGT	C	GTG	AGGG		
								ACA		
GAM2151	PF1 C	5'	GGGACGCAGACGGCGGCGGCGG	45604	ACA		_	CA		
				GCC	GCCGCCGT	GC	TCCC			
				CGG	CGGCGGCAG	CG	AGGG			
				CGG		A	C_			
GAM2151	PPI5PIV	3'	GGGGATCCGAGGGACTGTGGC	21277		CCG	G	CC		
				GCCACAG	CC	TCG	ATCCCC			
				CGGTGTC	GG	AGC	TAGGGG			
				A_	G	C_				
GAM2151	PTPNS1	3'	GGGATGGTGCAGCTGTG	28056	C	CGTC				
				CACAGC	GC	GCCATCCC				

GTGTCTG CG TGGTAGGG
 A ____
 GAM2151 PTR4 5' GGCGGCGGCGGCCGCGGC 36654 ACA
 GCC GCCGCCGTCGCC
 ||| |||||
 CGG CGGCGGCGGCGG
 CGC
 GAM2151 RPH3A 3' GGAGACAGCATGCTGGCTGTG 17307 C C CA _
 CACAGCCG CGT GC TC CC
 ||||| ||| || ||
 GTGTCTGGT GTA CG AG GG
 C _ AC A
 GAM2151 SLC21A11 5' GGAAAGCGGCAGCGGCGGCGGC 32208 ACA C A____
 GCC GCCGCCGT GCC TCC
 ||| ||||| ||| |||
 CGG CGGCGGCG CGG AGG
 ____ A CGAA
 GAM2151 SLIT1 5' GGGGATGGTCAGCGGCTGCTG 9030 C C_
 CAGC GCCGT GCCATCCCC
 ||| |||| |||||
 GTCG CGGCG TGGTAGGGG
 T AC
 GAM2151 SRF 5' GGGAAGCCGATGGCGGCGGCTG 9101 A ____ CA
 CGGC GCC CAGCCGCCGTC GC TCCC
 ||| ||||| || |||
 CGG GTCGGCGGCGG CG AGGG
 C TAGC A_
 GAM2151 SRF 5' GGGTTCGCAGCGGCGGCCGCGG 9102 ACA C CAT
 C GCC GCCGCCGT GC CCC
 ||| ||||| || |||
 CGG CGGCGGCG CG GGG
 CGC A CTT
 GAM2151 STIM2 5' GGGGATGCGCCGCGGCGGCGGC 21915 ACA C _
 GGC GCC GCCGCCGT GC CATCCCC
 ||| ||||| || |||||
 CGG CGGCGGCG CG GTAGGGG
 CGG C C
 GAM2151 STK39 5' GGGGACGGCGGCGGCGGCGGCG 14894 ACA A
 GC GCC GCCGCCGTCGCC TCCCC
 ||| ||||| |||||
 CGG CGGCGGCGGCGG AGGGG
 CGG C
 GAM2151 TU12B1-TY 3' GGGAATGACCATGGTCATGGC 18649 CA CC CCA
 GCCA GCCG GTCG TCCC
 ||| |||| ||||
 CGGT TGGT CAGT AGGG
 AC AC A____
 GAM2151 TUSP 3' GGAAACAGCTTGGCTGTGGT 21530 ____ C CG
 GCCACAGCC GC GT CC
 ||||| || || ||

			TGGTGTCTGG CG CA GG		
			TT A AA		
GAM2151	ULK2	5'	GGGAAGCGCGGGGCCGCGGC 16182	ACA G T CA	
			GCC GCC CCG CGC TCCC		
			CGG CGG GGC GCG AGGG		
			CGC _ _ A_		
GAM2151	WIT-1	3'	GGGGATGGAGGCCAGGCCGTGG 17991	A GCC G	
	C		GCCAC GCC GTC CCATCCCC		
			CGGTG CGG CGG GGTAGGGG		
			C AC_ A		
GAM2151	ZDHC3	5'	GGGAAGGCAGCGCGGCGCGGC 18689	ACA C A	
			GCC GCCGCCGT GCC TCCC		
			CGG CGGCGGCG CGG AGGG		
			_ _ A A		
GAM2151	ZF	5'	GGGGAGCCGCGGCGGCGTGGC 22191	A C CA	
			GCCAC GCCGCCGT GC TCCCC		
			CGGTG CGGCGGCG CG AGGGG		
			_ C _		
GAM2151	ZNF238	5'	GGGACATGTACCACGGCGGCCA 13044	CACA C_ CA_	
	AAGC		GC GCCGCCGT GC TCCC		
			CG CGGCGGCA TG AGGG		
			AAAC CCA TAC		
GAM2151	ZTL1	5'	GGAGCCGGCGACGGCGGCAGTG 23492	A A_	
	GC		GCCAC GCCGCCGTCGCC TCC		
			CGGTG CGGCGGCAGCGG AGG		
			A CCG		
GAM2151	ZTL1	5'	GGAGCCGGCGACGGCGGCAGTG 23188	A A_	
	GC		GCCAC GCCGCCGTCGCC TCC		
			CGGTG CGGCGGCAGCGG AGG		
			A CCG		
GAM2151	LOC115811	5'	GGGACCGCGGCGGTAAGTGTGG 28813	CC CA	
	C		GCCACAG GCCGTCGC TCCC		
			CGGTGTC TGGCGGCG AGGG		
			AA CC		
GAM2151	LOC118851	5'	GGGGACAGCTGCTGTGGC 37202	C C G	
			GCCACAGC GC GTC CC		
			CGGTGTCG CG CAG GG		
			T A G		
GAM2151	LOC121536	5'	GGGACCGCGGGGCAGCCAGGGC 36665	ACA C G CA	
			GCC GC GCC TCGC TCCC		

CGG CG CGG GGCG AGGG
 GAC A _ CC
 GAM2151 LOC122553 5' GGGATAGAATGGCGGCCTG 36690 _ CGCC
 CAG CCGCCGT ATCCC
 ||| ||||| ||||
 GTC GGCGGTA TAGGG
 C AGA_
 GAM2151 LOC122792 5' GGAGACGGCAGCGGCATGGC 29764 CA C CCA
 GCCA GCCGC GTCG TCC
 |||| |||| ||| |||
 CGGT CGGCG CGGC AGG
 A_ A AG_
 GAM2151 LOC125228 5' GGGAAGCGGCGGCGGCGGC 36792 ACA CA
 GCC GCCGCCGTCGC TCCC
 ||| ||||| ||||
 CGG CGGCGGCGGCG AGGG
 _ A_
 GAM2151 LOC126432 5' GGAGACGGCGGTGTGCC 36842 C G G
 G CACA CCGCCGTC CC
 | ||| ||||| ||
 C GTGT GGCGGCAG GG
 C _ A
 GAM2151 LOC134553 5' GGACCGTGCGCGGCGGCCGCGG 37077 ACA _ CA
 C GCC GCCGCCGT CGC TCC
 ||| ||||| ||| |||
 CGG CGGCGGCG GTG AGG
 CGC C CC
 GAM2151 LOC146057 5' GGGGACGAGGCGGCGGCGGCGG 38058 ACA A_
 C GCC GCCGCCGTCGCC TCCCC
 ||| ||||| ||||
 CGG CGGCGGCGGCGG AGGGG
 _ AGC
 GAM2151 LOC146439 5' GGGAGCCCCGGCGGCTTCGGC 38151 AC TC CA
 GCC AGCCGCCG GC TCCC
 ||| ||||| || ||||
 CGG TCGGCGGC CG AGGG
 CT C_ _
 GAM2151 LOC147895 5' GGGAGGTGGTGGCCACGGC 40861 CC _
 GCCG GTCGCCATC CCC
 |||| ||||| |||
 CGGC CGGTGGTGG GGG
 AC A
 GAM2151 LOC150113 5' GGAGATGGCGAGGCCTGC 42168 C_ G _
 GC GCC TCGCCATC CC
 || ||| ||||| ||
 CG CGG AGCGGTAG GG
 TC _ A
 GAM2151 LOC151610 3' GGGATGGCCCTCCTGGCTTCAG 39136 CAC CCGTC
 C GC AGCCG GCCATCCC
 || |||| |||||

		CG TCGGT CGGTAGGG		
		ACT CCTCC		
GAM2151	LOC152059 5'	GGAGCAAAACGGGGCTGTGGC 39208	G	CGCCA
		GCCACAGCC CCGT TCC		
		CGGTGTCGG GGCA AGG		
		_ AAACG		
GAM2151	LOC158654 3'	GAGGCGACAGCTGTGGC 39878	CGCC	A
		GCCACAGC GTCGCC TC		
		CGGTGTCG CAGCGG AG		
		A _ _		
GAM2151	LOC162022 5'	GACTGCGACGGCGTGCTGTGGC 40044	_	CA
		GCCACAGC CGCCGTCGC TC		
		CGGTGTCG GCGGCAGCG AG		
		T TC		
GAM2151	LOC199796 5'	GGAGAGCGGGAGGCGGCTG 36813	G_	CA
		CAGCCGCC TCGC TCC		
		GTCGGCGG GGCG AGG		
		AG AG		
GAM2151	LOC203069 5'	GGGGACGCCGAGGGCGGCTG 43001	G	CCA
		CAGCCGCC TCG TCCCC		
		GTCGGCGG AGC AGGGG		
		G CGC		
GAM2151	LOC221583 5'	GGGGATGGCAACAGCATTGGTG 44247	AGCC	C C
		CAC GC GT GCCATCCCC		
		GTG CG CA CGGTAGGGG		
		GTTA A A		
GAM2151	LOC254181 5'	GGGAATGGGCTATGGCAGCCCT 46598	CA C	C A _
	GGC	GCCA GC GCCGT GCC TCCC		
		CGGT CG CGGTA CGG AGGG		
		CC A T GTA		
GAM2151	LOC256586 5'	GAGGCGGCGGCGGCGGC 45514	ACA	A
		GCC GCCGCCGTCGCC TC		
		CGG CGGCGGCGGCGG AG		
		_ _		
GAM2151	LOC257438 3'	GGATTCCAAGTGCAGCTGTGGC 45108	C C	CGCC
		GCCACAGC GC GT ATCC		
		CGGTGTCG CG CA TAGG		
		A T CCT_		
GAM2151	LOC257612 5'	GATGGCACAGGGCTGTGG 46742	GCC	C
		CCACAGCC GT GCCATC		

GGTGTCCG CA CGGTAG
GA_ _

GAM2151 LOC51015 5' GGGAACAGTGGCGGCTTCGGC 18127 AC TCGCCA
GCC AGCCGCCG TCCC
||| ||||| |||
CGG TCGGCGGT AGGG
CT GACA_

GAM2151 LOC57107 3' GGGATGGCGCCAGGGCGGTGGC 21651 A GCC T
GCCAC GCC G CGCCATCCC
||||| ||| | |||||
CGGTG CGG C GCGGTAGGG
G GAC_

GAM2151 LOC84548 5' GGCGACGGCGACGGCGACGGC 35298 ACA _
GCC GCC GCCGTCGCC
||| ||| |||||
CGG CGG CGGCAGCGG
CAG CAG

GAM2151 LOC90620 5' GGAACAGACCTGGCTGTGGC 31804 CC GCCA
GCCACAGCCG GTC TCC
||||||| ||| |||
CGGTGTCCGT CAG AGG
C_ ACA_

GAM2151 LOC90835 5' GGACGACGGCGGCGGCGGC 32073 ACA _
GCC GCCGCCGTCG CC
||| ||||| ||| ||
CGG CGGCGGCAGC GG
CGG A

GAM2151 LOC90874 5' GAGAAGCCGCACGGCTGTGGC 32135 CC C CA_
GCCACAGCCG GT GC TC
||||||| ||| ||
CGGTGTCCGC CG CG AG
A_ C AAG

GAM2151 LOC91156 5' GGGGATGGCTACACGCGGCTGT 32465 C_ C
G CACAGCCGC GT GCCATCCCC
||||||| || |||||
GTGTCGGCG CA CGGTAGGGG
CA T

GAM2152 FLJ10748 5' CGGCGCCAAGTAGCCGGTGG 20087 GA_ _
TCACCGGC TTGGC CCG
||||||| ||||| |||
GGTGGCCG AACCG GGC
ATG C

GAM2152 LOC112937 5' GGCCTCGGGGCCAGCGG 44006 GCGA _
CCG TTGGCCC GACGCC
||| ||||| |||||
GGC GACCGGG CTGCGG
_ G

GAM2152 LOC158301 3' GGCCTCGGCGGCGGCGGCGA 39811 A G A GC
TC CCG CG TTG CCGACGCC
|| ||| ||| |||||

			AG GGC GC GGC GGCTGCGG		
			C G _ _		
GAM2153	CBFA2T3	3'	GTGGCTATCAGGAGTTCT 11692	CA	C T
			AGAACTCC GGT G CCAC		
			TCTTGAGG CTA C GGTG		
			A _ T _		
GAM2153	CLASP1	5'	GTGAATGCCATGAGAGTTCTGA 32540	C _	T C
			TCAGAACTC CA GG CGT CAC		
			AGTCTTGAG GT CC GTA GTG		
			A A _ A		
GAM2153	IL13RA1	3'	GCAATTTGGGAGTCCGA 7284	A A	C
			TC GA CTCCCAGGT GT		
			AG CT GAGGGTTTA CG		
			C _ A		
GAM2153	ITPR1	3'	ATGGCTAATGAGTTCTGA 7984	CCA	
			TCAGAACTC GGTCGT		
			AGTCTTGAG TCGGTA		
			TAA		
GAM2153	NBS1	3'	ATGAATGAGAGTTCTGG 34435	C	GG
			TCAGAACTC CA TCGT		
			GGTCTTGAG GT AGTA		
			A A _		
GAM2153	NDRG3	3'	TGAACCATCGCTGAGGTTCTGA 25725	_ CCA	C C
			TCAGAAC TC GGT GT CA		
			AGTCTTG AG CTA CA GT		
			G TCG C A		
GAM2153	NR2E3	3'	TGGTTCCATGGAGTTCTGA 18471	CA	TCGT
			TCAGAACTCC GG CCA		
			AGTCTTGAGG CC GGT		
			TA TT _		
GAM2153	RIG	3'	ATGGCTTGGCAGGAAGTCTGG 13103	A _ _	C
			TCAGA CT CCAGGTCGT		
			GGTCT GA GGTTCGGTA		
			CAAG C		
GAM2153	SLC22A3	3'	TGAACATCTGGGAATCCTG 22507	AAC	C C
			CAG TCCCAGGT GT CA		
			GTC AGGGTCTA CA GT		
			CTA _ A		
GAM2153	WIG1	5'	GCGTCCCGGGGGTTCCGA 45336	A	A T
			TC GAAGTCCC GG CGT		

			AG CTTGGGGG CC GCG			
			C C T			
GAM2153	ZNF202	3'	GTGTTGAACCTGGGACCCTGA 9509	AAC		_ TC
			TCAG TCCCAGGT CG CAC			
			AGTC AGGGTCCA GT GTG			
			CC_ A T_			
GAM2153	C9orf5	3'	GGACTTCTAAGAGTTTTGA 25715	CC		TC
			TCAGAACTC AGG GTCC			
			AGTTTTGAG TCT CAGG			
			AA T_			
GAM2153	CHODL	3'	GCTCTCTGAGGGTTCTGA 24490	C		TC
			TCAGAACTC CAGG GT			
			AGTCTTGGG GTCT CG			
			A CT			
GAM2153	CPR2	3'	ATGGCTGGGGGTTCTGA 25173	G		
			TCAGAACTCCCAG TCGT			
			AGTCTTGGGGGTC GGTA			
			—			
GAM2153	DKFZP586M1120	3'	GGAGGCTGGGAGTCTGA 25323	A		G G
			TCAGA CTCCCAG TC TCC			
			AGTCT GAGGGTC GG AGG			
			— — —			
GAM2153	DKFZp761K1423	5'	ATGTCTGGGACCTCTGA 20470	AC		T
			TCAGA TCCCAGG CGT			
			AGTCT AGGGTCT GTA			
			CC —			
GAM2153	DKFZp762E1312	5'	GCAGCCTGGGGTCCTGA 20451	A T		C
			TCAG AC CCCAGGT GT			
			AGTC TG GGGTCCG CG			
			C _ A			
GAM2153	EZF-2	3'	GAGGACCTGGGACCCCTGA 20341	AAC		G
			TCAG TCCCAGGTC TC			
			AGTC AGGGTCCAG AG			
			CCC G			
GAM2153	FLJ10520	5'	GGTGTCTAGTAGTTCTGA 19906	CCC		T T
			TCAGAACT AGG CG CC			
			AGTCTTGA TCT GT GG			
			TGA _ _			
GAM2153	FLJ13110	3'	GGGCTGCCAGAGGTTCTGA 23222	CCCA		C
			TCAGAACT GGT GTCC			

AGTCTTGG CCG CGGG
 AGA_ T
 GAM2153 FLJ13769 3' GTGGCCCATCTGGGAGTC 24596 A CGT
 GA CTCCCAGGT CCAC
 || ||||| |||
 CT GAGGGTCTA GGTG
 _ CCC
 GAM2153 FLJ20081 3' TGGGCCCGGGAGTTT 19182 A TC
 GAACTCCC GG GTCCA
 ||||| || |||
 TTTGAGGG CC CGGGT
 _ _
 GAM2153 FLJ20139 5' ACACCTGGGAATTATGA 19234 G C C
 TCA AA TCCCAGGT GT
 ||| || ||||| ||
 AGT TT AGGGTCCA CA
 A A _
 GAM2153 FLJ20477 5' GTGGCCCCTCTGGGAGGCCTGA 19503 AA _ TC T
 TCAG CTCCCAG G G CCAC
 ||| ||||| | |||
 AGTC GAGGGTC C C GGTG
 CG T CC _
 GAM2153 FLJ21916 3' GTGGAAACCGCCTGGGAATTCC 23381 A C CG_
 GG TC GAA TCCCAGGT TCCAC
 || || ||||| |||
 GG CTT AGGGTCCG AGGTG
 C A CCAA
 GAM2153 FLJ23510 3' GTGAACTGTCAGGAGTTCT 24053 CA TC C
 AGAACTCC GG GT CAC
 ||||| || |||
 TCTTGAGG CT CA GTG
 A_ GT A
 GAM2153 FLJ30294 5' GTGCTGGCTGGGAGTTCTGG 29451 G TC
 TCAGAACTCCCAG TCG CAC
 ||||| ||| |||
 GGTCTTGAGGGTC GGT GTG
 _ C_
 GAM2153 IKKE 5' GTGAGCCCTGAAAGCTCTGG 15204 A CC TC TC
 TCAGA CT CAGG G CAC
 |||| || ||| | |||
 GGTCT GA GTCC C GTG
 C AA _ GA
 GAM2153 KIAA0237 3' TGGGGCTTGGGAATTC 16458 C GT
 GAA TCCCAGGTC CCA
 || ||||| |||
 CTT AGGGTTCCG GGT
 A _
 GAM2153 KIAA0337 3' GTGGGCTGACCAGGACCTCTGA 16656 AC CA _
 TCAGA TCC GGTC GTCCAC
 |||| || |||| |||||

			AGTCT AGG CCAG CGGGTG		
			CC A_ T		
GAM2153	KIAA0390	3'	TGGACAACCTGGCTGG 16271	AACTC	C
			TCAG CCAGGT GTCCA		
			GGTC GGTCCA CAGGT		
			_____ A		
GAM2153	KIAA0451	3'	GGGCTTCAGGAGTTCTGA 16809	CA TC	
			TCAGAACTCC GG GTCC		
			AGTCTTGAGG CT CGGG		
			A_ T_		
GAM2153	KIAA0662	3'	TGGACAGTTGGGTTCTGA 39804	CT	GTC
			TCAGAA CCCAG GTCCA		
			AGTCTT GGGTT CAGGT		
			___ GA_		
GAM2153	KIAA1318	3'	TGGTGTATGAGGTTCTGA 33434	CC GGT T	
			TCAGAACT CA CG CCA		
			AGTCTTGG GT GT GGT		
			A_ AT_ _		
GAM2153	KIAA1503	5'	GCGCCTGGGATTCTGA 33917	C	T
			TCAGAA TCCCAGG CGT		
			AGTCTT AGGGTCC GCG		

GAM2153	KIAA1582	5'	ACTGCCTGGGAATTTGA 32580	AC	C
			TCAGA TCCCAGGT GT		
			AGTTT AGGGTCCG CA		
			A_ T		
GAM2153	KIAA1817	3'	GACTGTCCTTGGGAGTTT 33863	_ T _	
			GAACTCCCA GG C GTC		
			TTTGAGGGT CC G CAG		
			T T T		
GAM2153	MGC10765	3'	GTGGACATTTGGCAGGAGTTTT 23645	_____	C
	GA		TCAGAACTCC CAGGT GTCCAC		
			AGTTTTGAGG GTTTA CAGGTG		
			ACG _		
GAM2153	MGC13053	3'	ATGAACCGGGTGGGTTCTGA 26422	_ A _	
			TCAGAACTC CC GGT CGT		
			AGTCTTGGG GG CCA GTA		
			T G A		
GAM2153	MGC13168	3'	ATGGCTTGAAGTCCTGA 26460	A CC	
			TCAG ACT CAGGTCGT		

AGTC TGA GTTCGGTA
 C A_
 GAM2153 MGC2508 3' GGAACCTCTGGGGGCCCTGA 23619 AA TCG
 TCAG CTCCCAGG TCC
 |||| ||||| ||
 AGTC GGGGGTCT AGG
 CC CA_
 GAM2153 MGC2663 5' ATGAAAGGAGGGTTCTGA 23550 _ AGG
 TCAGAACTC CC TCGT
 ||||| || |||
 AGTCTTGGG GG AGTA
 A AA_
 GAM2153 PP1628 5' TGGATGACAGTCCTGA 24859 A CCCAG
 TCAG ACT GTCGTCCA
 ||| || |||||
 AGTC TGA CAGTAGGT
 C ____
 GAM2153 PQBP1 5' GGTTGGTGGGAGTTGCGA 12262 AG GG T
 TC AACTCCCA TCG CC
 || ||||| ||| ||
 AG TTGAGGGT GGT GG
 CG _ T
 GAM2153 RAB3-GAP150 3' GCCACCTGGGAGTTCTGG 14790 C
 TCAGAACTCCCAGGT GT
 ||||| ||||| ||
 GGTCTTGAGGGTCCA CG
 C
 GAM2153 SUPT4H1 3' ATGAACCTCGAGAAAGTTCTGA 9145 CCC__ _
 TCAGAACT AGGT CGT
 ||||| ||| |||
 AGTCTTGA TCCA GTA
 AAGAGC A
 GAM2153 VILL 5' TGGACGACGGCTCTGG 33948 ACT CAG
 TCAGA CC GTCGTCCA
 |||| || |||||
 GGTCT GG CAGCAGGT
 C_ _
 GAM2153 WSB1 3' TGGAATTGGGAGTCTGA 28619 A GGTCG
 TCAGA CTCCCA TCCA
 |||| ||||| |||
 AGTCT GAGGGT AGGT
 _ TA_
 GAM2153 YKT6 3' TGGTCCTTGGGAGCTCTG 13322 A TCGT
 CAGA CTCCCAGG CCA
 ||| ||||| |||
 GTCT GAGGGTTC GGT
 C CT_
 GAM2153 ZNF271 5' ACATTTTAGAGTTCTGA 45636 CC C
 TCAGAACTC AGGT GT
 ||||| ||| ||

	AGTCTTGAG TTTA CA	
	AT _	
GAM2153 LOC126392 5'	GTGGACGGGGAGAACTCTGA 37275	A__ AGGT
	TCAGA CTCCC CGTCCAC	
	AGTCT GAGGG GCAGGTG	
	CAA ____	
GAM2153 LOC144519 5'	GTGAGAAGTGAGAGATCTGA 37760	A C GG GTC
	TCAGA CTC CA TC CAC	
	AGTCT GAG GT AG GTG	
	A A GA A__	
GAM2153 LOC145899 5'	TGAACAGCGAGTTTTGA 40625	CCAG C C
	TCAGAACTC GT GT CA	
	AGTTTTGAG CG CA GT	
	____ A A	
GAM2153 LOC146243 5'	GCCGCCTGGAAGTTCTGA 40678	C C
	TCAGAACT CCAGGT GT	
	AGTCTTGA GGTCCG CG	
	A C	
GAM2153 LOC146802 3'	ATGGCGGAGTTCTGA 38246	CAG
	TCAGAACTCC GTCGT	
	AGTCTTGAGG CGGTA	

GAM2153 LOC147645 5'	GTGGAGCGCGGGGCCCTGA 38359	AA CAG T _
	TCAG CTCC G CG TCCAC	
	AGTC GGGG C GC AGGTG	
	CC ____ G	
GAM2153 LOC155038 3'	ATGAGTCTTGAGGTTCTGA 39533	TC _
	TCAGAAC CCAGG TCGT	
	AGTCTTG GTTC AGTA	
	GA TG	
GAM2153 LOC158117 3'	GCGGCCTCAAAGTTCTGA 39728	CCC
	TCAGAACT AGGTCGT	
	AGTCTTGA TCCGGCG	
	AAC	
GAM2153 LOC159199 5'	GCGGAAGTGAGGAGTTCTGG 39982	_ GG_
	TCAGAACTCC CA TCGT	
	GGTCTTGAGG GT GGCG	
	A GAA	
GAM2153 LOC161536 5'	ACGAAACAAGGGGAAGTTCTGA 40021	_ AGG__
	TCAGAACT CCC TCGT	

	AGTCTTGA GGG AGCA		
	A GAACAA		
GAM2153 LOC201514 5'	GGGCCACGGGAGTTCCGG 42583	A	AG C
	TC GAACTCCC GT GTCC		
	GG CTTGAGGG CA CGGG		
	C _ C		
GAM2153 LOC201707 5'	TGGGAGGCCTGAGGTTCTGA 42903	CC	GT
	TCAGAACT CAGGTC CCA		
	AGTCTTGG GTCCGG GGT		
	A_ AG		
GAM2153 LOC203275 3'	GCGGCCTCAAAGTTCTGA 43025	CCC	
	TCAGAACT AGGTCGT		
	AGTCTTGA TCCGGCG		
	AAC		
GAM2153 LOC221583 3'	ATGACTGAGTAAGAGTTTTGA 44244	CCA__	
	TCAGAACTC GGTCGT		
	AGTTTTGAG TCAGTA		
	AATGAG		
GAM2153 LOC253936 3'	TGAACGACCTGGTGTCTGA 45408	ACTC	C
	TCAGA CCAGGTCGT CA		
	AGTCT GGTCCAGCA GT		
	GT_ A		
GAM2153 LOC255565 3'	ACTCTCTGGAAGTTCTGG 45587	C	TC
	TCAGAACT CCAGG GT		
	GGTCTTGA GGTCT CA		
	A CT		
GAM2153 LOC255974 5'	TGGAGCTTGGGATCCTGA 46557	AAC	CG
	TCAG TCCCAGGT TCCA		
	AGTC AGGGTTCG AGGT		
	CT_ _		
GAM2153 LOC256021 3'	TGGAAGAGAGGGTTCTGA 46167	CCAGG G	
	TCAGAACTC TC TCCA		
	AGTCTTGGG AG AGGT		
	AG_ A		
GAM2153 LOC90010 3'	ACTCTCTGGAAGTTCTGG 30620	C	TC
	TCAGAACT CCAGG GT		
	GGTCTTGA GGTCT CA		
	A CT		
GAM2153 LOC90499 3'	TGGTGCAAGAGTTCTGA 31585	CCAG T T	
	TCAGAACTC G CG CCA		

			AGTCTTGAG C GT GGT		
			AA__ _		
GAM2154	TACSTD2	3'	TGTGTCCCAAGATATCCTA 8162	A	A
			TAG ATGTCTTG GATATA		
			ATC TATAGAAC CTGTGT		
			C C		
GAM2154	ELF1	3'	ACTATGAAGACATTCT 35401	GAGA	
			AGAATGTCTT TATAGT		
			TCTTACAGAA GTATCA		

GAM2154	MGC16202	5'	ATGCCTCAGGACATCCTA 26161	A	A
			TAG ATGTCTTGAG TAT		
			ATC TACAGGACTC GTA		
			C C		
GAM2154	LOC147219	5'	TGTACCATATGTGAAACATTCT 40824	C	AG A
	G		TAGAATGT TTG ATAT GTACA		
			GTCTTACA AGT TATA CATGT		
			A G_ C		
GAM2154	LOC153114	3'	TGTACTATACAGAAGGACA 41574	GAGA	
			TGTCTT TATAGTACA		
			ACAGGA ATATCATGT		
			AGAC		
GAM2155	FGFR2	3'	TAGAAAATTGAAACACAGA 5641	A	__
			TCTGTGT TCAAT TCTG		
			AGACACA AGTTA AGAT		
			A AA		
GAM2155	FGFR2	3'	TAGAAAATTGAAACACAGA 23237	A	__
			TCTGTGT TCAAT TCTG		
			AGACACA AGTTA AGAT		
			A AA		
GAM2155	FGFR2	3'	TAGAAAATTGAAACACAGA 23244	A	__
			TCTGTGT TCAAT TCTG		
			AGACACA AGTTA AGAT		
			A AA		
GAM2155	FGFR2	3'	TAGAAAATTGAAACACAGA 23291	A	__
			TCTGTGT TCAAT TCTG		
			AGACACA AGTTA AGAT		
			A AA		
GAM2155	FGFR2	3'	TAGAAAATTGAAACACAGA 23297	A	__
			TCTGTGT TCAAT TCTG		

AGACACA AGTTA AGAT
 A AA
 GAM2155 FGFR2 3' TAGAAAATTGAAACACAGA 23303 A ____
 TCTGTGT TCAAT TCTG
 ||||| |||| |||
 AGACACA AGTTA AGAT
 A AA
 GAM2155 GABRA5 3' ATATGTTAGATACACA 30212 TCAAT C
 TGTGTA TCTGACA AT
 ||||| ||||| ||
 ACACAT AGATTGT TA
 ____ A
 GAM2155 KCNJ6 3' CATGTGTTGTACAATACCAGA 8023 T CAATTCT
 TCTG GTAT GACACATG
 ||| ||| |||||
 AGAC CATA TTGTGTAC
 _ ACATG_
 GAM2155 FLJ14075 3' CATGTACGTTCTTGTACACAGA 24373 T TTCT ____
 TCTGTGTA CAA GAC ACATG
 ||||| ||| ||| |||||
 AGACACAT GTT TTG TGTAC
 _ C__ CA
 GAM2155 KIAA0626 3' GTGCAGAATTGATACCAGA 22314 T A
 TCTG GTATCAATTCTG CAC
 ||| ||||| ||||| |||
 AGAC CATAGTTAAGAC GTG

 GAM2156 FLJ22283 5' TGTGGCATCTGATATT 25947 ATCC A
 GATATCAGAT GT ACA
 ||||| || |||
 TTATAGTCTA CG TGT
 ____ G
 GAM2156 LOC219686 3' TGTGGATATCTAATTCTAA 43676 TATC
 TTAGA AGATATCCGTA
 |||| |||||
 AATCT TCTATAGGTGT
 TAA_
 GAM2157 FCN2 3' AAACCTGAATGGTCGCTACCTC 17950 C_ CAC
 GAGGTAGT TCAT CAGGTTT
 ||||| ||| |||||
 CTCCATCG GGTA GTCCAAA
 CT A_
 GAM2157 LOC90148 3' AAACCTGGCAGATACCACCTT 30890 A C ATCA
 GAGGT GT TC CCAGGTTT
 |||| || |||||
 TTCCA CA AG GGTCCAAA
 C T AC_
 GAM2158 DCT 5' AATACCAGCATAATA 7638 AATA
 TATTATGT TGGTGTT
 ||||| |||||

ATAATACG ACCATAA

GAM2158 EGFL5 3' ACATTATATTACATTATA 41876 T
TAT ATGTAATATGGTGT
||| |||||
ATA TACATTATATTACA
T

GAM2158 HIF1A 3' GTAAAGCCATTTACATAATA 7267 T G
TATTATGTAA ATGGT TTAC
||||||| |||||
ATAATACATT TACCG AATG
_ A

GAM2158 KCNMB3 5' GTAACACTTATTTACATA 15749 TAT
TATGTAA GGTGTTAC
||||| |||||
ATACATT TCACAATG
TAT

GAM2158 M17S2 3' TAACACCCAGAGCATGATA 25609 AATAT
TATTATGT GGTGTTA
||||| |||||
ATAGTACG CCACAAT
AGAC_

GAM2158 M17S2 3' TAACACCCAGAGCATGATA 25622 AATAT
TATTATGT GGTGTTA
||||| |||||
ATAGTACG CCACAAT
AGAC_

GAM2158 M17S2 3' TAACACCCAGAGCATGATA 12520 AATAT
TATTATGT GGTGTTA
||||| |||||
ATAGTACG CCACAAT
AGAC_

GAM2158 STCH 3' GTAAGTCCATATTATATAA 13834 _
TTATGTAATATGGT GTTAC
||||||| |||||
AATATATTATACCG CAATG
T

GAM2158 TNFRSF9 3' ACACCATCCTACATAATA 7288 AT
TATTATGTA ATGGTGT
||||||| |||||
ATAATACAT TACCACA
CC

GAM2158 C13orf1 3' GTAACATTTATTTACATAA 21693 TAT
TTATGTAA GGTGTTAC
||||| |||||
AATACATT TTACAATG
TAT

GAM2158 C3IP1 3' GCACTGAAGTATTACATAA 22275 _
TTATGTAATAT GGTGT
||||||| |||||

			AATACATTATG TCACG		
			AAG		
GAM2158	C5orf5	3'	GCACTATTACATAGTA 18699	AT	
			TATTATGTA ATGGTGT		
			ATGATACAT TATCACG		
			—		
GAM2158	HINT3	3'	ATACCATACTACACAATG 28878	A A	
			TATT TGTA TATGGTGT		
			GTAA ACAT ATACCATA		
			C C		
GAM2158	KIAA0416	3'	GTAACCTATTTTACATAGTA 17837	T T	
			TATTATGTAA ATGG GTTAC		
			ATGATACATT TATC CAATG		
			T _		
GAM2158	KIAA0781	3'	ACATTATATTACTAATA 33499	T	
			TATTA GTAATATGGTGT		
			ATAAT CATTATATTACA		
			—		
GAM2158	KIAA0871	3'	GTAACCTATGATAACATAATA 17332	AA_ T	
			TATTATGT TATGG GTTAC		
			ATAATACA GTATC CAATG		
			ATA _		
GAM2158	KIAA1505	5'	ACACTTTATTATATAATA 45190	T	
			TATTATGTAATA GGTGT		
			ATAATATATTAT TCACA		
			T		
GAM2158	KIAA1678	3'	GTAACATGATTACATAAT 35787	ATG	
			ATTATGTAAT GTGTAC		
			TAATACATTA TACAATG		
			G_		
GAM2158	MGC16063	3'	AACACTCTTCAGTACATAATA 27590	ATAT__	
			TATTATGTA GGTGTT		
			ATAATACAT TCACAA		
			GACTTC		
GAM2158	MSTP031	5'	TAACAGCATGTAACATAA 25734	A G	
			TTATGT ATATG TGTTA		
			AATACA TGTAC ACAAT		
			A G		
GAM2158	NAV3	3'	AACACCAGTTAACATAGTA 17088	AATA	
			TATTATGT TGGTGTT		

			ATGATACA ACCACAA		
			ATTG		
GAM2158	LOC51212	5'	TAACACCATACTTTGGCATA	18518	AA__
			TATGT TATGGTGTTA		
			ATACG ATACCACAAT		
			GTTTC		
GAM2159	ESPN	3'	AGAAACATGAAAACTGCCT	25548	A CTGG
			AG GTA TTTCATGTTTCT		
			TC CGT AAAGTACAAAGA		
			_ CA__		
GAM2159	GRLF1	3'	AGAAACGTTCCCAAACTC	38407	AC TTTC
			GAGT TGG ATGTTTCT		
			CTCA ACC TGCAAAGA		
			A_ CT__		
GAM2159	ITGA2	3'	AGAAACATGAAATGCTT	7962	ACTG
			GAGT GTTTCATGTTTCT		
			TTCG TAAAGTACAAAGA		

GAM2159	WT1	3'	AGAACTAACCAGTACCTC	23667	A TCATGT
			GAG GTACTGGTT TTCT		
			CTC CATGACCAA AAGA		
			_ TC_____		
GAM2159	WT1	3'	AGAACTAACCAGTACCTC	23675	A TCATGT
			GAG GTACTGGTT TTCT		
			CTC CATGACCAA AAGA		
			_ TC_____		
GAM2159	WT1	3'	AGAACTAACCAGTACCTC	23671	A TCATGT
			GAG GTACTGGTT TTCT		
			CTC CATGACCAA AAGA		
			_ TC_____		
GAM2159	WT1	3'	AGAACTAACCAGTACCTC	5951	A TCATGT
			GAG GTACTGGTT TTCT		
			CTC CATGACCAA AAGA		
			_ TC_____		
GAM2159	A2BP1	5'	AGTGCGTGAGAAACCAGCAC	20803	A _ TT
			GT CTGGTT TCATGT CT		
			CA GACCAA AGTGCG GA		
			C AG T_		
GAM2159	KIAA0993	3'	TAGAAGGTGGAAACCAAAACCC	32083	A AC ATG
			GAG GT TGGTTTC TTTCTA		
			TC		

			CTC CA ACCAAAG GAAGAT		
			C AA GTG		
GAM2159	KIAA1416	5'	AGAAACATGCAGCAGTCTC 41797	T G T	
			GAG ACTG TT CATGTTTCT		
			CTC TGAC GA GTACAAAGA		
			- - C		
GAM2159	My015	3'	AAATACCTAACCAGTACTT 33103	TCA	
			GAGTACTGGTT TGTTT		
			TTCATGACCAA ATAAA		
			TCC		
GAM2159	RASSF2	3'	AGAAGAGAACAGTACTCTC 16388	G ATGT	
			GAGAGTACTG TTTC TTCT		
			CTCTCATGAC AGAG AAGA		
			A _____		
GAM2159	TP53INP1	3'	AAACATGAAGGACTCC 36112	A A GGT	
			G GAGT CT TTCATGTTT		
			C CTCA GG AAGTACAAA		
			- - -		
GAM2159	TP53INP1	3'	AAACATGAAGGACTCC 27101	A A GGT	
			G GAGT CT TTCATGTTT		
			C CTCA GG AAGTACAAA		
			- - -		
GAM2159	LOC149711	5'	AAACATAAACCAGTACCTC 41065	A C	
			GAG GTACTGGTTT ATGTTT		
			CTC CATGACCAAAA TACAAA		
			- -		
GAM2159	LOC157503	3'	TAGAAACATGAAACCATGCACT 41815	A C	
			GAG GTA TGGTTTCATGTTTCTA		
			TTC CGT ACCAAAGTACAAAGAT		
			A -		
GAM2160	HUNK	3'	TCATACACTGAAGCAAATTCAG 15954	AATATA_	
			CTGAATTT TGTATGA		
			GACTTAAA ACATACT		
			CGAAGTC		
GAM2160	SFRS7	3'	TCATACATACCTACATTCAG 29900	T ATA	
			CTGAAT TA TATGTATGA		
			GACTTA AT ATACATACT		
			C CC_		
GAM2160	ARNTL2	3'	CACACATTAAATTCAGT 21412	ATAT A	
			ACTGAATTTA ATGT TG		

			TGACTTAAAT TACA AC		
			_____ C		
GAM2160	FLJ12592	3'	TCACACAGGGTTAAGTTCAGTA 25875	ATA	A
	A		TTACTGAATTTAAT TGT TGA		
			AATGACTTGAATTG ACA ACT		
			GG_ C		
GAM2160	HBXAP	3'	TCATACATAAGTCATTTAGTAA 18657	TTA	A
			TTACTGAAT AT TATGTATGA		
			AATGATTTA TG ATACATACT		
			C_ A		
GAM2160	KIAA0776	3'	TCATACACACACAATTCAGT 32363	TAATATA	
			ACTGAATT TGTATGA		
			TGACTTAA ACATACT		
			CACAC_		
GAM2161	DKFZp566D133	3'	CGCAAAGATGTACCTG 35545	AATAT	C
			TAGGT ATATCTTTTGC G		
			GTCCA TGTAGAAAACG C		
			_____ A		
GAM2161	SBBI31	3'	AAAGCATATATACTACCTA 15264	A	_
			TAGGTA TATATAT CTTT		
			ATCCAT ATATATA GAAA		
			C C		
GAM2161	LOC253959	3'	CGCAAAGATGTACCTG 45511	AATAT	C
			TAGGT ATATCTTTTGC G		
			GTCCA TGTAGAAAACG C		
			_____ A		
GAM2161	LOC57107	3'	ACAGCAAACAGATTTTATTACC 21647	TAT	_ C
	TA		TAGGTAATA ATCT TTTGC GT		
			ATCCATTAT TAGA AAACG CA		
			TT_ C A		
GAM2162	ESRRG	3'	TGATAATTTAGCAGCAA 32999	CCACA	
			TTGCTGCTAAA TGTCA		
			AACGACGATTT ATAGT		
			A_		
GAM2162	ITGAL	3'	GATTGACGTACTTAGCAGC 7972	ACCAC	
			GCTGCTAA ATGTCAATC		
			CGACGATT TGCAGTTAG		
			CA_		
GAM2162	NUFIP1	3'	ATTGAAGATAGGTTTAGCAGTA 14737	ACATG	
	A		TTGCTGCTAAACC TCAAT		

		AATGACGATTTGG AGTTA	
		ATAGA	
GAM2162	POU2AF1	3' GATTACAGTCCAGGCAGCAA 12892	AAACC A C
		TTGCTGCT AC TGT AATC	
		AACGACGG TG ACA TTAG	
		ACC__ _ T	
GAM2162	RAG2	5' ATTAATACCTGGTTTAGCGGCA 39985	CA C
	A	TTGCTGCTAAACCA TGT AAT	
		AACGGCGATTTGGT ATA TTA	
		CC A	
GAM2162	TNS	3' GGCATGTGGCTCAGCAGCAA 22903	AAA
		TTGCTGCT CCACATGTC	
		AACGACGA GGTGTACGG	
		CTC	
GAM2162	DKFZP434I092	3' ATTGACATTCCAGTAGAGCAA 33673	G AACCAC
		TTGCT CTA ATGTCAAT	
		AACGA GAT TACAGTTA	
		_ GACCT_	
GAM2162	FLJ10656	3' ATTAACATGGTAAGCCTTAGCA 19988	ACCA__ C
	GCAA	TTGCTGCTAA CATGT AAT	
		AACGACGATT GTACA TTA	
		CCGAATG A	
GAM2162	GABARAPL1	3' TGGCAGTCCAGCAGCAA 25392	AA CACA
		TTGCTGCT AC TGTCA	
		AACGACGA TG ACGGT	
		CC ____	
GAM2162	GABARAPL3	3' TGGCAGTCCAGCAGCAA 26300	AA CACA
		TTGCTGCT AC TGTCA	
		AACGACGA TG ACGGT	
		CC ____	
GAM2162	HT002	3' GACGGTGATGACCCAGCAGCAA 15281	AAAC__ A
		TTGCTGCT CAC TGTC	
		AACGACGA GTG GCAG	
		CCCAGTA _	
GAM2162	KIAA0475	3' GATTGGAAGTGGCCAGCAGCAA 16949	AAA ATG
		TTGCTGCT CCAC TCAATC	
		AACGACGA GGTG GGTTAG	
		CC_ AA_	
GAM2162	KIAA0712	5' ATGCAGTTTCAGCAGCAA 16262	_ CA
		TTGCTGCT AAAC CAT	

		AACGACGA TTTG GTA		
		C AC		
GAM2162 KIAA1301	3'	GATTGACATATGGTTTGCCAG 32978	C	C
		CTG TAAACCA ATGTCAATC		
		GAC GTTTGGT TACAGTTAG		
		C A		
GAM2162 SEZ6	3'	GACTTGCACCACAGTCCAGCAG 36774	AA	CA_____ T
	CAA	TTGCTGCT AC CA GTC		
		AACGACGA TG GT CAG		
		CC ACACCAC T		
GAM2162 VMP1	3'	ATGTGATGTTTCAGCAGCAA 25204	A	__
		TTGCTGCT AAC CACAT		
		AACGACGA TTG GTGTA		
		C TA		
GAM2162 LOC115110	3'	ACGTGAGTCAGCAGCAA 35503	AA	CA
		TTGCTGCT AC CATGT		
		AACGACGA TG GTGCA		
		C_ A_		
GAM2162 LOC132235	5'	TGACACGGGAGCTAGCAGCA 37483	AA_	ACA
		TGCTGCTA CC TGTCA		
		ACGACGAT GG ACAGT		
		CGA GC_		
GAM2162 LOC142941	3'	CATGTGGTTTGCAGCAA 40322	T	
		TTGCTGC AAACCACATG		
		AACGACG TTTGGTGTAC		
		-		
GAM2162 LOC158549	5'	GACGTGTTTAAACAGCAA 42007	C	CC
		TTGCTG TAAA ACATGTC		
		AACGAC ATTT TGTGCAG		
		A _		
GAM2162 LOC221882	5'	GATTGGTATGGTAATTTAAAGC 44434	GC	CCA_ GT
	AA	TTGCT TAAA CAT CAATC		
		AACGA ATTT GTA GTTAG		
		A_ AATG TG		
GAM2163 C9orf12	3'	ACCATGGAATTATATGAAA 22990	TGAA	
		TTTCATATAATTC GGT		
		AAAGTATATTAAGG CCA		
		TA__		
GAM2163 DKFZP564F013	3'	TTTTAGAAATTACATGAAA 45205	A	
		TTTCAT TAATTTCTGAAG		

AAAGTA ATTAAAGATTTT
 C
 GAM2163 LOC199923 3' ACTTCCCAGAAGTTATAT 42665 AA T
 ATATAATTTCTG GG AGT
 ||||| ||||
 TATATTGAAGAC CC TCA
 _ T
 GAM2164 IL6R 3' AAGATGCTTCTCACTGCC 6171 AAT GATG
 GGCAGTGA GT ATCTT
 ||||| || ||||
 CCGTCACT CG TAGAA
 CTT ____
 GAM2164 XT3 3' CAAGATCATGCCACTCCACTCC 21441 C AAAT _
 GG AGTG GTG ATGATCTTG
 || ||| || |||||
 CC TCAC CAC TACTAGAAC
 _ CT_ CG
 GAM2164 FBXO9 3' CAAGATCGTGCCATTCCACTCC 27257 C A TG
 GG AGTG AATG ATGATCTTG
 || ||| ||| |||||
 CC TCAC TTAC TGCTAGAAC
 _ C CG
 GAM2164 FLJ14840 5' CAAGATCAGCCTTCCTCGCCAC 26644 CA AATGTGA
 CG CGG GTGA TGATCTTG
 ||| ||| |||||
 GCC CGCT ACTAGAAC
 AC CCTTCCG
 GAM2164 Nup43 3' CAAGATCGTGCCACTTCACTCC 23932 C A TG
 GG AGTGAA TG ATGATCTTG
 || ||||| || |||||
 CC TCACTT AC TGCTAGAAC
 _ C CG
 GAM2164 PRPF8 3' GAGATCATCACCTCCACCACC 30684 CA AAAT
 GG GTG GTGATGATCTT
 || ||| |||||
 CC CAC CACTACTAGAG
 AC CTC_
 GAM2164 YME1L1 3' CAAGATCACAGGAGCCACTGC 29292 AAATG A
 GCAGTG TG TGATCTTG
 ||||| || |||||
 CGTCAC AC ACTAGAAC
 CGAGG _
 GAM2164 YME1L1 3' CAAGATCACAGGAGCCACTGC 15536 AAATG A
 GCAGTG TG TGATCTTG
 ||||| || |||||
 CGTCAC AC ACTAGAAC
 CGAGG _
 GAM2164 ZF5128 3' CAACACATGCTCACTGCC 15668 A_ A
 GGCAGTGA ATGTG TG
 ||||| ||||| ||

CCGTCACT TACAC AC
 CG A
 GAM2164 LOC147664 3' CAAGATCGTGCCATTCCACTCC 38352 C A TG
 GG AGTG AATG ATGATCTTG
 || ||| ||| |||||
 CC TCAC TTAC TGCTAGAAC
 _ C CG
 GAM2164 LOC51336 3' CAAGATCATTTACCTCACTCC 18755 C AA T
 GG AGTGA TG GATGATCTTG
 || ||| || |||||
 CC TCACT AC TTACTAGAAC
 _ CC T
 GAM2165 EFNB2 3' ATAGAACACAAGGGATATA 10295 ATA_
 TATGTCTCT TTCTAT
 ||||| |||
 ATATAGGGA AAGATA
 ACAC
 GAM2165 EPB41L1 3' ATAGATATATAGAGATATAGAT 34938 CA _
 A TATC TATGTCTCTATAT TCTAT
 ||| ||||| |||
 ATAG ATATAGAGATATA AGATA
 _ T
 GAM2165 GABARAPL3 3' AGAAGGTGAAGACATATAGA 26295 C C A
 TC ATATGTCT TAT TTCT
 || ||||| ||| |||
 AG TATACAGA GTG AAGA
 A A G
 GAM2165 KIAA0265 3' ATATAGAAACATATGGATA 34621 C
 TATCCATATGT TCTATAT
 ||||| |||||
 ATAGGTATACA AGATATA
 A
 GAM2165 MGC13105 3' ATAGAAGAGAAGACATATG 35407 CTATA
 CATATGTCT TTCTAT
 ||||| |||
 GTATACAGA AAGATA
 AGAG_
 GAM2165 LOC222681 3' AGAACATAGAGATAGGG 44606 ATA A
 TCC TGTCTCTAT TTCT
 || ||||| |||
 GGG ATAGAGATA AAGA
 _ C
 GAM2165 LOC255995 5' ATAGACATACAGAGATATA 46323 A _
 TATGTCTCT TAT TCTAT
 ||||| ||| |||
 ATATAGAGA ATA AGATA
 C C
 GAM2165 LOC257507 3' AGAACATAGAGATAGGG 46672 ATA A
 TCC TGTCTCTAT TTCT
 || ||||| |||

GGG ATAGAGATA AAGA
— C
GAM2165 LOC257625 3' AGAACATAGAGATAGGG 46728 ATA A
TCC TGTCTCTAT TTCT
||| ||||| |||
GGG ATAGAGATA AAGA
— C
GAM2165 LOC90777 3' ATAGAGAGCATATGGATA 31991 _
TATCCATATG TCTCTAT
||||||| |||||
ATAGGTATAC AGAGATA
G
GAM2166 BIG1 3' GTTAGATTTACTGGAAATGTA 13138 T TCT
TACATTTCCA GTA ATCTAAC
||||||| ||| |||||
ATGTAAAGGT CAT TAGATTG
— T—
GAM2166 E2F3 3' GTTAAGTGCCTACTGGAAATG 7669 T TC TC
CATTTCCA GTA TA TAAC
||||||| ||| || |||
GTAAAGGT CAT GT ATTG
— CC GA
GAM2166 KCNK6 3' TAGACAGTGCTGGAGA 11239 T T A
TTTCCA GTA CT TCTA
||||||| ||| || |||
AGAGGT CGT GA AGAT
— — C
GAM2166 RBM8A 3' AGATAGATGTTATAGAAATG 11577 CATG_
CATTTT TATCTATCT
||||| |||||
GTAAAG GTAGATAGA
ATATT
GAM2166 SCD 3' TAGATGGAATGGAAA 11494 GTA
TTTCCAT TCTATCTA
||||||| |||||
AAAGGTA AGGTAGAT
—
GAM2166 H2AV 3' ATGGATACATGAAAATTA 28909 C C
A ATTT CATGTATCTAT
| ||| |||||
A TAAA GTACATAGGTA
T A
GAM2166 KIAA0410 3' TAGATACATTTAGAAATGT 16621 C_
ACATTTT ATGTATCTA
||||||| |||||
TGTAAG TACATAGAT
ATT
GAM2166 KIAA0795 3' AGATAAGGACTGGAAATGTG 24582 T ATC
TACATTTCCA GT TATCT
||||||| || |||||

			GTGTAAAGGT CA ATAGA		
			_ GGA		
GAM2166	KIAA1786	3'	TAGATAAGGGAAAAATGTG 32846	___	ATG
			TACATT TCC TATCTA		
			GTGTAA AGG ATAGAT		
			AA GA_		
GAM2166	KIAA1900	3'	TAGATAGAATTTGGAAA 36262	T A	
			TTTCCA GT TCTATCTA		
			AAAGGT TA AGATAGAT		
			T _		
GAM2166	RAP140	3'	TAGACAGATACAGTGGAGAT 17559	_	A
			ATTTCCA TGTATCT TCTA		
			TAGAGGT ACATAGA AGAT		
			G C		
GAM2166	RBM7	3'	GTTAGATAAAATGGTAAAATGT 18179	___	GTATC
			ACATTT CCAT TATCTAAC		
			TGTAAA GGTA ATAGATTG		
			AT AA_		
GAM2166	LOC145820	3'	ATGGATACAGAGAAATGTA 37988	CA	
			TACATTTT TGTATCTAT		
			ATGTAAAG ACATAGGTA		
			AG		
GAM2166	LOC150587	3'	TAGATTGAACACATGGAATG 41213	T A_ T	
			CATT CCATGT TC ATCTA		
			GTAA GGTACA AG TAGAT		
			_ CA T		
GAM2166	LOC197003	3'	ATGGATACAATAGAAATGTA 42443	CA_	
			TACATTTT TGTATCTAT		
			ATGTAAAG ACATAGGTA		
			ATA		
GAM2166	LOC54505	5'	GTAGATACTGGAAATGTA 33696	T	
			TACATTTCCA GTATCTAT		
			ATGTAAAGGT CATAGATG		
			-		
GAM2167	FGF12	3'	TCAATAGCTTAACTCA 22020	ATTA C	
			TGAGT TGAGC ATTGA		
			ACTCA ATTCG TAACT		
			A_ A		
GAM2167	DKFZP434G1411	3'	TTCAGCTACAATACTCA 44233	ATG CAT	
			TGAGTATT AGC TGAA		

ACTCATAA TCG ACTT
 CA_ _
 GAM2167 GORASP2 3' ATATTCTATGCCTAATACTCA 17797 TGA C T
 TGAGTATTA GC AT GAATAT
 ||||| || |||||
 ACTCATAAT CG TA CTTATA
 C_ _ T
 GAM2167 KIAA1396 3' ATTCAATGGGTTGCATACCCA 31545 A TAT G
 TG GTAT GA CCATTGAAT
 || ||| || |||||
 AC CATA TT GGTAACCTA
 C CG_ G
 GAM2167 LOC220936 3' TCCATGAATTCATAATACTCA 43932 C_ T
 TGAGTATTATGAG CAT GA
 ||||| || ||
 ACTCATAATACTT GTA CT
 AA C
 GAM2168 ODF2 5' CCAGCAGCCAGAAATCTCACA 8386 AA CTTA
 TGTGA GTTTCTGGT CTGG
 |||| ||||| |||
 ACACT TAAAGACCG GACC
 C_ AC_
 GAM2168 SCA7 3' GAGACCAGAAACCTTCCA 5886 T A
 TG GAA GTTTCTGGTCTT
 || ||| |||||
 AC CTT CAAAGACCAGAG
 _ C
 GAM2168 SLC26A10 5' AGATGCAGGAACTTCCACA 28557 A _
 TGTG AAGTTTCTG GTCT
 |||| ||||| |||
 ACAC TTCAAGGAC TAGA
 C G
 GAM2168 LOC158236 5' CCAGTAAGACCATCTTTCA 41927 TTTC
 TGAAAG TGGTCTTACTGG
 |||| |||||
 ACTTTC ACCAGAATGACC
 T_
 GAM2168 LOC253264 5' CCACATTCCCAGAACTTCCAG 45417 GA_ TCTTAC
 CA TGT AAGTTTCTGG TGG
 || ||||| |||
 ACG TTCAAAGACC ACC
 ACC CTTAC_
 GAM2169 D10S170 3' TATATTTTATGACAAGAATGTG 11918 A _ C
 CACATTCTT TC TA GATATA
 ||||| || || |||||
 GTGTAAGAA AG AT TTATAT
 C T T
 GAM2169 DAZL 3' ATATCTTAAGAATGTG 33798 TCTAC
 CACATTCTTA GATAT
 ||||| |||||

			GTGTAAGAAT CTATA		
			T_____		
GAM2169	DBT	3'	ATATCCTGGGTAAGAATGT 7632	C	
			ACATTCTTATCTA GATAT		
			TGTAAGAATGGGT CTATA		
			C		
GAM2169	LOC256277	5'	ATATCTTGCAAGGATGTGATA 45424	ATC	C
			TATCACATTCTT TA GATAT		
			ATAGTGTAGGAA GT CTATA		
			C__ T		
GAM2170	ANGPT1	3'	TTCTTGGTGGCTTCTTCATAGC 6817	TA_	
	A		TGCT AAGAAGCCACCAAGAA		
			ACGA TTCTTCGGTGGTTCTT		
			TAC		
GAM2170	ATP1B2	3'	TTCTCTGGCTTCTTTTAGCAA 7397	T	CCA
			TTGCT AAAGAAGCCA AGAA		
			AACGA TTTCTTCGGT TCTT		
			T C__		
GAM2170	AP3M1	3'	TTCTTAAGGAGCTTTAAGC 14397	AAG	ACC
			GCTTAAAG CC AAGAA		
			CGAATTTC GG TTCTT		
			GA_ AA_		
GAM2170	BHC80	3'	GTTCTTTTTTTCTTTAAGGAA 18729	G	CCACC
			TT CTAAAGAAG AAGAAC		
			AA GAATTCTTT TTCTTG		
			G TT__		
GAM2170	FLJ21916	3'	TCTTCAATTTTTTAAGCAA 23383	GCCACC	
			TTGCTTAAAGAA AAGA		
			AACGAATTTTTT TTCT		
			AAC__		
GAM2170	KIAA0441	5'	CTTAGTGGCTTCTGAAG 16709	AA	C
			CTT AGAAGCCAC AAG		
			GAA TCTTCGGTG TTC		
			G_ A		
GAM2170	KIAA1157	3'	GTTCTCAGCTTTCCTTAAGCGA 35754	A_	CACCA
			TTGCTTAA GAAGC AGAAC		
			AGCGAATT TTTCG TCTTG		
			CC AC__		
GAM2170	PRO1580	5'	TCTTTGAATTCTTTAAGCAA 20567	GC	CC
			TTGCTTAAAGAA CA AAGA		

AACGAATTTCTT GT TTCT
 AA ____
 GAM2170 LOC257484 5' CTCAGTGGCTTCTTGGAGT 42814 A CA
 GCTT AAGAAGCCAC AG
 |||| ||||| ||
 TGAG TTCTTCGGTG TC
 G AC
 GAM2170 LOC91351 3' GTTCTGTGATTCTTTAAGCAA 32698 GC CA
 TTGCTTAAAGAA CAC AGAAC
 ||||| || ||||
 AACGAATTTCTT GTG TCTTG
 A ____
 GAM2171 CIT 3' AAGGATTTTCAGCAAACCACC 34559 TCACA _
 GGT TTGCT AAATCCTT
 || |||| |||||
 CCA AACGA TTTAGGAA
 CCA__ C
 GAM2171 KIAA0475 3' AAGGATTCAGAAAGAACCTTA 16944 ACATTG A
 TGAGGTTCT CT AATCCTT
 ||||| || |||||
 ATTCCAAG GA TTAGGAA
 AAA__ C
 GAM2171 KIAA1649 3' AAGGACCCAGGATTTGAACCCA 26100 A C G AAA
 TG GGTTCATT CT TCCTT
 || ||||| || ||||
 AC CCAAGT TAG GA AGGAA
 _ T _ CCC
 GAM2171 KIAA1649 3' AAGGACCCAGGATTTGAACCCA 33254 A C G AAA
 TG GGTTCATT CT TCCTT
 || ||||| || ||||
 AC CCAAGT TAG GA AGGAA
 _ T _ CCC
 GAM2171 KIAA1922 5' AAGGATCAGGTCAACACGGACC 36452 ACA _ AA
 TCA TGAGGTTCT TTG CT ATCCTT
 ||||| || |||||
 ACTCCAGG AAC GG TAGGAA
 CAC T AC
 GAM2171 TUSP 3' AAGAATTCAGCAATGTTATC 21520 TC A C
 GGT ACATTGCT AAT CTT
 || ||||| || ||||
 CTA TGTAACGA TTA GAA
 T_ C A
 GAM2171 ZNF384 3' AGGATTTGCTATGACCTCA 28544 TCA T T
 TGAGGT CAT GC AAATCCT
 ||||| || |||||
 ACTCCA GTA CG TTTAGGA
 _ T _
 GAM2171 LOC221656 3' AAGAATGTGCAGTGAACCTCA 44290 AT TAA C
 TGAGGTTCTAC TGC AT CTT
 ||||| || ||||

ACTCCAAGTG ACG TA GAA
 _ TG_ A
 GAM2172 ALDH3A2 3' AAAGTGAGGGAACCATTTCTC 34338 AATGG AC
 GAGGAAAT CC CACTTT
 ||||| || |||||
 CTCCTTTA GG GTGAAA
 CCAA_ GA
 GAM2172 FGF2 3' AAAGTAAACACATTAATTTCT 7730 _ GCCACC
 CA TGAGGAAAT AATG ACTTT
 ||||| || |||||
 ACTCCTTTA TTAC TGAAA
 A ACAA_
 GAM2172 HNRPK 3' TGGTGGCTGAATTTCCCA 7917 A AAT
 TG GGAAAT GGCCACCA
 || ||||| |||||
 AC CCTTTA TCGGTGGT
 _ AG_
 GAM2172 HNRPK 3' TGGTGGCTGAATTTCCCA 25281 A AAT
 TG GGAAAT GGCCACCA
 || ||||| |||||
 AC CCTTTA TCGGTGGT
 _ AG_
 GAM2172 PNUTL2 3' AAAGTGGTACCGACTTCCCA 27835 A ATAA CC
 TG GGAA TGG ACCACTTT
 || |||| || |||||
 AC CCTT GCC TGGTGAAA
 C CA_ A_
 GAM2172 PNUTL2 3' AAAGTGGTACCGACTTCCCA 27833 A ATAA CC
 TG GGAA TGG ACCACTTT
 || |||| || |||||
 AC CCTT GCC TGGTGAAA
 C CA_ A_
 GAM2172 FLJ23017 3' TAAAGTAGTGGTTTCTTCATTG 23131 _ C III
 TTTCTCA AATAATG GCCAC ACTTT A
 ||||| |||| |||| |
 TTGTTAC TGGTG TGAAA T
 TTCTT A III
 GAM2172 KIAA0660 3' GGTGGACATTATTTCCCA 14658 A G
 TG GGAAATAATG CCACC
 || ||||| |||||
 AC CCTTTATTAC GGTGG
 C A
 GAM2172 KIAA1054 3' TGGCCTTTACCTATTTCTTCA 33959 AT_
 TGAGGAAATA GGCCA
 ||||| |||||
 ACTTCTTTAT CCGGT
 CCATT
 GAM2172 KIAA1677 3' GTCTTCATTATTTCTCA 33292 _ CC
 TGAGGAAA TAATGG AC
 ||||| ||||| ||

ACTCCTTT ATTACT TG
 T TC
 GAM2172 LOC148946 3' AAAGTAATGTCGTATTATTTC 40935 A GC_ CC
 CCA TG GGAAATAATG CA ACTTT
 || ||||| || ||||
 AC CCTTTATTAT GT TGAAA
 C GCT AA
 GAM2172 LOC161829 5' GTGACTACCATTTCTCA 40039 AA C
 TGAGGAAAT TGG CAC
 ||||| || ||
 ACTCCTTTA ATC GTG
 CC A
 GAM2172 LOC219333 3' GTGGCTTTTTGTTTCCCCA 44935 A T_
 TG GGAAATAA GGCCAC
 || ||||| ||||
 AC CCTTTGTT TCGGTG
 C TT
 GAM2173 CACNG3 5' AGAAAGGAAATCCCAGCTTTCC 13291 GA G
 C GGGAAAGT GGGGT TCCTTTCT
 ||||| |||| |||||
 CCCTTTTCG CCCTA AGGAAAGA
 A_ A
 GAM2173 COL11A2 3' GGCACCCCTCACTTTCCC 27977
 GGGAAAGTGAGGGGTGTC
 |||||
 CCCTTTCACTCCCCACGG
 GAM2173 COL11A2 3' GGCACCCCTCACTTTCCC 27982
 GGGAAAGTGAGGGGTGTC
 |||||
 CCCTTTCACTCCCCACGG
 GAM2173 DUSP4 5' AGAAAGGGTGGCCACTTTCCC 27665 GAG G GT
 GGGAAAGT GG T CCTTTCT
 ||||| || |||||
 CCCTTTCA CC G GGAAAGA
 _ G TG
 GAM2173 HYOU1 3' AGGGTCCCACCCCTCACCCC 30002 AAA T_
 GGG GTGAGGGGTG CCTT
 || ||||| ||
 CCC CACTCCCCAC GGGA
 _ CCT
 GAM2173 MATK 5' AGAAGCAACACCCCTCTCCCTC 8193 AAGT CC
 CC GGA GAGGGGTGT TTTCT
 || ||||| ||||
 CCCT CTCCCCACA GAAGA
 CCCT AC
 GAM2173 PAX5 3' AAAAGACCTAGCCCACTTCCC 18788 A GA G_ C
 GGGAA GT GGG T GTC TTT
 |||| || || | || |||

CCCTT CA CCC A CAG AAA
 _ A_ GTC A
 GAM2173 PROK1 3' AGAAAGGACATTCCTCCCC 26196 AAAGT ____
 GGG GAGGGG TGTCTTTCT
 ||| ||||| |||||
 CCC CTCCCC ACAGGAAAGA
 ____ CTT
 GAM2173 TCF3 3' AGGACACCCCCACCCC 35004 AAA A
 GGG GTG GGGGTGTCCT
 ||| ||| |||||
 CCC CAC CCCCACAGGA
 ____ C
 GAM2173 XT3 3' AAAGTGGCTCTGACTTTCCC 21437 G GGT _
 GGGAAAGT AGG GTC CTTT
 ||||| ||| ||| |||
 CCCTTTCA TCT CGG GAAA
 G ____ T
 GAM2173 BIRC1 3' AAAGTCAACTCCCCTCCCC 10879 AAAGT T C__
 GGG GAGGGG GT CTTT
 ||| ||||| ||| |||
 CCC CTCCCC CA GAAA
 ____ T ACT
 GAM2173 CCR5 3' AGAAAAAATCGTCTCTCCCTCC 6181 AAGT GT TCC_
 C GGA GAGGG G TTTCT
 |||| |||| | ||||
 CCCT CTCTC C AAAGA
 CC__ TG TAAA
 GAM2173 DKFZP564D166 3' AAAGAAATGTTCTCTCCC 24988 AAGT GG C_
 GGA GAGG TGT CTTT
 |||| |||| ||| ||||
 CCCT CTCC GTA GAAA
 ____ TT AA
 GAM2173 FLJ20400 3' AGAAAGGATCTCCAGCCTCCC 33043 AA GA T
 GGA GT GGGG GTCCTTTCT
 |||| || ||||| |||||
 CCCT CG CCTC TAGGAAAGA
 C_ A_ _
 GAM2173 KIAA0193 3' AGAAAGGACAGAATCTCTCCC 16537 AAGT GG_
 GGA GAGG TGTCTTTCT
 |||| |||| |||||
 CCCT CTCT ACAGGAAAGA
 ____ AAG
 GAM2173 KIAA0648 3' GAAAAATCCCCACTCTTCC 40218 A A GTCC
 GGA AGTG GGGGT TTTC
 |||| |||| |||| ||||
 CCTT TCAC CCCTA AAAG
 C _ A__
 GAM2173 KIAA0903 3' AAAGAACAAAAACACTTCCC 35366 A AGGGG C
 GGGA GTG TGT CTTT
 ||||| ||| ||| ||||

		CCCTT CAC ACA GAAA		
		_ AAAA_ A		
GAM2173 KIAA1037	3'	AAAGGATGGGTCCCACCCTCCC 17384	AA A GT_	
		GGGA GTG GGG GTCCTTT		
		CCCT CAC CCT TAGGAAA		
		CC _ GGG		
GAM2173 KIAA1786	3'	AGAAAGAATTTATTCTCCTCCC 32844	AA T GT_ C	
		GGGA G GAGGG GT CTTTCT		
		CCCT C CTCTT TA GAAAGA		
		_ _ ATT A		
GAM2173 NSE1	3'	AGAAAGGACATGGCCTTCCCC 29736	AAAGT _	
		GGG GAGGG GTGTCCTTTCT		
		CCC CTTCC TACAGGAAAGA		
		_ _ _ GG		
GAM2173 P450RAI-2	3'	GACACCCCCACCTTCCC 21269	A A	
		GGGAA GTG GGGGTGTC		
		CCCTT CAC CCCCACAG		
		C _		
GAM2173 PSKH1	3'	AGAATTTCCCCCAGTTCCC 33866	AG A TGTCTT	
		GGGAA TG GGGG TTCT		
		CCCTT AC CCCC AAGA		
		G_ C TTT_		
GAM2173 RAB40A	5'	AGGTTTCATCCCTCACCTCCC 39927	AA T_	
		GGGA GTGAGGGGTG CCT		
		CCCT CACTCCCTAC GGA		
		CC TTT		
GAM2173 RHOBTB2	3'	AGAACTTCTCCCTCACCCCC 30557	AAA TGTCC	
		GGG GTGAGGGG TTTCT		
		CCC CACTCCCT AAAGA		
		C_ CTC_		
GAM2173 SEC15B	3'	AAAGGACAACTCACTCCCCC 33123	AA GGG	
		GGG AGTGAG TGTCTTT		
		CCC TCACTC ACAGGAAA		
		CC AA_		
GAM2173 WDR7	3'	AGAAAGAGCTTACCCCTTTCCC 17607	AAGT _ TC	
		GGGA GAGGGGT G CTTTCT		
		CCCT TTCCCCA C GAAAGA		
		_ _ TT GA		
GAM2173 LOC144558	5'	AGAATGAACCCTCACCTCCC 40436	AA GTGTCCT	
		GGGA GTGAGGG TTCT		

CCCT CACTCCC AAGA
 CC AAGT___
 GAM2173 LOC153196 5' AAAGCTGCCCCACCCACTCTCC 41584 A A__ TC
 C GGA AGTG GGGGTG CTTT
 |||| ||| ||||| ||||
 CCCT TCAC CCCCCT GAAA
 C CCA C_
 GAM2173 LOC219731 5' AGAAAGGCAGCTCCCTTCACCT 44714 A T __
 TCCC GGGAA GTGAGGGG GT CCTTTCT
 |||| | ||||| || |||||
 CCCTT CACTTCCC CG GGAAAGA
 C T AC
 GAM2173 LOC91759 3' AGAAAGCCCACCTCTCCTCCC 33302 AA T TC
 GGA G GAGGGGTG CTTTCT
 ||| | ||||| |||||
 CCCT C CTCTCCAC GAAAGA
 __ __ CC
 GAM2174 B4GALT5 3' AAGAAAGCAGTCCGATGA 11166 C GT
 TCA CGGATTGT TTTCTT
 ||| ||||| |||||
 AGT GCCTGACG AAAGAA
 A __
 GAM2174 ROBO1 3' TAAGGGAACAATCCATGTGA 28586 C_ GT TT
 TCAC GGATTGT T CTTA
 |||| ||||| | ||||
 AGTG CCTAACA A GAAT
 TA __ GG
 GAM2174 ROBO1 3' TAAGGGAACAATCCATGTGA 8850 C_ GT TT
 TCAC GGATTGT T CTTA
 |||| ||||| | ||||
 AGTG CCTAACA A GAAT
 TA __ GG
 GAM2174 KIAA0172 5' ATTAAGAAAACAGGGAATG 32409 GA G
 CG TT TGTTTTCTTAAT
 || || ||||| |||||
 GT GG ACAAAGAATTA
 AA G
 GAM2174 KIAA0276 3' TATTAAGAAAACCTCC 35139 TTGT
 GGA GTTTTCTTAATA
 ||| ||||| |||||
 CCT CAAAAGAATTAT

 GAM2174 KIAA0976 3' ATTAAGAAAATGCCAGT 17163 C ATT
 AC GG GTGTTTTCTTAAT
 || || ||||| |||||
 TG CC CGTAAAAGAATTA
 A ____
 GAM2174 PRO0618 3' TATTAAGAAATTATCCAGT 15399 C TGTGT
 AC GGAT TTTCTTAATA
 || |||| | ||||| |||||

		TG CCTA AAAGAATTAT	
		A TT___	
GAM2174	LOC90092	3' ATTAAGAAAACATGGTG 30783	GGATT
		CACC GTGTTTTCTTAAT	
		GTGG TACAAAAGAATTA	

GAM2175	ATP11B	3' AATACAGTGAGTTCTGCCA 39142	A A CT
		TG CA AATTC ACTGTATT	
		AC GT TTGAG TGACATAA	
		C C _	
GAM2175	EGLN3	3' AATGAAGACAGGAATTTTGT 22616	A_ G
		ACAAAATTCCT CT TATT	
		TGTTTAAAGGA GA GTAA	
		CA A	
GAM2175	PDE4D	3' TAATACAGTCTTGTTTGTC 36433	ATTCCT
		GACAAA ACTGTATTA	
		CTGTTT TGACATAAT	
		GTTC__	
GAM2175	ROBO1	3' TAATCAGAAAAGTAATTTTGTC 28587	C A__ T
	A	TGACAAAATT CT CTG ATTA	
		ACTGTTTAA GA GAC TAAT	
		T AAA _	
GAM2175	ROBO1	3' TAATCAGAAAAGTAATTTTGTC 8851	C A__ T
	A	TGACAAAATT CT CTG ATTA	
		ACTGTTTAA GA GAC TAAT	
		T AAA _	
GAM2175	TBX22	3' AATACAGTATTTCTTTGTTAT 18870	ATTCC
		ATGACAAA TACTGTATT	
		TATTGTTT ATGACATAA	
		CTTT_	
GAM2175	TTF2	3' AATACAGTGAGACCCTGTC 9652	AAAT C
		GACA TC TACTGTATT	
		CTGT AG GTGACATAA	
		CCC_ A	
GAM2175	DCTN4	3' AGTTTAAGACTTTTGTCATG 33663	T CT__
		CATGACAAAA TC ACT	
		GTACTGTTTT AG TGA	
		C AATT	
GAM2175	FLJ00001	3' CAGCAGGACCTTGTCATG 39773	AAT A
		CATGACAA TCCT CTG	

	GTACTGTT AGGA GAC		
	CC_ C		
GAM2175 LOC131308 3'	AATACAGTGTATTTTGTTAT 37012	TCC	
	ATGACAAAAT TACTGTATT		
	TATTGTTTTA GTGACATAA		
	T__		
GAM2175 LOC257319 3'	ACTACAGGGATTTTGT CAT 45830	ACT	
	ATGACAAAATTCCT GT		
	TACTGTTTTAGGGA CA		
	CAT		
GAM2176 FLJ00007 3'	TTGACAATGAATAAAGGGCACG 35315	GGAAC	C
	CG TTATTCAT GTCAA		
	GC AATAAGTA CAGTT		
	ACGGGA A		
GAM2176 FLJ20060 5'	ACAAGGAATCAGATTCCTCGT 19148	_ T	ATC
	ACGGGGAA CT ATTC GT		
	TGCCCTT GA TAAG CA		
	A C GAA		
GAM2176 LOC91250 5'	TTGACAATGAATAAGAGTTCCT 32549	A_	C
GT	ACGGGGA CTTATTCAT GTCAA		
	TGTCCTT GAATAAGTA CAGTT		
	GA A		
GAM2177 ITPR2 3'	CCGAGAACAATTTATAACTGTG 7990	TTACAC	
TT	AACACGGTTATAA CTCGG		
	TTGTGTCAATATT GAGCC		
	TAACAA		
GAM2177 LOC151878 5'	CCGAGGTGTACCCACAGTG 39170	G	TATAAT
	CAC GT TACACCTCGG		
	GTG CA ATGTGGAGCC		
	A CCC__		
GAM2178 RBBP9 3'	TAGGTCTATAAATCACCCA 34745	A	TAAAG G
	TG GTGATTAT AGAC TG		
	AC CACTAAATA TCTG AT		
	C _ G		
GAM2178 KIAA1056 3'	CACACCTCTTTAAGCTGACTC 17046	GATTTA	AC
	GAGT TTAAAGAG GTG		
	CTCA AATTCTC CAC		
	GTCG_ CA		
GAM2178 KIAA1199 3'	CACGTCTCTCTGGCCCACTCA 35898	ATTTA	A
	TGAGTG TTA AGAGACGTG		

		ACTCAC	GGT TCTCTGCAC		
		CC__	C		
GAM2178	KIAA1458	3'	CACTTGGTTTTAATAAATTACT 34203		AGAC
		CA	TGAGTGATTTATTAAAG GTG		
			ACTCATTAATAATTTT CAC		
			GGTT		
GAM2178	LOC151234	3'	TTTCTTTATAAATCACCCA 39080 A T		
			TG GTGATTTAT AAAGAGA		
			AC CACTAAATA TTTCTTT		
			C _		
GAM2178	LOC257443	3'	CACTTGGTTTTAATAAATTACT 45872		AGAC
		CA	TGAGTGATTTATTAAAG GTG		
			ACTCATTAATAATTTT CAC		
			GGTT		
GAM2179	LOC158865	5'	ACGATTGGAATTCATC 42037		ATAA
			GATGAATTCCAAT CGT		
			CTACTTAAGGTTA GCA		
GAM2180	ZNF387	3'	GGTATAGACAACCAGCT 16178 AAC		
			AGT GTTGTTTATACC		
			TCG CAACAGATATGG		
			AC_		
GAM2180	LOC157507	5'	AAAGGAGCTCAACAGCGTTACT 39603		TATAC
		TA	TAAGTAACGTTGTT CCTTT		
			ATTCATTGCGACAA GGAAA		
			CTCGA		
GAM2181	ITGA1	3'	GACAGCGAAGAACCTCCTG 31790 _ TAG		
			CAG AGGTTCTTC TGTT		
			GTC TCCAAGAAG ACAG		
			C CG_		
GAM2181	PDK4	3'	AACACTAGAAAAAAGAAATGT 46440 GAGG_ C		
			ACA TT TTCTAGTGTT		
			TGT AA AAGATCACAA		
			AAAGA A		
GAM2181	PODXL	3'	GAACACTAGAAGCTC 11875 GTT		
			GAG CTTCTAGTGTT		
			CTC GAAGATCACAA		
GAM2181	DUSP10	5'	GAACCATGAAAACCTCTGTGA 29556 C TAGT		
			TCACAGAGGTT TTC GTTC		

		AGTGTCTCCAA AAG CAAG		
		_ TAC_		
GAM2181	FLJ10342	5' GAGGCGGAAGAACCCCCCTG 19836	A__	A G
		CAG GGTTCCTTCT GT TT		
		GTC CCAAGAAGG CG AG		
		CCC _ G		
GAM2181	FLJ11267	3' GAACACTAGCATACCTGCATGA 21224	CAG	TCTT
		TCA AGGT CTAGTGTT		
		AGT TCCA GATCACAAG		
		ACG TAC_		
GAM2181	FLJ13340	3' GAACACTAGTCCTACCTCTG 27706	TCTT	
		CAGAGGT CTAGTGTT		
		GTCTCCA GATCACAAG		
		TCCT		
GAM2181	FLJ21777	5' GAGGCAGAAGAACCCCTTGA 25923	C A	A G
		TCA AG GGTTCCTTCT GT TT		
		AGT TC CCAAGAAGA CG AG		
		_ C _ G		
GAM2181	FLJ23153	3' AACACTAGAAAAAGCATTG 23907	AG C_	
		CAG GTT TTCTAGTGTT		
		GTT CGA AAGATCACAA		
		A_ AA		
GAM2181	FLJ31978	3' GAACACTAGAAAGCGCTGTGA 29488	AG C	
		TCACAG GTT TTCTAGTGTT		
		AGTGTC CGA AAGATCACAAAG		
		G_ _		
GAM2181	HSPCAL3	3' AACAAATGTTTGAGAACCTCTG 37615	CTAG__	
		CAGAGGTTCTT TGTT		
		GTCTCCAAGAG ACAA		
		TTTGTA		
GAM2181	KIAA0276	3' AACTGCTAAATACCTCTGT 35133	TCTTC _	
		ACAGAGGT TAGT GTT		
		TGTCTCCA ATCG CAA		
		TAAA_ T		
GAM2181	TBDN100	3' GAACACTAGTCCTACCTCTG 24697	TCTT	
		CAGAGGT CTAGTGTT		
		GTCTCCA GATCACAAG		
		TCCT		
GAM2181	THEA	3' AACACTTGAAGCTCTGTGA 32944	G TCT	
		TCACAGAG TTCT AGTGTT		

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AGTGTCTC AAGG TCACAA
      G T__
GAM2181 TUSP 5' AACACTGGGACCACTGT 21519 A TCT
      ACAG GGTTCT AGTGTT
      ||| ||||| |||||
      TGTCCAGGG TCACAA
      A ____
GAM2181 UBCE7IP5 3' ACTAGAAGAACCTCAGTGA 17269 A
      TCAC GAGGTTCTTCTAGT
      ||| ||||| |||||
      AGTG CTCCAAGAAGATCA
      A ____
GAM2181 LOC143196 3' AACACTCCTAACCTCTGT 40329 CTTCT
      ACAGAGGTT AGTGTT
      ||||| |||||
      TGTCTCCAA TCACAA
      TCC__
GAM2181 LOC147837 3' AGCAGAAAACTCTGTGA 38391 GTTC AGT
      TCACAGAG TTCT GTT
      ||||| ||| |||
      AGTGTCTC AAGA CGA
      AAA_ ____
GAM2181 LOC149111 3' AACACTAGACCTCTCCTGA 38646 C_ TTCT
      TCA AGAGG TCTAGTGTT
      || ||||| |||||
      AGT TCTCC AGATCACAA
      CC ____
GAM2181 LOC149420 3' AACACACTGGAACCTCATG 38746 _ TCTA
      CA GAGGTTCT GTGTT
      || ||||| |||||
      GTCTCCAAGG CACAA
      A TCA_
GAM2181 LOC151414 3' GAACACTAATAGCCCCCTGGA 39110 A A TT TC
      TC CAG GG CT TAGTGTT
      || ||| || |||||
      AG GTC CC GA ATCACAAG
      _ C CC TA
GAM2181 LOC87769 5' AACACCAGAAGGTGTGG 35335 GAGGT A
      TCACA TCTTCT GTGTT
      ||||| ||||| |||||
      GGTGT GGAAGA CACAA
      ____ C
GAM2182 KLHL1 3' TCAAAGCTGCATATCTCA 21920 CC ACCAT
      TGAGATA CA GTTTTGA
      ||||| || |||||
      ACTCTAT GT CGAAACT
      AC ____
GAM2182 BIRC1 3' CAAAACATGTTGAACATCCA 10882 A ACC C
      TG GAT CAAC ATGTTTTG
      || ||| ||||| |||||

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		AC CTA GTTG TACAAAAC	
		_ CAA _	
GAM2182	C20orf103	3' ATCAAACAGGCCTGGGTATCT 14569	A_ A T
		AGATACCCA CC TGTTT GAT	
		TCTATGGGT GG ACAA CTA	
		CC _ _	
GAM2182	KIAA1404	3' AGACATTTAGGTATCTCA 31048	C CC
		TGAGATACC AA ATGTTT	
		ACTCTATGG TT TACAGA	
		A _	
GAM2182	STK38L	3' ATCAAATTCTTTGGGTATCTC 34287	CCATGT
		GAGATACCCAA TTTGAT	
		CTCTATGGGTT AAATA	
		TCTT_	
GAM2183	ADAM12	3' TAAAACATCATTACTATAA 9545	
		TTATAGTGATGATGTTTTG	
		AATATCATTACTACAAAAT	
GAM2183	CALD1	3' AAAATCATCATCACTATAA 26990	_
		TTATAGTGATGATG TTTT	
		AATATCACTACTAC AAAA	
		T	
GAM2183	CALD1	3' AAAATCATCATCACTATAA 27008	_
		TTATAGTGATGATG TTTT	
		AATATCACTACTAC AAAA	
		T	
GAM2183	KIAA0265	3' TAAAACATCATCAACATAA 34627	AG
		TTAT TGATGATGTTTTG	
		AATA ACTACTACAAAAT	
		CA	
GAM2184	ANGPT1	3' ACACTGTTCCAGTGTCTAT 6813	AAC T_
		ATAGACAC GAAT TGT	
		TATCTGTG CTTG ACA	
		AC_ TC	
GAM2184	FLJ10970	3' TTCGCATATGTCTATGAAA 20279	CAA_
		TTTCATAGACA CGAA	
		AAAGTATCTGT GCTT	
		ATAC	
GAM2184	KIAA0976	3' TTCGTTGTGCCTTTGAAA 17168	T A
		TTTCA AG CACAACGAA	

		AAAGT TC GTGTTGCTT		
		T C		
GAM2184	LOC118491 5'	TTGGTTGTACTATGAAA 36595	AC	G
		TTTCATAG ACAAC AA		
		AAAGTATC TGTTG TT		
		A_ G		
GAM2185	ESRRG 3'	TGATAATTTAGCAGCAA 32999	CCACA	
		TTGCTGCTAAA TGTCA		
		AACGACGATTT ATAGT		
		A_____		
GAM2185	ITGAL 3'	GATTGACGTACTTAGCAGC 7972	ACCAC	
		GCTGCTAA ATGTCAATC		
		CGACGATT TGCAGTTAG		
		CA_____		
GAM2185	NUFIP1 3'	ATTGAAGATAGGTTTTCAGTA 14737	ACATG	
	A	TTGCTGCTAAACC TCAAT		
		AATGACGATTTGG AGTTA		
		ATAGA		
GAM2185	POU2AF1 3'	GATTTACAGTCCAGGCAGCAA 12892	AAACC A C	
		TTGCTGCT AC TGT AATC		
		AACGACGG TG ACA TTAG		
		ACC_ _ T		
GAM2185	RAG2 5'	ATTAATACCTGGTTTAGCGGCA 39985	CA C	
	A	TTGCTGCTAAACCA TGT AAT		
		AACGGCGATTTGGT ATA TTA		
		CC A		
GAM2185	TNS 3'	GGCATGTGGCTCAGCAGCAA 22903	AAA	
		TTGCTGCT CCACATGTC		
		AACGACGA GGTGTACGG		
		CTC		
GAM2185	DKFZP434I092 3'	ATTGACATTCCAGTAGAGCAA 33673	G AACCAC	
		TTGCT CTA ATGTCAAT		
		AACGA GAT TACAGTTA		
		_ GACCT_		
GAM2185	FLJ10656 3'	ATTAACATGGTAAGCCTTAGCA 19988	ACCA_ C	
	GCAA	TTGCTGCTAA CATGT AAT		
		AACGACGATT GTACA TTA		
		CCGAATG A		
GAM2185	GABARAPL1 3'	TGGCAGTCCAGCAGCAA 25392	AA CACA	
		TTGCTGCT AC TGTCA		

		AACGACGA TG ACGGT	
		CC ____	
GAM2185	GABARAPL3 3'	TGGCAGTCCAGCAGCAA 26300	AA CACA
		TTGCTGCT AC TGTC	
		AACGACGA TG ACGGT	
		CC ____	
GAM2185	HT002 3'	GACGGTGATGACCCAGCAGCAA 15281	AAAC____ A
		TTGCTGCT CAC TGTC	
		AACGACGA GTG GCAG	
		CCCAGTA _	
GAM2185	KIAA0475 3'	GATTGGAAGTGGCCAGCAGCAA 16949	AAA ATG
		TTGCTGCT CCAC TCAATC	
		AACGACGA GGTG GGTTAG	
		CC_ AA_	
GAM2185	KIAA0712 5'	ATGCAGTTTCAGCAGCAA 16262	_ CA
		TTGCTGCT AAAC CAT	
		AACGACGA TTTG GTA	
		C AC	
GAM2185	KIAA1301 3'	GATTGACATATGGTTTGCCAG 32978	C C
		CTG TAAACCA ATGTCAATC	
		GAC GTTTGGT TACAGTTAG	
		C A	
GAM2185	SEZ6 3'	GACTTGCACCACAGTCCAGCAG 36774	AA CA_____ T
	CAA	TTGCTGCT AC CA GTC	
		AACGACGA TG GT CAG	
		CC ACACCAC T	
GAM2185	VMP1 3'	ATGTGATGTTTCAGCAGCAA 25204	A ____
		TTGCTGCT AAC CACAT	
		AACGACGA TTG GTGTA	
		C TA	
GAM2185	LOC115110 3'	ACGTGAGTCAGCAGCAA 35503	AA CA
		TTGCTGCT AC CATGT	
		AACGACGA TG GTGCA	
		C_ A_	
GAM2185	LOC132235 5'	TGACACGGGAGCTAGCAGCA 37483	AA_ ACA
		TGCTGCTA CC TGTC	
		ACGACGAT GG ACAGT	
		CGA GC_	
GAM2185	LOC142941 3'	CATGTGGTTTGCAGCAA 40322	T
		TTGCTGC AAACCACATG	

AACGACG TTTGGTGTAC

GAM2185 LOC158549 5' GACGTGTTTAAACAGCAA 42007 C CC
TTGCTG TAAA ACATGTC
||||| ||| |||||
AACGAC ATTT TGTGCAG

A _
GAM2185 LOC221882 5' GATTGGTATGGTAATTTAAAGC 44434 GC CCA_ GT
AA TTGCT TAAA CAT CAATC
||||| ||| ||| |||||
AACGA ATTT GTA GTTAG

A_ AATG TG
GAM2186 GPM6A 3' GTGCTTCTCATCAATGATATGT 11778 C _
AA TTGCATATCA TGATG GGTAC
||||||| ||||| |||||
AATGTATAGT ACTAC TCGTG
A TCT

GAM2186 MS4A1 3' GTCCACAGTGATAAGCAA 5633 A A
TTGC TATCACTG TGGGT
||| ||||| |||||
AACG ATAGTGAC ACCTG
A _

GAM2186 NR3C1 3' AGGTACCAGCAATATGTAA 5684 CAC ATG
TTGCATAT TG GGTACCT
||||||| || |||||
AATGTATA AC CCATGGA
_ GA_

GAM2186 SMCX 3' GAGACAAGGCCAGTGTATATGC 10396 _ ATGG_ AC
AA TTGCATAT CACTG GT CTC
||||||| ||||| || |||
AACGTATA GTGAC CA GAG
T CGGAA _

GAM2186 CAPS2 3' TATTAAAGGATATGCAA 34954 A GATG
TTGCATATC CT GGTA
||||||| || |||||
AACGTATAG GA TTAT
_ AA_

GAM2186 DKFZP434I092 3' AGGATGGAATCAAACAATATGC 33672 CAC_ GGGTA
AA TTGCATAT TGAT CCT
||||||| ||||| |||
AACGTATA ACTA GGA
ACAA AGGTA

GAM2186 ICK 3' AGGTCACCATCAGTGAACGCAA 17192 ATA GT
TTGC TCACTGATGG ACCT
||| ||||| ||||| |||||
AACG AGTGACTACC TGGA
CA_ AC

GAM2186 KIAA0746 5' TCGACATCAGTGATACCCAA 34417 CA _
TTG TATCACTGATG GG
||| ||||| ||||| ||

AAC ATAGTGACTAC CT
 CC AGIII
 GAM2186 MMD 3' AGGTACCCAGTGATA 30075 GAT
 TATCACT GGGTACCT
 ||||| |||||
 ATAGTGA CCCATGGA

 GAM2186 VIT1 5' GGTACCTCAAAGCAACAGTGTA 20767 _ A _ TACC
 TATGCAA TAT CACTG TG GG TC
 || ||||| || || ||
 ATA GTGAC AC CT GG
 T A GAA||| CCAT
 GAM2186 LOC150311 5' ACCCCAAGGATATGCAA 38925 A GAT
 TTGCATATC CT GGGT
 ||||| || |||
 AACGTATAG GA CCCA
 _ AC_
 GAM2187 GJA1 3' GATATAGCAGTAATGCTATTA 5677 C _ TT
 TAATAGCA TTAC GTT TATC
 ||||| ||| || |||
 ATTATCGT AATG CGA ATAG
 _ A T_
 GAM2187 PCDH11X 3' AAATGGTTAGTGCTATTG 26783 TA_
 TAATAGCACT CGTTT
 ||||| |||
 GTTATCGTGA GTAAA
 TTG
 GAM2187 PCDH11X 3' AAATGGTTAGTGCTATTG 26798 TA_
 TAATAGCACT CGTTT
 ||||| |||
 GTTATCGTGA GTAAA
 TTG
 GAM2187 PCDH11Y 3' AAATGGTTAGTGCTATTG 26817 TA_
 TAATAGCACT CGTTT
 ||||| |||
 GTTATCGTGA GTAAA
 TTG
 GAM2187 FLJ20184 3' GATAAAAACCCCTTGCTATT 19273 CTTAC
 AATAGCA GTTTTTATC
 ||||| |||||
 TTATCGT CAAAATAG
 TCCC_
 GAM2187 STX3A 3' ATAAAAATGGAAGCTATTA 10386 ACTTA
 TAATAGC CGTTTTTAT
 ||||| |||||
 ATTATCG GTAAAAATA
 AAG_
 GAM2187 ZNF313 3' GATGGGGCTGCAAGTGCTA 20754 A T
 TAGCACTT CG TTTTATC
 ||||| || |||||

			ATCGTGAA GT GGGGTAG		
			C C		
GAM2187	LOC130026	3'	GATAAAAACGTAGCTA 28819	ACT	
			TAGC TACGTTTTTATC		
			ATCG ATGCAAAAATAG		
			—		
GAM2187	LOC144438	3'	GATAGGAGGTAAGTGACCATTA 37737	AG_ G	
			TAAT CACTTAC TTTTATC		
			ATTA GTGAATG GAGGATAG		
			CCA _		
GAM2187	LOC149722	5'	GATAAATTGTAAGTGCTA 41042	TT	
			TAGCACTTACG TTTATC		
			ATCGTGAATGT AAATAG		
			T_		
GAM2187	LOC220988	3'	ATAAAAATCATGTGTTATTA 43681	TTAC	
			TAATAGCAC GTTTTAT		
			ATTATTGTG TAAAAATA		
			TAC_		
GAM2188	CALCRL	3'	TAAACAAATTAGCAATCATT 12377	CCT C	
			AATG TTGCTAAT TGTTTA		
			TTAC AACGATTA ACAAAT		
			T_ A		
GAM2188	DSC1	3'	TAAATACTTTAGCAAAAACATT 11389	CC TC	
			AATG TTTGCTAA TGTTTA		
			TTAC AAACGATT ATAAAT		
			AA TC		
GAM2188	DSC1	3'	TAAATACTTTAGCAAAAACATT 23659	CC TC	
			AATG TTTGCTAA TGTTTA		
			TTAC AAACGATT ATAAAT		
			AA TC		
GAM2188	FZD10	3'	AAACAGATCAGGAAGCA 14048	CT G A	
			TGC TT CT ATCTGTTT		
			ACG AA GA TAGACAAA		
			_ G C		
GAM2188	RUNX3	3'	TAGGTCCTAGCAGAAGGCATTG 10551	_ _	
	A		TCAATGCCT TTGCTA ATCTG		
			AGTTACGGA GACGAT TGGAT		
			A CC		
GAM2188	KIAA0731	5'	TAAACAGCGCAAAGGCA 33242	TAAT	
			TGCCTTTGC CTGTTTA		

ACGGAAACG GACAAAT
 C____
 GAM2188 KLF5 3' AAATCAGTTGGCAGGCA 7459 TT T _
 TGCCT GCTAA CTG TTT
 |||| |||| ||||
 ACGGA CGGTT GAC AAA
 _ _ T
 GAM2188 LOC149773 5' AAAAGGAAAAACAAAGGCATT 38799 CTAA G
 AATGCCTTTG TCT TTT
 ||||| ||||
 TTACGGAAAC AGG AAA
 AAA_ A
 GAM2188 LOC153387 5' TAAACAGATTTTTTAAAAACATT 41634 CC CT
 GA TCAATG TTTG AATCTGTTTA
 |||| ||| |||||
 AGTTAC AAAT TTAGACAAAT
 AA TT
 GAM2188 LOC51157 5' AAACAGATTTAGGGATTGA 18296 G TTGCT
 TCAAT CCT AATCTGTTT
 |||| ||| |||||
 AGTTA GGA TTAGACAAA
 G T____
 GAM2189 F3 3' ATTGTTCTATTTGTATATAT 33298 T_
 ATATGTACAAATAG CGAT
 ||||| ||||
 TATATATGTTTATC GTTA
 TT
 GAM2189 C1orf24 3' ATATAATCAAAGAATTTTCTGT 27528 AATAG_ ____
 ACATAT TATGTACA TC GATTATAT
 ||||| || |||||
 ATACATGT AG CTAATATA
 CTTTTA AAA
 GAM2189 EPN2 3' ATATAATTTATCATTTGTAC 17345 A C
 GTACAAAT GT GATTATAT
 ||||| || |||||
 CATGTTTA TA TTAATATA
 C T
 GAM2189 STAF65(gamma) 3' ATCAGACTATCTGTATATAT 16922 A _
 ATATGTACA ATAGTC GAT
 ||||| ||||| |||
 TATATATGT TATCAG CTA
 C A
 GAM2190 RRM2 3' CTAATGGGAGCCAATTCA 6699 CTA
 TGAA GTTCCTGTTAG
 ||| |||||
 ACTT CGAGGGTAATC
 AAC
 GAM2190 KIAA1762 3' CTCACAGGAACTGTTCA 31910 T T
 TGAAC AGTTCCTGT AG
 |||| ||||| ||

			ACTTG TCAAGGACA TC		
			— C		
GAM2190	LOC157623	5'	CTAATACAAACAGGAACT 39614	AGC	
			AGTTCCTGTT ATTAG		
			TCAAGGACAA TAATC		
			ACA		
GAM2190	LOC91759	5'	AATGCTAATGAACAGCTCA 33299	A A CT	
			TGA CT GTTC GTTAGCATT		
			ACT GA CAAG TAATCGTAA		
			C _ _		
GAM2191	EFG1	3'	TGTCTATCTCAACTCTATT 45397	ATC TC	
			AATAGAGTT GAT AGACA		
			TTATCTCAA CTA TCTGT		
			CT_ _		
GAM2191	SLC6A3	3'	TGTCTGTTGACCAATCTCTATT 6713	TTA_ TT	
	CA		TGAATAGAG TCGA CAGACA		
			ACTTATCTC AGTT GTCTGT		
			TAACC _		
GAM2191	H2AV	3'	TGCCTGACAATTAGCTCTATT 28912	TCGAT A	
	A		TGAATAGAGTTA TCAG CA		
			ACTTATCTCGAT AGTC GT		
			TAAC_ C		
GAM2191	HMP19	3'	GTCTGAACCGATATTTCT 42273	T A	
			AGAG TATCG TTCAGAC		
			TCTT ATAGC AAGTCTG		
			T C		
GAM2192	BACH1	3'	AAGTTGTAATGCAGATGGA 6855	A TC	
			TC CATCT CGTTACAACTT		
			AG GTAGA GTAATGTTGAA		
			_ C_		
GAM2192	ESR1	3'	AAGTTAAAATGTAAAAGATGTG 5597	C_ AC	
	AT		ATCACATCTT CGTT AACTT		
			TAGTGTAGAA GTAA TTGAA		
			AAT AA		
GAM2192	IDI2	3'	AAGCAGTACGGAAGATG 27089	T AA	
			CATCTTCCGT AC CTT		
			GTAGAAGGCA TG GAA		
			_ AC		
GAM2192	KIAA1979	3'	AATGTGAAGAATGTGATA 42587	_ _	
			TATCACAT CTTC CGTT		

			ATAGTGTA GAAG GTAA		
			A T		
GAM2192	LBP-9	3'	TAAGTTCCAAAAGAAGATGTAA 15880	C	CG AC
	TA		TAT ACATCTTC TT AACTTA		
			ATA TGTAGAAG AA TTGAAT		
			A AA CC		
GAM2192	LHFPL2	3'	AAGTTTGTGTGAAAGATGTG 34656	CCGT	_
			CACATCTT TACAA CTT		
			GTGTAGAA GTGTT GAA		
			AGT_ T		
GAM2192	SDCCAG43	3'	AAGTTGCAGAGATGTGA 34844	CCGTTA	
			TCACATCTT CAACTT		
			AGTGTAGAG GTTGAA		
			AC____		
GAM2192	TRAD	3'	TAAGTTGTAAGTGAAGATTGCAA 13928	CA TC C	
	TA		TAT CA TTC GTTACAACCTTA		
			ATA GT GAG CAATGTTGAAT		
			AC TA T		
GAM2192	LOC135293	3'	GTTGTAACAGAAGAGTGA 37495	A C	
			TCAC TCTTC GTTACAAC		
			AGTG AGAAG CAATGTTG		
			_ A		
GAM2193	NCOA3	3'	TCCGAAAACCTTCCATTG 13286	GATA	
			TAATGGAAGTTTT GGA		
			GTTACCTTCAAAA CCT		
			G____		
GAM2193	PAH	3'	ATCCCCATAACTTCCA 5823	T ATA A	
			TGGAAGTT TG GG GAT		
			ACCTTCAA AC CC CTA		
			T ____ _		
GAM2193	SIAT9	3'	TCAGAACAAAACCTTCTATTA 9977	ATAG	
			TAATGGAAGTTTTG GA		
			ATTATCTTCAAAAC CT		
			AAGA		
GAM2193	LOC51075	3'	ATCCCCTGGACTTTCA 18068	TTGA A	
			TGGAAGTT TAGG GAT		
			ACTTTCAG GTCC CTA		
			____ C		
GAM2194	ADAM12	3'	TACATAATTCACCTCTGAGTGTT 9546	_ GT_ A	
	TTA		TAAAA ACTT GTGAA TTATGTA		

		ATTTT TGAG CACTT AATACAT	
		G TCT _	
GAM2194	ADD3	3' ACATAATTTTTTAAAAAGTTTT 18817	GTGT_
		AAAACCTT GAAATTATGT	
		TTTTGAA TTTTAATACA	
		AAATT	
GAM2194	C9orf12	3' ACATATCAACACAGGTTTTTA 22989	GAAAT
		TAAAAACTTGTGT TATGT	
		ATTTTTGGACACA ATACA	
		ACT__	
GAM2194	KIAA1813	5' ACATGATGTTTTTCACACACATT 34807	CT ____
	TT	AAAA TGTGTGAA ATTATGT	
		TTTT ACACACTT TAGTACA	
		AC TTG	
GAM2194	OAZIN	3' TACATACAAGAACACAGTTTTT 18023	T GAAAT
	A	TAAAAACT GTGT TATGTA	
		ATTTTTGA CACA ATACAT	
		_ AGAAC	
GAM2194	OSMR	3' ACATAATTCCAGTCACAGTTTT 10149	T _ A
	TG	TAAAAACT GTG TG AATTATGT	
		GTTTTTGA CAC AC TTAATACA	
		_ TG C	
GAM2194	TSPAN-2	3' TACATGTGAAAACACAAGTCTT 12281	A GAAAT
	TG	TAAA ACTTGTGT TATGTA	
		GTTT TGAACACA GTACAT	
		C AAAGT	
GAM2195	LOC256846	5' AACTTGAAGATCTCACAGACCT 45695	TA_ A_
	AA	TTAGGTCTGT ATT TAAGTT	
		AATCCAGACA TAG GTTCAA	
		CTC AA	
GAM2196	TRIM34	3' ATATTTTCAGAGAAAGTTACCT 22248	A
	AA	TTGGGTAACCTTTTTTT AAAATAT	
		AATCCATTGAAAGAGA TTTTATA	
		C	
GAM2196	TRIM34	3' ATATTTTCAGAGAAAGTTACCT 28172	A
	AA	TTGGGTAACCTTTTTTT AAAATAT	
		AATCCATTGAAAGAGA TTTTATA	
		C	
GAM2196	LOC197287	3' ATTTCTTTAGGAAGTTACCCA 30521	TTAA
		TGGGTAACCTTTTT AAAT	

ACCCATTGAAGGA TTTA
 TTTC
 GAM2197 CARD4 3' TTTTCATTGAAGAGTTGA 12742 CTTC C
 TCAACTC TTCAAT AAAA
 ||||| ||||| |||||
 AGTTGAG AAGTTA TTTT
 _____ C
 GAM2197 CXCR6 3' TTGATTGGGACTGGGGCTGA 13334 A T_ T
 TCA CTCC TCT CAATCAA
 ||| ||||| ||| |||||
 AGT GGGG AGG GTTAGTT
 C TC _
 GAM2197 PRPSAP1 3' CTTATTGATACTAAAGAGGAGT 8659 TC CA_ A
 T AACTCCT TT ATCAA AAG
 ||||| || ||||| |||
 TTGAGGA AA TAGTT TTC
 GA TCA A
 GAM2197 SHANK2 3' CTTTTTAATTGAAGATGTCTTG 14683 CTCCT C
 A TCAA TCTTCAAT AAAAAG
 ||||| ||||| |||||
 AGTT AGAAGTTA TTTTTC
 CTGT_ A
 GAM2197 SMURF1 3' TTTGAAAGGAGAAGGAATTGG 44417 C AA
 TCAA TCCTTCTTC TCAAA
 ||||| ||||| |||||
 GGTT AGGAAGAGG AGTTT
 A AA
 GAM2197 TEM6 3' CTTTTTGGGTAGAAGAAG 22962 AA_
 CTTCTTC TCAAAAAG
 ||||| |||||
 GAAGAAG GGTTTTTC
 ATG
 GAM2197 C1orf9 3' CTTTTTGAAAGGGAGAGAATTG 18340 C _ CAA
 A TCAA TC CTTCTT TCAAAAAG
 ||||| || ||||| |||||
 AGTT AG GAGGGA AGTTTTTC
 A A A_
 GAM2197 C20orf4 3' TGAATGAGAAGGAATTGA 17773 C T A
 TCAA TCCTTCT CA TCA
 ||||| ||||| || |||
 AGTT AGGAAGA GT AGT
 A _ A
 GAM2197 DIO2 3' TGCATTGAGAAGGAAGTGA 6463 AC T _
 TCA TCCTTCT CAAT CA
 ||| ||||| ||||| |||
 AGT AGGAAGA GTTA GT
 CA _ C
 GAM2197 DIO2 3' TGCATTGAGAAGGAAGTGA 15174 AC T _
 TCA TCCTTCT CAAT CA
 ||| ||||| ||||| |||

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AGT AGGAAGA GTTA GT
CA _ C
GAM2197 FLJ20548 3' TTTTGTATCTGGGAGATGA 19546 A TCTTCA
TCA CTCCT ATCAAAAA
||| ||||| |||||
AGT GAGGG TAGTTTTT
A TC____
GAM2197 HSH2 3' TGTTTTGAAGAAGAGACTGA 26655 AC _ T_
TCA TC CTTCTTCAA CA
||| || ||||| |||
AGT AG GAAGAAGTT GT
C_ A TT
GAM2197 KIAA0322 3' CTTCTTGATTGAGGTAGCATGA 44561 ACTC T A
TCA CT CTTCAATCAA AAG
||| || ||||| |||
AGT GA GGAGTTAGTT TTC
AC_ T C
GAM2197 KIAA0700 3' TGACAAGGAAGGAGTTGA 35661 CAA
TCAACTCCTTCTT TCA
||||||| |||
AGTTGAGGAAGGA AGT
AC_
GAM2197 KIAA1045 3' CTTTTTGTTGAGAAAGGA 35197 CT
TCCTT TCAATCAAAAAG
||||| |||||
AGGAA AGTTGGTTTTTC
AG
GAM2197 KIAA1163 3' CTTTTTAATTGGAGAATTGA 38558 CTCC C
TCAA TTCTTCAAT AAAAAG
||||| ||||| |||||
AGTT AAGAGGTTA TTTTTC
_____ A
GAM2197 KIAA1673 3' TTTTGTTTTGAAGAGTTGA 35028 CTTC T_
TCAACTC TTCAA CAAAA
||||| ||||| |||||
AGTTGAG AAGTT GTTTT
_____ TT
GAM2197 MGC4172 3' TTTGACATGGGAAAGGAGTTG 23602 CT A_
CAACTCCTT TCA TCAAA
||||||| ||| |||||
GTTGAGGAA GGT AGTTT
AG AC
GAM2197 LOC132332 3' TTGATGAAGAAGAAGATGA 37489 A C A
TCA CT CTTCTTCA TCAA
||| || ||||| |||
AGT GA GAAGAAGT AGTT
A A _
GAM2197 LOC138654 5' CTTTTTGAAATTCGAGGAGCTG 37398 A CTTCAA
A TCA CTCCTT TCAAAAAG
||| ||||| |||||

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			AGT GAGGAG	AGTTTTTC		
			C	CTTAA_		
GAM2197	LOC149670	3'	TTGGAAGAGGAAGAGAAGTTGA	38807	__	AA
			TCAACT C CTTCTTC	TCAA		
			AGTTGA G	GAAGGAG GGT		
			A A	AA		
GAM2197	LOC157695	5'	GATTAAAAGAAGAGTTGA	41831	C	C_
			TCAACTC TTCTT	AATC		
			AGTTGAG AAGAA	TTAG		
			_	AA		
GAM2198	COL4A5	3'	ATAAAGGTGTTAAGCTTA	6108	C	C
			TAA CTTAACACCT	TAT		
			ATT GAATTGTGGA	ATA		
			C	A		
GAM2198	COL4A5	3'	ATAAAGGTGTTAAGCTTA	27211	C	C
			TAA CTTAACACCT	TAT		
			ATT GAATTGTGGA	ATA		
			C	A		
GAM2198	COL4A5	3'	ATAAAGGTGTTAAGCTTA	27214	C	C
			TAA CTTAACACCT	TAT		
			ATT GAATTGTGGA	ATA		
			C	A		
GAM2198	USP9Y	5'	CTATTAATAGAATGAGG	32016	ACACC	
			CCTTA	TCTATTAATAG		
			GGAGT	AGATAATTATC		
			A	_____		
GAM2198	MGC10646	3'	AGTGGGAAAAGGTGTTAAG	26413	_____	
			CTTAACACCT	CTATT		
			GAATTGTGGA	GGTGA		
			AAAG			
GAM2199	LOC219672	5'	ATATACTAGGCATAATATCA	43888	C	T
			TGATA TATGCTTA	TATAT		
			ACTAT ATACGGAT	ATATA		
			A	C		
GAM2200	ENDOFIN	3'	TGTAGTCCTGTCATTAA	16368	A_	
			TTAAATGACG	ACTATA		
			AATTTACTGT	TGATGT		
			CC			
GAM2200	FLJ10498	3'	ATATTTAGTTCATCATTGA	19886	C	T
			TTAAATGA GAACTA	ATGT		

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AGTTTACT CTTGAT TATA
      A   T
GAM2200 KIAA0534 3' CAAATAGTTCGTATTTAA 35381      A   A
      TTAAATG CGAACTAT TG
      ||||| ||||| ||
      AATTTAT GCTTGATA AC
            A
GAM2201 AMACR 3' GGAACAGTATTACAGTGTCTTA 34016      _ ACA CA
      TAGGACAC GTA GTAT TTCC
      ||||| || ||| |||
      ATCCTGTG CAT TATG AAGG
            A ____ AC
GAM2201 ATP6V1G2 3' AATGATACTGTGTTCC 28222      C GTA
      GGA AC ACAGTATCATT
      ||| || |||||
      CCT TG TGTCATAGTAA
            _ ____
GAM2201 ATP6V1G2 3' AATGATACTGTGTTCC 28696      C GTA
      GGA AC ACAGTATCATT
      ||| || |||||
      CCT TG TGTCATAGTAA
            _ ____
GAM2201 DKFZP434P211 3' GAATGTTCTCAGTGTCTTA 15867      GTAAC TAT
      TAGGACAC AG CATT
      ||||| || |||
      ATCCTGTG TC GTAAG
            AC ____ TT ____
GAM2201 FLJ00007 3' GAATAACACTGTTGCTTCCTG 35309      CAC ATC
      TAGGA GTAACAGT ATTC
      |||| ||||| |||
      GTCCT CGTTGTCA TAAG
            T ____ CAA
GAM2201 FLJ13105 3' AATGATACTTTCAATGTGCC 24570      A AAC ____
      GG CACGT AGTATCATT
      || |||| |||||
      CC GTGTA TCATAGTAA
            _ ACTT
GAM2201 PTPRR 3' GGAATGATATAATCTGTCC 28381      C AACA
      GGACA GT GTATCATTCC
      |||| || |||||
      CCTGT TA TATAGTAAGG
            C A ____
GAM2201 PTPRR 3' GGAATGATATAATCTGTCC 8742      C AACA
      GGACA GT GTATCATTCC
      |||| || |||||
      CCTGT TA TATAGTAAGG
            C A ____
GAM2201 LOC150174 3' GAATGTTCTCAGTGTCTTA 38873      GTAAC TAT
      TAGGACAC AG CATT
      ||||| || |||

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		ATCCTGTG TC GTAAG	
		AC__ TT_	
GAM2201	LOC150213 3'	GAATGTTCTCAGTGCCTA 36958	GTAAC TAT
		TAGGACAC AG CATT	
		ATCCTGTG TC GTAAG	
		AC__ TT_	
GAM2201	LOC151742 3'	AATGATACTGAATGAGTC 29240	A AA
		GAC CGT CAGTATCATT	
		CTG GTA GTCATAGTAA	
		A A_	
GAM2202	ACTN2 3'	ATATAACACGGCTAAAATG 6754	C G
		TATTTTAGCT TG TATAT	
		GTAAAATCGG AC ATATA	
		C A	
GAM2202	SYT1 3'	ATATTTACAAAGCTAAAATA 12168	C GT_
		TATTTTAGCT TG ATAT	
		ATAAAATCGA AC TATA	
		A ATT	
GAM2202	FLJ22173 5'	ATATAATCCAGAGCTAAGA 24635	_
		TTTAGCTCTGG TATAT	
		AGAATCGAGACC ATATA	
		TA	
GAM2202	SH3BGRL2 3'	ATATAATATATATGCTAAAGTA 25524	TCTG C
		TATTTTAGC GTATAT ATAT	
		ATGAAATCG TATATA TATA	
		TA__ A	
GAM2202	LOC146823 3'	ATATGATACACCAGAGCTG 40745	A
		TAGCTCTGGT TATCATAT	
		GTCGAGACCA ATAGTATA	
		C	
GAM2202	LOC255231 3'	ATATGATATATTTTCTCTAAA 45671	CTCT
		TTTAG GGTATATCATAT	
		AAATC TTATATAGTATA	
		TCTT	
GAM2203	ESPN 3'	AGAAACATGAAAACCTGCCT 25548	A CTGG
		AG GTA TTTCATGTTTCT	
		TC CGT AAAGTACAAAGA	
		_ CA_	
GAM2203	GRLF1 3'	AGAAACGTTCCCAAACCTC 38407	AC TTTC
		GAGT TGG ATGTTTCT	

			CTCA ACC TGCAAAGA			
			A_ CT__			
GAM2203	ITGA2	3'	AGAAACATGAAATGCTT	7962	ACTG	
			GAGT GTTTCATGTTTCT			
			TTCG TAAAGTACAAAGA			
GAM2203	WT1	3'	AGAACTAACCAGTACCTC	23671	A	TCATGT
			GAG GTACTGGTT TTCT			
			CTC CATGACCAA AAGA			
			TC__			
GAM2203	WT1	3'	AGAACTAACCAGTACCTC	23675	A	TCATGT
			GAG GTACTGGTT TTCT			
			CTC CATGACCAA AAGA			
			TC__			
GAM2203	WT1	3'	AGAACTAACCAGTACCTC	23667	A	TCATGT
			GAG GTACTGGTT TTCT			
			CTC CATGACCAA AAGA			
			TC__			
GAM2203	WT1	3'	AGAACTAACCAGTACCTC	5951	A	TCATGT
			GAG GTACTGGTT TTCT			
			CTC CATGACCAA AAGA			
			TC__			
GAM2203	A2BP1	5'	AGTGCGTGAGAAACCAGCAC	20803	A	__ TT
			GT CTGGTT TCATGT CT			
			CA GACCAA AGTGCG GA			
			C AG T_			
GAM2203	KIAA0993	3'	TAGAAGGTGGAACCAAAACCC	32083	A AC	ATG
	TC		GAG GT TGGTTTC TTTCTA			
			CTC CA ACCAAAG GAAGAT			
			C AA GTG			
GAM2203	KIAA1416	5'	AGAAACATGCAGCAGTCTC	41797	T G T	
			GAG ACTG TT CATGTTTCT			
			CTC TGAC GA GTACAAAGA			
			_ _ C			
GAM2203	My015	3'	AAATACCTAACCAGTACTT	33103	TCA	
			GAGTACTGGTT TGTTT			
			TTCATGACCAA ATAAA			
			TCC			
GAM2203	RASSF2	3'	AGAAGAGAACAGTACTCTC	16388	G ATGT	
			GAGAGTACTG TTTC TTCT			

CTCTCATGAC AGAG AAGA
A _____
GAM2203 TP53INP1 3' AAACATGAAGGACTCC 27101 A A GGT
G GAGT CT TTCATGTTT
||||| || |||||
C CTCA GG AAGTACAAA

— — —
GAM2203 TP53INP1 3' AAACATGAAGGACTCC 36112 A A GGT
G GAGT CT TTCATGTTT
||||| || |||||
C CTCA GG AAGTACAAA

— — —
GAM2203 LOC149711 5' AAACATAAACCAGTACCTC 41065 A C
GAG GTACTGGTTT ATGTTT
||| ||||| |||||
CTC CATGACCAAAA TACAAA

— — —
GAM2203 LOC157503 3' TAGAAACATGAAACCATGCACT 41815 A C
T GAG GTA TGGTTTCATGTTTCTA
||| ||| |||||
TTC CGT ACCAAAGTACAAAGAT
A _

GAM2204 FLJ20094 3' ACTCACAATTTGTGCTCA 19207 TA T
TGA CACAAATTGT AGT
||| ||||| |||
ACT GTGTTTAACA TCA
C_ C

GAM2204 TNKS2 3' GCTGTCAGTTTGTGCACCATA 24913 ATA T
TATG CACAAATTG TAGT
|||| ||||| |||
ATAC GTGTTTGAC GTCG
CAC T

GAM2204 LOC202025 5' ATTGGCAATCTGTGATCA 43400 A A
TGAT CACA ATTGTTAGT
|||| ||| |||||
ACTA GTGT TAACGGTTA
_ C

GAM2205 ANK3 3' TTCCACACATTAATGGCATG 21984 A TC_
CAT TT AATGTGTGGAA
||| || |||||
GTA GG TTACACACCTT
C TAA

GAM2205 CD2AP 3' CACATATAAAATATGTA 14433 CA
TACATATTT ATGTGTG
||||| |||||
ATGTATAAA TATACAC
A_

GAM2205 CDH6 3' TTTCCAATACGACACTGAAATA 11378 A_ _
TGTG TACATATTTCA TGTGT GGAAA
||||| ||| |||||

		GTGTATAAAGT GCATA CCTTT	
		CACA A	
GAM2205	MAP3K7	3' TTCCATCCGTAAAATATGTA 9165	CA TG
		TACATATTT ATG TGGAA	
		ATGTATAAA TGC ACCTT	
		A_ CT	
GAM2205	PSA	3' TCACTGATATATGTAGA 22131	T ATGT
		TCTACATAT TCA GTGG	
		AGATGTATA AGT CACT	
		T ____	
GAM2205	PSA	3' TCACTGATATATGTAGA 27740	T ATGT
		TCTACATAT TCA GTGG	
		AGATGTATA AGT CACT	
		T ____	
GAM2205	SEL1L	3' CCACTATAAATATGTAGA 11502	CA T
		TCTACATATTT ATG GTGG	
		AGATGTATAAA TAT CACC	
		— —	
GAM2205	TGFBR3	3' TTTCCACTCAAAATATGT 9253	CAA T
		ACATATTT TG GTGGAAA	
		TGTATAAA AC CACCTTT	
		— T	
GAM2205	FLJ20136	3' TCAAGACTCTGAAATATGTA 19231	AT G_
		TACATATTTCA GT TGG	
		ATGTATAAAGT CA ACT	
		CT GA	
GAM2205	IL-23R	3' TTCCCTCATTGAAAGATG 29526	A TGT
		CAT TTTCAATG GGAA	
		GTA AAAGTTAC CCTT	
		G TC_	
GAM2205	KIAA0007	3' TTCCACCTGTGAATATGTA 39047	T AT_ T
		TACATATT CA GTG GGAA	
		ATGTATAA GT CAC CCTT	
		_ GTC _	
GAM2205	MGC5576	3' TTCCACACAGCGCCTGTAGA 23494	TATTTCAA
		TCTACA TGTGTGGAA	
		AGATGT ACACACCTT	
		CCGCG_	
GAM2205	OSBPL5	3' TTCCACACCTTGAAATAAACAG 35993	ACA T
	A	TCT TATTTCAA GTGTGGAA	

		AGA ATAAAGTT CACACCTT		
		CAA C		
GAM2205	PEGASUS	3' TTTCCACAAGAGGAAATGT 22816	AATG	
		ATATTTTC TGTGGAAA		
		TGTAAAG ACACCTTT		
		GAGA		
GAM2205	PURG	3' TCCAGACTATTGAAGTATG 15007	_ G	
		CATATTTCAAT GT TGGA		
		GTATGAAGTTA CA ACCT		
		T G		
GAM2205	SMOC2	3' TTCCACATGTTAACAGTAGA 35838	ATATTTTC	
		TCTAC AATGTGTGGAA		
		AGATG TTGTACACCTT		
		ACAA__		
GAM2205	LOC122773	3' TTTCTATATTGAAATAT 36712	T	
		ATATTTCAATGTG GGAA		
		TATAAAGTTATAT CTTT		
		-		
GAM2205	LOC144305	3' TACAAAAATATGTAGA 40402	CAA	
		TCTACATATTT TGTG		
		AGATGTATAAA ACAT		
		A__		
GAM2205	LOC145845	3' TCTAATATTGAAATATG 40617	G	
		CATATTTCAATGT TGGA		
		GTATAAAGTTATA ATCT		
		-		
GAM2205	LOC152185	3' TTTCCATCAAGTGAAATAT 29540	ATG _	
		ATATTTCA TG TGGA		
		TATAAAGT AC ACCTTT		
		GA_ T		
GAM2205	LOC153688	3' TTCCATGTATTGAAATATCCAG 41663	AC	TG
	A	TCT ATATTTCAATG TGGA		
		AGA TATAAAGTTAT ACCTT		
		CC GT		
GAM2205	LOC196527	3' TTTAGCATATTGAAACATTAGA 42402	C A	G
		TCTA AT TTTCAATGTGT GAA		
		AGAT TA AAAGTTATACG TTT		
		_ C A		
GAM2205	LOC221271	3' TTTCCACACACCAACATGTG 44128	TTCAA	
		CATAT TGTGTGGAAA		

GTGTA ACACACCTTT
 CAACC
 GAM2206 DKFZp434G179 3' AATCATTTCCATTCCCATA 39039 TATCTA
 TATGG GGAAATGATT
 |||| |||||
 ATACC CCTTTACTAA
 CTTA__
 GAM2206 ORMDL2 3' ATCACTCTCCTCCATAGCA 15466 TATCT AA_
 TGCTATGG AGGA TGAT
 ||||| ||| |||
 ACGATACC TCCT ACTA
 _____ CTC
 GAM2206 TUB 3' CATTCCCAAGCCATGGCA 9321 ATCTA A
 TGCTATGGT GGAA TG
 ||||| ||| ||
 ACGGTACCG CCTT AC
 AAC__ _
 GAM2206 LOC115265 3' CATTTACCATGGCA 36307 ATCTAG
 TGCTATGGT GAAATG
 ||||| ||||
 ACGGTACCA CTTTAC

 GAM2206 LOC157657 3' AATCATTCCCCAAGTTGTAGCA 39624 TG TATCTA A
 TGCTA G GGAA TGATT
 |||| | ||| ||||
 ACGAT T CCTT ACTAA
 GT CAACC_ _
 GAM2207 PARG 3' TTTTTTTATACCAAGTTTGGAG 9693 GTCG_
 A TCTC TTGGTATAAAAAA
 ||| |||||
 AGAG GACCATATTTTTTT
 GTTTT
 GAM2207 ST7 3' TTTTATACTGACACAAGA 22433 C C TG
 TCT GT GT GTATAAAA
 ||| || |||||
 AGA CA CA CATATTTT
 A _ GT
 GAM2207 BMF 3' TTTTTCATACCTAGTGGGATA 27284 TCGTT A
 TATCTCG GGTAT AAAAA
 ||||| |||| ||||
 ATAGGGT CCATA TTTT
 GAT__ C
 GAM2207 FLJ11274 3' TTTATACTCAAAGAGATA 20402 GTCG _
 TATCTC TTG GTATAAA
 ||||| ||| |||||
 ATAGAG AAC CATATTT
 AA__ T
 GAM2207 FLJ20457 3' TTATGCCAACAAGATG 19498 CGTC
 TATCT GTTGGTATAA
 |||| |||||

			GTAGA CAACCGTATT		
			A__		
GAM2207	KIAA1165	3'	TTTCTTATACCAATGTGA 33479	T	A
			TCG CGTTGGTATAA AAA		
			AGT GTAACCATATT TTT		
			— C		
GAM2207	MRPL13	5'	TTTTTCCACCAAGCGAGATA 15305	CG	AT
			TATCTCGT TTGGT AAAAA		
			ATAGAGCG AACCA TTTTT		
			— CC		
GAM2207	LOC220565	3'	TTTTTCTATACCAATCGC 43636	C	A
			GT GTTGGTATA AAAAA		
			CG TAACCATAT TTTTT		
			C C		
GAM2208	KCNK1	3'	TAAAATTCATATGTGACA 8032	C	
			TGTCACGTA GAATTTTG		
			ACAGTGTAT CTAAAAAT		
			A		
GAM2209	FLJ10620	3'	CGTGCCAAAGCACTTACCA 19973	A	CCGAT
			TGGTAAGT CTT CACG		
			ACCATTCA GAA GTGC		
			C ACC__		
GAM2209	FLJ25415	3'	GTCACGACCAGAAGCATTACC 29535	A	_____ ATCA
	ACA		TGGTAAGT CTTC CG C		
			ACCATTTA GAAG GC G		
			C ACCIIIA ACTA		
GAM2210	TNFSF15	5'	CATACGTAAACAAGAGAGGC 11600	ATGGCGC	
			GCCT GTTTACGTATG		
			CGGA CAAATGCATAC		
			GAGAA__		
GAM2210	KIAA1497	5'	CATACCCCTGGCCATAGGC 33525	G	TTTAC
			GCCTATGGC CG GTATG		
			CGGATACCG GT CATAC		
			— CCC__		
GAM2211	CNTN2	3'	TCTGAGATAGTCACAACCCAGG 11527	TTC	AG AG__
	TGA		TCACCTGG GT T TCAGA		
			AGTGGACC CA G AGTCT		
			CAA CT ATAG		
GAM2211	DKFZP566I1024	3'	CTGGGAGAACCAGATGAT 34734	C	GTAGTAG
			ATCA CTGGTTC TCAG		

			TAGT GACCAAG	GGTC		
			A AG_____			
GAM2211	FLJ12078	3'	GATTGCTAACCAAGTGAT	24536	C	TCG
			ATCAC TGGT TAGTAGTC			
			TAGTG ACCA ATCGTTAG			
			A _____			
GAM2211	GK001	3'	CTGATACCACGAACCAGTGA	21430	C	A G
			TCAC TGGTTCGT GTA TCAG			
			AGTG ACCAAGCA CAT AGTC			
			- C -			
GAM2211	SCIN	5'	TCTGAAGGCCAAACCAGGT	26972	C	AGTAG
			ACCTGGTT GT TCAGA			
			TGGACCAA CG AGTCT			
			A GA_____			
GAM2211	ZNF323	3'	ACTTGTCTACAAACCAGGTG	25167	C	T__
			CACCTGGTT GTAG AGT			
			GTGGACCAA CATC TCA			
			A TGT			
GAM2211	LOC152925	3'	TCTGTAAACTAAAAACCAGGT	39337	CG	AGT
			ACCTGGTT TAGT CAGA			
			TGGACCAA ATCA GTCT			
			AA AAT			
GAM2212	PRKAR2A	5'	CGTGC GC GAAGAGACCTCG	10370	TA	GACA
			CGA TCTC CGCGCACG			
			GCT AGAG GCGCGTGC			
			CC AA_____			
GAM2213	ECM2	3'	TGTTTATAAACTTTACTC	7088	G	CTCCAT
			GAG TAAAGT TAAACA			
			CTC ATTCA ATTTGT			
			- AAT -			
GAM2213	PRDM2	5'	TAATGGAGCCCTACCTC	14536	AA	T
			GAGGTA G CTCCATTA			
			CTCCAT C GAGGTAAT			
			CC _			
GAM2213	PRDM2	5'	TAATGGAGCCCTACCTC	18006	AA	T
			GAGGTA G CTCCATTA			
			CTCCAT C GAGGTAAT			
			CC _			
GAM2213	DKFZp547G183	3'	CTGTTTAACAATTTTTCCTC	20789	T	CTCCA
			GAGG AAAGT TTAAACAG			

		CTCC TTTTA AATTTGTC		
		T AC__		
GAM2213	FLJ10139	3' TTTGATAAAGACTTTACC 19736	CC	
		GGTAAAGTCT ATTAAA		
		CCATTTTCAGA TAGTTT		
		AA		
GAM2213	KIAA1165	3' CTGCTTAATGGAaaaaaATACT 33475	AAGTC	A
		GGTA TCCATTAA CAG		
		TCAT AGGTAATT GTC		
		AAAAA C		
GAM2213	mPA-PLA1	3' CTGTTTGAAAGCTTCACCTC 29250	A T CCA	
		GAGGT AAG CT TTAAACAG		
		CTCCA TTC GA AGTTTGTC		
		C _ A__		
GAM2213	MTCH1	3' CTGTTTAATGGTGATGCCTCG 15661	AAA T	
		CGAGGT GTC CCATTAAACAG		
		GCTCCG TAG GGTAATTTGTC		
		_ T		
GAM2213	LOC158364	5' CTGTTTAGTAACCTCCACCTC 39817	AA CTCC	
		GAGGT AGT ATTAACAG		
		CTCCA TCA TGATTTGTC		
		CC A__		
GAM2213	LOC221773	3' AGTGAAGATTTACCTCG 43760	G C	
		CGAGGTAAA TCT CATT		
		GCTCCATTT AGA GTGA		
		_ A		
GAM2214	ATP5B	5' TTA CTGCGGGCCGCTCCG 30008	AACA T A_	
		CGGA G CG TCGCAGTAA		
		GCCT C GC GGCGTCATT		
		_ _ CG		
GAM2214	RS1	3' CGAATCGACTGTCTCTGT 5877	A _	
		ACGGA ACAGTCGAT CG		
		TGTCT TGTCAGCTA GC		
		C A		
GAM2214	ARFD1	3' TACTTCAAACGTGTTTCC 7372	C_ TCGC	
		GGAAACAGT GA AGTA		
		CCTTTGTCA CT TCAT		
		AA _		
GAM2214	FLJ20666	3' TTACCACAGATACTGTTTCC 19586	CG GCA_	
		GGAAACAGT ATC GTAA		

		CCTTTGTCA TAG CATT	
		— ACAC	
GAM2214	FLJ20666	3' TTACCACAGATACTGTTTCC 20337	CG GCA_
		GGAAACAGT ATC GTAA	
		CCTTTGTCA TAG CATT	
		— ACAC	
GAM2214	KIAA1274	3' CTGGGATCCACTGTTTCC 43909	C G
		GGAAACAGT GATC CAG	
		CCTTTGTCA CTAG GTC	
		C G	
GAM2214	MRPL20	3' TTA CTGCGCCTCACC ACTCCCG 19701	AAACA C T_
	T	ACGG GT GA CGCAGTAA	
		TGCC CA CT GCGTCATT	
		CTCAC _ CC	
GAM2214	phospho1	3' ACCGCGACCCACACTATTTCT 40058	C CGA___ A
	GTG	CACGGAAA AGT TCGC GT	
		GTGTCTTT TCA AGCG CA	
		A CACCCC C	
GAM2214	UNC5D	3' TGAATGACCACCGTTTCCGT 28118	A___ A
		ACGGAAAC GTCG TCG	
		TGCCTTTG CAGT AGT	
		CCAC A	
GAM2214	LOC130639	5' TACTGCAGGTGTTTCC 37003	G GATC
		GGAAACA TC GCAGTA	
		CCTTTGT GG CGTCAT	
		_ A___	
GAM2215	ADRBK2	3' AACAGATTGCCCTAAGCATTG 11641	CTTT_ T
		CAATGC GC AATCTGTT	
		GTTACG CG TTAGACAA	
		AATCC _	
GAM2215	EGFL5	3' AACAGACCTTAAAAGGTATTGA 41872	GCTAA
		TCAATGCCTTT TCTGTT	
		AGTTATGGAAA AGACAA	
		ATTCC	
GAM2215	PARG	3' AACAGATTCCAAGAGAATTGA 9692	GC GCT
		TCAAT CTTT AATCTGTT	
		AGTTA GAGA TTAGACAA	
		A_ ACC	
GAM2215	PRKCN	3' AACAAACCATAGAGGCATTGA 12394	CTAATC
		TCAATGCCTTTG TGTT	

		AGTTACGGAGAT	ACAA		
		ACCAA_			
GAM2215	RUNX3	3'	AGGTCCTAGCAGAAGGCATTGA	10546	_ _
			TCAATGCCT TTGCTA ATCT		
			AGTTACGGA GACGAT TGGA		
			A CC		
GAM2215	FLJ20004	3'	AGCAGTGCAAAGGCCCTGA	45642	AT TAAT
			TCA GCCTTTGC CTGTT		
			AGT CGGAAACG GACGA		
			CC T__		
GAM2215	HTCD37	3'	AACAGATTAGAGGCCATTG	33616	_ TTG
			CAATG CCT CTAATCTGTT		
			GTTAC GGA GATTAGACAA		
			C _		
GAM2215	KIAA0841	3'	AACAGCACATGCAAAGGCCCTG	35357	AT TAAT_
	A		TCA GCCTTTGC CTGTT		
			AGT CGGAAACG GACAA		
			CC TACAC		
GAM2215	KIAA0855	3'	AACAGATTTGCCGGCATT	17371	TTT T
			AATGCC GC AATCTGTT		
			TTACGG CG TTAGACAA		
			C_ T		
GAM2215	KIAA1843	3'	AACAGATTAACACTGGTA	31160	TT C
			TGCC TG TAATCTGTT		
			ATGG AC ATTAGACAA		
			TC A		
GAM2215	MGC2827	3'	ACAGATTAAGCATTGA	23423	CTTTGC
			TCAATGC TAATCTGT		
			AGTTACG ATTAGACA		
			A__		
GAM2215	NXP-2	3'	AACAGAAAAAAGGTATTGA	35228	GCTAA
			TCAATGCCTTT TCTGTT		
			AGTTATGGAAA AGACAA		
			AA__		
GAM2215	LOC148809	3'	AACAGAATGAGAGCAAAGGCAC	38591	AA AA__
	AGA		TC TGCCTTTGCT TCTGTT		
			AG ACGGAAACGA AGACAA		
			AC GAGTA		
GAM2215	LOC153387	5'	AACAGATTTTTTAAAAACATTGA	41633	CC CT
			TCAATG TTTG AATCTGTT		

AGTTAC AAAT TTAGACAA
 AA TT
 GAM2215 LOC169225 5' AACTGACAGCAAGGGCACTGA 42203 A AA T
 TCA TGCCTTTGCT TC GTT
 ||| ||||| |||
 AGT ACGGGAACGA AG CAA
 C C_ T
 GAM2215 LOC169966 3' AACAGATTCAGAAGACATT 40163 C GCT
 AATG CTTT AATCTGTT
 ||| ||| |||||
 TTAC GAAG TTAGACAA
 A AC_
 GAM2215 LOC51157 5' ACAGATTTAGGGATTGA 18297 G TTGCT
 TCAAT CCT AATCTGT
 |||| ||| |||||
 AGTTA GGA TTAGACA
 G T____
 GAM2216 CYP3A4 3' ACCCAACTGTCTCGATGCAATG 18931 _ TATCA
 TATTGCATCG GGCA GGT
 ||||| ||| |||
 GTAACGTAGC CTGT CCA
 T CAAC_
 GAM2216 ICOS 3' ACCCGATATGTCATTATGCA 14382 CG_ A
 TGCAT GGCATATC GGT
 |||| ||||| |||
 ACGTA CTGTATAG CCA
 TTA C
 GAM2216 LOC256790 5' CCTGATATGTTGCTATA 45459 T TCGG
 TAT GCA GCATATCAGG
 ||| ||| |||||
 ATA CGT TGTATAGTCC
 T ____
 GAM2216 LOC91421 3' CCTAGGCCGATGCAATG 32827 G ATATC
 TATTGCATCGG C AGG
 ||||| ||| |||
 GTAACGTAGCC G TCC
 _ GA____
 GAM2217 SLC22A3 3' CGCAATGTGAACAGGTCA 22503 A AGTA
 TGACC GTT ACATTGCG
 |||| ||| |||||
 ACTGG CAA TGTAACGC
 A G____
 GAM2217 SLC6A12 3' CGATATTGCTAACTGATCA 9010 C C
 TGA CAGTTAGTAA ATTG
 ||| ||||| |||
 ACT GTCAATCGTT TAGC
 A A
 GAM2217 C22orf23 3' CAATGATTAAGTGGCCA 26287 A AA
 TG CCAGTTAGT CATTG
 || ||||| |||||

		AC GGTCAATTA GTAAC		
		C —		
GAM2217	FLJ10159	3' CAATGACACCAGCTGGTCA	19748	A AA
		TGACCAGTT GT CATTG		
		ACTGGTCGA CA GTAAC		
		C CA		
GAM2217	KIAA1323	3' GTATCTATTA ACTGGCCA	31566	A ACAT
		TG CCAGTTAGTA TGC		
		AC GGTCAATTAT ATG		
		C CT—		
GAM2218	FLJ13072	5' ATGTGTGATTAGAAACGATGA	43233	C —
		TCA CGTTTTTA ACACGT		
		AGT GCAAAGAT TGTGTA		
		A TAG		
GAM2219	PCDHB16	3' ATGCTCACCACCACCAATAA	21945	A TA CA
		TTAT TGGT GT GTGAGCAT		
		AATA ACCA CA CACTCGTA		
		— C_ C_		
GAM2219	LOC221474	5' TATGATTAGGATAACCATATAA	44382	G AG G
		TTATATGGTTA TC TGA CATA		
		AATATACCAAT AG ATT GTAT		
		— G_ A		
GAM2220	PRO2435	5' AATGTCACAGAGACTAGTTCA	20598	C TA
		TGA ACTAGTC CTGT GCATT		
		ACTTGATCAG GACA TGTA		
		A C_		
GAM2220	LOC143425	3' CTAATGCAAGGAGGGCTAGTTC	42354	T G A
	A	TGA ACTAG CCCT TT GCATTAG		
		ACTTGATC GGGA GA CGTAATC		
		— G A		
GAM2221	CHD2	3' TACCTTGAATTTACAGTGGGAA	6936	A GAA
	A	TTTC CACTGTAAA TGGGGTA		
		AAAG GTGACATTT GTTCCAT		
		G AA_		
GAM2221	COQ7	3' TACCTCATCCTCTCCACAGTGT	18222	AA —
	GAGA	TTTCACACTGT AGA ATGGGGTA		
		AGAGTGTGACA TCT TACTCCAT		
		CC CC		
GAM2221	KIAA1969	3' ACCCCACAAGTGTGAAA	38490	GTAAAGAA
		TTTCACACT TGGGGT		

		AAAGTGTGA	ACCCCA		
		AC_____			
GAM2221	LOC153196 5'	ACCCCATTTAACAATGTGAAG	41586	C	AAA
		TTTCACA TGT GAATGGGGT			
		GAAGTGT ACA TTTACCCCA			
		A A__			
GAM2221	LOC169026 3'	ACCCCATTCCTGTGAAA	40260	CTGTAAA	
		TTTCACA GAATGGGGT			
		AAAGTGT CTTACCCCA			
		C_____			
GAM2222	CSE-C 3'	TGCAGTTTACTGATGGATTAA	43982	AAA	TA
		TTAATCCAT TAAAT TGTA			
		AATTAGGTA ATTTG ACGT			
		GTC _			
GAM2222	DKFZP434N178 3'	TACAGCTTTTATTTGTGAATTA	35599	C	TTA
	A	TTAAT CATAAATAAA TGTA			
		AATTA GTGTTTATTT ACAT			
		A TCG			
GAM2222	LOC203411 3'	TAGTGTTATTTATGGATTAG	43566	_	
		TTAATCCATAAATAA ATTA			
		GATTAGGTATTTATT TGAT			
		G			
GAM2223	EGFL5 5'	AAAGCAAAGGCAAATAGTGC	41871	AC	A
		GTACTATT TCTTT CTTT			
		CGTGATAA GGAAA GAAA			
		AC C			
GAM2223	EGLN1 5'	GGTAGAATAATAGTAC	22586	CTC	
		GTACTATTA TTTACT			
		CATGATAAT AGATGG			
		A__			
GAM2223	ERBB2IP 3'	AAAGTAAAAGGAAACAGTAC	20769	A A	TC
		GTACT TT C TTTACTTT			
		CATGA AA G AAATGAAA			
		C A GA			
GAM2223	FOG2 3'	AAGAGTAGCAATACTGCA	14371	CTA	
		TGCAGTA TTA CTCTT			
		ACGTCAT GATGAGAA			
		AAC			
GAM2223	TRAF5 3'	AAAGCAGAAAGTACTGCA	10963	A A	_
		TGCAGTACT TT CT CTTT			

ACGTCATGA AA GA GAAA
 _ _ C
 GAM2223 KIAA0643 3' AAGTAGAGTAATAGCACT 24172 A TT
 AGT CTATTACTCT ACTT
 ||| ||||| ||||
 TCA GATAATGAGA TGAA
 C _
 GAM2223 KIAA1676 3' AAGAGGAATGGTACTACA 44725 C A
 TG AGTACTATT CTCTT
 || ||||| ||||
 AC TCATGGTAA GAGAA
 A G
 GAM2223 LOC199725 3' AAAGTAAAGAAAGTAC 43240 ATTAC
 GTACT TCTTTACTTT
 |||| |||||
 CATGA AGAAATGAAA
 A _
 GAM2223 LOC200347 5' AAAGTAAAGAATATGATGAGTA 42805 _ C _
 C GTACT ATTA TCTTTACTTT
 |||| ||| |||||
 CATGA TAGT AGAAATGAAA
 G ATA
 GAM2224 ADCY6 3' CCTACCGAGAGGATTATGCAA 17586 C C A TTTT
 TTGCA AA CCTC TC TAGG
 |||| || ||| |||
 AACGT TT GGAG AG ATCC
 A A _ CC _
 GAM2224 ADCY6 3' CCTACCGAGAGGATTATGCAA 21974 C C A TTTT
 TTGCA AA CCTC TC TAGG
 |||| || ||| |||
 AACGT TT GGAG AG ATCC
 A A _ CC _
 GAM2224 DUOX2 3' CCTAAAAAGCTGAGCTGTAA 15307 CAACC T
 TTGCA CTCA CTTTTTAGG
 |||| ||| |||||
 AATGT GAGT GAAAAATCC
 C _ C
 GAM2224 ZNF36 3' CCAAAAAAGATTTCGGTTGTCAA 45102 C CTC A
 TTG ACAACC ATCTTTT GG
 ||| |||| ||||| ||
 AAC TGTTGG TAGAAAAA CC
 _ CT _ A
 GAM2224 AKAP11 3' TATAAAGATTGTGCAG 18371 ACCCTC T
 TTGCACA ATCTTT TA
 ||||| ||||| ||
 GACGTGT TAGAAA AT
 _ T
 GAM2225 EXTL3 3' CTGACTTGTATTCCTTT 7166 A G
 AAAG AATA CAAGTCAG
 |||| ||| |||||

TTTC TTAT GTTCAGTC
 C _
 GAM2225 LANCL1 3' CAATTTTCTGACTTGCTTTTCT 12693 T T_
 AGAAA AGCAAGTCAGA ATTG
 |||| ||||| ||||
 TCTTT TCGTTCAGTCT TAAC
 _ TT
 GAM2225 LPL 3' CAATATCTGACAGTTACTCTT 5750 AA AA
 AAGA TAGC GTCAGATATTG
 ||| ||| |||||
 TTCT ATTG CAGTCTATAAC
 C_ A_
 GAM2225 FLJ22746 3' CAATATGGACTGCTATTTACT 24162 _ A AG
 AG AAATAGCA GTC ATATTG
 || ||||| ||| |||||
 TC TTTATCGT CAG TATAAC
 A _ G_
 GAM2225 LOC128077 3' CTGCTTGCTATCCCTTT 36917 AA T
 AAAG ATAGCAAG CAG
 ||| ||||| |||
 TTTC TATCGTTC GTC
 CC _
 GAM2225 LOC151201 5' ATTTTCTTGCTATTTT 41320 TC
 AGAAATAGCAAG AGAT
 ||||| |||
 TTTTATCGTTC TTTA
 TT
 GAM2225 LOC152286 3' ATCTACTTGCTACTTCT 41460 A C
 AGAA TAGCAAGT AGAT
 ||| ||||| |||
 TCTT ATCGTTCA TCTA
 C _
 GAM2225 LOC221747 3' ATGTGACTTGCTCCTCTTT 44364 AAT G
 AAAGA AGCAAGTCA AT
 |||| ||||| ||
 TTTCT TCGTTCAGT TA
 CC_ G
 GAM2226 BCL6 3' AACAAAAAGAACAAAAAATCT 7428 CAG__ A
 GCAG TTGCA TTT TTCTTTTGT
 |||| ||| |||||
 GACGT AAA AAGAAAAACAA
 CTA AAA C
 GAM2226 BCL6 3' AACAAAAAGAACAAAAAATCT 29055 CAG__ A
 GCAG TTGCA TTT TTCTTTTGT
 |||| ||| |||||
 GACGT AAA AAGAAAAACAA
 CTA AAA C
 GAM2226 BMPR1B 5' AACAAAAAGTTAACTTACAAG 6868 CAC TT
 CTTG AGTTTA CTTTTGT
 ||| |||| |||||

			GAAC TCAAAT GAAAAACAA		
			AT_ T_		
GAM2226	DGKG	5'	AAGGGAATAAACCGCGA 7024	ACA	
			TTGC GTTTATTCTTTT		
			AGCG CAAATAAGGGAA		
			C_		
GAM2226	HNRPD	3'	AACAAATCTGGATAAATGTGCA 7913	G	TT_
	A		TTGCACA TTTATTC TTTGTT		
			AACGTGT AAATAGG AAACAA		
			_ TCT		
GAM2226	HNRPD	3'	AACAAATCTGGATAAATGTGCA 25363	G	TT_
	A		TTGCACA TTTATTC TTTGTT		
			AACGTGT AAATAGG AAACAA		
			_ TCT		
GAM2226	DKFZP434D193	5'	AACAAAAAAGGCAGATGTGCAA 42849	G	A TC
	G		CTTGCACA TTT T TTTTGT		
			GAACGTGT AGA G AAAAACAA		
			_ C GA		
GAM2226	PDGFC	3'	AGGAAAAAACTGTGCAAG 18300	A_	
			CTTGCACAGTTT TTCTT		
			GAACGTGTCAAA AAGGA		
			AA		
GAM2226	SENPD	3'	AACAAAAAATTTTACCTGTGCA 21821	TTTATTC	
	A		TTGCACAG TTTTGT		
			AACGTGTC AAAAACAA		
			CATTTTA		
GAM2226	SNRK	3'	AACAAAAAGATGCTCTGTGTAA 19305	TTTAT	
			TTGCACAG TCTTTTGT		
			AATGTGTC AGAAAAACAA		
			TCGT_		
GAM2226	TBX19	3'	AACAAAAAGAATAAAGCT 11622	_	
			AGTTT ATTCTTTTGT		
			TCGAA TAAGAAAAACAA		
			A		
GAM2226	LOC154282	3'	AACAAAAAGGAGGACCACGCAA 41695	ACA	A
			TTGC GTTT TTCTTTTGT		
			AACG CAGG AGGAAAAACAA		
			CAC _		
GAM2226	LOC92539	3'	AACAAAAAGGACGACCATGCAA 34495	CA	TA
			TTGCA GTT TTCTTTTGT		

			AACGT CAG AGGAAAAACAA	
			AC C_	
GAM2227 AKAP13	3'	TGGATGTCCTTGGGAATG	43183	AA CAT
		TATTCCAA ACA TCCA		
		GTAAGGTT TGT AGGT		
		CC ____		
GAM2227 ALDH8A1	3'	TGTGGACGTCTTTGGAAT	22890	A ACAT
		ATTCCAAA AC TCCACA		
		TAAGGTTT TG AGGTGT		
		C C ____		
GAM2227 ATP1B2	3'	TGTGGATGCTCCTGGAATG	7396	AAAACA T
		TATTCCA CAT CCACA		
		GTAAGGT GTA GGTGT		
		CCTC__ _		
GAM2227 CLASP1	3'	TGTGTGGGGTGCAGTTTTT	32543	A_
		AAAAAC CATTCCACACA		
		TTTTTG GTGGGGTGTGT		
		AC		
GAM2227 KCNA3	3'	TGTGTGGAACGTGCCCCCTTGG	8014	AAA__ A
		CCAA CAC TTCCACACA		
		GGTT GTG AAGGTGTGT		
		CCCC C		
GAM2227 LEP	3'	GAATGTGTTTTCTGAATA	5737	CA
		TATTC AAAACACATTC		
		ATAAG TTTTGTGTAAG		
		TC		
GAM2227 MAML1	3'	TGTGAGCTGTTTTTGGAA	16501	CATTC
		TTCCAAAAACA CACA		
		AAGGTTTTTGT GTGT		
		CGA__		
GAM2227 NET1	3'	TGGAATGTATGTCTGGAGTA	12475	AAAAC
		TATTCCA ACATTCCA		
		ATGAGGT TGTAAGGT		
		CTGTA		
GAM2227 POLQ	3'	GAATGTATTTGGAATA	13366	AAC
		TATTCCAAA ACATTC		
		ATAAGGTTT TGTAAG		
		A__		
GAM2227 RAD50	5'	GTGCGGAGTTTTGGAATA	28553	AACAC A
		TATTCCAAA ATTCC CAC		

			ATAAGGTTT	TGAGG	GTG	
			_____	C		
GAM2227	AD022	3'	TGGTTGTGTTTTCAGAAT	43738	CA	TT
			ATTC AAAACACA	CCA		
			TAAG TTTTGTGT	GGT		
			AC	T_		
GAM2227	BTN2A2	3'	TGTGAGTGTGTTTCCAGAA	13862	CAA	C
			TTC AAACACATTC	ACA		
			AAG TTTGTGTGAG	TGT		
			ACC	_		
GAM2227	C21orf42	5'	TGTATGAACAAGTGTTTTTGGA	27750	ATTC_	C
	AT		ATTCCAAAAACAC	CA ACA		
			TAAGGTTTTTGTG	GT TGT		
			AACAA	A		
GAM2227	DKFZp547D155	3'	TGTGTAAGAATGTGTTTT	34871	C_	
			AAAACACATTC	ACACA		
			TTTTGTGTAAG	TGTGT		
			AA			
GAM2227	FBXO30	3'	GTGTGAAATTTTTGGAA	25838	ACAC	C
			TTCCAAAA	ATT CACAC		
			AAGGTTTT	TAA GTGTG		
			_____	A		
GAM2227	FLJ31978	3'	TGTGGGAAGGGCGTGTTTTT	29491	A_____	
			AAAAACAC	TTCCACA		
			TTTTTGTG	AGGGTGT		
			CGGGA			
GAM2227	HSU24186	5'	GTGTGGGACTTTTAGAATG	14991	C	ACACA
			TATTC AAAA	TTCCACAC		
			GTAAG TTTT	AGGGTGTG		
			A	C_____		
GAM2227	KIAA0939	3'	TGTGTGGAACGAGTTCTTGGA	31070	A	ACA
	TG		TATTCCAA AAC	TTCCACACA		
			GTAAGGTT TTG	AAGGTGTGT		
			C	AGC		
GAM2227	KIAA1145	5'	TGGTAGGTGCTGTTTGAATA	32681	AA_	ATT
			TATTCCAAA	CAC CCA		
			ATAAGGTTT	GTG GGT		
			GTC	GAT		
GAM2227	KIAA1432	5'	TGGAGTGTTTTTGGAG	33158	AT	
			TTCCAAAAACAC	TCCA		

GAGGTTTTTTGTG AGGT

GAM2227 KIAA1950 3' TGTGGTGATGTTTTTGGA 44493 CATT
TTCCAAAAACA CCACA
||||||| ||||
AGGGTTTTTGT GGTGT
AGT_

GAM2227 MFN2 3' TGTGTAGATCTGTTTTGGAA 17013 A CAT C
TTCCAAAA CA TC ACACA
||||||| || |||||
AAGGTTTT GT AG TGTGT
_ CT_ A

GAM2227 MGC21738 3' TGTGGGGTGTATTTCTGGA 29678 A C
TCCA AAA ACATTCCACA
||| ||| |||||
AGGT TTT TGTGGGGTGT
C A

GAM2227 STAT5A 3' TGTGTAAACAGTGTTTTGAAT 9130 A ATTCC
A TATTCCAAAA CAC ACACA
||||||| ||| |||||
ATAAGGTTTT GTG TGTGT
_ AAAAA

GAM2227 LOC143872 3' TGTGAAAAATGTGTTTTTGA 37655 CCA
TCCAAAAACACATT CACA
||||||| |||
AGGTTTTTGTGTAA GTGT
AAA

GAM2227 LOC144321 3' TGTCTTTGTGGTTTTTGAATA 40410 A TCC_
TATTCCAAAAAC CAT ACA
||||||| ||| |||
ATAAGGTTTTTG GTG TGT
_ TTTC

GAM2227 LOC145482 3' TGTGTAACAGTTTTTGGGATA 37878 ACATTCC
TATTCCAAAAAC ACACA
||||||| |||||
ATAGGGTTTTTG TGTGT
ACAA_

GAM2227 LOC146782 5' GTGGGCACGTTTTTGGAA 37525 ACAT
TTCCAAAAAC TCCAC
||||||| |||||
AAGGTTTTTG GGGTG
CAC_

GAM2227 LOC221474 3' GTGTAGGAGTTTTTGA 44381 CAC _
TCCAAAAA ATTCC ACAC
||||||| ||||| |||||
AGGTTTTT TGAGG TGTG
_ A

GAM2227 LOC90092 5' TCGTGGAAGTGGATGTGTCCCC 30792 CAAAA _ A
AGAAT ATT C ACACAT TCCAC CA
||| ||||| ||||| ||

			TAAG	TGTGTA	AGGTG	GT		
			ACCCC	GGTC	C			
GAM2227	LOC92344	3'	TGGTTG	GAGTGT	TTTTTAGA	34210	C	AT CA
			TC	AAAAACAC	TCCA	CA		
			AG	TTTTTG	TG	AGGT	GT	
			A	__	TG			
GAM2228	CACNG7	3'	TGCCTTTT	AGGGGG	CTCTTG	25641		ATAA A
			TAAGA	TTCCTAAA	AG	CA		
			GTTCT	GGGGATT	TTTC	GT		
			CG__		C			
GAM2228	GRINL1A	3'	TGTCCTTTT	AAGAATT	ATTTT	34447	C	_
			AGAATAATTC	TAAAAG	ACA			
			TTTTATTAAG	ATTTTC	TGT			
			A		C			
GAM2228	HS3ST4	3'	TGTTATTAGGAATAATCCTTA			36372	A A	AA
			TAAG	AT	ATTCCTAA	GACA		
			ATTC	TA	TAAGGATT	TTGT		
			C	A		A_		
GAM2228	ITGB3	3'	CTTGTGAAGGAATTATTC			5708		AAAAG
			GAATAATTCCT		ACAAG			
			CTTATTAAGGA		TGTTC			
			AG__					
GAM2228	PBX2	3'	CTTGTCTTTTTTTTTTTTATTTCT			8448		TAATTCCT
	TA		TAAGAA		AAAAGACAAG			
			ATTCTT		TTTCTGTTC			
			TATTTTTT					
GAM2228	ZNF264	3'	TCTCAGGAATTATTTT			9461		AAA
			TAAGAATAATTCCT		AGA			
			ATTTTATTAAGGA		TCT			
			C_					
GAM2228	CG012	3'	TGTCTTTTAGTCATTTCTT			40489		TAATTC
			AAGAA		CTAAAAGACA			
			TTCTT		GATTTTCTGT			
			TACT__					
GAM2228	FLJ12604	3'	CTTGTCTTTCAGAATTACTTA			32190	AA	CTA
			TAAG	TAATTC	AAAGACAAG			
			ATTC	ATTAAG	TTTCTGTTC			
			_	AC_				
GAM2228	IL1RAPL1	5'	CTTATTTT	TAAAGAATT	TATTCT	15553	C	C
	TA		TAAGAATAATTC	TAAAAGA	AAG			

		ATTCTTATTAAG ATTTTTT TTC		
		A A		
GAM2228 KIAA1069	3'	CTTGCCTTTTAGGATGTTCTTA 33724	AT	A
		TAAGAATA TCCTAAAAG CAAG		
		ATTCTTGT AGGATTTTC GTTC		
		— C		
GAM2228 KIAA1318	3'	CTTGTCCCTCAGTGGGGGTTCT 33432	AT	AAA—
	CT	AGA AATTCCTA GACAAG		
		TCT TTGGGGGT CTGTTC		
		C_ GACTCC		
GAM2228 KIAA1468	3'	CTTGTCTTTCAGAATAATTTTT 44100	A	CTA
	A	TAAGAAT ATTC AAAGACAAG		
		ATTTTATA TAAG TTTCTGTTC		
		A AC_		
GAM2228 SAE1	3'	CTTGTCTTTCAAGGCCAGGTTC 12005	AATT	A_
		GAAT CCT AAAGACAAG		
		CTTG GGA TTTCTGTTC		
		GACC AC		
GAM2228 ZFP36L2	3'	CTTGTCTTTTTTTTTTTTATTTT 13754	TTCCT	
	TA	TAAGAATAA AAAAGACAAG		
		ATTTTATT TTTCTGTTC		
		TTTTT		
GAM2228 LOC151571	5'	CTTGCCTTTGATGATTATTCTT 41373	CCTA	A
	A	TAAGAATAATT AAAG CAAG		
		ATTCTTATTAG TTTC GTTC		
		TAG_ C		
GAM2228 LOC158219	3'	TTTAGGAATTTTCTTA 39764	T	
		TAAGAA AATTCCTAAAA		
		ATTCTT TTAAGGATTTT		
		T		
GAM2228 LOC257415	3'	CTTGGGAGAGGAATTATTTT 45959	AAAAGA	
		AGAATAATTCCT CAAG		
		TTTTATTAAGGA GTTC		
		GAGG_		
GAM2228 LOC57019	3'	TTGTCTTTCAGAGTTGTT 21570	CTA	
		AATAATTC AAAGACAA		
		TTGTTGAG TTTCTGTT		
		AC_		
GAM2229 PLAG1	3'	ATCTTCTTAAAGGTCTAA 8516	T	A
		TTAGA CCTTTAAGAA GAT		

AATCT GGAAATTCTT CTA

GAM2229 FLJ10140 3' ACCATCTTCCCTCTGGGGGGAT 19737 TA ____ A
T GATCCTT AGA AAGAT GT
||||| ||| ||||| ||
TTAGGGG TCT TTCTA CA
GG CCC C

GAM2230 BIG1 3' TGGTAAAAGATATTTAGCAA 13139 C GGG
TTGCTAGA ATTT TACCA
||||| ||| |||||
AACGATTT TAGA ATGGT
A AA_

GAM2230 CADPS 3' GTGGTACCAAGATTAGCAA 32508 GAC G
TTGCTA ATTT GGTACCAC
||||| ||| |||||
AACGAT TAGA CCATGGTG
____ A

GAM2230 CENTD1 3' GGAGTTAAATGTCCTGCAA 29201 TA GTA
TTGC GACATTTGG CC
||| ||||| ||
AACG CTGTAAATT GG
TC GA_

GAM2230 CENTD1 3' GGAGTTAAATGTCCTGCAA 17563 TA GTA
TTGC GACATTTGG CC
||| ||||| ||
AACG CTGTAAATT GG
TC GA_

GAM2230 POLS 3' GTGGTACCCAGTTTTAGGAA 13866 G CAT
TT CTAGA TTGGGTACCAC
|| ||||| |||||
AA GATTT GACCCATGGTG
G T_

GAM2230 PPP3CA 3' TGGTTAGCATGTTTAGCAA 6646 TTGGGT
TTGCTAGACAT ACCA
||||| |||
AACGATTTGTA TGGT
CGAT_

GAM2230 PRPS2 3' TGGGAAGTGTCCAGCAA 8657 A GGGTA
TTGCT GACATTT CCA
||||| |||
AACGA CTGTGAA GGT
C G_

GAM2230 RBM8A 3' GTAATAAGGTGTCCAGCAG 11581 A GGG
TTGCT GACATTT TAC
||||| |||
GACGA CTGTGGA ATG
C ATA

GAM2230 YES1 3' GTGGTTTGAGTGTCTAGCAA 11915 TG GT
TTGCTAGACATT G ACCAC
||||| |||

			AACGATCTGTGA T TGGTG		
			GT _		
GAM2230	CLGN	3'	GTTTCTAATATCTAGCAA 10569	CAT	T
			TTGCTAGA TTGGG AC		
			AACGATCT AATCT TG		
			AT_ T		
GAM2230	CNNM1	3'	GTGGTCTTTTCAAATGTC 21610	T_	
			GACATTTGGG ACCAC		
			CTGTAAACTT TGGTG		
			TTC		
GAM2230	DKFZp434C0923	5'	GTGACAAATTCTAGCAA 19066	C	GG
			TTGCTAGA ATTTG TAC		
			AACGATCT TAAAC GTG		
			_ A_		
GAM2230	FLJ10704	3'	GTGGTACCCGTAGTGCCCAGCA 20034	AGA	_
			TGCT CATT TGGGTACCAC		
			ACGA GTGA GCCCATGGTG		
			CCC T		
GAM2230	FLJ11267	5'	TGGCTCTAGAATGTCTAGGAA 21225	G	G TA
			TT CTAGACATTT GG CCA		
			AA GATCTGTAAG TC GGT		
			G A TC		
GAM2230	FLJ13962	3'	GTATCAAATATCTGGCAA 24298	C	G
			TTGCTAGA ATTTGG TAC		
			AACGGTCT TAACT ATG		
			A _		
GAM2230	FLJ20413	3'	TGGGAGAAAATGTCTGCAA 19455	T	GGGTA
			TTGC AGACATTT CCA		
			AACG TCTGTAAA GGT		
			_ AGAG_		
GAM2230	FLJ20729	3'	GTGTTTTGATATGTCTAGCAA 19657	TT_	GG
			TTGCTAGACAT G TAC		
			AACGATCTGTA T GTG		
			TAGT TT		
GAM2230	KIAA0237	3'	GTGATACCCAGACCAGCAG 16453	AGACA	C
			TTGCT TTTGGGTA CAC		
			GACGA AGACCCAT GTG		
			CC_ A		
GAM2230	KIAA0746	5'	GTGATACCCAAAGCTGAGCAG 34415	AGACA	C
			TTGCT TTTGGGTA CAC		

			GACGA	AAACCCAT	GTG	
			GTCG_	A		
GAM2230	KIAA0788	3'	GTGGTACCCACACATCAGCA	35344	A	CATT
			TGCT GA	TGGGTACCAC		
			ACGA CT	ACCCATGGTG		
			_ ACAC			
GAM2230	KIAA0795	3'	GTGATCATGTCTAGTAA	24586	TT	GG
			TTGCTAGACA TG	TAC		
			AATGATCTGT AC	GTG		
			_ TA			
GAM2230	KIAA1977	5'	GGCTGGCCATGTCTAGCA	36746	TT	G _
			TGCTAGACA TGG	TA CC		
			ACGATCTGT ACC	GT GG		
			_ G C			
GAM2230	KR18	3'	TACCTGTTGTTTAGCAA	27121	TT	
			TTGCTAGACA TGGGTA			
			AACGATTTGT GTCCAT			
			T_			
GAM2230	LIG-1	3'	TATTGAAGTGTCTAACAA	31954	C	G
			TTG TAGACATTT	GGTA		
			AAC ATCTGTGAA	TTAT		
			A	G		
GAM2230	NUP133	3'	TGGGAAATGTCTAGTAA	20168	GGGTA	
			TTGCTAGACATTT	CCA		
			AATGATCTGTAAA	GGT		
			G_			
GAM2230	PLAGL2	3'	TATTAATGTCTGGCAA	34880	GG	
			TTGCTAGACATTT	GTA		
			AACGGTCTGTAAA	TAT		
			AT			
GAM2230	RAN	3'	GTATTTCAAATATCTAAGCAA	13017	_ C	_
			TTGCT AGA ATTTGGG	TAC		
			AACGA TCT TAACTT	ATG		
			A A	T		
GAM2230	ROBO2	3'	ACTCTAGAATATCTAGCAA	31317	C	_
			TTGCTAGA ATTT	GGGT		
			AACGATCT TAAG	CTCA		
			A	AT		
GAM2230	SEC15B	3'	GTACCCAGTATCAGCAA	33125	A	CAT
			TTGCT GA	TTGGGTAC		

			AACGA CT GACCCATG		
			_ AT_		
GAM2230	SH3BGRL	3'	TGGCATTCTCTAGCAA	31027	CATT T A
			TTGCTAGA GGGT CCA		
			AACGATCT CTTA GGT		
			_____ C		
GAM2230	TRIP-Br2	3'	TACTCAAAGTCTAACAA	16494	C A
			TTG TAGAC TTTGGGTA		
			AAC ATCTG AAACATCAT		
			A _		
GAM2230	LOC157507	5'	TATCCAAGTGTCCAGCAA	39607	A
			TTGCT GACATTTGGGTA		
			AACGA CTGTGAACCTAT		
			C		
GAM2230	LOC161742	3'	TGGTATTCAACCAGCAA	40028	AGACAT
			TTGCT TTGGGTACCA		
			AACGA AACTTATGGT		
			CC_____		
GAM2230	LOC162239	3'	GGGTACCACATGAATTGTCTAG	40053	TT_____ GTA
	CAA		TGCTAGACA TGG CC		
			ACGATCTGT ACC GG		
			TAAGTAIIIC ATG		
GAM2230	LOC199704	3'	GTGACAATGTCTAGTAA	42602	T GG
			TTGCTAGACATT G TAC		
			AATGATCTGTAA C GTG		
			_ A_		
GAM2230	LOC220469	5'	GTAATCAGATGTGTAGCAA	37554	G GG
			TTGCTA ACATTTG TAC		
			AACGAT TGTAGAC ATG		
			G TA		
GAM2230	LOC221002	3'	GTGACAATGTGTCCAGCAA	43975	A _ GG
			TTGCT GACAT TTG TAC		
			AACGA CTGTG AAC GTG		
			C T A_		
GAM2230	LOC56965	3'	GTGGATCATCTCTAGCAA	21454	CATT TG A
			TTGCTAGA GGT CCAC		
			AACGATCT CTA GGTG		
			CTA_____		
GAM2230	LOC91050	3'	GCCTGCAAATGTCCAGCA	32337	A _
			TGCT GACATTTG GGT		

		ACGA CTGTAAAC CCG	
		C GT	
GAM2231	ATP1A2	3' GACGATCATTGTGCCCCACTTA 6367	T T _ A
		TGAGT G GT CAATGATC TC	
		ATTCA C CG GTTACTAG AG	
		_ C T C	
GAM2231	PCDHA9	3' TGTCTATCAGCACAACCTCA 15214	CAA CAT
		TGAGTTGTGT TGAT CA	
		ACTCAACACG ACTA GT	
		___ TCT	
GAM2231	PTPRA	5' TGACAAGAGGTGACACAACCT 8715	ATGA A__
		AGTTGTGTCA TC TCA	
		TCAACACAGT AG AGT	
		GG__ AAC	
GAM2231	SFRS1	3' TGATGACAGACATAACTCA 13803	AA A
		TGAGTTGTGTC TG TCATCA	
		ACTCAATACAG AC AGTAGT	

GAM2231	SLC22A3	3' GATGAAATAAACACAACCTC 22504	CA GA
		GAGTTGTGT AT TCATC	
		CTCAACACA TA AGTAG	
		AA A_	
GAM2231	VNN1	3' TGACATTACACAACCTCA 11040	C A
		TGAGTTGTGT AATG TCA	
		ACTCAACACA TTAC AGT	

GAM2231	ZNF124	3' TTGATGGTATAACATAACTCA 9484	CAATG
		TGAGTTGTGT ATCATCAA	
		ACTCAATACA TGGTAGTT	
		ATA__	
GAM2231	C22orf19	3' TGATCCTTGAACAACCTCA 9776	G T
		TGAGTTGT TCAA GATCA	
		ACTCAACA AGTT CTAGT	
		_ C	
GAM2231	C8orf2	3' TGATCACCACAACCTCA 14024	TCAA
		TGAGTTGTG TGATCA	
		ACTCAACAC ACTAGT	
		C__	
GAM2231	C8orf2	3' TGATCACCACAACCTCA 14025	TCAA
		TGAGTTGTG TGATCA	

			ACTCAACAC	ACTAGT		
			C__			
GAM2231	FADS1	3'	TGAGATCCAGCACA	ACTCA 15069	CAAT	A
			TGAGTTGTGT	GATC TCA		
			ACTCAACACG	CTAG AGT		
			AC__ _			
GAM2231	FLJ23132	3'	GATGACTAACACA	ACT 45982	CAA	A
			AGTTGTGT	TG TCATC		
			TCAACACA	AT AGTAG		
			__ C			
GAM2231	HRD1	3'	TGGCAACCACACA	ACTCA 34475	CAA	A
			TGAGTTGTGT	TG TCA		
			ACTCAACACA	AC GGT		
			CCA _			
GAM2231	KIAA0009	3'	ATGATCATTTAGCATTCA	16022	T	GTC
			TGAGT GT	AATGATCAT		
			ACTTA CG	TTACTAGTA		
			_ AT_			
GAM2231	MGC13523	5'	TGGCATTGACAAACCCA	27234	A	G A
			TG GTT TGTCAATG	TCA		
			AC CAA ACAGTTAC	GGT		
			C _ _			
GAM2231	LOC150481	3'	GAGACACTGGACACAACCCA	38979	A	AA_ A A
			TG GTTGTGTC	TG TC TC		
			AC CAACACAG	AC AG AG		
			C GTC _ _			
GAM2231	LOC158191	3'	GAGACACTGGACACAACCCA	39758	A	AA_ A A
			TG GTTGTGTC	TG TC TC		
			AC CAACACAG	AC AG AG		
			C GTC _ _			
GAM2231	LOC201516	5'	TGACAACCCATACA	ACTCA 42582	CAA_	A
			TGAGTTGTGT	TG TCA		
			ACTCAACATA	AC AGT		
			CCCA _			
GAM2231	LOC219672	5'	TGATGATCATGGAGAAAC	43890	GTG	A
			GTT TC	ATGATCATCA		
			CAA AG	TACTAGTAGT		
			AG_ G			
GAM2231	LOC219988	5'	ATGTTTAGACCGGACACA	ACTC 44042	AA__	T
			TGAGTTGTGTC	TGA CAT		

			ACTCAACACAG	ATT GTA		
			GCCAG	T		
GAM2231	LOC90190	3'	TGACAGGGACACAACCA	30947	A	AA A
			TG GTTGTGTC	TG TCA		
			AC CAACACAG	AC AGT		
			_	GG _		
GAM2231	LOC91380	3'	GTGGCATTAACTCA	32758		C A
			TGAGTTGTGT	AATG TCAT		
			ACTCAATACA	TTAC GGTG		
			A	_		
GAM2232	ATP7A	3'	TACAGGAGAAAGAGGTGA	5494		CA ACGCAG
			TCACCTCT	CT CTGTA		
			AGTGGAGA	GA GACAT		
			AA G	_____		
GAM2232	BCAT1	3'	ACAGCAGGAAGAGGTGA	32894		CA ACGCA
			TCACCTCT	CT GCTGT		
			AGTGGAGA	GA CGACA		
			AG	_____		
GAM2232	FZD4	3'	ACAGCTGCAGTTAGGAAGGG	14481	TC A	_ _
			CC TC CTA	C GCAGCTGT		
			GG AG GAT	G CGTCGACA		
			GA	_ T A		
GAM2232	MAPK1	3'	TTACAGCTTTCTGTGCAGAGAT	8618	C	_ TACGC
	GA		TCA CTCT	CAC AGCTGTAA		
			AGT GAGA	GTG TCGACATT		
			A	C TCTT_		
GAM2232	RAD52	3'	ACAGCTGCAGCAGGTGA	28641	_	CACTAC
			TCACCT	CT GCAGCTGT		
			AGTGGA	GA CGTCGACA		
			C	_____		
GAM2232	RAD52	3'	ACAGCTGCAGCAGGTGA	28651	_	CACTAC
			TCACCT	CT GCAGCTGT		
			AGTGGA	GA CGTCGACA		
			C	_____		
GAM2232	RAD52	3'	ACAGCTGCAGCAGGTGA	28660	_	CACTAC
			TCACCT	CT GCAGCTGT		
			AGTGGA	GA CGTCGACA		
			C	_____		
GAM2232	C21orf93	3'	ACAGCCCAGCGAGGGTGA	29738	T A	ACGCA
			TCACC CTC	CT GCTGT		

AGTGG GAG GA CGACA
 _ C CC_
 GAM2232 DKFZP434C171 3' ACAGCCAAATGGGGGAAGAGGT 17881 CA TA CA_
 GA TCACCTCT C CG GCTGT
 ||||| | || ||||
 AGTGGAGA G GT CGACA
 AG GG AAAC
 GAM2232 KIAA0285 5' ATGGCAGTGGAGGTGA 16747 T ACGCA
 TCACCTC CACT GCTGT
 ||||| ||| ||||
 AGTGGAG GTGA CGGTA
 _ _
 GAM2232 KIAA0408 5' TTACAGCTTTGCCGGAAGT 16237 C ACTA C
 AC TCTC CG AGCTGTAA
 || ||| || |||||
 TG AGGG GT TCGACATT
 A CC_ T
 GAM2232 KIAA1871 3' TTACAATGCTGTACAGTGAGAG 30707 AC _
 CTCTCACT GCAGC TGTA
 ||||| |||| ||||
 GAGAGTGA TGTCG ACATT
 CA TA
 GAM2232 phospho1 3' TTACAACTATAAAGGAGGTGA 40065 CACTACGC C
 TCACCTCT AG TGTA
 ||||| || ||||
 AGTGGAGG TC ACATT
 AAATA_ A
 GAM2232 PPI5PIV 3' ACAGCTGCAACGTGGGGTGA 21273 T T TAC
 TCACC C CAC GCAGCTGT
 |||| | ||| |||||
 AGTGG G GTG CGTCGACA
 _ CAA
 GAM2232 THTPA 3' TTACAGCTGAGTTAGAAGATGA 23621 C _ C ACG
 TCA CT CT ACT CAGCTGTAA
 ||| || ||| |||||
 AGT GA GA TGA GTCGACATT
 A A T _
 GAM2232 TSPEAR 3' ACAGGCAGTGAGGATGA 29594 C T AC AG
 TCA C CTCACT GC CTGT
 ||| | |||| || |||
 AGT G GAGTGA CG GACA
 A _ _ _
 GAM2232 ZNF297B 3' ACACTTAGTGAGAAGG 39769 _ CGC C
 CCT CTCACTA AG TGT
 ||| ||||| || |||
 GGA GAGTGAT TC ACA
 A _ _ _
 GAM2232 ZNF297B 3' ACACTTAGTGAGAAGG 15218 _ CGC C
 CCT CTCACTA AG TGT
 ||| ||||| || |||

GGA GAGTGAT TC ACA
 A _ _
 GAM2232 LOC146227 3' GCAGGTAACAGAGGTGA 38089 CAC GCAG
 TCACCTCT TAC CTGT
 ||||| || |||
 AGTGGAGA ATG GACG
 CA_ _
 GAM2232 LOC146520 5' TACAGCTGCGAAGAAGGCAG 38188 _ CA A
 CT CT CT CGCAGCTGTA
 || || || |||||
 GA GG GA GCGTCGACAT
 C AA A
 GAM2232 LOC149566 3' ACAGCTCAGAAAGGAGAGGTGA 41013 ACTACGC
 TCACCTCTC AGCTGT
 ||||| |||||
 AGTGGAGAG TCGACA
 GAAAGAC
 GAM2232 LOC155435 3' ACAGCTGCGTTGGAGTGGTGA 39565 T ACT
 TCACC CTC ACGCAGCTGT
 |||| || |||||
 AGTGG GAG TCGTCGACA
 T GT_
 GAM2232 LOC202460 5' CAGCCGCACAGCAGGAGGTGA 42981 CA AC A
 TCACCTCT CT GC GCTG
 ||||| || |||||
 AGTGGAGG GA CG CGAC
 AC CA C
 GAM2232 LOC203080 5' CTGAACGTAGTGGAGATGA 43003 C T _
 TCA CTC CACTACG CAG
 || || ||||| |||
 AGT GAG GTGATGC GTC
 A _ AA
 GAM2233 SOX12 3' CACACTCTCATTACACA 13829 CA A
 TGTG AA GAGAGTGTG
 |||| || |||||
 ACAC TT CTCTCACAC
 AC A
 GAM2233 BRPF3 3' AACCACCACAATTCTTATACA 44344 CAA AG
 TGTG AAGAG TGTGGTGGTT
 |||| |||| |||||
 ACAT TTCTT ACACCACCAA
 A_ CA
 GAM2233 KIAA1202 3' ACCCACTCTCCTTCCCACA 35638 CA A
 TGTG AA GAGAGTGTGGT
 |||| || |||||
 ACAC TT CTCTCACACCA
 CC C
 GAM2233 LHFPL2 3' ACCATGCTCTTCCACACA 34658 CAAAA
 TGTG GAGAGTGTGGT
 |||| |||||

ACAC TTCTCGTACCA
 ACC__
 GAM2233 MGC1842 3' AACCACTAACACCTCTGCACA 32684 AAA A _
 TGTGCA GAG GTGT GGTGGTT
 ||||| ||| ||| |||||
 ACACGT CTC CACA TCACCAA
 ____ _ A
 GAM2233 PAK7 3' ACCATTCTTTTGCACA 34509 GAGT
 TGTGCAAAAGA GTGGT
 ||||| ||||
 ACACGTTTTCT TACCA

 GAM2233 RALGPS1A 3' ACTCACTCTCTTTTGCCA 16014 T T
 TG GCAAAAGAGAGTG GGT
 || ||||| ||||| |||
 AC CGTTTTCTCTCAC TCA
 _ _
 GAM2233 SPINLW1 3' AATTGGCACACTCTCTTCCACA 21666 CAA G
 TGTG AAGAGAGTGTG TGGTT
 ||| ||||| ||||| |||||
 ACAC TTCTCTCACAC GTTAA
 C__ G
 GAM2233 LOC127435 3' AACCAACACAGTCTCTGTCACA 37460 CAAA G
 TGTG AGAGA TGTGGTGGTT
 ||| |||| ||||| |||||
 ACAC TCTCT ACACCACCAA
 TG__ G
 GAM2233 LOC144866 5' ACCACCTGTCTTTTGCATA 40474 G T
 TGTGCAAAAGA AG GTGGT
 ||||| || |||||
 ATACGTTTTCT TC CACCA
 G _
 GAM2233 LOC163231 5' AACCTCTTCACTCTCTCCAC 40091 CAAA T T
 GTG AGAGAGTG GG GGTT
 ||| ||||| || |||||
 CAC TCTCTCAC TC CCAA
 CC__ T T
 GAM2233 LOC201952 5' AACCACTGTGCCTCTCACACA 43393 CAAA A TG
 TGTG AGAG GTG GTGGTT
 |||| ||| ||| |||||
 ACAC TCTC CGT CACCAA
 AC__ _ GT
 GAM2233 LOC253675 5' GCTCACACTCTCCTCTCACA 46264 CAAAA _
 TGTG GAGAGTGTG GT
 |||| ||||| ||
 ACAC CTCTCACAC CG
 TCTC_ T
 GAM2233 LOC92080 5' AATCGCCACCCCCTCCTGCCA 33756 T AAA AGT
 TG GCA GAG GTGGTGGTT
 || ||| ||| |||||

		AC CGT CTC CACCGCTAA	
		_ C_ CCC	
GAM2234 ANK3	3'	CCTAGTCGATTATTTAAGCAT 21982	_ G
		ATGCTTAGATAA CGG TAGG	
		TACGAATTTATT GCT ATCC	
		A G	
GAM2234 EPB72	3'	CTAGCCTTCCAAGCATGAA 10305	A TAAC A
		TTCATGCTT GA GGGT GG	
		AAGTACGAA CT TCCG TC	
		C _ _ _ A	
GAM2234 AKAP6	3'	CCTCCCCAAGCATGAA 10489	AGATAAC T
		TTCATGCTT GGG AGG	
		AAGTACGAA CCC TCC	
		C	
GAM2234 KLHL8	3'	CCTACCCGTAAAATATGAA 31476	CTTAGATA
		TTCATG ACGGGTAGG	
		AAGTAT TGCCCATCC	
		AAAA_	
GAM2234 LOC200150	3'	CCTACACAGTCAGCTAAGCATG 42711	ATA GG_
AA		TTCATGCTTAG AC GTAGG	
		AAGTACGAATC TG CATCC	
		GAC ACA	
GAM2234 LOC257319	3'	GCCTTTGTTTATTTAAACATGA 45834	C _ GT
A		TTCATG TTAGATAA CGG AGGC	
		AAGTAC AATTTATT GTT TCCG	
		A T _	
GAM2234 LOC89932	3'	CTGTTATCTGAGCATGAA 30491	
		TTCATGCTTAGATAACGG	
		AAGTACGAGTCTATTGTC	
GAM2235 ALOX15	3'	AGAACTAGGACTGAACTATTTT 6808	CCA GA_ C
A		TAAAATAG TCAG TAGT CT	
		ATTTTATC AGTC ATCA GA	
		A_ AGG A	
GAM2235 ATP8B2	5'	GATGCCACTGATGACTATTT 32515	C GATA
		AAATAG CATCAG GTC	
		TTTATC GTAGTC TAG	
		A ACCG	
GAM2235 COL19A1	3'	GTAGTCCTAAGATGCTGGCTAT 7598	T A_ ATAGT
TTTA		AATAGCCA C GG C	

		TTATCGGT G	CC	G	
		C TAGAIIIT	TGATA		
GAM2235	CPN1	5'	AGGAGAGATGAGTGGCTATT	6990	_ GGATAG
			AATAGCCA TCA	TCCT	
			TTATCGGT AGT	AGGA	
			G AGAG__		
GAM2235	CTNND2	3'	AGGAAATATTAAGAGCTATTTT	7014	CA AG G_
	A		TAAAATAGC TC	GATA TCCT	
			ATTTTATCG AG	TTAT AGGA	
			__ AA	AA	
GAM2235	IL12RB2	3'	AGGACCATTTCATGCAATGACTA	7279	C __ _ A
	TTT		AAATAG CAT	CA GGAT GTCCT	
			TTTATC GTA	GT CTTA CAGGA	
			A AC A	C	
GAM2235	PBX3	3'	GTCCTGTAGCTATTTTA	12868	CAT
			TAAAATAGC	CAGGAT	
			ATTTTATCG	GTCCTG	
			AT_		
GAM2235	PPP3CA	3'	GACTATCCCAAGGTTATTTTA	6643	ATCA
			TAAAATAGCC	GGATAGTC	
			ATTTTATTGG	CCTATCAG	
			AAC_		
GAM2235	PXF	3'	AGGAAATTAATGGCTATT	8750	C GATAG
			AATAGCCAT AG	TCCT	
			TTATCGGTA TT	AGGA	
			A AA__		
GAM2235	RFXAP	3'	ATGTTGATGGCTATTTTG	6134	G
			TAAAATAGCCATCAG	AT	
			GTTTATCGGTAGTT	TA	
			G		
GAM2235	HSA243666	3'	AGGACAATGATGGCTATTCTA	19019	A GGATA
			TA AATAGCCATCA	GTCCT	
			AT TTATCGGTAGT	CAGGA	
			C	AA__	
GAM2235	MCM10	3'	AGGTTATGTCCTAATAACTATT	20592	CC C GT_
			AATAG AT AGGATA	CCT	
			TTATC TA TCCTGT	GGA	
			AA A	ATT	
GAM2235	NETO1	3'	GACTATCCCAACTTTATTTT	29070	CCATCA
			AAAATAG	GGATAGTC	

		TTTTATT CCTATCAG		
		TCAAC_		
GAM2235	PEPP3	3' AGAACACACCTGTGGCTATCTT 17233	A	T ATA C
	A	TAA ATAGCCA CAGG GT CT		
		ATT TATCGGT GTCC CA GA		
		C _ ACA A		
GAM2235	ZID	3' ACTATGACTGTATGATTATTTT 13414	GC	_ G_
	A	TAAAATA CAT CAG ATAGT		
		ATTTTAT GTA GTC TATCA		
		TA T AG		
GAM2235	ZNF237	3' AGAACTATCTTATGGGATATTT 15504	G_	C C
	TA	TAAAATA CCAT AGGATAGT CT		
		ATTTTAT GGTA TTCTATCA GA		
		AG _ A		
GAM2235	LOC122786	3' AGGATCATTTAATGACTGTTTT 36697	C	CA A
	A	TAAAATAG CAT GGAT GTCCT		
		ATTTTGTC GTA TTTA TAGGA		
		A A_ C		
GAM2235	LOC124801	3' AGGGTTCCTGATGGCTTTTTTA 36762	T	TAG
		TAAAA AGCCATCAGGA TCCT		
		ATTTT TCGGTAGTCCT GGGA		
		_ T_		
GAM2236	AKAP2	3' GGTGCAGCCTACATGGCA 14062	AGCAAT	_
		TGCCA TGTAG CTGCACC		
		ACGGT ACATC GACGTGG		
		_ C		
GAM2236	AMFR	3' GTATTATCTACAATTATTGGCA 29067	GC	C_
		TGCCAA AATTGTAG TGC		
		ACGGTT TTAACATC ATG		
		A_ TATT		
GAM2236	AMFR	3' GTATTATCTACAATTATTGGCA 6811	GC	C_
		TGCCAA AATTGTAG TGC		
		ACGGTT TTAACATC ATG		
		A_ TATT		
GAM2236	BCL2L2	3' GTGGTTTTCAAACCTGCTTGGCA 10263	A_	T_ TG
		TGCCAAGCA TTG AGC C		
		ACGGTTCGT AAC TTG G		
		CA TT GT		
GAM2236	DPH2L2	3' GTGCAGCTACAGGATATGC 7060	A_	
		GCA TTGTAGCTGCAC		

CGT GACATCGACGTG
 ATAG
 GAM2236 HBE1 5' CAGCTGCAATCACTAGCA 11805 CA CA
 TGC AG ATTGTAGCTG
 ||| || |||||
 ACG TC TAACGTCGAC
 A_ AC
 GAM2236 HSPA4 3' TGGAGAACAATTGCTTAGG 42975 _ AG G
 CC AAGCAATTGT CT CA
 || ||||| ||
 GG TTCGTTAACA GA GT
 A A_ G
 GAM2236 SKI 3' GGTGCAGCTCCGCCCGGC 8990 AA AATT T
 GCC GC G AGCTGCACC
 ||| || | |||||
 CGG CG C TCGACGTGG
 CC _ C
 GAM2236 TMPRSS2 3' TGGTGCAGGTCTCCACCTGC 12196 AT T _
 GCA TG AG CTGCACCA
 ||| ||| |||||
 CGT AC TC GACGTGGT
 CC C TG
 GAM2236 C20orf150 3' TGGTGCAGGACAGCTGCCAGCA 32599 CAA A AG
 TGC GCA TTGT CTGCACCA
 ||| ||| ||| |||||
 ACG CGT GACA GACGTGGT
 AC_ C G_
 GAM2236 CSTF1 5' GCGCAGCGGTCGCTTGGC 7009 A A T
 GCCAAGC ATTGT GC GC
 ||||| |||| ||
 CGGTTTCG TGGCG CG CG
 C A _
 GAM2236 FLJ12700 3' GGGGCAAACCTGCTTGGCA 24414 ATT AGC A
 TGCCAAGCA GT TGC CC
 ||||| || |||
 ACGGTTTCGT CA ACG GG
 _ A_ G
 GAM2236 FLJ20320 5' GGTGCAGCCCTGCCTGGC 19383 A ATTGTA
 GCCA GCA GCTGCACC
 ||| ||| |||||
 CGGT CGT CGACGTGG
 C CC_
 GAM2236 GP5 3' TGGTGCAGCCAACCAACCTGGC 10821 AGCAA_ TA
 A TGCCA TTG GCTGCACCA
 |||| ||| |||||
 ACGGT AAC CGACGTGGT
 CCAACC _
 GAM2236 KIAA0649 3' CAGCGGCAGCTGCTCGGCA 16773 A A A
 TGCC AGCA TTGT GCTG
 |||| |||| |||| |||

		ACGG TCGT GACG CGAC		
		C C G		
GAM2236	KIAA1383	3' TAGCACAATTCCTGGCA	34585	A C A
		TGCCA G AATTGT GCTG		
		ACGGT C TTAACA CGAT		
		_ C _		
GAM2236	PA26	3' GCAGTGA CTGTTTGGCA	15808	ATT A
		TGCCAAGCA GT GCTGC		
		ACGGTTTGT CA TGACG		
		_ _ G		
GAM2236	SLC5A7	3' TGGAGACTACAATTCCTGGCA	22394	A C _ G
		TGCCA G AATTGTAG CT CA		
		ACGGT C TTAACATC GA GT		
		_ C A G		
GAM2236	LOC118987	3' TGCAGCTGCACCTAAGCA	36609	CA CAAT
		TGC AG TG TAGCTGCA		
		ACG TC ACGTCGACGT		
		AA C _		
GAM2236	LOC150245	3' TAGTTACAGCTACTTGGCA	41164	CAA
		TGCCAAG TTGTAGCTG		
		ACGGTTC GACATTGAT		
		ATC		
GAM2236	LOC151162	5' TAGCACAGTGCTTGGCA	41309	A A
		TGCCAAGCA TTGT GCTG		
		ACGGTTCGT GACA CGAT		
		_ _		
GAM2236	LOC158056	5' GTGCAGCTGCTGCTGGGCA	39719	A ATT
		TGCC AGCA GTAGCTGCAC		
		ACGG TCGT CGTCGACGTG		
		G _		
GAM2236	LOC202134	3' TGCAGCTACAAGGCCACTGGC	43414	A _ AA
		GCCA GC TTGTAGCTGCA		
		CGGT CG AACATCGACGT		
		CAC G _		
GAM2236	LOC203377	5' TAGCACAGTGCTTGGCA	43544	A A
		TGCCAAGCA TTGT GCTG		
		ACGGTTCGT GACA CGAT		
		_ _		
GAM2236	LOC220988	3' TAGCACAGTTGCTTAGTA	43683	C A
		TGC AAGCAATTGT GCTG		

		ATG TTCGTTGACA CGAT		
		A _		
GAM2236	LOC221271 3'	CAGTAGCAGTTACTTGGCA	44123	C A
		TGCCAAG AATTGT GCTG		
		ACGGTTC TTGACG TGAC		
		A A		
GAM2236	LOC92370 3'	TGGTACGTGAATTGCTTGGTA	34259	GTA T C
		TGCCAAGCAATT GC G ACCA		
		ATGGTTCGTAA TG C TGGT		
		G _ _ A		
GAM2236	LOC93048 5'	TGCAGCTGCACCTAAGCA	35296	CA CAAT
		TGC AG TGTAGCTGCA		
		ACG TC ACGTCGACGT		
		AA C _		
GAM2237	CBFA2T3 3'	CCGACACACCTCTGCT	11689	G A
		AGCAG AGGTGTGTT GG		
		TCGTC TCCACACAG CC		
		_ G		
GAM2237	DBY 3'	AACTCTTCCCCTCCTGCTT	11025	TGTGTT _
		AAGCAGGAGG AG GTT		
		TTCGTCCTCC TC CAA		
		CCT _ T		
GAM2237	DFNA5 3'	AACAGTAACACACCCTGCTT	10654	A G _
		AAGCAGG GGTGTGTTA GTT		
		TTCGTCC CCACACAAT CAA		
		_ GA		
GAM2237	HNMT 5'	AACCTTGCTTCCTGCT	13767	TGTT
		AGCAGGAGGTG AGGTT		
		TCGTCCTTCGT TCCAA		
		_		
GAM2237	JPH2 5'	TTGAACCTTTCCTTCCTGCTT	45333	TGTGTT
		AAGCAGGAGG AGGTTCAA		
		TTCGTCCTTC TCCAAGTT		
		CTT _		
GAM2237	NBEA 3'	TTGAACCTAACCTGCATCCC	45494	A _
		GG GGTGT GTTAGGTTCAA		
		CC CTACG CAATCCAAGTT		
		_ TC		
GAM2237	TSN 3'	TTAAAACACCTCTGCTT	10987	G G
		AAGCAG AGGTGT TTAG		

			TTCGTC TCCACA AATT		
			— A		
GAM2237	VCL	3'	TGAAGGACACTTCCTGC 9406	G	TAGG
			GCAGGAGGTGT T TTCA		
			CGTCCTTCACA G AAGT		
			G —		
GAM2237	VCL	3'	TGAAGGACACTTCCTGC 15195	G	TAGG
			GCAGGAGGTGT T TTCA		
			CGTCCTTCACA G AAGT		
			G —		
GAM2237	C9orf14	5'	TGAAGATGACACCTCCTCT 41912	C	GT GG
			AG AGGAGGTGT TA TTCA		
			TC TCCTCCACA GT AAGT		
			— — AG		
GAM2237	CASPR3	5'	TGAACCTGCCGCCTCCGTGC 24317	—	T T
			GCA GGAGGTG GT AGGTTCA		
			CGT CCTCCGC CG TCCAAGT		
			G — —		
GAM2237	CASPR3	5'	TGAACCTGCCGCCTCCGTGC 27388	—	T T
			GCA GGAGGTG GT AGGTTCA		
			CGT CCTCCGC CG TCCAAGT		
			G — —		
GAM2237	DATF1	3'	GGCCACACACTCCTGCTT 28063	G	TA
			AAGCAGGAG TGTGT GGTT		
			TTCGTCCTC ACACA CCGG		
			— —		
GAM2237	DATF1	3'	GGCCACACACTCCTGCTT 22652	G	TA
			AAGCAGGAG TGTGT GGTT		
			TTCGTCCTC ACACA CCGG		
			— —		
GAM2237	DKFZp434F142	3'	AACAGGCCCAGCTCCTGC 25991	G T	AG
			GCAGGAG TG GTT GTT		
			CGTCCTC AC CGG CAA		
			G C A_		
GAM2237	FLJ11320	3'	TTGAACCCCTTCCTTCTGC 20430	TGTGTTA	
			GCAGGAGG GGTTCAA		
			CGTCTTCC CCAAGTT		
			TTCC_		
GAM2237	FLJ12529	3'	AATCCCACACCTCCTGTTT 24190	TTA	
			AAGCAGGAGGTGTG GGTT		

	TTTGTCTCCACAC	CTAA	
	C__		
GAM2237 KIAA0408	3' AACCTGCCTGACTTCCTGCT	16228	GTGT
	AGCAGGAGGT TAGGTT		
	TCGTCCTTCA GTCCAA		
	GTCC		
GAM2237 KIAA0618	3' AACCCCATGTCCTCCTCCT	16831	C _ TTA
	AG AGGAGG TGTG GGTT		
	TC TCCTCC GTAC CCAA		
	C T C__		
GAM2237 KIAA1191	3' TGAACCTTGAGTCCCCCTGCTT	21683	A TG GTT
	AAGCAGG GG T AGGTTCA		
	TTCGTCC CC G TCCAAGT		
	_ CT AGT		
GAM2237 KIAA1944	3' TTGAACCTATCTTCTCCCTGCT	37232	AG TGTGT
T	AAGCAGG G TAGGTTCAA		
	TTCGTCC C ATCCAAGTT		
	CT TTCT_		
GAM2237 MGC2668	3' AGCCACACCCCTCCTGCT	30379	T TA
	AGCAGGAGG GTGT GGTT		
	TCGTCCTCC CACA CCGA		
	C _		
GAM2237 NIN283	3' CTATTCACAGCACCTCCTGCTT	26013	GT_____
	AAGCAGGAGGTGT TAG		
	TTCGTCCTCCACG ATC		
	ACACTT		
GAM2237 TRABID	5' AACCTCGTTATATCTCCTGC	33992	TT_
	GCAGGAGGTGTG AGGTT		
	CGTCCTCTATAT TCCAA		
	TGC		
GAM2237 LOC139770	3' TTGAACCTAAATTTGACCATGC	37150	_ AGGTGTG
	GCA GG TTAGGTTCAA		
	CGT CC AATCCAAGTT		
	A AGTTTA_		
GAM2237 LOC146268	3' GACCCACGCCTCCCGC	38124	A TTA
	GC GGAGGTGTG GGTT		
	CG CCTCCGCAC CCAG		
	C _		
GAM2237 LOC147136	3' AACCCAGACCCACCTCCTGC	38298	T A_
	GCAGGAGGTG GTT GGTT		

		CGTCCTCCAC CAG CCAA	
		C AC	
GAM2237	LOC219793 5'	AACCCCTGGCACCTACTGCTT 43915	G GTTA
		AAGCAG AGGTGT GGT	
		TTCGTC TCCACG CCAA	
		A GTCC	
GAM2237	LOC219920 5'	TGAACCCACCATCTTCCTGCT 44812	T TTA
		AGCAGGAGG GTG GGTTC	
		TCGTCCTTC TAC CCAAGT	
		_ CAC	
GAM2238	ADCY7 3'	GCAAAAAGCCAGGTTTTGG 6784	CAA T C_
		TCAAAACC TG GCT TTGC	
		GGTTTTGG AC CGA AACG	
		_ _ AA	
GAM2238	ATP8A2 3'	GCAAGAGTATAGGACATTGA 44921	AAC AA
		TCAA CC TGTGCTCTTGC	
		AGTT GG ATATGAGAACG	
		ACA _	
GAM2238	BCL6 5'	GCCGGACACCAGGTTTTGA 7431	CAAT C T
		TCAAAACC GTG TCT GC	
		AGTTTTGG CAC AGG CG	
		AC_ _ C	
GAM2238	MLLT4 3'	GCAAGGACTCTCATTGGGTT 35887	TGC_
		AACCCAATG TCTTGC	
		TTGGGTTAC GGAACG	
		TCTCA	
GAM2238	PSME3 5'	GCAAGGGCGGTCGGGTCCCGA 12371	AAA A G
		TC ACCC AT TGCTCTTGC	
		AG TGGG TG GCGGGAACG	
		CCC C _	
GAM2238	RAB23 3'	GCAAAATGAGCTTGGGTTT 18400	TGT _
		AAACCCAA GCTC TTGC	
		TTTGGGTT CGAG AACG	
		_ TAA	
GAM2238	SLC1A1 3'	CAAGTGTTTTGGGTTTT 10377	TGT T
		AAAACCCAA GC CTTG	
		TTTTGGGTT TG GAAC	
		T_ T	
GAM2238	ATP9A 3'	GCAAGGCATTCTTGGGTTTT 31085	T_ T
		AAAACCCAA GTGC CTTGC	

			TTTTGGGTT TACG GAACG		
			CT _		
GAM2238	DGKD	3'	GCAAGGAGTTGGGTTTGA 29883	A	GTGC
			TC AAACCCAAT TCTTGC		
			AG TTTGGGTTG GGAACG		
			G A__		
GAM2238	FLJ10520	3'	GCATTAGTACATTAAATTTGG 19905	ACCC	CT
			TCAA AATGTGCT TGC		
			GGTTT TTACATGA ACG		
			AAA_ TT		
GAM2238	FLJ20618	3'	GCAAGAGTAGGGGCCTGA 19569	AAA	AATG
			TCA CCC TGCTCTTGC		
			AGT GGG ATGAGAACG		
			CCG _		
GAM2238	GRIN3A	3'	GCAAGAGCCATGTTTTTGA 28536	CCCA	T
			TCAAAA ATG GCTCTTGC		
			AGTTTT TAC CGAGAACG		
			TG__ _		
GAM2238	H2AFJ	3'	CAAAATGCATATATGGTTTTGA 20237	CA	TC_
			TCAAAACC ATGTGC TTG		
			AGTTTTGG TATACG AAC		
			TA TAA		
GAM2238	KIAA0565	5'	CAAGAGCATAGGAGTTTT 33216	_	AA
			AAAAC CC TGTGCTCTTG		
			TTTTG GG ATACGAGAAC		
			A _		
GAM2238	KIAA0677	3'	GCAAGAGCACTCTGGGTT 16110	AT	
			AACCCA GTGCTCTTGC		
			TTGGGT CACGAGAACG		
			CT		
GAM2238	KIAA0794	3'	CAAGATGTGGTGGGTTTT 39177	ATGT	_
			AAAACCCA GC TCTTG		
			TTTTGGGT TG AGAAC		
			GG_ T		
GAM2238	KIAA0979	3'	CCTTGACATACATTGGTTTTG 17387	C	T_____ TCTT
	A		CAAAACC AATG GC G		
			GTTTTGG TTAC CG C		
			_ ATACA TTCT		
GAM2238	LHFP	3'	CAAGGGTTTGGGTTTT 12356	TGT	
			AAAACCCAA GCTCTTG		

TTTTGGGTT TGGGAAC

GAM2238 MKP-7 5' GCAAGAGCACATCAACGGG 33007 A____
CCC ATGTGCTCTTGC
||| |||||
GGG TACACGAGAACG
CAAC

GAM2238 PORIMIN 3' CAAGGGTTTGGGTTTGA 27491 TGT
TCAAAACCCAA GCTCTTG
||||||| |||||
AGTTTGGGTT TGGGAAC

GAM2238 PTK9 3' GCAAGAGCCATAACTTTGA 8691 ACCCA T
TCAAA ATG GCTCTTGC
|||| | |||||
AGTTT TAC CGAGAACG
CAA__ _

GAM2238 SNPH 3' GCAAGAGCTGATGAGGTCCTGA 16295 AA _ ATGT
TCA ACC CA GCTCTTGC
||| ||| || |||||
AGT TGG GT CGAGAACG
CC A AGT_

GAM2238 LOC115509 3' GCAAACAGGCACTGGGTTTT 36364 AT C__
AAAACCCA GTGCT TTGC
|||||| |||| ||||
TTTTGGGT CACGG AACG
_ ACA

GAM2238 LOC134266 3' GCAAGGAGCATCGAAATTTGA 37068 ACCCAAT _
TCAAA GTGCTC TTGC
|||| ||||| ||||
AGTTT TACGAG AACG
AAAGC__ G

GAM2238 LOC145439 5' GCAAGAGCTCATGGGCCATGA 37865 AAA A T
TCA CCCA TG GCTCTTGC
||| |||| || |||||
AGT GGGT AC CGAGAACG
ACC _ T

GAM2238 LOC146819 3' GCTCTTGCACAAATTTTGGGT 38254 ____ T__ TCTT
TTTG AAACCCAA TG GC GC
|||||| || || ||
TTTGGGTT AC CG CG
TTTAA A||| TTCT

GAM2238 LOC146821 3' GCTCTTGCACAAATTTTGGGT 38252 ____ T__ TCTT
TTTG AAACCCAA TG GC GC
|||||| || || ||
TTTGGGTT AC CG CG
TTTAA A||| TTCT

GAM2238 LOC150142 5' GCAAGAGCACTGGCTGTTGTGA 38853 A __ AT
TCA AAC CCA GTGCTCTTGC
||| ||| || |||||

AGT TTG GGT CACGAGAACG
 G TC ____
 GAM2238 LOC201287 5' CAAGAGCATAGGAGTTTT 42559 _ AA
 AAAAC CC TGTGCTCTTG
 ||||| || |||||
 TTTTG GG ATACGAGAAC
 A ____
 GAM2238 LOC219627 5' AAGGGCTGGGTTTTGA 44271 ATGT
 TCAAAACCCA GCTCTT
 ||||| || |||||
 AGTTTTGGGT CGGGAA

 GAM2238 LOC220705 3' GCAGTAACATTGGGTCCTGG 43834 AA GCTC
 TCA ACCCAATGT TTGC
 || ||||| |||||
 GGT TGGGTTACA GACG
 CC AT____
 GAM2238 LOC221895 3' AGAGCACATTAAGTCTGA 44442 AA CC
 TCA AC AATGTGCTCT
 || || |||||
 AGT TG TTACACGAGA
 C_ AA
 GAM2238 LOC222060 5' GCAAGATTTGTGTTGTTTGA 45160 C TG GC_
 TCAAAACC AA T TCTTGC
 ||||| || | |||||
 AGTTTTGG TT G AGAACG
 _ GT TTT
 GAM2238 LOC256207 5' CAAGAGCATAGGAGTTTT 45617 _ AA
 AAAAC CC TGTGCTCTTG
 ||||| || |||||
 TTTTG GG ATACGAGAAC
 A ____
 GAM2238 LOC86651 3' CCTTGCGCAGACATTGGTTTTG 34098 C T_____ TCTT
 A CAAAACC AATG GC G
 ||||| || || |
 GTTTTGG TTAC CG C
 _ AGACG||| TTCT
 GAM2238 LOC91151 5' GCAAGAGCCAGACAGGACTTTG 27053 AC AA__ T
 CAAA CC TG GCTCTTGC
 |||| || || |||||
 GTTT GG AC CGAGAACG
 CA ACAG _
 GAM2239 ABCA1 3' GCTTTGATTCCCTCTGATA 12015 T _ T
 TATCAGAGG AA CAA GT
 ||||| || || ||
 ATAGTCTCC TT GTT CG
 C A T
 GAM2239 EIF1A 3' ATATTGATACCTCTGATA 42719 A
 TATCAGAGGTA CAATGT
 ||||| || |||||

		ATAGTCTCCAT GTTATA	
		A	
GAM2239	PCDH12	5' GGCAGTTTACCTCTGATG 18658	CAA
		TATCAGAGGTAA TGTT	
		GTAGTCTCCATT ACGG	
		TG_	
GAM2239	RRM2B	3' CTTAACATTTAAACTGATA 33689	AGG CA
		TATCAG TAA ATGTTAAG	
		ATAGTC ATT TACAATTC	
		AAA _	
GAM2239	AKT3	3' ACATTTATCACCTCTGATG 11957	AAC_
		TATCAGAGGT AATGT	
		GTAGTCTCCA TTACA	
		CTAT	
GAM2239	DNAJC6	3' GCTTGAATGCCACCTTCTGA 16661	_ AA ATG
		TCAGA GGT CA TTAAGC	
		AGTCT CCA GT AGTTCG	
		T CC A_	
GAM2239	KIAA0694	3' CTTAACAAACCTTTGA 35928	AACAA
		TCAGAGGT TGTTAAG	
		AGTTTCCA ACAATTC	
		A_	
GAM2239	KIAA0892	3' CTTAACATCTGTCCTGATG 35169	A GT ACA
		TATCAG G A ATGTTAAG	
		GTAGTC C T TACAATTC	
		_ TG C_	
GAM2239	LRP1B	3' CTTTTTGTTCTCTGATA 20639	T TGTT
		TATCAGAGG AACAA AAG	
		ATAGTCTCC TTGTT TTC	
		_ T_	
GAM2239	NR6A1	3' GCCCGGCTGCTACCTCTG 27181	A AT AA
		CAGAGGTA CA GTT GC	
		GTCTCCAT GT CGG CG	
		C _ CC	
GAM2239	NR6A1	3' GCCCGGCTGCTACCTCTG 27187	A AT AA
		CAGAGGTA CA GTT GC	
		GTCTCCAT GT CGG CG	
		C _ CC	
GAM2239	NR6A1	3' GCCCGGCTGCTACCTCTG 7233	A AT AA
		CAGAGGTA CA GTT GC	

	GTCTCCAT GT CGG CG		
	C _ CC		
GAM2239 RAB3GAP 3'	CTAAATGTATTACTTCTGATA 33244	CA	A
	TATCAGAGGTAA ATGTT AG		
	ATAGTCTTCATT TGTA TC		
	A_ A		
GAM2239 LOC147632 5'	GCTATGCGTTACCTCTGAT 28826	AAT	TA
	ATCAGAGGTAA GT AGC		
	TAGTCTCCATTG CG TCG		
	_ TA		
GAM2239 LOC148894 3'	GCTTTTTTTGCCACTCTGATA 40919	GTAA	TGTT
	TATCAGAG CAA AAGC		
	ATAGTCTC GTT TTCG		
	ACC_ TTT_		
GAM2239 LOC151473 3'	CTTAATATTACCTCCAATG 39120	CA	ACA
	TAT GAGGTA ATGTTAAG		
	GTA CTCCAT TATAATTC		
	AC _		
GAM2239 LOC151521 5'	GCCCAACATCCCTTTACCTCT 41370	CA_	AA
	AGAGGTAA ATGTT GC		
	TCTCCATT TACAA CG		
	TCCC CC		
GAM2239 LOC157349 5'	CTGAGCATTACTCTGATA 39594	GTAAC	A
	TATCAGAG AATGTT AG		
	ATAGTCTC TTACGA TC		
	A_ G		
GAM2239 LOC200150 3'	TTTGTATTTGTTACCTCTGA 42713	TGT	
	TCAGAGGTAACAA TAAG		
	AGTCTCCATTGTT GTTT		
	TAT		
GAM2239 LOC51185 3'	GCTTTGGAAATTATTGCCTCTG 18424	C	GTT_
ATA	TATCAGAGGTAA AAT AAGC		
	ATAGTCTCCGTT TTA TTCG		
	A AAGGT		
GAM2239 LOC56906 3'	CTCAACATCAAATGCTCTGATG 21343	GTAACA	A
	TATCAGAG ATGTT AG		
	GTAGTCTC TACAA TC		
	GTAAAC C		
GAM2239 LOC92539 5'	ATATTGCTTCCTCTGATA 34500	TAA	
	TATCAGAGG CAATGT		

			ATAGTCTCC GTTATA		
			TTC		
GAM2240	SLC39A1	3'	GTAATGTGGCACTGAGC 15794	CGAACA	
			GCTCA GCCACATTAC		
			CGAGT CGGTGTAATG		
			CA_____		
GAM2240	SOX12	5'	AATGTGTGTTGTGAGC 13828	G GC	
			GCTCAC AACA CACATT		
			CGAGTG TTGT GTGTAA		
			— —		
GAM2240	RASSF2	3'	ATGTGCTGCTCGTGAGC 16391	A C	
			GCTCACGA CAGC ACAT		
			CGAGTGCT GTCG TGTA		
			C —		
GAM2240	SSR3	3'	TAATGTGGAGTGACTA 13973	C GAACAG	
			TAG TCAC CCACATTA		
			ATC AGTG GGTGTAAT		
			— A_____		
GAM2240	LOC152200	3'	AATGTGGCCTGGCCAAGCTG 41436	CACGAA _	
			TAGCT CAG CCACATT		
			GTCGA GTC GGTGTAA		
			ACCG_ C		
GAM2241	POPX1	3'	ATGGTGTGAAAAATAACTGTT 17117	CGGA_	
			GACA TTTTCAACACCAT		
			TTGT AAAAGTTGTGGTA		
			CAATA		
GAM2241	PRO2714	5'	ATGGTGTTAATGTGTGCCT 20603	A G TTC	
			AG CACG ATT AACACCAT		
			TC GTGT TAA TTGTGGTA		
			C G _		
GAM2241	SLC11A2	3'	ATGGTGTTGAAGGACTTCTC 6223	CAC A	
			GA GG TTTTCAACACCAT		
			CT TC GGAAGTTGTGGTA		
			CT_ A		
GAM2241	LOC254228	3'	ATGGTGTTGAGTGGCATGCTC 45918	_ CGGATT	
			GA CA TTCAACACCAT		
			CT GT GAGTTGTGGTA		
			C ACGGT_		
GAM2241	LOC90736	3'	TTGAAGATATGTGCTTA 31959	A G	
			TAAG CACG ATTTCAA		

ATTC GTGT TAGAAGTT
 _ A
 GAM2242 ALDH1A3 3' GTGTCCAGCAGTTGCTTGAA 6354 _
 TTCAAGCA CTGCTGGACAC
 ||||| |||||
 AAGTTCGT GACGACCTGTG
 T
 GAM2242 ANXA9 5' CCACACCGGAGCAGTGCT 9622 _ ACAC
 AGCACTGCT GG TGTGG
 ||||| || ||||
 TCGTGACGA CC ACACC
 GG ____
 GAM2242 CARD6 3' CCACAGTGCCCAGCCCGAATTG 26321 GCACT A
 GA TTCAA GCTGG CACTGTGG
 |||| |||| |||||
 AGGTT CGACC GTGACACC
 AAGCC C
 GAM2242 DKFZp434C0923 3' CCACAGACGCTCAGCCAATGCT 19062 CT_ _ACA
 TGAA TTCAAGCA GCTG G CTGTGG
 ||||| ||| | |||||
 AAGTTCGT CGAC C GACACC
 AAC T GCA
 GAM2242 FLJ13491 3' CCACAGTACCACAGTGT 23886 C AC
 GCACTG TGG ACTGTGG
 ||||| || |||||
 TGTGAC ACC TGACACC
 _ A_
 GAM2242 KIAA1229 3' CCACAGTGCCCTGCTTACCTGC 31096 CT___ T A
 GCA GC GG CACTGTGG
 || || || |||||
 CGT CG CC GTGACACC
 CCATT T C
 GAM2242 LOC157798 5' TGATCCAGCAGTGTGCGAA 41853 AA _
 TTC GCACTGCTGGA CA
 || ||||| ||
 AAG TGTGACGACCT GT
 C_ A
 GAM2242 LOC92912 5' CCATTTTCCAGCAGCGCTCGA 35083 A A CACT
 TC AGC CTGCTGGA GTGG
 || || ||||| ||||
 AG TCG GACGACCT TACC
 C C TT_
 GAM2243 EXTL2 3' CCAAACACTTGCATTCACAACT 7161 A_ A C
 TTA TGAAGTTGTGGAT AA TGT TGG
 ||||| || || ||||
 ATTTCAACACTTA TT ACA ACC
 CG C A
 GAM2243 LRRC2 3' CAAACATTTTATTCTCAA 23702 T C
 TTG GGATAAAATGT TG
 || ||||| ||

			AAC CTTATTTTACA AC		
			T A		
GAM2243	MKI67	3'	CCAGACATCTTTCTCCAGCTTC 8253	TG	TAAA
	A		TGAAGTTG GA ATGTCTGG		
			ACTTCGAC CT TACAGACC		
			CT TTC_		
GAM2243	HML2	5'	CAGACCTCCCACAGCTCCA 13041 A	ATAAAAT	
			TG AGTTGTGG GTCTG		
			AC TCGACACC CAGAC		
			C CTC_		
GAM2243	KIAA0057	3'	CAGAGACGCCACAACCTTCA 14617	ATAAAATG	
			TGAAGTTGTGG TCTG		
			ACTTCAACACC AGAC		
			GCAG_		
GAM2243	LOC145757	5'	CATTTTAACCACAACCTTCA 37971	A	
			TGAAGTTGTGG TAAAATG		
			ACTTCAACACC ATTTTAC		
			A		
GAM2243	LOC149506	3'	CATTTTTCTCCACCCCAACTTC 41004	_ T_	
	A		TGAAGTT GTGGA AAAATG		
			ACTTCAA CACCT TTTTAC		
			CCC CT		
GAM2244	XK	3'	GTCCAGCACTACAACCTTA 22060	A _	
			TGAGTTGTA TGCTG AC		
			ATTCAACAT ACGAC TG		
			C C		
GAM2244	POF1B	3'	CCACTTTAAAGTATTACAACCTC 24454	GA	CTCTA
	A		TGAGTTGTAATGCT TGG		
			ACTCAACATTATGA ACC		
			AATTTC_		
GAM2244	LOC158156	3'	CCACAAAGTCAGCATTTAAAT 39738	GT	CTA
			GTT AATGCTGACT TGG		
			TAA TTACGACTGA ACC		
			AT AAC		
GAM2245	ALTE	3'	GTAAGCTGAGATCGCTGCA 11106	G	CTG T
			TG AGCG CT CAGCTTAC		
			AC TCGC GA GTCGAATG		
			G TA_ _		
GAM2245	BAG2	5'	AGCCCAAGGAGCGCTCCA 43752	G	CA
			TGGAGCGCT CTT GCT		

ACCTCGCGA GAA CGA
 G CC
 GAM2245 DKFZp547D155 3' TGGGCAAAGCAGCCACCCCA 34870 AGC_ CA
 TGG GCTGCTT GCTTA
 ||| ||||| ||||
 ACC CGACGAA CGGGT
 CCAC A_
 GAM2245 DKFZP586A011 3' GGTGAAAACAGCACTCC 17717 C C CAGC
 GGAG GCTG TT TTACC
 |||| |||| || ||||
 CCTC CGAC AA AGTGG
 A A ____
 GAM2245 FLJ10719 3' TGGTAAATATCCAGCGCTTCA 31342 CTCACG
 TGGAGCGCTG TTACCA
 ||||| ||||
 ACTTCGCGAC AATGGT
 CTATA_
 GAM2245 KLK15 3' GGCTTGAAGCAGGGCTCCAT 23266 G _
 ATGGAGC CTGCTTCA GCT
 ||||| ||||| |||
 TACCTCG GACGAAGT CGG
 G T
 GAM2245 KLK15 3' GGCTTGAAGCAGGGCTCCAT 28864 G _
 ATGGAGC CTGCTTCA GCT
 ||||| ||||| |||
 TACCTCG GACGAAGT CGG
 G T
 GAM2245 LR8 5' TGGGTCAAGCAGCGCCCA 15237 A CA
 TGG GCGCTGCTT GCTTA
 ||| ||||| ||||
 ACC CGCGACGAA TGGGT
 C C_
 GAM2245 SDFR1 3' TAAGCTGGAACAGTCCA 14803 AGC C
 TGG GCTG TTCAGCTTA
 ||| ||| |||||
 ACC TGAC AGGTCGAAT
 _ A
 GAM2245 SDFR1 3' TAAGCTGGAACAGTCCA 18930 AGC C
 TGG GCTG TTCAGCTTA
 ||| ||| |||||
 ACC TGAC AGGTCGAAT
 _ A
 GAM2245 ZAK 3' AAGAGGATAAAACAACGCTCCA 18775 C CT__ AG
 T ATGGAGCG TG TC CTT
 ||||| || |||
 TACCTCGC AC AG GAA
 A AAAAT GA
 GAM2245 LOC146540 3' GTAAGCTGAGATGGCTCCAT 38199 GCTG T
 ATGGAGC CT CAGCTTAC
 ||||| || |||||

		TACCTCG GA GTCGAATG	
		GTA_ _	
GAM2245	LOC152485 3'	AAGCTGAAGCACGCCCCA 39280	A C
		TGG GCG TGCTTCAGCTT	
		ACC CGC ACGAAGTCGAA	
		C _	
GAM2245	LOC91300 5'	AGGCGGAAACAGCACTTCAT 45385	C C A
		ATGGAG GCTG TTC GCTT	
		TACTTC CGAC AAG CGGA	
		A A G	
GAM2245	LOC91300 5'	AGGCGGAAACAGCACTTCAT 29004	C C A
		ATGGAG GCTG TTC GCTT	
		TACTTC CGAC AAG CGGA	
		A A G	
GAM2246	FY 5'	GACCTTGTCTCCACCCGAC 7792	ACA A TTT
		GTC TGG AG AACAAAGGTC	
		CAG ACC TC TTGTTCCAG	
		CCC C _	
GAM2246	PACE4 3'	ACCCTGGGCCATCCTCACATGT 8429	GA TTAA_ A
	GAC	GTCACATG AG CA GGT	
		CAGTGTAC TC GT CCA	
		AC CTACCGG C	
GAM2246	PACE4 3'	ACCCTGGGCCATCCTCACATGT 28718	GA TTAA_ A
	GAC	GTCACATG AG CA GGT	
		CAGTGTAC TC GT CCA	
		AC CTACCGG C	
GAM2246	SURF6 3'	GACCTCGGCCTCTCCATGTGA 13611	A TTAAACA
		TCACATGGA G AGGTC	
		AGTGTACCT C TCCAG	
		TCCGGC	
GAM2246	TIMP3 3'	GACCTCTGTCTTGATGTGAC 5929	G TTAA _
		GTCACATG AAG ACA AGGTC	
		CAGTGTAC TTC TGT TCCAG	
		G _ C	
GAM2246	FLJ10620 3'	GACCCTGTCATTAATTCCATGT 19974	GTTTA_ A
	G	CACATGGAA ACA GGTC	
		GTGTACCTT TGT CCAG	
		AATTAC C	
GAM2246	FLJ12355 3'	GGCCTAACCCCATGTGAC 24544	AA TAACA
		GTCACATGG GTT AGGTC	

CAGTGTACC CAA TCCGG
 CC _____
 GAM2246 KIAA0515 3' ACCTTGTTAAACGTTGAC 31917 CATGGAA
 GTCA GTTTAACAAGGT
 ||| |||||
 CAGT CAAATTGTTCCA
 TG_____

GAM2246 KIAA1165 3' GACCTCACTAAACTGTTTATGT 33476 _ ACA
 GAC GTCACATGGA AGTTTA AGGTC
 ||||| ||||| |||
 CAGTGTATTT TCAAAT TCCAG
 G CAC

GAM2246 LOC137964 3' ACCCTGAACTCCCCATGTGAT 37109 A_ ACAA
 GTCACATGG AGTTTA GGT
 ||||| ||||| |||
 TAGTGTACC TCAAGT CCA
 CC C_____

GAM2246 LOC145474 5' GACCTTGTTAGTGACATGT 37868 GAAGT
 ACATG TTAACAAGGTC
 ||| |||||
 TGTAC GATTGTTCCAG
 AGT_____

GAM2246 LOC158654 3' ACTCAAGCTTCCATGTGAC 39873 AACAA
 GTCACATGGAAGTTT GGT
 ||||| ||||| |||
 CAGTGTACCTTCGAA TCA
 C_____

GAM2246 LOC253897 3' ACCCTGAACTCCCCATGTGAT 45966 A_ ACAA
 GTCACATGG AGTTTA GGT
 ||||| ||||| |||
 TAGTGTACC TCAAGT CCA
 CC C_____

GAM2247 SYNJ2 3' ATTTGTACTGAAATTGTACATG 30943 C TC
 AT ATCA GTACAATTTTCG ACAGAT
 ||| ||||| |||||
 TAGT CATGTTAAAGT TGTTTA
 A CA

GAM2247 LOC125704 3' ATCTGTGACAAAATATTTTCG 36797 TACA C
 CG ATTT GTCACAGAT
 || ||| |||||
 GC TAAA CAGTGTCTA
 TTTA A

GAM2247 LOC132321 3' ATCTGTGGCAAATTGTATATGA 37025 CG C
 T ATCA TACAATTT GTCACAGAT
 ||| ||||| |||||
 TAGT ATGTTAAA CGGTGTCTA
 AT _

GAM2247 LOC219894 5' ATCTGTGAGTTATTGTCAC 44793 _ TTCG
 GT ACAAT TCACAGAT
 || ||||| |||||

		CA TGTTA AGTGTCTA		
		C TTG_		
GAM2248	KIAA0731	5' AACCCGTGGACTAAGAACGCA 33238		G G GAAA
		TGCGTTCTTAG T CA GGTT		
		ACGCAAGAATC A GT CCAA		
		_ G GC_		
GAM2248	LOC256112	3' CCTTACTAAACATCTAAGAACA 46104	C	C_ A
	CA	TG GTTCTTAGGTG AG AAGG		
		AC CAAGAATCTAC TC TTCC		
		A AAA A		
GAM2249	ATP7A	3' TGTTTCTTTTCTACATTT 5499	T	
		AAATGTAGAAAA GAAACA		
		TTTACATCTTTT CTTTGT		
		-		
GAM2249	EPB72	3' TAATGTTCAATTTATTTTCTA 10306		___
		TAGAAAATGAA ACATTA		
		ATCTTTTATTT TGTAAT		
		ACT		
GAM2249	FHL1	3' TGATGCCTCATTTCTACATT 7180	A	AA
		AATGTAGAAA TGA CATTA		
		TTACATCTTT ACT GTAGT		
		_ CC		
GAM2249	KIT	3' GTTCCCCCTTCTACATTT 5733	AAT_	
		AAATGTAGAA GAAAC		
		TTTACATCTT CTTTG		
		CCCC		
GAM2249	CRNKL1	3' CTTAATTTTCATTTTCCTCATT 18773	TA	C
		AATG GAAAATGAAA ATTAAG		
		TTAC CTTTACTTT TAATTC		
		TC _		
GAM2249	DKFZp434E2220	3' TGTTTTCCCTTTCTACATTT 19114		AT_
		AAATGTAGAAA GAAACA		
		TTTACATCTTT TTTTGT		
		CCC		
GAM2249	FLJ11259	3' ATGCTTCATTTTCACAT 20382	A	A
		ATGT GAAAATGAA CAT		
		TACA CTTTACTT GTA		
		_ C		
GAM2249	FLJ14775	3' TGTATATTTTCTACATTT 26619		AA
		AAATGTAGAAAATG ACA		

TTTACATCTTTTAT TGT
 A_
 GAM2249 LOC131873 5' TGGCTTCATTTTCTACAT 37367 A_
 ATGTAGAAAATGAA CA
 ||||| ||
 TACATCTTTTACTT GT
 CG
 GAM2249 LOC255798 3' TGTTAATCCATTTTACATTT 46352 A____
 AAATGTAGAAAATG AACAA
 ||||| |||
 TTTACATTTTAC TTGT
 CTAA
 GAM2250 OPA1 3' ATCCTAAGCATGCTTTA 28319 CGGTCACA
 TAAAGCA CTTAGGAT
 ||||| |||||
 ATTTTCGT GAATCCTA
 AC_____
 GAM2250 OPA1 3' ATCCTAAGCATGCTTTA 28327 CGGTCACA
 TAAAGCA CTTAGGAT
 ||||| |||||
 ATTTTCGT GAATCCTA
 AC_____
 GAM2250 OPA1 3' ATCCTAAGCATGCTTTA 28335 CGGTCACA
 TAAAGCA CTTAGGAT
 ||||| |||||
 ATTTTCGT GAATCCTA
 AC_____
 GAM2250 OPA1 3' ATCCTAAGCATGCTTTA 28343 CGGTCACA
 TAAAGCA CTTAGGAT
 ||||| |||||
 ATTTTCGT GAATCCTA
 AC_____
 GAM2250 OPA1 3' ATCCTAAGCATGCTTTA 28351 CGGTCACA
 TAAAGCA CTTAGGAT
 ||||| |||||
 ATTTTCGT GAATCCTA
 AC_____
 GAM2250 PTMA 3' CTTGTGGTGTGACCATGTTCA 8692 A C _
 A AGCA GGTCACACT TAGG
 | ||| ||||| |||
 A TTGT CCAGTGTGG GTTC
 C A T
 GAM2250 KIAA1096 3' AGTAGTGACCGTGCTTTA 33996 _
 TAAAGCACGGTCAC ACT
 ||||| |||
 ATTTTCGTGCCAGTG TGA
 A
 GAM2250 MGC16142 3' ATCCTAAGCAGTTACTCTG 26506 C C A_
 CA GGT AC CTTAGGAT
 || ||| || |||||

			GT TCA TG GAATCCTA		
			C T AC		
GAM2250	PCDH19	3'	AAGTGTGACATGCTTTA 31858	CG	
			TAAAGCA GTCACACTT		
			ATTCGT CAGTGTGAA		
			A_		
GAM2250	RODH-4	5'	ATCCTAGACAAGCCTGACCGTG 9807	CA	_____
	C		GCACGGTCA CT TAGGAT		
			CGTGCCAGT GA ATCCTA		
			CC ACAG		
GAM2250	LOC145123	3'	CTTGTGGTGTGACCATGTTCA 33532	A C	_
			A AGCA GGTCACACT TAGG		
			A TTGT CCAGTGTGG GTTC		
			C A T		
GAM2250	LOC147791	3'	ATGCTGAGTGTGGCCGCGCCTT 40857	A A	G
	A		TAA GC CGGTCACACTTAG AT		
			ATT CG GCCGGTGTGAGTC TA		
			C C G		
GAM2251	ADH5	3'	TCTTGTTTTATGCTGTCA 6324	G G	
			TGACA G ATAGAACAAGA		
			ACTGT C TATTTTGTCT		
			_G		
GAM2251	FLRT2	3'	TCTTGTCTTGGTCTTGTCAA 14886	AT_	
			TTGACAGGG AGAACAAGA		
			AACTGTTCT TCTTGTCT		
			GGT		
GAM2251	FOSB	3'	TCTGACTGTCCCTGCCAATG 13583	A	AACA
			CATTG CAGGGATAG AGA		
			GTAAC GTCCCTGTC TCT		
			C AG_		
GAM2251	IRTA2	3'	CTGCTCATGTGTCAGTGT 25297	_____	A
			ACATTGACA GGG TAG		
			TGTGACTGT CTC GTC		
			GTA _		
GAM2251	MME	3'	TCTTGCTCTATCTCTCAA 14160	CA	A
			TTGA GGGATAGA CAAGA		
			AACT CTCTATCT GTTCT		
			_ C		
GAM2251	MME	3'	TCTTGCTCTATCTCTCAA 14155	CA	A
			TTGA GGGATAGA CAAGA		

			AACT CTCTATCT GTTCT		
			— C		
GAM2251	MME	3'	TCTTGCTCTATCTCTCAA 14151	CA	A
			TTGA GGGATAGA CAAGA		
			AACT CTCTATCT GTTCT		
			— C		
GAM2251	MME	3'	TCTTGCTCTATCTCTCAA 6603	CA	A
			TTGA GGGATAGA CAAGA		
			AACT CTCTATCT GTTCT		
			— C		
GAM2251	PIP5K1A	3'	TCCTGTTCTATCCCTTC 9604	C	A
			GA AGGGATAGAACA GA		
			CT TCCCTATCTTGT CT		
			— C		
GAM2251	POLQ	3'	TCCTGTTCTGTAAGATCAGATG 13367	GACAGGG	A
	TT		AACATT ATAGAACA GA		
			TTGTAG TGTCTTGT CT		
			ACTAGAA C		
GAM2251	ROBO1	3'	CTTGTTCTATTTTCAAT 28585	CA	
			ATTGA GGGATAGAACAAG		
			TAACT TTTTATCTTGTTT		
			—		
GAM2251	ROBO1	3'	CTTGTTCTATTTTCAAT 8849	CA	
			ATTGA GGGATAGAACAAG		
			TAACT TTTTATCTTGTTT		
			—		
GAM2251	SERPINB5	3'	TCTTGTTCTGAGATTCAAT 8496	CAGGGA	
			ATTGA TAGAACAAGA		
			TAACT GTCTTGTCT		
			TAGA_		
GAM2251	SNCA	3'	TTCAATCCTGTCAATGTT 5897	G A	
			AACATTGACAGG AT GAA		
			TTGTAAGTGTCC TA CTT		
			— A		
GAM2251	SVIL	3'	TCTTGTTCCAGCTAGGCAATG 9150	ACAG ATA	
			CATTG GG GAACAAGA		
			GTAAC TC CTTGTTCT		
			GGA_ GAC		
GAM2251	SVIL	3'	TCTTGTTCCAGCTAGGCAATG 22347	ACAG ATA	
			CATTG GG GAACAAGA		

GTAAC TC CTTGTTCT
 GGA_ GAC
 GAM2251 TCF1 3' CTTGTTCTGTCACCAATGT 6149 ACAGG
 ACATTG GATAGAACAAG
 ||||| |||||
 TGTAAC CTGTCTTGTTT
 CA__
 GAM2251 VSNL1 3' TCTTGTTTCATGTTTGTCTAATG 9417 A ATA
 CATTG CAGGG GAACAAGA
 ||||| ||||| |||||
 GTAAT GTTTT CTTGTTCT
 C GTA
 GAM2251 ARPP-19 3' TCTCACTCTGTCATTGTT 13424 T AT
 AACA TGACAGGG AGA
 ||| ||||| |||
 TTGT ACTGTCTC TCT
 T AC
 GAM2251 C21orf7 3' CTTGTTCTACCTATCA 21362 C GA
 TGA AGG TAGAACAAG
 ||| ||| |||||
 ACT TCC ATCTTGTTT
 A _
 GAM2251 DKFZP586J0619 3' CTTGCCCCTGGTCAGCGT 39582 A _ ATAGAA
 AC TTGAC AGGG CAAG
 || ||||| ||| |||||
 TG GACTG TCCC GTTC
 C G C____
 GAM2251 FKSG42 3' CTTGTTCTGGTCACTGTT 25733 _ GA
 GACAG G TAGAACAAG
 ||||| | |||||
 TTGTC C GTCTTGTTT
 A TG
 GAM2251 FLJ10352 3' TTATCCACAAAACAGTCAATGT 25830 AG_____
 T AACATTGAC GGATAG
 ||||| |||||
 TTGTAAGT CCTATT
 ACAAACA
 GAM2251 FLJ20275 3' CTTGCCATCTGTCAGTGT 19321 GATAGAA
 ACATTGACAGG CAAG
 ||||| ||||| |||||
 TGTGACTGTCT GTTC
 ACC____
 GAM2251 FLJ23074 3' TCTTATCAAGTTCTGTCAAT 24649 ATA AC
 ATTGACAGGG GA AAGA
 ||||| || |||||
 TAACTGTCTT CT TTCT
 GAA A_
 GAM2251 IL22R 3' CTGCCTCTTCTGTCATTGTT 22235 T GAT ACA
 AACA TGACAGG AGA AG
 ||| ||||| ||| ||

			TTGT ACTGTCT TCT TC			
			T ____ CCG			
GAM2251	KIAA0296	3'	TCCTTCCCTGTCAGTGTT 16223		TA	
			AACATTGACAGGGA GA			
			TTGTGACTGTCCCT CT			
			TC			
GAM2251	KIAA0376	3'	TCCTGTTCTGTTAGTACCAAAG 32676	A	ACAGG	A
		TT	AAC TTG GATAGAACA GA			
			TTG AAC TTGTCTTGT CT			
			A CATGA C			
GAM2251	M96	3'	CTTAACATGTACCTGTCAATGT 14287	G	GAAC	
		T	AACATTGACAGG ATA AAG			
			TTGTAAGTGTCC TGT TTC			
			A ACAA			
GAM2251	mPA-PLA1	3'	CTTGTTCCGACCTGTCAAT 29251		GATA	
			ATTGACAGG GAACAAG			
			TAACTGTCC CTTGTTC			
			AGC_			
GAM2251	LOC149910	3'	TCTTCCCTGTCAGTGTT 38829		T	
			AACATTGACAGGGA AGA			
			TTGTGACTGTCCCT TCT			
			—			
GAM2251	LOC206426	3'	TCCTGTTCTATCCCTTC 43121	C	A	
			GA AGGGATAGAACA GA			
			CT TCCCTATCTTGT CT			
			C			
GAM2251	LOC220963	3'	CTCATTCTTTAGTCCCTGTCAA 43957	A	____	CA
		GGTT	AAC TTGACAGGGAT AGAA AG			
			TTG AACTGTCCCTG TCTT TC			
			G ATT AC			
GAM2251	LOC91012	5'	CTTGTTCCAGTTTCTGTCACTG 32281	T	GG A_	
			CA TGACAG AT GAACAAG			
			GT ACTGTC TG CTTGTTC			
			C TT AC			
GAM2252	CRAT	3'	CTGTGGATAACATTGCTAGCGA 6408	A	AACA	G
			TC CTAGCAAT TGTCTA GG			
			AG GATCGTTA ATAGGT TC			
			C CA_ G			
GAM2252	CRAT	3'	CTGTGGATAACATTGCTAGCGA 10153	A	AACA	G
			TC CTAGCAAT TGTCTA GG			

			AG GATCGTTA ATAGGT TC		
			C CA__ G		
GAM2252	MPL	3'	CCCTACTACACTTTGCTAGTGA 11847		TAACA C_
			TCACTAGCAA TGT TAGGG		
			AGTGATCGTT ACA ATCCC		
			TC__ TC		
GAM2252	ADAM9	3'	ACATGTTATTGCAGTGA 9906	A	
			TCACT GCAATAACATGT		
			AGTGA CGTTATTGTACA		
			—		
GAM2252	CDV-1	3'	CCTGACACCCCATTGCTAGT 25540		AACA T
			ACTAGCAAT TGTC AGG		
			TGATCGTTA ACAG TCC		
			CCCC _		
GAM2252	MAPK8IP2	3'	CTAGACGCTGCTAGGA 29156	A	ATAACA
			TC CTAGCA TGTCTAG		
			AG GATCGT GCAGATC		
			_ C_____		
GAM2252	MAPK8IP2	3'	CTAGACGCTGCTAGGA 14705	A	ATAACA
			TC CTAGCA TGTCTAG		
			AG GATCGT GCAGATC		
			_ C_____		
GAM2252	MAPK8IP2	3'	CTAGACGCTGCTAGGA 18553	A	ATAACA
			TC CTAGCA TGTCTAG		
			AG GATCGT GCAGATC		
			_ C_____		
GAM2252	LOC202025	5'	CCCATTACATGTTATCATAG 43401	GCA	CTA
			CTA ATAACATGT GGG		
			GAT TATTGTACA CCC		
			AC_ TTA		
GAM2252	LOC221641	5'	CCCAACATGCATTGCTAGT 45008	AA	CTA
			ACTAGCAAT CATGT GGG		
			TGATCGTTA GTACA CCC		
			C_ A__		
GAM2253	AKAP2	3'	TTCAAGAAACCTTGGGCC 14064	G	_
			GGT CAA TTTCTTGAA		
			CCG GTT AAAGAACTT		
			G CC		
GAM2253	DYRK1A	3'	TTCAAGATTACAACATCTGTGA 7095		CAATT_
			TAACAGGTG TCTTGAA		

		ATTGTCTAC	AGAACTT		
		AACATT			
GAM2253	DYRK1A	3'	TTCAAGATTACAACATCTGTTA	28167	CAATT_
			TAACAGGTG	TCTTGAA	
			ATTGTCTAC	AGAACTT	
			AACATT		
GAM2253	DYRK1A	3'	TTCAAGATTACAACATCTGTTA	28190	CAATT_
			TAACAGGTG	TCTTGAA	
			ATTGTCTAC	AGAACTT	
			AACATT		
GAM2253	ELAVL2	5'	TTGGGAGAACTGCACCGTTA	10718	A A_ TG
			TAAC GGTGCA	TTTCT A	
			ATTG CCACGT	AGAGG T	
			_ CA	GT	
GAM2253	ITGA1	3'	G TTCAGAAATCATACCT	31791	CA T
			AGGTG	ATTTCT GAAC	
			TCCAT	TAAAGA CTTG	
			AC	_	
GAM2253	LPHH1	3'	TCTTG GTTGACATGTTA	14670	G TCTT
			TAACA GTGCAATT	GA	
			ATTGT CACGTTGG	CT	
			A	TT__	
GAM2253	MAP3K7IP2	3'	G TTCAGAAACTAGTCTGT	17487	GCAA
			ACAGGT	TTTCTTGAAC	
			TGTCTG	AAAGAACTTG	
			ATC_		
GAM2253	AD-020	3'	G TTCAGCATGTTTGCACTTGTT	29871	TTTC_
	A		TAACAGGTGCAA	TTGAAC	
			ATTGTTACGTT	GACTTG	
			TGTAC		
GAM2253	AD-020	3'	G TTCAGCATGTTTGCACTTGTT	21341	TTTC_
	A		TAACAGGTGCAA	TTGAAC	
			ATTGTTACGTT	GACTTG	
			TGTAC		
GAM2253	BIKE	3'	TTCAGCAACACCTGTTA	19041	CAAT C
			TAACAGGTG	TT TTGAA	
			ATTGTCCAC	AA GACTT	
			__ C		
GAM2253	FLJ11101	3'	TCAAGAAGGGAGACCTGTT	20314	GCAA
			AACAGGT	TTTCTTGA	

TTGTCCA GAAGAACT
 GAGG
 GAM2253 FLJ21144 3' GTTCAAGAGCAACCTG 23038 _ AATT
 CAGGT GC TCTTGAAC
 ||||| || |||||
 GTCCA CG AGAACTTG
 A ____
 GAM2253 GALNT6 3' GTTCAAGAAAAGTACTTCA 14073 C AA
 A AGGTGC TTTCTTGAAC
 | ||||| |||||
 A TTCATG AAAGAACTTG
 C A_
 GAM2253 KIAA1240 3' TTCAATTTCAAATTGCACC 33144 C____
 GGTGCAATTT TTGAA
 ||||| |||||
 CCACGTTAAA AACTT
 CTTT
 GAM2253 MGC22014 3' TCAAGAAATCATCATCTG 32224 CA_
 CAGGTG ATTTCTTGA
 ||||| |||||
 GTCTAC TAAAGAACT
 TAC
 GAM2253 LOC143173 5' TCAAGAAATCAAGTACTTCA 30272 C A_
 A AGGTGC ATTTCTTGA
 | ||||| |||||
 A TTCATG TAAAGAACT
 C AAC
 GAM2253 LOC149722 5' GTTCATGATCTGCACCTG 41043 ATT T
 CAGGTGCA TC TGAAC
 ||||| || |||||
 GTCCACGT AG ACTTG
 CT_ T
 GAM2253 LOC152627 5' GTTCATTATTATCACACCTGTT 39295 CA TTCT_
 A TAACAGGTG AT TGAAC
 ||||| || |||||
 ATTGTCCAC TA ACTTG
 AC TTATT
 GAM2253 LOC257482 3' AAGACTGCACCTGTTA 45233 ATT
 TAACAGGTGCA TCTT
 ||||| |||||
 ATTGTCCACGT AGAA
 C_
 GAM2253 LOC257485 3' TCAGCACATTGCACCAGTTA 32670 A TTC
 TAAC GGTGCAAT TTGA
 ||| ||||| |||||
 ATTG CCACGTTA GACT
 A CAC
 GAM2253 LOC90670 3' GTTCCCATAATCCGCACCTGT 31883 A_ TCTT
 ACAGGTGC ATT GAAC
 ||||| ||| |||||

			TGTCCACG TAA CTTG		
			CC TACC		
GAM2254	ACPT	3'	TCTTCTACCGCAATGACT 28045	AATAG	
			AGTCAT GGTAGAAGA		
			TCAGTA CCATCTTCT		
			ACG__		
GAM2254	ACPT	3'	TCTTCTACCGCAATGACT 28048	AATAG	
			AGTCAT GGTAGAAGA		
			TCAGTA CCATCTTCT		
			ACG__		
GAM2254	ARHGDIB	5'	CTTCCTTCCTGTTCTAACTG 6850	CAT	TA
			CAGT AATAGGG GAAG		
			GTCA TTGTCCT CTTC		
			ATC TC		
GAM2254	CAPZA1	3'	CTTCTCCCTCTGACTG 35951	TAAT	T
			CAGTCA AGGG AGAAG		
			GTCAGT TCCC TCTTC		
			C__ _		
GAM2254	ERBB4	3'	CTTCCTTCTACCCCAAGGC 11745	ATAATA	A
			GTC GGGTAGAAG AAG		
			CGG CCCATCTTC TTC		
			AAC__ C		
GAM2254	FLRT2	3'	TCTCTTGCTGTCATTATGAT 14885	AG_	GA
			GTCATAAT GGTA AGA		
			TAGTATTA TCGT TCT		
			CTG TC		
GAM2254	NOS1	3'	TTTCTCCTTTTTTATGAT 6235	T_	T
			GTCATAA AGGG AGAAG		
			TAGTATT TTCC TCTTT		
			TT _		
GAM2254	SLC4A7	3'	CTTCTTTTGACTACTTGACTG 9670	TAA	GG
			CAGTCA TAG TAGAAGAAAG		
			GTCAGT ATC GTTTTCTTTC		
			TC_ A_		
GAM2254	C21orf108	3'	CTTCTGCCATGACTG 42769	AATAG	
			CAGTCAT GGTAGAAG		
			GTCAGTA CCGTCTTC		

GAM2254	DKFZp434C0328	5'	CTTCCTCTATTATGC 19011	T	TA
			G CATAATAGGG GAAG		

C GTATTATCTC CTTC

GAM2254 FLJ10971 3' CTTTCTTCTCAAGATTCATGAC 20280 _ AGGGT
T AGTCAT AAT AGAAGAAAG

||||| ||| |||||
TCAGTA TTA TCTTCTTTC
C GAAC_

GAM2254 FLJ13397 3' CTTTCTTCTATATTTATAAAC 24500 C_ TAGG
GT ATAA GTAGAAGAAAG

|| ||| |||||
CA TATT TATCTTCTTTC
AA TA_

GAM2254 FLJ14249 3' TTCCCCTACCCTAAGCTG 28171 CATAA AA
CAGT TAGGGTAG GAA

||| ||||| |||
GTCG ATCCCATC CTT
A_ CC

GAM2254 FLJ14249 3' TTCCCCTACCCTAAGCTG 22801 CATAA AA
CAGT TAGGGTAG GAA

||| ||||| |||
GTCG ATCCCATC CTT
A_ CC

GAM2254 KIAA0063 3' TTTCTCCCCCCTGTGACTG 17019 AAT TA A
CAGTCAT AGGG GA GAAA

||||| ||| || |||
GTCAGTG TCCC CT CTTT
_ CC _

GAM2254 KIAA1361 3' CTTCTTTGTATTATGAT 31168 G T
GTCATAATA GG AGAAG

||||||| || |||
TAGTATTAT TT TCTTC
G _

GAM2254 KPNA6 3' TCTCCTATTATCTATTATCACT 14689 C _ A
G CAGT ATAATAGG GTAG AGA

||| ||||| ||| |||
GTCA TATTATCT TATC TCT
C AT C

GAM2254 NMU2R 3' TTTCCACTATCCTAACTG 21385 CATAA AA
CAGT TAGGGTAG GAAA

||| ||||| |||
GTCA ATCCTATC CTTT
_ AC

GAM2254 RAB14 3' CTTTCTTCCCATCCTTAACTG 18447 CATAAT A_
CAGT AGGGT GAAGAAAG

||| ||| |||||
GTCA TCCTA CTTCTTTC
AT_ CC

GAM2254 TBX19 3' TCTCCCTATTAGACTG 11624 A T
CAGTC TAATAGGG AGA

||||| ||||| |||

GTCAG ATTATCCC TCT

GAM2254 LOC129831 3' TCTTCTACCCTAGATCTGAT 36981 TAA_
GTCA TAGGGTAGAAGA
|||| |||||
TAGT ATCCCATCTTCT
CTAG

GAM2254 LOC146545 5' TCTGCCTGCCCTATCCTGAC 38201 TA A_
GTCA ATAGGGTAG AGA
|||| ||||| ||
CAGT TATCCCGTC TCT
CC CG

GAM2254 LOC149111 3' CTTTCTTCCAAGCCATGGC 38648 AATAG A_
GTCAT GGT GAAGAAAG
|||| || |||||
CGGTA CCG CTTCTTTC
AAC

GAM2254 LOC152897 5' TCCTTCTTGTCTGTGACTG 39327 _ TA
CAGTCATA ATAGGG GA
||||| ||||| ||
GTCAGTGT TGTCT CT
C TC

GAM2254 LOC199676 5' TCTTCCTGGCCATGGCTG 43225 AATA G _
CAGTCAT GG TAG AAGA
||||| || ||| ||||
GTCGGTA CC GTC TTCT
G C

GAM2254 LOC221814 3' CTTTCCATTGACCATTATGACT 45093 A G AA
AGTCATAAT GG TAG GAAAG
||||||| || ||| |||||
TCAGTATTA CC GTT CTTTC
A AC

GAM2254 LOC253868 3' CTTCTGCCATGACTG 45750 AATAG
CAGTCAT GG TAGAAG
||||| |||||
GTCAGTA CCGTCTTC

GAM2254 LOC255515 3' CTTCCCTTGATCTATTATGACT 45961 GTA_
AGTCATAATAGG GAAG
||||||| |||
TCAGTATTATCT CTTC
AGTTC

GAM2254 LOC56181 3' CTTTCTTCCAGGCCCTTGACTG 45740 TAAT A_
CAGTCA AGGGT GAAGAAAG
||||| ||||| |||||
GTCAGT TCCCG CTTCTTTC
GAC

GAM2255 NTRK2 3' TTGTCACTTCTGCTGTACA 12849 C _
TG ATAGCAGAA ACAA
|| ||||| |||

		AC TGTCGTCTT TGTT		
		A CAC		
GAM2255	TNFSF4	3' CAGGGATATTTCTGCTATGCA 9329	CA	
		TGCATAGCAGAAA ATCTTTG		
		ACGTATCGTCTTT TAGGGAC		
		A_		
GAM2255	FLJ10352	3' TCAGAGGCTTCTGCTCGCA 25829	AT	ACAA
		TGC AGCAGAA TCTTTGA		
		ACG TCGTCTT GGAGACT		
		C_ C__		
GAM2255	JK	3' TCATAATCATTTCTGCTGTGCA 18407	CA	CTT
		TGCATAGCAGAAA AT TGA		
		ACGTGTCGTCTTT TA ACT		
		AC AT_		
GAM2255	LOC115574	3' GTCAGAGATGTCCCCTGCCATG 36366	A	AAACA
	CA	TGCAT GCAG ATCTTTGAC		
		ACGTA CGTC TAGAGACTG		
		C CCCTG		
GAM2255	LOC149711	3' GTCAAAAAGGTTTCTGCCCAC 41072	ATA_	AATC
	GCA	TGC GCAGAAAC TTTGAC		
		ACG CGTCTTTG AAAGT		
		CACC GAAA		
GAM2255	LOC149837	3' GTCATGGAAATCCCAGCTATGC 41100	AGAAACAA	T
	A	TGCATAGC TCT TGAC		
		ACGTATCG AGG ACTG		
		ACCCTAA_ T		
GAM2255	LOC220766	5' CATGGATATTTCTGCTATGC 43650	CA	T
		GCATAGCAGAAA ATCT TG		
		CGTATCGTCTTT TAGG AC		
		A_ T		
GAM2255	LOC221272	5' TTGTTATCTCTGCTTGCA 44965	T	__
		TGCA AGCAGA AACAA		
		ACGT TCGTCT TTGTT		
		_ CTA		
GAM2256	FAT2	3' CCATCAAGTATTACCTGCAGCG 7172	AG	CC
	A	TC TGCAGG GGTGTTTGATGG		
		AG ACGTCC TTATGAACTACC		
		CG A_		
GAM2256	KIAA0930	3' CCACGAACACCAGCCCAAACTG 34913	GCA	C A
	A	TCAGT GGC GGTGTTTG TGG		

			AGTCA CCG CCACAAGC ACC		
			AAC A _		
GAM2256	PADI1	3'	CATACCCCAGCCTGCACTGA 31054	C T T	
			TCAGTGCAGGC GG GT TG		
			AGTCACGTCCG CC CA AC		
			A C T		
GAM2256	LOC144600	5'	CCACGAACACCAGCCCAAAGT 40446	GCA C A	
	A		TCAGT GGC GGTGTTTG TGG		
			AGTCA CCG CCACAAGC ACC		
			AAC A _		
GAM2257	CHRM1	5'	CCTCCCCGCTAAGGCTGGCGTG 45441	G _ _ AA_	
	C		GCACGCC AGCC GC GAGG		
			CGTGCGG TCGG CG CTCC		
			_ AAT CCC		
GAM2257	FCN2	3'	TCCTCCCACGGCTTGTGGCTG 17954	A C CAA	
			TAGC CGC GAGCCG GAGGA		
			GTCG GTG TTCGGC CTCCT		
			_ _ ACC		
GAM2257	MAP3K8	5'	TCCCAGTGCCCCGGCGTGCT 11706	A AAGA	
			AGCACGCCG GCCGC GGA		
			TCGTGCGGC CGGTG CCT		
			C AC_		
GAM2257	PCDH9	5'	TCCTCTTGCAATTTGTGC 40296	CC GCC	
			GCACG GA GCAAGAGGA		
			CGTGT TT CGTTCTCCT		
			_ AA_		
GAM2257	STK10	3'	CCTCTTGCGTCTGTGC 12614	GCCG C	
			GCAC AG CGCAAGAGG		
			CGTG TC GCGTTCTCC		
			_ T		
GAM2257	TEAD3	5'	CCCCTTGCGGCTCCCTCGGGC 9210	A CC_ A	
			GC CG GAGCCGCAAG GG		
			CG GC CTCGGCGTTC CC		
			G TCC C		
GAM2257	WHSC1L1	5'	TTCCTCTTCCCGCAGCACGC 23318	C A C _	
			GC G GC GC AAGAGGAA		
			CG C CG CG TTCTCCTT		
			_ A A CCC		
GAM2257	WHSC1L1	5'	TTCCTCTTCCCGCAGCACGC 19411	C A C _	
			GC G GC GC AAGAGGAA		

CG C CG CG TTCTCCTT
 _ A A CCC
 GAM2257 DKFZP434C131 3' TCCCCTTGC GGCCCCCTGCT 34246 CGCCGA A
 AGCA GCCGCAAG GGA
 ||| ||||| |||
 TCGT CGGCGTTC CCT
 CCC__ C
 GAM2257 LOC203871 5' TCCCCAGGGCAGGCCAGCGTG 43080 CGA _ AAGA_
 CTG TAGCACGC GCC GC GGA
 ||||| ||| |||
 GTCGTGCG CGG CG CCT
 ACC A GGACC
 GAM2257 LOC221250 5' CCTCGCGGCTCGGTCCGGC 44120 AC_ AA
 GC GCCGAGCCGC GAGG
 || ||||| |||
 CG TGGCTCGGCG CTCC
 GCC _
 GAM2257 LOC253805 3' CTGGCACTACTCAGCGTGCTA 46135 C CC_ A
 TAGCACGC GAG GC AG
 ||||| ||| |||
 ATCGTGCG CTC CG TC
 A ATCA G
 GAM2257 LOC91145 3' TCCTTAAGTCAAGTGTGCTA 32451 C CCGCAA
 TAGCACGC GAG GAGGA
 ||||| ||| |||||
 ATCGTGTG CTC TTCCT
 A AA____
 GAM2258 ETV5 3' CCTTGGCCATGTGAA 10747 A TCG
 TTCA CATGGCCA AGG
 ||| ||||| |||
 AAGT GTACCGGT TCC
 _ _
 GAM2258 HNF4G 5' CCTAGGCCAGGCCGTGTTGAA 10346 A_ G
 TTCAACATGGCC TC AGG
 ||||| ||| |||
 AAGTTGTGCCGG GG TCC
 ACC A
 GAM2258 ITS1 3' CTCGGTTGGCAGCCATGTTGGA 8955 C____
 TTCAACATGGC ATCGAG
 ||||| ||| |||||
 AGGTTGTACCG TGGCTC
 ACGGT
 GAM2258 TNFSF4 3' CTCCTTTACTATGTTGAA 9332 CCATC
 TTCAACATGG GAGGAG
 ||||| ||| |||||
 AAGTTGTATC TTCCTC
 AT____
 GAM2258 C20orf12 5' CTCCTGAAGACAATGTTGAA 19958 GGCCA G
 TTCAACAT TC AGGAG
 ||||| ||| |||||

		AAGTTGTA AG TCCTC		
		ACAGA _		
GAM2258	CLIC4	3' CTCCTCAAGCCGTAATGTTGAA 15129	___	CATC
		TTCAACAT GGC GAGGAG		
		AAGTTGTA CCG CTCCTC		
		ATG AA__		
GAM2258	DKFZp434A171	5' CCAGTGGCCATGTGAA 35037	A	CGA
		TTCA CATGGCCAT GG		
		AAGT GTACCGGTG CC		
		_ A__		
GAM2258	IPLA2(GAMMA)	3' CTCATAATCATGTTGAA 30445	CC	C
		TTCAACATGG AT GAG		
		AAGTTGTACT TA CTC		
		AA _		
GAM2258	KIAA0171	3' CTCCCCATGTTATGTTGAA 16122	CATCGA	
		TTCAACATGGC GGAG		
		AAGTTGTATTG CCTC		
		TACC__		
GAM2258	KIAA1879	5' COTTGTCACCATGTTGAG 36414	CCAT	
		TTCAACATGG CGAGG		
		GAGTTGTACC GTTCC		
		ACT_		
GAM2258	KLHL4	3' CTCGAAAACATCATGTTGAA 21195	CCA_	
		TTCAACATGG TCGAG		
		AAGTTGTACT AGCTC		
		CAAA		
GAM2258	LANCL2	3' CTTTGATGGCCACACTGT 20777	___	
		ACA TGGCCATCGAGG		
		TGT ACCGGTAGTTTC		
		CAC		
GAM2258	LEC3	3' CTCATTGTGGCCTTGTTGAA 17569	T T G	
		TTCAACA GGCCA CGA GAG		
		AAGTTGT CCGGT GTT CTC		
		T _ A		
GAM2258	MGC21688	3' CTCCTCGGATAATGTGAA 29454	A	GGCCA
		TTCA CAT TCGAGGAG		
		AAGT GTA GGCTCCTC		
		_ ATA__		
GAM2258	MGC5566	3' CTCAGCCGGTCATGTTGAA 23486	ATC_	
		TTCAACATGGCC GAG		

		AAGTTGTA	CTG		
		CCGA			
GAM2258	MRPS21	5'	CCTGAGCATGTTGAA	21070	G CA G
			TTCAACATG C TC AGG		
			AAGTTGTAC G AG TCC		
			— — —		
GAM2258	NCOA2	3'	CTCTAAAGACCATGTTGGA	13295	CCA GA_
			TTCAACATGG TC GGAG		
			AGGTTGTACC AG TCTC		
			— AAA		
GAM2258	RP4-622L5	3'	CTCCTCGATGCCCAGTGAA	21201	A A C
			TTCA C TGG CATCGAGGAG		
			AAGT G ACC GTAGCTCCTC		
			— — C		
GAM2258	TACTILE	3'	CTCTTTGACCATACTGA	12412	AC CCA
			TCA ATGG TCGAGGAG		
			AGT TACC AGTTTCTC		
			CA —		
GAM2258	LOC112840	3'	CTCCCTGGCCATGCTGAA	27957	A TC
			TTCA CATGGCCA GAG		
			AAGT GTACCGGT CTC		
			C CC		
GAM2258	LOC127702	3'	CCAGGCGGTCCATGTTGAA	37181	_ AT GA
			TTCAACATGG CC C GG		
			AAGTTGTACC GG G CC		
			T CG A_		
GAM2258	LOC146287	5'	CTCCTCGAGCTCTTTGAA	40689	CAT CA
			TTCAA GGC TCGAGGAG		
			AAGTT TCG AGCTCCTC		
			TC_ —		
GAM2258	LOC150933	3'	CTTGTGGCCATGCCGAA	41271	AA T
			TTC CATGGCCA CGAG		
			AAG GTACCGGT GTTC		
			CC _		
GAM2258	LOC255374	5'	CTCCTCGGGCACACGGTGAA	45955	ACA _ AT
			TTCA TG GCC CGAGGAG		
			AAGT AC CGG GCTCCTC		
			GGC A _		
GAM2258	LOC90906	5'	CTCCTCTAGGA	ACTATGTTGAA 32150	_ ATC
			TTCAACATGG CC GAGGAG		

AAGTTGTATC GG CTCCTC
 AA AT_
 GAM2258 LOC92080 3' CTCCCTGATGGCCATGCTGAG 33758 A A
 TTCA CATGGCCATCG GGAG
 |||| |||||
 GAGT GTACCGGTAGT CCTC
 C C
 GAM2259 ADPRT 3' TGAACATGGGAGCTCTTG 7326 A
 CGAGAGCTCCTG GTTCA
 |||||
 GTTCTCGAGGGT CAAGT
 A
 GAM2259 DPH2L1 3' TGAATATGGTTGGAGAGCCCTG 7055 G A _TG GT
 G C AG GCTC C A TCATATTCA
 | |||| | |||||
 G TC CGAG G T GGTATAAGT
 G C A GT _
 GAM2259 GBP1 3' TATCAACTCAGGAAATCTC 7811 GC C
 GAGA TCCTGAGTT ATA
 |||| |||||
 CTCT AGGACTCAA TAT
 AA C
 GAM2259 NTRK2 3' GACTCCGAGAAGCTCTCG 12844 C _
 CGAGAGCT CT GAGTT
 ||||| || ||||
 GCTCTCGA GA CTCAG
 A GC
 GAM2259 PDE4B 3' AATAGCAGCTCAGGAAATC 8464 GC CA
 GA TCCTGAGTT TATT
 || ||||| ||||
 CT AGGACTCGA ATAA
 AA CG
 GAM2259 PRO0149 5' TATGGACTCAAACTCTC 15370 CTCC
 GAGAG TGAGTTCATA
 |||| |||||
 CTCTC ACTCAGGTAT
 AAA_
 GAM2259 PRPF8 3' TGAACACCCAAGAGCTCTTG 30688 C A_
 CGAGAGCTC TG GTTCA
 ||||| || ||||
 GTTCTCGAG AC CAAGT
 A CCA
 GAM2259 LOC127428 3' GAATACGCTGGCGCTCTC 36899 T TG TCA
 GAGAGC CC AGT TATTC
 ||||| || || ||||
 CTCTCG GG TCG ATAAG
 C _ C_
 GAM2259 LOC149175 3' AATATGAACTGGTATTCTC 38659 CT TG
 GAGAG CC AGTTCATATT
 |||| || |||||

		CTCTT GG TCAAGTATAA		
		AT _		
GAM2259	LOC158318 5'	GAATGGAAGCCAGGAGCTC 41956	A	CA
		GAGCTCCTG GTT TATTC		
		CTCGAGGAC CGA GTAAG		
		_ AG		
GAM2259	LOC158450 5'	TGAATATAAAAATCAGCTCTTG 39845	CCT	GTTC_
		CGAGAGCT GA ATATTCA		
		GTTCTCGA CT TATAAGT		
		_ AAAAA		
GAM2259	LOC158504 5'	TGAATATAAAAATCAGCTCTTG 39856	CCT	GTTC_
		CGAGAGCT GA ATATTCA		
		GTTCTCGA CT TATAAGT		
		_ AAAAA		
GAM2259	LOC51170 3'	TGAATATCATGAACTCTC 18364	C C	_
		GAGAG TC TGA GTTCA		
		CTCTC AG ACT TAAGT		
		A T A		
GAM2259	LOC90249 3'	TGAATATGCAATGGGAGT 31015	GA	_
		GCTCCT GTT CATATTCA		
		TGAGGG TAA GTATAAGT		
		_ C		
GAM2260	SCG3 3'	GTGGTTAAACATAGCTTT 14902	C	A
		AAAGCTATGTTT AA TAC		
		TTTCGATACAAA TT GTG		
		A G		
GAM2260	C11orf23 3'	GTATTTGAAACATAACTTT 20302	C	
		AAAG TATGTTTCAAATAC		
		TTTC ATACAAAGTTTATG		
		A		
GAM2260	COAS3 3'	CAAATACATTTTGAAACTAGCT 29119	T	TAC_
	TT	AAAGCTA GTTTCAA GTTTG		
		TTTCGAT CAAAGTTT TAAAC		
		_ TACA		
GAM2260	FLJ12076 3'	CAAACGTGTTGAAACACAGCTT 24822	A	ATAC
	T	AAAGCT TGTTCAA GTTTG		
		TTTCGA ACAAAGTT CAAAC		
		C GGT_		
GAM2260	KIAA1550 3'	CAAACGTATTTAACACAG 33069	A	TC
		CT TGTT AAATACGTTTG		

			GA ACAA TTTATGCAAAC		
			C _		
GAM2260	NRBF-2	3'	TATTTGAAACATGCTTT 25043	T	
			AAAGC ATGTTTCAAATA		
			TTTCG TACAAAGTTTAT		
			-		
GAM2260	SE57-1	3'	CAAACATATTTGAAAGTTAACT 24887	C TG	C
	TT		AAAG TA TTTCAAATA GTTTG		
			TTTC AT AAAGTTTAT CAAAC		
			A TG A		
GAM2260	WWP1	5'	AACGATAGATTTGAAACAAGCT 39190	A	A_
			AGCT TGTTTCAAAT CGTT		
			TCGA ACAAAGTTTA GCAA		
			- GATA		
GAM2261	ATP2A3	3'	CCACCTGCTGACCTGCTGTT 11672	C ACT	CAC
			AACAGCAGG CA GC TGG		
			TTGTCGTCC GT CG ACC		
			A _ TCC		
GAM2261	GABRP	3'	CCAGTGGCAGATCCCCTGT 15478	CCAA	
			GCAGG CTGCCACTGG		
			TGTCC GACGGTGACC		
			CCTA		
GAM2261	NDST1	5'	CCAGTGTCTCTGGCCTGCTG 7270	ACTGC	
			CAGCAGGCCA CACTGG		
			GTCGTCCGGT GTGACC		
			CTCCT		
GAM2261	PPP2R2B	5'	CCACGCAAGTAAGCCTGCTGT 10923	CA _	CAC
			ACAGCAGGC ACT GC TGG		
			TGTCGTCCG TGA CG ACC		
			AA A C_		
GAM2261	RYP3	3'	TGTCAGTCAACTGCTGTTA 6700	GCCA	C
			TAACAGCAG ACTG CA		
			ATTGTCGTC TGAC GT		
			AAC_ T		
GAM2261	SLC9A1	3'	CCAGTCCTGCTGGCCTGCTCTT 34857	C	ACT C_
	A		TAA AGCAGGCCA GC ACTGG		
			ATTTCGTCCGGT CG TGACC		
			C _ TCC		
GAM2261	TYRO3	3'	CCAGCCTGGTGGCCAGCT 12984	A_	AACT _
			AGC GGCC GCCA CTGG		

		TCG CCGG TGGT GACC	
		AC ____ CC	
GAM2261	ALK7	5' CCAGTGGCAGGAGCGCCGCGC 37294	A_ CAA_
		GC GGC CTGCCACTGG	
		CG CCG GACGGTGACC	
		CG CGAG	
GAM2261	C6orf37	3' CCATAACAATAACCTGCTGTTA 33512	CCAAC CCAC
		TAACAGCAGG TG TGG	
		ATTGTCGTCC AC ACC	
		AATA_ AAT_	
GAM2261	DC-TM4F2	3' CCAGGGCTGGCTGGCCTGC 25197	A _ A
		GCAGGCCA CT GCC CTGG	
		CGTCCGGT GG CGG GACC	
		C T _	
GAM2261	DCTN4	3' CCAAAGGTAGACCTGCTGTTA 33664	CCAA AC
		TAACAGCAGG CTGCC TGG	
		ATTGTCGTCC GATGG ACC	
		A____ AA	
GAM2261	FLJ22127	3' CAGTGGCAGCTGGTGACTG 23041	CAG A
		CAG GCCA CTGCCACTG	
		GTC TGGT GACGGTGAC	
		AG_ C	
GAM2261	FLJ23447	5' CCAGTGGCCGAGCCTGCTG 24217	CAACT
		CAGCAGGC GCCACTGG	
		GTCGTCCG CGGTGACC	
		AGC__	
GAM2261	KIAA0323	3' CAGACCAACTCTGCTGTTA 31689	CCAAC CCA
		TAACAGCAGG TG CTG	
		ATTGTCGTCT AC GAC	
		CA____ CA_	
GAM2261	KIAA1045	3' GCAGTCAGCTGCTGTTA 35198	G CA
		TAACAGCAG C ACTGC	
		ATTGTCGTC G TGACG	
		_ AC	
GAM2261	KIAA1509	3' CCAGAGTCAGGCCTGCTGTTA 30873	A_ GCCA
		TAACAGCAGGCC ACT CTGG	
		ATTGTCGTCCGG TGA GACC	
		AC ____	
GAM2261	MESDC2	3' CAGTGGAAGCTGCTGTTA 35890	GCCAA G
		TAACAGCAG CT CCACTG	

	ATTGTCGTC	GA GGTGAC	
	_____ A		
GAM2261 MGC11352	5' CCAGGGCTGGCTGGCCTGC	32355	A _ A
	GCAGGCCA CT GCC CTGG		
	CGTCCGGT GG CGG GACC		
	C T _		
GAM2261 LOC147645	3' CCAGCAGCAGCCAGGGCCTGCT	38358	AA__ CA
	AGCAGGCC CTGC CTGG		
	TCGTCCGG GACG GACC		
	GACC AC		
GAM2261 LOC151742	3' CCAGTGGCAACTGCCTGC	29242	CAAC
	GCAGGC TGCCACTGG		
	CGTCCG ACGGTGACC		
	TCA_		
GAM2261 LOC154790	5' CCAGGGGCTGCCCTGCTGT	39490	C ACT A
	ACAGCAGG CA GCC CTGG		
	TGTCGTCC GT CGG GACC		
	C _ _ G		
GAM2261 LOC219914	5' CCAACAGCAGTTGGGGTGTCC	44815	A GG CAC
	C GCA CCAACTGC TGG		
	C TGT GGTGACG ACC		
	C GG ACA		
GAM2261 LOC222008	3' CCATTGCCAGCCTTGCTGT	45123	CCAA C C
	ACAGCAGG CTG CA TGG		
	TGTCGTTC GAC GT ACC		
	C _ _ C T		
GAM2261 LOC256979	5' CCAGTGGCAATGCTTTGTTA	45951	CA CAAC
	TAACAG GGC TGCCACTGG		
	ATTGTT TCG ACGGTGACC		
	_ TA_		
GAM2261 LOC56181	5' CCAGTGGCAGCTTTTCCTGT	45738	CC _
	GCAGG AA CTGCCACTGG		
	TGTCC TT GACGGTGACC		
	TT C		
GAM2262 CASP9	3' ACTTTCCTCGCCTGACAACCAC	6898	C TACC TA
T	AGTGGTTG CA AG AAAGT		
	TCACCAAC GT TC TTTCA		
	A CCGC C_		
GAM2262 DKFZP586A011	3' ACTGGCATGGGCTAACCACT	17716	_ ATA_
	AGTGGTT GCC CCAGT		

		TCACCAA CGG GGTCA	
		T GTAC	
GAM2262	HSU24186 5'	ACTTTTAGAATGTAGCAACCAC 14990	C CCAG
	T	AGTGGTTGC ATA TAAAAGT	
		TCACCAACG TGT ATTTTCA	
		A AAG_	
GAM2262	KIAA1497 5'	ACTTGTCACTGTGACAACCACT 33523	C T__ C
		AGTGGTTG CA AC AGT	
		TCACCAAC GT TG TCA	
		A CTAC T	
GAM2262	MAN1C1 5'	ACTCTCAGGGTTGGCAACCCT 21643	T T AGTAAA
		AG GGTTGCCA ACC AGT	
		TC CCAACGGT TGG TCA	
		_ _ GACTC_	
GAM2262	PRO0902 5'	ACTGGTGATAATAACAGCAACC 27605	CA_____
	ACT	AGTGGTTGC TACCAGT	
		TCACCAACG GTGGTCA	
		ACAATAATA	
GAM2262	LOC222159 5'	CTTTTAACTGCAACCAC 45147	CATACC _
		GTGGTTGC AGT AAAAG	
		CACCAACG TCA TTTTC	
		_____ A	
GAM2263	GCH1 3'	CCACAGAAACACAAACACA 5665	G _
		TGTGT TTGTG TCTGTGG	
		ACACA AACAC AGACACC	
		_ AA	
GAM2263	RANBP2L1 5'	CCACAGACACAACCTGGCCAC 26004	T__
		GTG GTTGTGTCTGTGG	
		CAC CAACACAGACACC	
		CGGT	
GAM2263	SIM1 3'	CCTCAAACACACAAACTA 11510	C GTGTC T
		TAG TTGTGTGTT TG GG	
		ATC AACACACAA AC CC	
		A _____ T	
GAM2263	KCNS1 5'	TCCACAGACAGGGAAACAAGC 8045	GTG G
		GCTTGT TT TGTCTGTGGA	
		CGAACA GG ACAGACACCT	
		AA_ G	
GAM2263	KIAA0446 5'	TCCACAGACACACTAGGAAAGC 34155	GTG T
		GCTT TG TGTGTCTGTGGA	

		CGAA AT ACACAGACACCT		
		AGG C		
GAM2263	KIAA1828	5' CCACACACACACACAA	36525	T C
		TTGTGTGT GTGT TGTGG		
		AACACACA CACA ACACC		
		_ C		
GAM2263	ZDHC3	3' TCCACAGACACACCTAAGC	18691	T TGT
		GCTTG GTGT GTCTGTGGA		
		CGAAT CACA CAGACACCT		
		C _		
GAM2263	LOC130813	3' CCACACTGACACACAAACAA	37308	G T _
		TTGT TGT GTGTC TGTGG		
		AACA ACA CACAG ACACC		
		A _ TC		
GAM2263	LOC150759	3' TCCACAGACACTACCCAAAGC	39014	G T T
		GCTT TG GT GTGTCTGTGGA		
		CGAA AC CA CACAGACACCT		
		_ C T		
GAM2263	LOC151323	3' TCCACAGACACTACCCAAAGC	39103	G T T
		GCTT TG GT GTGTCTGTGGA		
		CGAA AC CA CACAGACACCT		
		_ C T		
GAM2263	LOC200399	3' TCCACAGACACTACCCAAAGC	42811	G T T
		GCTT TG GT GTGTCTGTGGA		
		CGAA AC CA CACAGACACCT		
		_ C T		
GAM2264	COX11	3' GACTATTCAATACCATACTGAA	10593	C C _
	GA	TCT TCAG ATGGTATTGAAT GTC		
		AGA AGTC TACCATAACTTA CAG		
		_ A T		
GAM2264	CXCL13	3' GACATTCAATAAAGTTGAG	13135	ATGG
		CTCAGC TATTGAATGTC		
		GAGTTG ATAACCTACAG		
		AA_		
GAM2264	MTMR6	3' GACATTCAGTTCTGTAAGA	44937	CA T T
		TCT GCA GG ATTGAATGTC		
		AGA TGT CT TGACTTACAG		
		A_ _ _		
GAM2264	HEY2	3' GACATTTTAATACCATGCCAGA	14565	CA _
	GA	TCTCT GCATGGTATTGAA TGTC		

		AGAGA CGTACCATAATTT ACAG	
		C_ T	
GAM2264 KIAA0546	3'	GACACTCTCTGATGCCTGAGAG 35330	_ GGTATT A
A		TCTCTCAG CAT GA TGTC	
		AGAGAGTC GTA CT ACAG	
		C GTCT_ C	
GAM2264 KIAA1511	3'	ACATTTGTCCACCCTGAGAGA 34755	CA TATT
		TCTCTCAG TGG GAATGT	
		AGAGAGTC ACC TTTACA	
		CC TG_	
GAM2264 PDE1C	3'	ACATTCATCACCGCAAAGA 11458	CA AT AT
		TCT GC GGT TGAATGT	
		AGA CG CCA ACTTACA	
		AA _ CT	
GAM2264 PDE1C	3'	GACATCCTGGATATGCTGGGAG 11459	GTATT A
A		TCTCTCAGCATG GA TGTC	
		AGAGGGTCGTAT CT ACAG	
		AGGTC _	
GAM2264 LOC128344	3'	ACACTCAGGCCTGAGAGA 36921	GCAT A A
		TCTCTCA GGT TTGA TGT	
		AGAGAGT CCG GACT ACA	
		_ _ C	
GAM2264 LOC169436	5'	GACACCCAACATTTGAGAGA 40277	C GTA AA
		TCTCTCAG ATG TTG TGTC	
		AGAGAGTT TAC AAC ACAG	
		_ _ CC	
GAM2264 LOC92399	3'	GACTGTCACCATGCTGACAGA 29012	C ATT AT
		TCT TCAGCATGGT GA GTC	
		AGA AGTCGTACCA CT CAG	
		C _ GT	
GAM2265 ARHGAP6	3'	AAAACAAACAGAACCCAAAC 6839	GGAGGCC
		GTTTGGG TTTGTTTT	
		CAAACCC AAACAAAA	
		AAGAC_	
GAM2265 ARHGAP6	3'	AAAACAAACAGAACCCAAAC 15083	GGAGGCC
		GTTTGGG TTTGTTTT	
		CAAACCC AAACAAAA	
		AAGAC_	
GAM2265 HOXC9	3'	AAAACAAAAACCCACAAA 30718	_ AGGCC
		TTTG GGGG TTTGTTTT	

		AAAC CCCC AAACAAAA	
		A AA__	
GAM2265 PSMB9	3'	AAAACAAAAGGGACTAACTA 8674	GGGAGG _
		TAGTTTGG CCTTT GTTTT	
		ATCAAATC GGAAA CAAAA	
		AG__ A	
GAM2265 CGGBP1	3'	AAACAAAAGCCACAAAC 9736	GGGGA C
		GTTTG GGC TTTGTTT	
		CAAAC CCG AAACAAA	
		A__ A	
GAM2265 DUSP10	3'	AAAACAAAAACCCAACCAAAC 14070	GGGA CC
		GTTTGG GG TTTGTTTT	
		CAAACC CC AAACAAAA	
		AAC_ AA	
GAM2265 DUSP10	3'	AAAACAAAAACCCAACCAAAC 29554	GGGA CC
		GTTTGG GG TTTGTTTT	
		CAAACC CC AAACAAAA	
		AAC_ AA	
GAM2265 IMP-2	3'	AAAACAGGAACCCACCAAAC 13301	_ AGG TT
		GTTTGG GGG CCT GTTTT	
		CAAACC CCC GGA CAAAA	
		A AA_ _	
GAM2265 KIAA0140	3'	AAAACAAAACAAACCCCTAACTA 16106	T GAGGCC
		TAGTT GGGG TTTGTTTT	
		ATCAA TCCC AAACAAAA	
		_ AAACA_	
GAM2265 KIAA1211	3'	AAACAACCCCCCAAGC 34157	AGGCCT
		GTTTGGGGG TTGTTT	
		CGAACCCCC AACAAA	
		C__	
GAM2265 KIAA1676	3'	AAAACAAAAGGATTACCCAAA 44723	GG GG _
C		GTTTGGG A CCTT TGTTTT	
		CAAACCC T GGAA ACAAAA	
		AT A_ AA	
GAM2265 MACF1	3'	AAAACAAAGGGCATGCCCAAAG 26933	GG AG_ _
C		GTTT GGG GCC TTTGTTTT	
		CGAA CCC CGG AAACAAAA	
		A_ GTA G	
GAM2265 MKRN2	3'	AAAACAAAATTAACCCAAAT 35855	GGAGGCC
		GTTTGGG TTTGTTTT	

		TAAACCC	AAACAAAA		
		AAAATTA			
GAM2265	POPX1	3'	AAACAAAGGCAGCAGACTA	17114	GGGGAG
			TAGTTTG GCCTTTGTTT		
			ATCAGAC CGGAAACAAA		
			GA_____		
GAM2265	TRIP-Br2	3'	AAAACAAAAACCCCAA	16478	GAGGCC
			TTTGGGG TTTGTTTT		
			AAACCCC AAACAAAA		
			AA_____		
GAM2265	LOC144997	3'	AAAACAAAAGCAAAAACAAAC	40481	GGGGAG C
			GTTTG GC TTTGTTTT		
			CAAC CG AAACAAAA		
			AAAAA_ A		
GAM2265	LOC159053	3'	AAAACAAAACCCACAAAAC	42059	GGG A CC
			GTTT GG GG TTTGTTTT		
			CAAA CC CC AAACAAAA		
			ACA _ AA		
GAM2266	IKBBK	3'	TGGTGTTCTGCTGCACTGA	31662	TA TG
			TCAGT CAGCAGGAAT TTA		
			AGTCA GTCGTCCTTG GGT		
			C_ GT		
GAM2266	NORE1	3'	TGGCTCCTGCTGCAAC	25444	A ATT
			GTT CAGCAGGA GTTA		
			CAA GTCGTCCT CGGT		
			C _____		
GAM2266	HSPCAL3	3'	CAGTGCTGCTGTAAGTGA	37617	GA
			TCAGTTACAGCAG ATTG		
			AGTCAATGTCGTC TGAC		
			G_ _____		
GAM2266	RTBDN	5'	ATTTTTCCTGCTGCACTGA	25424	TA TT
			TCAGT CAGCAGGAA GT		
			AGTCA GTCGTCCTT TA		
			C_ TT		
GAM2267	HRH1	3'	CTGGTAAGCAAAAAGTAGTAA	6524	C _____
			TTAC AGTTTTTGT ACCAG		
			AATG TCAAAAACG TGGTC		
			A AA		
GAM2267	DKFZP564I122	3'	ACTGAGACTTTAACTGGTAA	31643	TTT AC
			TTACCAGTT GT CAGT		

			AATGGTCAA CA GTCA		
			TTT GA		
GAM2267	ITGA10	5'	TCATACTGGACAGAAAC 29866	A	C
			GTTTTTTGT CCAGTA GA		
			CAAAGACA GGTCAT CT		
			— A		
GAM2267	YKT6	3'	TCGTACCAGCAAGTAGACTAGG 13321	—	— ACCA
			CC AGTTT TTGT GTACGA		
			GG TCAGA AACG CATGCT		
			A TG AC—		
GAM2267	ZFD25	3'	TCATACTGGAGAGAAACT 18324	GTA	C
			AGTTTTT CCAGTA GA		
			TCAAAGA GGTCAT CT		
			GA_ A		
GAM2268	IRTA1	3'	TGCACAGCTTACACTGTCA 25304	C	A_
			TGACAGTG AAGT TGCG		
			ACTGTCAC TTCG ACGT		
			A AC		
GAM2268	MTAP	3'	TTTCATGCCCTTGCCTATCA 8288	C T	TAT
			TGA AG GCAAG GCGTGAAA		
			ACT TC CGTTC CGTACTTT		
			A _ C—		
GAM2268	PROX1	5'	TTTCCAGAATCACTTGCACTGT 8652		_ GCGT
	C		GACAGTGCAAGT AT GAAA		
			CTGTCACGTTCA TA CTTT		
			C AGAC		
GAM2268	RNPEPL1	3'	TCCCAGTCTCTTGCCTGCA 20164	A	TAT GT_
			TG CAGTGCAAG GC GA		
			AC GTCACGTTT CG CT		
			— TCT ACC		
GAM2268	AKT3	3'	TTCTGCTACTTCACTGTCA 11961	C	T T
			TGACAGTG AAGTA GCG GAA		
			ACTGTCAC TTCAT CGT CTT		
			— — —		
GAM2268	C20orf38	3'	TTCACCTAGGTACACTGTCA 20324	CAAGTA	C
			TGACAGTG TG GTGAA		
			ACTGTCAC AT CACTT		
			ATGG_ C		
GAM2268	KIAA1160	3'	TTATTTTGACTTGCACTGCCA 21851	A	ATGC
			TG CAGTGCAAGT GTGA		

			AC GTCACGTTCA TATT		
			C GTTT		
GAM2268	KIAA1198	3'	TCACGTCAGTGCATGTCA 31715	G	AGTAT
			TGACA TGCA GCGTGA		
			ACTGT ACGT TGCACT		
			_ GAC_		
GAM2268	KOC1	3'	CATGGGGCCAGCACTGTCA 43779	AA	ATG
			TGACAGTGC GT CGTG		
			ACTGTCACG CG GTAC		
			AC GG_		
GAM2268	LMOD1	3'	CACTGTCAGCCCTCACTGTCA 14445	CAA	AT _
			TGACAGTG GT GC GTG		
			ACTGTCAC CG TG CAC		
			TCC AC T		
GAM2268	POLM	3'	CATGCATACCTGCACTGCA 43783	A	A
			TG CAGTGCA GTATGCGTG		
			AC GTCACGT CACACGTAC		
			_ C		
GAM2268	PRPF8	3'	CACAGACTCGCACTGTCA 30676	A	ATGC
			TGACAGTGC AGT GTG		
			ACTGTCACG TCA CAC		
			C GA_		
GAM2268	RFX4	3'	TTCTGTCATACCCACATCTGTC 26243	_	CAA _ T
	A		TGACAG TG GTATG CG GAA		
			ACTGTC AC CACAC GT CTT		
			T ACC T _		
GAM2268	RHOBTB3	3'	TATGTATACCAACACTGCCA 17077	A	CAA
			TG CAGTG GTATGCGTG		
			AC GTCAC CATATGTAT		
			C AAC		
GAM2268	RLUCL	3'	CACACAGCCATGCATTGTCA 27753	AGTA	C
			TGACAGTGCA TG GTG		
			ACTGTTACGT AC CAC		
			ACCG A		
GAM2268	RNF8	3'	TTTTCATTGTGTATTTGCACCA 10102	CA	_
	TCA		TGA GTGCAAGTATGCG TGAAAA		
			ACT CACGTTTATGTGT ACTTTT		
			AC T		
GAM2268	USP8	3'	TTTATTGCATACTTGACAC 11632	_	
			GTGCAAGTATGCG TGAA		

		CACGTTTCATACGT ATTT	
		T	
GAM2268	LOC144438 3'	TTTTCATGTTGTATCACACTGT 37741	CAAGTAT
	CA	TGACAGTG GCGTGAAAA	
		ACTGTCAC TGTACTTTT	
		ACTATGT	
GAM2268	LOC196955 5'	TTCCAGTGCGCCCCACTGTCA 37942	CAA_ GCGT
		TGACAGTG GTAT GAA	
		ACTGTCAC CGTG CTT	
		CCCG AC__	
GAM2268	LOC200488 5'	TTCTGCTACTTACACTGTCA 43317	C T T
		TGACAGTG AAGTA GCG GAA	
		ACTGTCAC TTCAT CGT CTT	
		A _ _	
GAM2268	LOC200940 5'	TTCCTGCCTACCCGCACTGTC 42875	AA T T
		GACAGTGC GTA GCG GAA	
		CTGTCACG CAT CGT CTT	
		CC C C	
GAM2268	LOC255057 3'	TCACGTCTGTGCACTGTC 45662	AGTAT
		GACAGTGCA GCGTGA	
		CTGTCACGT TGCACT	
		GTC__	
GAM2269	AKAP13 3'	TCCCTCAGCCCTTTCA 43180	C TGC GAA
		TGAAAG G CTGAGGGA	
		ACTTTC C GACTCCCT	
		C _____	
GAM2269	ALDH3B1 3'	TCCCTCAGCCGCTCCCA 44000	AA T GAAC
		TG AGCG GC TGAGGGA	
		AC TCGC CG ACTCCCT	
		CC _ _ _	
GAM2269	BCAT1 3'	TTCCCTCAGTCCTCATAACTT 32897	AGC CGA
	C	GAA GTG ACTGAGGGAAA	
		CTT TAC TGA TCCCTTT	
		CAA TCC	
GAM2269	RET 3'	TTCCCTTACCCACCTTCA 21789	A C CGAAC
		TGAA G GTG TGAGGGAA	
		ACTT C CAC ATTCCCTT	
		_ _ CC__	
GAM2269	RGS5 3'	TTCCCTTGGACCACCTTCA 9680	A C CGAA TG
		TGAA G GTG C AGGGAA	

			ACTT C CAC G TCCCTT		
			__ CA__ GT		
GAM2269	ROBO1	5'	TCCCTCAGCAGCTCTCA	28588	A G GAAC
			TGA AGC TGC TGAGGGA		
			ACT TCG ACG ACTCCCT		
			C _ ____		
GAM2269	SDC4	3'	TTCATTCTCTCGCACATTTT	8894	GC ACT G
			GAAA GTGCGA GAG GAA		
			CTTT CACGCT CTT CTT		
			A_ CT_ A		
GAM2269	SLC21A2	3'	TTCCCTCAGCTCTTACCT	12160	C C A
			AG GTG GA CTGAGGGAA		
			TC CAT CT GACTCCCTT		
			_ T C		
GAM2269	TAL1	3'	TTCCCTCAGTCCCAAATCCTTC	9174	AGCG_ C A
			GAA TG GA CTGAGGGAA		
			CTT AC CT GACTCCCTT		
			CCTAA C _		
GAM2269	UBE2L3	3'	TCCCTCGGCACACTTT	9362	C GAAC
			AAAG GTGC TGAGGGA		
			TTTC CACG GCTCCCT		
			A ____		
GAM2269	CLSTN1	5'	TCCCGGGCCCGCGCGCTCCCA	17258	AA AA GA
			TG AGCGTGCG CT GGGA		
			AC TCGCGCGC GG CCCT		
			CC CC G_		
GAM2269	D21S2056E	3'	TTTCCCTCAGCCAGGTCACCCT	9790	A C _ GAA_
	CA		A AG GTG C CTGAGGGAAA		
			A TC CAC G GACTCCCTTT		
			C C T GACC		
GAM2269	FADS2	3'	TCCCTCAGCCGTCAGCCATCA	10470	AA GT AA
			TGA GC GCG CTGAGGGA		
			ACT CG TGC GACTCCCT		
			AC AC C_		
GAM2269	FLJ13265	3'	TTTCCCTCAGCCTGTGCAC	24314	AA__
			GTGCG CTGAGGGAAA		
			CACGT GACTCCCTTT		
			GTCC		
GAM2269	KIAA1854	3'	TTCCCTCAGCTCCAACTCTTC	35538	AGCG C A
			GAA TG GA CTGAGGGAA		

CTT AC CT GACTCCCTT
 CTCA _ C
 GAM2269 KIAA1855 3' TTCCCTCAGCTCACCCTTCA 44363 A C CGAA
 TGAA G GTG CTGAGGGAA
 ||||| ||| |||||
 ACTT C CAC GACTCCCTT
 _ C TC_
 GAM2269 MGC15854 5' TCCCTCAGATCCAGGCCCTCA 29646 AA G C A
 TGA GC TG GA CTGAGGGA
 ||| ||||| |||||
 ACT CG AC CT GACTCCCT
 CC G _ A
 GAM2269 TNFAIP3 3' TCCCCCAGCATCTCTCA 12980 A C GAAC A
 TGA AG GTGC TG GGGA
 ||| ||||| |||||
 ACT TC TACG AC CCCT
 C _ _ C
 GAM2269 TRAF6 3' TTTCCTGGGAATCCACACGTT 10970 C_ A_ G
 AGCGTG GA CT AGGGAA
 ||||| || |||||
 TTGCAC CT GG TCCTTT
 AC AA G
 GAM2269 VPS39 3' TTCCCTCAACTCTCTGCCCTC 31474 AA TGC AC
 GA GCG GA TGAGGGAA
 || ||| || |||||
 CT CGT CT ACTCCCTT
 CC CT_ CA
 GAM2269 WIT-1 3' TCCCCCAGTTCGCGAGTGC 17992 _ A
 GCG TGC GAACTG GGGA
 ||| ||||| |||||
 CGT ACGCTTGAC CCCT
 G C
 GAM2269 LOC129607 3' TCCCTCAGTCCCAAATTC 36976 AGCG C A
 GAA TG GA CTGAGGGA
 ||| ||||| |||||
 CTT AC CT GACTCCCT
 AA_ C _
 GAM2269 LOC144308 3' TTTCCCTCAACACCTGCTC 40409 A_ C CGAAC
 GA AG GTG TGAGGGAAA
 || ||||| |||||
 CT TC CAC ACTCCCTTT
 CG _ A_
 GAM2269 LOC145761 5' TTTCCCTCACC GCAGCTCTCA 40586 A G AAC
 TGA AGC TGCG TGAGGGAAA
 ||| ||||| |||||
 ACT TCG ACGC ACTCCCTTT
 C _ C_
 GAM2269 LOC158310 5' CCCTCAGTCAACGTTTCA 41945 G GC A
 TGAAA CGT GA CTGAGGG
 ||||| ||| |||||

ACTTT GCA CT GACTCCC
 _ A _
 GAM2269 LOC199986 5' CCCTCTCCACCCTTCA 43270 A C C ACT
 TGAA G GTG GA GAGGG
 |||| | ||| || ||||
 ACTT C CAC CT CTCCC
 _ C _ _ _
 GAM2269 LOC201952 5' TTCCCTCAGTTCCTGCTGCCA 43396 AA TGC
 TG AGCG GAACTGAGGGAA
 || |||| |||||
 AC TCGT CTTGACTCCCTT
 CG C _
 GAM2269 LOC219404 3' TTTCCCCCAGTATTGGTTTTCA 44911 GTG _ A
 TGAAAGC CGA ACTG GGGAAA
 ||||| ||| |||| |||||
 ACTTTTG GTT TGAC CCCTTT
 _ _ A C
 GAM2269 LOC219653 3' CCCTCAGTATCCACCTT 43868 C C _
 AAG GTG GA ACTGAGGG
 ||| ||| || |||||
 TTC CAC CT TGACTCCC
 _ _ A
 GAM2269 LOC221178 3' CCTCCTGCCTGCACGCCTTCA 44927 A AACT_
 TGAA GCGTGCG GAGG
 |||| ||||| |||
 ACTT CGCACGT CTCC
 C CCGTC
 GAM2269 LOC245812 3' TCCCTGCTCCACAGCTTTCA 45100 _ C ACTG
 TGAAAGC GTG GA AGGGA
 ||||| ||| || |||||
 ACTTTCG CAC CT TCCCT
 A _ CG _
 GAM2269 LOC91660 5' CCCTCAGTATTATGATCTCA 33208 AAG CGA
 TGA CGTG ACTGAGGG
 ||| |||| |||||
 ACT GTAT TGACTCCC
 CTA TA _
 GAM2269 LOC92689 3' TCCTGAGCTCCACGCCTTCA 34785 A C A G
 TGAA GCGTG GA CT AGGG
 |||| |||| || |||||
 ACTT CGCAC CT GA TCCT
 C _ C G
 GAM2269 LOC92906 5' CCCTCAGTCCGTCGCGCTT 28762 _ A
 AAGCGT GCG ACTGAGGG
 ||||| ||| |||||
 TTCGCG TGC TGACTCCC
 CC C
 GAM2270 HEF1 3' ACACATGATGGCCAAGTGCCA 13110 CTG CA
 TGGCAC GGTTATTA TGT
 ||||| ||||| |||

ACCGTG CCGGTAGT ACA
 AA_ AC
 GAM2271 PPP3CA 3' CAGATAAGAGAAGCCTGTTT 6642 A CAC
 AAGCAGGCT TCTCT CTG
 ||||| |||| ||
 TTTGTCCGA AGAGA GAC
 _ ATA
 GAM2271 cerk 3' CAGGTGAAAGGGCAGCTTTAA 23012 AG AT C
 TTAAAGC GCT CT TCACCTG
 ||||| || |||||
 AATTTCG CGG GA AGTGGAC
 A_ _ A
 GAM2271 DKFZP434P0111 3' CAGGTGAGAAATTGTGCT 33453 GGCT C
 AGCA AT TCTCACCTG
 ||| |||||
 TCGT TA AGAGTGGAC
 GT_ A
 GAM2271 FLJ11004 5' CAGGTGAGAGCTCTGC 20286 CTAT
 GCAGG CTCTCACCTG
 |||| |||||
 CGTCT GAGAGTGGAC
 C_
 GAM2271 FLJ21276 3' CAGGATAGCAGATAACCTGCTT 23900 C _ CA
 TGA TTAAAGCAGG TATCT CT CCTG
 ||||| |||| ||
 AGTTTCGTCC ATAGA GA GGAC
 A C TA
 GAM2271 IDI2 3' AGACATACTTGCTTTAA 27090 C C
 TTAAAGCAGG TAT TCT
 ||||| ||||
 AATTTCGTTC ATA AGA
 _ C
 GAM2271 RAB-R 3' CAGGTGAAAGGTGGCTGC 12720 G C
 GCAG CTATCT TCACCTG
 ||| |||| |||||
 CGTC GGTGGA AGTGGAC
 _ A
 GAM2271 LOC165693 3' CAGGCAAGAGAGATGCCTGC 40186 T A_
 GCAGGC ATCTCTC CCTG
 |||| ||||| |||
 CGTCCG TAGAGAG GGAC
 _ AAC
 GAM2271 LOC255042 3' GTAAGAGACAACCTGGGTCTGTT 45649 A_____ C
 T AAGCAGGCT TCTCT AC
 ||||| |||| ||
 TTTGTCTGG AGAGA TG
 GTCAAC A
 GAM2272 FPRL1 5' GGTGGCCAATTGAGCTTCAA 7195 CACC _
 TTGA CAATTGGCC CT
 ||| ||||| ||

			AACT GTTAACCGG GG		
			TCGA T		
GAM2272	LIMK1	3'	CTACAAGGACAAGAGGCTCAA 18800	CAC AA GC	
			TTGA CC TTG CCTTGTAG		
			AACT GG AAC GGAACATC		
			C_ AG A_		
GAM2272	MCL1	3'	CTACAAATTAATGTTGGTTGTC 22486	C TGGCCC	
	AA		TTGACA CCAAT TTGTAG		
			AACTGT GGTTG AACATC		
			T TAATTA		
GAM2272	C5orf4	3'	ACAAGGGGAGGGGTCAA 18472	A AATTGG	
			TTGAC CCC CCCTTGT		
			AACTG GGG GGGAACA		
			_ AG_		
GAM2272	C5orf4	3'	ACAAGGGAAGGGGTCAA 26177	A AATTGG	
			TTGAC CCC CCCTTGT		
			AACTG GGG GGGAACA		
			_ AA_		
GAM2273	TLX1	3'	ACACATCCCAGCCCAATC 12042	A TC	
			GATTGGGTT GGA TGTGT		
			CTAACCCGA CCT ACACA		
			C _		
GAM2273	DKFZP434C128	3'	GCCTGAACCCCAACCCAACCCT 32374	A_ A_ A T_	
	A		TAG TTGGGTT GG TC GT		
			ATC AACCCAA CC AG CG		
			CC CC A TC		
GAM2273	IMP-2	3'	ACACACAAACCAGCCTCAACT 13302	A _ A ATC	
			AG TTG GGTT GG TGTGTGT		
			TC AAC CCGA CC ACACACA		
			_ T _ AA_		
GAM2273	TOB2	3'	CACACAGGCACCCACCCA 45764	TA A_	
			TGGGT GG TCTGTGTG		
			ACCCA CC GGACACAC		
			C_ AC		
GAM2273	LOC147671	3'	CACACAGGCACCCACCCA 38376	TA A_	
			TGGGT GG TCTGTGTG		
			ACCCA CC GGACACAC		
			C_ AC		
GAM2273	LOC158819	3'	ACACACAGACCCCTCCCCAATC 42024	TTA A	
	TG		TAGATTGGG GG TCTGTGTGT		

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GTCTAACCC CC AGACACACA
CTC C
GAM2273 LOC200014 3' GGTTCCTAACCCAACCTA 42693 A T
TAG TTGGGTTAGGA CT
||| ||||| ||
ATC AACCCAATCCT GG
C T
GAM2274 ATRX 3' CAGTTCTGCAAAAATGACCTAT 6094 CT AA
AA TTA GGTCAATTTT GGGACTG
||| ||||| |||||
AAT CCAGTAAAAA TCTTGAC
AT CG
GAM2274 ATRX 3' CAGTTCTGCAAAAATGACCTAT 28683 CT AA
AA TTA GGTCAATTTT GGGACTG
||| ||||| |||||
AAT CCAGTAAAAA TCTTGAC
AT CG
GAM2274 JDD1 3' CAGTCCCTTAAAAATTCCA 31671 TC
TGG ATTTTAAAGGGACTG
||| ||||| |||||
ACC TAAAAATTCCCTGAC
T_
GAM2274 KIAA1102 3' CAGCCCCTGGTCTGTGATCAG 34211 TTTTA A
CTGGTCAT AGGG CTG
||||| ||| |||
GACTAGTG TCCC GAC
TCTGG C
GAM2275 COL6A2 3' ACCCGCTCCACCTGCA 27726 ACAGACA _
TGTAG GTG AGCGGGT
||| ||| |||||
ACGTC CAC TCGCCCA
C
GAM2275 DKFZP434H132 5' CACCCAAACCTGTCTAC 36445 ACA GAGC
GTAGACAG GT GGGTG
||||| || |||||
CATCTGTC CA CCCAC
AA_
GAM2275 DKFZP586I2223 3' GCTCACTGTCTTCCACA 28017 A C
TGT GA AGACAGTGAGC
||| || ||||| |||||
ACA CT TCTGTCACTCG
C _
GAM2275 DKFZP586I2223 3' GCTCACTGTCTTCCACA 28019 A C
TGT GA AGACAGTGAGC
||| || ||||| |||||
ACA CT TCTGTCACTCG
C _
GAM2275 DKFZP586I2223 3' GCTCACTGTCTTCCACA 17730 A C
TGT GA AGACAGTGAGC
||| || ||||| |||||

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ACA CT TCTGTCACTCG
C _

GAM2275 FBXO21 3' GCACCTGTCTGTCCATCTGCA 27323 CA TGA
TG TAGA GACAG GCGGGTGC
||||| |||| |
ACGTCT CTGTC TGTCCACG
AC _

GAM2275 FLJ00007 3' GCACCTGCCCCACCTGCCACACA 35310 AGA ACA A_
TGT CAG GTG GCGGGTGC
||| ||| ||| |
ACA GTC CAC CGTCCACG
CCC _ CC

GAM2275 FLJ23231 3' GCACCTCTAGCTGTCTGCCTCA 24679 T A G C
TG AG CAGACAGT AG GGGTGC
|| || ||||| || |||||
AC TC GTCTGTCTG TC TCCACG
_ C A _

GAM2275 MIG2 3' GCATAATCACTGTCTGCCTA 35863 A GCGG
TAG CAGACAGTGA GTGC
||| ||||| |||
ATC GTCTGTCACT TACG
C AA_

GAM2275 PRO0650 5' GCACCCGCCCTGTGACGCTCCA 15403 T ACAG TGA
TG AG ACAG GCGGGTGC
|| || ||| |
AC TC TGTC CGCCCACG
C GCAG C_

GAM2275 LOC165140 5' GCTCACTGCCTTCCTACA 40117 AC A
TG TAG AG CAGTGAGC
|||| | |||||
ACATC TC GTCAC TCG
CT C

GAM2275 LOC197414 3' CGCCACCGTCTGTCTCA 42514 T A A
TG AGACAGAC GTG GCG
|| ||||| ||| |||
AC TCTGTCTG CAC CGC
_ C _

GAM2275 LOC199923 3' GCACCCGCTTCAACTGCCTGCA 42669 A ACAGT
TG TAG CAG GAGCGGGTGC
|||| ||| |
ACGTC GTC TTCGCCCACG
C AAC_

GAM2275 LOC222160 3' GCACTTAGCACTGCCTACCTCA 45167 T AC A AGC
TG AG AG CAGTG GGGTGC
|| || || |||| |
AC TC TC GTCAC TTCACG
_ CA C GA_

GAM2275 LOC255645 3' GCCTCCTCACTGTCTACCTCCA 46221 T AC C
TG AG AGACAGTGAG GGGT
|| || ||||| |||||

				AC TC TCTGTCACTC TCCG			
				C CA C			
GAM2275	LOC90092	5'	GCACCCAGCAGCATCTGCCTCA	30787	T A	CA GA	_
			TG AG CAGA GT GC GGGTGC				
			AC TC GTCT CG CG CCCACG				
			_ C A_ A_ A				
GAM2276	ANKH	5'	CCCTGCTAGAGCAGCCGCGC	27635	A	AC_	
			GC CGGCT CTGGTAGGG				
			CG GCCGA GATCGTCCC				
			C CGA				
GAM2276	ANKH	5'	CCCTGCTAGAGCAGCCGCGC	21252	A	AC_	
			GC CGGCT CTGGTAGGG				
			CG GCCGA GATCGTCCC				
			C CGA				
GAM2276	CRKL	5'	CCCCCGGCTCTGCCGTGCA	11707		TAC_	TA
			TGCACGGC CTGG GGG				
			ACGTGCCG GGCC CCC				
			TCTC _				
GAM2276	DLEC1	3'	CCCTACCAGCAGCTGTGCA	14264		AC	
			TGCACGGCT CTGGTAGGG				
			ACGTGTCGA GACCATCCC				
			C_				
GAM2276	DLEC1	3'	CCCTACCAGCAGCTGTGCA	14271		AC	
			TGCACGGCT CTGGTAGGG				
			ACGTGTCGA GACCATCCC				
			C_				
GAM2276	IFNW1	5'	TCCTATTAAGCCATGCA	7937	C	ACC	
			TGCA GGCT TGGTAGGG				
			ACGT CCGA ATTATCCT				
			A AA_				
GAM2276	LENG4	3'	TCCCTGCCACAACCTGCA	23586	C	CTACC	
			TGCA GG TGGTAGGGA				
			ACGT CC ACCGTCCCT				
			_ AAC_				
GAM2276	LPL	3'	TCCCTACCATGGCCTGCA	5753	C	CC	
			TGCA GGCTA TGGTAGGGA				
			ACGT CCGGT ACCATCCCT				
			_ T_				
GAM2276	MAN2C1	5'	TCCCTACCAGGAGGCAGTCCA	36102	C G	A	
			TG AC GCT CCTGGTAGGGA				

			AC TG CGG GGACCATCCCT		
			C A A		
GAM2276	MPP2	3'	CCCGCTGGCAGCCAGGCA 30082	AC A T A	
			TGC GGCT CC GGT GGG		
			ACG CCGA GG TCG CCC		
			GA C _ _		
GAM2276	PABPC1	5'	CCCTGCGGGCAGCCGTGC 8419	A G	
			GCACGGCT CCTG TAGGG		
			CGTGCCGA GGGC GTCCC		
			C _		
GAM2276	SLC13A3	3'	CCCTGCCGATAACCAGCA 30329	AC C CC	
			TGC GG TA TGGTAGGG		
			ACG CC AT GCCGTCCC		
			A_ A A_		
GAM2276	STAR	3'	TCCCTACTGGAAGCCTGCA 5904	C A T	
			TGCA GGCT CC GGTAGGGA		
			ACGT CCGA GG TCATCCCT		
			_ A _		
GAM2276	SUFU	3'	TCCCTGCCTGCAGCCTGCA 18258	C ACCT	
			TGCA GGCT GGTAGGGA		
			ACGT CCGA CCGTCCCT		
			_ CGT_		
GAM2276	TEGT	3'	TCCCTATTCAACAGTGCA 32275	_ CTACCT	
			TGCAC GG GGTAGGGA		
			ACGTG CC TTATCCCT		
			A AACAC_		
GAM2276	DKFZp434K2435	3'	TCAGGTAGAGAAGCCGTGCA 26000	_____	
			TGCACGGCT ACCTGG		
			ACGTGCCGA TGGACT		
			AGAGA		
GAM2276	DKFZp547E052	3'	CCCTATTATTAAGTGTGCA 26031	C CC	
			TGCACGG TA TGGTAGGG		
			ACGTGTC AT ATTATCCC		
			A T_		
GAM2276	FLJ12287	3'	CCTTACCAGTCGTGCA 22755	ACCT	
			TGCACGGCT GGTAGGG		
			ACGTGCTGA CCATTCC		

GAM2276	FLJ13162	3'	CCCGCCGGGCAGCCGTGCA 24573	A A	
			TGCACGGCT CCTGGT GGG		

ACGTGCCGA GGGCCG CCC
 C _
 GAM2276 FLJ14743 3' CCCCACCAGGTGGCAGCA 33761 ACG A
 TGC GCTACCTGGT GGG
 ||| ||||| |||
 ACG CGGTGGACCA CCC
 A_ C
 GAM2276 FLJ20739 3' CCCTACCAGATGCCAGCA 33703 AC TAC
 TGC GGC CTGGTAGGG
 ||| ||| |||||
 ACG CCG GACCATCCC
 A_ TA_
 GAM2276 KIAA0082 3' CCCTGAGGGTAGCCATGC 44264 C GG
 GCA GGCTACCT TAGGG
 ||| ||||| |||||
 CGT CCGATGGG GTCCC
 A A_
 GAM2276 KIAA0494 3' CCCTACCAAGTTTGGCA 16588 AC ACC
 TGC GGCT TGGTAGGG
 ||| ||| |||||
 ACG TTGA ACCATCCC
 GT _
 GAM2276 KIAA0872 3' TCCCTGCCCAGTCATGCA 17248 C ACCT
 TGCA GGCT GGTAGGGA
 |||| ||| |||||
 ACGT CTGA CCGTCCCT
 A C_
 GAM2276 KIAA1344 3' TCCTGCTAAATAACCTGCA 35873 C C CC
 TGCA GG TA TGGTAGGG
 |||| || || |||||
 ACGT CC AT ATCGTCCT
 _ A AA
 GAM2276 KIAA1416 5' CCCTACCAGCAGCAGCA 41804 ACG AC
 TGC GCT CTGGTAGGG
 ||| ||| |||||
 ACG CGA GACCATCCC
 A_ C_
 GAM2276 KIAA1821 3' TCCACACGGTTAGCCGTGCA 35554 C GTAG
 TGCACGGCTA CTG GGA
 ||||| ||| |||
 ACGTGCCGAT GGC CCT
 T ACA_
 GAM2276 KIAA1870 5' TCCCTACCAAGCCTTCGGC 26712 AC_ ACC
 GC GGCT TGGTAGGGA
 || ||| |||||
 CG CCGA ACCATCCCT
 GCTT _
 GAM2276 MGC10334 5' CCCCCGGAGCAGGCCGTGCA 24949 AC_ TA
 TGCACGGCT CTGG GGG
 ||||| ||| |||

			ACGTGCCGG	GGCC	CCC		
			ACGA	___			
GAM2276	PALM	3'	CCCGAACCAGAGCCGTGCA	8438	AC	A_	
			TGCACGGCT	CTGGT	GGG		
			ACGTGCCGA	GACCA	CCC		
			___	AG			
GAM2276	PLAC3	5'	CCAGCACAGGTAGCCAGCA	34365	AC	_ A	
			TGC	GGCTACCTG	GT GG		
			ACG	CCGATGGAC	CG CC		
			A_	A A			
GAM2276	PRO2015	5'	TCCCTGACTGCAGGTAGCC	20586	G___		
			GGCTACCTG	TAGGGA			
			CCGATGGAC	GTCCCT			
			GTCA				
GAM2276	SIRPB1	3'	TCCCTGTCCCAGCCAGCA	12711	AC	ACCT _	
			TGC	GGCT	GG TAGGGA		
			ACG	CCGA	CC GTCCCT		
			A_	C___	T		
GAM2276	TU3A	5'	TCGTGGAAGTGGCCGTGCA	14036	C GG	G	
			TGCACGGCTAC	T TA GG			
			ACGTGCCGGTG	A GT CT			
			_	AG G			
GAM2276	ZFP100	3'	TCCCTACCAGTGTCTTGT	34707	C	TAC	
			GCA	GGC	CTGGTAGGGA		
			TGT	CTG	GACCATCCCT		
			T	T___			
GAM2276	LOC129642	5'	CCCTCAGCAACGCCGTGCA	29021	TAC_	GT	
			TGCACGGC	CTG AGGG			
			ACGTGCCG	GAC TCCC			
			CAAC	___			
GAM2276	LOC143666	5'	TCCTGAGGATGCCGCGCA	40371	A	TA GG	
			TGC	CGGC	CCT TAGGG		
			ACG	GCCG	GGA GTCCT		
			C	TA	___		
GAM2276	LOC147229	3'	TCCCTGCCCCAGGCGTGCA	38322	G	ACCT	
			TGCACG	CT	GGTAGGGA		
			ACGTGC	GA	CCGTCCCT		
			G	CC___			
GAM2276	LOC150319	3'	CCTTGCGGTAGCCGGCA	38892	A	TG	
			TGC	CGGCTACC	G TAGGG		

ACG GCCGATGG CGTTCC

GAM2276 LOC157918 3' CCCCACCCACCCAGCCGTGTA 41895 ACCT__ A
TGCACGGCT GGT GGG
||||||| ||| |||
ATGTGCCGA CCA CCC
CCCACC C

GAM2276 LOC157919 5' CCCCACCCACCCAGCCGTGTA 39682 ACCT__ A
TGCACGGCT GGT GGG
||||||| ||| |||
ATGTGCCGA CCA CCC
CCCACC C

GAM2276 LOC200197 3' TCCCCACCAGGTGATCCG 42731 C_ A
CGG TACCTGGT GGGA
||| ||||| |||||
GCC GTGGACCA CCCT
TA C

GAM2276 LOC200583 5' CCCTGTGGGCAGCCGTGC 42822 A GGT
GCACGGCT CCT AGGG
||||||| ||| |||||
CGTGCCGA GGG TCCC
C TG_

GAM2276 LOC202052 3' TCCCTACCATGCCTCTGCA 43409 C_ TACC
TGCA GGC TGGTAGGGA
||| ||| ||||| |||||
ACGT CCG ACCATCCCT
CT T__

GAM2276 LOC220827 3' CCCTGCCAGCACCCGTGCA 43844 CTAC
TGCACGG CTGGTAGGG
||||||| ||||| |||||
ACGTGCC GACCGTCCC
CAC_

GAM2276 LOC222008 3' TCTGAAGGCAGCTGTGCA 45126 A GG
TGCACGGCT CCT TAGG
||||||| ||| |||||
ACGTGTCGA GGA GTCT
C A_

GAM2276 LOC92017 3' TCCCTGGCTTAGCCGTCA 33710 C CCT _
TG ACGGCTA GGT AGGGA
|| ||||| ||| |||||
AC TGCCGAT TCG TCCCT
_ _ _ G

GAM2277 ATP8A2 3' GAGACTAATATCAGAGTACCCA 44920 CAA T_____ GAGA
GCA C GTACTCTGG AG C
| ||||| || |
G CATGAGACT TC G
ACC ATAA||| AGAG

GAM2277 FLNB 3' AGTCTCCTACTTCCCTACCGGC 31138 AA CTCT
A TGCC GTA GGTAGGAGACT
||| ||| ||||| |||||

ACGG CAT TCATCCTCTGA
 C_ CCCT
 GAM2277 MX2 3' AGTCTCCTGCACAGCACCTGCA 8294 CAA ACT _
 TGC GT CTG GTAGGAGACT
 ||| || ||| |||||
 ACG CA GAC CGTCCTCTGA
 TC_ C_ A
 GAM2277 PAG 3' TCTCCCCAAAGTACTTG 20511 C TA
 CAAGTACT TGG GGAGA
 ||||| ||| ||||
 GTTCATGA ACC CCTCT
 A _
 GAM2277 PCDH9 5' CCTCCAGAGTATTTGACA 40293 C T
 TG CAAGTACTCTGG AGG
 || ||||| ||| |||
 AC GTTTATGAGACC TCC
 A _
 GAM2277 RNH 5' AGTCCCCAGGCCAGTGCTTGGC 8843 CT A_ A
 A TGCCAAGTACT GGT GG GACT
 ||||| ||| || |||
 ACGGTTTCGTGA CCG CC CTGA
 _ GA C
 GAM2277 TNFSF8 3' GAGACTAGTACCAGAGCAGCTA 6915 CA A_ T_____ GAGA
 GCA AGT CTCTGG AG C
 ||| ||||| || |
 TCG GAGACC TC G
 A_ AC ATGAI|| AGAG
 GAM2277 ACTR3 3' GAGACTAGCCTCATGAGACTTG 12273 A T_ T_ GAGA
 GCA CAAGT CTC GG AG C
 ||||| || || |
 GTTCA GAG CC TC G
 _ TACT GAI|| AGAG
 GAM2277 ERp44 3' AGTCATAAGACAGAACATTTGG 39721 AC GTAGGA
 CA TGCCAAGT TCTG GACT
 ||||| ||| |||
 ACGGTTTA AGAC CTGA
 CA AGAATA
 GAM2277 FLJ10330 3' TCTTTATTAGAATACTTG 19832 C G
 CAAGTA TCTGGTAG AGA
 ||||| ||||| |||
 GTTCAT AGATTATT TCT
 A _
 GAM2277 FLJ10849 3' AGTCTCCTTTTCAGTATTTGGCA 20203 CT T
 TGCCAAGTACT GG AGGAGACT
 ||||| || |||||
 ACGGTTTATGA CT TCCTCTGA
 _ T
 GAM2277 FLJ23121 3' GAGACTAGGACCAGAGTCCTTA 24003 C T T_____ GAGA
 GCA C AAG ACTCTGG AG C
 | ||| ||||| || |

G TTC TGAGACC TC G
 A C AGGAIII AGAG
 GAM2277 FLJ23519 5' AGTCCCCAGGCCAGTGCTTGGC 25973 CT A_ A
 A TGCCAAGTACT GGT GG GACT
 ||||| ||| || ||||
 ACGGTTCTGTGA CCG CC CTGA
 _ GA C
 GAM2277 FLJ23519 5' AGTCCCCAGGCCAGTGCTTGGC 34306 CT A_ A
 A TGCCAAGTACT GGT GG GACT
 ||||| ||| || ||||
 ACGGTTCTGTGA CCG CC CTGA
 _ GA C
 GAM2277 KIAA0523 3' TCCATACAGCAAGACACCTGGC 33646 A A_ _ GTA
 A TGCCA GT CT CTG GGA
 |||| || || ||| |||
 ACGGT CA GA GAC CCT
 C CA AC ATA
 GAM2277 KIAA1130 3' AGTCTCCACCAACCCTGCTGGC 31279 A CTC A
 GCCA GTA TGGT GGAGACT
 ||| ||| ||| |||||
 CCGT CGT ACCA CCTCTGA
 _ CCC C
 GAM2277 KIAA1238 3' CCAACAAGAGACTTGGCA 35216 A G A
 TGCCAAGT CTCT GT GG
 ||||| ||| || ||
 ACGGTTCA GAGA CA CC
 _ A A
 GAM2277 LAP1B 5' AGTCTCCTACACGCAGTCAAC 32262 _ C _
 GT ACT TG GTAGGAGACT
 || ||| || |||||
 CA TGA GC CATCCTCTGA
 AC C A
 GAM2277 MGC14289 3' GAGACTAATCCTAGAGTACTTT 27947 C TA_____ GAGA
 GCA C AAGTACTCTGG G C
 | ||||| | |
 G TTCATGAGATC C G
 T CTAIIIT AGAG
 GAM2277 P2RX1 3' AGTCTCCTACCCTCTCAGC 33351 CA TACTCT
 GC AG GGTAGGAGACT
 || || |||||
 CG TC CCATCCTCTGA
 AC TC_____
 GAM2277 SYNCOILIN 3' CTAGTGCCAGAACTTGGCA 25080 AC T_____
 TGCCAAGT TCTGG AG
 ||||| ||| ||
 ACGGTTCA AGACC TC
 A_ GTGAIII
 GAM2277 LOC132880 5' CTACCAGGACACCTGGCA 37030 A AC
 TGCCA GT TCTGGTAG
 |||| || |||||

		ACGGT CA GGACCATC			
		C CA			
GAM2277	LOC158014 5'	CCTCCGGAGTAACTGGCA	39691	AG	T
		TGCCA TACTCTGG AGG			
		ACGGT ATGAGGCC TCC			
		CA _			
GAM2277	LOC158357 3'	TCCTATATTCAGAGTACT	39819	___	
		AGTACTCTG GTAGGA			
		TCATGAGAC TATCCT			
		TTA			
GAM2277	LOC162137 3'	CCTCCAGGTACACTTGGCA	42113	___ T	T
		TGCCAAGT AC CTGG AGG			
		ACGGTTCA TG GACC TCC			
		CA _ _			
GAM2277	LOC253596 5'	AGCCTCCTACTAGTAC	45722	CT	A
		GTACT GGTAGGAG CT			
		CATGA TCATCCTC GA			
		___ C			
GAM2278	LOC200339 3'	TGCAAGGTCTTCCGTTATA	43301	C	_
		TATAACGGAA ACCT GCA			
		ATATTGCCTT TGGA CGT			
		C A			
GAM2278	LOC200339 3'	TGCAAGGTGTTCCATTATA	43302	C	_
		TATAA GGAACACCT GCA			
		ATATT CCTTGTGGA CGT			
		A A			
GAM2278	LOC90777 3'	CCGAGTCTCAGATATTCTGTTA	31992	CAC	CA__
	TA	TATAACGGAA CTG TCGG			
		ATATTGTCTT GAC AGCC			
		ATA TCTG			
GAM2279	GNAZ 3'	AAGACTTGAGAAGCTGTCACA	7844	A A	TG AT
		TGT GACA CTTCT AG TCTT			
		ACA CTGT GAAGA TC AGAA			
		_ C GT _			
GAM2279	ZNF265 3'	AAGAATCTTGTGATGTCTACA	11939	ACT	T
		TGTAGACA TC TGAGATTCTT			
		ACATCTGT AG GTTCTAAGAA			
		___ T			
GAM2279	BAG2 3'	AAGAATCTTTCCAAAGTTGTCT	43751	T	CTT_
	CA	TG AGACAACTT GAGATTCTT			

			AC TCTGTTGAA TTCTAAGAA		
			— ACCT		
GAM2279	DEFCAP	3'	AAGGAATAAGAAGTTACCTAC 26891	AC	AGA
			GTAG AACTTCTTG TTCTT		
			CATC TTGAAGAAT AGGAA		
			CA A__		
GAM2279	DEFCAP	3'	AAGGAATAAGAAGTTACCTAC 26892	AC	AGA
			GTAG AACTTCTTG TTCTT		
			CATC TTGAAGAAT AGGAA		
			CA A__		
GAM2279	DEFCAP	3'	AAGGAATAAGAAGTTACCTAC 17200	AC	AGA
			GTAG AACTTCTTG TTCTT		
			CATC TTGAAGAAT AGGAA		
			CA A__		
GAM2279	DGCR8	5'	GGTTCTAAAAGCTGTCTACA 22919	A	CTTG TT
			TGTAGACA CTT AGA C		
			ACATCTGT GAA TCT G		
			C AA__ TG		
GAM2279	FLJ21140	5'	AAGAATCTCAGCAGTATTATCA 24138	A	CA__ T T
			CA TGT GA ACT CT GAGATTCTT		
			ACA CT TGA GA CTCTAAGAA		
			_ ATTA C _		
GAM2279	RALGPS1A	3'	AGTTATAGAAAGCTGTCTACA 16015	A	CT A
			TGTAGACA CTT TG GATT		
			ACATCTGT GAA AT TTGA		
			C AG A		
GAM2279	THEA	3'	AAGAACAGATCAAGAAGCTGTC 32945	A	A GA__
			ACA TGT GACA CTTCTTGA TTCTT		
			ACA CTGT GAAGAACT AAGAA		
			_ C AGAC		
GAM2279	LOC146515	3'	AATCTCATTGTACTACA 38191	_	CTTCT
			TGTAG ACAA TGAGATT		
			ACATC TGTT ACTCTAA		
			A _____		
GAM2280	ATP7A	3'	CAGTGCCGGTTCAGACTCACCT 5491	CT	AAAA
			A TAGG AGTCTGGAC CACTG		
			ATCC TCAGACTTG GTGAC		
			AC GCC_		
GAM2280	DACH	3'	TGTCTAAGAAAAGTAGCTTA 28043	___	_
			TAGGCTAG TCT GGACA		

		ATTCGATC AGA TCTGT		
		AAA A		
GAM2280 FGD1	3'	CAGTATTTTATCGTCCAGACCC 10767	CTA	___ C
		GG GTCTGGAC AAAA ACTG		
		CC CAGACCTG TTTT TGAC		
		___ CTA A		
GAM2280 GYG	3'	CAGTGTTCTGCTTTTAAATCCT 10337	CTAGTCT A A	
A		TAGG GG CA AACACTG		
		ATCC TC GT TTGTGAC		
		TAATTTT _ C		
GAM2280 PCTK1	3'	CAGCCAGGGGTCCAGAGCTAGC 12871	_	AAAACA
C		GGCTAG TCTGGAC CTG		
		CCGATC AGACCTG GAC		
		G GGGACC		
GAM2280 PCTK1	3'	CAGCCAGGGGTCCAGAGCTAGC 26906	_	AAAACA
C		GGCTAG TCTGGAC CTG		
		CCGATC AGACCTG GAC		
		G GGGACC		
GAM2280 PCTK1	3'	CAGCCAGGGGTCCAGAGCTAGC 26912	_	AAAACA
C		GGCTAG TCTGGAC CTG		
		CCGATC AGACCTG GAC		
		G GGGACC		
GAM2280 PRY	5'	CAGTGTTTCACTGTCTCAAC 30234	CT	___
		GT GGACA AAACACTG		
		CA TCTGT TTTGTGAC		
		AC CAC		
GAM2280 RALBP1	3'	CAGTGTTTGTGTTTCCAGCTCA 13658	T T	___
		C AG CTGGA CAAAACACTG		
		A TC GACCT GTTTTGTGAC		
		C _ TT		
GAM2280 SLC35A1	3'	CAGTATTTTGTCTAGCAGC 13125	A CT	C
		GCT GT GGACAAAA ACTG		
		CGA CG CCTGTTTT TGAC		
		_ AT A		
GAM2280 TRPV1	3'	CAGTGCTCTGTCAGCAGCCTG 27993	A T G	AAA
		TAGGCT G CTG ACA CACTG		
		GTCCGA C GAC TGT GTGAC		
		_ _ _ CTC		
GAM2280 TRPV1	3'	CAGTGCTCTGTCAGCAGCCTG 28001	A T G	AAA
		TAGGCT G CTG ACA CACTG		

			GTCCGA C GAC TGT GTGAC		
			__ _ CTC		
GAM2280	TRPV1	3'	CAGTGCTCTGTCAGCAGCCTG 28009	A T G	AAA
			TAGGCT G CTG ACA CACTG		
			GTCCGA C GAC TGT GTGAC		
			__ _ CTC		
GAM2280	TRPV1	3'	CAGTGCTCTGTCAGCAGCCTG 20813	A T G	AAA
			TAGGCT G CTG ACA CACTG		
			GTCCGA C GAC TGT GTGAC		
			__ _ CTC		
GAM2280	KIAA0680	3'	CAGTGTTTCAATCCAGCC 16284	AGTCT	CA_
			GGCT GGA AAACACTG		
			CCGA CCT TTTGTGAC		
			_____ AAC		
GAM2280	OSBPL10	3'	CAGTGTTTTGTCTGTCCGCGCC 19415	TAGTCT	
			GGC GGACAAAACACTG		
			CCG TCTGTTTTGTGAC		
			CGCCTG		
GAM2280	TLE4	3'	CAGTACTTTGTCCATTTGGGAC 33719	_ AGTC	AC
	CT		AGG CT TGGACAAA ACTG		
			TCC GG ACCTGTTT TGAC		
			A GTTT CA		
GAM2280	UHRF1	3'	CAGTACTTTGTCCAGATT 14950	AC	
			AGTCTGGACAAA ACTG		
			TTAGACCTGTTT TGAC		
			CA		
GAM2280	LOC126133	5'	CAGTGCCTTGCCAGGATCCC 36804	CTAG	A AA
			GG TCTGG CAA CACTG		
			CC GGACC GTT GTGAC		
			CTA_ _ CC		
GAM2280	LOC142948	3'	CAGTGCTCTGTGTCTAGCTTA 40325	TCTGG	AAA
			TAGGCTAG ACA CACTG		
			ATTCGATC TGT GTGAC		
			TG_ _ CTC		
GAM2280	LOC159160	5'	CAGTGTTTCACTGTCTCAAC 30358	CT	_
			GT GGACA AAACACTG		
			CA TCTGT TTTGTGAC		
			AC CAC		
GAM2280	LOC91947	3'	CAGTGTTTTACCGTCCCCAGCC 33570	AGTCT	_
			GGCT GGAC AAAACACTG		

CCGA CCTG TTTTGTGAC
 CC__ CCA
 GAM2281 FOXD2 5' TTCTGTGAAAAGGGTTGCA 10791 C CT
 TGCAACCC TT GCGGAG
 ||||| || |||||
 ACGTTGGG AA TGTCTT
 A AG
 GAM2281 GBAS 3' CTCCAGAAGGGGTCCACG 7226 CA GC
 CGTG ACCCCTTCT GGAG
 ||| ||||| |||
 GCAC TGGGGAAGA CCTC
 C_ _
 GAM2281 HAS3 3' TCCCCCAGATGCAGGGCTGCAG 11804 G A CT_ C A
 G C TGCA CCC TCTG GG GA
 | ||| ||| ||| |||
 G ACGT GGG AGAC CC CT
 G C ACGT _ C
 GAM2281 PAICS 3' TCTCTGTAGAAAACCGCAC 13164 AACCCC
 GTGC TTCTGCGGAGA
 ||| |||||
 CACG AAGATGTCTCT
 CCAA_
 GAM2281 CLONE24945 3' CTCGAGGAACAAGGTTGCAC 17906 CC_ GCG
 GTGCAACC TTCT GAG
 ||||| ||| |||
 CACGTTGG AAGG CTC
 AAC AG_
 GAM2281 CRMP5 3' TCTCCAGCCGAAGCTGCAGG 21333 G ACCC T _
 C TGCA CTTC GC GGAGA
 | ||| ||| ||| |||||
 G ACGT GAAG CG CCTCT
 G C_ C A
 GAM2281 KIAA0420 3' ATTCCCTGCAGAAGCCGCAGCA 31725 AACCC A
 TGC CTTCTGCGG GAAT
 ||| ||||| |||||
 ACG GAAGACGTC CTTA
 ACGCC C
 GAM2281 KIAA1198 3' ATTCTCCGTTTTCTGAATTGCA 31705 CCCCTTCT
 T GTGCAA GCGGAGAAT
 ||||| |||||
 TACGTT TGCCTCTTA
 AAGTCTTT
 GAM2281 KIAA1198 3' TCTCCTGCGGGATTGCA 31717 C TTCT _
 TGCAA CCC GC GGAGA
 ||||| ||| ||| |||||
 ACGTT GGG CG CCTCT
 A _ T
 GAM2281 LOC146782 5' TCCCTGCAGGGATTTCAC 37526 C C TCT A
 GTG AA CCCT GCGG GA
 ||| ||| ||||| |||

CAC TT GGGG CGTC CT
T A _ C
GAM2281 LOC148114 5' ATTCTCCGCCTGAGTTGCA 38464 CCCT T_
TGCAAC TC GCGGAGAAT
||||| || |||||
ACGTTG AG CGCCTCTTA
_ TC
GAM2281 LOC257354 3' ATTCCCTGCAGAAGCCGCAGCA 45578 AACCC A
TGC CTTCTGCGG GAAT
||| ||||| |||
ACG GAAGACGTC CTTA
ACGCC C
GAM2282 ARHGEF6 3' ATTACTGCCCTATGTTGTC 33844 C A_
GACAACA AGG GGTAAT
||||| ||| |||||
CTGTTGT TCC TCATTA
A CG
GAM2282 BAZ1B 3' AGTGAGAATCCTGTGTTCCCA 26191 AC GGTA
TG AACACAGGA TACT
|| ||||| |||
AC TTGTGTCCT GTGA
CC AAGA_
GAM2282 CSNK1G3 3' AGTATTACTGATGGTACTGTTA 10610 AC AGGA
TGACA AC GGTAATACT
||||| || |||||
ATTGT TG TCATTATGA
CA GTAG
GAM2282 GLS 3' TATTACCTCGTGCATTGT 17108 CA G
ACAA CA GAGGTAATA
||||| || |||||
TGTT GT CTCCATTAT
AC G
GAM2282 LENG4 5' AGTATTGCCCCCGTGTTG 23580 A A
CAACAC GG GGTAATACT
||||| || |||||
GTTGTG CC CCGTTATGA
C _
GAM2282 PKD2 3' AGTATTCTTGATCCTGTGTTTC 30177 C _ T
A TGA AACACAGGA GG AATACT
||| ||||| || |||||
ACT TTGTGTCCT TC TTATGA
_ AGT _
GAM2282 SNAP25 3' TGTTGTCCTGTGTCATC 28318 CA GG
GA ACACAGGA TAATA
|| ||||| |||
CT TGTGTCCT GTTGT
AC _
GAM2282 SNAP25 3' TGTTGTCCTGTGTCATC 9055 CA GG
GA ACACAGGA TAATA
|| ||||| |||

		CT TGTGTCCT GTTGT		
		AC —		
GAM2282	TCTE1L	3' TATTATCTTCCTGTGCTGT	35143	A —
		ACA CACAGGA GGTAATA		
		TGT GTGTCCT CTATTAT		
		C T		
GAM2282	WASF3	3' AGTATTACCAATGCTGTTGT	13440	— GGA
		ACAACA CA GGTAATACT		
		TGTTGT GT CCATTATGA		
		C AA_		
GAM2282	WHSC1	3' AGTAAGATTCTCCTGTATTTCA	17176	C C TAA_
		TGA AA ACAGGAGG TACT		
		ACT TT TGTCTCT ATGA		
		_ A TAGA		
GAM2282	ARHGEF3	3' TATTACCCTGTGTTGT	21211	AG
		ACAACACAGG GTAATA		
		TGTTGTGTCC CATTAT		
		—		
GAM2282	BCE-1	5' TATGTTGCTGTGTTGTTA	13868	— G
		TGACAACACAG GA GTA		
		ATTGTTGTGTC TT TAT		
		G G		
GAM2282	C19orf7	3' AGTATTACCCACCTGTCC	30635	C A_
		A ACAGG GGTAATACT		
		C TGTCC CCATTATGA		
		C ACC		
GAM2282	C20orf36	3' GTATTTCTGTGTTGTCA	20222	GGTA
		TGACAACACAGGA ATAC		
		ACTGTTGTGTCTT TATG		
		—		
GAM2282	CHCR	3' AGTACCATTCTTGTGTTGT	20421	AA
		ACAACACAGGAGGT TACT		
		TGTTGTGTTCTTTA ATGA		
		CC		
GAM2282	ELOVL2	3' TATTACCTCAGATACCTGTTGT	19388	CAG_____
	CA	TGACAACA GAGGTAATA		
		ACTGTTGT CTCCATTAT		
		CCATAGA		
GAM2282	ERAP140	5' AGTATTTGCCTCCTGTGT	37083	—
		ACACAGGAGGTAA TACT		

TGTGTCCTCCGTT ATGA
 T
 GAM2282 FLJ10781 3' TATTACCTTGTGTTCA 20139 CAAC G
 TGA ACA GAGGTAATA
 ||| ||| |||||
 ACT TGT TTCCATTAT
 ____ G
 GAM2282 FLJ13162 3' ATTGTCTCCTGTGTTCTCA 24572 C GT
 TGA AACACAGGAG AAT
 ||| ||||| |||
 ACT TTGTGTCCTC TTA
 C TG
 GAM2282 FLJ20130 3' AGTCTGGTCTCCTGTGTTTCA 19226 C AAT
 TGA AACACAGGAGGT ACT
 ||| ||||| |||
 ACT TTGTGTCCTCTG TGA
 _ GTC
 GAM2282 FLJ20344 3' AGTATTATATCCATGCTGT 19402 _ _ G
 ACA CA GGA GTAATACT
 ||| ||| |||||
 TGT GT CCT TATTATGA
 C A A
 GAM2282 FLJ20972 3' AGTGCACATCCTGTGTCATCA 24623 CA G AA
 TGA ACACAGGA GT TACT
 ||| ||||| || |||
 ACT TGTGTCCT CA GTGA
 AC A C_
 GAM2282 FLJ23462 3' ATCCCTGGCCTGTTGTCA 24262 ____ A
 TGACAACA CAGG GGT
 ||||| ||| |||
 ACTGTTGT GTCC CTA
 CCG _
 GAM2282 GOLGA1 5' GCCAGATCCTGTGTTGCCA 7861 A ____
 TG CAACACAGGA GGT
 || ||||| |||
 AC GTTGTGTCCT CCG
 C AGA
 GAM2282 KIAA0820 3' AGTACTACTTGATTTGTGTT 34217 ____ A
 AACACAGG AGGTA TACT
 ||||| ||| |||
 TTGTGTTT TTCAT ATGA
 AG C
 GAM2282 KIAA1281 3' AGTACCACAAAACTGTGTTGT 42960 GAG__ AA
 ACAACACAG GT TACT
 ||||| || |||
 TGTTGTGTC CA ATGA
 AAAAA CC
 GAM2282 KIAA1775 3' AGTACTTTCCAGCCTGTGTTTC 26938 C A_ TAA_
 A TGA AACACAGG GG TACT
 ||| ||||| || |||

ACT TTGTGTCC CC ATGA
 _ GA TTTC
 GAM2282 KIAA1925 5' AGTAACTGCCCTGTGTTGTCA 44207 A_ AA
 TGACAACACAGG GGT TACT
 ||||| ||| ||||
 ACTGTTGTGTCC TCA ATGA
 CG _
 GAM2282 KIAA1987 3' ACCTCAGCTTTGTTGTCA 42492 C _
 TGACAACA AG GAGGT
 ||||| || ||||
 ACTGTTGT TC CTCCA
 T GA
 GAM2282 NAPG 3' TATTAAATGTGTTGTTA 46253 GGAGG
 TGACAACACA TAATA
 ||||| ||||
 ATTGTTGTGT ATTAT
 AA_
 GAM2282 PEX12 3' AGTATTGCGCTGTAATGTCA 5831 AC GAG
 TGACA ACAG GTAATACT
 |||| ||| |||||
 ACTGT TGTC CGTTATGA
 AA G_
 GAM2282 PSR 3' AGCATTGCTCCTGTGCTGCCA 32497 A A G A
 TG CA CACAGGAG TAAT CT
 || || ||||| ||| ||
 AC GT GTGTCCTC GTTA GA
 C C _ C
 GAM2282 SES2 3' ATTACCTCCTACTTGCCA 25480 A CAC
 TG CAA AGGAGGTAAT
 || ||| |||||
 AC GTT TCCTCCATTA
 C CA_
 GAM2282 THEA 3' AGTATTGCTGCCCGCATGTCA 32947 ACACA A_
 TGACA GG GGTAATACT
 |||| || |||||
 ACTGT CC TCGTTATGA
 ACG_ CG
 GAM2282 USP24 3' AGTGAGGGTTTCTGTGCTGTCA 43814 A GTAA
 TGACA CACAGGAG TACT
 |||| ||||| ||||
 ACTGT GTGTCTTT GTGA
 C GGA
 GAM2282 LOC145815 5' TGTTCCCTCTGTGTTGTCA 40607 G T
 TGACAACACAG AGG AATA
 ||||| ||| ||||
 ACTGTTGTGTC TCC TTGT
 _ _
 GAM2282 LOC146449 3' TACCTTGCAGCTGTATTGCTCA 30611 _ C _
 TGA CAA ACAG GAGGTA
 ||| ||| ||| ||||

		ACT GTT TGTC TTCCAT		
		C A GACG		
GAM2282	LOC197414	3' GTCTCCCCTGTGTTTCA 42515	C	A TA
		TGA AACACAGG GG AT		
		ACT TTGTGTCC CC TG		
		— — TC		
GAM2282	LOC221002	3' GTTCCACTGTATTGTCA 43976	C	GA T
		TGACAA ACAG GG AAT		
		ACTGTT TGTC CC TTG		
		A A_ _		
GAM2282	LOC83693	3' TTATCTCCTGTGTTTCA 25498	C	
		TGA AACACAGGAGGTAA		
		ACT TTGTGTCCTCTATT		
		—		
GAM2283	FZD10	3' CATTTGTGAACTCAAACGATGT 14052	C	A C
		GCA CGTTTGA TTCACAAG TG		
		TGT GCAAACCT AAGTGTTT AC		
		A C _		
GAM2283	C17orf31	5' CAGCCTGCACAGCGGTGC 18997	_	AATTCA A
		GCACCGTT TG CA GCTG		
		CGTGGCGA AC GT CGAC		
		C _ _ _ C		
GAM2283	CL683	3' CCAATGCAAACCTCAAATGGTGC 17925		A CA AGC
		GCACCGTTTGA TT CA TGG		
		CGTGGTAAACT AA GT ACC		
		C AC A_ _		
GAM2283	FLJ13710	3' CCAACTTGTGAAGCACACAGC 24203	ACC T AA	C
		GC GT TG TTCACAAG TGG		
		CG CA AC AAGTGTTT ACC		
		A_ C G_ A		
GAM2283	KIAA1679	3' CAGACCTGTGAATTCAAA 34749	AG_	
		TTTGAATTCACA CTG		
		AAACTTAAGTGT GAC		
		CCA		
GAM2283	PLU-1	3' AGCCTGTAAACGGTGC 42250	GAATTC	A
		GCACCGTTT ACA GCT		
		CGTGGCAAA TGT CGA		
		_ _ _ C		
GAM2283	PLU-1	3' AGCCTGTAAACGGTGC 13401	GAATTC	A
		GCACCGTTT ACA GCT		

		CGTGGCAAA	TGT CGA	
		_____ C		
GAM2284	AGL	5' TCTTCAGACTTGAACAAGA	6307	G CA T
		TC TG CA GTCTGAAGA		
		AG AC GT CAGACTTCT		
		A AA T		
GAM2284	HNRPU	3' TCAGCATTGTGCACGATAA	10836	_ T
		TTATCGTGCACA TG CTGA		
		AATAGCACGTGT AC GACT		
		T _		
GAM2284	HNRPU	3' TCAGCATTGTGCACGATAA	25580	_ T
		TTATCGTGCACA TG CTGA		
		AATAGCACGTGT AC GACT		
		T _		
GAM2284	KIAA1155	3' CTTCTTCAGACACTGAACAT	31195	CA _
		GTG CA TGTCTGAAGAAG		
		TAC GT ACAGACTTCTTC		
		AA C		
GAM2284	LOC148254	3' CTTCTCAGACATCTCCAT	38501	CAC A
		GTG ATGTCTGA GAAG		
		TAC TACAGACT CTTC		
		CTC C		
GAM2285	ADRA2B	3' GCTGCTCCCCGCAATGCTG	6339	A__ TGGA
		CAGTATTGC GAGT GGC		
		GTCGTAACG CTCG TCG		
		CCC _____		
GAM2285	BCL2	3' CCCCCAACTCCCAATACTG	6254	CA A
		CAGTATTG GAGTTGG GG		
		GTCATAAC CTCAACC CC		
		C_ C		
GAM2285	CLOCK	3' TATGCCTTCACTACAACATT	11334	A C AGT
		AGT TTG AG TGGAGGCATA		
		TTA AAC TC ACTTCCGTAT		
		C A _____		
GAM2285	CNTNAP2	3' ATGCCTCCAAACAACACTG	15415	A CAGAG
		CAGT TTG TTGGAGGCAT		
		GTCA AAC AACCTCCGTA		
		C A_____		
GAM2285	HGF	3' ATGTATCCTGCAATACTG	45218	GAGTT G
		CAGTATTGCA GGA GCAT		

		GTCATAACGT	CCT TGTA	
		_____ A		
GAM2285	KCNN2	5' ATGCCTCCGGT	GCAACAGCTG 22242	A_ GAG
		CAGT TTGCA	TTGGAGGCAT	
		GTCG AACGT	GGCCTCCGTA	
		AC	_____	
GAM2285	RNPEPL1	3' ATGCCTCCTGTCTCA	AACTG 20159	A C GTT
		CAGT TTG AGA	GGAGGCAT	
		GTCA AAC TCT	CCTCCGTA	
		C	_____ GT_	
GAM2285	TM7SF3	3' CCTGTAATCCCA	ATACTG 30010	CAGA G
		CAGTATTG	GTTG AGG	
		GTCATAAC	TAAT TCC	
		CC	_____ G	
GAM2285	FLJ10388	3' TGTACCATGCA	ATACT 19844	GAGT AG
		AGTATTGCA	TGG GCA	
		TCATAACGT	ACC TGT	
		_____ A_		
GAM2285	KIAA1879	3' ATGCCTATAGTCCCTG	CAACTC 36409	TA AGTTGG_
	TG	CAG TTGCAG	AGGCAT	
		GTC AACGTC	TCCGTA	
		TC	CCTGATA	
GAM2285	LOC157697	5' TTCCA	ACTCTGTAACACTG 39647	A
		CAGT TTGCAG	AGTTGGAG	
		GTCA AATGTCTCA	ACCTT	
		C		
GAM2285	LOC219894	3' ATGCTGTCTCTGC	AGTACTG 44794	TTGGA
		CAGTATTGCAGAG	GGCAT	
		GTCATGACGTCTC	TCGTA	
		TG	_____	
GAM2286	FLJ14346	3' CAGGAAGTCTGGAGGCTG	AAAC 24620	CG G _
	A	TGT CAGC CTTCA	ACTTCCTG	
		ACA GTCG GAGGT	TGAAGGAC	
		AA	_____ C	
GAM2286	FLJ20366	3' CAGGAAGTCAATCATCTG	TGAC 19418	CGCTTCA
	A	TGTCGCAG	ACTTCCTG	
		ACAGTGTC	TGAAGGAC	
		TACTAAC		
GAM2286	NIR3	3' GCAGGAAGTTGCTTGG	CCCGAC 32928	CA GCTT
	A	TGTCG GC	CAACTTCCTGC	

ACAGC CG GTTGAAGGACG
 C_ GTTC
 GAM2286 LOC92492 5' GCAGGAGGCAAGGGCTGCAACA 34452 C G CAA
 TGT GCAGC CTT CTTCCTGC
 ||| ||||| ||| |||||
 ACA CGTCG GAA GGAGGACG
 A G C__
 GAM2287 FLJ13646 3' CAAACTAGCTAAAGGAAACCAA 23811 GCACG TC A
 TTGG C TTA CTAGTTTG
 |||| | ||| |||||
 AACC G AAT GATCAAAC
 AAA__ GA C
 GAM2287 KIAA1937 3' CAGAGAGTTAAGAGGCGCCCAA 36482 ACG AG
 TTGGGC CTCTTAACT TTTG
 ||||| ||||| |||||
 AACCCG GAGAATTGA AGAC
 CG_ G_
 GAM2287 NGEF 3' CAAACTGGATAAAGGGTGCCCA 34275 G C A
 A TTGGGCAC CT TTA CTAGTTTG
 ||||| || ||| |||||
 AACCCGTG GA AAT GGTCAAAC
 G _ A
 GAM2287 LOC152765 3' GGTTAAGAACATGCCCAG 39318 CGC
 TTGGGCA TCTTAACT
 ||||| |||||
 GACCCGT AGAATTGG
 ACA
 GAM2287 LOC255045 3' CAAACTAGCTAAAGGAAACCAA 46030 GCACG TC A
 TTGG C TTA CTAGTTTG
 |||| | ||| |||||
 AACC G AAT GATCAAAC
 AAA__ GA C
 GAM2288 ATP1A2 3' TCTACCAAAAACAATACTTT 6370 C CAAA
 AAAGTATTGT TTTG TGGA
 ||||| ||||| |||||
 TTTCATAACA AAAC ATCT
 A C__
 GAM2288 HCA4 3' TCCATTTGCAAATACCATACT 38027 T C
 AGTAT GT TTTGCAAATGGA
 ||||| || |||||
 TCATA CA AAACGTTTACCT
 C T
 GAM2288 KIAA0247 3' TCCATTTGCAAACAGATCTT 16379 T GTC
 AAG ATT TTTGCAAATGGA
 ||| ||| |||||
 TTC TAG AAACGTTTACCT
 _ AC_
 GAM2288 KIAA0319 3' CCACCCACAAAGCAGTACT 16760 T CAAA
 AGTATTG CTTTG TGG
 ||||| ||||| |||

		TCATGAC GAAAC ACC		
		_ ACCC		
GAM2288 KIAA0794	3'	TCCATTCAGAAGACAACATTT	39185	A GCA
		AAGT TTGTCTTT AATGGA		
		TTTA AACAGAAG TTACCT		
		C AC_		
GAM2288 LOC153810	3'	CCATTTGCAACAGGAACA	39411	_ _
		TGT CT TTGCAAATGG		
		ACA GG AACGTTTACC		
		A AC		
GAM2288 LOC253272	5'	TCCATTTGCAAAGGTTACTT	45664	TTG
		AAGTA TCTTTGCAAATGGA		
		TTCAT GGAAACGTTTACCT		
		T_		
GAM2288 LOC90643	3'	TCCATTTGCAATGAGAAAC	31855	A G T
		GT TT TC TTGCAAATGGA		
		CA AA AG AACGTTTACCT		
		_ G T		
GAM2288 LOC93206	3'	TCCATCAGAAATAATACTTTA	35518	C CAA
		TAAAGTATTGT TTTG ATGGA		
		ATTCATAATA AGAC TACCT		
		A _		
GAM2289 NORE1	3'	TGTGTGGTACTTAGTCA	25445	T CAA
		TGACT AG TATTACACG		
		ACTGA TC ATGGTGTGT		
		T _		
GAM2289 FLJ13117	3'	GCGGGTGGATCACTAGGTCA	23327	CA A A
		TGACTTAG AT TTAC CGC		
		ACTGGATC TA GGTG GCG		
		AC _ G		
GAM2289 KIAA0212	3'	CGTGTTTTATGTTAAGTCA	16143	A TT
		TGACTTAGCA TA ACACG		
		ACTGAATTGT AT TGTGC		
		_ TT		
GAM2289 KIAA0982	3'	CGTGTGTGTGGCTAAATTA	15248	C A T
		TGA TTAGC ATAT ACACG		
		ATT AATCG TGTG TGTGC		
		A G _		
GAM2289 KIAA1164	3'	TGTAATATTTCCAAGTCA	34442	AGC
		TGACTT AATATTACA		

			ACTGAA TTATAATGT		
			CCT		
GAM2289	MGC13090	3'	GCGCAGTATTTATTGCTAAATT 26428	C	T_ A_
	A		TGA TTAGCAATA TAC CGC		
			ATT AATCGTTAT ATG GCG		
			A TT AC		
GAM2289	OSBPL8	3'	CGTGTAATAAGTTGAGT 21906	AA	
			ACTTAGC TATTACACG		
			TGAGTTG ATAATGTGC		
			A_		
GAM2289	PTK6	3'	GCGTGTGAAATAGTAAGTCA 12601	G A A	
			TGACTTA C AT TTACACGC		
			ACTGAAT G TA AGTGTGCG		
			_ A A		
GAM2289	SB52	3'	GCGTGTAAATAAATAAGTTA 28734	GCAA	
			TGACTTA TATTACACGC		
			ATTGAAT ATAATGTGCG		
			AA_		
GAM2289	SLC5A7	3'	GCATGTAATATTCTGAGCA 22393	A C C	
			TG CTTAG AATATTACA GC		
			AC GAGTC TTATAATGT CG		
			_ _ A		
GAM2290	FLJ13912	3'	CTTTAACCCAAGAACCCA 23030	CAT ATAC	
			TGGGTTCT GGT TAAAG		
			ACCCAAGA CCA ATTTC		
			AC_ _		
GAM2290	JAM1	5'	CCTCTAGCTCCAAGTGAAGACC 29338	_ TATA A	
	CA		TGGGTTCTCA TGG CTA AGG		
			ACCCAAGAGT ACC GAT TCC		
			CA TC_ C		
GAM2290	JAM1	5'	CCTCTAGCTCCAAGTGAAGACC 29349	_ TATA A	
	CA		TGGGTTCTCA TGG CTA AGG		
			ACCCAAGAGT ACC GAT TCC		
			CA TC_ C		
GAM2290	KIAA1958	3'	CCTTTAGTTTGCTAAACACCCA 39829	TCTCA T	
			TGGGT TGGTA ACTAAAGG		
			ACCCA ATCGT TGATTTC		
			CAA_ T		
GAM2290	MAPK8IP3	3'	CCTCTGAGAGACCGGAACC 27219	A ATA AA_	
	CA		TGGGTTCTC TGGT CT AGG		

ACCCAAGGG ACCA GA TCC
 C GA_ GTC
 GAM2290 OR2C3 5' TTCAGATGAGAATCCA 37178 GGTATA A
 TGGGTTCTCAT CT AA
 ||||| ||
 ACCTAAGAGTA GA TT
 _____ C
 GAM2290 PPP1R10 3' CCTTAATGCTTGAGAACCTA 8576 T ACTA
 TGGGTTCTCA GGTAT AAGG
 ||||| |||| ||
 ATCCAAGAGT TCGTA TTCC
 _____ A____
 GAM2291 TRPM8 3' CCAGGCTCCTATTGAAGG 23515 CA _
 CCT TAATAG AGCCTGG
 || |||| |||||
 GGA GTTATC TCGGACC
 A_ C
 GAM2291 PMX2B 5' CCAAGTTTATTATGAGG 10015 G C
 CCTCATAATAGA C TGG
 ||||| ||||
 GGAGTATTATTT G ACC
 _____ A
 GAM2291 LOC130813 3' CCAGGCCTGGTCCATGAGACA 37309 C AA__ A
 TG CTCAT TAG GCCTGG
 || |||| || |||||
 AC GAGTA GTC CGGACC
 A CCTG _
 GAM2291 LOC135818 3' CCAAGTTTTATTGAGGCAT 37092 TA C
 ATGCCTCA ATAGAGC TGG
 ||||| ||||| ||
 TACGGAGT TATTTTG ACC
 _____ A
 GAM2291 LOC196528 3' CCACTGGCTCATTATGAGTCAT 42405 C A _
 ATG CTCATAAT GAGCC TGG
 || ||||| |||| ||
 TAC GAGTATTA CTCGG ACC
 T _ TC
 GAM2292 DKFZP564D0478 3' TGCACCGGGTACACTTAACGTG 25811 _____ G
 TACGTTAA ATT GGTGCA
 ||||| || |||||
 GTGCAATT TGG CCACGT
 CACA G
 GAM2292 DKFZP566G1424 3' TGCACCTATGCAACTTAACGTG 41118 AT____
 TACGTTAA TGGGTGCA
 ||||| |||||
 GTGCAATT ATCCACGT
 CAACGT
 GAM2293 MAP1A 3' GCCCTGCCAGACTACTGCCAGA 8185 CGA ATTAA A
 TTTGGCAG TC CA GGC
 ||||| || ||||

		AGACCGTC AG GT CCG	
		ATC ACC__ C	
GAM2293	VIL2	3' CCTTATTAATGATCAGCT 9410 _ C	
		AGC GATCATTA AAGG	
		TCG CTAGTAATT TTCC	
		A A	
GAM2293	ABCA10	5' CCCTGTTAATGAACAGGACAAA 27825 GCAGCGA A	
		TTTG TCATTAACA GG	
		AAAC AGTAATTGT CC	
		AGGACA_ C	
GAM2293	C11orf23	3' CCTTGTTAACAAGCATCACCAA 20301 CA__ GATCA	
		TTGG GC TTAACAAGG	
		AACC CG AATTGTTCC	
		ACTA AAC__	
GAM2293	KIAA0472	3' CCTGGAAGAGTCCACTGCCAAA 35575 C_ CA AACA	
		TTTGGCAG GAT TT AGG	
		AAACCGTC CTG AA TCC	
		AC AG GG__	
GAM2293	KIAA0847	3' CCTTGTGTTTGCTGCCAAA 38047 TCATTA	
		TTTGGCAGCGA ACAAGG	
		AAACCGTCGTT TGTTCC	
		TG____	
GAM2293	LBP-9	3' CCTTGTTGAACCGCTGCTAAA 15876 ATCA	
		TTTGGCAGCG TTAACAAGG	
		AAATCGTCGC AGTTGTTCC	
		CA__	
GAM2293	LOC143914	5' CCTTGTCAAGACTGTCAAA 37634 CGA A A	
		TTTGGCAG TC TT ACAAGG	
		AAACTGTC AG AA TGTTCC	
		__ _ C	
GAM2294	ADAM19	3' ACCAGTTCCAAAGTCAGTAATT 27093 ACA TCGA	
		AATTAC ACTTTGGG GGT	
		TTAATG TGAAACCT CCA	
		AC_ TGA_	
GAM2294	LOC92228	3' ACCGCAGAGTTGTATAAT 34002 C _	
		ATTA ACAACTTTG GGT	
		TAAT TGTTGAGAC CCA	
		A G	
GAM2295	TAF9	5' AAAATCAGGACTGAAATACATT 9163 ATG_	
		AATGTATTT TCTGATTTT	

			TTACATAAA	GGA	CTAAAA	
			GTCA			
GAM2295	KIAA1866	3'	AGACACAAACACATGGA	30554	A A A	
			TCCA TGT TTT TGTCT			
			AGGT ACA AAA ACAGA			
			_ C C			
GAM2295	LOC200269	3'	AAAATCAGACATTTGAATAT	42757	__	
			GTATTT ATGTCTGATTTT			
			TATAAG TACAGACTAAAA			
			TT			
GAM2295	LOC255461	5'	AAAATCAGGAACTATCATTGGA	46461	T TTATG	
			TCCAATG AT TCTGATTTT			
			AGGTTAC TA GGA	CTAAAA		
			_ TCAA_			
GAM2295	LOC255516	5'	AAAATCAGGAACTATCATTGGA	46467	T TTATG	
			TCCAATG AT TCTGATTTT			
			AGGTTAC TA GGA	CTAAAA		
			_ TCAA_			
GAM2296	CDH11	3'	CACTCATTGTCTTTGAGGAA	27392	G A GT	
			TT CTCAAA ACGATG AGTG			
			AA GAGTTT TGTTAC TCAC			
			G C _			
GAM2296	ENO2	5'	CACTACCACCGTCTGAG	7704	AAA A	
			CTCA ACG TGGTAGTG			
			GAGT TGC ACCATCAC			
			C_ C			
GAM2296	KL	3'	TACACCATTTTGTGAGCAG	11203	AAC A	
			TTGCTCAAA GATGGT GTG			
			GACGAGTTT TTACCA CAT			
			__ _			
GAM2296	CLDN1	3'	ACCGTCTGTGTTTGAGCAA	22079	A _	
			TTGCTCAAA AC GATGGT			
			AACGAGTTT TG CTGCCA			
			G T			
GAM2296	GGA2	3'	CACTACCAGAGTTCTCTAGCAA	28918	CAAA GA	
			TTGCT AAC TGGTAGTG			
			AACGA TTG ACCATCAC			
			TCTC AG			
GAM2296	GGA2	3'	CACTACCAGAGTTCTCTAGCAA	17398	CAAA GA	
			TTGCT AAC TGGTAGTG			

			AACGA TTG ACCATCAC		
			TCTC AG		
GAM2296 KIAA0268	3'	GCCACTGATTTTTGAGGAA	34687	G	_ A
		TT CTCAAAAA CG TGGT			
		AA GAGTTTTT GT ACCG			
		G A C			
GAM2296 KIAA0323	3'	GCTGCATCCCTTTTGAGCAA	31694		AC G
		TTGCTCAAAA GATG TAGT			
		AACGAGTTTT CTAC GTCG			
		CC _			
GAM2296 KIAA1582	5'	CACTACCACGAGCAA	32585		AAAAAC A
		TTGCTC G TGGTAGTG			
		AACGAG C ACCATCAC			

GAM2296 phorbolin-1	5'	ACACCACGCCTTGAGCAA	42797		AAA A A
		TTGCTCAA CG TGGT GT			
		AACGAGTT GC ACCA CA			
		CC_ _ _			
GAM2296 PRRG1	3'	GCCACCACTGTACCTTGAGCAA	6654		AA_ A A
		TTGCTCAA ACG TGGT GT			
		AACGAGTT TGT ACCA CG			
		CCA C C			
GAM2296 TREX1	5'	TCACATTTTCTTCTTGAGCAA	27339		A C TG A
		TTGCTCAA AA GA GT GTGA			
		AACGAGTT TT CT TA CACT			
		C _ TT _			
GAM2296 LOC219653	3'	ATCATTCGTTTGTGAGCAA	43866		_ _
		TTGCTCAA AAACGA TGGT			
		AACGAGTT TTTGCT ACTA			
		G T			
GAM2296 LOC51285	3'	CACTGCCATCTGAACAA	18635	C	AAAAC
		TTG TCA GATGGTAGTG			
		AAC AGT CTACCGTCAC			
		A _____			
GAM2297 MAPK14	3'	TCCCAATAACTAATGCTA	7005		CATAAAC
		TAGCATTAGT TTGGGA			
		ATCGTAATCA AACCCT			
		AT_____			
GAM2297 MAPK14	3'	TCCCAATAACTAATGCTA	29109		CATAAAC
		TAGCATTAGT TTGGGA			

		ATCGTAATCA	AACCCT	
		AT_____		
GAM2297	MAPK14	3' TCCCAATAACTAATGCTA	29116	CATAAAC
		TAGCATTAGT	TTGGGA	
		ATCGTAATCA	AACCCT	
		AT_____		
GAM2297	ATP10B	3' TCCCCTATAACATAATGCTA	31736	_ C AACTT
		TAGCATTAGT	GT ATA GGGA	
		ATCGTAAT	CA TAT CCCT	
		A A C_____		
GAM2297	FLJ25415	5' ATCCCAAGCCTGATAAATCTA	29532	C A TAAA
		TAG ATT GTCA	CTTGGGAT	
		ATC TAA TAGT	GAACCCTA	
		_ A CC_____		
GAM2297	PRO2032	3' TTCTTTTTTAATACTAATGCTA	20686	CA CTT
		TAGCATTAGT	TAAA GGGA	
		ATCGTAATCA	ATTT TCTT	
		_____ TT_____		
GAM2297	PRO2730	5' CCCAAGTTCATGACTTTTGC	24899	TT A
		GCA AGTCAT	AACTTGGG	
		CGT TCAGTA	TTGAACCC	
		TT	C	
GAM2297	LOC149830	3' ATCCCAAGTGGGCCCAAAGCTA	41094	A A_ ATAA
		TAGC TT GTC	ACTTGGGAT	
		ATCG AA CGG	TGAACCCTA	
		A CC G_____		
GAM2298	FKBP14	3' CTACAATAACATTGTATCA	19643	TTT CC
		TGATATAA	TGT ATTGTAG	
		ACTATGTT	ACA TAACATC	
		_____ A_____		
GAM2298	MDS028	3' ACCACAATCAGAATTATATC	20533	TCC A
		GATATAATTTTG	ATTGT GT	
		CTATATTAAGAC	TAACA CA	
		_____ C		
GAM2298	LOC203429	3' ACTACATGATGACAGAATTATA	43047	CAT_
		TCA	TGATATAATTTTGTG	
		ACTATATTAAGACAG	ACATCA	
		TAGT		
GAM2299	TYRO3	5' AAAATCAGTTAACTATACTCC	12983	CCT _
		GGAGTATAG	ATT ATTTT	

				CCTCATATC TGA TAAAA		
				AAT C		
GAM2300	RAD17	5'	ATATAGAGGAAAGGGGC	8783	AG	A
			GCT CCTT TCCTCTATAT			
			CGG GGAA AGGAGATATA			
GAM2300	RAD17	5'	ATATAGAGGAAAGGGGC	28480	AG	A
			GCT CCTT TCCTCTATAT			
			CGG GGAA AGGAGATATA			
GAM2300	RAD17	5'	ATATAGAGGAAAGGGGC	28484	AG	A
			GCT CCTT TCCTCTATAT			
			CGG GGAA AGGAGATATA			
GAM2300	RAD17	5'	ATATAGAGGAAAGGGGC	28486	AG	A
			GCT CCTT TCCTCTATAT			
			CGG GGAA AGGAGATATA			
GAM2300	RAD17	5'	ATATAGAGGAAAGGGGC	28488	AG	A
			GCT CCTT TCCTCTATAT			
			CGG GGAA AGGAGATATA			
GAM2300	RAD17	5'	ATATAGAGGAAAGGGGC	28490	AG	A
			GCT CCTT TCCTCTATAT			
			CGG GGAA AGGAGATATA			
GAM2300	KIAA0416	3'	ATAGCCAAGGCTAGCGA	17831		ATCCT
			TCGCTAGCCTT CTAT			
			AGCGATCGGAA GATA			
			CC__			
GAM2300	TTY2	5'	GGACACAGAGTTTGAGCAGC	42071	A C TC	ATA
			GCT GC TTA CTCT TCC			
			CGA CG AGT GAGA AGG			
			_ _ TT CAC			
GAM2300	LOC149606	3'	GGACATAGAAAAAGAGGCTGGC	38783	ATCC	A
			GCTAGCCTT TCTAT TCC			
			CGGTCTGGAG AGATA AGG			
			AAAA C			
GAM2300	LOC159148	5'	GGACACAGAGTTTGAGCAGC	42078	A C TC	ATA
			GCT GC TTA CTCT TCC			

CGA CG AGT GAGA AGG
 _ _ TT CAC

GAM2301 ANKRD6 3' TCACATGAAAAGTTATCAGAT 17252 C ____
 ATC GATAACTTTTT TGA
 ||| ||||| |||
 TAG CTATTGAAAAG ACT
 A TAC

GAM2301 DKFZP564O1863 3' TTCAAAAAAAAGTTCCGGAT 34044 AT GAC
 ATCCG AACTTTTTT GAA
 |||| ||||| |||
 TAGGC TTGAAAAAA CTT
 C_ AAA

GAM2302 CA12 3' GATGTCAAATCGTGGTTTA 6881 A _
 TAAACCAC ATTTG CGTC
 ||||| |||| |||
 ATTTGGTG TAAAC GTAG
 C T

GAM2302 CLASP2 3' TGGAAAAATTGTGTTTACA 32270 C GCG
 TGTAAC ACAATTT TCCG
 ||||| ||||| |||
 ACATTTG TGTTAAA AGGT
 _ A_

GAM2302 CYP24 3' GACTTAAAAATTGTGTTTACA 6427 C GC_
 TGTAAC ACAATTT GTC
 ||||| ||||| |||
 ACATTTG TGTTAAA CAG
 _ AATT

GAM2302 GPR48 3' GCAGACTGTAAATTGTGGTTT 20549 _ _ C
 ATA TGTAACCACAATTTG C GTC GC
 ||||| ||||| ||| ||
 ATATTGGTGTAAAT G CAG CG
 T T A

GAM2302 PIGA 3' GCAGCCAGTTGTGGTTTACA 21710 T _
 TGTAACCACAATT GC GT
 ||||| ||||| || ||
 ACATTTGGTGTGTA CG CG
 C A

GAM2302 PIGA 3' GCAGCCAGTTGTGGTTTACA 21717 T _
 TGTAACCACAATT GC GT
 ||||| ||||| || ||
 ACATTTGGTGTGTA CG CG
 C A

GAM2302 RBAK 3' GATTCAAATTGTATTTACA 22142 CC C
 TGTAAC ACAATTTG GTC
 ||||| ||||| |||
 ACATTT TGTTAAAC TAG
 A_ T

GAM2302 TOMM70A 3' ACGAATTATAATTATGGTTTAC 16787 C TG____
 A TGTAACCA AATT CGT
 ||||| |||| |||

			ACATTTGGT TTAA	GCA		
			A TATTAA			
GAM2302	LOC145815	5'	GACGAAGATCTGGTTTACA	40606	CA	G
			TGTAAACCA ATTT CGTC			
			ACATTTGGT TAGA GCAG			
			C_ A			
GAM2303	ACTN2	3'	GAAGTTTTTACAGTATATGACA	6757	A	TGA
	TA		TATGTCATA ACTGTAAA	TTC		
			ATACAGTAT TGACATTT	AAG		
			A TTG			
GAM2303	CENTD1	3'	CAGGACAGTTTATGAAATA	17561	G	AAA
			TAT TCATAAACTGT	TG		
			ATA AGTATTTGACA	AC		
			A GG_			
GAM2303	CENTD1	3'	CAGGACAGTTTATGAAATA	29199	G	AAA
			TAT TCATAAACTGT	TG		
			ATA AGTATTTGACA	AC		
			A GG_			
GAM2303	SYN3	3'	GAATCAACAGATCAATGACATA	28592	AAA_	AAA
			TATGTCAT CTGT TGATTC			
			ATACAGTA GACA ACTAAG			
			ACTA _			
GAM2303	SYN3	3'	GAATCAACAGATCAATGACATA	28594	AAA_	AAA
			TATGTCAT CTGT TGATTC			
			ATACAGTA GACA ACTAAG			
			ACTA _			
GAM2303	SYN3	3'	GAATCAACAGATCAATGACATA	9583	AAA_	AAA
			TATGTCAT CTGT TGATTC			
			ATACAGTA GACA ACTAAG			
			ACTA _			
GAM2303	FLJ20546	3'	GAATCATTTTTAGATTGTGACA	19543	A	T
	TA		TATGTCATAA CTG AAATGATTC			
			ATACAGTGTT GAT TTTACTAAG			
			A T			
GAM2303	LOC145790	3'	GAATATAAACAGTTTATGA	37979	AAATG	
			TCATAAACTGT	ATTC		
			AGTATTTGACA	TAAG		
			AAATA			
GAM2303	LOC219688	5'	ATCCTGTGCAGTTTACAACA	44697	CA	AAT
			TGT TAACTGTA	GAT		

ACA ATTTGACGT CTA
 AC GTC
 GAM2303 LOC255533 5' GAATCACACTATAGTTTAATGA 46331 _ AA_
 CATA TATGTCAT AAAGTGTG TGATTC
 ||||| ||||| |||||
 ATACAGTA TTTGATAT ACTAAG
 A CAC
 GAM2304 CSMD1 3' CTATGAATTACAGAACTGTCC 36188 T A GTA
 GGAC AGT TC TAATTCATAG
 ||| ||| || |||||
 CCTG TCA AG ATTAAGTATC
 _ _ AC_
 GAM2304 DRIL2 3' ATGAACCCAGGCCACTAGTCT 13182 ATC ATAA_
 GGAAGT GT TTCAT
 ||||| || |||||
 TCTGATCA CG AAGTA
 C_ GACCC
 GAM2304 LOC158187 3' AATTATACAATACTTGTCC 41919 T C
 GGAC AGTAT GTATAATT
 ||| |||| |||||
 CCTG TCATA CATATTAA
 T A
 GAM2305 GA 5' TGTCTCGCTCGCTCCGCCC 14936 _ _
 GGGCGGAGC CGA ACA
 ||||| ||| |||
 CCCGCCTCG GCT TGT
 CTC C
 GAM2305 KIAA0753 3' TGGAGAAGGGATGGCACCACCC 16737 C A AACA
 GGG GG GCCG TTCTCCA
 ||| ||| |||||
 CCC CC CGGT AAGAGGT
 A A AGGG
 GAM2305 KIAA1130 3' TGGGAGCCCAGGCTCCGCCC 31289 GAACA T
 GGGCGGAGCC TTC CCA
 ||||| ||| |||
 CCCGCCTCGG GAG GGT
 ACCC_ _
 GAM2305 RPL36 5' GAGCCGGTACTCACCTCCGCCC 17715 CC _ ATT
 GGGCGGAG GA AC CTC
 ||||| || |||
 CCCGCCTC CT TG GAG
 CA CA GCC
 GAM2305 LOC56920 3' AGAGCTGCAGCCAGCTCTGCCC 21381 CGAA_ _
 GGGCGGAGC CA TTCT
 ||||| || |||
 CCCGTCTCG GT GAGA
 ACCGAC C
 GAM2306 BUB3 3' CTAATATCATTTTGTGACTG 11094 AGTC
 CAGTCA AATGATATTAG
 ||||| |||||

			GTCAGT TTACTATAATC		
			GTT_		
GAM2306 MME	3'	TAATATCATTCACTAGCT	14159	CA C	
		AGT AGT AATGATATTA			
		TCG TCA TTACTATAAT			
		A_ C			
GAM2306 MME	3'	TAATATCATTCACTAGCT	6602	CA C	
		AGT AGT AATGATATTA			
		TCG TCA TTACTATAAT			
		A_ C			
GAM2306 MME	3'	TAATATCATTCACTAGCT	14150	CA C	
		AGT AGT AATGATATTA			
		TCG TCA TTACTATAAT			
		A_ C			
GAM2306 MME	3'	TAATATCATTCACTAGCT	14154	CA C	
		AGT AGT AATGATATTA			
		TCG TCA TTACTATAAT			
		A_ C			
GAM2306 SHOC2	5'	CTAATGAATCATTGATTGAC	14304	G	—
		GTCAA TCAATGAT ATTAG			
		CAGTT AGTTACTA TAATC			
		— AG			
GAM2306 LOC126669	3'	AATATCATTAGGCATTGGC	37154	—	—
		GTCAA GTC AATGATATT			
		CGGTT CGG TTACTATAA			
		A A			
GAM2306 LOC154789	5'	AATACGTGGGCTTGACT	39485	A A	
		AGTCAAGTC ATG TATT			
		TCAGTTCGG TGC ATAA			
		G —			
GAM2306 LOC220963	3'	TATGTTTGACTTGCTAGTA	43958	C T	TG
		TAC AG CAAGTCAA ATA			
		ATG TC GTTCAGTT TAT			
		A _ TG			
GAM2307 CDH6	3'	TAGTTATTATCCAGAGGA	11375	A A	
		TC TCTG ATAATAACTA			
		AG AGAC TATTATTGAT			
		G C			
GAM2307 CPD	3'	ACACATGGTTTTCAGATGA	6981	TAAT	A
		TCATCTGAA AACTAT TGT			

		AGTAGACTT TTGGTA ACA	
		_____ C	
GAM2307	NDP	3' GCTATAATTATTATTCAGA 5808	C T
		TCTGAATAATAA TATA GT	
		AGACTTATTATT ATAT CG	
		A _	
GAM2307	SOCS5	3' TACCTGCTGTTACTTATTCAGA 15230	_ TA T
	T	ATCTGAATAA TAAC TA GTA	
		TAGACTTATT ATTG GT CAT	
		C TC C	
GAM2307	HSA250839	3' ACACAGGTGTCCATTCAGATGA 20436	AATA ATA
		TCATCTGAAT ACT TGT	
		AGTAGACTTA TGG ACA	
		CCTG AC_	
GAM2307	LOC149372	5' TACATATAAATGATATCAAGAT 38732	GA A AC
	GA	TCATCT ATA TA TATATGTA	
		AGTAGA TAT GT ATATACAT	
		AC A AA	
GAM2307	LOC149844	5' CACATAGTCATTTAGATGA 38820	AATA A
		TCATCTGAAT ACTAT TG	
		AGTAGATTTA TGATA AC	
		C___ C	
GAM2307	LOC51133	5' TACATATAGTTACTGTGACA 18205	A_ A
		TG ATA TAACTATATGTA	
		AC TGT ATTGATATACAT	
		AG C	
GAM2307	LOC89135	5' CACATAGTCATTTAGATGA 30249	AATA A
		TCATCTGAAT ACTAT TG	
		AGTAGATTTA TGATA AC	
		C___ C	
GAM2308	GAN	3' CATATGAAAAACATCACTTA 22561	T TA
		TAAGTGAT GTTTTTT ATG	
		ATTCACTA CAAAAAG TAC	
		_ TA	
GAM2308	DKFZP434F0318	3' CCATTAAAAAATAATCCTTA 25139	T
		TAAG GATTGTTTTTTTAATGG	
		ATTC CTAATAAAAAAATTACC	
		_	
GAM2308	DKFZP761E2110	3' CATTAACAAAACAATCACT 25223	T
		AGTGATTGTTTT TTAATG	

		TCACTAACAAAA AATTAC	
		C	
GAM2308 KIAA1393	3'	CCATTAATAGGCAATCATTTA 35686	TT
		TAAGTGATTGTTT TTAATGG	
		ATTTACTAACGGA AATTACC	
		T_	
GAM2308 KIAA1495	3'	CCATTAAAAACACAGCAATCAT 36224	—
	T	AGTGATTGTT TTTTAAATGG	
		TTACTAACGA AAAAATTACC	
		CAC	
GAM2308 KIAA1954	3'	CCATTAAAAAATTAAC TTG 38096	GATT
		TAAGT GTTTTTTAAATGG	
		GTTCA TAAAAAATTACC	
		AT_	
GAM2308 KPNA6	3'	CCATTAAAAACCATTCTCTTA 14686	T T T
		TAAG GA TG TTTTTTAAATGG	
		ATTC CT AC AAAAATTACC	
		T T C	
GAM2308 RAP140	5'	CCATTAAAAATTGCACTTA 17555	ATTGTT
		TAAGTG TTTTAAATGG	
		ATTCAC AAAAATTACC	
		GTT_	
GAM2308 SPTLC2	3'	CCATTAAAAAACATTTTATTT 11275	T_
		AAGTGA TGTTTTTTAAATGG	
		TTTATT AAAAAAAATTACC	
		TT	
GAM2308 LOC115219	3'	CATTTAAAAACAATTACT 36277	TT
		AGTGATTGTTTTT AATG	
		TCATTAACAAAA TTAC	
		T_	
GAM2308 LOC202451	5'	GAAAAACAAGTCACTTA 43438	—
		TAAGTGATT GTTTTTT	
		ATTCAGTGA CAAAAAG	
		A	
GAM2308 LOC51185	3'	CCAAAAAAGACATGTCAC 18423	— AA
		GTGAT TGTTTTTTT TGG	
		CACTG ACAGAAAAA ACC	
		T _	
GAM2309 FLJ23189	3'	ATTTACGTGGACAAC TTTCATA 24656	TAAT A_ G
		TATGA GT TC ACGTAAAT	

		ATACT CA AG TGCATTTA	
		TT__ AC G	
GAM2310 CALD1	3'	ATCAATATGTTTTCAATGCCTG 26991	CAT _
AT		ATCA CATT AAAACATATTGAT	
		TAGT GTAA TTTTGTATAACTA	
		CC_ C	
GAM2310 CALD1	3'	ATCAATATGTTTTCAATGCCTG 27009	CAT _
AT		ATCA CATT AAAACATATTGAT	
		TAGT GTAA TTTTGTATAACTA	
		CC_ C	
GAM2310 NBEA	3'	ATCATTATTTATTGATGTGAT 45491	T AAC T
		ATCACATCA TAA ATA TGAT	
		TAGTGTAGT ATT TAT ACTA	
		T _ _ T	
GAM2310 SFRP4	3'	ATGTTTTAAAATGTGAT 8937	CA
		ATCACAT TTAAAACAT	
		TAGTGTA AATTTTGTA	
		A_	
GAM2310 CG018	3'	TCTTTATTTTAAATGATGT 27404	AC TT
		ACATCATTA AAA ATA GA	
		TGTAGTAATTT TAT CT	
		_ TT	
GAM2310 HIC2	3'	ATCAATATGTTTGTGCAGTGAT 32524	AT TA
		ATCAC CAT AAACATATTGAT	
		TAGTG GTG TTTGTATAACTA	
		AC _	
GAM2310 HTGN29	3'	ATCAATATGTAAATATGTGAT 21431	C AAA
		ATCACAT ATT ACATATTGAT	
		TAGTGTA TAA TGTATAACTA	
		_ A_	
GAM2310 KIAA1257	3'	TCAATATGTTTTGATGAT 31438	
		ATCATTA AAAACATATTGA	
		TAGTAGTTTTGTATAACT	
GAM2310 LOC201725	3'	ATCAAATTTAAATGATGTGAT 42904	A CATA
		ATCACATCATT AAA TTGAT	
		TAGTGTAGTAA TTT AACTA	
		A A_	
GAM2310 LOC221810	3'	ATCATTTGTTAATGATGT 45082	AA TAT
		ACATCATTA ACA TGAT	

			TGTAGTAAT TGT ACTA		
			__ TT_		
GAM2310	LOC256073	3'	ATCAATGTGATTCATTGATGT 46228	TTAAAA	
			ACATCA CATATTGAT		
			TGTAGT GTGTAAC TA		
			TACTTA		
GAM2311	MTMR8	3'	GGATAGTTTATGAGTAATCTTT 17746	TAA__	
			AAAGATTACTC TATCC		
			TTTCTAATGAG ATAGG		
			TATTTG		
GAM2311	PRDM4	3'	GGAAGGGAATAATCTTTTA 14786	C AATA	
			TGAAAGATTA TCT TCC		
			ATTTTCTAAT AGG AGG		
			A GA__		
GAM2311	SLC35A3	3'	AGGAATATTAGAGGAACTT 14548	ATTA C	
			AAG CTCTAATAT CCT		
			TTC GAGATTATA GGA		
			AAAG A		
GAM2311	SON	3'	AGGCATCAGAGTAATCTTCA 27744	A A ATC	
			TGAA GATTACTCT AT CCT		
			ACTT CTAATGAGA TA GGA		
			_ C C__		
GAM2311	SON	3'	AGGCATCAGAGTAATCTTCA 29040	A A ATC	
			TGAA GATTACTCT AT CCT		
			ACTT CTAATGAGA TA GGA		
			_ C C__		
GAM2311	SON	3'	AGGCATCAGAGTAATCTTCA 29045	A A ATC	
			TGAA GATTACTCT AT CCT		
			ACTT CTAATGAGA TA GGA		
			_ C C__		
GAM2311	COP9	3'	GAGAAATACTGAGCAAGTCTTT 13534	A_ TAA CC	
	CA		TGAAAGATT CTC TAT CTC		
			ACTTTCTGA GAG ATA GAG		
			AC TC_ AA		
GAM2311	KIAA1600	3'	AGAGATATTAGATATTTCTT 35390	TTAC C	
			AAGA TCTAATATC CT		
			TTCT AGATTATAG GA		
			TTAT A		
GAM2311	MGC4737	5'	GAAGGATATTACAGGAATCTCT 25507	A A C C	
	C		GA AGATT CT TAATATCC TC		

		CT TCTAA GA ATTATAGG AG	
		C G C A	
GAM2311	LOC126964 3'	GAGGGATGATATCATCTCTCA 36884	A TACTC A
		TGA AGAT TA TATCCCTC	
		ACT TCTA AT GTAGGGAG	
		C CT__ A	
GAM2311	LOC128344 3'	GGGGATAGAACATCTTTCA 36923	TAC ATA
		TGAAAGAT TCTA TCCCT	
		ACTTTCTA AGAT AGGGG	
		CA_ _	
GAM2311	LOC152245 3'	GATATTCGGTAATCTTTTA 41451	CT
		TGAAAGATTACT AATATC	
		ATTTTCTAATGG TTATAG	
		CC	
GAM2312	HNRPD L 3'	TCATCTTCTCCCTGTAAGT 11956	AAA A
		TAGTTGCA AGAA ATGA	
		GTCAATGT TCTT TACT	
		CCC C	
GAM2312	HTR4 3'	TCATTTTCCCCTGCAGCT 6544	AAAA
		AGTTGCA GAAAATGA	
		TCGACGT CTTTACT	
		CCC_	
GAM2312	SRC 3'	CATGGCCTCTGCAACTGCTCA 11887	A AAA AAA
		TGA TAGTTGCA AG ATG	
		ACT GTCAACGT TC TAC	
		C C_ CGG	
GAM2312	SULT1C1 3'	CATTTTCCCAACTATTC 6720	CAAAAA
		GAATAGTTG GAAAATG	
		CTTATCAAC CTTTAC	
		C_	
GAM2312	TCF2 3'	TCATTTTCTTTTGATCT 13202	TTG
		AG CAAAAAGAAAATGA	
		TC GTTTTCTTTTACT	
		TA_	
GAM2312	TEGT 3'	TCATTTCTTTTGCACAC 32274	_ A
		GT TGCAAAAAG AAATGA	
		CA ACGTTTTTC TTTACT	
		C C	
GAM2312	VSNL1 3'	TTCAGTCTGCAGCTATTCA 9418	AAAA
		TGAATAGTTGCA GAA	

ACTTATCGACGT CTT
 CTGA
 GAM2312 DCOHM 3' CATTTTCTCTTGGGGTATTCA 25844 G G AA
 TGAATA TT CAA AGAAAATG
 ||||| || ||| |||||
 ACTTAT GG GTT TCTTTTAC
 _ G C_
 GAM2312 EFS2 3' TTTCTTCAACAACTATTCA 12480 CAAA
 TGAATAGTTG AAGAAA
 ||||| |||||
 ACTTATCAAC TTCTTT
 AAC_
 GAM2312 FLJ10511 3' TCATTTTCTTTTCAAGCCTCA 19901 ATA GCA
 TGA GTT AAAAGAAAATGA
 ||| ||| |||||
 ACT CGA TTTTCTTTTACT
 C__ AC_
 GAM2312 FLJ20040 3' TCATTTTCTTTGTATAACTATG 21067 A CAA
 CA TG ATAGTTG AAAGAAAATGA
 || ||||| |||||
 AC TATCAAT TTTCTTTTACT
 G ATG
 GAM2312 FLJ22569 5' TCATCCTGATGGAACCTATTCA 23401 G AAA AAA
 TGAATAGTT CA AG ATGA
 ||||| || || |||||
 ACTTATCAA GT TC TACT
 G AG_ C__
 GAM2312 FLJ23053 3' TCATTTTCTTTTATAC 23208 TGC
 GT AAAAAGAAAATGA
 || |||||
 CA TTTTCTTTTACT
 TA_
 GAM2312 GRID1 3' CATTTTCTTTTCAAAATTA 33978 GCA
 TAGTT AAAAGAAAATG
 |||| |||||
 ATTAA TTTTCTTTTAC
 AAC
 GAM2312 KIAA0268 3' CATTTTCTCGTTATATTCA 34684 GTT AAAA
 TGAATA GC AGAAAATG
 |||| || |||||
 ACTTAT TG TCTTTTAC
 AT_ C__
 GAM2312 MGC12466 3' TCATTTTCTTTCTTTTATTC 38610 TTGCAA
 GAATAG AAAGAAAATGA
 |||| |||||
 CTTATT TTTCTTTTACT
 TCC__
 GAM2312 LOC145135 5' TCACCTTCTTTTGTCTTTCTA 40498 TT_ AA
 TAG GCAAAAAGAA TGA
 || ||||| |||

		ATC CGTTTTTCTT ACT	
		TTT CC	
GAM2312	LOC196528 3'	TCATTTTCCTTTAGCTTCTGCT 42407	A TT A A
	CA	TGA TAG GC AAA GAAAATGA	
		ACT GTC CG TTT CTTTACT	
		C TT A C	
GAM2312	LOC92303 3'	CATTCCCCTTTGCAGCTAT 34135	AAGAA
		ATAGTTGCAAA AATG	
		TATCGACGTTT TTAC	
		CCCC_	
GAM2312	LOC93587 3'	TCATTTTCTTTTCATTTTATATT 35964	GTTGCAA
	C	GAATA AAAGAAAATGA	
		CTTAT TTTCTTTTACT	
		ATTTTAC	
GAM2313	GCNT1 3'	AAAATGAGAAGATGTGACCT 7236	GGA C
		AGGT GCATCTTC CATTTT	
		TCCA TGTAAG GTAAAA	
		G_ A	
GAM2313	STK6 3'	AAAATAGGAACACGTGCTCTAC 9653	C_ C
	CTC	GAGGTGGAGCAT TTCC ATTTT	
		CTCCATCTCGTG AAGG TAAAA	
		CAC A	
GAM2313	FLJ12595 5'	AAAATGGGAAGAAAGCAACCTC 24555	GGA A_
		GAGGT GC TCTTCCCATTTT	
		CTCCA CG AGAAGGGTAAAA	
		A_ AA	
GAM2313	HSPC031 3'	AAAACGGGTTCAAACCCCACTT 18183	AGCATCTT A
	CT	AGAGGTGG CCC TTTT	
		TCTTCACC GGG AAAA	
		CCAAACTT C	
GAM2313	KIAA1719 3'	AAAACGGGGCACCCACTCCCAC 33815	_ CATCT_ A
	CTC	GAGGTGG AG TCCC TTTT	
		CTCCACC TC GGGG AAAA	
		C ACCCAC C	
GAM2313	pcnp 3'	AAAATAAGAAGATGCACTTTCT 21624	T A CC
		AGG GG GCATCTTC ATTTT	
		TCT TC CGTAGAAG TAAAA	
		T A AA	
GAM2313	PTPRU 3'	AAAATGGGGCAGGCCACACC 12253	GA ATCT
		GGTG GC TCCCATTTT	

		CCAC CG GGGGTAAAA	
		AC GAC_	
GAM2313	PTPRU	3' AAAATGGGGCAGGCCACACC 28403	GA ATCT
		GGTG GC TCCCATTTT	
		CCAC CG GGGGTAAAA	
		AC GAC_	
GAM2313	PTPRU	3' AAAATGGGGCAGGCCACACC 28398	GA ATCT
		GGTG GC TCCCATTTT	
		CCAC CG GGGGTAAAA	
		AC GAC_	
GAM2313	TPD52	3' AAAATGAAAATATCTTCACCTC 11528	C C CC
	T	AGAGGTGGAG AT TT CATTTT	
		TCTCCACTTC TA AA GTAAAA	
		_ T AA	
GAM2313	LOC202108	5' AAATGGGAAAATGGCTTT 42964	_ C
		GGAGC AT TTCCCATT	
		TTTCG TA AAGGGTAAA	
		G A	
GAM2314	ATP2A2	3' AGGCCTCCAGTTCATT 7399	G AAAAA
		AAATGAAC GGA GTCT	
		TTTACTTG CCT CGGA	
		A C____	
GAM2314	CRTAP	3' AAGAGACTTCCTCTTGCGTTC 13059	____ AAA
		GAACG GGA AAGTCTCTT	
		CTTGC TCT TTCAGAGAA	
		GGT CC_	
GAM2314	CSNK2A1	3' GGTCTTTTCCCTGTTCAT 7622	AA T
		ATGAACGGG AAAAG CT	
		TACTTGTC TTTTC GG	
		C_ T	
GAM2314	HPCAL1	3' GGCTGCCCCCCCCGTTTCATT 7929	AAAAA
		AAATGAACGGG AGTC	
		TTTACTTGCCC TCGG	
		CCCCG	
GAM2314	HPCAL1	3' GGCTGCCCCCCCCGTTTCATT 28636	AAAAA
		AAATGAACGGG AGTC	
		TTTACTTGCCC TCGG	
		CCCCG	
GAM2314	NPEPPS	3' GGCTTCTCCCGTTTCATT 13000	_ AAA
		AAATGAAC GGGA AAGTC	

		TTTACTTG CCCT TTCGG		
		G C__		
GAM2314	SIM1	5' AAGAACATATTTTCCGTTCA 11507	AAA	C
		TGAACGGGAAA GT TCTT		
		ACTTGCCTTTT CA AGAA		
		ATA _		
GAM2314	SLC22A12	3' AAGAGACTTCTTCTGTTC 29401	AAA	
		GAACGGGA AAGTCTCTT		
		CTTGTCTT TTCAGAGAA		
		C__		
GAM2314	TGFA	3' AAGAGACGGACTCCTGTTCA 9229	AAAAA	
		TGAACGGGA GTCTCTT		
		ACTTGCCT CAGAGAA		
		CAGG_		
GAM2314	UBE2B	3' AAGAGACTTTGTCATTATTT 9344	CG	AAA_
		GAA GG AAAGTCTCTT		
		TTT TC TTTCAGAGAA		
		AT ACTG		
GAM2314	FLJ10468	3' AGAGACTTCTCCCTTCA 19872	C	AA
		TGAA GGGAA AAGTCTCT		
		ACTT CCCTT TTCAGAGA		
		_ C_		
GAM2314	FLJ14146	3' AAGAGACTTCTTTTGT 24028	AAA	
		ACGGGA AAGTCTCTT		
		TGTTTT TTCAGAGAA		
		C__		
GAM2314	FLJ20651	3' AAGAGACTTTCTCTTTCAT 19573	C	AAA
		ATGAA GGGAA AGTCTCTT		
		TACTT CTCTT TCAGAGAA		
		T _		
GAM2314	FLJ21162	5' AAGAGACTTTTCCCCTGTTT 24305	AA	
		GAACGGG AAAAGTCTCTT		
		TTTGTCC TTTTCAGAGAA		
		CC		
GAM2314	KIAA0164	3' ACCTTTTCCCCCCCATT 16402	AAC	A
		AAATG GGGAAAAA GT		
		TTTAC CCCTTTT CA		
		CCC C		
GAM2314	KIAA0356	3' AAGGTGGGTTTTTCCCATTTCAT 32889	C	AG _
		ATGAA GGGAAAAA TC TCTT		

			TACTT CCCTTTTT GG GGAA		
			A G_ T		
GAM2314	KIAA0514	3'	AAGAGACTTTCTTCTGTGTCA	16199	_ AA
			TGA ACGGGA AAAGTCTCTT		
			ACT TGTCTT TTTCAGAGAA		
			G C_		
GAM2314	KIAA1610	3'	GCTTCTTCCAGTTCATTT	33341	G AA
			AAATGAAC GGAA AAGT		
			TTTACTTG CCTT TTCG		
			A C_		
GAM2314	KIAA1954	3'	AAGAGGAGAATTTTCCCGTTAA	38090	G AAG_
		TTT	AAAT AACGGGAAAA TCTCTT		
			TTTA TTGCCCTTTT GGAGAA		
			A AAGA		
GAM2314	PEX12	5'	GGTCTTTTTTTCCAGTTCATT	5832	_ _T
		T	AAATGAAC GGGAAAAAA G CT		
			TTTACTTG CCCTTTTTT C GG		
			A TT		
GAM2314	RAP2B	3'	AAGAACTTTTTTTCCTTC	45858	C C
			GAA GGGAAAAAAGT TCTT		
			CTT CCTTTTTTCA AGAA		
			_ A		
GAM2314	LOC151877	3'	ATTTTTTCCCCATTCAT	41392	C_
			ATGAA GGGAAAAAAGT		
			TACTT CCCTTTTTTTA		
			AC		
GAM2314	LOC168489	5'	AAGAGACTTTCTGCTTTCA	40249	CG AAA
			TGAA GG AAAGTCTCTT		
			ACTT TC TTTCAGAGAA		
			_ GTC		
GAM2314	LOC197319	3'	AAGTTTAGTTTTTCCCATTCG	42474	C AGTCT
			TGAA GGGAAAAA CTT		
			GCTT CCCTTTTT GAA		
			A GATT		
GAM2314	LOC221773	3'	AAGAGACTCTCCTGCCTCA	43758	A_ AAAA
			TGA CGGGA AGTCTCTT		
			ACT GTCCT TCAGAGAA		
			CC C__		
GAM2314	LOC90591	3'	AGGCCTCTCTCCCGTTCATTT	31757	AAAAA_
			AAATGAACGGG GTCT		

		TTTACTTGCCC CGGA	
		CTCTCTC	
GAM2315 TRPM8	3'	TAAATATCTATTTATTATTA 23518	C
		TAATAGTA ATAGATATTTA	
		ATTATTAT TATCTATAAAT	
		T	
GAM2315 UGDH	3'	AAATATCTATCTGCTATTA 9386	C
		TAATAGTA ATAGATATTT	
		ATTATCGT TATCTATAAA	
		C	
GAM2315 FLJ23259	3'	GTATCATTACTATTACTA 24063	C A
		TAGTAATAGTA AT GATAT	
		ATCATTATCAT TA CTATG	
		— —	
GAM2316 B4GALT1	3'	TGCCAGACCTCGGGGAGGATA 7248	TTT _ CGA
		TATCCTCT CC AGGTC CA	
		ATAGGAGG GG TCCAG GT	
		___ C ACC	
GAM2316 DMD	5'	TGTCAGACAGAAAAAAGAGG 10200	CCAG C
		CCTCTTTT GTC GACA	
		GGAGAAAA CAG CTGT	
		AAGA A	
GAM2316 DMD	5'	TGTCAGACAGAAAAAAGAGG 10227	CCAG C
		CCTCTTTT GTC GACA	
		GGAGAAAA CAG CTGT	
		AAGA A	
GAM2316 DMD	5'	TGTCAGACAGAAAAAAGAGG 10239	CCAG C
		CCTCTTTT GTC GACA	
		GGAGAAAA CAG CTGT	
		AAGA A	
GAM2316 FGFR2	3'	TCAGATCCTTTGAAAAGAG 23238	C_ _ C
		CTCTTTTC AGG TC GA	
		GAGAAAAG TCC AG CT	
		TT T A	
GAM2316 FGFR2	3'	TCAGATCCTTTGAAAAGAG 23245	C_ _ C
		CTCTTTTC AGG TC GA	
		GAGAAAAG TCC AG CT	
		TT T A	
GAM2316 FGFR2	3'	TCAGATCCTTTGAAAAGAG 23292	C_ _ C
		CTCTTTTC AGG TC GA	

			GAGAAAAG TCC AG CT		
			TT T A		
GAM2316 FGFR2	3'	TCAGATCCTTTGAAAAGAG	5642	C_ _ C	
		CTCTTTTC AGG TC GA			
		GAGAAAAG TCC AG CT			
		TT T A			
GAM2316 FGFR2	3'	TCAGATCCTTTGAAAAGAG	23298	C_ _ C	
		CTCTTTTC AGG TC GA			
		GAGAAAAG TCC AG CT			
		TT T A			
GAM2316 FGFR2	3'	TCAGATCCTTTGAAAAGAG	23304	C_ _ C	
		CTCTTTTC AGG TC GA			
		GAGAAAAG TCC AG CT			
		TT T A			
GAM2316 MSL3L1	5'	TGTCGGTCTAAAAGAGGA	13672	CCA T	
		TCCTCTTTT GG CCGACA			
		AGGAGAAAA TC GGCTGT			
		___ T			
GAM2316 NDUFS2	5'	GCCTGAGAAAAGAGGGTA	10896	_	
		TATCCTCTTTTC CAGGT			
		ATGGGAGAAAAG GTCCG			
		A			
GAM2316 PART1	3'	TTGTCGGAGGGGAAAAGG	18667	AGG	
		TCTTTTCC TCCGACAA			
		GGAAAAGG AGGCTGTT			
		GG_			
GAM2316 PTGS1	3'	GTTTCCTGGAAGAAGA	6676	C	TCC
		TC TCTTTTCCAGG GAC			
		AG AGAAAAGGTCC TTG			
		A T__			
GAM2316 PTGS1	3'	GTTTCCTGGAAGAAGA	27897	C	TCC
		TC TCTTTTCCAGG GAC			
		AG AGAAAAGGTCC TTG			
		A T__			
GAM2316 FLJ21816	5'	GTCATCAAAAAGAGGAT	23984	CCA CC	
		ATCCTCTTTT GGT GAC			
		TAGGAGAAAA CTA CTG			
		A__ _			
GAM2316 FLJ22174	5'	TCGATGACTGGAAAAGAGG	22468	GTC_	
		CCTCTTTTCCAG CGA			

			GGAGAAAAGGTC	GCT		
			AGTA			
GAM2316	KIAA0222	3'	TTGAGACACTGGAAAAAAGAT	16048	CTC	_ _
	A		TATC TTTTCCAG	GTC CGA		
			ATAG AAAAGGTC	CAG GTT		
			AAA A A			
GAM2316	RAB10	3'	TGGGTTTGGAAAAAGGA	41282	C	GT
			TCCT TTTTCCAG	CCG		
			AGGA AAAAGGTT	GGT		
			_ TG			
GAM2316	SEMA4G	5'	CGCATCCTGGAAAAAAGGA	45411	C	TC_
			TCCT TTTTCCAGG	CG		
			AGGA AAAAGGTCC	GC		
			A TAC			
GAM2316	ZAK	3'	ACCAAAGGAGCAAAGAGGATA	18776	_	A_
			TATCCTCTTT	TCC GGT		
			ATAGGAGAAA	AGG CCA		
			CG AAA			
GAM2316	LOC131363	5'	TGAAGGCTGGAAAAGAG	37353		GT GA
			CTCTTTTCCAG	CC CA		
			GAGAAAAGGTC	GG GT		
			_ AA			
GAM2316	LOC147057	3'	TGCCGGACCTGGTGGGGAG	40785	TT	A
			CTCTT CCAGGTCCG	CA		
			GAGGG GGTCCAGGC	GT		
			GT C			
GAM2316	LOC152580	5'	ATCTTAAGGAAAAGAGGA	41521	_	
			TCCTCTTTTCC	AGGT		
			AGGAGAAAAGG	TCTA		
			AAT			
GAM2316	LOC221751	5'	TCGATGACTGGAAAAGAGG	44191		GTC_
			CCTCTTTTCCAG	CGA		
			GGAGAAAAGGTC	GCT		
			AGTA			
GAM2316	LOC89932	3'	TGGCTGGAAAAGGGA	30495	T	GT
			TCC CTTTTCCAG	CCG		
			AGG GAAAAGGTC	GGT		
			_ _			
GAM2317	CARKL	3'	CCAGGCTCAGGCAGGCCTGGCC	14937	A A	TC _
	CA		TG GCCA GTCTGCCTG	GTC GG		

AC CGGT CGGACGGAC CGG CC
 C C T_ A
 GAM2317 MAP3K11 5' ACAGGCAGTCTCGGCCCA 8256 A A T
 TG GCC AG CTGCCTGT
 || ||| || |||||
 AC CGG TC GACGGACA
 C C T
 GAM2317 P114-RHO-GEF 3' CCGACGACCTCAACTCTGCCCA 17639 A CA C CCT
 TG GC AGT TG GTCGTCGG
 || || ||| || |||||
 AC CG TCA AC CAGCAGCC
 C TC _ TC_
 GAM2317 LOC144347 3' GACAAAGACTTGGCTCA 37722 GCC
 TGAGCCAAGTCT TGTC
 ||||| |||
 ACTCGGTTTCAGA ACAG
 A_
 GAM2317 LOC146243 3' CCAACTGAGAAGACTTGGGCCCA 40675 A GC GTC C
 TG GCCAAGTCT CT GT GG
 || ||||| || |||
 AC CGGTTTCAGA GA CA CC
 C A_ GT_ A
 GAM2317 LOC255231 3' CCTAGGCAGGCAGACTGAGCTC 45673 CA GTC
 A TGAGC AGTCTGCCTGTC GG
 |||| ||||| ||
 ACTCG TCAGACGGACGG CC
 AG AT_
 GAM2318 DVL3 3' CCCTTTTGTCTCTGGGACCAGA 10694 CA C A
 C GTC GTCCC GAGGCAAGA GGG
 || |||| ||||| |||
 CAG CAGGG CTCTGTTTT CCC
 AC T _
 GAM2318 EFNB1 3' CCCTTCTTGAAGGCAGGGCTG 10707 _ GAGG
 GAC GTCCAGTCC CC CAAGAAGGG
 ||||| || |||||
 CAGGTCGGG GG GTTCTTCCC
 AC AAG_
 GAM2318 LHX5 5' CCAGAGATTGCCCAAGGACTGG 22749 CCGA GAAG_
 AC GTCCAGTCC GGCAA GG
 ||||| ||| ||
 CAGGTCAGG CCGTT CC
 AAC_ AGAGA
 GAM2318 MASP1 3' CCTTCTTGGGAAACTGGGC 7606 CC GAGG
 GTCCAGT CC CAAGAAGG
 ||||| || |||||
 CGGGTCA GG GTTCTTCC
 AA ____
 GAM2318 MYOG 3' CCCCCAGCAAGGGACTGGAC 29847 CGAG AAGAA
 GTCCAGTCCC GC GGG
 ||||| || |||

			CAGGTCAGGG CG CCC		
			AA__ ACCC_		
GAM2318	PTBP1	3'	CCCTCCACACCCGGGGCCAGAC 8684	CA T	A CAAGA
			GTC G CCCC GG AGGG		
			CAG C GGGG CC TCCC		
			AC _ _ ACACC		
GAM2318	PTBP1	3'	CCCTCCACACCCGGGGCCAGAC 25704	CA T	A CAAGA
			GTC G CCCC GG AGGG		
			CAG C GGGG CC TCCC		
			AC _ _ ACACC		
GAM2318	TUFT1	3'	CCCTTCTGTTGTAGACTGGAC 21315	CC AG	A
			GTCCAGTC CG GCA GAAGGG		
			CAGGTCAG GT TGT CTTCCC		
			AT _ _		
GAM2318	ARFGAP1	3'	CCCTCACCTCCCCGAGGACTGG 20108	C A	CAAGA
	AT		GTCCAGTCC CG GG AGGG		
			TAGGTCAGG GC CC TCCC		
			A C TCCAC		
GAM2318	BLR1	5'	CCCTTGCAAGTTCTGGGAAGTGG 26775	C	AG AAG
	AC		GTCCAGT CCG GC AAGGG		
			CAGGTCA GGGT TG TTCCC		
			A CT ACG		
GAM2318	C20orf110	3'	CCCTTCTTGTGGTGAGACTG 38837	CC AG	
			CAGTC CG GCAAGAAGGG		
			GTCAG GT TGTCTTCCC		
			A_ GG		
GAM2318	COL4A3BP	5'	CCCTTCACCCCGAGGACTGGGC 12266	C A	CAA
			GTCCAGTCC CG GG GAAGGG		
			CGGGTCAGG GC CC CTTCCC		
			A _ CA_		
GAM2318	CTSO	3'	CCCTTCTTGTAGAGAGATGGAC 7016	G	CCCGAG
			GTCCA TC GCAAGAAGGG		
			CAGGT AG TGTCTTCCC		
			_ AGAGA_		
GAM2318	FLJ10743	3'	CCCTCCCTGCCTCGGCTCTG 20077	TCC	AGA
			CAG CCGAGGCA AGGG		
			GTC GGCTCCGT TCCC		
			TC_ CCC		
GAM2318	FLJ14124	3'	CCTTCCATGAGGCCTGGAC 24304	T C A	CAAG
			GTCCAG CC CG GG AAGG		

CAGGTC GG GT CC TTCC
 C A A ____
 GAM2318 FLJ14824 3' CCCTTCTTAAGTAGACCTAGAC 26641 CA_ CCCG GC
 GTC GTC AG AAGAAGGG
 ||| ||| || |||||
 CAG CAG TC TTCTTCCC
 ATC A__ AA
 GAM2318 HSU79303 3' CCCCTCGAGTGGGGGACTGTAC 14960 C GAG AA A
 GT CAGTCCCC GC GA GGG
 || ||||| || |||
 CA GTCAGGGG TG CT CCC
 T G__ AG C
 GAM2318 ICB-1 3' CCTCCCCGAGGCTGGAC 11258 C A CAAGA
 GTCCAGTC CCG GG AGG
 ||||| ||| |||
 CAGGTCGG GGC CC TCC
 A C ____
 GAM2318 KIAA0010 5' CCCCTCCCGCCCCAGGGCAGGG 16129 A CCGA AA A
 C GTCC GTCC GGC GA GGG
 ||| ||| ||| |||
 CGGG CGGG CCG CT CCC
 A ACC_ CC C
 GAM2318 KIAA0121 5' CCCTCCCTGCCTCGGCAGCGCG 35969 A_ CC AGA
 G CC GT CCGAGGCA AGGG
 || || ||||| |||
 GG CG GGCTCCGT TCCC
 CG AC CCC
 GAM2318 KIAA0194 3' CCCTTCTATGAAGGGGAAGCAG 32822 CAG_ GAGG _
 AC GTC TCCCC CA AGAAGGG
 ||| |||| || |||||
 CAG AGGGG GT TCTTCCC
 ACGA AA__ A
 GAM2318 KIAA1691 3' CCCTTCCCCCAGGAGAGACTG 44467 CCCGA__ CAA
 GGC GTCCAGTC GG GAAGGG
 ||||| || |||||
 CGGGTCAG CC CTTCCC
 AGACCCA CC_
 GAM2318 NGEF 3' CCCTGGCCCCCAGGGACTGGA 34276 CGA_ AAGA
 TCCAGTCCC GGC AGGG
 ||||| ||| |||
 AGGTCAGGG CCG TCCC
 ACCC G__
 GAM2318 REPRIMO 3' CCCCTCACTATCAGAGACTGGG 21248 CCC GGCAA A
 C GTCCAGTC GA GA GGG
 ||||| || |||
 CGGGTCAG CT CT CCC
 AGA ATCA_ C
 GAM2318 ZF5128 3' CCCTCCTCAATTGGAGGCTGGA 15669 C GGCA A
 C GTCCAGTC CCGA AG AGGG
 ||||| ||| |||

CAGGTCGG GGTT TC TCCC
 A AAC_ C
 GAM2318 LOC147136 3' CCCCTCTTGCCTCAGGA 38302 CC A
 TCC GAGGCAAGA GGG
 ||| ||||| |||
 AGG CTCCGTTCT CCC
 A_ C
 GAM2318 LOC153196 5' CCCTTCTGCAAGCCTGGAGACT 41589 C G A____
 GGAC GTCCAGTC CC AGGC AGAAGGG
 ||||| || ||| |||||
 CAGGTCAG GG TCCG TCTTCCC
 A _ AACG
 GAM2318 LOC158654 3' CCTAGCCCAGGGACTGGA 39877 CGA AAGA
 TCCAGTCCC GGC AGG
 ||||| ||| |||
 AGGTCAGGG CCG TCC
 AC_ A____
 GAM2319 PTPN18 3' GGCAGAACTAAGCCAGGCATA 15704 ACAACGA C
 TATG GCTTAGTTC GCC
 ||| ||||| |||
 ATAC CGAATCAAG CGG
 GGAC____ A
 GAM2319 TNFRSF11A 3' GCAGAACTAAGCTCAGTATGT 9932 _ _ C
 ACA AC GAGCTTAGTTC GC
 ||| || ||||| |||
 TGT TG CTCGAATCAAG CG
 A A A
 GAM2319 AFAP 3' GGCAGCTGGGCCCACTTCATA 22293 CAACGA _
 TATGA GCTTAGTT CC
 |||| ||||| |||
 ATACT CGGGTCGA GG
 TCACC_ C
 GAM2319 LOC221362 3' GGCAAATAAGCCTGCATTGTCA 45022 _ A GTTCC
 TA TATGACAA CG GCTTA GCC
 ||||| || ||| |||
 ATACTGTT GT CGAAT CGG
 AC C AAA____
 GAM2320 DEK 3' CCACTCCTGAATGAGACTTAAT 9537 CA TCTTT
 ATTA TCTCATTG TGG
 ||| ||||| |||
 TAAT AGAGTAAG ACC
 TC TCCTC
 GAM2320 HFE 5' CCAAAAGAAGCGGAGATTTAA 29098 C ATTC
 TTA ATCTC TCTTTTGG
 ||| ||| |||||
 AAT TAGAG AGAAAACC
 T GCGA
 GAM2320 HFE 5' CCAAAAGAAGCGGAGATTTAA 29100 C ATTC
 TTA ATCTC TCTTTTGG
 ||| ||| |||||

			AAT TAGAG AGAAAACC		
			T GCGA		
GAM2320 HFE	5'	CCAAAAGAAGCGGAGATTTAA	29101	C	ATTC
		TTA ATCTC TCTTTTGG			
		AAT TAGAG AGAAAACC			
		T GCGA			
GAM2320 HFE	5'	CCAAAAGAAGCGGAGATTTAA	29102	C	ATTC
		TTA ATCTC TCTTTTGG			
		AAT TAGAG AGAAAACC			
		T GCGA			
GAM2320 HFE	5'	CCAAAAGAAGCGGAGATTTAA	29103	C	ATTC
		TTA ATCTC TCTTTTGG			
		AAT TAGAG AGAAAACC			
		T GCGA			
GAM2320 HFE	5'	CCAAAAGAAGCGGAGATTTAA	5984	C	ATTC
		TTA ATCTC TCTTTTGG			
		AAT TAGAG AGAAAACC			
		T GCGA			
GAM2320 PSEN1	3'	CCACAGCAAATGAGATGTA	14234		CT TT
		TACATCTCATT CT TGG			
		ATGTAGAGTAA GA ACC			
		AC C_			
GAM2320 PSEN1	3'	CCACAGCAAATGAGATGTA	5456		CT TT
		TACATCTCATT CT TGG			
		ATGTAGAGTAA GA ACC			
		AC C_			
GAM2320 DKFZP564B1162	3'	CCAAAAGAGAAATGTAA	25335		CTCA _
		TTACAT TTCTCTTTT GG			
		AATGTA AAGAGAAAA CC			
		_ A			
GAM2320 FLJ12568	3'	CCAAAAGAAATGATATGTA	24552	C	C
		TACAT TCATT TCTTTTGG			
		ATGTA AGTAA AGAAAACC			
		T _			
GAM2320 FLJ14640	5'	CCAGAAAGAATGAGATATAA	26585	C	C
		TTA ATCTCATTCT TTTTGG			
		AAT TAGAGTAAGA AAGACC			
		A _			
GAM2320 FLJ22635	3'	CAAGAACAAGATGTGAT	24715	CA	CTTT
		ATTACATCT TTCT TG			

				TAGTGTAGA AAGA AC AC ____	
GAM2320	GABARAPL1	3'	CCAAAAGAGACCCACTGTAAT	25389	TCTCAT
			ATTACA TCTCTTTTGG		
			TAATGT AGAGAAAACC		
			CACCC_		
GAM2320	KIAA0441	3'	CCAAAAGAAATGTCGTG	16708	CT C
			CAT CATT TCTTTTGG		
			GTG GTAA AGAAAACC		
			CT _		
GAM2320	KIAA0494	3'	CCAAAAAGGCTGTGAGATG	16587	T_TC
			CATCTCAT C TTTTGG		
			GTAGAGTG G AAAACC		
			TC GA		
GAM2320	MGC27277	3'	CCAAAAGATGATGATGTGAT	29592	_ TTC
			ATTACATC TCA TCTTTTGG		
			TAGTGTAG AGT AGAAAACC		
			T ____		
GAM2320	LOC129530	5'	CCAAAATAGGATGAGATG	36971	C
			CATCTCATTCT TTTTGG		
			GTAGAGTAGGA AAAACC		
			T		
GAM2320	LOC145678	3'	CCAGCCAATGAGATGTAA	40555	CTCTT
			TTACATCTCATT TTGG		
			AATGTAGAGTAA GACC		
			CC____		
GAM2321	CD4	3'	AGTGCCGGACTAGCAAGTGCTG	6218	C CCTC ____
	GA		TCCAGCACT GT GTC GCACT		
			AGGTCGTGA CG CAG CGTGA		
			A AT__ GC		
GAM2321	MAFK	5'	AGCGCGACAGTGAGCGCCGG	8172	A A TC C A
			CC GC CTCG CT GTCGC CT		
			GG CG GAGT GA CAGCG GA		
			C C _ _ C		
GAM2321	MEN1	5'	GTGGGAAACGAGTGCTG	28298	CCTCG G
			CAGCACTCGT TC CAC		
			GTCGTGAGCA AG GTG		
			A__ G		
GAM2321	MEN1	5'	GTGGGAAACGAGTGCTG	28302	CCTCG G
			CAGCACTCGT TC CAC		

			GTCGTGAGCA	AG GTG		
			A _ G			
GAM2321	PTPRJ	5'	GCGGGACGAGCGCGGGA	8731	A A	T
			TCC GC CTCGTCC CGT			
			AGG CG GAGCAGG GCG			
			G C _			
GAM2321	USH3A	5'	GCACACGAGTGAACGAGTGCAG	27562	A	_ _ C_
	GA		TCC GCACTCGT C CTCGT GC			
			AGG CGTGAGCA G GAGCA CG			
			A A T CA			
GAM2321	GMEB2	3'	AGCGCGACCCTGCAGGTGCTGG	14738	TC CCTC	A
	A		TCCAGCAC GT GTCGC CT			
			AGGTCGTG CG CAGCG GA			
			GA TCC_ C			
GAM2321	R3HDM	3'	TGCATTTGATGAGTGCTGGA	17662	CTC C	
			TCCAGCACTCGTC GT GCA			
			AGGTCGTGAGTAG TA CGT			
			TT_ _			
GAM2321	LOC145216	3'	TGGGAGGACGAGAGCCGGA	40509	A A	G
			TCC GC CTCGTCCTC TCG			
			AGG CG GAGCAGGAG GGT			
			C A _			
GAM2321	LOC148697	3'	GCAATGGATGAGTGCTGGA	38572	TCGTC	
			TCCAGCACTCGTCC GC			
			AGGTCGTGAGTAGG CG			
			TAA_			
GAM2321	LOC152580	5'	GTGCAACGAGGACTTGGA	41523	CACTC	C
			TCCAG GTCCTCGT GCAC			
			AGGTT CAGGAGCA CGTG			
			_ _ A			
GAM2321	LOC254431	3'	GTGGGGGGCCGAGTGCTG	46292	T G	
			CAGCACTCG CCTC TCGC			
			GTCGTGAGC GGGG GGTG			
			C _			
GAM2322	APG5L	3'	AGTGTCAGGCCTTTGCAGT	11261	ACCA _	
			ACTGCAAAGGC GC CT			
			TGACGTTTCCG TG GA			
			GAC_ T			
GAM2322	B4GALT5	3'	TTGATACCTTTGCGGTCA	11171	CAC	
			TGACTGCAAAGG CAG			

			ACTGGCGTTTCC GTT		
			ATA		
GAM2322	EGR2	3'	GTGTTACCTTTGTAGTCA 5970	___	
			TGACTGCAAAGG CAC		
			ACTGATGTTTCC GTG		
			ATT		
GAM2322	FUS1	3'	AAGGCTGGTGCCAGTAGTTA 14136	AAA	
			TGACTGC GGCACCAGCCTT		
			ATTGATG CCGTGGTCGGAA		
			A_		
GAM2322	KCNK4	5'	AAGGCTGGCCCCTGCTGCA 27150	A_ CA	
			TGCA AGG CCAGCCTT		
			ACGT TCC GGTCGGAA		
			CG CC		
GAM2322	MUS81	5'	AAGGCTGGCTGGAGTGGAGCCA 24771	A G AAGG _	
			TG CT CA CA CCAGCCTT		
			AC GA GT GT GGTCGGAA		
			C G GAG_ C		
GAM2322	NBS1	3'	GAGGCTGGCCTCTACATCA 34437	C CAA AC	
			TGA TG AGGC CAGCCTT		
			ACT AC TCCG GTCGGAG		
			_ ATC _		
GAM2322	NUMB	3'	AAGGCTGGAAGCTGCAG 9832	AAG A_	
			CTGCA GC CCAGCCTT		
			GACGT CG GGTCGGAA		
			_ AA		
GAM2322	OPHN1	3'	AAGGTCTTGGTGCCTCTGCAGT 8398	A _	
			ACTGCA AGGCACCA GCCTT		
			TGACGT TCCGTGGT TGGAA		
			C TC		
GAM2322	PRKCM	3'	CTGTGCCTTTGCAAATCA 8613	C_ C	
			TGA TGCAAAGGCAC AG		
			ACT ACGTTTCCGTG TC		
			AA _		
GAM2322	RXRA	3'	CTGGTGCCTTTTGCAGCCA 8868	A _	
			TG CTGCAAA GGCACCAG		
			AC GACGTTT CCGTGGTC		
			C T		
GAM2322	SIP	3'	AAGGCTGGCGCCCGTAATC 15756	C AAA A	
			GA TGC GGC CCAGCCTT		

CT ATG CCG GGTCGGAA
 A C_ C
 GAM2322 ZHX1 3' AAGACTGGTGCTGTTCATTCA 14090 C C A C
 TGA TG AA GGCACCAG CTT
 ||| || ||||| |||
 ACT AC TT TCGTGGTC GAA
 T _ G A
 GAM2322 FLJ20257 3' AAGGCTGGCTGTGCTGGAGTCA 21219 G AAG _
 TGA CT CA GCA CCAGCCTT
 ||||| || ||| |||||
 ACTGA GT TGT GGTCGGAA
 G CG_ C
 GAM2322 FLJ21865 3' AAGGCTGGGTACTCAGCAGCCA 22999 A AA GCA
 TG CTGC AG CCAGCCTT
 || |||| || |||||
 AC GACG TC GGTCGGAA
 C AC ATG
 GAM2322 FLJ22160 3' TTGGTGCCTTTTCAGCCA 23821 A C
 TG CTG AAAGGCACCAG
 || ||| |||||
 AC GAC TTTCCGTGGTT
 C T
 GAM2322 KIAA1328 3' GTTGGTGCCCCTGCCATCA 30887 CT AA
 TGA GCA GGCACCAGC
 ||| ||| |||||
 ACT CGT CCGTGGTTG
 AC CC
 GAM2322 KIAA1354 3' AAGGTGTAACACCTTTGCAGT 30539 CACCA_
 ACTGCAAAGG GCCTT
 ||||| |||||
 TGACGTTTCC TGGAA
 ACAATG
 GAM2322 KIAA1554 3' GGACTGGTGCCTTTGCATTCA 45611 C _
 TGA TGCAAAGGCACCAG CC
 ||| ||||| ||||| ||
 ACT ACGTTTCCGTGGTC GG
 T A
 GAM2322 OS4 3' CTGTGCCTTTACGATCA 12288 C C C
 TGA TG AAAGGCAC AG
 ||| || ||||| ||
 ACT GC TTTCCGTG TC
 A A _
 GAM2322 OSBPL3 3' AAGGCTGGTATTCCTTGAGTCA 17812 G A C_
 TGA CT CAA GG ACCAGCCTT
 ||||| ||| || |||||
 ACTGA GTT CC TGGTCGGAA
 _ _ TTA
 GAM2322 PRO0365 5' AGGCTGGTTTACAGTC 15384 C AGGC
 GACTG AA ACCAGCCT
 ||||| || |||||

CTGAC TT TGGTCGGA
 A ____
 GAM2322 RAB20 3' CTGGTCCTTTGCAGCCA 19465 A C
 TG CTGCAAAGG ACCAG
 || ||||| ||||
 AC GACGTTTCC TGGTC
 C _
 GAM2322 TRIP-Br2 3' AAGGCTGGGCTTCAAAATCA 16480 CTGCAA A
 TGA AGGC CCAGCCTT
 || |||| |||||
 ACT TTCG GGTTCGAA
 AAAAC_ _
 GAM2322 LOC118978 5' AAGGCTGGGCTGCAGCCA 37412 A AAG A
 TG CTGCA GC CCAGCCTT
 || |||| || |||||
 AC GACGT CG GGTTCGAA
 C _ G
 GAM2322 LOC159110 3' CTTGTGTTACCTTTGCAGCCA 39943 A _ C
 TG CTGCAAAGG CAC AG
 || ||||| ||||
 AC GACGTTTCC GTG TC
 C ATT T
 GAM2322 LOC159116 3' CTTGTGTTACCTTTGCAGCCA 39941 A _ C
 TG CTGCAAAGG CAC AG
 || ||||| ||||
 AC GACGTTTCC GTG TC
 C ATT T
 GAM2322 LOC203221 5' AAGGCCCTGTGGACACTTTGCA 43126 GCA _
 GTCA TGA CTGCAAAG CCA GCCTT
 ||||| ||||
 ACTGACGTTTC GGT CGGAA
 ACA GTCC
 GAM2322 LOC90844 3' AAGGCTGGAGTTTGAATCA 32118 CTGCAA A
 TGA AGGC CCAGCCTT
 || |||| |||||
 ACT TTTG GGTTCGAA
 AAGG_ A
 GAM2323 KIAA0620 3' CAGGACATGACGCCGCTCAGCG 31120 CA G A
 CGT GGGTGG CGTCAT TCCTG
 || |||| ||||| ||||
 GCG CTCGCC GCAGTA AGGAC
 A_ _ C
 GAM2323 KIAA1023 3' CAGGACCCGCCCCACCCTGCG 19087 T C CATA
 CG CAGGGTGGG GT TCCTG
 || ||||| || ||||
 GC GTCCCAACC CG AGGAC
 _ _ CCC_
 GAM2323 LOC127534 3' CAGAACCACACCTCCACCCTAA 37164 C C CATATC
 C GT AGGGTGGG GT CTG
 || ||||| || |||

		CA TCCCACCT CA GAC	
		A C CACCAA	
GAM2323	LOC155179 3'	CAGGACCCGCCCCACCCTGCG 39554	T C CATA
		CG CAGGGTGGG GT TCCTG	
		GC GTCCACCC CG AGGAC	
		_ _ CCC_	
GAM2324	FLJ20298 3'	TATCTAAAATATTACCATT 19363	C A
		GATGGTAATAT TTA GATA	
		TTACCATTATA AAT CTAT	
		A _	
GAM2324	LOC152445 5'	AAATATCTCATCCTTACCATC 41508	TATCTTA
		GATGGTAA AGATATTT	
		CTACCATT TCTATAAA	
		CCTAC_	
GAM2325	BCLG 3'	CATAGAAAGACTACTGTCAA 25050	G G
		TTGACAGTAG CTT TTGTG	
		AACTGTCATC GAA GATAC	
		A A	
GAM2325	BCLG 3'	CATAGAAAGACTACTGTCAA 28966	G G
		TTGACAGTAG CTT TTGTG	
		AACTGTCATC GAA GATAC	
		A A	
GAM2325	BCLG 3'	CATAGAAAGACTACTGTCAA 28968	G G
		TTGACAGTAG CTT TTGTG	
		AACTGTCATC GAA GATAC	
		A A	
GAM2325	CLCN3 3'	CCACAACAAAGGCTCATCAA 7566	CAGT G _
		TTGA AG CTT GTTGTGG	
		AACT TC GAA CAACACC	
		AC_ G A	
GAM2325	LDB2 3'	CCAGAATCCACTGTCAA 6969	A CTT G
		TTGACAGT GG GTT TGG	
		AACTGTCA CC TAA ACC	
		_ _ _ G	
GAM2325	PODXL 3'	CCAGGACACCTATGTCAA 11872	G CT G
		TTGACA TAGG TGTT TGG	
		AACTGT ATCC ACAG ACC	
		_ _ _ G	
GAM2325	TR2 3'	CACATTTAACCTACTGTCAA 35793	C T_
		TTGACAGTAGG TTG TGTG	

			AACTGTCATCC AAT ACAC		
			— TT		
GAM2325	C20orf18	3'	CCACAACACTCATCTGTCAA 25275		TAGGCT
			TTGACAG TGTTGTGG		
			AACTGTC ACAACACC		
			TACTC_		
GAM2325	DCTN4	3'	CTGCTAGAGCCTACTGTGAA 33666	G	GTT TG
			TTACAGTAGGCTT G G		
			AA TGTCATCCGAG C C		
			G AT_GT		
GAM2325	KIAA1855	3'	CACCCTGGAAGCCACTGTCAA 44353	A	GTT__
			TTGACAGT GGCTT GTG		
			AACTGTCA CCGAA CAC		
			— GTCC		
GAM2325	LOC158402	5'	TGCCAATACCACCTACTGT 41977		CTT TG
			ACAGTAGG GT TGGCA		
			TGTCATCC CA ACCGT		
			AC_ TA		
GAM2325	LOC56963	3'	GCCAGGGACCGCCTGCTGCCAA 35400	A	TTG G
			TTG CAGTAGGC TT TGGC		
			AAC GTCGTCCG GG ACCG		
			C CCA G		
GAM2326	BCL6	5'	GAAAGTTTTTAAGTAAACCTCC 29057		ACTTT GG
	CA		TGGGAG CT GAGACTTTC		
			ACCCTC GA TTTTGAAAG		
			CAAAT AT		
GAM2326	STAU	3'	CCTTGAATAAGTCTCCCA 18925	—	T
			TGGGAGACTT TC GGG		
			ACCCTCTGAA AG TCC		
			TA T		
GAM2326	STAU	3'	CCTTGAATAAGTCTCCCA 10941	—	T
			TGGGAGACTT TC GGG		
			ACCCTCTGAA AG TCC		
			TA T		
GAM2326	STAU	3'	CCTTGAATAAGTCTCCCA 18913	—	T
			TGGGAGACTT TC GGG		
			ACCCTCTGAA AG TCC		
			TA T		
GAM2326	STAU	3'	CCTTGAATAAGTCTCCCA 18919	—	T
			TGGGAGACTT TC GGG		

ACCCTCTGAA AG TCC
 TA T
 GAM2326 CLIPR-59 3' GAAAATCCAATCCCAAGTCCCC 17788 A TTC ____ C
 A TGGG GACT TGGGA GA TTTC
 |||| ||| |||| || ||||
 ACCC CTGA ACCCT CT AAAG
 _ ____ AAC A
 GAM2326 HAPIP 3' AAAGTTTTAAAAGTCCTCCA 10065 GA CTGG
 TGG GACTTT GAGACTTT
 || ||||| |||||
 ACC CTGAAA TTTTGAAA
 TC A____
 GAM2326 KIAA0092 3' AAAGTCTCATTTTTTAAATCTCC 16151 C TCTGG_
 C GGGAGA TT GAGACTTT
 ||||| || |||||
 CCCTCT AA CTCTGAAA
 A TTTTTA
 GAM2326 KIAA0217 3' GAAAGTCTTATTAAAAGCCTCC 33282 A CTGG
 GGAG CTTT GAGACTTTC
 |||| ||| |||||
 CCTC GAAA TTCTGAAAG
 C ATTA
 GAM2326 LIMK2 3' GAAAACCTCCATCTTGGCTCCC 18785 A TTCTG AC
 A TGGGAG CT GGAG TTTC
 ||||| || ||| ||||
 ACCCTC GG CCTC AAAG
 _ TTCTA CA
 GAM2326 LIMK2 3' GAAAACCTCCATCTTGGCTCCC 12095 A TTCTG AC
 A TGGGAG CT GGAG TTTC
 ||||| || ||| ||||
 ACCCTC GG CCTC AAAG
 _ TTCTA CA
 GAM2326 PRO1331 5' AAAGTCTTCTGCAGAATCTCCC 25065 CT ____
 A TGGGAGA TTCTG GGAGACTTT
 ||||| |||| |||||
 ACCCTCT AAGAC CTTCTGAAA
 ____ GT
 GAM2326 LOC150225 3' AAAGCCCCCGAGACCTCCCA 41185 AC T AGA
 TGGGAG TTTC GGG CTTT
 ||||| |||| ||| ||||
 ACCCTC AGAG CCC GAAA
 C_ C C_
 GAM2326 LOC158191 5' AAAGCCTTGGGAGATCCCCCA 39757 A C TG AGA
 TGGG GA TTTC GG CTTT
 ||| || |||| || ||||
 ACCC CT AGAG TC GAAA
 C _ GT C_
 GAM2326 LOC196446 3' GAAAGCCACAGAGAAATCTCCC 42372 C_ _ AGA
 A TGGGAGA TTTCTG GG CTTTC
 ||||| ||||| || ||||

ACCCTCT AGAGAC CC GAAAG
 AA A ____
 GAM2326 LOC222182 3' AAAGTCTCCCAACCCCA 45195 AGACTTTC
 TGGG TGGGAGACTTT
 ||| |||||
 ACCC ACCCTCTGAAA
 CA_____
 GAM2326 LOC90841 5' GAAAGCTGGGCTAGAAAATCTC 32111 C G__ A
 TCA TGGGAGA TTTCTGG AG CTTTC
 ||||| ||||| || |||||
 ACTCTCT AAAGATC TC GAAAG
 A GGG _
 GAM2326 LOC91056 3' AAAATCTCCTTTCTGCTTCCCA 45438 ACTTTCT C
 TGGGAG GGGAGA TTT
 ||||| ||||| |||
 ACCCTT TCCTCT AAA
 CGTCTT_ A
 GAM2327 GPR61 5' ACCCTAAAACTGAGGCACT 38562 _ AG A
 AG GC TAGTTTTAG GT
 || || ||||| ||
 TC CG GTCAAAATC CA
 A GA C
 GAM2327 PLSCR1 3' ACTCTAAAACTCTGGTATTATA 22085 CAGG T
 TATAA CAG AGTTTTAGAGT
 |||| || |||||
 ATATT GTC TCAAAATCTCA
 ATG_ _
 GAM2327 SLC21A2 3' ACCCTGGGCCACTGCCTG 12154 A T A
 CAGGCAGT GTTT AG GT
 ||||| ||| || ||
 GTCCGTCA CGGG TC CA
 C _ C
 GAM2327 FLJ10702 3' ACTCTAGACCTGCCTG 20024 TAGT
 CAGGCAG TTTAGAGT
 ||||| |||||
 GTCCGTC AGATCTCA
 C____
 GAM2327 FLJ12287 3' ACCCTAAAAACCTGCCTGT 22753 TAG A
 ACAGGCAG TTTTAG GT
 ||||| ||||| ||
 TGTCCGTC AAAATC CA
 CAA C
 GAM2327 MGC20253 3' CTCTGGAGCTACTCCTGCTA 29396 A C
 TA CAGG AGTAGTTTTAGAG
 || ||| |||||
 AT GTCC TCATCGAGGTCTC
 C _
 GAM2327 PRDM10 3' ACTCTAAAACTAATTTGT 21495 GCAG
 ACAG TAGTTTTAGAGT
 ||| |||||

			TGTT ATCAAAATCTCA		
			TA__		
GAM2328	AKAP13	5'	TCCAAGAAAGATTCTGA 29559	TACCA	C
			TCAGAGTCTT TCT GGA		
			AGTCTTAGAA AGA CCT		
			_____ A		
GAM2328	DLX4	3'	TCCAGCTGGACAAAGACTCTGG 28694	A_	T C
			TCAGAGTCTTT CCA CT GGA		
			GGTCTCAGAAA GGT GA CCT		
			CA C _		
GAM2328	DLX4	3'	TCCAGCTGGACAAAGACTCTGG 7646	A_	T C
			TCAGAGTCTTT CCA CT GGA		
			GGTCTCAGAAA GGT GA CCT		
			CA C _		
GAM2328	KCNJ1	5'	CCGAATAATAAAGACTT 5726	CC	C
			GAGTCTTTA AT TCGG		
			TTCAGAAAT TA AGCC		
			AA _		
GAM2328	MEIS2	3'	TCTGGAAAAAGACTCCGA 21349	A	ACCA T
			TC GAGTCTTT TC CGGA		
			AG CTCAGAAA AG GTCT		
			C A__ _		
GAM2328	NDP	3'	TCTAGTAATAAAGACTCT 5810	CCAT	C
			AGAGTCTTTA CT GGA		
			TCTCAGAAAT GA TCT		
			AAT_ _		
GAM2328	NFRKB	5'	TTTCCGAGACGGACACTTT 12824	CTTTA	A
			AGAGT CC TCTCGGAAA		
			TTTCA GG AGAGCCTTT		
			CA__ C		
GAM2328	UC28	3'	TTCCCAAGTGTAAGACTCTG 22282	TAC	CTC
			CAGAGTCTT CAT GGAA		
			GTCTCAGAA GTG CCTT		
			T__ AAC		
GAM2328	C1QTNF7	3'	TCCCTGTGGTAAACACTCTGA 25668	C	CTC
			TCAGAGT TTTACCAT GGA		
			AGTCTCA AAATGGTG CCT		
			C TC_		
GAM2328	KIAA1416	3'	CGAGAACAAAGACTCTGA 41805	ACCA	
			TCAGAGTCTTT TCTCG		

		AGTCTCAGAAA AGAGC		
		CA__		
GAM2328	KIAA1493	3' TTTCCATCGCTGAAGACTCT 32096		CCATCTC
		AGAGTCTTTA GGAAA		
		TCTCAGAAGT CCTTT		
		CGCTA__		
GAM2328	KIAA1524	3' TCTAATTTAGTAAAGACCCTGA 36361	A	CATCTC
		TCAG GTCTTTAC GGA		
		AGTC CAGAAATG TCT		
		C ATTTAA		
GAM2328	KIAA1904	3' TTCCAAAGAGCAGGACTCTGA 36384		TACCA C_
		TCAGAGTCTT TCT GGAA		
		AGTCTCAGGA AGA CCTT		
		CG__ AA		
GAM2328	TUSP	3' TTTGAGATATAAAGACCCTGA 21538	A	CC
		TCAG GTCTTTA ATCTCGGA		
		AGTC CAGAAAT TAGAGTTT		
		C A_		
GAM2328	LOC128989	3' CCTGATAATAAACTCTGA 36942	C	CC TC
		TCAGAGT TTTA ATC GG		
		AGTCTCA AAAT TAG CC		
		_ AA T_		
GAM2328	LOC146455	3' CCGAGATGGAGTCTTACTCTG 38157		CTTTA_
		CAGAGT CCATCTCGG		
		GTCTCA GGTAGAGCC		
		TTCTGA		
GAM2328	LOC150282	5' TTTGTTGGGCAAAGACTCTGA 38919	A	ATCT
		TCAGAGTCTTT CC CGGA		
		AGTCTCAGAAA GG GTTT		
		C GTT_		
GAM2328	LOC219731	5' TCCGAAACTGAAGACTCT 44719		CCATC
		AGAGTCTTTA TCGGA		
		TCTCAGAAGT AGCCT		
		CAA__		
GAM2328	LOC254024	5' CCGTGTCTGACAAAGACTCTG 46040		AC TCT_
		CAGAGTCTTT CA CGG		
		GTCTCAGAAA GT GCC		
		CA CTGT		
GAM2329	APM1	3' ACTGAGGTCAAGATTTC 11205	_	
		TGAGATCTTGAT TCAGT		

		ACTTTAGAACTG AGTCA	
		G	
GAM2329	B4GALT3	5' AGCTTGAACCTAGATCTCA 9863	TGA T
		TGAGATCT TTCAG GTT	
		ACTCTAGA AAGTT CGA	
		TCC _	
GAM2329	CKTSF1B1	3' AACACTGAATTTCTC 15020	TCTT
		GAGA GATTCAGTGT	
		CTCT TTAAGTCACAA	

GAM2329	KCNJ3	3' AAACACTGAATCATGTT 8021	CT
		GAT TGATTCAGTGTTT	
		TTG ACTAAGTCACAAA	
		T_	
GAM2329	MME	3' AAACAGTTGTGAACCAAGATCT 14157	A G__
		AGATCTTG TTCA TGTTT	
		TCTAGAAC AAGT ACAA	
		C GTTG	
GAM2329	MME	3' AAACAGTTGTGAACCAAGATCT 14153	A G__
		AGATCTTG TTCA TGTTT	
		TCTAGAAC AAGT ACAA	
		C GTTG	
GAM2329	MME	3' AAACAGTTGTGAACCAAGATCT 14149	A G__
		AGATCTTG TTCA TGTTT	
		TCTAGAAC AAGT ACAA	
		C GTTG	
GAM2329	MME	3' AAACAGTTGTGAACCAAGATCT 6601	A G__
		AGATCTTG TTCA TGTTT	
		TCTAGAAC AAGT ACAA	
		C GTTG	
GAM2329	PRKAA2	3' AAACCTGCCTCCAAGATTTCA 12926	ATT_ T
		TGAGATCTTG CAG GTTT	
		ACTTTAGAAC GTC CAAA	
		CTCC _	
GAM2329	RANBP2	3' AACACTGGTGATTTCA 12947	TTGAT
		TGAGATC TCAGTGT	
		ACTTTAG GGTCACAA	
		T_____	
GAM2329	RPL10	3' AAACACTGAAGTGCTTTTCA 12621	TCTTGA
		TGAGA TTCAGTGTTT	

ACTTT AAGTCACAAA
 TCGTG_
 GAM2329 TAL1 5' AAACACTGAACCGACCGATC 9167 ____ A
 GATC TTG TTCAGTGTTT
 |||| ||| |||||
 CTAG GAC AAGTCACAAA
 CCA C
 GAM2329 TNFRSF1B 3' ACCCTGGAATCAAGATGTCA 6733 G _ T
 TGA ATCTTGATTG AG GT
 ||| ||||| || ||
 ACT TAGAACTAAG TC CA
 G G C
 GAM2329 C1orf24 3' AAACATAGCAAGATCTCA 27525 ATTCA
 TGAGATCTTG GTGTTT
 ||||| |||||
 ACTCTAGAAC TACAAA
 GA_
 GAM2329 DKFZP564O123 3' ACTGAAATCAAGGCCTCA 29904 AT _
 TGAG CTTGATT CAGT
 |||| ||||| ||||
 ACTC GAACTAA GTCA
 CG A
 GAM2329 KIAA1560 3' AAACACTGATAGTATCTCA 32097 C AT
 TGAGAT TTG TCAGTGTTT
 ||||| ||| |||||
 ACTCTA GAT AGTCACAAA
 T _
 GAM2329 MGC3222 3' AAACACTGAAGATGTC 23640 G TGAT
 GA ATCT TCAGTGTTT
 || |||| |||||
 CT TAGA AGTCACAAA
 G _
 GAM2329 PXMP4 3' AAACACTGATTTTAAATC 14110 C T_
 GAT TTGA TCAGTGTTT
 ||| |||| |||||
 CTA AATT AGTCACAAA
 A TT
 GAM2329 Rab11-FIP2 3' AAACACTGAGAGTATCT 17093 _ GAT
 AGAT CTT TCAGTGTTT
 |||| ||| |||||
 TCTA GAG AGTCACAAA
 T _
 GAM2329 Rabip4R 3' AAACACTGAACAGTTATC 19714 C_ A
 GAT TTG TTCAGTGTTT
 ||| ||| |||||
 CTA GAC AAGTCACAAA
 TT _
 GAM2329 RHOBTB1 3' AAACACCAGATAGAAGATCTTA 43948 G_ CA
 TGAGATCTT ATT GTGTTT
 ||||| ||| |||||

			ATTCTAGAA TAG CACAAA		
			GA AC		
GAM2329	SLC1A7	3'	AAACACTTGTCCAAGGTCTCA	13487	ATTC
			TGAGATCTTG AGTGTTT		
			ACTCTGGAAC TCACAAA		
			CTGT		
GAM2329	SMT3H2	3'	AAACACTGAACCATTCT	13818	TCT A
			AGA TG TTCAGTGTTT		
			TCT AC AAGTCACAAA		
			T__ C		
GAM2329	LOC112687	3'	AAACACTGAATCCATC	36063	CTT
			GAT GATTCAGTGTTT		
			CTA CTAAGTCACAAA		
			C__		
GAM2329	LOC143154	3'	AAACACTGTCAAGGATTTC	37583	GATT
			TGAGATCTT CAGTGTTT		
			ACTTTAGGA GTCACAAA		
			ACT_		
GAM2329	LOC144262	5'	AAACACCTGAAGATCTCA	37703	TGAT _
			TGAGATCT TCAG TGTTT		
			ACTCTAGA AGTC ACAA		
			____ C		
GAM2329	LOC151632	5'	AAACACATATCAAGATCCA	41380	A TCA
			TG GATCTTGAT GTGTTT		
			AC CTAGAACTA CACAAA		
			_ TA_		
GAM2329	LOC152271	3'	AAACACATATCAAGATCCA	39237	A TCA
			TG GATCTTGAT GTGTTT		
			AC CTAGAACTA CACAAA		
			_ TA_		
GAM2329	LOC158434	5'	AAGTGTGAAATCAAGATGTCA	41980	G CA TG
			TGA ATCTTGATT G TTT		
			ACT TAGAACTAA T GAA		
			G AG GT		
GAM2329	LOC158662	5'	AAACACTGAAAAACATC	39879	C GA
			GAT TT TTCAGTGTTT		
			CTA AA AAGTCACAAA		
			C A_		
GAM2329	LOC200904	5'	AAACACATATCAAGATCCA	43359	A TCA
			TG GATCTTGAT GTGTTT		

			AC CTAGAACTA CACAAA		
			— TA_		
GAM2329	LOC201824	3'	AAACACTGATGTTGATTTC	42919	TTGAT
			— TGAGATC TCAGTGTTT		
			ACTTTAG AGTCACAAA		
			TTGT_		
GAM2329	LOC203083	5'	AAACACATATCAAGATCCA	43476	A TCA
			— TG GATCTTGAT GTGTTT		
			AC CTAGAACTA CACAAA		
			— TA_		
GAM2329	LOC219294	3'	AAACACTGTCAAGGATTTC	44684	GATT
			— TGAGATCTT CAGTGTTT		
			ACTTTAGGA GTCACAAA		
			ACT_		
GAM2329	LOC219300	5'	AAACACTGAACAACCTC	45287	ATC A
			— GAG TTG TTCAGTGTTT		
			CTC AAC AAGTCACAAA		
			C_ _		
GAM2329	LOC219919	5'	AAACACATATCAAGATCCA	44798	A TCA
			— TG GATCTTGAT GTGTTT		
			AC CTAGAACTA CACAAA		
			— TA_		
GAM2329	LOC254176	5'	AAACACATATCAAGATCCA	46473	A TCA
			— TG GATCTTGAT GTGTTT		
			AC CTAGAACTA CACAAA		
			— TA_		
GAM2329	LOC255327	5'	AAACACTGAAAAACATC	46021	C GA
			— GAT TT TTCAGTGTTT		
			CTA AA AAGTCACAAA		
			C A_		
GAM2329	LOC256594	5'	AAACACATATCAAGATCCA	46376	A TCA
			— TG GATCTTGAT GTGTTT		
			AC CTAGAACTA CACAAA		
			— TA_		
GAM2329	LOC51301	5'	AAACACTGTAGGGAACCTC	18668	A_ GATT
			— GAG TCTT CAGTGTTT		
			CTC AGGG GTCACAAA		
			CA AT_		
GAM2329	LOC90826	3'	AAACACTGAAAGGCTTC	32047	AT GAT
			— GAG CTT TCAGTGTTT		

		CTT GAA AGTCACAAA		
		CG ____		
GAM2329	LOC93206	3' AAACACTGACTCAATCTT	35514	CT T
		GAGAT TGA TCAGTGTTT		
		TTCTA ACT AGTCACAAA		
		__ C		
GAM2330	AF5Q31	5' GCCCCCGCCTGCCTCA	15778	TTGCCA
		TGAGGTAGGCGG	GGC	
		ACTCCGTCCGCC	CCG	
		C ____		
GAM2330	CENPB	3' TCTGCCTGCTTTCCACCTCCCC	34465	A T C TT_ C
	A	TG GG AGG GG GC AGGCAGA		
		AC CC TCC CC CG TCCGTCT		
		_ C A TTT _		
GAM2330	CSRP1	3' TCTGCCTGAGGTCCCACCCCA	10279	A A C GT GC
		TG GGT GG G T CAGGCAGA		
		AC CCA CC C G GTCCGTCT		
		C _ _ TG A_		
GAM2330	EPHA8	3' TCTGCCTGGGTGAGCCCAACCC	21750	A A GGTTG
	G	TG GGT GGC CCAGGCAGA		
		GC CCA CCG GGTCCGTCT		
		C C AGTG_		
GAM2330	GAD1	5' CTGCCCCCGCCTACCCCG	6480	A TTGCCA
		TG GG TAGGCGG	GGCAG	
		GC CCATCCGCC	CCGTC	
		C C ____		
GAM2330	HOXC9	3' CCTACCCAGCCTGCTGCCTCA	30719	GC CC_
		TGAGGTAG GGTTG AGG		
		ACTCCGTC CCGAC TCC		
		GT CCA		
GAM2330	KAI1	3' CTGCCTGGCCCCCAACCTCA	8012	A C TT
		TGAGGT GG GG GCCAGGCAG		
		ACTCCA CC CC CGGTCCGTC		
		A _ _		
GAM2330	PAX2	3' CTGCCTTGCCCCTACCTCA	10139	C TGCC
		TGAGGTAGG GGT AGGCAG		
		ACTCCATCC CCG TCCGTC		
		_ T ____		
GAM2330	PAX2	3' CTGCCTTGCCCCTACCTCA	10145	C TGCC
		TGAGGTAGG GGT AGGCAG		

			ACTCCATCC CCG TCCGTC		
			— T —		
GAM2330	PCTK1	3'	CTGCCTGCCCCACCTGCCTCA 26908	C TT C	
			TGAGGTAGG GG GC AGGCAG		
			ACTCCGTCC CC CG TCCGTC		
			A C _ _		
GAM2330	PCTK1	3'	CTGCCTGCCCCACCTGCCTCA 26914	C TT C	
			TGAGGTAGG GG GC AGGCAG		
			ACTCCGTCC CC CG TCCGTC		
			A C _ _		
GAM2330	PCTK1	3'	CTGCCTGCCCCACCTGCCTCA 12873	C TT C	
			TGAGGTAGG GG GC AGGCAG		
			ACTCCGTCC CC CG TCCGTC		
			A C _ _		
GAM2330	PDE4A	5'	CTGCCCGGCACCCCCTCCCCA 12875	A T C T A	
			TG GG AGG GG TGCC GGCAG		
			AC CC TCC CC ACGG CCGTC		
			_ C _ C C		
GAM2330	PFN2	3'	TCTACCTAGCAACTGTCTTC 27583	T C C	
			GG AGGCGGTTGC AGG AGA		
			CT TCTGTCAACG TCC TCT		
			_ A A		
GAM2330	PFN2	3'	TCTACCTAGCAACTGTCTTC 8489	T C C	
			GG AGGCGGTTGC AGG AGA		
			CT TCTGTCAACG TCC TCT		
			_ A A		
GAM2330	PIAS3	3'	TCTGCCTGACAAGGCCAGCACC 12745	A A _ GG C	
	CA		TG GGT GGC TTG CAGGCAGA		
			AC CCA CCG AAC GTCCGTCT		
			_ CGA G _ A		
GAM2330	PRSS8	5'	CTGCCTTCGACACCACCCA 8664	A A CG CC	
			TG GGT GG GTTG AGGCAG		
			AC CCA CC CAGC TCCGTC		
			C _ A _ T _		
GAM2330	SERPINB9	3'	CCTCAAGCAATCCGCCTACCTC 10363	_ C _	
	A		TGAGGTAGGCGG TTGC AGG		
			ACTCCATCCGCC AACG TCC		
			T AAC		
GAM2330	SKI	3'	GCCTTACTGCCGCCTACCCCG 8989	A TGCC	
			TG GGTAGGCGGT AGGC		

GC CCATCCGCCG TCCG
 C TCAT
 GAM2330 TAZ 3' TCTGCCTGAGCTTCCCCCCC 5588 TA C TT _
 GG GG GG GC CAGGCAGA
 || || || || |||||
 CC CC CC CG GTCCGTCT
 C_ _ TT A
 GAM2330 TIMM23 3' CTGCCCCGGCTGCCACCCC 30197 TA C T A
 GG GG GGT GCC GGCAG
 || || || || |||||
 CC CC CCG CGG CCGTC
 _ A T C
 GAM2330 C4orf6 5' CCTGCCAGCCTCCTACCTCA 12311 C C
 TGAGGTAGG GGTTG CAGG
 ||||| |||| ||||
 ACTCCATCC CCGAC GTCC
 T C
 GAM2330 DKFZP434K1772 3' GCCCAGCCCCTAGCCCCA 33633 A _ C CCA
 TG GGT AGG GGTTG GGC
 || || || |||| ||
 AC CCG TCC CCGAC CCG
 C A _ _
 GAM2330 DKFZP564D172 3' CCCGCACGCCTCCTCA 25750 T GT CA
 TGAGG AGGCG TGC GG
 |||| |||| || ||
 ACTCC TCCGC ACG CC
 _ _ C_
 GAM2330 ELF4 3' CTACCTGGCTCTATCTCA 7122 CGGTT C
 TGAGGTAGG GCCAGG AG
 ||||| |||| ||
 ACTCTATCT CGGTCC TC
 _ A
 GAM2330 FLJ10206 5' CTGCCTGGGACGGCCTACC 19767 G G
 GG TAGGC GTT CCAGGCAG
 ||||| || |||||
 CCATCCG CAG GGTCCGTC
 G _
 GAM2330 FLJ13710 3' CTGCCTCAGCCGCCTCCCCCA 24205 A T CC
 TG GG AGGCGGTTG AGGCAG
 || || ||||| |||||
 AC CC TCCGCCGAC TCCGTC
 C C _
 GAM2330 KIAA0022 3' CTGCCTGGTTTTCTACCCA 17027 A CGGTT
 TG GG TAGG GCCAGGCAG
 || |||| |||||
 AC CCATCC TGGTCCGTC
 _ TTT_
 GAM2330 KIAA0173 3' CTGCCTGGCTGGCACCTCA 16039 AG GGTT
 TGAGGT GC GCCAGGCAG
 |||| || |||||

ACTCCA CG CGGTCCGTC
 __ GT__
 GAM2330 KIAA0515 3' CCTACCAACAGCGCCACCCCA 31922 A A __ CC
 TG GGT GGCG GTTG AGG
 || ||| ||| |||
 AC CCA CCGC CAAC TCC
 C C GA CA
 GAM2330 KIAA0774 5' CCTAAACCATCTACCTCA 44090 GC GCC
 TGAGGTAG GGTT AGG
 ||||| ||| |||
 ACTCCATC CCAA TCC
 TA A__
 GAM2330 KIAA0819 3' CACCCGGTGCCTGCCTCA 31807 GGTT A CA
 TGAGGTAGGC GCC GG G
 ||||| ||| |||
 ACTCCGTCCG TGG CC C
 __ C AC
 GAM2330 KIAA1437 5' TCTGCCTGACCCAGCCACCCC 30387 TA C C__
 GG GG GGTTG CAGGCAGA
 || ||| |||||
 CC CC CCGAC GTCCGTCT
 __ A CCA
 GAM2330 MGC20470 3' CTGCCTGCTGACCCACCTG 29685 C_ GC
 TAGG GGTT CAGGCAG
 ||| ||| |||||
 GTCC CCAG GTCCGTC
 AC TC
 GAM2330 MGC4796 3' CTGCCTGGCCCTGCTCCCC 30831 TA TT
 GG GGCGG GCCAGGCAG
 || ||| |||||
 CC TCGTC CGGTCCGTC
 CC C_
 GAM2330 PRPF8 3' CTGCCTGGCCAGCTGCCCC 30681 TA _
 GG GGCGGTTG CCAGGCAG
 || ||||| |||||
 CC CCGTCGAC GGTCCGTC
 __ C
 GAM2330 RAB40C 3' CTGCCCATGCCTGCCCCA 22146 A GTTGCCA
 TG GG TAGGCG GGCAG
 || ||||| |||
 AC CCGTCCGT CCGTC
 C AC____
 GAM2330 RER1 3' CCGCCAGCCGCCTTCCCCA 13903 A T CCA
 TG GG AGGCGGTTG GG
 || || ||||| ||
 AC CC TCCGCCGAC CC
 C T CG_
 GAM2330 SDC3 3' TCTGCCTGGCAGGCCAACCTCA 16090 A GG
 TGAGGT GGC TTGCCAGGCAGA
 ||||| ||| |||||

ACTCCA CCG GACGGTCCGTCT
 A _
 GAM2330 LOC116411 5' CTGCCTGGCAACTGCCCC 36569 TA
 GG GGC GGTTGCCAGGCAG
 || |||||
 CC CCGTCAACGGTCCGTC
 —
 GAM2330 LOC129880 3' CTGCCTGATTCTCCTGCCTCA 36983 C TTGC
 TGAGGTAGG GG CAGGCAG
 ||||| || |||||
 ACTCCGTCC CT GTCCGTC
 T TA_
 GAM2330 LOC149422 3' CTTGGGCCGCCAGCCTCA 38744 A_ TG
 TGAGGT GGC GGTT CCAGG
 ||||| ||||| |||||
 ACTCCG CCGCCG GGTTT
 AC _
 GAM2330 LOC154043 3' CTGCCTGGCTCCTGCCCC 39459 TA TT
 GG GGC GG GCCAGGCAG
 || ||||| |||||
 CC CCGTC CGGTCCGTC
 _ CT
 GAM2330 LOC155382 3' TCTGCCAGCCGGCCCCCACCT 41766 A C _ CA
 C GAGGT GG GGTTG C GGCAGA
 ||||| || ||||| |||||
 CTCCA CC CCGGC G CCGTCT
 C _ C AC
 GAM2330 LOC158364 5' CTGCCTGGCCCCACCTC 39816 A CGGTT
 GAGGT GG GCCAGGCAG
 ||||| || |||||
 CTCCA CC CGGTCCGTC
 C _
 GAM2330 LOC170393 3' CTGCCTGGTCCTGCCACCTCA 40312 A TT
 TGAGGT GGC GG GCCAGGCAG
 ||||| ||||| |||||
 ACTCCA CCGTC TGGTCCGTC
 C C_
 GAM2330 LOC202868 5' CTGCCTGCCTGCCTGCCTCA 43449 TT C
 TGAGGTAGGCGG GC AGGCAG
 ||||| ||||| |||||
 ACTCCGTCCGTC CG TCCGTC
 — —
 GAM2330 LOC219649 3' CTGCCTGGGTCTCCTCCCTCA 44665 T C TTG
 TGAGG AGG GG CCAGGCAG
 ||||| ||||| |||||
 ACTCC TCC TC GGTCCGTC
 C _ TG_
 GAM2330 LOC253664 5' TCTGCCTGGCAACCTGATCTCG 45451 AGGC
 TGAGGT GGTTGCCAGGCAGA
 ||||| |||||

GCTCTA CCAACGGTCCGTCT
 GT__
 GAM2330 LOC256306 5' TCTGCCTGGCAGCCTAGCCTCA 46238 AGGC
 TGAGGT GGTGCCAGGCAGA
 ||||| |||||
 ACTCCG CCGACGGTCCGTCT
 AT__
 GAM2330 LOC90198 5' TCTGCCTGAGATCCCACCCCA 30959 A A C GC
 TG GGT GG GGTT CAGGCAGA
 || ||| ||| |||||
 AC CCA CC CTAG GTCCGTCT
 C _ _ A_
 GAM2330 LOC90249 3' CTGCCCGAACTCCCACCTC 31009 A C GCCA
 GAGGT GG GGTT GGCAG
 ||||| ||| |||
 CTCCA CC TCAA CCGTC
 _ C GC_
 GAM2330 LOC91064 5' GCTTGGTGACCTCCCTCA 32341 TA C TG
 TGAGG GG GGT CCAGGC
 ||||| ||| |||
 ACTCC CT CCA GGTTCCG
 _ _ GT
 GAM2330 LOC91355 5' CTGCCTGGGAGCCCCCCC 32703 TA C G
 GG GG GGTT CCAGGCAG
 || ||| |||||
 CC CC CCGA GGTCCGTC
 C_ _ G
 GAM2330 LOC92697 5' CTGCCTGATTCTCCTGCCTCA 34802 C TTGC
 TGAGGTAGG GG CAGGCAG
 ||||| || |||||
 ACTCCGTCC CT GTCCGTC
 T TA__
 GAM2330 LOC92697 5' CTGCCTGGCCACCACCCC 34803 TA C T
 GG GG GGT GCCAGGCAG
 || ||| |||||
 CC CC CCA CGGTCCGTC
 _ A C
 GAM2331 GPRC5B 3' ACCATCACATTTGGAAAGTGAT 18349 ACC C
 C GATCACT TCGGGTGTGA GGT
 ||||| ||||| |||
 CTAGTGA GGTTTACACT CCA
 AA_ A
 GAM2331 PGF 3' ACCGTCACACTCTTCAGTGA 8490 ACCTC
 TCACT GGGTGTGACGGT
 ||||| |||||
 AGTGA CTCACACTGCCA
 CTT__
 GAM2331 ORCTL3 3' ACCACCATCTGAGACAGGA 10442 A AC TGAC
 TC CT CTCGGGTG GGT
 || ||| ||||| |||

AG GA GAGTCTAC CCA
 _ CA CA_
 GAM2331 LOC202459 5' CCATCACACCCAGTGCTC 29815 T ACCTC C
 GA CACT GGGTGTGA GG
 || ||| ||||| ||
 CT GTGA CCCACACT CC
 C _ A
 GAM2332 HTR6 5' ACCCCAGGGAGCCCATCCGACC 6547 A CCT_ C
 TC GAGGTC GG CTCCC GGGGT
 ||||| || ||||| |||||
 CTCCAG CC GAGGG CCCCA
 _ TACCC A
 GAM2332 FLJ10043 3' GGGAGAGACTGACCTCA 19708 GC
 TGAGGTCAG CTCTCCC
 ||||| |||||
 ACTCCAGTC GAGAGGG
 A_
 GAM2332 FLJ20694 3' ACCCCAAAGAAAATGACTTCA 19605 GGCC CCCC
 TGAGGTCA TCT GGGGT
 ||||| || |||||
 ACTTCAGT AGA CCCCA
 AAA_ AA_
 GAM2332 KIAA0798 3' ACCCCGGGCGGTCCACCGCCT 16066 CA_ TCTC
 CA TGAGGT GGCC CCCGGGGT
 ||||| ||| |||||
 ACTCCG CTGG GGGCCCCA
 CCCAC C_
 GAM2332 KLK15 3' CCGGGGTACAAGAGGCCCAATC 28862 CA T_ CCGG
 TCA AGGT GGCCTC CC G
 ||| |||| || |
 TCTA CCGGAG GG C
 AC AACAIIT GGCC
 GAM2332 KLK15 3' CCGGGGTACAAGAGGCCCAATC 23264 CA T_ CCGG
 TCA AGGT GGCCTC CC G
 ||| |||| || |
 TCTA CCGGAG GG C
 AC AACAIIT GGCC
 GAM2332 Rpo1-2 3' ACCCTGTCTTAAAGACCCTGAC 21095 CC CCC_
 CTCA TGAGGTCAGG TCT CGGGGT
 ||||| || |||||
 ACTCCAGTCC AGA GTCCCA
 C_ AATTCT
 GAM2332 LOC121838 5' CCGGGGTAAAAGAAGCATGACC 37418 G C T_ CCGG
 TCA AGGTCA GC TC CC G
 ||||| || || || |
 TCCAGT CG AG GG C
 A A AAAAIIT GGCC
 GAM2332 LOC220739 3' ACCCCAGAAGCCCTGACCTCA 44654 _ C CCCC
 TGAGGTCAGG C TCT GGGGT
 ||||| || || |||||

		ACTCCAGTCC G AGA C C C C C A	
		C A _ _ _ _	
GAM2332	LOC222066 3'	CCGGGGTACAGAGACCTGACCT 44555	C T _ _ _ _ CCGG
	CA	GAGGTCAGG CTC CC G	
		CTCCAGTCC GAG GG C	
		A ACAIIT GGCC	
GAM2332	LOC254685 5'	ACCCCACTCCCGGCCTGACACC 46152	AG TCTCCCC
	A	TG GTCAGGCC GGGGT	
		AC CAGTCCGG C C C C A	
		CA CCCTCA _	
GAM2333	GLI2 5'	TGAAGTTCGTGGACTCCTACAA 24937	CCCG A C
	TA	TGTTGTAG TCAC AACT CA	
		ATAACATC GGTG TTGA GT	
		CTCA C A	
GAM2333	SLC19A2 3'	AGTTTGTGGCATAACAAC 34193	GCCC
		GTTGTA GTCACAAACT	
		CAACAT CGGTGTTTGA	
		A _ _ _	
GAM2333	FLJ11210 3'	GAATTTGTGACGAAAGCTG 29973	C _ _ C
		TAGC CGTCACAAA TC	
		GTCG GCAGTGTTT AG	
		AAA A	
GAM2333	FLJ22167 5'	TGGAGCCCATGCTGCCTACAGC 23744	CC T CAAA
	A	TGTTGTAG CG CA CTCCA	
		ACGACATC GT GT GAGGT	
		C _ C ACCC	
GAM2333	KIAA0285 3'	TGGAGTTTATAAACTGGACAAC 16755	AG C CAC _
		GTTGT CC GT AAACTCCA	
		CAACA GG CA TTTGAGGT	
		_ T AATA	
GAM2333	KIAA0635 5'	GAGTTGCCTGGGCTACAA 16057	TCACA
		TTGTAGCCCG AACTC	
		AACATCGGGT TTGAG	
		CCG _ _	
GAM2333	KIAA1656 3'	TGGAACTAAGGAGGCTACAGCA 32737	CG ACAAAC
		TGTTGTAGCC TC TCCA	
		ACGACATCGG AG AGGT	
		_ GAATCA	
GAM2333	LIG-1 3'	TGGAATTTATAGAGGCTACAAC 31956	CGTCAC C
		GTTGTAGCC AAA TCCA	

			CAACATCGG	TTT AGGT		
			AGATA_	A		
GAM2333	PFTK1	3'	AGTTTGCTTAGTTACAACA	14750	CCGTCA	
			TGTTGTAGC	CAAAC		
			ACAACATTG	GTTTGA		
			ATTC_			
GAM2333	LOC255565	5'	GGAGCGCCTGACGGGCCCAACA	45592	TA	CAAA
			TGTTG	GCCCGTCA	CTCC	
			ACAAC	CGGGCAGT	GAGG	
			C_	CCGC		
GAM2334	EIF3S10	3'	ACACAGAACTTGCTGCTGTGT	35499	CTTG	C
			AACACAGCA	AAGT	CTGTGT	
			TTGTGTCGT	TTCA	GACACA	
			CG_	A		
GAM2334	GJB3	3'	ACAGCCTGCTCCCAGTGCTGTG	23435	TGA	C_
	T		ACACAGCACT	AGT	CTGT	
			TGTGTCGTGA	TCG	GACA	
			CCC	TCC		
GAM2334	GNA15	5'	ACACAGGACCCAGTCTGC	30102	C_	AA
			GCA	TTG	GTCCTGTGT	
			CGT	GAC	CAGGACACA	
			CT	C_		
GAM2334	HIP1	3'	CACTGACCAAGTGCTG	11810	AA	CT
			CAGCACTTG	GTC	GTG	
			GTCGTGAAC	CAG	CAC	
			_	T_		
GAM2334	HIVEP3	5'	ACACAGGACCAGTTTGC	23697	C_	AA
			GCA	TTG	GTCCTGTGT	
			CGT	GAC	CAGGACACA	
			TT	_		
GAM2334	STK10	3'	ACACAGGACTTGGTCTGCTG	12612	CTTG	
			CAGCA	AAGTCCTGTGT		
			GTCGT	TTCAGGACACA		
			CTGG			
GAM2334	AKAP7	3'	ACACAGCTATCAAGTGCTAAGT	11252	AC	AGTC
	T		AAC	AGCACTTGA	CTGTGT	
			TTG	TCGTGAACT	GACACA	
			AA	ATC_		
GAM2334	AKAP7	3'	ACACAGCTATCAAGTGCTAAGT	18515	AC	AGTC
	T		AAC	AGCACTTGA	CTGTGT	

			TTG TCGTGAAC	T	GACACA	
			AA ATC_			
GAM2334	AKAP7	3'	ACACAGCTATCAAGTGCTAAGT	28905	AC	AGTC
		T	AAC AGCACTTGA CTGTGT			
			TTG TCGTGAAC	T	GACACA	
			AA ATC_			
GAM2334	BRD4	3'	ACACAGGACATCGTTGCTG	27772	CT	A
			CAGCA TGA GTCCTGTGT			
			GTCGT GCT CAGGACACA			
			T_ A			
GAM2334	C5orf7	3'	ACACAGGAAAGTCGTACTGTTC	31939	C	CACT AG_
			A ACAG TGA TCCTGTGT			
			C TGTC GCT AGGACACA			
			T AT_ GAA			
GAM2334	FLJ10081	3'	CACAGAATTAGGCTGTGTT	19721	A	TGA C
			AACACAGC CT AGT CTGTG			
			TTGTGTCTG GA TTA GACAC			
			_ _ _ A			
GAM2334	FLJ13491	5'	ACACAGGACTTGGCCATG	23885	CA	ACTTG
			CA GC AAGTCCTGTGT			
			GT CG TTCAGGACACA			
			AC G_			
GAM2334	FLJ21308	5'	ACACAGGACCTTTGGCCGCTCC	23877	C	AC TG _
			A AGC T AAG TCCTGTGT			
			C TCG G TTC AGGACACA			
			C CC GT C			
GAM2334	FLJ21918	3'	ACACAGGACCCTTAACCTTGC	24481	C_	A_
			GCA TTGA GTCCTGTGT			
			CGT AATT CAGGACACA			
			TTC CC			
GAM2334	FLJ22173	5'	ACACAGGGCAAAGTACTATG	24634	C C	GAA
			CA AG ACTT GTCCTGTGT			
			GT TC TGAA CGGGACACA			
			A A A_			
GAM2334	KIAA1155	3'	ACACCCATTTCAAGTGT	31193		CCT
			GCACTTGAAGT GTGT			
			TGTGAACTTTA CACA			
			CC_			
GAM2334	KIAA1560	3'	ACACAGAAATGTAGCTGTGTT	32098	_	TTGAAGTC
			AACACAGC AC CTGTGT			

		TTGTGTCG TG	GACACA	
		A TAAA_____		
GAM2334	KIAA1764	5' ACACAGGAGTTAGAAATGC	34351	C G_ G
		GCA TT AA TCCTGTGT		
		CGT AA TT AGGACACA		
		A GA G		
GAM2334	KIAA1936	5' ACACAGGAGCTGCAGTGCTGT	36362	TGA _
		ACAGCACT AG TCCTGTGT		
		TGTCGTGA TC AGGACACA		
		CG_ G		
GAM2334	LOC150605	5' ACACAGGACCCCTCAGCACACT	41227	CAC_ A__
	G	CAG TTGA GTCCTGTGT		
		GTC GACT CAGGACACA		
		ACAC CCC		
GAM2334	LOC157858	5' ACAGTCTCAGGTGCTGTGTT	41864	A TC
		AACACAGCACTTGA G CTGT		
		TTGTGTCGTGGACT C GACA		
		_ T_		
GAM2334	LOC254057	5' ACACAGGAGGCGGTGCTG	46341	T AAG
		CAGCACT G TCCTGTGT		
		GTCGTGG C AGGACACA		
		_ GG_		
GAM2334	LOC90485	3' ACACAGGGCTAAGACTGT	31552	CA GA
		ACAG CTT AGTCCTGTGT		
		TGTC GAA TCGGGACACA		
		A_ _		
GAM2335	CARPX	3' CCCCAAGCCTCATTCA	21396	GGAGTC
		TGAATGAGGTT GGGG		
		ACTTACTCCGA CCCC		
		A_____		
GAM2335	PLAB	5' CTGGGCCCCAACCTCATCCAA	32753	A A G
		TTG ATGAGGTTGG GTC GG		
		AAC TACTCCAACC CGG TC		
		C C G		
GAM2335	FLJ21916	3' CCCC GACTCCGCACCCCA	23379	A _
		TG GGT TGGAGTCGGGG		
		AC CCA GCCTCAGCCCC		
		C C		
GAM2335	FLJ23233	3' CCAGCGTTTCAACCTCATTCAA	24000	T G_
		TTGAATGAGGTTGGAG CG GG		

			AACTTACTCCAAC TTT GC CC		
			_ GA		
GAM2335	RNF8	3'	CCAGATGCCCACCTCATCAA 10094	A	T A G
			TTG ATGAGGT GG GTC GG		
			AAC TACTCCA CC TAG CC		
			C C G A		
GAM2335	LOC149461	3'	CCCCCGACCCACAGCTCA 38762	GT_	A
			TGAG TGG GTCGGGGG		
			ACTC ACC CAGCCCCC		
			GAC C		
GAM2335	LOC152018	3'	CCCTCCAACCTCCCCAA 41420	AAT	GTC
			TTG GAGGTTGGA GGG		
			AAC CTCCAACCT CCC		
			CCC _		
GAM2335	LOC164684	3'	CCTGTCTTCCCATCCTCATTCA 40160	T _	T
	A		TTGAATGAGG TGG AG CGGG		
			AACTTACTCC ACC TC GTCC		
			T CT T		
GAM2335	LOC203083	5'	CCCCAGCAACCTCAGCCAA 43477	AA	GAGTC
			TTG TGAGGTTG GGGG		
			AAC ACTCCAAC CCCC		
			CG GA_		
GAM2335	LOC254176	5'	CCCCAGCAACCTCAGCCAA 46474	AA	GAGTC
			TTG TGAGGTTG GGGG		
			AAC ACTCCAAC CCCC		
			CG GA_		
GAM2336	ATP8A2	3'	GCCCTTCTCGTTCTGTAAAGAA 44922	AC	_ CACGC
	A		TTTC TACAGAAC AG GGC		
			AAAG ATGTCTTG TC CCG		
			AA C TTC_		
GAM2336	KIAA0218	3'	GTGCTGTTGCACAGTGAAA 16517	ACAG	
			TTTCACT AACAGCAC		
			AAAGTGA TTGTCGTG		
			CACG		
GAM2336	KIAA0570	3'	TGCTGTTCTTTAGTGAAA 16255	C	
			TTTCACTA AGAACAGCA		
			AAAGTGAT TCTTGTCGT		
			T		
GAM2336	RHOBTB2	3'	GCACTGACCTGTAGTGAAA 30560	AA	CAC
			TTTCACTACAG CAG GC		

AAAGTGATGTC GTC CG
 CA A_
 GAM2336 LOC149910 3' CCATCTTGTGTTCTGTTATGAA 38826 CT G CGC_
 A TTTCA ACAGAACA CA GG
 |||| ||||| || ||
 AAAGT TGTCTTGT GT CC
 AT _ TCTA
 GAM2336 LOC151361 3' GCCACGCACCGGTTAGTGAGA 41330 CAGA AGCA_ C
 TTTCATA AC CG GGC
 ||||| || ||||
 AGAGTGAT TG GC CCG
 _ GCCAC A
 GAM2337 BAP1 3' CCATGGCCTCTGCCAG 11023 AACTCT C
 CTGGCAGAG GCCA GG
 ||||| |||| ||
 GACCGTCTC CGGT CC
 _ A
 GAM2337 FCN2 3' CCTGTGATCTCTGCCA 17951 ACTCTGC
 TGGCAGAGA CACGGG
 ||||| ||||
 ACCGTCTCT GTGTCC
 A_
 GAM2337 FCN2 3' CCTGTGATCTCTGCCA 17953 ACTCTGC
 TGGCAGAGA CACGGG
 ||||| ||||
 ACCGTCTCT GTGTCC
 A_
 GAM2337 STX1A 3' CCCCATGCTCCCTTCTCTGCCA 10945 CTCT CAC
 TGGCAGAGAA GC GGGG
 ||||| || ||||
 ACCGTCTCTT CG CCCC
 CCCT TA_
 GAM2337 BIKE 3' CCCCTCAAGAGTTTCTCACCAG 19040 CA GCCAC
 CTGG GAGAACTCT GGGG
 ||| ||||| ||||
 GACC CTCTTGAGA CCCC
 A_ ACT_
 GAM2337 BLR1 3' CCCCATTTCTAGAACATCCCTG 26774 A AC_ CCAC_
 CCAG CTGGCAG GA TCTG GGGG
 ||||| || ||||
 GACCGTC CT AGAT CCCC
 C ACA CTTTA
 GAM2337 BLR1 3' CCCCATTTCTAGAACATCCCTG 7445 A AC_ CCAC_
 CCAG CTGGCAG GA TCTG GGGG
 ||||| || ||||
 GACCGTC CT AGAT CCCC
 C ACA CTTTA
 GAM2337 CSEN 3' CCCCGTAGCCACTCTCTGCC 15089 ACTCT C
 GGCAGAGA GC ACGGGG
 ||||| || |||||

		CCGTCTCT	CG TGCCCC		
		CAC__ A			
GAM2337	CSMD1	3'	CTGGGCAAAGTCCTCTGCTAG 36191	A C A	
			CTGGCAGAG ACT TGCC CGG		
			GATCGTCTC TGA ACGG GTC		
			C A _		
GAM2337	FLJ20435	3'	CCCCACTCAGCACTCTGCCAG 19469	AACT CCAC	
			CTGGCAGAG CTG GGGG		
			GACCGTCTC GAC CCCC		
			AC__ TCA_		
GAM2337	MAD4	3'	CTGGGCAGAGTCCCCTGC 13170	AGA A	
			GCAG ACTCTGCC CGG		
			CGTC TGAGACGG GTC		
			CCC _		
GAM2337	MGC2721	3'	CCCCGGGGGATACCCTCTGCCAG 26463	AACTCTG A	
			CTGGCAGAG CC CGGGG		
			GACCGTCTC GG GCCCC		
			CCATA__ G		
GAM2337	NXN	3'	CCCCACTCAGCACTCTGCCAG 22808	AACT CCAC	
			CTGGCAGAG CTG GGGG		
			GACCGTCTC GAC CCCC		
			AC__ TCA_		
GAM2337	P2RXL1	3'	CCCCGTGGGGGTGCCTGTGCCA 11929	G A_ TG	
	G		CTGGCA AG ACTC CCACGGGG		
			GACCGT TC TGGG GGTGCCCC		
			G CG _		
GAM2337	TACTILE	3'	CCCCATGGCAGAACTCTGCTGG 12410	TG AAC C	
			C GCAGAG TCTGCCA GGGG		
			G CGTCTC AGACGGT CCCC		
			GT A__ A		
GAM2337	ZNF213	5'	CCCGCGCCGCTCTGCCAG 32463	AACTCT CA	
			CTGGCAGAG GC CGGG		
			GACCGTCTC CG GCCC		
			GC__ C_		
GAM2337	LOC257482	3'	CCCTCACAGAGTTTTCCACCA 45236	CA CCAC	
			TGG GAGAACTCTG GGG		
			ACC CTTTTGAGAC CCC		
			AC ACT_		
GAM2338	AQP1	3'	CATGATGGGAGGTGTGCCAG 5960	_ GG _	
			CTG CACACCT TA CATG		

		GAC GTGTGGA GT GTAC	
		C GG A	
GAM2338	B4GALT6	3' CATGTACCTCTGGTGTGTCAGG 30092	_ T__
	GA	TCCCTG CACACC GGTACATG	
		AGGGAC GTGTGG CCATGTAC	
		T TCT	
GAM2338	BCL2	3' CATGTATCACTGTAGAGGGA 6252	GC CC
		TCCCT ACA TGGTACATG	
		AGGGA TGT ACTATGTAC	
		GA C_	
GAM2338	CASR	5' CATGTGTCCCCACTGCAGGGA 5961	CACCT _
		TCCCTGCA GG TACATG	
		AGGGACGT CC GTGTAC	
		CACC_ T	
GAM2338	CERD4	3' TGCTGGTGTGTGCAGGGA 14351	_ TG
		TCCCTGCACAC C GTA	
		AGGGACGTGTG G CGT	
		T GT	
GAM2338	DGAT2	3' CATGCACCATTGCAGGGA 26289	CACC A
		TCCCTGCA TGGT CATG	
		AGGGACGT ACCA GTAC	
		T__ C	
GAM2338	IHPK3	5' TAGCAGACTGTGCAGGGA 27659	C_ G
		TCCCTGCACA CTG TA	
		AGGGACGTGT GAC AT	
		CA G	
GAM2338	IL17E	5' CATGTACCAGGTCAGTGCAG 23070	__
		CTGCAC ACCTGGTACATG	
		GACGTG TGGACCATGTAC	
		AC	
GAM2338	IL1RN	3' CATGGCAAGGACTGCAGGGA 6178	CA G A
		TCCCTGCA CCT GT CATG	
		AGGGACGT GGA CG GTAC	
		CA A _	
GAM2338	MBNL	5' CATGTACTTTTAAAGCAGGGA 22026	ACACCT
		TCCCTGC GGTACATG	
		AGGGACG TCATGTAC	
		AAATTT	
GAM2338	PDGFB	3' CATGTAAGGTTGTGCAGGG 8468	_ GG
		CCCTGCACA CCT TACATG	

GGGACGTGT GGA ATGTAC
T ____
GAM2338 PIK3R3 3' ACCAGCGGTGTGCAGGGA 30600 ____
TCCCTGCACACC TGGT
||||| |||
AGGGACGTGTGG ACCA
CG
GAM2338 PNUTL1 3' ACCGCTGTGGTGTGCCGGA 8546 T ____
TCCC GCACACC TGGT
||| ||||| |||
AGGG CGTGTGG GCCA
C TGTC
GAM2338 SFRP1 3' CATTTGAAAGGTGTGCTAG 8928 _ GG C
CT GCACACCT TA ATG
|| ||||| || |||
GA CGTGTGGA GT TAC
T AA T
GAM2338 TDGF1 3' CATCTGCGTGTGTGCAGGGA 9209 CTG C
TCCCTGCACAC GTA ATG
||||| ||| |||
AGGGACGTGTG CGT TAC
TG_ C
GAM2338 XK 3' GTTCAGGTGTATAGGGA 22061 C T
TCCCTG ACACCTGG AC
||||| ||||| ||
AGGGAT TGTGGACT TG
A _
GAM2338 C11orf11 5' CATGTACCTGATGCGG 44782 _ CCT
CTGCA CA GGTACATG
||||| || |||||
GGCGT GT CCATGTAC
A ____
GAM2338 DKFZP434E2135 3' GTATAGGCAGGTGTGAGGGA 25116 G ____
TCCCT CACACCTG GTAC
||||| ||||| |||
AGGGA GTGTGGAC TATG
_ GGA
GAM2338 EFA6R 3' CATGTGCTCAGTCTGCAGG 17623 C CT
CCTGCA AC GGTACATG
||||| || |||||
GGACGT TG TCGTGTAC
C AC
GAM2338 FLJ10829 3' CATGACCGATGCAGGGA 20179 CACC A
TCCCTGCA TGGT CATG
||||| ||| |||
AGGGACGT GCCA GTAC
A____ _
GAM2338 FLJ11608 3' CATGAATAAGGTGCCAGG 23776 CA G A
CCTG CACCT GT CATG
||| ||||| || |||

GGAC GTGGA TA GTAC
C_ A A
GAM2338 FLJ20073 3' CATGTGCTTGGA CTCAAGGA 19164 C CACA T
TCC TG CC GGTACATG
||| || || |||||
AGG AC GG TCGTGTAC
A TCAC T
GAM2338 FLJ20274 3' CATGTGCTGCTGTTGCAAAGA 31385 CC _ CCT
TC TGCA CA GGTACATG
|| ||| || |||||
AG ACGT GT TCGTGTAC
AA T CG_
GAM2338 GABARAPL3 3' CATGTATCAGGACAGAGA 26297 C CACA
TC CTG CCTGGTACATG
|| ||| |||||
AG GAC GGA CTATGTAC
A A_
GAM2338 GMPPB 5' ACTGGTGGGCTGCAGGGA 45809 _ T
TCCCTGCA CACC GGT
||||| ||| |||
AGGGACGT GTGG TCA
CGG _
GAM2338 KIAA0143 3' CATGTATTGCATGTAAAGG 32350 GC CC
CCT ACA TGGTACATG
||| ||| |||||
GGA TGT GTTATGTAC
AA AC
GAM2338 KIAA0161 3' CATGGCAGCAGGATGCAGGGA 16429 CA GTA_
TCCCTGCA CCTG CATG
||||| ||| |||
AGGGACGT GGAC GTAC
A_ GACG
GAM2338 KIAA0495 3' TGTGCAAATGTGCAGGGA 31367 CCTG
TCCCTGCACA GTACA
||||| |||
AGGGACGTGT CGTGT
AAA_
GAM2338 KIAA0542 3' CATCTGCAGTGTGTCAGG 32858 _ CTG C
CCTG CACAC GTA ATG
||| ||| ||| |||
GGAC GTGTG CGT TAC
T A_ C
GAM2338 KIAA0774 5' CATGTACTGCAGGTGTGCAGTG 44089 C _
A TC CTGCACACCTG GTACATG
|| ||||| |||||
AG GACGTGTGGAC CATGTAC
T GT
GAM2338 KIAA1223 3' CATGTACTGTTGATGAGG 35244 G _ CCT
CCT CA CA GGTACATG
||| ||| |||||

		GGA GT GT TCATGTAC		
		_ A TG_		
GAM2338	LHPP	3' CATGCCCCGGTGTGTGCAGG	22673	_ TA
		CCTGCACAC CTGG CATG		
		GGACGTGTG GGCC GTAC		
		T C_		
GAM2338	MGC14161	5' CATGTAAGGACGTGTCAGG	26719	_ A_ GG
		CCTG CAC CCT TACATG		
		GGAC GTG GGA ATGTAC		
		T CA _		
GAM2338	NECL1	3' CATGCAGCCATGCAGGGA	22164	CACC A_
		TCCCTGCA TGGT CATG		
		AGGGACGT ACCG GTAC		
		_ AC		
GAM2338	PRRG1	3' CATGTTATGCTAGGTGCACA	6652	CA _
		TG CACCTGGT ACATG		
		AC GTGGATCG TGTAC		
		AC TAT		
GAM2338	SEC14L1	3' TGTGTGCCCGTGCAGGGA	8908	ACCT
		TCCCTGCAC GGTACATG		
		AGGGACGTG CCGTGTGT		
		CC_		
GAM2338	SFXN5	3' GTGTGAGGGTGCAGGGA	29387	A GG
		TCCCTGCAC CCT TAC		
		AGGGACGTG GGA GTG		
		_ GT		
GAM2338	UNC5D	3' CATGAGGTGGTGTGCAGAGG	28111	_ TGGTA
		CC CTGCACACC CATG		
		GG GACGTGTGG GTAC		
		A TGA_		
GAM2338	LOC122553	3' CATGTATTTGTGTGACAGGGA	36688	_ CT
		TCCCTG CACAC GGTACATG		
		AGGGAC GTGTG TTATGTAC		
		A T_		
GAM2338	LOC126823	5' CATGCACCGAACTGCGGGGA	36864	CACC A
		TCCCTGCA TGGT CATG		
		AGGGGCGT GCCA GTAC		
		CAA_ C		
GAM2338	LOC132338	5' TGTTTCAGATGTGCAGGGA	37368	C T
		TCCCTGCACA CTGG ACA		

AGGGACGTGT GACT TGT
 A T
 GAM2338 LOC146774 3' CATGTACCAGGTGTCCCAG 38233 C_
 CTG ACACCTGGTACATG
 ||| |||||
 GAC TGTGGACCATGTAC
 CC
 GAM2338 LOC149577 3' CATGCACTTCTGCAGGGG 41021 CACCT A
 TCCCTGCA GGT CATG
 ||||| ||| |||
 GGGGACGT TCA GTAC
 CT__ C
 GAM2338 LOC158288 5' CATGTGGCTCGTGCTGGGA 41928 T ACCT _
 TCCC GCAC GGT ACATG
 ||| ||| ||| |||
 AGGG CGTG TCG TGTAC
 T C__ G
 GAM2338 LOC163231 5' CATGTACCAAATGCAGGG 40098 CACC
 CCCTGCA TGGTACATG
 ||||| |||||
 GGGACGT ACCATGTAC
 AA__
 GAM2338 LOC255742 5' ACTTAGTGTGTGCAGAGA 46054 C _ _
 TC CTGCACAC CTG GT
 || ||||| ||| ||
 AG GACGTGTG GAT CA
 A T T
 GAM2338 LOC85414 3' CATGCACTGGAATGCGGGGA 26948 CAC TG A
 TCCCTGCA C GT CATG
 ||||| | ||| |||
 AGGGGCGT G CA GTAC
 AA_ GT C
 GAM2338 LOC90268 5' CATGTACCGTGCTGCAG 31040 _ CT
 CTGCA CAC GGTACATG
 ||||| ||| |||||
 GACGT GTG CCATGTAC
 C _
 GAM2338 LOC91801 3' CATGTGTTCCGTGAGGGA 29008 G ACCT _
 TCCCT CAC GG TACATG
 ||||| ||| || |||||
 AGGGA GTG CC GTGTAC
 _ ____ TT
 GAM2339 KCN15 3' AGCTGTGCTCTGGACAGTGTTTC 8030 A C _ TT
 TCA TGA AACAC GTCCGGAG AC CT
 ||| ||||| ||||| || ||
 ACT TTGTG CAGGTCTC TG GA
 C A G TC
 GAM2339 PEA15 3' AGAAGTTAACTACAGTGTTTTTC 9846 C CCGGA
 GAAAACAC GT GACTTCT
 ||||| || |||||

			CTTTTGTG CA TTGAAGA	
			A TCAA_	
GAM2339	SFRS2IP	5'	AGAAGTCTCCTTTCTGTTTCA 11084	A CCGTCC
			TGAAA CA GGAGACTTCT	
			ACTTT GT CCTCTGAAGA	
			_ CTTT_	
GAM2339	SURF6	3'	AGAAGTCTTAAGATATTTC 13609	ACACC CG
			TGAAA GTC GAGACTTCT	
			ACTTT TAG TTCTGAAGA	
			A_ AA	
GAM2339	UBE2V1	3'	AGAAGTTTTAAACAGGGCTTTC 22519	ACA GTCCG
	A		TGAAA CC GAGACTTCT	
			ACTTT GG TTTTGAAGA	
			CG_ ACAA	
GAM2339	UBE2V1	3'	AGAAGTTTTAAACAGGGCTTTC 22766	ACA GTCCG
	A		TGAAA CC GAGACTTCT	
			ACTTT GG TTTTGAAGA	
			CG_ ACAA	
GAM2339	UBE2V1	3'	AGAAGTTTTAAACAGGGCTTTC 9367	ACA GTCCG
	A		TGAAA CC GAGACTTCT	
			ACTTT GG TTTTGAAGA	
			CG_ ACAA	
GAM2339	BLZF1	5'	AGAAGTCTTGGAGTGCATTTTC 9748	_ CG G
	A		TGAAAA CAC TCCG AGACTTCT	
			ACTTTT GTG AGGT TCTGAAGA	
			AC _ _	
GAM2339	KIAA0217	3'	AAGCCTCCAGATGTTTTC 33275	CCG C A
			TGAAAACA TC GGAG CTT	
			ACTTTTGT AG CCTC GAA	
			_ A C	
GAM2339	MCF2L	3'	CTCTGGACGGTGCTTTC 30507	A
			TGAAA CACCGTCCGGAG	
			ACTTT GTGGCAGGTCTC	
			C	
GAM2339	LOC116028	3'	AGAAGTCTCATGTTGCATTTTC 36491	CAC TCCG
			GAAAA CG GAGACTTCT	
			CTTTT GT CTCTGAAGA	
			AC_ TGTA	
GAM2339	LOC149013	3'	AGAAGTCTCCACCTGGTCTTC 38631	AAC TCC
			GAA ACCG GGAGACTTCT	

		CTT TGGT CCTCTGAAGA	
		C__ CCA	
GAM2340 KAL1	3'	ACACCCAAGCCAGAGGA	T AG AAACA
		ACTCA 5714	
		TGAGTTC CT GG GGTGT	
		ACTCAAG GA CC CCACA	
		_ GA GAAC_	
GAM2340 PDGFRB	3'	GTTCCCCCAGGGA	A A
		ACTCA 32816	
		TGAGTTCTCT GGG AAC	
		ACTCAAGGGA CCC TTG	
		C C	
GAM2340 PRY	5'	ACACCCACCTCTAAGG	C AAACA
		ACTCA 30233	
		TGAGTTCT TAGGG GGTGT	
		ACTCAGGA ATCTC CCACA	
		_ CAC__	
GAM2340 WNT8B	3'	ACACCTAGGTCTGAGA	TAG AAC
		ACTCA 29982	
		TGAGTTCTC GGA AGGTGT	
		ACTCAAGAG TCT TCCACA	
		_ GGA	
GAM2340 DKFZP547L112	5'	ACACCTGCACTAGAGA	GGAAA
		ACTCA 33054	
		GTTCTCTAG CAGGTGT	
		CAAGAGATC GTCCACA	
		AC__	
GAM2340 FLJ20694	3'	ACACCTGTCTAGGTGA	TC TAG_ AA
		ACTCA 19604	
		TGAGT TC GGA CAGGTGT	
		ACTCA AG TCT GTCCACA	
		GA TGGA _	
GAM2340 KIAA1169	3'	TGTTTCCTAGAAAACCCA	A C G
		ACTCA 19567	
		TG GTT TCTAGG AAACA	
		AC CAA AGATCC TTTGT	
		C A _	
GAM2340 KIAA1817	3'	ACACCTGTCCCCCTTCCCA	A CTCT_ AA
		ACTCA 33860	
		TG GTT AGGG ACAGGTGT	
		AC CAA TCCC TGTCCACA	
		_ CCCCT CC	
GAM2340 LHFPL2	3'	ACACCTGTTTACAAAAAGA	G CTAGGG
		ACTCA 34657	
		TGA TTCT AAACAGGTGT	
		ACT AAGA TTTGTCCACA	
		_ AAAACA	
GAM2340 NR2F1	3'	GTCCCCCTAGAGACTCA	T AA
		ACTCA 45915	
		TGAGT CTCTAGGG AC	

			ACTCA GAGATCCC TG	
			— CC	
GAM2340	LOC159160	5'	ACACCCACCTCTAAGGACTCA 30357	C AAACA
			TGAGTTCT TAGGG GGTGT	
			ACTCAGGA ATCTC CCACA	
			— CAC__	
GAM2341	ADCY6	3'	CATGCCAGCACTTGAAGTGA 21973	CA A_
			CAGTTTAAG CTG ATG	
			GTCAAGTTC GAC TAC	
			AC CG	
GAM2341	ADCY6	3'	CATGCCAGCACTTGAAGTGA 17585	CA A_
			CAGTTTAAG CTG ATG	
			GTCAAGTTC GAC TAC	
			AC CG	
GAM2341	ADH4	5'	TGATACACAAGCTTAAAT 6322	AC AA
			GTTTAAGC TG TGTATCA	
			TAAATTCG AC ACATAGT	
			A_ _	
GAM2341	CNTN3	3'	TTGATATAAATGTTCTTAAACT 33134	C TGAA
			AGTTTAAG AC TGTATCAA	
			TCAAATTC TG ATATAGTT	
			T TAA_	
GAM2341	DAPP1	3'	TGATAGAAAGTGCTTAAAC 15733	GAATG
			GTTTAAGCACT TATCA	
			CAAATTCGTGA ATAGT	
			AAG__	
GAM2341	ITGA6	3'	TTGATACATTTTTGTACTAACT 5705	TAA CT
			AGTT GCA GAATGTATCAA	
			TCAA TGT TTTACATAGTT	
			TCA T_	
GAM2341	PCK1	3'	ATATTGTGCTTAAATT 30116	TG
			AGTTTAAGCAC AATGT	
			TTAAATTCGTG TTATA	
			—	
GAM2341	TDG	3'	TTGATACTCTCATTTAAACTG 9207	CAC AT
			CAGTTTAAG TGA GTATCAA	
			GTCAAATTT ACT CATAGTT	
			__ CT	
GAM2341	ZNF80	3'	ACGTCAGAGAACTTAAACTG 13984	CA__ A
			CAGTTTAAG CTGA TGT	

		GTCAAATTC GACT GCA	
		AAGA _	
GAM2341	BTN2A2	3' TGAGGCTTTTCAGACTTAAACTG 13860	CA T A
		CAGTTTAAG CTGAA GT TCA	
		GTCAAATTC GACTT CG AGT	
		A_ T G	
GAM2341	FLJ20288	5' GATAACCCAGTGCTTAAA 23972	AATG
		TTTAAGCACTG TATC	
		AAATTCGTGAC ATAG	
		CCA_	
GAM2341	KIAA1086	3' ACATTTGTGCTTAAATTG 35010	T
		CAGTTTAAGCAC GAATGT	
		GTTAAATTCGTG TTTACA	
		-	
GAM2341	KIAA1600	3' TTGATATATGAGTATTTAAACT 35396	C GA
		AGTTTAAG ACT ATGTATCAA	
		TCAAATTT TGA TATATAGTT	
		A G_	
GAM2341	PDE3A	3' TGATACATCCTGCCAACACTG 6633	TTAA CT A
		CAGT GCA GA TGTATCA	
		GTCA CGT CT ACATAGT	
		CAAC C_ _	
GAM2341	RHOBTB1	3' TGAGTTTTCAGTGTTAAACT 43954	G TGTA
		AGTTTAA CACTGAA TCA	
		TCAAATT GTGACTT AGT	
		_ TTG_	
GAM2341	USP25	3' TTGATACAGCGTCGCCAAAACT 15050	AA _ TGAA
		AGTTT GC AC TGTATCAA	
		TCAA CG TG ACATAGTT	
		AC C CG_	
GAM2341	LOC147077	3' GGTGCAGCACTTAAACTG 38291	CAC AA
		CAGTTTAAG TG TGTATC	
		GTCAAATTC AC ACGTGG	
		_ G_	
GAM2341	LOC153077	3' TTGATACATTCTCACAAAC 41572	AAGCACT
		GTTT GAATGTATCAA	
		CAAA CTTACATAGTT	
		CACT_	
GAM2341	LOC255177	3' TTGATACATTATTATAAACT 46204	AGCACTG
		AGTTTA AATGTATCAA	

			TCAAAT	TTACATAGTT		
			ATTA__			
GAM2341	LOC92379	3'	TTGACACATTTCAGTAACT	34269	TAAGC	A
			AGTT ACTGAATGT TCAA			
			TCAA TGACTTACA AGTT			
			_____ C			
GAM2342	ALDH3A2	5'	CTCGGCTCCCCGCACTGCT	34341	ATA GT T	
			AGCAGTGC GA GCC GG			
			TCGTCACG CT CGG TC			
			CC_ _ C			
GAM2342	MAP3K14	3'	CTTCAGGCCCCAGCACTGC	10092	ATAGAGT	
			GCAGTGC GCCTGGAG			
			CGTCACG CGGACTTC			
			ACC_____			
GAM2342	MEN1	5'	TCCAGCCCTGCACTGC	44848	TAGA T C	
			GCAGTGCA G GC TGGA			
			CGTCACGT C CG ACCT			
			_____ C _			
GAM2342	NEO1	3'	CTCCAGGCATGGCCACCTGC	8315	_ CATAGA	
			GCAG TG GTGCCTGGAG			
			CGTC AC TACGGACCTC			
			C CGG_____			
GAM2342	ADMP	3'	TCTTCTCTATGCACTCTT	29659	C TGCCT	
			AAG AGTGCATAGAG GGA			
			TTC TCACGTATCTC TCT			
			_ T_____			
GAM2342	BRD4	3'	CTCCAGACACAATGGCACTGCT	27776	A GA C	
	T		AAGCAGTGC TA GTG CTGGAG			
			TTCGTCACG GT CAC GACCTC			
			_ AA A			
GAM2342	DKFZP434B205	3'	CTCCAGGCACCTCGCCCCACGGC	37126	A CATA _	
			GC GTG GAG TGCCTGGAG			
			CG CAC CTC ACGGACCTC			
			G CCG_ C			
GAM2342	DKFZp547O146	5'	CCAGGCACCCCTCTTTTTACT	21482	CAT ____	
			AGTG AGA GTGCCTGG			
			TCAT TCT CACGGACC			
			TTT CCC			
GAM2342	FLJ10781	5'	CTCCAGGCAGGAAGCAGTGC	20135	G ATAGAG	
			GCA TGC TGCCTGGAG			

		CGT ACG ACGGACCTC	
		G AAGG__	
GAM2342	FLJ12387	3' CCCGGCCTTATGCACTGC 23101	A T T
		GCAGTGCAT GAG GCC GG	
		CGTCACGTA TTC CGG CC	
		_ _ C	
GAM2342	FLJ14810	3' CCAGGCACCCTCTGCCCTGC 26633	T T A
		GCAG GCA AG GTGCCTGG	
		CGTC CGT TC CACGGACC	
		C C C	
GAM2342	FLJ22059	5' CCAGGCACCTACCGCTGC 22975	CA A
		GCAGTG TAG GTGCCTGG	
		CGTCGC ATC CACGGACC	
		C_ _	
GAM2342	FLJ23462	3' CTCCAAACACTCCTCTAAGCAC 24265	A ____ CC
	T	AGTGC TAGA GTG TGGAG	
		TCACG ATCT CAC ACCTC	
		A CCT AA	
GAM2342	HZFW1	3' CCAACCTCCTATGACTGCTT 24915	G _ TGCC
		AAGCAGT CATAG AG TGG	
		TTCGTCA GTATC TC ACC	
		_ C CA__	
GAM2342	KIAA0014	3' CCAGGCACTCACGCCTCTT 16113	C T ATA
		AAG AG GC GAGTGCCTGG	
		TTC TC CG CTCACGGACC	
		_ _ CA_	
GAM2342	KIAA0237	3' CTCCAGGCACCCACCTGC 16445	_ CATAGA
		GCAG TG GTGCCTGGAG	
		CGTC AC CACGGACCTC	
		C C_____	
GAM2342	KIAA0514	3' CCTTTTCTCCATGCATTGCT 16206	A TGCCT
		AGCAGTGCAT GAG GG	
		TCGTTACGTA CTC CC	
		C TTTT_	
GAM2342	KIAA0672	5' CCAGGCATTGCTCTGC 16918	T TAGA
		GCAG GCA GTGCCTGG	
		CGTC CGT TACGGACC	
		T _____	
GAM2342	KIAA1196	3' CTCCAGGCCTGCCCCACT 30821	CA AGT
		AGTG TAG GCCTGGAG	

		TCAC GTC CGGACCTC	
		CC ____	
GAM2342 KIAA1468	3'	CTCCAAAGATATTTGCACTGCT 44098	TAGAGTGCC
	T	AAGCAGTGCA TGGAG	
		TTCGTCACGT ACCTC	
		TTATAGAA_	
GAM2342 KIAA1762	3'	CTCCAGGGACAGGCACTGC 31911	ATAGA G
		GCAGTGC GT CCTGGAG	
		CGTCACG CA GGACCTC	
		GA__ G	
GAM2342 LGI3	3'	CTCCAGGCATTGTTTACCTGCT 29277	TGCATAG
		AGCAG AGTGCCTGGAG	
		TCGTC TTACGGACCTC	
		CATTG_	
GAM2342 MGC13170	5'	TCCAGACACTCTGCTGTTT 26434	GCAT C
		AAGCAGT AGAGTG CTGGA	
		TTTGTCTG TCTCAC GACCT	
		____ A	
GAM2342 RI58	3'	CTCCAGGAAGAGTTAAGCACTG 14795	A AGTG_
	CTT	AAGCAGTGCT TAG CCTGGAG	
		TTCGTCACG ATT GGACCTC	
		A GAGAA	
GAM2342 SP329	5'	CTCCAGCTCACACAACACTGCT 25096	CATAGA C_
	T	AAGCAGTG GTG CTGGAG	
		TTCGTCAC CAC GACCTC	
		AACA__ TC	
GAM2342 UBCE7IP5	3'	CCAGGCACAGAGCTGCCTGCT 17270	T TAGA_
		AGCAG GCA GTGCCTGG	
		TCGTC CGT CACGGACC	
		_ CGAGA	
GAM2342 LOC123591	5'	CTCCAGGCCCGCACGTGCT 37252	_ ATAGAGT
		AGCA GTGC GCCTGGAG	
		TCGT CACG CGGACCTC	
		G CCC____	
GAM2342 LOC145371	3'	CCAGGCACGCCACCTGCT 37845	_ CATAGA
		AGCAG TG GTGCCTGG	
		TCGTC AC CACGGACC	
		C CG____	
GAM2342 LOC149478	5'	CTCCTCACCTACGCACCGC 38752	A A A CCT
		GC GTGC TAG GTG GGAG	

CG CACG ATC CAC CCTC
C C C T__

GAM2342 LOC152762 3' CTCTTCCGCTCTCTGCACTGCT 39306 T CCT
T AAGCAGTGCA AGAGTG GGAG
||||||| ||||| ||||
TTCGTCACGT TCTCGC TCTC
C CT_

GAM2342 LOC153516 3' CCAGGCACTGCACAGC 28841 A TAGA
GC GTGCA GTGCCTGG
|| |||| | |||||
CG CACGT CACGGACC
A ____

GAM2342 LOC163412 5' CTCCAGGCCCTGGACACCCTGC 39952 __ CA AGT
GCA GTG TAG GCCTGGAG
||| ||| ||| |||||
CGT CAC GTC CGGACCTC
CC AG C__

GAM2342 LOC222182 3' CCAGTCCTTCTGCACTGCT 45196 TA TG C
AGCAGTGCA GAG C TGG
||||||| ||| | |||
TCGTCACGT TTC G ACC
CC CT_

GAM2343 CDT6 5' CAGAGTGAAAGCGTAAGGTT 22119 A CGGG
AACCTTAC CT GCTCTG
||||||| || |||||
TTGGAATG GA TGAGAC
C AAG_

GAM2343 P114-RHO-GEF 3' CAGAGCCCCACGCAGGTTTAC 17637 A TACACTC
GT AACCT GGGGCTCTG
|| |||| | |||||
CA TTGA CCCCAGAGAC
C CGCA__

GAM2343 ZFD25 5' CAGAGTAATATATAGGGTTTAC 18321 CACTCGGG
GTAAACCTTA GCTCTG
||||||| |||||
CATTTGGGAT TGAGAC
ATATAA__

GAM2343 LOC151414 3' AGCTCAAGTGTAAGATTTAT 39107 C CG
GTAAA CTTACACT GGGCT
||||| ||||| |||||
TATTT GAATGTGA CTCGA
A A_

GAM2343 LOC90550 3' AGGAAGATGTAAGGTTTAC 36176 C GGGG T
GTAAACCTTACA TC C CT
||||||| || | |||
CATTTGGAATGT AG G GA
_ AA__

GAM2344 DAPP1 3' ATAGAAAGTGCTTAAAC 15730 C TC
GTTTAAGCAC TTT AT
||||||| ||| ||

CAAATTCGTG AAA TA
 _ GA
 GAM2344 FLJ23189 3' GGTCATGGGGGCAATCTTAAAC 24657 CACC TT
 GTTTAAG TT CATGACC
 ||||| || |||||
 CAAATTC GG GTACTGG
 TAAC GG
 GAM2344 KIAA0063 3' TATGCAAAGACGCTTAAAC 17017 AC T
 GTTTAAGC CTTT CATG
 ||||| ||| |||
 CAAATTCG GAAA GTAT
 CA C
 GAM2344 KIAA0802 5' GGCAAGGTGCTCAAACCTG 31351 A T
 TAGTTT AGCACCTT TC
 ||||| ||||| ||
 GTCAAA TCGTGGAA GG
 C C
 GAM2344 KIAA1560 3' ATGGAAGGTATTAAACTA 32101 GC T
 TAGTTTAA ACCTTT CAT
 ||||| ||||| |||
 ATCAAATT TGAAG GTA
 A_ _
 GAM2344 SLC25A21 3' GGTCTAGAAATGCTTAAACTA 24967 CCT AT
 TAGTTTAAGCA TTTC GACC
 ||||| ||| |||
 ATCAAATTCGT AAAG CTGG
 _ AT
 GAM2345 ETV3 3' AACCACAGATAGTACCA 11750 CAT AC
 TGG CTATCTGT GGTT
 || ||||| |||
 ACC GATAGACA CCAA
 AT_ _
 GAM2345 NR5A2 3' AACTCACAGATGGATACCA 9912 C AC
 TGG ATCTATCTGT GGTT
 || ||||| |||
 ACC TAGGTAGACA TCAA
 A C_
 GAM2345 UCP3 3' AACCAAGATAGATCCA 9383 C GTAC
 TGG ATCTATCT GGTT
 || ||||| |||
 ACC TAGATAGA CCAA
 _ A_
 GAM2345 DKFZp762K2015 3' AGCAGAAGATAGATGCCA 35884 GTACG
 TGGCATCTATCT GTT
 ||||| |||
 ACCGTAGATAGA CGA
 AGA_
 GAM2345 FLJ13340 3' AACTGGGACATATAGATACCA 27703 C C A_
 TGG ATCTAT TGT CGGTT
 || ||||| ||| |||||

		ACC TAGATA ACA GTCAA	
		A T GG	
GAM2345 HTEX4	5'	AGTAACCACAAATTGCCA 44215	TCTATC AC
		TGGCA TGT GGTTACT	
		ACCGT ACA CCAATGA	
		TAA__ _	
GAM2345 HTEX4	5'	AGTAACCACAAATTGCCA 46651	TCTATC AC
		TGGCA TGT GGTTACT	
		ACCGT ACA CCAATGA	
		TAA__ _	
GAM2345 HTEX4	5'	AGTAACCACAAATTGCCA 46720	TCTATC AC
		TGGCA TGT GGTTACT	
		ACCGT ACA CCAATGA	
		TAA__ _	
GAM2345 KIAA0907	3'	AGCTAAACAACAGATGCCA 17275	ATC AC
		TGGCATCT TGT GGTT	
		ACCGTAGA ACA TCGA	
		CA_ AA	
GAM2345 TBDN100	3'	AACTGGGACATATAGATACCA 24692	C C A_
		TGG ATCTAT TGT CGGTT	
		ACC TAGATA ACA GTCAA	
		A T GG	
GAM2345 TU3A	3'	AACTGCCACAGATAGCTGCCA 14031	T A_
		TGGCA CTATCTGT CGGTT	
		ACCGT GATAGACA GTCAA	
		C CC	
GAM2345 ZNF-U69274	3'	TAACCATGAGAGATGCCA 15761	A TGTAC
		TGGCATCT TC GGTTA	
		ACCGTAGA AG CCAAT	
		G TA__	
GAM2345 LOC201627	3'	AACAGTAGCAAAAGATGCCA 42893	ATC _ G
		TGGCATCT TGT AC GTT	
		ACCGTAGA ACG TG CAA	
		AA_ A A	
GAM2345 LOC255777	5'	GAGTTCACAGAAACAGATGCCA 46041	A_ ACGGTT
		TGGCATCT TCTGT ACTC	
		ACCGTAGA AGACA TGAG	
		CAA CT__	
GAM2346 AQP6	5'	GGGCAGCTGCAGGCCACAGTG 27616	CA A_ T C
		CACTG GG TGT GGC GCCC	

			GTGAC CC ACG TCG CGGG		
			A_ GG _ A		
GAM2346	ARHGAP6	3'	GGCCCACCCTGCGGTG 6846	AT T	
			CACTGCAGG GT GGCC		
			GTGGCGTCC CA CCGG		
			_ C		
GAM2346	CHI3L1	3'	GGAGCCAAACATCCTACA 6942	C _ CG	
			TG AGGATGTT GGC CC		
			AC TCCTACAA CCG GG		
			A A A_		
GAM2346	COL6A3	3'	CGGGAGGGAACATCCTGC 27671	GG GC	
			GCAGGATGTT CC CCCG		
			CGTCCTACAA GG GGGC		
			G_ A_		
GAM2346	COL6A3	3'	CGGGAGGGAACATCCTGC 10587	GG GC	
			GCAGGATGTT CC CCCG		
			CGTCCTACAA GG GGGC		
			G_ A_		
GAM2346	CXX1	5'	GGCCCGCCCTGCAGTG 10024	AT T	
			CACTGCAGG GT GGCC		
			GTGACGTCC CG CCGG		
			_ C		
GAM2346	DDX20	5'	CGGGGCGGTGCCCCCACC GCA 14067	A A TT _	
			TGC GG TG GGC CGCCCCG		
			ACG CC AC CCG GCGGGGC		
			_ _ CC TG		
GAM2346	DVL1	3'	GGGGCAACCCCCTGCGGTG 29843	AT GGCC	
			CACTGCAGG GTT GCCCC		
			GTGGCGTCC CAA CGGGG		
			CC _ _		
GAM2346	GGT2	5'	CGGGACGGTGGCTCTGCAGTG 36490	AT G C	
			CACTGCAGG GTTG CCG CCCG		
			GTGACGTCT CGGT GGC GGGC		
			_ _ A		
GAM2346	MGAT1	5'	GGGCGGCCGCGGCAG 8227	AGGA T C	
			CTGC TGT GGCCGCC C		
			GACG GCG CCGGCGG G		
			_ _ A		
GAM2346	NCOR2	3'	GGGCGGCCAGGGACCCAAAGCA 13004	A_ ATG	
			TGC GG TTGGCCGCC		

		ACG CC GACCGGCGGG	
		AAAC AGG	
GAM2346	PMM2	3' GGACAGGCCATCTGCAGTG 35681	ATGT GCC
		CACTGCAGG TGGCC CC	
		GTGACGTCT ACCGG GG	
		_____ ACA	
GAM2346	PPP1R8	5' CGGGGCGGCCAGGGCTAGAGTG 28854	GCA ATG
		CACT GG TTGGCCGCCCG	
		GTGA TC GACCGGCGGGGC	
		GA_ GG_	
GAM2346	PPP1R8	5' CGGGGCGGCCAGGGCTAGAGTG 8568	GCA ATG
		CACT GG TTGGCCGCCCG	
		GTGA TC GACCGGCGGGGC	
		GA_ GG_	
GAM2346	BRD4	3' GGGCGACTGTCCTGCGTG 27778 T	GTT C C
		CAC GCAGGAT GG CGCC C	
		GTG CGTCCTG TC GCGG G	
		_ ____ A A	
GAM2346	C20orf175	5' GGGCAGCTTTGGCCAGCAGTG 28094	A ATGTT C
		CACTGC GG GGC GCCC	
		GTGACG CC TCG CGGG	
		A GGTT_ A	
GAM2346	CSMD1	5' CGGAGCAGCTCAGCCCTGCAGT 27069	AT _ C C
	G	CACTGCAGG GTTG GC GC CCG	
		GTGACGTCC CGAC CG CG GGC	
		____ T A A	
GAM2346	CSMD1	5' CGGAGCAGCTCAGCCCTGCAGT 36187	AT _ C C
	G	CACTGCAGG GTTG GC GC CCG	
		GTGACGTCC CGAC CG CG GGC	
		____ T A A	
GAM2346	DKFZP547L112	3' GGCAGGAATCCCGCCCTGCAGT 33058	AT T ____ _
	G	CACTGCAGG GT GG CC GCC	
		GTGACGTCC CG CC GG CGG	
		____ C TAA A	
GAM2346	DKFZP564B147	5' GGGGCCAGCCCTGCAGTG 39935	AT G
		CACTGCAGG GTTGGCC CC	
		GTGACGTCC CGACCGG GG	
		____ _	
GAM2346	DOCK3	3' GGAGCCTGCAAACCCTGCAGTG 33038	A__ T CG
		CACTGCAGG TGT GGC CC	

GTGACGTCC ACG CCG GG
 CAA T A_
 GAM2346 FLJ13153 5' GGGGTCACATTCTGCAG 24166 T G
 CTGCAGGATGT GGCC CC
 ||||| ||||
 GACGTCTTACA CTGG GG

 - -
 GAM2346 FLJ14621 5' GCGGCCAAGGCCACGGTG 26580 CA ATG
 CACTG GG TTGGCCGC
 |||| || |||||
 GTGGC CC AACCGGCG
 A_ GG_
 GAM2346 FLJ20752 5' GGGCTGAGCCATCCCGCGTG 21129 T A TGT __
 CAC GC GGA TGGC C GCCC
 ||| ||| |||||
 GTG CG CCT ACCG G CGGG
 _ C _ A T
 GAM2346 FLJ21709 3' TGACCAACATCCTAGAGCA 38172 _ C
 TGC AGGATGTTGG CG
 ||| ||||| ||
 ACG TCCTACAACC GT
 AGA A
 GAM2346 FLJ22477 5' CGGCGGCGGCCGACAGC 24075 AGGA _
 GC TGTTGGCCGCC CCG
 || ||||| |||
 CG ACAGCCGGCGG GGC
 _ C
 GAM2346 FLJ32865 3' GCTCAACATCCTGCAATG 29429 C _
 CA TGCAGGATGTTG GC
 || ||||| ||
 GT ACGTCCTACAAC CG
 A T
 GAM2346 HGC6.1.1 3' GCAACTGATGTCCTGCGTG 15685 T TG CC
 CAC GCAGGATGT G GC
 ||| ||||| | ||
 GTG CGTCCTGTA C CG
 _ GT AA
 GAM2346 KIAA0010 5' CGAGGCAGGGCCGCCCTCCAG 16131 C AT T _ C
 T ACTG AGG GT GGCC GCC CG
 |||| ||| || ||| ||| ||
 TGAC TCC CG CCGG CGG GC
 C C_ _ GA A
 GAM2346 KIAA1881 3' GGGCTCTTCCAGTCCTGCAG 45657 GT CC_
 CTGCAGGAT TGG GCCC
 ||||| ||| |||
 GACGTCCTG ACC CGGG
 _ TTCT
 GAM2346 MGC20486 5' CGGGGCGGCCAGGGCCGCTGCA 27422 GATG_
 TGCAG TTGGCCGCCCGG
 |||| |||||

ACGTC GACCGGCGGGGC
 GCCGG
 GAM2346 PRPF8 3' GGCCCGGACAATCCTGCAG 30685 _ _
 CTGCAGGAT GTT GGCC
 ||||| ||| |||
 GACGTCCTA CAG CCGG
 A GC
 GAM2346 ZD52F10 5' CGGAATAACTTCCTGCAG 27155 T G_
 CTGCAGGA GTTG CCG
 ||||| ||| |||
 GACGTCCT CAAT GGC
 T AA
 GAM2346 LOC150538 3' CGGGGCGGCCCTGCTGCCAGC 38992 A AT T_
 GC GG GT GGCCGCCCCG
 || || || |||||
 CG CC CG CCGGCGGGGC
 A GT TC
 GAM2346 LOC157740 5' CGAGGCGGTTACCCCGCCGCA 39648 A ATGT_ C
 TGC GG TGGCCGCC CG
 ||| || ||||| ||
 ACG CC ATTGGCGG GC
 _ GCCC A
 GAM2346 LOC158117 3' GGGCGGTTTCCTGAAGTG 39729 G TGTTG
 CACT CAGGA GCCGCC
 ||| ||| |||||
 GTGA GTCCT TGGCGGG
 A _
 GAM2346 LOC158972 3' CGGAGCGGCCAGGACACAG 42043 CAGGA _ C
 CTG TGT TGGCCGC CCG
 ||| ||| ||||| |||
 GAC ACA ACCGGCG GGC
 _ GG A
 GAM2346 LOC203275 3' GGGCGGTTTCCTGAAGTG 43027 G TGTTG
 CACT CAGGA GCCGCC
 ||| ||| |||||
 GTGA GTCCT TGGCGGG
 A _
 GAM2346 LOC219513 3' CGAGGCCTGGTCAGCCTGCAGT 45293 ATG _ C
 ACTGCAGG TTGGCC GCC CG
 ||||| ||||| ||| ||
 TGACGTCC GACTGG CGG GC
 _ TC A
 GAM2346 LOC221271 5' CGGGGCAGCGGCTCCTGCAG 44124 T G C
 CTGCAGGA GTTG C GCCCG
 ||||| ||| | |||||
 GACGTCCT CGGC G CGGGGC
 _ _ A
 GAM2346 LOC256812 5' GGGGCGGCCTCGCCGCGCA 46579 A_ A TT
 TGC GG TG GGCCGCCCC
 ||| ||| |||||

			ACG CC GC CCGGCGGGG		
			CG _ T_		
GAM2346	LOC257422	5'	GCGGCCAACATTCCAG	46190	CA
			CTG GGATGTTGGCCGC		
			GAC CTTACAACCGGCG		
			—		
GAM2346	LOC57228	5'	CGGAGCGGCCGAAGCTCAGC	21706	A_ ATG C
			GC GG TTGGCCGC CCG		
			CG TC AGCCGGCG GGC		
			AC GA_ A		
GAM2347	CSNK1A1	3'	TCTTCAGCCACAGTTGTGA	7620	AAC CA
			TCACAACT GGCT GAGGG		
			AGTGTTGA CCGA CTTCT		
			CA_ _		
GAM2347	MADD	3'	GTCCCTCTGAGTGTGTCTTG	9788	CTA G
			CAA ACG CTCAGAGGGAC		
			GTT TGT GAGTCTCCCTG		
			CTG _		
GAM2347	MADD	3'	GTCCCTCTGAGTGTGTCTTG	28237	CTA G
			CAA ACG CTCAGAGGGAC		
			GTT TGT GAGTCTCCCTG		
			CTG _		
GAM2347	MADD	3'	GTCCCTCTGAGTGTGTCTTG	28243	CTA G
			CAA ACG CTCAGAGGGAC		
			GTT TGT GAGTCTCCCTG		
			CTG _		
GAM2347	MADD	3'	GTCCCTCTGAGTGTGTCTTG	28248	CTA G
			CAA ACG CTCAGAGGGAC		
			GTT TGT GAGTCTCCCTG		
			CTG _		
GAM2347	MADD	3'	GTCCCTCTGAGTGTGTCTTG	28253	CTA G
			CAA ACG CTCAGAGGGAC		
			GTT TGT GAGTCTCCCTG		
			CTG _		
GAM2347	MADD	3'	GTCCCTCTGAGTGTGTCTTG	28258	CTA G
			CAA ACG CTCAGAGGGAC		
			GTT TGT GAGTCTCCCTG		
			CTG _		
GAM2347	MATN3	3'	CTAAAGAGCACTAGTTGTGA	8196	ACG AG_
			TCACAACTA GCTC AG		

AGTGTTGAT CGAG TC
 CA_ AAA
 GAM2347 CMRF-35H 3' TCCCTCTGTTGCCATCAGCTTG 34861 _ AAC T_
 CAA CT GGC CAGAGGGA
 ||| || ||| |||||
 GTT GA CCG GTCTCCCT
 C CTA TT
 GAM2347 CNOT3 5' CCCTCTGAGTAGGAAGTGTGA 15843 A AACG
 TCACA CT GCTCAGAGGG
 ||||| || |||||
 AGTGT GA TGAGTCTCCC
 _ AGGA
 GAM2347 DKFZP564D172 3' TCCTTTTGCCAGCTAATTGTGA 25753 CTAAC _
 TCACAA GGCT CAGAGGGA
 ||||| ||| |||||
 AGTGTT TCGA GTTTTCCT
 AA_ CC
 GAM2347 FLJ14327 3' TCCCTCAGGCTGGTTGTGA 24430 TAA CA
 TCACAAC CGGCT GAGGGA
 ||||| ||||| |||||
 AGTGTTG GTCGG CTCCCT
 _ A_
 GAM2347 FLJ22233 3' CCCTCTGAGAAGGGCTGGA 24514 A A AACGG
 TC CA CT CTCAGAGGG
 || ||| |||||
 AG GT GG GAGTCTCCC
 _ C GAA_
 GAM2347 NEU4 5' GTCCCTCTGGGAGGTCAACTGC 28028 A ACTA GG
 GG TC CA AC CTCAGAGGGAC
 || || || |||||
 GG GT TG GGGTCTCCCTG
 C CAAC GA
 GAM2347 LOC112868 3' CCCTCTGAGCTGGCCTGTGG 36079 ACTAA
 TCACA CGGCTCAGAGGG
 ||||| |||||
 GGTGT GTCGAGTCTCCC
 CCG_
 GAM2347 LOC151826 3' CTAAAGCAGTTAGTTGTGA 39165 G CAG
 TCACA ACTAAC GCT AG
 ||||| ||| ||
 AGTGTTGATTG CGA TC
 A AA_
 GAM2347 LOC152313 3' TCCCCGCTCCCAGTTGTGA 41478 AAC TCAGA
 TCACA ACT GGC GGGA
 ||||| || |||
 AGTGTTGA TCG CCCT
 CCC C_
 GAM2347 LOC152313 5' TCCCTGCTCCCAGTTGTGA 41479 AAC TCAG
 TCACA ACT GGC AGGGA
 ||||| || |||||

		AGTGTGA TCG TCCCT	
		CCC _____	
GAM2347	LOC161498 5'	TCCCTCTGGTCACTGTGA 42108	ACTAAC T
		TCACA GGC CAGAGGGA	
		AGTGT CTG GTCTCCCT	
		CA_____	
GAM2347	LOC92568 3'	TCCCTCTGAGCCCACGATTGGA 34580	A CTAAC
		TC CAA GGCTCAGAGGGA	
		AG GTT CCGAGTCTCCCT	
		_ AGCAC	
GAM2348	IDH1 3'	TGAGGTAGAGCTGTGCATTAA 30800	TCCC TA
		TTAATGCACA CTAT CTCA	
		AATTACGTGT GATG GAGT	
		CGA_ _	
GAM2348	FLJ20060 3'	TGAGTAATCTTGTAAAGCATTAA 19150	_ TCCCCT
		TTAATGC ACA ATTACTCA	
		AATTACG TGT TAATGAGT	
		AA TC_____	
GAM2348	GHITM 3'	TAATGGGGCAGATATGCATTAA 15727	C _
		TTAATGCA ATC CCCTATTA	
		AATTACGT TAG GGGGTAAT	
		A AC	
GAM2348	GNG4 3'	GAGCATTGGTGTGCATTAA 10812	CCCTATTA
		TTAATGCACATC CTC	
		AATTACGTGTGG GAG	
		TTAC_____	
GAM2348	KIAA1228 3'	TGAGTAGACAGGATATTGCATT 32447	C_ CCTA
	AA	TTAATGCA ATCC TTAATCA	
		AATTACGT TAGG GATGAGT	
		TA ACA_	
GAM2348	KIAA1361 3'	AGTTGTGTGAGGATTGCATTAA 31166	C CC_ T
		TTAATGCA ATCC TAT ACT	
		AATTACGT TAGG GTG TGA	
		_ AGT T	
GAM2348	LOC222001 3'	TGAGTAATCTTGTAAAGCATTAA 44641	_ TCCCCT
		TTAATGC ACA ATTACTCA	
		AATTACG TGT TAATGAGT	
		AA TC_____	
GAM2349	ABCD1 5'	GCCCTGACCTCAGGGGCCA 5471	A GA A A
		TG CTCCTGA GG CAG GGC	

			AC GGGGACT CC GTC CCG		
			C _ A _		
GAM2349	ANK1	3'	GCCCCGGTGGATCTCAGGAGT 30286	GG_	AGA
			ACTCCTGAGA AC GGC		
			TGAGGACTCT TG CCG		
			AGG GC_		
GAM2349	AXL	3'	CTCCCTCTCAGGATCCA 22444 AC	ACA	
			TG TCCTGAGAGG GAG		
			AC AGGACTCTCC CTC		
			CT _		
GAM2349	AXL	3'	CTCCCTCTCAGGATCCA 7423 AC	ACA	
			TG TCCTGAGAGG GAG		
			AC AGGACTCTCC CTC		
			CT _		
GAM2349	COL11A2	3'	CCCCTGTCCTCCCCTGGGCA 27976	A CTGA	A
			TG CTC GAGGACAG GG		
			AC GGG CTCCTGTC CC		
			_ TCCC C		
GAM2349	COL11A2	3'	CCCCTGTCCTCCCCTGGGCA 27981	A CTGA	A
			TG CTC GAGGACAG GG		
			AC GGG CTCCTGTC CC		
			_ TCCC C		
GAM2349	DAP	3'	GCCCCCTCAATTCCAGGAGTCA 35917	A GAC A	
			TGACTCCTG GAG AG GGC		
			ACTGAGGAC CTT TC CCG		
			_ AAC C		
GAM2349	DHCR24	3'	GCCAGAATCCTCTCAGAGTCA 16523	C	CAGA
			TGACTC TGAGAGGA GGC		
			ACTGAG ACTCTCCT CCG		
			_ AAGA		
GAM2349	DLG5	3'	GCCCCCTGTCCCCTCTGTCA 40338	TCCT A	A
			TGAC GAG GGACAG GGC		
			ACTG CTC CCTGTC CCG		
			T_ C C		
GAM2349	FGFRL1	3'	GCCTCTGTCCCCGCCTCAG 22450	A_	
			CTGAG GGACAGAGGC		
			GA CTC CCTGTCTCCG		
			CGCC		
GAM2349	GTF2I	5'	GCCTCTGTCCCCCAGTGATC 26886	C _	AGA
			GA TC CTG GGACAGAGGC		

			CT AG GAC CCTGTCTCCG		
			_ T CC_		
GAM2349	GTF2I	5'	GCCTCTGTCCCCCAGTGATC 26890	C _	AGA
			GA TC CTG GGACAGAGGC		
			CT AG GAC CCTGTCTCCG		
			_ T CC_		
GAM2349	HKE4	5'	GCCTCTGTCCCTCTGGTCA 13840	CCT	A
			TGACT GAG GGACAGAGGC		
			ACTGG CTC CCTGTCTCCG		
			T__ _		
GAM2349	HOXD3	5'	GCCCAGCTCTCTCAGGATTCA 13773	C	ACAGA
			TGA TCCTGAGAGG GGC		
			ACT AGGACTCTCT CCG		
			T CGAC_		
GAM2349	KIF3C	3'	GTCCCCTCCGAGGAGTCA 8059	_	A
			TGACTCCT GAG GGAC		
			ACTGAGGA CTC CCTG		
			GC C		
GAM2349	MLLT7	3'	CCCCCTCTCAGGAGCCA 12576	A	ACAGA
			TG CTCCTGAGAGG GG		
			AC GAGGACTCTCC CC		
			C C__		
GAM2349	MLLT7	3'	CCCCTGCCTTTGGGAGCA 12577	A G A A	
			TG CTCCT AGAGG CAG GG		
			AC GAGGG TTTCC GTC CC		
			_ _ _ C		
GAM2349	MME	5'	GCCTCTGCCTTGGGGAGTTA 14158	GA	A
			TGACTCCT GAGG CAGAGGC		
			ATTGAGGG TTCC GTCTCCG		
			G_ _		
GAM2349	MVK	3'	GCCCCCTGTCTCTCAGGG 30426	G A_	
			TCCTGAGAG ACAG GGC		
			GGGACTCTC TGTC CCG		
			_ CC		
GAM2349	MYLK2	3'	GCCCCCATCTTGGGGGTCA 26965	TG _	ACAGA
			TGACTCC AGA GG GGC		
			ACTGGGG TCT CC CCG		
			GT A C__		
GAM2349	MYO15A	3'	CTGAACCTCTCAGGATCA 18354	C	A_
			TGA TCCTGAGAGG CAG		

			ACT AGGACTCTCC GTC	
			— AA	
GAM2349 NOVA1	3'	GCCTTTGTTCCCAAGACCCA	13216	AC C AGA
		TG TC TG GGACAGAGGC		
		AC AG AC CTTGTTTCCG		
		CC A C__		
GAM2349 NOVA1	3'	GCCTTTGTTCCCAAGACCCA	8347	AC C AGA
		TG TC TG GGACAGAGGC		
		AC AG AC CTTGTTTCCG		
		CC A C__		
GAM2349 PCSK2	3'	GCCTCTGTCCCGAAGAGTCA	8458	__ AGA
		TGACTC CTG GGACAGAGGC		
		ACTGAG GGC CCTGTCTCCG		
		AA __		
GAM2349 PCTK1	5'	GCCTCTCCTCGAAAAGTCA	26910	CCTGA CA
		TGACT GAGGA GAGGC		
		ACTGA CTCCT CTCCG		
		AAAG__ __		
GAM2349 PIGR	3'	GCCCCTGCCCTCTGTTGGAG	35939	TG__ A__ A
		CTCC AGAGG CAG GGC		
		GAGG TCTCC GTC CCG		
		TTG CC C		
GAM2349 RET	3'	GCAGGTGCCTCTCAGAGGCCA	21784	A TC A GAG
		TG C CTGAGAGG CA GC		
		AC G GACTCTCC GT CG		
		C GA __ GGA		
GAM2349 RFP	5'	GCCCGGTGCCTCTCAGGA	13259	__ AGA
		TCCTGAGAGG AC GGC		
		AGGACTCTCC TG CCG		
		G GC__		
GAM2349 SEZ6L	5'	CCTCCTGCCCTCAGGAG	22093	A A __
		CTCCTGAG GG CAG AGG		
		GAGGACTC CC GTC TCC		
		__ __ C		
GAM2349 SGT	3'	GCCTCCGCGGCTCAGGAGCCG	8941	A AGGACA
		TG CTCCTGAG GAGGC		
		GC GAGGACTC CTCCG		
		C GGCGC__		
GAM2349 TEGT	3'	GCCTGACCCTCAGGGAGTCA	32273	GA ACAG
		TGACTCCT GAGG AGGC		

			ACTGAGGG CTCC TCCG		
			A_ CAG_		
GAM2349	TNS	5'	CCCCCTGTCCTGGGAGTC 22902	GAG	A
			GACTCCT AGGACAG GGC		
			CTGAGGG TCCTGTC CCG		
			_____ C		
GAM2349	TOP3B	5'	CCAGTCTCACAGGAGTCA 10037	A	ACAGA
			TGACTCCTG GAGG GG		
			ACTGAGGAC CTCT CC		
			A GA_____		
GAM2349	ATF3	3'	CCCCCGGTGTGTCCCAGGAGTC 10244	AGA	GA_____
			GACTCCTG GGACA GGC		
			CTGAGGAC CCTGT CCG		
			_____ GTGGCC		
GAM2349	C20orf178	3'	GCCTCTGTCCTTGTAAGTCA 36935	CCTGA	
			TGACT GAGGACAGAGGC		
			ACTGA TTCCTGTCTCCG		
			ATG_____		
GAM2349	CSNK1G1	3'	CCAGTGCCTCCCAGGAGTC 22569	A	A GA
			GACTCCTG GAGG CA GG		
			CTGAGGAC CTCC GT CC		
			C _ GA		
GAM2349	CSR1	3'	GCCTCTGCCCTTCAGGAGCA 18359	A	A A
			TG CTCCTGAG GG CAGAGGC		
			AC GAGGACTT CC GTCTCCG		
			_____ C _		
GAM2349	DGKD	3'	GCCTCCGCCCTCTCAGCCTGT 29885	TC_	ACA
			AC CTGAGAGG GAGGC		
			TG GACTCTCC CTCCG		
			TCC CGC		
GAM2349	DGKD	3'	GCCTCTGTCCTCTCAGCCTGT 29886	TC_	
			AC CTGAGAGGACAGAGGC		
			TG GACTCTCCTGTCTCCG		
			TCC		
GAM2349	DKFZP434N1511	5'	GCCTGGCTGCCTCAGGAGCCA 43937	A	GA A _
			TG CTCCTGA GG CAG AGGC		
			AC GAGGACT CC GTC TCCG		
			C _ _ GG		
GAM2349	DKFZP564O0423	3'	GCCTGAGCCCTCTCAGAAGCA 44067	A C	ACAG
			TG CT CTGAGAGG AGGC		

AC GA GACTCTCC TCCG
 _ A CGAG
 GAM2349 DKFZP761D0211 3' CTCTGTCCCCCAAGGAGTCA 25736 GAGA
 TGACTCCT GGACAGAG
 ||||| |||||
 ACTGAGGA CCTGTCTC
 ACCC
 GAM2349 FLJ10597 3' GCCCCTGTTCTTCGCTCAGGAG 19953 A _ A
 CA TG CTCCTGAG AGGACAG GGC
 || ||||| ||||| ||
 AC GAGGACTC TCTTGTC CCG
 _ GCT C
 GAM2349 FLJ10661 3' GCCTCTGGCCCAGGAGTTA 19997 AGA A
 TGACTCCTG GG CAGAGGC
 ||||| || |||||
 ATTGAGGAC CC GTCTCCG
 _ G
 GAM2349 FLJ21276 3' GCCTGTGGTCTCTCAGAAGCCA 23902 A C GA G
 TG CT CTGAGAG CA AGGC
 || || ||||| || ||||
 AC GA GACTCTC GT TCCG
 C A TG G
 GAM2349 GGA2 3' GCCTCTGTCCCAATTCTGAGT 28921 CT A_
 ACTC GAG GGACAGAGGC
 ||| || |||||
 TGAG CTT CCTGTCTCCG
 T_ AAC
 GAM2349 GGA2 3' GCCTCTGTCCCAATTCTGAGT 17400 CT A_
 ACTC GAG GGACAGAGGC
 ||| || |||||
 TGAG CTT CCTGTCTCCG
 T_ AAC
 GAM2349 GR6 5' GCCCCTTGCTCTCAGGAG 14285 GAC A
 CTCCTGAGAG AG GGC
 ||||| || |||
 GAGGACTCTC TC CCG
 GT_ C
 GAM2349 H326 5' GCCTATTTCTCAGGAG 17939 A CAG
 CTCCTGAG GGA AGGC
 ||||| || |||
 GAGGACTC CTT TCCG
 _ TA_
 GAM2349 KIAA0153 3' GCCTCTGTCTGCGAGCCA 17498 A CT AG
 TG CTC G AGGACAGAGGC
 || ||| | |||||
 AC GAG C TCCTGTCTCCG
 C _ CG
 GAM2349 KIAA0527 3' CCATTTCTCTCAGAAGCA 45843 A C C A
 TG CT CTGAGAGGA AG GG
 || || ||||| || ||

				AC GA GACTCTCCT TT CC			
				_ A _ A			
GAM2349	KIAA0819	3'	GCCTCTGTCCCTGGCGGCCA	31808	A C G A		
			TG CT CT AG GGACAGAGGC				
			AC GG GG TC CCTGTCTCCG				
			C C _ _				
GAM2349	KIAA1110	3'	GCCTGAAACTCTCAGGAGTC	30985		GACAG	
			GACTCCTGAGAG AGGC				
			CTGAGGACTCTC TCCG				
			AAAG_				
GAM2349	KIAA1228	3'	GCCCCTGCTGTTCTCAGCAGCC	32445	A C _ A A		
	A		TG CT CTGAGA GG CAG GGC				
			AC GA GACTCT TC GTC CCG				
			C C TG _ C				
GAM2349	KIAA1538	3'	GCCCCTGGAGCTCAGGGGTCA	35430		AGGA A	
			TGACTCCTGAG CAG GGC				
			ACTGGGGACTC GTC CCG				
			GAG_ C				
GAM2349	KIAA1559	3'	GCCTCCTGTACCTCTCAG	36163	_ _		
			CTGAGAGG ACAG AGGC				
			GACTCTCC TGTC TCCG				
			AC C				
GAM2349	KIAA1751	3'	CCTCCGTCTCCTCCTGTGTC	35497	TCCT _ A		
			GAC GAG AGGAC GAGG				
			CTG CTC TCCTG CTCC				
			TC__ C C				
GAM2349	KIAA1755	5'	GCCTCTATCCTCCTTTCGAG	30751	CT _ C		
			CTC GAG AGGA AGAGGC				
			GAG TTC TCCT TCTCCG				
			CT C A				
GAM2349	KIAA1784	3'	GCCTCCAGCCTCAGGAGCA	32485	A GA ACA		
			TG CTCCTGA GG GAGGC				
			AC GAGGACT CC CTCCG				
			_ _ GAC				
GAM2349	KIAA1870	5'	GCCCTGCACCCCGGGAGTCA	26710		AGA A_ A	
			TGACTCCTG GG CAG GGC				
			ACTGAGGGC CC GTC CCG				
			CC_ AC _				
GAM2349	KIAA1957	3'	CCCCCTCCAGGGGTCA	37277	A ACAGA		
			TGACTCCTG GAGG GG				

		ACTGGGGAC CTCC CC		
		C C____		
GAM2349	MGC16279	3' GCCTCTGGCCCAGGAGTTA 26732	AGA	A
		TGACTCCTG GG CAGAGGC		
		ATTGAGGAC CC GTCTCCG		
		____ G		
GAM2349	MGC33182	5' GCCTCCATCCTCCCCTAGAGGG 37233	GA____	CA
		GTCA TGACTCCT GAGGA GAGGC		
		ACTGGGGA CTCCT CTCCG		
		GATCCC AC		
GAM2349	MGC4415	3' CCCCTGGCTCAGGAGCCG 25568	A	AGGA A
		TG CTCCTGAG CAG GG		
		GC GAGGACTC GTC CC		
		C G____ C		
GAM2349	MGC4677	5' GCCTCAGGGCCCATCAGGAGTC 27452	GA ACA_	
		A TGACTCCTGA GG GAGGC		
		ACTGAGGACT CC CTCCG		
		AC GGGA		
GAM2349	MYT1L	5' GCCTGCGTCCTGCCAGGAGTCA 33185	AG	AG
		TGACTCCTG AGGAC AGGC		
		ACTGAGGAC TCCTG TCCG		
		CG CG		
GAM2349	PIP5K2B	3' GCCCCTGGAGTTCAGAAGTC 9613	C	AGGA A
		GA CTGAG CAG GGC		
		CTGA GACTT GTC CCG		
		A GAG_ C		
GAM2349	PLA2G6	3' CCTCAGCTCTCAAAGGTCA 33031	CC	GACA
		TGACT TGAGAG GAGG		
		ACTGG ACTCTC CTCC		
		AA GA____		
GAM2349	SCN12A	3' GCCTCTGAGCTCCAGGGGTCA 15411	A	GA
		TGACTCCTG GAG CAGAGGC		
		ACTGGGGAC CTC GTCTCCG		
		_ GA		
GAM2349	STMN3	3' CCCCTGCAGGGCTCAGGGGTCA 18038	AGGA_	A
		TGACTCCTGAG CAG GG		
		ACTGGGGACTC GTC CC		
		GGGAC C		
GAM2349	TUSP	5' CCTTTGTCTCTGGAATCA 21525	C TG	G
		TGA TCC AGAG ACAGAGG		

ACT AGG TCTC TGTTTC
 A _ _
 GAM2349 VI 3' CCTTTGTCTGGAGTCA 15107 TGAGA
 TGA CTCC GGACAGAGG
 ||||| |||||
 ACTGAGG TCTGTTTC

 GAM2349 VIT1 3' CCTTTGTCAGAAGTCA 20765 C GAGAG
 TGA CT CT GACAGAGG
 ||||| || |||||
 ACTGA GA CTGTTTC
 A _ _
 GAM2349 VT12 5' CCGCTCCCTCAGGAGTC 13057 A CAGA
 GACTCCTGAG GGA GG
 ||||| || |||||
 CTGAGGACTC CCT CC
 _ CG _
 GAM2349 ZFP95 3' CCTCACCCAGGAGTCA 15919 AGA ACA
 TGA CTCTG GG GAGG
 ||||| || |||||
 ACTGAGGAC CC CTCC
 _ A _
 GAM2349 ZFP95 3' CCTCACCCAGGAGTCA 29709 AGA ACA
 TGA CTCTG GG GAGG
 ||||| || |||||
 ACTGAGGAC CC CTCC
 _ A _
 GAM2349 LOC114987 3' GCCTCTGTCTGTGAAAGTCA 29754 CCTGAGA
 TGA CT GGACAGAGGC
 ||||| |||||
 ACTGA TCTGTCTCCG
 AAGTG _
 GAM2349 LOC115073 5' CCCCCGTTTCAGGGTCA 36239 T _ ACAGA
 TGAC CCTGAGA GG GG
 ||||| ||||| || |||||
 ACTG GGACTTT CC CC
 _ G C _
 GAM2349 LOC121274 3' GCCGGTGCTACCAGGAGTCA 36656 AG G AGA
 TGA CTCTG AG AC GGC
 ||||| || || |||||
 ACTGAGGAC TC TG CCG
 CA G G _
 GAM2349 LOC135763 3' CCTCTGTCTGTCAGCAG 28881 C AG
 CT CTG AGGACAGAGG
 || ||||| |||||
 GA GAC TCCTGTCTCC
 C G _
 GAM2349 LOC144231 5' GCCTGCTGCTCTCAGGA 40393 GA _
 TCCTGAGAG CAG AGGC
 ||||| |||||

		AGGACTCTC GTC TCCG		
		— G		
GAM2349	LOC144465 3'	CCTCTGTACACAGGAGCA 37751	A	AGAG
		TG CTCCTG GACAGAGG		
		AC GAGGAC CTGTCTCC		
		— ACA—		
GAM2349	LOC145945 5'	GCCCCTGTCCTTGGCCAGTC 40632	CCTGA	A
		GACT GAGGACAG GGC		
		CTGA TTCCTGTC CCG		
		CCGG— C		
GAM2349	LOC148760 3'	CCTCTGTGAAAGGAGTTA 40896	GAGAGG	
		TGACTCCT ACAGAGG		
		ATTGAGGA TGTCTCC		
		AAG—		
GAM2349	LOC149194 3'	GCCCAGTTCCTTCCAGGAGTCA 38670	AG	CAGA
		TGACTCCTG AGGA GGC		
		ACTGAGGAC TCCT CCG		
		CT TGAC		
GAM2349	LOC151162 5'	CCTCCTGTCCTCAGGGATCA 41305	C	GA —
		TGA TCCT GAGGACAG AGG		
		ACT AGGG CTCCTGTC TCC		
		— A— C		
GAM2349	LOC154449 5'	CCTCTGTCCCCTTGAAGT 39475	C	TG A
		ACT C AG GGACAGAGG		
		TGA G TC CCTGTCTCC		
		A GT C		
GAM2349	LOC157450 3'	GCCTCTGGCCCAGGAGTTA 35147	AGA	A
		TGACTCCTG GG CAGAGGC		
		ATTGAGGAC CC GTCTCCG		
		— G		
GAM2349	LOC157860 3'	CTGTCCTCTGAGAAGCCA 41859	A	C G
		TG CT CT AGAGGACAG		
		AC GA GA TCTCCTGTC		
		C A G		
GAM2349	LOC158490 3'	GCCTCTGGCCCAGGAGTTA 39851	AGA	A
		TGACTCCTG GG CAGAGGC		
		ATTGAGGAC CC GTCTCCG		
		— G		
GAM2349	LOC158819 5'	CCTCTGTTGAGCAGTCA 42025	C	GAGAG
		TGACT CT GACAGAGG		

	ACTGA GA	TTGTCTCC		
	C G			
GAM2349	LOC168489 5'	CCTCATCTGCAGGAGTCA 40250	AG	ACA
		TGACTCCTG AGG GAGG		
		ACTGAGGAC TCT CTCC		
		G_ A_		
GAM2349	LOC203377 5'	CCTCCTGTCCTCAGGGATCA 43540	C	GA _
		TGA TCCT GAGGACAG AGG		
		ACT AGGG CTCCTGTC TCC		
		_ A_ C		
GAM2349	LOC221692 3'	GCCCCTGTTCTGTCCAGCAGCC 44298	A C _ G	A
	A	TG CT CTG A AGGACAG GGC		
		AC GA GAC T TCTTGTC CCG		
		C C C G C		
GAM2349	LOC221715 5'	CTCCCTCTCAGAAGCCA 45017	A C	ACA
		TG CT CTGAGAGG GAG		
		AC GA GACTCTCC CTC		
		C A _		
GAM2349	LOC254205 5'	GCCAGCCTCTCGGGAGTCA 46218		ACAGA
		TGACTCCTGAGAGG GGC		
		ACTGAGGGCTCTCC CCG		
		GA_		
GAM2349	LOC255101 5'	GCCTGAGTCCCAGGAGTC 46339	AGA	AG
		GACTCCTG GGAC AGGC		
		CTGAGGAC CCTG TCCG		
		_ AG		
GAM2349	LOC256337 3'	GCCTCTGTTAAGGAGGAGTC 45421		GAGAG
		GACTCCT GACAGAGGC		
		CTGAGGA TTGTCTCCG		
		GGAA_		
GAM2349	LOC90309 5'	CTGTCCTTTCAAGAGCCA 31151	A C	
		TG CTC TGAGAGGACAG		
		AC GAG ACTTTCCTGTC		
		C A		
GAM2349	LOC91960 3'	GCCAGATGCCTCTCAGGAG 33612	A	GA_
		CTCCTGAGAGG CA GGC		
		GAGGACTCTCC GT CCG		
		_ AGA		
GAM2349	LOC92340 3'	CCTCAACCCTGAGGAGTCA 34198	G A	ACA
		TGACTCCT AG GG GAGG		

		ACTGAGGA TC CC CTCC		
		G _ AA_		
GAM2349	LOC92822	3' GCCTCTGTCCCCAGGTGT 34985	T	AGA
		AC CCTG GGACAGAGGC		
		TG GGAC CCTGTCTCCG		
		T CC_		
GAM2349	LOC93320	3' GCCTCTGGCCCAGGAGTTA 35656		AGA A
		TGACTCCTG GG CAGAGGC		
		ATTGAGGAC CC GTCTCCG		
		___ G		
GAM2350	ADAM8	3' GCCTGCTGAGCCGGCTGCC 6766		GTCCCC
		GGCAGC CTCAGCAGGC		
		CCGTCTG GAGTCGTCCG		
		GCC___		
GAM2350	BMP1	3' GCCCCCTCGGGGACGCCCCCA 12771	CA	CTC CA
		TGG GCGTCCCC AG GGC		
		ACC CGCAGGGG TC CCG		
		CC C__ CC		
GAM2350	BMP1	3' GCCCCCTCGGGGACGCCCCCA 12774	CA	CTC CA
		TGG GCGTCCCC AG GGC		
		ACC CGCAGGGG TC CCG		
		CC C__ CC		
GAM2350	CENTD2	5' GCCCACTAAGGAGGAGGAGTCA 29195	AGCG	C C CA
		TGGC TCC CCT AG GGC		
		ACTG AGG GGA TC CCG		
		AGG_ A A AC		
GAM2350	ITGAL	3' CCTGCTGAGGGACCAGCCA 7970	AGC	CC
		TGGC GTCCC TCAGCAGG		
		ACCG CAGGG AGTCGTCC		
		AC_ _		
GAM2350	LAMC1	5' GCCTCCGGGGGACGCCGCTA 8076	A	TCAGC
		TGGC GCGTCCCC AGGC		
		ATCG CGCAGGGGG TCCG		
		C CC___		
GAM2350	P3	5' GCCTGCCAGGCAGACGCTGC 21255	CC	CA
		GCAGCGTC CCT GCAGGC		
		CGTCGCAG GGA CGTCCG		
		AC C_		
GAM2350	PSEN2	5' GCCTGCTGAGAAGAAGAAACCA 6034	CAGCG	CCC
		TGG TC CTCAGCAGGC		

ACC AG GAGTCGTCCG
 AAAGA AA_
 GAM2350 PSEN2 5' GCCTGCTGAGAAGAAGAAACCA 14864 CAGCG CCC
 TGG TC CTCAGCAGGC
 ||| || |||||
 ACC AG GAGTCGTCCG
 AAAGA AA_
 GAM2350 SH3BP2 3' GCCTGCTGAGGGGGCAGTGCCA 8948 GC T
 TGGCA G CCCCTCAGCAGGC
 |||| | |||||
 ACCGT C GGGGGAGTCGTCCG
 GA_
 GAM2350 TGM2 3' GCCTGCTGAGAGCCCCCA 10955 CA GTCCCC
 TGG GC CTCAGCAGGC
 ||| || |||||
 ACC CG GAGTCGTCCG
 CC A____
 GAM2350 TIC 3' GCCCACTGAGGGGACAGCC 14826 AGC C CA
 GGC GTCCCC TCAG GGC
 ||| ||||| ||| |||
 CCG CAGGGG AGTC CCG
 A__ _ AC
 GAM2350 TIC 3' GCCCGCCAAGAGGGGGCCTCTG 14827 CGT A__ A
 CTA TGGCAG CCCCTC GC GGC
 ||||| ||||| || |||
 ATCGTC GGGGGAG CG CCG
 TCC AAC C
 GAM2350 TK1 3' CCTACTGGACGCTGCC 9269 CCCTC C
 GGCAGCGTCC AG AGG
 ||||| || |||
 CCGTCGCAGG TC TCC
 _____ A
 GAM2350 Apg4B 3' GCCTGCCGAGGGGCTGCGC 14976 CC A
 GCGT CCCTC GCAGGC
 ||| ||||| |||||
 CGCG GGGAG CGTCCG
 TC C
 GAM2350 C11orf9 3' CCTGCTGGAAGCTGCCA 14945 G CCCTC
 TGGCAGC TCC AGCAGG
 ||||| ||| |||||
 ACCGTCG AGG TCGTCC
 A _____
 GAM2350 CACNA1H 5' CCCGCGGGGACGCCGCC 22077 A CTCA A
 GGC GCGTCCCC GC GG
 ||| ||||| || |||
 CCG CGCAGGGG CG CC
 C _____ C
 GAM2350 CECR7 5' GCCTGGCGCCAGGGACGCTGCC 38878 CCTCA _
 A TGGCAGCGTCCC GC AGGC
 ||||| || |||

ACCGTCGCAGGG CG TCCG
 ACCG_ G
 GAM2350 CGB7 5' CCAGGCAGGGGACGCACCA 26993 CA CTCA A_
 TGG GCGTCCCC GC GG
 ||| ||||| || ||
 ACC CGCAGGGG CG CC
 A_ A__ GA
 GAM2350 CRMP5 3' GCCTGCTGAGAGAGGGTCG 21332 T C__
 CG CCC CTCAGCAGGC
 || ||| |||||
 GC GGG GAGTCGTCCG
 T AGA
 GAM2350 FLJ11160 3' GCCCTTCAAAGATGCTGCCA 20352 CCCCTC CA
 TGGCAGCGTC AG GGC
 ||||| || |||
 ACCGTCGTAG TC CCG
 AACT_ __
 GAM2350 FLJ12438 5' CCTGCTGAGAGAGGCCCA 22455 CA G CCC
 TGG GC TC CTCAGCAGG
 ||| ||| |||||
 ACC CG AG GAGTCGTCC
 _ G A_
 GAM2350 FLJ14957 3' GCCTGCTGAGAGAAGCC 26682 AGCG CCC
 GGC TC CTCAGCAGGC
 ||| || |||||
 CCG AG GAGTCGTCCG
 A__ A_
 GAM2350 FLJ22195 5' GCCTGCTGAGAAGCGTGGTGC 22998 _ CCCC
 GCA GCGT CTCAGCAGGC
 ||| ||| |||||
 CGT TGCG GAGTCGTCCG
 GG AA_
 GAM2350 FLJ23306 5' GCTCTCAAGGAGATGCTGCCA 23734 _ CCTC_
 TGGCAGCGTC CC AGC
 ||||| || |||
 ACCGTCGTAG GG TCG
 A AACTC
 GAM2350 JAM1 5' CCTGCTGAAGGAGTCC 29339 CA G CCC
 GG GC TCC TCAGCAGG
 || ||| |||||
 CC TG AGG AGTCGTCC
 _ _ A_
 GAM2350 K-ALPHA-1 5' GCAAGGAAGATGCTGCCA 37743 CC CA
 TGGCAGCGTC CCT GC
 ||||| ||| ||
 ACCGTCGTAG GGA CG
 AA A_
 GAM2350 KIAA0544 3' CCTGCTGACATCTACCTGCCA 35111 C CCCCC
 TGGCAG GT TCAGCAGG
 ||||| || |||||

		ACCGTC CA AGTCGTCC		
		_ TCTAC		
GAM2350 KIAA0789	5'	GCCTGCTGAGCTCAGCTGGCA 31847	G	GTCCCC
		TG CAGC CTCAGCAGGC		
		AC GTCG GAGTCGTCCG		
		G ACTC__		
GAM2350 KIAA0945	3'	CCTGCTGAGCTGCAGCCA 17295	A	TCCCC
		TGGC GCG CTCAGCAGG		
		ACCG CGT GAGTCGTCC		
		A C__		
GAM2350 KIAA1055	3'	CCTGCAAGGGGGACCCTGCCA 32851	C	CA
		TGGCAG GTCCCCCT GCAGG		
		ACCGTC CAGGGGGA CGTCC		
		C A_		
GAM2350 KIAA1762	3'	GCCTGGACTCTAGGGGATGCCG 31912	A	CTC _
		CCA TGGC GCGTCCCC AG CAGGC		
		ACCG CGTAGGGG TC GTCCG		
		C ATC AG		
GAM2350 KIAA1906	3'	CCTGCTGAGGGAGACACCA 36228	CAGC	C
		TGG GTC CCCTCAGCAGG		
		ACC CAG GGGAGTCGTCC		
		A__ A		
GAM2350 MAP3K3	3'	GCCCCGCGATGTGGAAGTCTGC 8221		__ CCC A A
		CA TGGCAGCG TCC TC GC GGC		
		ACCGTCGT AGG AG CG CCG		
		CA TGT _ C		
GAM2350 MDN1	3'	GCCTTGAGGAGATGCTGCCA 31410	CC	GC
		TGGCAGCGTC CCTCA AGGC		
		ACCGTCGTAG GGAGT TCCG		
		A_ _		
GAM2350 MGC13170	5'	GCCATGGCTAGGAAAGCGCTGC 26433		CCC C A__
		CA TGGCAGCGT CCT AGC GGC		
		ACCGTCGCG GGA TCG CCG		
		AAA _ GTA		
GAM2350 NPTXR	3'	CCTGCTGAGACCTAGGTTGCCA 27733		GTCCCC
		TGGCAGC CTCAGCAGG		
		ACCGTTG GAGTCGTCC		
		GATCCA		
GAM2350 NPTXR	3'	CCTGCTGAGACCTAGGTTGCCA 15585		GTCCCC
		TGGCAGC CTCAGCAGG		

		ACCGTTG GAGTCGTCC		
		GATCCA		
GAM2350	RAB35	3' CCTGGCGAGGACGCTGCC 13733	CCC	AG
		GGCAGCGTCC TC CAGG		
		CCGTCGCAGG AG GTCC		
		___ CG		
GAM2350	STARD7	3' CTGTAGAAGGGGGACATGCCA 21357	GC	_ A
		TGGCA GTCCCCCT C GCAG		
		ACCGT CAGGGGGA G TGTC		
		A_ A A		
GAM2350	STARD7	5' GCCATTTAGGGGGACGCTGC 21358	CAGCA	
		GCAGCGTCCCCCT GGC		
		CGTCGCAGGGGGA CCG		
		TTTA_		
GAM2350	STARD7	3' CTGTAGAAGGGGGACATGCCA 29260	GC	_ A
		TGGCA GTCCCCCT C GCAG		
		ACCGT CAGGGGGA G TGTC		
		A_ A A		
GAM2350	TRAF3	5' CCTGCTGAGGGGAAGCCA 30043	AGCGTC	
		TGGC CCCCTCAGCAGG		
		ACCG GGGGAGTCGTCC		
		AA___		
GAM2350	LOC120425	3' GCCTGCTGAGGGGAGGGGAGC 36621	GT	___
		GC CCC CCTCAGCAGGC		
		CG GGG GGAGTCGTCCG		
		AG AGG		
GAM2350	LOC146823	3' CTCAGCAGGCACAGGAAGCGCT 40747	C_ _____	CAGC
		GCCA GCAGCGT CC CCT AG		
		CGTCGCG GG GGA TC		
		AA ACAIIC CGAC		
GAM2350	LOC150372	3' GCCTGCTGAAGCCCTCCTTGCC 38941	CGTCCCCC	
		A TGGCAG TCAGCAGGC		
		ACCGTT AGTCGTCCG		
		CCTCCCGA		
GAM2350	LOC151176	3' CCTGCTGAGGAAGAGTTAACC 41314	C_ G CC	
		GG AGC TC CCTCAGCAGG		
		CC TTG AG GGAGTCGTCC		
		AA _ AA		
GAM2350	LOC153577	3' CCTGCAGGACGCTGGCA 41644	G	CCCTCA
		TG CAGCGTCC GCAGG		

AC GTCGCAGG CGTCC
 G A____
 GAM2350 LOC157653 5' GCCTGCTGAAGGGAAGCCA 39634 AGCG CC
 TGGC TCCC TCAGCAGGC
 |||| ||| |||||
 ACCG AGGG AGTCGTCCG
 A__ A_
 GAM2350 LOC163682 5' GCCTGCTGAAAGAGCCTCC 42095 CA G CCCC
 GG GC TC TCAGCAGGC
 || ||| |||||
 CC CG AG AGTCGTCCG
 TC _ AA_
 GAM2350 LOC222681 5' CCATGAGGGGGAGGCTGCCA 44615 G GCA
 TGGCAGC TCCCCCTCA GG
 ||||| ||||| ||
 ACCGTCG AGGGGGAGT CC
 G A_
 GAM2350 LOC253216 3' CCTACTGGGCCGCTGCCA 45518 T CCTC C
 TGGCAGCG CCC AG AGG
 ||||| ||| || |||
 ACCGTCGC GGG TC TCC
 C _ A
 GAM2350 LOC257507 5' CCATGAGGGGGAGGCTGCCA 46681 G GCA
 TGGCAGC TCCCCCTCA GG
 ||||| ||||| ||
 ACCGTCG AGGGGGAGT CC
 G A_
 GAM2350 LOC257625 5' CCATGAGGGGGAGGCTGCCA 46737 G GCA
 TGGCAGC TCCCCCTCA GG
 ||||| ||||| ||
 ACCGTCG AGGGGGAGT CC
 G A_
 GAM2351 ADAMTS4 3' TGAGATTATAGGCACCTACCAC 11569 GG C
 GTGGTAGGTGCTTA AA CTCA
 ||||| ||||| || |||
 CACCATCCACGGAT TT GAGT
 A_ A
 GAM2351 ATF7 3' GAGGTTTCCTTTGTTCTACC 13725 T TT
 GGTAGG GC AGGAACCTC
 ||||| || |||||
 CCATCT TG TCCTTGAG
 _ TT
 GAM2351 G6PC 3' TGAGACGGCGCACCTATCAC 5658 TTAGGAAC
 GTGGTAGGTGC CTCA
 ||||| ||||| |||
 CACTATCCACG GAGT
 CGGCA_
 GAM2351 HD 3' TGAGACCCCCAAGCTTCCACC 7897 A T_ A AAC
 GGT GG GCTT GG CTCA
 ||| || ||| || |||

CCA CC CGAA CC GAGT
 _ TT C CCA
 GAM2351 IRAK4 3' AGGTTCTAAACAACTCACT 30691 TAGG C
 AGTGG TG TTAGGAACCT
 |||| ||||||||
 TCACT AC AATCCTTGGA
 CA_ A
 GAM2351 NDRG3 3' TGAGACTACAGGCACCTGCCAC 25726 AGGAAC
 GTGGTAGGTGCTT CTCA
 |||||||| ||||
 CACCGTCCACGGA GAGT
 CATCA_
 GAM2351 REGL 3' AGGCTCCCACTGCTACTACT 13256 _ CTTA A
 AGTGGTAG GTG GGA CCT
 |||||| || ||||
 TCATCATC CAC CCT GGA
 GT _ C
 GAM2351 SMT3H1 3' TGAGGCCCAGGACCCACC 30126 A G TA AA
 GGT GGT CT GG CCTCA
 || || || || ||||
 CCA CCA GA CC GGAGT
 C G _ C_
 GAM2351 FLJ13102 3' TGAGGCTGGCCACCTGCCACT 24344 C GAA
 AGTGGTAGGTG TTAG CCTCA
 |||||||| |||| ||||
 TCACCGTCCAC GGTC GGAGT
 C _
 GAM2351 FLJ20320 3' TGAGGCTGCCCCTCCTACCAC 19384 TGCTTA AA_
 GTGGTAGG GG CCTCA
 |||||| || ||||
 CACCATCC CC GGAGT
 TCC_ GTC
 GAM2351 FLJ20584 3' GAGGCTCCTCCCCACCAC 19562 A TGCTT A
 GTGGT GG AGGA CCTC
 |||| || |||| ||||
 CACCA CC TCCT GGAG
 C C_ C
 GAM2351 GIT1 3' AGGCCAGCACCCACCAT 15256 A TA AA
 GTGGT GGTGCT GG CCT
 |||| |||| || ||||
 TACCA CCACGA CC GGA
 C _ _
 GAM2351 KIAA0980 3' TTCCAGTTTTTGCCACT 24812 T TA
 AGTGGTAGG GCT GGAA
 |||||| || ||||
 TCACCGTTT TGA CCTT
 _ C_
 GAM2351 KIAA1553 3' GAAACTCCCATCTACCCCT 44144 T CTTA ACC
 AG GGTAGGTG GGA TC
 || |||||| || ||

		TC CCATCTAC	CCT	AG		
		C	___	CAA		
GAM2351	KIAA1854	3'	TAAGTAAAACACTACCACT	35535	___	___
			AGTGGTAG GT	GCTTA		
			TCACCATC CA	TGAAT		
			A	AAA		
GAM2351	OSBPL8	3'	TTCAAGCACTACCACT	21910	G	A
			AGTGGTAG TGCTT	GGA		
			TCACCATC ACGAA	CTT		
			___	___		
GAM2351	PHRET1	3'	TGAAGTCTTCACATCTACCACT	22178	CTT	ACC
			AGTGGTAGGTG	AGGA TCA		
			TCACCATCTAC	TTCT AGT		
			AC_	GA_		
GAM2351	USP2	5'	GAGGCTCCAGTCCCCACT	10401	TA T	TA A
			AGTGG	GG GCT GGA CCTC		
			TCACC	CC TGA CCT GGAG		
			___	___	C_	C
GAM2351	LOC130412	5'	TGAAGTTTGCACCTGGCACCTAC	37293	TAG_	C
			CAC	GTGGTAGGTGCT	GAAC TCA	
			CACCATCCACGG	TTTG AGT		
			TCACG	A		
GAM2351	LOC146337	3'	TCCAAAACCTACCACT	40693	GC	A
			AGTGGTAGGT	TT GGA		
			TCACCATCCA	AA CCT		
			A_	___		
GAM2351	LOC152794	5'	TGAGACTACAGGCACGCACCAC	39322	AG	AGGAAC
			GTGGT	GTGCTT CTCA		
			CACCA	CACGGA GAGT		
			CG	CATCA_		
GAM2351	LOC206012	5'	TGAACTTCAGCTGCACCCACA	43110	___	A TTAG CC_
			CAC	GTG GT GGTGC GAA TCA		
			CAC CA	CCACG CTT AGT		
			A C	TCGA CAA		
GAM2351	LOC254251	5'	TTCCCAACAGCTTCCACT	45901	T G C	A
			AGTGG	AG TG TT GGAA		
			TCACC	TC AC AA CCTT		
			T G	_ C		
GAM2351	LOC257480	5'	GAGGTTCCCCCAGCTGCCAC	38146	G	CTTA
			GTGGTAG	TG GGAACCTC		

CACCGTC AC CCTTGGAG
G CC__
GAM2351 LOC257612 5' TGAGGTTCTGGGCCCCGCACCA 46743 A_ T
C GTGGT GG GCTTAGGAACCTCA
||||| || |||||
CACCA CC CGGGTCCTTGGAGT
CG _
GAM2351 LOC91156 5' TCCAGACCTACCACT 32466 G TA
AGTGGTAGGT CT GGA
||||||| || |||
TCACCATCCA GA CCT

GAM2352 ATP7B 3' ACCAAAAAACCTCACTGGGC 5503 CTCTC
GCCCAGTGGGGT TGGT
||||||| |||
CGGGTCACTCCA ACCA
AAAA_
GAM2352 B3GAT1 3' ACCAGAGAGCAGCCACGGGCA 20715 A GT_
TGCCC GTGGG CTCTCTGGT
||||| ||| |||||
ACGGG CACCC GAGAGACCA
_ GAC
GAM2352 B3GAT1 3' ACCAGAGAGCAGCCACGGGCA 27627 A GT_
TGCCC GTGGG CTCTCTGGT
||||| ||| |||||
ACGGG CACCC GAGAGACCA
_ GAC
GAM2352 CA7 3' ACCAGAGAGACTCAAGCA 30214 CCAGTG
TGC GGGTCTCTCTGGT
||| |||||
ACG CTCAGAGAGACCA
AA__
GAM2352 CERD4 3' ACCAGAGAGGGAGGCCACTG 14342 GG_
CAGTGG TCTCTCTGGT
||||| |||||
GTCACC GGAGAGACCA
GGAG
GAM2352 DPYSL3 3' ACCAGAGAAAAGTACACACTGG 7069 GG ____
GC GCCCAGTG GT C TCTCTGGT
||||| || |||||
CGGGTCAC CA G AGAGACCA
A_ T AAA
GAM2352 GNB1 3' CCAGAGAGTCTAGGGCA 7848 AGTG T
TGCCC GGG CTCTCTGG
||||| || |||||
ACGGG TCT GAGAGACC
A__ _
GAM2352 IL2RA 3' ACCAAAAAGGGATCCGTAC 5997 _ C_
GTG GGGTCTCT TGGT
||| ||||| |||

			CAT CCTAGGGA ACCA		
			G AAA		
GAM2352	LRP1	3'	ACCAGAACGCACCCCACTGGG 8135	CTC_	
			CCCAGTGGGGT TCTGGT		
			GGGTCACCCCA AGACCA		
			CGCA		
GAM2352	MGA	3'	ACCAGAGATTTTACTGGG 31453	TC	
			CCCAGTGGGG TCTCTGGT		
			GGGTCATTTT AGAGACCA		
			T_		
GAM2352	MSN	3'	ACCAGAGAGCTGCTGGG 30224	TG GGT	
			CCCAG G CTCTCTGGT		
			GGGTC C GAGAGACCA		
			GT _		
GAM2352	RANBP3	3'	ACCACACACCCCACTGGGC 9687	CTCTC	
			GCCCAGTGGGGT TGGT		
			CGGGTCACCCCA ACCA		
			CAC_		
GAM2352	RANBP3	3'	ACCACACACCCCACTGGGC 14239	CTCTC	
			GCCCAGTGGGGT TGGT		
			CGGGTCACCCCA ACCA		
			CAC_		
GAM2352	RUNX3	3'	CCAGAGACACACTGGCA 10548	C GGGTC	
			TGCC AGTG TCTCTGG		
			ACGG TCAC AGAGACC		
			_ AC_		
GAM2352	ZNF141	3'	ACCAGAGAGAAACCCTAC 9496	_	
			GTGGGG TCTCTCTGGT		
			CATCCC AGAGAGACCA		
			AA		
GAM2352	AFAP	3'	ACCAGCTTCCTCACCAGGCA 22289	CA TCTCT	
			TGCC GTGGGG CTGGT		
			ACGG CACTCC GACCA		
			AC TTC_		
GAM2352	DDR1	3'	ACCTGGGGCCCCACTGGACA 15178	C CTCT	
			TG CCAGTGGGGTCT GGT		
			AC GGTACCCCCGGG CCA		
			A T_		
GAM2352	DDR1	3'	ACCTGGGGCCCCACTGGACA 15180	C CTCT	
			TG CCAGTGGGGTCT GGT		

AC GGTCACCCCGGG CCA
 A T____
 GAM2352 DDR1 3' ACCTGGGCCCCACTGGACA 7677 C CTCT
 TG CCAGTGGGGTCT GGT
 || ||||| ||
 AC GGTCACCCCGGG CCA
 A T____
 GAM2352 FLJ00001 3' ACCAGGGCAGACCCCACTAAGC 39770 CC _
 GC AGTGGGGTCT CTCTGGT
 || ||||| |||||
 CG TCACCCCAAGA GGGACCA
 AA C
 GAM2352 FLJ12895 5' ACCACCTGAGCCCACTGGGCA 23403 G TCTC
 TGCCCACTGGG TC TGGT
 ||||| || |||
 ACGGGTCACCC AG ACCA
 G TCC_
 GAM2352 FLJ13150 3' ACCAGAAAGCAGCCCACTGG 24200 GT_ C
 CCAGTGGG CT TCTGGT
 ||||| || |||||
 GGTCAACC GA AGACCA
 GAC A
 GAM2352 FLJ20209 3' ACCAGAAAGACATTGGGC 41402 GGG C
 GCCCAGT GTCT TCTGGT
 ||||| ||| |||||
 CGGGTTA CAGA AGACCA
 _ A
 GAM2352 FLJ20209 3' ACCAGAGAGTTTCACTAGGG 41403 _ _ T
 CCC AGTG GGG CTCTCTGGT
 || ||| || |||||
 GGG TCAC CTT GAGAGACCA
 A A _
 GAM2352 FLJ20241 5' ACCAATTCACCCAGCTGGGCA 19312 G CTCTC
 TGCCCACTGGG TGGT
 ||||| ||| |||
 ACGGGTCG CCA ACCA
 A CTTA_
 GAM2352 HIG2 3' ACCAGAGAACTATTACTAGGC 14977 C _ C
 GCC AGTGG GGT TCTCTGGT
 || |||| || |||||
 CGG TCATT TCA AGAGACCA
 A A _
 GAM2352 KIAA0355 3' ACCAAAAAGAGGCTGGGC 16187 GGGGT C_
 GCCCAGT CTCT TGGT
 ||||| ||| |||
 CGGGTCG GAGA ACCA
 _ AAA
 GAM2352 KIAA0514 3' ACCAGAGGGAGTCACAGGCA 16200 CA G G
 TGCC GTG G TCTCTCTGGT
 ||| ||| |||||

		ACGG CAC T AGGGAGACCA		
		A _ _ G		
GAM2352	KIAA0545	3' CCGCGAACCCCACTGG	31633	C TC
		CCAGTGGGGT TC TGG		
		GGTCACCCCA AG GCC		
		_ C _		
GAM2352	KIAA1272	3' ACCAGAGATGAACCCACTG	34759	G _
		CAGTGGG TC TCTCTGGT		
		GTCACCC AG AGAGACCA		
		A T		
GAM2352	KIAA1871	3' ACCAGAAAATCCCACTGG	30702	_ CTC
		CCAGTG GGGT TCTGGT		
		GGTCAC CCTA AGACCA		
		A AA _		
GAM2352	KIAA1879	5' CCAGAGGCGCCAGGCA	36412	CAG G CT
		TGCC TGG GT CTCTGG		
		ACGG ACC CG GAGACC		
		_ G _		
GAM2352	PCYT2	3' CCACCTCCCACTGGGCA	8761	TCTCTC
		TGCCCAGTGGGG TGG		
		ACGGGTCACCCT ACC		
		CC _ _		
GAM2352	USP22	3' ACCAGAGAAACAGAGATGGGC	33750	GTGGG C
		GCCCA GT TCTCTGGT		
		CGGGT CA AGAGACCA		
		AGAGA A		
GAM2352	LOC112476	3' ACCAAAGCGCCCACTGGCA	29749	C GTCT C
		TGCC AGTGGG CT TGGT		
		ACGG TCACCC GA ACCA		
		_ GC _ A		
GAM2352	LOC144501	3' ACCAGCCTCCCACTGCACA	40422	CC TCTCT
		TG CAGTGGGG CTGGT		
		AC GTCACCCT GACCA		
		AC CC _		
GAM2352	LOC150935	3' CCAGGTCCCCACTGGCA	39018	C T TCT
		TGCC AGTGGGG C CTGG		
		ACGG TCACCCC G GACC		
		_ T _		
GAM2352	LOC151178	5' ACCACTGCACTCCACTAAGCA	39068	CC CTCTC
		TGC AGTGGGGT TGGT		

ACG TCACCTCA ACCA
 AA CGTC_
 GAM2352 LOC155435 3' ACCACTCAGTACCCACTGGGCA 39567 GT CTC
 TGCCCAGTGGG CT TGGT
 ||||| || |||
 ACGGGTCACCC GA ACCA
 AT CTC
 GAM2352 LOC163115 3' ACCAGAGAATTACACTGG 40088 _ C
 CCAGTG GGGT TCTCTGGT
 ||||| ||| |||||
 GGTCAC CTTA AGAGACCA
 A _
 GAM2352 LOC163682 5' ACCAGAGAATGGAAGCCAGGC 42083 CAG GG ____
 GCC TGG TC TCTCTGGT
 ||| ||| || |||||
 CGG ACC AG AGAGACCA
 ____ GA GTA
 GAM2352 LOC197259 3' ACCAGAAGAACCACTCAAGCA 42471 CC_ GG C
 TGC AGTGG TCT TCTGGT
 ||| ||||| ||| |||||
 ACG TCACC AGA AGACCA
 AAC A_ _
 GAM2352 LOC201895 5' ACCAGAGAGTGGGTCTCTCAGCA 42924 CCAG T____
 TGC TGGGG CTCTCTGGT
 ||| ||||| |||||
 ACG ACTCC GAGAGACCA
 ____ TGGGT
 GAM2352 LOC220758 3' ACCAGAGAACAAATTCTGGCCA 43641 C TGGG_ C
 TG CCAG GT TCTCTGGT
 || |||| || |||||
 AC GGTC CA AGAGACCA
 C TTAAA _
 GAM2352 LOC221272 3' ACCAGAGAAGTGCTAGGC 44961 CAG G TC
 GCC TGG G TCTCTGGT
 ||| ||| || |||||
 CGG ATC T AGAGACCA
 ____ G GA
 GAM2352 LOC221584 5' ACCAAAGAACAGATCCTGG 45040 GTG ____ C
 CCA GGGTC TCT TGGT
 ||| |||| ||| ||||
 GGT CCTAG AGA ACCA
 ____ ACA A
 GAM2352 LOC254181 5' ACCAAAGACCCTACTGGGCA 46596 CTC
 TGCCCAGTGGGGTCT TGGT
 ||||| ||||| |||||
 ACGGGTCATCCCAGA ACCA
 A_
 GAM2352 LOC51152 3' ACCAGGTCCCCACTGAGG 18282 _ T TCT
 CC CAGTGGGG C CTGGT
 || ||||| || |||||

			GG GTCACCCC G GACCA		
			A T__		
GAM2352	LOC51580	3'	ACCAGAAAATCCACTGGG	18009	GTCTC
			CCCAGTGGG TCTGGT		
			GGGTCACCT AGACCA		
			AAA__		
GAM2352	LOC56963	3'	ACCAGAGACACACTGGG	35398	GGGTC
			CCCAGTG TCTCTGGT		
			GGGTCAC AGAGACCA		
			AC__		
GAM2352	LOC90317	3'	ACCAGAGAATCCACACTGG	31205	_ C
			CCAGTG GGGT TCTCTGGT		
			GGTCAC CCTA AGAGACCA		
			A _		
GAM2353	ALX3	3'	GACACTGCCCTGCTTCCTC	13223	_ GGCC
			GAGGAAGC GGGCGG GTC		
			CTCCTTCG CCCGTC CAG		
			T A__		
GAM2353	ATBF1	5'	GCCCCGCCCCGCCCCCTT	13749	AA_
			GAGG GCGGGCGGGGC		
			TTCC CGCCCCGCCCG		
			CCC		
GAM2353	ATP7B	3'	GGACGGCCCTGCCTGCCTCT	5507	GAA
			AGAG GCGGGCGGGGCCGTCC		
			TCTC CGTCCGTCCCGGCAGG		
			__		
GAM2353	AXL	5'	GGGACAGCCCGGCCCTGCCCCC	7424	AA _ G C
	TC		GAGG GC GGGC GGGC GTCCC		
			CTCC CG CCCG CCCG CAGGG		
			CC T G A		
GAM2353	AXL	5'	GGGACAGCCCGGCCCTGCCCCC	22445	AA _ G C
	TC		GAGG GC GGGC GGGC GTCCC		
			CTCC CG CCCG CCCG CAGGG		
			CC T G A		
GAM2353	BTG2	3'	GGAATCTTACCCCCACTTCCTC	13629	C CG CCG
	T		AGAGGAAG GGG GGG TCC		
			TCTCCTTC CCC CTT AGG		
			A CA CTA		
GAM2353	C1orf6	5'	GGCCCGCCCGCCCCTC	21329	AA G
			GAGG GCGGGCGGG CC		

			CTCC CGCCCGCCC GG		
			C_ _		
GAM2353 CIT	3'	GGGACGGGGGCACCCACTTCCT 34564	C CGGGG		
T		GAGGAAG GGG CCGTCCC			
		TTCCTTC CCC GGCAGGG			
		A ACGGG			
GAM2353 DBH	3'	GGAACGCCCCCGCCCCGCC 6440	AAGC C _		
		GG GGGCGGGG CGT CC			
		CC CCGCCCC GCA GG			
		GCC_ C A			
GAM2353 FOXE1	5'	GGGACGCCAGGCCCGCCCCC 10784	AA GG C		
		GG GCGGGC GGC GTCCC			
		CC CGCCCG CCG CAGGG			
		CC GA _			
GAM2353 GAB2	3'	GGGACAGCTACCACTGTCCTCT 27849	AA GC _ C		
		AGAGG GCGG GG GGC GTCCC			
		TCTCC TGTC CC TCG CAGGG			
		_ A_ A A			
GAM2353 GAB2	3'	GGGACAGCTACCACTGTCCTCT 14654	AA GC _ C		
		AGAGG GCGG GG GGC GTCCC			
		TCTCC TGTC CC TCG CAGGG			
		_ A_ A A			
GAM2353 GPR4	5'	GGTGCCGCCGCCCGCCCC 30099	AA _ CGT		
		GG GCGGGCGG GGC CC			
		CC CGCCCGCC CCG GG			
		C_ G T_			
GAM2353 HCFC1	3'	GGACAGCCAGCTCCGCCCT 35159	AA _ GG C		
		AGG GCGG GC GGC GTCC			
		TCC CGCC CG CCG CAGG			
		_ T A_ A			
GAM2353 HHLA1	5'	ACGGCCCCACCCTTATCTC 12263	A C C		
		GAGG AG GGG GGGGCCGT			
		CTCT TT CCC CCCC GGCA			
		A _ A			
GAM2353 HK2	5'	GGACCGCGCCGCCCGCCTCCCC 5690	A A G C		
T		AG GGA GCGGGCGG GC GTCC			
		TC CCT CGCCCGCC CG CAGG			
		C C G C			
GAM2353 HLCS	5'	GGACAGCCAGGGCTTCCTT 5991	GGGCGG C		
		GAGGAAGC GGC GTCC			

			TTCCTTCG	CCG CAGG		
			GGA__	A		
GAM2353	IRS1	5'	GGGACTTGGCAACCCGCCTCC	12068	A	CGGG _
			GGA GCGGG	GCC GTCCC		
			CCT CGCCC	CGG CAGGG		
			C	AA__ TT		
GAM2353	IRS2	5'	CGCCCCCGCCCGCGCCCCCT	30031	A AA	C
			AG GG	GCGGGCGGGG CG		
			TC CC	CGCCCGCCCC GC		
			C CG	C		
GAM2353	KCNC3	3'	GGTCCCCCCCGCCCCTTCC	11421	C	CCGT
			GGAAG	GGGCGGGG CC		
			CCTTC	CCCGCCCC GG		
			_	CCCT		
GAM2353	KCNK4	5'	GGAGCCCCCGCCCGGCCCTC	27151	AAG	CCG
			GAGG	CGGGCGGGG TCC		
			CTCC	GCCCGCCCC AGG		
			CCG	CCG		
GAM2353	KCNK4	5'	GGAGCCCCCGCCCGGCCCTC	27152	AAG	CCG
			GAGG	CGGGCGGGG TCC		
			CTCC	GCCCGCCCC AGG		
			CCG	CCG		
GAM2353	LAG3	5'	GGGACACCCCGCCCCCACCT	8067	AAGC	CC
			AGG	GGGCGGGG GTCCC		
			TCC	CCCGCCCC CAGGG		
			ACC_	CA		
GAM2353	LMO2	5'	GGCCGCGCGCCCCTCT	12101	AAGC	_
			AGAGG	GGGCGG GGCC		
			TCTCC	CCCGCC CCGG		
			_	G		
GAM2353	LNK	5'	GGGCCCGCCCGCCCCCTC	11975	AA	G
			GAGG	GCGGGCGGG CC		
			CTCC	CGCCCGCCC GG		
			CC	G		
GAM2353	MATK	5'	GGCCGTCCCGAGCCCCGCTTC	29304	C_____	CCG
	CTC		AGGAAGCGGG	GGGG TC		
			TCCTTCGCCC	CCCT GG		
			CCGAG	GCC		
GAM2353	MGAT2	5'	GGCCGCGCGCCCGCCCCCT	8232	A AA_	_
			AG GG	GCGGGCGG GGCC		

			TC CC CGCCCGCC CCGG		
			C GCC G		
GAM2353	MUCDHL	3'	GGGAGCCCGCCCCGCTTCC 42209	CG	CG
			GGAAGCGGG GGGC TCCC		
			CCTTCGCCC CCGG AGGG		
			CG _		
GAM2353	MUCDHL	3'	GGGAGCCCGCCCCGCTTCC 25284	CG	CG
			GGAAGCGGG GGGC TCCC		
			CCTTCGCCC CCGG AGGG		
			CG _		
GAM2353	NDRG1	3'	GGCCAGCCGCCCCACTTCC 29969	C	_
			GGAAG GGGCGG GGCC		
			CCTTC CCCGCC CCGG		
			A GA		
GAM2353	NRXN2	5'	GGAGCGCCCGGCCCCCTC 17469	AAGC	G CG
			GAGG GGGC GGGC TCC		
			CTCC CCGG CCGG AGG		
			_ G CG		
GAM2353	NRXN2	5'	GGAGCGCCCGGCCCCCTC 28985	AAGC	G CG
			GAGG GGGC GGGC TCC		
			CTCC CCGG CCGG AGG		
			_ G CG		
GAM2353	OCLN	5'	GGACCGCGTCTCCCGCCCCCT 8382	AA	C _ C
	C		GAGG GCGGG GGG GC GTCC		
			CTCC CGCCC CCT CG CAGG		
			CC T G C		
GAM2353	PAFAH1B1	5'	GGAGCCCGCCCGCTCCCCTC 6011	A_	G_
			GAGG AGCGGGCGGG CC		
			CTCC TCGCCCGCCC GG		
			CC GA		
GAM2353	PCBP1	5'	GGA CTCCCGCCCGCTCCCGCT 12869	A A	CC
			AG GG AGCGGGCGGGG GTCC		
			TC CC TCGCCCGCCCT CAGG		
			G C _		
GAM2353	PCDH9	5'	GGACAACCACCTCGTTCCTCT 40295	G	CG GCC
			AGAGGAA CGGG GG GTCC		
			TCTCCTT GCTC CC CAGG		
			_ CA AA_		
GAM2353	PKIA	5'	GGGAGCGGCCCGCTCCCC 13701	AAGC	_
			GG GGGCGGGGCCG TCCC		

			CC CTCGCCCCGGC AGGG		
			CC__ G		
GAM2353	RAD50	5'	GGCTCCATCCCCGCCCCCTCT 12295	AA	C__
			AGAGG GCGGG GGGGCC		
			TCTCC CGCCC CCTCGG		
			CC CCTA		
GAM2353	RAD50	5'	GGCTCCATCCCCGCCCCCTCT 28552	AA	C__
			AGAGG GCGGG GGGGCC		
			TCTCC CGCCC CCTCGG		
			CC CCTA		
GAM2353	SECTM1	3'	GGACGCATGCCCCTCCCTCT 8912	A C	GG C
			AGAGG AG GGGCG GC GTCC		
			TCTCC TC CCCGT CG CAGG		
			C _ A _		
GAM2353	SLC22A3	3'	GGAGTCCCTCCCGTCCACCTCC 22505	A__	C CG
	TCT		AGAGGA GCGGG GGGGC TCC		
			TCTCCT TGCCC CCCTG AGG		
			CCACC T _		
GAM2353	SMAC	5'	GGACAGCCCCGCCTCCGCCCCC 29053	AA	_ C
	T		AGG GCGG GCGGGG GTCC		
			TCC CGCC CGCCCCG CAGG		
			CC TC A		
GAM2353	SMG1	5'	GGAACGGCCGTCCTCTTCC 17479	C GG	_
			GGAAG GGGC GGCCGT CC		
			CCTTC CCTG CCGGCA GG		
			T _ A		
GAM2353	SOX10	5'	GGGCCCCCGGCCCTCCCTC 13824	A C	CC
			GAGG AG GGGCGGGG GTCC		
			CTCC TC CCGCCCC CGGG		
			C _ C_		
GAM2353	SRP46	5'	GCTCCGCCGCCCGCCTCT 25791	AA_	G
			AGAGG GCGG CGGGGC		
			TCTCC CGCC GCCTCG		
			GCC _		
GAM2353	TACC1	5'	GGCTCTCCCCACCCATTCCCCT 12967	A GC C	CC_
			AG GGAA GGG GGGG GTC		
			TC CCTT CCC CCCC CGG		
			C A_ A TCT		
GAM2353	TK1	3'	GGGCCGCCCGCTCCCTT 9270	A	G G
			GAGG AGCGGGCG G CC		

TTCC TCGCCCGC C GG
 C _ G
 GAM2353 VIPR2 3' GCGTCCCGAGACGCCGGCTTCC 9414 G _____ CCGT
 TC AGGAAGC GGCG GGG C
 ||||| ||| ||| |
 TCCTTCG CCGC CCC G
 G AGAG||| TGCC
 GAM2353 BRUNOL6 5' GGCTCCGCCCCCTCCCCCT 27421 A A C
 AG GG AG GGGCGGGGCC
 || || |||||
 TC CC TC CCCGCCTCGG
 C C C
 GAM2353 C21orf108 3' GGCCGCCCTTCCTCT 42771 C GG
 AGAGGAAG GGGC GGCC
 ||||| ||| |||
 TCTCCTTC CCCG CCGG

 GAM2353 CAPN13 5' GGAACCTGCCCGTCTCCCCT 29380 A AG G_
 AG GGA CGGGCGGG CC
 || || ||||| ||
 TC CCT GCCCGTCC GG
 C CT AA
 GAM2353 CDT1 5' GCGCGCCCGCCCGCCCCC 38066 AA _ C
 GG GCGGGCGGG GC GT
 || ||||| || ||
 CC CGCCCGCCC CG CG
 CC G _
 GAM2353 DKFZP434N1511 5' GGTGTCCCGCCCGCCGCCTC 43939 AA CGT
 GAGG GCGGGCGGGGC CC
 ||| ||||| ||
 CTCC CGCCCGCCCTG GG
 GC T_
 GAM2353 DKFZP586J1624 3' GGACCCTCCCTGCCACCCCT 17798 AAGC CC_
 C GAGG GGGCGGGG GTCC
 ||| ||||| |||
 CTCC CCCGTCCC CAGG
 CCCA TCC
 GAM2353 DKFZP727G051 3' GCCCACCCACTTTCCTCT 34430 _C CG
 AGAGGAA G GGG GGGC
 ||||| ||| |||
 TCTCCTT C CCC CCCG
 T A A_
 GAM2353 EHM2 5' GGGACGGCCCCGAGCGCGCCCT 21190 AA GG
 C GAGG GCG CGGGGCCGTCCC
 ||| || |||||
 CTCC CGC GCCCCGGCAGGG
 CG GA
 GAM2353 EPN2 3' GACAGCCCCCTGCCCATCT 17348 AGC _ C
 GGA GGGC GGGGC GTC
 || ||| ||||| |||

TCT CCCG CCCCG CAG
 AC_ TC A
 GAM2353 FLJ00001 3' GACGCCACCGGCTCCCTC 39780 A G CG C
 GAGG AGC GG GGGC GTC
 |||| ||| || |||| ||||
 CTCC TCG CC CCCG CAG
 C G A_ _
 GAM2353 FLJ13441 3' GGTTCGCCCCACTTCTTC 23395 C
 GAGGAAG GGGCGGGGCC
 |||||| ||||||||
 CTTCTTC CCCGCCTTGG
 A
 GAM2353 FLJ20085 3' GGACGGCCGCGCCGCCCCC 19186 AA GG
 GG GCGGGC GGCCGTCC
 || ||||| ||||||
 CC CGCCCG CCGGCAGG
 CC G_
 GAM2353 FLJ20898 5' GGCCGTCCCAAACAACCATTT 23851 C GC_____ CCG
 CCTCT GGAAG GG GGGG TC
 ||||| || |||| ||
 CCTTT CC CCCT GG
 A AACAAAAIII GCC
 GAM2353 FLJ22246 5' GGGACAGCCGGATCGCCCTCT 24909 AAGCG ____ C
 AGAGG GCGGG GGC GTCCC
 |||| |||| || ||||
 TCTCC CCGCT CCG CAGGG
 _____ AGG A
 GAM2353 FLJ22408 5' CCGAGCCGCGCCGCTCTTC 24173 A _____
 GAGGA GCGGGCGG GG
 |||| |||||| ||
 CTTCT CGCCCGCC CC
 C GAGIII
 GAM2353 HRD1 3' GGGACCCCTGCCCGCCCTCCC 34473 A C C_
 GG AG GGGCGGGGC GTCCC
 || || |||||| ||||
 CC TC CCCGCCCG CAGGG
 C _ TCC
 GAM2353 HSPC195 5' GCCCCGCCCTCCCCCT 39422 A A C
 AG GG AG GGGCGGGGC
 || || || ||||||
 TC CC TC CCCGCCCG
 C C _
 GAM2353 KHSRP 3' GGCCCCGCCCGTCCCCCT 9796 A AA
 AG GG GCGGGCGGGGCC
 || || ||||||||
 TC CC TGCCCGCCCGG
 C CC
 GAM2353 KIAA0420 3' GGGCCGCCCGCTCGCCTCC 31728 A G C
 GGA GCGGGCGGG C GTCC
 || |||||| | |||

CCT CGCTCGCCC G CGGG
 C _ C
 GAM2353 KIAA0513 3' GGCTGCGCCCGCTCCCTC 16359 A G
 GAGG AGCGGGCG GGCC
 |||| ||||| ||||
 CTCC TCGCCCGC TCGG
 C G
 GAM2353 KIAA0545 3' ACAGCCTTCATCTCCTCCTCT 31632 A C C_ C
 AGAGGA G GGG GGGGC GT
 ||||| | ||| ||||| ||
 TCTCCT C CTC TTCCG CA
 _ _ TAC A
 GAM2353 KIAA0668 3' GCACCCCGCGCTTCC 33050 G CC
 GGAAGCGG CGGGG GT
 ||||| ||||| ||
 CCTTCGCC GCCCC CG
 _ A_
 GAM2353 KIAA0672 5' GGACGGCCCCAGGCATTGCTCT 16920 G _ GGGC
 AGAG AA GC GGGGCCGTCC
 ||| || ||| ||||| |||||
 TCTC TT CG CCCCAGCAGG
 G A GA_
 GAM2353 KIAA0987 3' GACAGCCGCTGCTTCC 14677 G GG C
 GGAAGCGG C GGC GTC
 ||||| | ||| |||
 CCTTCGTC G CCG CAG
 _ _ A
 GAM2353 KIAA1170 3' GGTGATCCGCCCGCCTCC 34612 A _
 GGA GCGGGCGGG GCC
 ||| ||||| |||
 CCT CGCCCGCCT TGG
 C AG
 GAM2353 KIAA1867 3' GCCTCCCCACCCACCTCCTGCT 45455 _ AGC C CC
 AG AGGA GGG GGGG GT
 || |||| ||| |||| ||
 TC TCCT CCC CCCC CG
 G CCA A TC
 GAM2353 KIAA1904 3' GACTCCCCCGCCCCCTCT 36377 AAGC CC
 AGAGG GGGCGGGG GTC
 |||| ||||| |||
 TCTCC CCGCCCC CAG
 _ CT
 GAM2353 KIAA1906 3' GACAACCCCGCCTCCTCT 36231 AGCG CC
 AGAGGA GGCGGGG GTC
 |||| ||||| |||
 TCTCCT CCGCCCC CAG
 _ AA
 GAM2353 KIAA1924 3' GCGTCCCAGGACGCCCGCTTCC 36479 _ CCGT
 T AGGAAGCGGGCG GGG C
 ||||| ||| |

TCCTTCGCCCCG CCC G
 AGGAIII TGCC
 GAM2353 LHPP 3' GAGAGCCCCGCCTCCTC 22678 AGCG CG
 GAGGA GGCGGGGC TC
 IIII IIIIII II
 CTCCT CCGCCCCG AG
 _____ AG
 GAM2353 MANBAL 3' GGGCAATCCACCACTTCCTCT 22620 C GC GCC
 AGAGGAAG GG GGG GTCC
 IIIIII II III II
 TCTCCTTC CC CCT CGGG
 A A_ AA_
 GAM2353 MAPKAPK2 5' GGCCGTCCCAAAGCGGCCGCT 11150 G _____ CCGT
 TCC GAAGCGG CG GGG CC
 IIIIII II III II
 CTTGCGC GC CCC GG
 G GAAAAIII TGCC
 GAM2353 MAPKAPK2 5' GGCCGTCCCAAAGCGGCCGCT 26764 G _____ CCGT
 TCC GAAGCGG CG GGG CC
 IIIIII II III II
 CTTGCGC GC CCC GG
 G GAAAAIII TGCC
 GAM2353 NIN283 3' GACGACTCCACCGCCTCTCT 26014 AA GC C
 AGAGG GCGG GGGG CGTC
 IIII III IIII II
 TCTCT CGCC CCTC GCAG
 C_ A_ A
 GAM2353 NS1-BP 5' GATTCCCGCCCGCTTCCTC 35913 CC
 GAGGAAGCGGGCGGGG GTC
 IIIIIIIIII III
 CTCCTTCGCCCCGCCCT TAG

 GAM2353 OBTP 3' GGACAGCCCCGTCCCC 19080 AAGC C
 GG GGGCGGGGC GTCC
 II IIIIII II
 CC CCTGCCCCG CAGG
 _____ A
 GAM2353 PADI1 3' GCCCCACCCGCCATCCTCT 31055 A_ C_
 AGAGGA GCGGG GGGGC
 IIII IIII II
 TCTCCT CGCCC CCCC
 AC AC
 GAM2353 PAK6 3' GGA CTGCTGCCTCCTC 21391 A G
 GAGGA GCGGGCGGG CC
 IIII IIIIII II
 CTCCT CGTCCGTTC GG
 C A
 GAM2353 QKI 5' GGGCTCGCCCCGCCCCTCCCT 32619 A C C T_
 C GAGG AG GGGCGGGG CG CCC
 II II IIIIII II III

CTCC TC CCCGCCCC GC GGG
 C _ C TC
 GAM2353 RAB3IL1 3' GACCCCTCCCCGCTTCCTC 15063 C CC
 GAGGAAGCGGG GGGG GTC
 ||||| ||| ||
 CTCCTTCGCCC CCTC CAG
 _ CC
 GAM2353 RAI 3' GGGACAGGAAACCACTTCCTTT 13471 C GCGGGG _
 AGAGGAAG GG CC GTCCC
 ||||| || || ||||
 TTTCTTC CC GG CAGGG
 A AAA _ A
 GAM2353 RAI17 3' GGACACCCACTTCCCTCT 43862 AAGC C GCC
 AGAGG GGG GGG GTCC
 |||| ||| ||| ||||
 TCTCC TTC CCC CAGG
 C _ A A _
 GAM2353 RHOBTB1 5' GGGGGCCCCCGCTCCC 43952 A C G
 GG AGCGGG GGGGCC TCC
 || ||||| ||||| |||
 CC TCGCCC CCGCGG GGG
 C _ _
 GAM2353 SCAM-1 3' GGACCCCGGCCACATCCTC 12350 AGC CC
 GAGGA GGGCGGGG GTCC
 |||| ||||| ||||
 CTCCT CCGCCCC CAGG
 ACA _
 GAM2353 SLC26A10 5' GGTAGTCAGCCACCTCCTCT 28560 AGC GG CG
 AGAGGA GGGC GGC TC
 |||| ||| ||| ||
 TCTCCT CCG CTG GG
 CCA A _ AT
 GAM2353 TBX21 3' GAAGGCCCGCTCCCTCT 14997 A CGG G
 AGAGG AGCGGG GGCC TC
 |||| |||| ||| ||
 TCTCC TCGCCC CCGG AG
 C _ A
 GAM2353 TEX27 3' GGGCCCCCGCCCCCTCCTCT 22460 A C CC
 AGAGGA G GGGCGGGG GTCC
 ||||| | ||||| ||||
 TCTCCT C CCGCCCC CGGG
 _ C C _
 GAM2353 TUB 3' GACAGCCCTGCCTATCCTCT 9324 AGC C
 AGAGGA GGGCGGGG GTC
 |||| ||||| ||||
 TCTCCT TCGTCCCG CAG
 A _ A
 GAM2353 WSB1 5' GGCCGCCCGCCCGTCTCCTC 28617 AG C T
 T AGAGGA CGGGCGGGG CG CC
 ||||| ||||| || ||

			TCTCCT	GCCCGCCCC	GC	GG		
			CT	C	C			
GAM2353	WSB1	5'	GGCCGCCCCCGCCCGTCTCCTC	28623	AG	C	T	
	T		AGAGGA	CGGGCGGGG	CG	CC		
			TCTCCT	GCCCGCCCC	GC	GG		
			CT	C	C			
GAM2353	LOC112937	5'	GGCCCTCCCGCTTCCCCT	44005	A	C		
			AG	GGAAGCGGG	GGGGCC			
			TC	CCTTCGCCC	TCCCGG			
			C	_				
GAM2353	LOC115073	5'	GGGCACCGCCCCGCTCCCCC	36242	AAGC	C	_	
			GG	GGGCGGGG	GT	CCC		
			CC	CTCGCCCCG	CA	GGG		
			CC_	C	C			
GAM2353	LOC126917	3'	GACGGCCCTTCTCTCTCC	36871	A	C	C	
			GGA	G	GGG	GGGGCCGTC		
			CCT	C	CTC	TCCCGGCAG		
			_	T	T			
GAM2353	LOC127702	3'	GACGGCTCCCACTTCCTTT	37183	C	CGG		
			AGAGGAAG	GGG	GGCCGTC			
			TTTCCTTC	CCC	TCGGCAG			
			A	_				
GAM2353	LOC144347	3'	GGGACGGCTGCCACTCC	37724	AGCG	GG		
			GGA	GGC	GGCCGTCCC			
			CCT	CCG	TCGGCAGGG			
			CA_	_				
GAM2353	LOC145438	5'	GCGCCCGCCCGCCCCGCCCT	40537	A	AA_	_	
			AG	GG	GCGGGCGGG	GC		
			TC	CC	CGCCCGCCC	CG		
			_	GCCC	G			
GAM2353	LOC145980	5'	GGACGACCCTGCCTCCGTCT	40650	_	AGCG	C	
			AGA	GGA	GGCGGGG	CGTCC		
			TCT	CCT	CCGTCCC	GCAGG		
			G	_	A			
GAM2353	LOC146237	3'	GGACTTTTCCCCACCTCCTC	40669	AGCG	C	CC_	
			GAGGA	GG	GGGG	GTCC		
			CTCCT	CC	CCCC	CAGG		
			_	A	TTTT			
GAM2353	LOC148014	3'	GATGCCCTGCCACCTC	38440	AAGC	C		
			GAGG	GGGCGGGG	GTC			

CTCC CCGTCCCG TAG
A_____
GAM2353 LOC149182 5' GCGTCCCAGAACCCGCTCT 40971 GA C _____ CCGTC
CTCT G AGCGGG GG GG C
| ||||| || || |
C TCGCCC CC CC G
TC A AAGAI|| CTGCC
GAM2353 LOC150208 5' ACGGTGACCGCCTCCTGCT 41155 _ AGCG G_
AG AGGA GGCGG GCCGT
|| ||| |||| ||||
TC TCCT CCGCC TGGCA
G _____ AG
GAM2353 LOC151278 3' GGCCGTCCCAAAACACCCATTT 39096 C C_____ CCG
CCTCT GGAAG GGG GGGG TC
||||| ||| ||| ||
CCTTT CCC CCCT GG
A ACAAAA||| GCC
GAM2353 LOC155064 5' GGGCCGCCCGCTCCCTC 39530 A G G
GAGG AGCGGGCG G CC
||| ||||| |||
CTCC TCGCCCGC C GG
C _ G
GAM2353 LOC159199 5' GGACGGCCACCGCCTCT 39983 GAA GCG
AGAG GCGG GGGCCGTCC
||| ||| |||||
TCTC CGCC CCGGCAGG
_____ A_____
GAM2353 LOC170127 3' GGGATCGCCCGCTTCCTT 40176 GG
GAGGAAGCGGGCGG CC
||||||| |||
TTCCTTCGCCCGCT GG
AG
GAM2353 LOC199786 3' GACAAGCTTTTACCGACTTCCT 42620 _ GC C_
CT AGAGGAAG CGG GGGGC GTC
||||| ||| ||| |||
TCTCCTTC GCC TTTCG CAG
A AT AA
GAM2353 LOC200081 3' GGGACAGCCAGGCACCTGCTCC 42705 A _ _ GG C
GGA GC GG GC GGC GTCCC
||| ||| ||| |||
CCT CG CC CG CCG CAGGG
_ T A GA A
GAM2353 LOC200982 3' GGACAGCTTCACTTCCTCT 43376 CGGGC C
AGAGGAAG GGGGC GTCC
||||| ||| |||
TCTCCTTC CTTCG CAGG
A_____ A
GAM2353 LOC201229 3' GCCCCGCCCCCTCCTCT 42543 A C
AGAGGA G GGGCGGGGC
||||| | |||||

TCTCCT C CCCGCCCG
_ C
GAM2353 LOC203378 5' GGCCGTCCCAGAAGCGCCTGCT 43555 A _____ CCGT
CCCCCT G AGCGGGCG GGG CC
| ||||| ||| ||
C TCGTCCGC CCC GG
C GAAGAI|| TGCC
GAM2353 LOC219920 5' GGACCAGCCACTTCCTCT 44809 CG G G
AGAGGAAG GGC GG CC
||||| ||| |||
TCTCCTTC CCG CC GG
A_ A A
GAM2353 LOC221399 5' GGACAACATGTCCTTCCTCT 45052 GC GGGCC
AGAGGAA GGGCG GTCC
||||| |||| |||
TCTCCTT CCTGT CAGG
_ ACAA_
GAM2353 LOC221424 5' GGAACGCGCCGCCGCTCGCTC 44980 GA _ CCG
T AGAG AGCGGGCGG GG TCC
||| ||||| || |||
TCTC TCGCCCGCC CT AGG
GC G CA_
GAM2353 LOC221794 5' GGGACGGCCCCACCACCACC 45073 AAGCG C
GG GG GGGGCCGTCCC
|| || |||||
CC CC CCCCGGCAGGG
ACCA_ A
GAM2353 LOC254351 5' GGGTGATCCACCCGCCTCC 45542 A C GC T
GGA GCGGG GGG CG CCC
||| ||||| ||| |||
CCT CGCCC CCT GT GGG
C A A_ _
GAM2353 LOC254617 5' GGACCCTCCCTGCCACCCCT 46519 AAGC CC_
C GAGG GGGCGGG GTCC
||||| ||||| |||
CTCC CCCGTCCC CAGG
CCCA TCC
GAM2353 LOC257354 3' GGGCCGCCCGCTCGCCTCC 45581 A G C
GGA GCGGGCGGG C GTCC
||| ||||| ||| |||
CCT CGCTCGCCC G CGGG
C _ C
GAM2353 LOC51083 5' GGACGACCACGCGCTTCCT 18070 G G_ C
AGGAAGCGG CG GG CGTCC
||||| || ||| |||
TCCTTCGCC GC CC GCAGG
_ ACA A
GAM2353 LOC92078 3' CCAAGCCACCTGCTTCCTC 33744 C _____
GAGGAAGCGGG GG GG
||||||| || ||

CTCCTTCGTCC CC CC
 A GAAIII
 GAM2353 LOC92661 3' GGCCGTCCCAGACCCCGCTTC 34724 A C_____ CCG
 CCCT GGAAGCGGG GGGG TC
 ||||| ||| ||
 CCTTCGCCC CCCT GG
 C CCAGAIII GCC
 GAM2354 BCL7B 3' AGAAGAGAGAGATGTGGAAGGC 7433 ____ T C
 ACCTT AAGGTGCT TAT TCTCTCTCT CT
 ||||| || ||||| ||
 TTCCACGG GTG AGAGAGAGA GA
 AAG T A
 GAM2354 CEP1 5' AGGAAAGAGAGGAAACATC 13875 CTTA C
 GGTG TTTCTCTCT TCCT
 ||| ||||| |||
 CTAC AAGGAGAGA AGGA
 A____ A
 GAM2354 EHD4 3' AGAAGAAAGAGAAATTGTCC 29255 T TT C C
 GG GC ATTTCTCT TCT CT
 || || ||||| ||| ||
 CC TG TAAAGAGA AGA GA
 _ T_ A A
 GAM2354 GNAI1 5' AGGAGAGAGAGAAAGGATTCCCCT 7838 TGCTTA C
 AGG TTT TCTCTCTCCT
 ||| ||| ||||| |||
 TCC GAA AGAGAGAGGA
 CCTTAG _
 GAM2354 HAL 5' AGAGAGAGAGAAATTGGGGACC 7889 G _
 GGT CTTA TTTCTCTCTCT
 ||| ||| ||||| |||
 CCA GGGT AAAGAGAGAGA
 G T
 GAM2354 HAP1 3' AGAGAGGGGTGGATAAGCTCC 10073 T _
 GG GCTTATTT CTCTCTCT
 || ||||| |||||
 CC CGAATAGG GGGAGAGA
 T T
 GAM2354 MADH2 3' AGAGAGAAAACAGCACTT 12521 TA
 AGGTGCT TTTCTCTCT
 ||||| |||||
 TTCACGA AAAGAGAGA
 CA
 GAM2354 PIK3R1 3' AGGAGAGAGAGGCAGAAGAACC 34035 G ATT
 GGT CTT TCTCTCTCTCCT
 ||| ||| ||||| |||
 CCA GAA GGAGAGAGAGGA
 A GAC
 GAM2354 RGS9 5' AGAAAGAAAAAATGGGCATT 9927 C__ C
 GGTGCTTATTT TCT TCT
 ||||| ||| |||

			TTACGGGTAAA AGA AGA		
			AAA A		
GAM2354	SHOX2	3'	AGGAGAGAGAAAAATAATGGCA 13747	___	C
			TGCT TATTT TCTCTCTCCT		
			ACGG ATAAA AGAGAGAGGA		
			TA A		
GAM2354	SHOX2	3'	AGGAGAGAGAAAAATAATGGCA 8973	___	C
			TGCT TATTT TCTCTCTCCT		
			ACGG ATAAA AGAGAGAGGA		
			TA A		
GAM2354	ZNF38	5'	AGAAGAGAAAGGCAAGTACCTT 45310	A__	C
			AAGGTGCTT TTTCTCT TCT		
			TTCCATGAA AAAGAGA AGA		
			CGG _		
GAM2354	ABLM	3'	AGAAGAAAGAGAAACCTTCACT 8112	CTTA	C C
	TT		AAGGTG TTTCTCT TCT CT		
			TTTCAC AAAGAGA AGA GA		
			TTCC A A		
GAM2354	ABLM	3'	AGAAGAAAGAGAAACCTTCACT 13545	CTTA	C C
	TT		AAGGTG TTTCTCT TCT CT		
			TTTCAC AAAGAGA AGA GA		
			TTCC A A		
GAM2354	AD-020	3'	AGGAAAGAGAGTTACACCTT 21338	CTTATTT	C
			AAGGTG CTCTCT TCCT		
			TTCCAC GAGAGA AGGA		
			ATT___ A		
GAM2354	AD-020	3'	AGGAAAGAGAGTTACACCTT 29868	CTTATTT	C
			AAGGTG CTCTCT TCCT		
			TTCCAC GAGAGA AGGA		
			ATT___ A		
GAM2354	ARHGEF9	5'	GAAGGGGGGAACCAAGCACC 17541	AT	TC
			GGTGCTT TTCTCTC TC		
			CCACGAA AAGGGGG AG		
			CC GA		
GAM2354	DKFZP564K0822	3'	GGAGAGAGCAAGCCCCTT 45140	T	ATTTCT
			AAGG GCTT CTCTCTCC		
			TTCC CGAA GAGAGAGG		
			C C___		
GAM2354	DKFZP586M1120	3'	AGGAGAGAAAGGGCAGCTCC 25318	T	TAT C
			GG GCT TTCT TCTCTCCT		

			CC CGA GGA AGAGAGGA		
			T C_ A		
GAM2354	FLJ10769	3'	AGAAGTAAACAGGCACCTT 20111	_____	
			AAGGTGCT TATTTCT		
			TTCCACGG ATGAAGA		
			ACAA		
GAM2354	FLJ20015	3'	GGAACAGAAACAAGCACTT 21069	A	CTCTC
			AGGTGCTT TTTCT TCC		
			TTCACGAA AAAGA AGG		
			C CA_		
GAM2354	FLJ20420	3'	GGAGAGAAAATGTACCT 19460	TTA	
			AGGTGC TTTCTCTCT		
			TCCATG AAAGAGAGG		
			TA_		
GAM2354	HAND1	3'	GAGAAAGAGAAATATATAT 11236	CT	C
			GTG TATTTCTCT TCTC		
			TAT ATAAAGAGA AGAG		
			AT A		
GAM2354	KIAA0716	3'	AGTGTGAAAAAAGCACCTT 16245	A	TCT
			AAGGTGCTT TTTC CT		
			TTCCACGAA AAAG GA		
			A TGT		
GAM2354	KIAA1095	3'	AGAGAGAGAAAAACACC 33505	C A	
			GGTG TT TTTCTCTCTCT		
			CCAC AA AAAGAGAGAGA		
			- -		
GAM2354	KIAA1416	3'	AGAGAGAATCAGGTACCTT 41798	AT	
			AAGGTGCTT TTCTCTCT		
			TTCCATGGA AAGAGAGA		
			CT		
GAM2354	KIAA1582	3'	GGAACAGAAACAAGCACTT 32590	A	CTCTC
			AGGTGCTT TTTCT TCC		
			TTCACGAA AAAGA AGG		
			C CA_		
GAM2354	KIAA1841	3'	AGAGAGAAGGCACTCTT 39024	_	TAT
			AAG GTGCT TTCTCTCT		
			TTC CACGG AAGAGAGA		
			T _		
GAM2354	KIAA1889	3'	GAAAGAGGGAAACATC 36387	CTTA	C
			GGTG TTTCTCTCT TC		

			CTAC	AAAGGGAGA	AG		
			_____	A			
GAM2354	MGC13183	3'	AGAGAGAGAAGCACT	26144	TATT		
			GGTGCT	TCTCTCTCT			
			TCACGA	AGAGAGAGA			

GAM2354	OLFM3	3'	AGGACCCTGAAAATAAGCAC	39958	C TCTC		
			GTGCTTATTT	TC TCCT			
			CACGAATAAA	AG AGGA			
			_____	TCCC			
GAM2354	PDE10A	3'	AGAGAGAGAAGTACC	13460	TATT		
			GGTGCT	TCTCTCTCT			
			CCATGA	AGAGAGAGA			

GAM2354	PDE4DIP	3'	AGAGCCCAAATAAGCATC	16049	CT_		
			GGTGCTTATTT	CTCT			
			CTACGAATAAA	GAGA			
			_____	CCC			
GAM2354	SH3BGRL	3'	AGGAGAAAGAGAAATAACCT	31023	GCT C		
			AGGT	TATTTCTCT TCTCCT			
			TCCA	ATAAAGAGA AGAGGA			
			_____	A			
GAM2354	SLC31A2	3'	GGAAAGAGAGAGAAAATCACT	30192	CTTA C		
			GGTG	TTTCTCTCT TCC			
			TCAC	AAAGAGAGA AGG			
			_____	TA_ A			
GAM2354	STC2	3'	GAGAGAGAGAGAAAAGAGCCTC	9811	T A		
			GG	GCTT TTTCTCTCTCTC			
			CT	CGAG AAAGAGAGAGAG			
			_____	C A			
GAM2354	TBLR1	3'	AGAAGAGAGAGAAAAATATACATT	23965	CT C C		
			GGTG	TATTT TCTCTCT CT			
			TTAC	ATAAA AGAGAGA GA			
			_____	AT A A			
GAM2354	TOB2	3'	AGAGGAGAGAAATAAACCTT	45761	GC T		
			AAGGT	TTATTTCTC CTCT			
			TTCCA	AATAAAGAG GAGA			
			_____	A_ _			
GAM2354	TP53INP1	3'	AGTGAGAGAAATAAGACCT	36115	G T		
			AGGT	CTTATTTCTC CT			

TCCA GAATAAAGAG GA
 — T
 GAM2354 TP53INP1 3' AGTGAGAAATAAGACCT 27104 G T
 AGGT CTTATTTCTC CT
 |||| ||||| ||
 TCCA GAATAAAGAG GA
 — T
 GAM2354 VILL 5' GGAGAGAAAGGCTCCTT 33947 T TA
 AAGG GCT TTTCTCTCT
 |||| || |||||
 TTCC CGG AAAGAGAGG
 T —
 GAM2354 LOC115110 3' AGAGAGAAACACACACCTT 35504 CTTA
 AAGGTG TTTCTCTCT
 |||| |||||
 TTCCAC AAAGAGAGA
 ACAC
 GAM2354 LOC126669 3' AGAAGAGAGAGTAAAGGACCTT 37155 G ATTT C
 AAGGT CTT CTCTCTCT CT
 |||| || ||||| ||
 TTCCA GAA GAGAGAGA GA
 G AT__ A
 GAM2354 LOC127396 3' GGAGAGAAAGGCACTT 36895 TA
 AGGTGCT TTTCTCTCT
 ||||| |||||
 TTCACGG AAAGAGAGG
 —
 GAM2354 LOC147671 3' AGAGGAGAAATAAAACCTT 38375 GC T
 AAGGT TTATTTCTC CTCT
 |||| ||||| ||||
 TTCCA AATAAAGAG GAGA
 A_ —
 GAM2354 LOC150185 3' AGAGAGGCTGGCATCTT 41151 TATT
 AAGGTGCT TCTCTCT
 ||||| |||||
 TTCTACGG GGAGAGA
 TC__
 GAM2354 LOC154739 5' AGGAAAGAGAAATAGGCCCTT 41712 T CTC
 AAGG GCTTATTTCTCT TCCT
 |||| ||||| ||||
 TTCC CGGATAAAGAGA AGGA
 — A__
 GAM2354 LOC160717 5' GGAAAGGAACAAGCACCTT 40009 A C
 AAGGTGCTT TTTCT TCT
 ||||| |||| ||||
 TTCCACGAA AAGGA AGG
 C A
 GAM2354 LOC169426 5' AGAGAGAGACCCAGCATC 42206 TATT
 GGTGCT TCTCTCTCT
 ||||| |||||

		CTACGA AGAGAGAGA		
		CCC_		
GAM2354	LOC200150 3'	GGAGAGAAAAAACACTTT	42712	C A
		AAGGTG TT TTTCTCTCT		
		TTTCAC AA AAAGAGAGG		
		_ A		
GAM2354	LOC219731 5'	AGGAGAGAAAGGCAGCTCC	44715	T TATT C
		GG GCT TCT TCTCTCCT		
		CC CGA GGA AGAGAGGA		
		T C__ A		
GAM2354	LOC221069 5'	GAGAGAGAGAAAAAACCT	44767	GCTTA
		AGGT TTTCTCTCTCTC		
		TCCA AAAGAGAGAGAG		
		AA__		
GAM2354	LOC221294 5'	AGAAAGAGTGGAAGCACTT	44112	ATTT C
		AGGTGCTT CTCT TCT		
		TTCACGAA GAGA AGA		
		GGT_ A		
GAM2354	LOC221550 5'	AGAAGAAAAGAGCACCT	44238	A C
		AGGTGCTT TTTCT TCT		
		TCCACGAG AAAGA AGA		
		A _		
GAM2354	LOC222008 3'	GGAGAGAAAAAAGTGACT	45125	GT A
		AG GCTT TTTCTCTCT		
		TC TGAA AAAGAGAGG		
		AG A		
GAM2354	LOC222256 3'	AGAAGAAAACCTCAGTAGGCACC	45247	TCTCTC C
	TT	AAGGTGCTTATT TCT CT		
		TTCCACGGATGA AGA GA		
		CTCAAA A		
GAM2354	LOC253263 3'	AGGAAAGAAAAAAGGAAAGGA	46359	G A C__ C
	ACCTT	AGGT CTT TTTCT TCT TCCT		
		TCCA GGA AAGGA AGA AGGA		
		A _ AAAAA A		
GAM2354	LOC256021 3'	AGGAAAGAGAAATGTCACC	46163	CT CTC
		GGTG TATTTCTCT TCCT		
		CCAC GTAAAGAGA AGGA		
		T_ A__		
GAM2354	LOC256118 5'	AGGAAAAAGAGAAATGCTTCAC	46601	CT_ CTC
	T	GGTG TATTTCTCT TCCT		

			TCAC GTAAAGAGA AGGA		
			TTC AAA		
GAM2354	LOC257495	5'	AGAAGAAAAGAGCACCT 46655	A	C
			AGGTGCTT TTTCT TCT		
			TCCACGAG AAAGA AGA		
			A _		
GAM2354	LOC257576	5'	AGAAGAAAAGAGCACCT 46715	A	C
			AGGTGCTT TTTCT TCT		
			TCCACGAG AAAGA AGA		
			A _		
GAM2354	LOC92078	3'	AGAAGAGAGAGCAGAGCCCCTT 33740	T	ATTT C
			AAGG GCTT CTCTCTCT CT		
			TTCC CGAG GAGAGAGA GA		
			C AC_ A		
GAM2354	LOC92303	3'	AGAGAGGGAAAGACC 34133	G	ATT
			GGT CTT TCTCTCTCT		
			CCA GAA AGGGAGAGA		
			_ _		
GAM2355	BAZ2B	3'	GATAGCTATACAGTCTGTACA 15124	C	CT A C
			TGT ACAGACTG TA GC ATC		
			ACA TGTCTGAC AT CG TAG		
			_ AT _ A		
GAM2355	GPR85	3'	ATGGTACCAGCCTGTCACA 21042	C	A CTTAA
			TGT ACAG CTG GCCAT		
			ACA TGTC GAC TGGTA		
			C C CA_		
GAM2355	NTRK2	3'	GATGGCTTAAGCCTGTGTATA 12845	_	ACT
			TGT CACAG GCTTAAGCCATC		
			ATA GTGTC CGAATTCGGTAG		
			T _		
GAM2355	UBE2L3	3'	GCTTGGTCTGGTCTGTGCA 9360	T	_ T
			TG CACAGACT GCT AAGC		
			AC GTGTCTGG TGG TTCG		
			_ TC _		
GAM2355	DKFZP761G1913	3'	GATGCAAGGAGCTGCCTGTGAC 25545		ACT AAGC
			TGTCACAG GCTT CATC		
			ACAGTGTC CGAG GTAG		
			CGT GAAC		
GAM2355	EIF5	3'	ATGGCTTAACATCATGCTACA 7698	CA	_ C C
			TGT CA GA TG TTAAGCCAT		

ACA GT CT AC AATTCGGTA
 TC A _ _
 GAM2355 FLJ12586 3' ATGATTCAGTCTGTACCA 23881 TC CTT GC
 TG ACAGACTG AA CAT
 || ||||| || ||
 AC TGTCTGAC TT GTA
 CA _ _ A_
 GAM2355 FLJ14494 3' GATGGCTTTGGTTGGTCCGTGA 43693 A _ T
 TCAC GACTG CT AAGCCATC
 ||| |||| || |||||
 AGTG CTGGT GG TTCGGTAG
 C T T
 GAM2355 HSPC031 3' GCTTATTGTTATCTGTGATA 18184 CT T_
 TGTACAGA GC TAAGC
 ||||| || ||||
 ATAGTGTCT TG ATTCG
 AT TT
 GAM2355 KIAA1423 3' ATGGCTTAATTCTGACA 30919 CA CTGC
 TGTCA GA TTAAGCCAT
 |||| || |||||
 ACAGT CT AATTCGGTA
 _ T_
 GAM2355 PAK2 5' GATGGCTTCCCTTCTGGAACA 33062 CA CTGCTT
 TGT CAGA AAGCCATC
 || ||| |||||
 ACA GTCT TTCGGTAG
 AG TCCC_
 GAM2355 PIP5K2B 3' ATGAGACTGCAGCCTGTGACA 9606 A TTAAGC
 TGTACAG CTGC CAT
 ||||| ||| ||
 ACAGTGTC GACG GTA
 C TCAGA_
 GAM2355 LOC134265 3' GATGGCTTCTTTCTGTCACA 37075 C CTGCTT
 TGT ACAGA AAGCCATC
 || |||| |||||
 ACA TGTCT TTCGGTAG
 C TTC_
 GAM2355 LOC144438 3' TTTAAGCAGTCTATGCA 37740 T C
 TG CA AGACTGCTTAAG
 || || |||||
 AC GT TCTGACGAATTT
 _ A
 GAM2355 LOC147071 5' ATGGAGCAGATCTGTGACA 36133 _ TAAG
 TGTACAGA CTGCT CCAT
 ||||| |||| ||
 ACAGTGTCT GACGA GGTA
 A _
 GAM2355 LOC201173 5' ATGGAGCAGATCTGTGACA 42212 _ TAAG
 TGTACAGA CTGCT CCAT
 ||||| |||| ||

ACAGTGTCT GACGA GGTA
 A ____
 GAM2355 LOC51706 3' GATGAAAGGAACAGTCTGTGCA 34816 T C AAGC
 TG CACAGACTG TT CATC
 || ||||| || |||
 AC GTGTCTGAC AG GTAG
 _ A GAAA
 GAM2355 LOC91291 5' ATGGGTAAGGAACAGTCTGTGA 32629 ____ AG
 TCACAGACTG CTTA CCAT
 ||||| ||| |||
 AGTGTCTGAC GAAT GGTA
 AAG G_
 GAM2356 DMD 5' GTTGCCCCTGCGCCAGGGA 10196 GTA A
 TCCC CGCA GGGGCAAC
 ||| ||| |||||
 AGGG GCGT CCCC GTTG
 ACC _
 GAM2356 DMD 5' GTTGCCCCTGCGCCAGGGA 10223 GTA A
 TCCC CGCA GGGGCAAC
 ||| ||| |||||
 AGGG GCGT CCCC GTTG
 ACC _
 GAM2356 DMD 5' GTTGCCCCTGCGCCAGGGA 10235 GTA A
 TCCC CGCA GGGGCAAC
 ||| ||| |||||
 AGGG GCGT CCCC GTTG
 ACC _
 GAM2356 DSCAM 5' CCGGCTGGCGCACGGGAGG 7077 A A ____
 TCTCCCGT CGC AG GG
 ||||| ||| || ||
 GGAGGGCA GCG TC CC
 C G GGIII
 GAM2356 GCK 5' GCCCCTTG GCTGGCAGA 27285 _ C ACG
 TCT CC GT CAAGGGGC
 ||| ||| |||||
 AGA GG CG GTTCCCCG
 C T ____
 GAM2356 HLCS 3' GGTCGCCCCTTGCCCTGGAG 5992 CGTAC A
 CTCC GCAAGGGGC ACC
 ||| ||||| |||
 GAGG CGTTCCCCG TGG
 TCC__ C
 GAM2356 INPP5B 3' GGGCAACCAGTCGTGAAGACAC 45736 ACG__ A _____ GCAA
 GGGAGA CCGT CA G GG CC
 ||| ||| || ||
 GGCA GT C CC GG
 CAGAA G TGAI|| AACG
 GAM2356 MAP3K7IP1 3' GCCAGGCGTGCGGGAGA 12761 AAGG
 TCTCCCGTACGC GGC
 ||||| |||

			AGAGGGCGTGCG	CCG		
			GA__			
GAM2356	MCF2	5'	TGTAATTGCGTACAGGCGA	11841	T C	GGG
			TC CC GTACGCAA	GCA		
			AG GG CATGCGTT	TGT		
			C A	AA_		
GAM2356	PGF	5'	GCCGCCCAGCTACGGGAGG	8492	C AA	_
			TCTCCCGTA	GC GG GGC		
			GGAGGGCAT	CG CC CCG		
			_ AC	G		
GAM2356	DDX17	5'	GCGTCTGCGACGGGAGA	13090	A A	G
			TCTCCCGT	CGCA GG GC		
			AGAGGGCA	GCGT CT CG		
			_ _	G		
GAM2356	FLJ00024	5'	GCTCTTTGCAAACGAAAGA	31896	CC	AC
			TCT CGT	GCAAGGGGC		
			AGA GCA	CGTTTCTCG		
			AA	AA		
GAM2356	FLJ14871	5'	GCAACCGACTGGCATCACGGGA	26652	AC_ A	_____ GCAA
			GA	CTCCCGT	GC AG GG C	
			GAGGGCA	CG TC CC G		
			CTA G	AG AACG		
GAM2356	FLJ21687	3'	GTTCCCGGCACGGGAGA	24292	AC	AA
			TCTCCCGT	GC GGGGC		
			AGAGGGCA	CG CCTTG		
			_ GC			
GAM2356	KIAA1196	3'	GGTTGCCCTCCTCATGGGA	30823	ACGCA	
			TCCCGT	AGGGGCAACC		
			AGGGTA	TCCCGTTGG		
			CTCC_			
GAM2356	NPTXR	3'	GCCACCCAGCTGGACACGGGAG	27734	AC_	AA _
			A	TCTCCCGT	GC GG GGC	
			AGAGGGCA	CG CC CCG		
			CAGGT	AC A		
GAM2356	NPTXR	3'	GCCACCCAGCTGGACACGGGAG	15586	AC_	AA _
			A	TCTCCCGT	GC GG GGC	
			AGAGGGCA	CG CC CCG		
			CAGGT	AC A		
GAM2356	LOC152633	5'	GTTGCCCTGCGCCAAGGGA	41534	GTA_	A
			TCCC	CGCA GGGGCAAC		

AGGG GCGT CCCC GTTG
 AACCC _
 GAM2356 LOC256222 5' GGTGCCCCCTCTACTCAGAGA 46428 CC_ CGCA
 TCTC GTA AGGGGCAACC
 |||| ||| ||||||||
 AGAG CAT TCCCCGTTGG
 ACT C__
 GAM2357 ABCE1 3' AAATCTTGAAAAGGGTTTCTG 29939 TGTGG
 TAGAG TCTTTTCAAGATT
 |||| ||||||||
 GTCTT GGAAAAGTTCTAAA
 TG__
 GAM2357 PLOD2 3' CTTGAAAATCAGATTCTA 6640 G CT
 TAGAGT TGGT TTTCAAG
 |||| ||| |||||
 ATCTTA ACTA AAAGTTC
 G _
 GAM2357 DKFZP586P0123 3' AATCCTAGGGCCACCTC 45462 T TTCAA
 GAG GTGGTCTT GATT
 || ||||| |||
 CTC CACCGGGA CTAA
 _ TC__
 GAM2357 WNT2B 3' AAATCTTAGGCTACCACATTCT 10390 CT C
 A TAGAGTGTGGT TTT AAGATTT
 |||||||| || |||||
 ATCTTACACCA GGA TTCTAAA
 TC _
 GAM2357 WNT2B 3' AAATCTTAGGCTACCACATTCT 23691 CT C
 A TAGAGTGTGGT TTT AAGATTT
 |||||||| || |||||
 ATCTTACACCA GGA TTCTAAA
 TC _
 GAM2357 LOC196202 5' AAATCCCAAAAGTCACACTT 43078 T CAA
 GAGTGTGG CTTTT GATTT
 ||||| |||| ||||
 TTCACACT GAAAA CTAAA
 _ CC_
 GAM2357 LOC220672 3' AAATCTTGAAAAGGGTTTCTG 30306 TGTGG
 TAGAG TCTTTTCAAGATT
 |||| ||||||||
 GTCTT GGAAAAGTTCTAAA
 TG__
 GAM2358 ADH1B 3' CTCTCATTTGTTAATGCTTTCC 35962 A CA
 A AAAGCGTTAACAAG GGAG
 | |||||||| |||
 C TTTCGTAATTGTTT TCTC
 C AC
 GAM2358 AICDA 3' TCCTAAAGTGTCAACGTTTTT 21833 A AGC_
 AAAAGCGTT ACA AGGA
 |||||| || |||

			TTTTTGCAA TGT TCCT		
			C GAAA		
GAM2358	APPBP2	3'	TTCTCCTGCCTCAGCCTT 13085	C	AACAA
			AAG GTT GCAGGAGAA		
			TTC CGA CGTCCTCTT		
			_ CTC_		
GAM2358	ATP2B4	5'	CTCCTGCACCCTTTT 34825	C	TAACAA
			AAAAAG GT GCAGGAG		
			TTTTTC CA CGTCCTC		
			C _____		
GAM2358	BRIP1	3'	TTCTCCTGCCTCAGCCTT 25758	C	AACAA
			AAG GTT GCAGGAGAA		
			TTC CGA CGTCCTCTT		
			_ CTC_		
GAM2358	CASP2	3'	TTCTCCTGCCTCAGCCTT 26856	C	AACAA
			AAG GTT GCAGGAGAA		
			TTC CGA CGTCCTCTT		
			_ CTC_		
GAM2358	CASP2	3'	TTCTCCTGCCTCAGCCTT 26861	C	AACAA
			AAG GTT GCAGGAGAA		
			TTC CGA CGTCCTCTT		
			_ CTC_		
GAM2358	CASP2	3'	TTCTCCTGCCTCAGCCTT 26866	C	AACAA
			AAG GTT GCAGGAGAA		
			TTC CGA CGTCCTCTT		
			_ CTC_		
GAM2358	CASP2	3'	TTCTCCTGCCTCAGCCTT 6893	C	AACAA
			AAG GTT GCAGGAGAA		
			TTC CGA CGTCCTCTT		
			_ CTC_		
GAM2358	CBFA2T3	3'	TCCTGTAATGTAAACTCTTT 11693	C	_ A_
			AAAG GTT AACA GCAGGA		
			TTTC CAA TTGT TGTCTT		
			T A AA		
GAM2358	CBFB	3'	TTCCCCTGAGGGAATCGCTTTT 7508	TTAACAAG	A
	T		AAAAAGCG CAGG GAA		
			TTTTTCGC GTCC CTT		
			TAAGGGA_ C		
GAM2358	CBFB	3'	TTCCCCTGAGGGAATCGCTTTT 23149	TTAACAAG	A
	T		AAAAAGCG CAGG GAA		

TTTTTCGC GTCC CTT
 TAAGGGA_ C
 GAM2358 CD164 3' TTCTAGGTCATTAACGTTTTTT 12632 CAA AGG
 AAAAAGCGTTAA GC AGAA
 ||||||| || |||
 TTTTTTGCAATT TG TCTT
 AC_ GA_
 GAM2358 CORO2B 5' TTCTCCTGCTTCAGCCT 32257 C AAC
 AG GTT AAGCAGGAGAA
 || ||| |||||
 TC CGA TTCGTCCTCTT
 _ C_
 GAM2358 EIF1A 3' TTCTCCTGCTTGTCTCAGCTTC 42728 A GTTA
 A AAGC ACAAGCAGGAGAA
 | ||| |||||
 A TTCG TGTTCGTCCTCTT
 C ACTC
 GAM2358 HOXB3 5' TTCTCCTGCCTGTTGCTTTT 7923 TTA A
 AAAAGCG ACA GCAGGAGAA
 ||||| ||| |||||
 TTTTCGT TGT CGTCCTCTT
 _ C
 GAM2358 ISLR 3' CTCCTGCTCCTTGCTGTTTT 12071 T CA
 AAAGCG TAA AGCAGGAG
 ||||| ||| |||||
 TTTTGT GTT TCGTCCTC
 C CC
 GAM2358 MLANA 3' TTCTCCTGCCTTAGCCT 12029 C CAA
 AG GTTAA GCAGGAGAA
 || ||| |||||
 TC CGATT CGTCCTCTT
 _ C_
 GAM2358 MYCL2 3' TTCTCCTGCCTGAGCCTT 11858 C AA A
 AAG GTT CA GCAGGAGAA
 ||| ||| ||| |||||
 TTC CGA GT CGTCCTCTT
 _ _ C
 GAM2358 SERPIND1 3' CTCCTGCTGTTGCCT 5687 C T A
 AG GT AACA GCAGGAG
 || ||| |||||
 TC CG TTGT CGTCCTC
 _ _ _
 GAM2358 SLC13A1 3' TTCTCCTGCCTCAGCCAAACCT 22776 C AACAA_
 TT AAAG GTT GCAGGAGAA
 |||| ||| |||||
 TTTC CAA CGTCCTCTT
 _ ACCGACTC
 GAM2358 SURF5 3' TTCTCCTGGACAAACCTTTCC 13607 A C AACAAAG
 A AAAG GTT CAGGAGAA
 | ||| ||| |||||

C TTTC CAA GTCCTCTT
 C _ ACAG__
 GAM2358 TRIM 3' TTCTGATTGTTAAGACTTTCC 18533 A CG G
 A AAAG TTAACAA CAGGA
 | ||| ||||| ||||
 C TTTC AATTGTT GTCTT
 C AG A
 GAM2358 WASF3 3' CTCCCCTTTGGTAATGCTT 13441 A CA
 AAGCGTTA CAAG GGAG
 ||||| ||| |||
 TTCGTAAT GTTT CCTC
 G CC
 GAM2358 WBSCR1 3' TTCTCCTGCTCCTTGTTTTCC 22727 A TTAACA
 A AAAGCG AGCAGGAGAA
 | |||| |||||
 C TTTTGT TCGTCCTCTT
 C TCC__
 GAM2358 WBSCR1 3' TTCTCCTGCTCCTTGTTTTCC 25710 A TTAACA
 A AAAGCG AGCAGGAGAA
 | |||| |||||
 C TTTTGT TCGTCCTCTT
 C TCC__
 GAM2358 CEP3 3' TTCTCCAGTGTTAAACTTTT 13160 CG AGCA
 AAAAG TTAACA GGAGAA
 |||| |||| ||||
 TTTTC AATTGT CCTCTT
 AA GA__
 GAM2358 COLEC12 3' TTCTCCTGCCTTAGCCT 25073 C CAA
 AG GTTAA GCAGGAGAA
 || |||| |||||
 TC CGATT CGTCCTCTT
 _ C__
 GAM2358 CRMP5 3' CTCCTGCTGTAGTCCTTT 21331 CG A A
 AAAG TTA CA GCAGGAG
 ||| ||| |||||
 TTTC GAT GT CGTCCTC
 CT _ _
 GAM2358 DDM36 3' TTCTCCTGCTCCCAGATACTCT 21957 C TAACA__
 TT AAAG GT AGCAGGAGAA
 ||| || |||||
 TTTC CA TCGTCCTCTT
 T TAGACCC
 GAM2358 FLJ11710 3' TCTCCTGCGTCAGCCT 24276 C A AA
 AG GTT AC GCAGGAGA
 || ||| || |||||
 TC CGA TG CGTCCTCT
 _ C _
 GAM2358 FLJ12078 3' CTCCTTTGTTAAACTTTT 24535 CG GC
 AAAAG TTAACAA AGGAG
 |||| ||||| ||||

TTTTC AATTGTT TCCTC
 AA _
 GAM2358 FLJ13910 3' CTCCTGCTTTTACTTTT 23054 CGT C
 AAAAG TAA AAGCAGGAG
 |||| ||| |||||
 TTTTC ATT TTCGTCCTC
 _ _
 GAM2358 FLJ20651 3' TTGCCTTACTTAACGCTTTT 19577 CAA_
 AAAAAGCGTTAA GCAG
 ||||| |||
 TTTTTCGCAATT CGTT
 CATTG
 GAM2358 FLJ20671 3' TTCTCCTGCCTCAACCTT 19593 C AACAA
 AAG GTT GCAGGAGAA
 ||| ||| |||||
 TTC CAA CGTCCTCTT
 _ CTC_
 GAM2358 FLJ23024 3' TTCTCCTGCCTTAGCCT 24474 C CAA
 AG GTTAA GCAGGAGAA
 || |||| |||||
 TC CGATT CGTCCTCTT
 _ C_
 GAM2358 FLJ23056 3' TTCAGCACTTTAACGCTTT 23809 CAA A
 AAAGCGTTAA GC GGA
 ||||| || |||
 TTTTCGCAATT CG CTT
 TCA A
 GAM2358 FREQ 3' CTCCCCTGAAATGCTTTT 15562 AACA CA
 AAAAGCGTT AG GGAG
 ||||| || |||
 TTTTCGTAA TC CCTC
 AG_ C_
 GAM2358 GTPBP1 3' CTCCTGCTTGCGGACTGCT 10497 _ AA
 AGC GTT CAAGCAGGAG
 ||| ||| |||||
 TCG CAG GTTCGTCCTC
 T GC
 GAM2358 JM11 3' TCCTGGCGTTAAGCTTTT 27330 G AAG
 AAAAGC TTAAC CAGGA
 |||| |||| ||||
 TTTTCG AATTG GTCCT
 _ CG_
 GAM2358 KIAA0026 3' TCCTGTATCTGTAAACACTTTT 14616 C A A_
 T AAAAAG GTT ACA GCAGGA
 |||| ||| ||| |||||
 TTTTTC CAA TGT TGTCTC
 A A CTA
 GAM2358 KIAA0152 3' TTCTCCTGCCTCTAGCCT 16342 C ACAA
 AG GTTA GCAGGAGAA
 || |||| |||||

		TC CGAT CGTCCTCTT	
		_ CTC_	
GAM2358 KIAA0285	3'	TCGCCGCCTTATCAAGCGCTTT 16753	AAC_ CA A
	T	AAAAGCGTT AAG GG GA	
		TTTTCGCGA TTC CC CT	
		ACTA CG G	
GAM2358 KIAA0513	5'	TTCTCCTGCCTCAGCCTT 16365	C AACAA
		AAG GTT GCAGGAGAA	
		TTC CGA CGTCCTCTT	
		_ CTC_	
GAM2358 KIAA0767	3'	TCTCCTGTAACATTTTTT 30410	C AACAA
		AAAAAG GTT GCAGGAGA	
		TTTTTT CAA TGTCCTCT	
		A _____	
GAM2358 KIAA1200	3'	TCTCCTGCCTCAGCCTTCG 31265	A C AACAA
		A AAG GTT GCAGGAGA	
		G TTC CGA CGTCCTCT	
		C _ CTC_	
GAM2358 KIAA1257	3'	TCTCCTGCATTAGCCTTCC 31440	A C CAA
		A AAG GTTAA GCAGGAGA	
		C TTC CGATT CGTCCTCT	
		C _ A_	
GAM2358 KIAA1257	3'	TCTCCTGCTTCAACCT 31441	C AAC
		AG GTT AAGCAGGAGA	
		TC CAA TTCGTCCTCT	
		_ C_	
GAM2358 KIAA1536	3'	TCTCCTACCTGGCTCTTTT 21924	C ACAAGC
		AAAAG GTTA AGGAGA	
		TTTTC CGGT TCCTCT	
		T CCA_	
GAM2358 KIAA1649	3'	TCTCTACGTTAACGTTT 33259	AAGCA
		AAGCGTTAAC GGAGA	
		TTTGCAATTG TCTCT	
		CA_	
GAM2358 KIAA1649	5'	TCTCTACGTTAACGTTT 26111	AAGCA
		AAGCGTTAAC GGAGA	
		TTTGCAATTG TCTCT	
		CA_	
GAM2358 KIAA1710	3'	CTCCCTTCACTAATGCTTTTT 31330	AC_ CA
		AAAAAGCGTTA AAG GGAG	


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          TTTTTCGTAAT TTC CCTC
              CAC ____
GAM2358 KLF12  5' TTCTCCTGCTCTGCAGCTT 18411  _ TAACA
              AAGC GT  AGCAGGAGAA
              ||| ||  |||||
              TTCG CG  TCGTCCTCTT
              A TC____
GAM2358 KLF12  5' TTCTCCTGCTCTGCAGCTT 14120  _ TAACA
              AAGC GT  AGCAGGAGAA
              ||| ||  |||||
              TTCG CG  TCGTCCTCTT
              A TC____
GAM2358 LAMP3  3' TTCTCCTGCTTCAGCTT 29921  GTTAAC
              AAGC  AAGCAGGAGAA
              |||  |||||
              TTCG  TTCGTCCTCTT
              AC____
GAM2358 MANBAL 5' TTCTCCTGCCTCAGCCTT 22622  C AACAA
              AAG GTT  GCAGGAGAA
              ||| |||  |||||
              TTC CGA  CGTCCTCTT
              _ CTC____
GAM2358 MGC14836 3' TTCTCCTGCCTTAGCCT 27237  C CAA
              AG GTTAA GCAGGAGAA
              || ||||  |||||
              TC CGATT CGTCCTCTT
              _ C____
GAM2358 MGC3222 3' TTCTCCTGCTGTTTCCTT 23642  CGTT A
              AAG  AACA GCAGGAGAA
              |||  ||||  |||||
              TTC  TTGT CGTCCTCTT
              CT____ _
GAM2358 moblak 3' TTCTCCTGCTTCAGCCT 28313  C AAC
              AG GTT  AAGCAGGAGAA
              || |||  |||||
              TC CGA  TTCGTCCTCTT
              _ C____
GAM2358 NICE-3 3' TTCCCCAGTAGCGCTTTT 17735  ACAAGCA
              AAAAAGCGTTA  GGAG
              ||||| |||
              TTTTTCGCGAT  CCTT
              GACCC____
GAM2358 PILR(ALPHA) 5' TCTCCTGCCTGGACGGCT 15103  _ AA A
              AGC GTT  CA GCAGGAGA
              ||| |||  |||||
              TCG CAG  GT CGTCCTCT
              G  _ C
GAM2358 PIP3-E 3' TCTCCTGCTTTATGTTTTT 33182  TAAC
              AAAAGCGT  AAGCAGGAGA
              |||||  |||||

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			TTTTTGTA	TTCGTCCTCT		
			T___			
GAM2358	QSCN6	3'	TCTCCTGCTTGGTCTTGGCCCT	8699	C	___
			AG GTTAA	CAAGCAGGAGA		
			TC CGGTT	GTTTCGTCCTCT		
			C	CTG		
GAM2358	Rpo1-2	3'	CTCCTGCCCCCTTTGTTTTTT	21100	TTAACAA	
			AAAAAGCG	GCAGGAG		
			TTTTTTGT	CGTCCTC		
			TTCCC__			
GAM2358	Rpo1-2	3'	CTCCTGCCCCCTTTGTTTTTT	25933	TTAACAA	
			AAAAAGCG	GCAGGAG		
			TTTTTTGT	CGTCCTC		
			TTCCC__			
GAM2358	SHARP	3'	TTCTCCTGCTGCCACCGTCTT	17370	_	TTAACA
			AAG CG	AGCAGGAGAA		
			TTC GC	TCGTCCTCTT		
			T	CACCG_		
GAM2358	SLC31A2	3'	TCTCCTGCTTTGTGCCTT	30193	C	TA _
			AAG GT	ACAA GCAGGAGA		
			TTC CG	TGTT CGTCCTCT		
			_ _	T		
GAM2358	WBSCR20A	5'	TTCTCCTGCTTCAGCCTT	25861	C	AAC
			AAG GTT	AAGCAGGAGAA		
			TTC CGA	TTCGTCCTCTT		
			_	C_		
GAM2358	ZFD25	5'	TCTCCTGCCTGCCTTATCCTT	18325	C	TAA_ A
			AAG GT	CA GCAGGAGA		
			TTC TA	GT CGTCCTCT		
			C	TTCC C		
GAM2358	LOC113675	5'	TTCTCCTGCCTCAGCCTT	28798	C	AACAA
			AAG GTT	GCAGGAGAA		
			TTC CGA	CGTCCTCTT		
			_	CTC_		
GAM2358	LOC115294	3'	TCCCCTGCTTGTTTTTTTTTT	36147	CGTT	A
			T	AAAAAG	AACAAGCAGG	GA
			TTTTTT	TTGTTCGTCC	CT	
			TTTT	C		
GAM2358	LOC130813	3'	TTCTCCTGCTTCTGCCT	37316	C	TAAC
			AG GT	AAGCAGGAGAA		

TC CG TTCGTCCTCTT
 _ TC_
 GAM2358 LOC143241 5' TTCTCCTGCCTCAGCCTT 29037 C AACAA
 AAG GTT GCAGGAGAA
 ||| ||| |||||
 TTC CGA CGTCCTCTT
 _ CTC_
 GAM2358 LOC144248 5' TTCTCCTGCCTTAGCCT 37701 C CAA
 AG GTTAA GCAGGAGAA
 || ||||| |||||
 TC CGATT CGTCCTCTT
 _ C_
 GAM2358 LOC144453 3' CCTCCTTCCTAACGTTTTT 37746 AC C
 AAAAGCGTTA AAG AGG
 ||||| ||| |||
 TTTTTCGAAT TTC TCC
 CC C
 GAM2358 LOC144571 3' CTCCTGCTTTAACCTTTCC 40441 A C CA
 A AAAG GTTAA AGCAGGAG
 | ||| ||||| |||||
 C TTTC CAATT TCGTCCTC
 C _ _
 GAM2358 LOC144742 5' TTCTCCTGCCTCAGCCTT 37781 C AACAA
 AAG GTT GCAGGAGAA
 ||| ||| |||||
 TTC CGA CGTCCTCTT
 _ CTC_
 GAM2358 LOC145216 3' TCTCCTGCCTTTGACCT 40508 C CAA
 AG GTTAA GCAGGAGA
 || ||||| |||||
 TC CAGTT CGTCCTCT
 _ TC_
 GAM2358 LOC146909 3' TTCTCCTGCCTCAGCTTTCC 38273 A GTTAACAA
 A AAAGC GCAGGAGAA
 | ||||| |||||
 C TTTCG CGTCCTCTT
 C ACTC_
 GAM2358 LOC148709 3' TTCTCCTGCTTCAGCCT 38585 C AAC
 AG GTT AAGCAGGAGAA
 || ||| |||||
 TC CGA TCGTCCTCTT
 _ C_
 GAM2358 LOC150054 5' TTCTCCTGCCTCAGCCTT 41127 C AACAA
 AAG GTT GCAGGAGAA
 ||| ||| |||||
 TTC CGA CGTCCTCTT
 _ CTC_
 GAM2358 LOC150319 3' TCTCCTGCTCTGCCCACCCTT 38897 C TAA _
 AAG GT CA AGCAGGAGA
 ||| || |||||

TTC CA GT TCGTCCTCT
 C CCC C
 GAM2358 LOC151475 5' TTCTCCTGCCTTAGCCT 41361 C CAA
 AG GTTAA GCAGGAGAA
 || |||| |||||
 TC CGATT CGTCCTCTT
 _ C_
 GAM2358 LOC152445 3' TTCTCCTGCCTTAGCCT 41514 C CAA
 AG GTTAA GCAGGAGAA
 || |||| |||||
 TC CGATT CGTCCTCTT
 _ C_
 GAM2358 LOC153196 3' CTCCTGCTCTTACTGTTT 41590 T CA
 AAGCG TAA AGCAGGAG
 |||| || |||||
 TTTGT ATT TCGTCCTC
 C C_
 GAM2358 LOC158310 5' TTCTCCTGCCTCAGCCTT 41951 C AACAA
 AAG GTT GCAGGAGAA
 ||| || |||||
 TTC CGA CGTCCTCTT
 _ CTC_
 GAM2358 LOC158382 3' TCTCCTGAAAATGCTTTTT 41968 AACAAAG
 AAAAAGCGTT CAGGAGA
 ||||| |||||
 TTTTTCGTAA GTCCTCT
 AA____
 GAM2358 LOC169611 3' TTCTCCTGCCTTAGCCT 40289 C CAA
 AG GTTAA GCAGGAGAA
 || |||| |||||
 TC CGATT CGTCCTCTT
 _ C_
 GAM2358 LOC170082 5' TTCTCCTGCTTCAGCCT 40172 C AAC
 AG GTT AAGCAGGAGAA
 || || |||||
 TC CGA TTCGTCCTCTT
 _ C_
 GAM2358 LOC200059 3' TTCATTTGCCAGACGCTTTTT 42701 AACAA A
 AAAAAGCGTT GCAGG GAA
 ||||| |||||
 TTTTTCGCAG CGTTT CTT
 AC__ A
 GAM2358 LOC200301 3' TTCTCCTGCTTCTTTGCTTTCC 42785 A TTAAC
 A AAAGCG AAGCAGGAGAA
 | |||| |||||
 C TTTCGT TTCGTCCTCTT
 C TTC_
 GAM2358 LOC220705 3' TCTCCCATGGCTTAATGCTT 43836 ACA A_
 AAGCGTTA AGC GGAGA
 ||||| || ||||

		TTCGTAAT TCG CCTCT	
		___ GTAC	
GAM2358	LOC221354 3'	TCTCCTGCTACATTCCTTTT 44394	CGTTAACA
		AAAAAG AGCAGGAGA	
		TTTTTC TCGTCCTCT	
		CTTACA__	
GAM2358	LOC255454 5'	CTCTTGCTTATCAACATTTT 46613	GC AAC
		AAAAA GTT AAGCAGGAG	
		TTTTT CAA TTCGTTCTC	
		A_ CTA	
GAM2358	LOC255919 3'	TTCTCCTGCTTCAGCCTT 45558	C AAC
		AAG GTT AAGCAGGAGAA	
		TTC CGA TTCGTCCTCTT	
		_ C__	
GAM2358	LOC51008 5'	TTCTCCTGCTTCAGCCT 18066	C AAC
		AG GTT AAGCAGGAGAA	
		TC CGA TTCGTCCTCTT	
		_ C__	
GAM2358	LOC90141 3'	TTCTCCTGCCTTAGCCT 30883	C CAA
		AG GTTAA GCAGGAGAA	
		TC CGATT CGTCCTCTT	
		_ C__	
GAM2358	LOC90333 5'	TTCTCCTGCCTCAGCCTT 31229	C AACAA
		AAG GTT GCAGGAGAA	
		TTC CGA CGTCCTCTT	
		_ CTC__	
GAM2358	LOC90371 5'	TTCTCCTACTCCATTGCTTTT 31324	TTAACA C
		AAAAAGCG AG AGGAGAA	
		TTTTTCGT TC TCCTCTT	
		TACC__ A	
GAM2358	LOC91923 5'	TTCTCCACATTTTGCACACGC 33545	AA CA__
	TT	AAGCGTT CAAG GGAGAA	
		TTCGCAA GTTT CCTCTT	
		CC TTACA	
GAM2359	BTG2 3'	ATCCCTTTGAGAGGTGGCTCA 13622	AGCA CC_
		TGAGC TGCC CAAAGGGAT	
		ACTCG GTGG GTTCCCTA	
		___ AGA	
GAM2359	GRIK3 3'	TCCCTCTGGGGCTGTTCA 6486	ATGCC A
		TGAGCAGC CCCA AGGGA	

			ACTTGT	CG	GGGT	TCCCT	
				_____	C		
GAM2359	MSF	3'	CCCTTCGACATGCTGCCA	42522	A	CCCCCA	
			TG GCAGCATG	AAGGG			
			AC CGTCGTAC	TTCCC			
			_____	AGC_____			
GAM2359	ZNF36	3'	TTGGGACATGCTGCTCA	45105		CC	
			TGAGCAGCATG	CCCAA			
			ACTCGTCGTAC	GGGTT			
				A_____			
GAM2359	KIAA0469	3'	CCCACGGAAGGACATGCTGTCC	16888	AG	_____C_____AAA	
	A		TG CAGCATG	CC CC GGG			
			AC GTCGTAC	GG GG CCC			
			CT	A AA CA_____			
GAM2359	SMARCF1	3'	CCCAGGGCTGCTGCTCA	20518	T	CCAAA	
			TGAGCAGCA	GCCC GGG			
			ACTCGTCGT	CGGG CCC			
				A_____			
GAM2359	LOC115708	3'	ATCCCCTCGGCCCTGCTGCTC	36403	T_____	CCCAA	
			GAGCAGCA	GCC GGGAT			
			CTCGTCGT	CGG CCCTA			
				CC CTC_____			
GAM2359	LOC51754	5'	CTTTTGGGGACCACTGCCCA	35179	A	CATGC	
			TG GCAG	CCCCAAAGG			
			AC CGTC	GGGGTTTTC			
				C ACCA_____			
GAM2360	GTF2I	3'	CTGTGAATTAAAGAGCAGAGT	26885	CA	GGAC	
			ACTC CTC	GATTCACAG			
			TGAG GAG	TTAAGTGTC			
				AC AAA_____			
GAM2360	GTF2I	3'	CTGTGAATTAAAGAGCAGAGT	26889	CA	GGAC	
			ACTC CTC	GATTCACAG			
			TGAG GAG	TTAAGTGTC			
				AC AAA_____			
GAM2360	FLJ10314	5'	CTGTGAATACAGGAACATAGTC	19816		CCAC GGACG	
	A		TGACT	TC ATTCACAG			
			ACTGA	AG TAAAGTGTC			
				TACA GACA_____			
GAM2360	FLJ13441	3'	GTGAACCCTGAGGAGTGGAGTC	23397		GGACGA_____	
	A		TGACTCCACTC	TTCAC			

		ACTGAGGTGAG	AAGTG		
		GAGTCCC			
GAM2360	FLJ13441	3' GTGAACCCTGAGGAGTGGAGTC	23398		GGACGA_
	A	TGACTCCA	CTC	TTCAC	
		ACTGAGGTGAG	AAGTG		
		GAGTCCC			
GAM2360	KIAA0481	3' GTGGCCAAGTGGAGCA	35571	A	C ACGAT
		TG CTCCACT	GG	TCAC	
		AC GAGGTGA	CC	GGTG	
		_ A _			
GAM2360	KIAA1904	3' CTGTGAATGACAAGAGGAGCCA	36376	A	AC GGACG
		TG CTCC	TC	ATTCACAG	
		AC GAGG	AG	TAAGTGTC	
		C _	AACAG		
GAM2360	POPX1	3' CTGTGAGTTTCAAAGGGAGTCA	17120	A	CG C
		TGACTCC	CT	GA GATTCACAG	
		ACTGAGG	GA	CT TTGAGTGTC	
		_ AA _			
GAM2360	SLC1A7	3' CTGTGCGTCCAAGTGGAGTCA	13489	C	ATT
		TGACTCCA	CT	GGACG CACAG	
		ACTGAGGTGA	CCTGC	GTGTC	
		A _			
GAM2361	APBA2	3' CCTGGCCACGCAGCCAGGA	12017	A	GG
		TCCTGGCT	TG	GGCCAGG	
		AGGACCGA	GC	CCGGTCC	
		C A_			
GAM2361	EPHA8	3' GCCCCCCTCCCCATAGCCAG	21747		CCA_
		CTGGCTATGGGGG	GGGC		
		GACCGATA	CCCCCT	CCCG	
		CCCC			
GAM2361	EVC	3' GCCCCTCTCACCACAGCCAGGA	15890	A	_ CCA
		TCCTGGCT	TGG GGG	GGGC	
		AGGACCGA	ACC CTC	CCCG	
		C A TC_			
GAM2361	EVC	3' GCCCCTCTCACCACAGCCAGGA	15891	A	_ CCA
		TCCTGGCT	TGG GGG	GGGC	
		AGGACCGA	ACC CTC	CCCG	
		C A TC_			
GAM2361	EVC	3' GCCCTGGTCTAATCCAGGA	15892		CTATGG
		TCCTGG	GGGCCAGGGC		

AGGACC TCTGGTCCCG
 TAA____
 GAM2361 EVC 3' GCCCTTCACACCACAGCCAGGA 15893 A GGGCC
 TCCTGGCT TGG AGGGC
 ||||| || ||||
 AGGACCGA ACC TCCCG
 C ACACT
 GAM2361 EVC 3' GCCCCTCACACCACAGCCAGGA 15888 A GGGCCA
 TCCTGGCT TGG GGGC
 ||||| || ||||
 AGGACCGA ACC CCGG
 C ACACTC
 GAM2361 EVC 3' GCCCCTCACACCACAGCCAGGA 15889 A GGGCCA
 TCCTGGCT TGG GGGC
 ||||| || ||||
 AGGACCGA ACC CCGG
 C ACACTC
 GAM2361 EVC 3' GCCCCTCACACCACAGCCAGGA 15887 A GGGCCA
 TCCTGGCT TGG GGGC
 ||||| || ||||
 AGGACCGA ACC CCGG
 C ACACTC
 GAM2361 EVC 3' GCCCCACACACCACAGCCAGGA 15886 A GGGCCA
 TCCTGGCT TGG GGGC
 ||||| || ||||
 AGGACCGA ACC CCGG
 C ACACAC
 GAM2361 ICOS 3' CCCTGGCCCTTCAAGATA 14386 C CTATG
 TATC TGG GGGGCCAGGG
 ||| ||| |||||
 ATAG ACT TCCCGGTCCC
 A ____
 GAM2361 KCNJ10 5' CCCCCGCCCCCGCCCCCGGA 8025 T__ ATG A
 TCC GGCT GGGGCC GGG
 || ||| ||||| |||
 AGG CCGG CCCCCG CCC
 CCC ____ C
 GAM2361 KCNQ1 3' GCCCTGGCCCCCACATGGTGAT 5724 CTG ____
 G TATC GCTA TGGGGGCCAGGGC
 ||| ||| |||||
 GTAG TGGT ACCCCCGGTCCCG
 ____ AC
 GAM2361 LOH11CR2A 5' GCCCCATGAGTAGCCAGGATA 15988 G____
 TATCCTGGCTAT GGGGC
 ||||| |||
 ATAGGACCGATG CCGG
 AGTA
 GAM2361 MAP3K14 3' CCCCCGCCCCCAGCACA 10091 _ AT A
 TG GCT GGGGGCC GGG
 || ||| ||||| |||

AC CGA CCCCCGG CCC
 A _ C
 GAM2361 NTSR1 3' GCCCTGGCCCCGGCC 8369 ATG
 GGCT GGGGCCAGGGC
 |||| |||||
 CCGG CCCCAGTCCCG

 GAM2361 SOX10 3' GCCCTAACCCTTGGCTCCAGGA 13823 CTA CC
 TCCTGG TGGGGG AGGGC
 ||||| ||||| |||||
 AGGACC GTTCCC TCCCG
 TCG AA
 GAM2361 SPHK2 3' GCCCTGGCCCCGTCTCAGGAT 21313 CTATG
 ATCCTGG GGGGCCAGGGC
 ||||| |||||
 TAGGACT CCCCAGTCCCG
 CTG_
 GAM2361 COLEC10 3' GCCCTGGCCCCAAAGCCAG 13146 ATGG
 CTGGCT GGGGCCAGGGC
 ||||| |||||
 GACCGA CCCCAGTCCCG
 AA_
 GAM2361 DKFZP434L0117 3' GCCCTAGGGATTATAGCCAGGA 23051 GGG _
 TCCTGGCTATGG CC AGGGC
 ||||| || |||||
 AGGACCGATATT GG TCCCG
 AG_ A
 GAM2361 FLJ20123 5' GCCCTCAGGGCCAGCCAGGA 19218 ATGGG _
 TCCTGGCT GGCC AGGGC
 ||||| ||| |||||
 AGGACCGA CCGG TCCCG
 _ GAC
 GAM2361 FLJ20160 3' GCCCCCAGCCAGGATA 19258 AT
 TATCCTGGCT GGGGGC
 ||||| |||||
 ATAGGACCGA CCCCCG
 C_
 GAM2361 KIAA0855 5' CAGGGCACCCAGGACACCCAG 17372 CTA_ _ CAGG
 GATA CCTGG TGGGG GC G
 |||| |||| || |
 GGACC ACCCC CG C
 CACAGG AIII GGAC
 GAM2361 KIAA1086 3' CCCACCTCCACAGCCAGGATG 35012 A CCA
 TATCCTGGCT TGGGGG GGG
 ||||| ||||| |||
 GTAGGACCGA ACCTCC CCC
 C A_
 GAM2361 PPP1R16B 3' GCACCCCAATGCCAGGATA 30775 TA _
 TATCCTGGC TGGGG GC
 ||||| |||| ||

		ATAGGACCG ACCCC CG		
		TA AIII		
GAM2361	RAI1	5' CCCCACCCCCATGGCCA 30253	CCA	
		TGGCTATGGGGG GGG		
		ACCGGTACCCCC CCC		
		AGC		
GAM2361	LOC112476	3' GCCCTGGCCCCACCCCTAAGG 29751	___ CTA	
	A	TCCT GG TGGGGGCCAGGGC		
		AGGA CC ACCCCCGGTCCCG		
		AT CC_		
GAM2361	LOC149464	5' GCCCTGGCAGGCAGCCAGGG 40993	ATGGGG	
		TCCTGGCT GCCAGGGC		
		GGGACCGA CGGTCCCG		
		CGGA_		
GAM2361	LOC151959	5' GCCCTGGCCTAGAGACCAG 41408	_ ATGG	
		CTGG CT GGGCCAGGGC		
		GACC GA TCCGGTCCCG		
		A GA_		
GAM2361	LOC158969	3' CCTCCCCCATAATCAAGA 39921	C GC CC	
		TC TG TATGGGGG AGG		
		AG AC ATACCCCC TCC		
		A TA _		
GAM2361	LOC166206	5' GCCCCGGCCCCCATTCCCG 40208	CT A	
		TGG ATGGGGGCC GGGC		
		GCC TACCCCCGG CCCG		
		CT C		
GAM2361	LOC197196	3' GCCCTGGCAGACAAGCCA 43202	A GGG	
		TGGCT TG GCCAGGGC		
		ACCGA AC CGGTCCCG		
		_ AGA		
GAM2361	LOC200081	3' CCCCAGCCCCTGTGCCAGG 42704	T CA	
		CCTGGC ATGGGGGC GGG		
		GGACCG TGTCCCCG CCC		
		_ AC		
GAM2361	LOC220045	5' GCCCTGGCCCCACAGGCTCAG 44860	_ A_	
		CTG GCT TGGGGGCCAGGGC		
		GAC CGG ACCCCCGGTCCCG		
		T AC		
GAM2361	LOC221042	3' GCGCCCCGGCAGTCAGGATA 44757	A_ _	
		TATCCTGGCT TGGGG GC		

		ATAGGACTGA GCCCC CG		
		CG GIII		
GAM2361	LOC253842	3' CCCTGGCCTCTCAGCAGGA 46502	G AT	
		TCCTG CT GGGGGCCAGGG		
		AGGAC GA TCTCCGGTCCC		
		_ C_		
GAM2361	LOC257479	5' CCCCGGTCCCCGCAGCCAGGA 46051	A A	
		TCCTGGCT TGGGGGCC GGG		
		AGGACCGA GCCCCTGG CCC		
		C C		
GAM2362	DDOST	3' TCTAAAATAGGGACGTGGCCA 11712	G CCCG	
		TGGCCACGTC CT TAGA		
		ACCGGTGCAG GA ATCT		
		G TAAA		
GAM2362	FZD1	5' TCTACGGGGCCGCGGCCA 9595	A TC T	
		TGGCC CG GC CCCGTAGA		
		ACCGG GC CG GGGCATCT		
		C _ _		
GAM2362	HDAC4	3' CTGCAGCCACGTGGCCA 12664	C CCC	
		TGGCCACGT GCT GTAG		
		ACCGGTGCA CGA CGTC		
		C _ _		
GAM2362	NAV2	5' CGCTGAGCGCCGTGGCCA 30204	T C_	
		TGGCCACG CGCTC CG		
		ACCGGTGC GCGAG GC		
		C TC		
GAM2362	PEX10	3' TCTACGGGAGTCTGAACGCCA 8481	CACGTC	
		TGGC GCTCCCGTAGA		
		ACCG TGAGGGCATCT		
		CAAGTC		
GAM2362	C11orf11	3' TCTGACAAGCACCGTGGCCA 44788	TC CCCG	
		TGGCCACG GCT TAGA		
		ACCGGTGC CGA GTCT		
		CA ACA_		
GAM2362	DKFZp434F1719	3' TCTGAAGCTACGTGGCCA 25990	C CCCG	
		TGGCCACGT GCT TAGA		
		ACCGGTGCA CGA GTCT		
		T A_		
GAM2362	FLJ20013	3' TCCACCTGGACCGTGGCCA 19122	TCGC C_ A	
		TGGCCACG TCC GT GA		

			ACCGGTGC AGG CA CT	
			C___ TC C	
GAM2362	GIT2	3'	CGGTGGAATGACGTGGCCA 16602	___ TC
			TGGCCACGTCTG C CCG	
			ACCGGTGCAGT G GGC	
			AA GT	
GAM2362	GIT2	3'	CGGTGGAATGACGTGGCCA 27684	___ TC
			TGGCCACGTCTG C CCG	
			ACCGGTGCAGT G GGC	
			AA GT	
GAM2362	GIT2	3'	CGGTGGAATGACGTGGCCA 27697	___ TC
			TGGCCACGTCTG C CCG	
			ACCGGTGCAGT G GGC	
			AA GT	
GAM2362	IDN3	5'	TCTACGGGAAATGGGTCA 28511	A CGC
			TGGCC CGT TCCCGTAGA	
			ACTGG GTA AGGGCATCT	
			_ A_	
GAM2362	IDN3	5'	TCTACGGGAAATGGGTCA 17684	A CGC
			TGGCC CGT TCCCGTAGA	
			ACTGG GTA AGGGCATCT	
			_ A_	
GAM2362	KIAA1649	3'	CTGCAGCCACGTGGCCA 26105	C CCC
			TGGCCACGT GCT GTAG	
			ACCGGTGCA CGA CGTC	
			C _	
GAM2362	KIAA1649	3'	CTGCAGCCACGTGGCCA 33257	C CCC
			TGGCCACGT GCT GTAG	
			ACCGGTGCA CGA CGTC	
			C _	
GAM2362	KIAA1884	3'	TCTACAGTAGCACTGTGGCCA 36297	TC CCC
			TGGCCACG GCT GTAGA	
			ACCGGTGT CGA CATCT	
			CA TGA	
GAM2362	KIAA1944	5'	TCTACGGAAGATGTGGC 37231	GCTC
			GCCACGTC CCGTAGA	
			CGGTGTAG GGCATCT	
			AA_	
GAM2362	LOC151162	5'	CTACAGGCTGGGGTGGCC 41306	G CT C
			GGCCAC TCG CC GTAG	

		CCGGTG GGT GG CATC	
		G C_ A	
GAM2362	LOC203377 5'	CTACAGGCTGGGGTGGCC 43541	G CT C
		GGCCAC TCG CC GTAG	
		CCGGTG GGT GG CATC	
		G C_ A	
GAM2362	LOC221576 3'	TCTGGTTGAACCACGTGGCCA 45000	CGC CCG
		TGGCCACGT TC TAGA	
		ACCGGTGCA AG GTCT	
		CCA TTG	
GAM2362	LOC253573 3'	TCTACAAGGTGTTGTGGCCA 46366	T CCC
		TGGCCACG CGCT GTAGA	
		ACCGGTGT GTGG CATCT	
		T AA_	
GAM2362	LOC257515 3'	TCTGGTTGAACCACGTGGCCA 46684	CGC CCG
		TGGCCACGT TC TAGA	
		ACCGGTGCA AG GTCT	
		CCA TTG	
GAM2362	LOC257572 3'	TCTGGTTGAACCACGTGGCCA 46745	CGC CCG
		TGGCCACGT TC TAGA	
		ACCGGTGCA AG GTCT	
		CCA TTG	
GAM2363	MATK 5'	GGAGAAGCAACACCCCTCT 8194	A ACGA A
		AGAGGGGT GTT TT CTCC	
		TCTCCCCA CAA AA GAGG	
		_ CG_ _	
GAM2363	FADS2 3'	GGAGCAATCTGACCCTTCT 10469	AGTTAC A
		AGAGGGGT GATT CTCC	
		TCTTCCA CTAA GAGG	
		GT_ C	
GAM2363	FKBP9 3'	TGGAATAACCACATGGCTACCT 45146	G CGA_ C
	TCT	AGAGGG TAGTTA TTA TCCA	
		TCTTCC ATCGGT AAT AGGT	
		_ ACACC A	
GAM2363	KIAA0318 3'	GAGTAAAAGTCTACCCCTCT 34187	TT GA
		AGAGGGGTAG AC TTA CTC	
		TCTCCCCATC TG AATGAG	
		_ AA	
GAM2363	KIAA1524 5'	TAATCCCATAACTACCCTCT 36360	G C_
		AGAGGG TAGTTA GATTA	

			TCTCCC ATCAAT CTAAT		
			— ACC		
GAM2364	ABCD4	3'	CCTGAGGCAGGTAAATGGGGC 21590	AC	GGGG_
			GCCC CGT TGCCTCAGG		
			CGGG GTA ACGGAGTCC		
			— AATGG		
GAM2364	CELSR1	3'	CCGTCACCCACACAGGCTG 15512	CACC	CCTCA
			CAGCC GTGGGGTG GG		
			GTCGG CACCCAC CC		
			ACA_ TG__		
GAM2364	HSD17B1	5'	CCTGAGGCACCCCAACATG 5995	CCG	
			CA TGGGGTGCCTCAGG		
			GT ACCCCACGGAGTCC		
			ACA		
GAM2364	ITGA4	5'	CCGAACGTCCGCCGCGGTGGG 6581	GT_	CTCA
	C		GCCACCGTGGG GC GG		
			CGGGTGGCGCCC TG CC		
			GCC CAAG		
GAM2364	MBP	3'	CCCAAGGCACAGAGACACGGGC 43220	ACC	GG__ CA
			GCCC GTG GTGCCT GG		
			CGGG CAC CACGGA CC		
			— AGAGA AC		
GAM2364	PRDM2	5'	CCTGAGGCACCCACTTGGG 18000	CC	G
			CCCA GTGGG TGCCTCAGG		
			GGGT CACCC ACGGAGTCC		
			T_ _		
GAM2364	PRDM2	5'	CCTGAGGCACCCACTTGGG 14532	CC	G
			CCCA GTGGG TGCCTCAGG		
			GGGT CACCC ACGGAGTCC		
			T_ _		
GAM2364	RAP1GA1	3'	CCTGGAGCCCCAGGTGGGCTG 8798	G	GC T
			CAGCCCACC TGGGGT C CAGG		
			GTCGGGTGG ACCCCG G GTCC		
			_ A__		
GAM2364	SYNGR1	3'	CGAGGTCACGGTGAGT 11064	C	GGGT A
			GC CACCGTG GCCTC G		
			TG GTGGCAC TGGAG C		
			A ____ C		
GAM2364	FLJ11053	5'	CCTGAGGCCTTCAAACAGTGG 42777	CG__	T
			CCAC TGGGG GCCTCAGG		

GGTG ACTTC CGGAGTCC
 ACAA _

GAM2364 FLJ11539 5' CTAGGCACCCACGATTAGCTG 24087 CCAC C
 CAGC CGTGGGGTGCCT AG
 ||| ||||| ||
 GTCG GCACCCACGGA TC
 ATTA _

GAM2364 FLJ12505 5' CCCGAGGCACCGCCGTAAGC 24093 CC TGG A
 GC ACCG GGTGCCTC GG
 || ||| ||||| ||
 CG TGGC CCACGGAG CC
 AA CG_ C

GAM2364 FLJ14129 3' GCCTCCCACGGTCAGCTG 25163 CC T
 CAGC ACCGTGGGG GC
 ||| ||||| ||
 GTCG TGGCACCT CG
 AC C

GAM2364 FLJ20004 5' CCTGGGCCACCCACAGCGGGC 45644 ACC C
 GCCC GTGGGGTG CTCAGG
 ||| ||||| |||||
 CGGG CACCCAC GGGTCC
 CGA C

GAM2364 FLJ21709 3' CTGAGGCTCTGGTAGGCTG 38171 C GTGG T
 CAGCC ACC GG GCCTCAG
 |||| || || |||||
 GTCGG TGG TC CGGAGTC
 A _ T

GAM2364 KIAA0084 3' CCCAAGGCATCTTACCAACAGC 33804 CCACC CA
 TG CAGC GTGGGGTGCCT GG
 ||| ||||| ||
 GTCG CATTCTACGGA CC
 ACAAC AC

GAM2364 KIAA0376 5' CCTGAGGCAGTCCGATGGGGCT 32673 ACCG G
 AGCCC TGGG TGCCTCAGG
 |||| ||| |||||
 TCGGG GCCT ACGGAGTCC
 GTA_ G

GAM2364 KLF5 5' CTGAGAGCACGGTGGGGC 7462 _ GTGGG _
 GCCC ACC GTGC CTCAG
 ||| || ||| |||||
 CGGG TGG CACG GAGTC
 G _ A

GAM2364 MGC15631 3' CCTGAGGCATGGGATGGG 26493 _ GTGGG
 CCCA CC GTGCCTCAGG
 ||| || |||||
 GGGT GG TACGGAGTCC
 A G_

GAM2364 MGC20727 5' CTGAGGCCCGGCGAGGT 27436 CAC G GT
 GCC CGT GG GCCTCAG
 || ||| || |||||

TGG GCG CC CGGAGTC
 A_ G_
 GAM2364 MGC2605 5' CCTGAAGGGGCACCGTGGGCTG 26086 CGTGG ____
 CAGCCAC GGTGCC TCAGG
 ||||| ||||| |||||
 GTCGGGTG CCACGG AGTCC
 ____ GGA
 GAM2364 PP1665 3' CTGAGGCCAGCTGGGC 25090 CC GG T
 GCCCA GT GG GCCTCAG
 |||| | | |||||
 CGGGT CG CC CGGAGTC
 ____ A_ _
 GAM2364 PTDSS2 5' CTAAGACCCGCGGGC 25076 ACC GC C
 GCCC GTGGGGT CT AG
 ||| ||||| |||
 CGGG CGCCCCA GA TC
 ____ _ A
 GAM2364 SAST 5' CCTACCAGCCACGGTGG 31539 G CCTC
 CCACCGTGGG TG AGG
 ||||| || |||
 GGTGGCACCC AC TCC
 G CA_
 GAM2364 SSH2 3' CCTGAGGCATCGAATGGGCT 31179 CCGTGG
 AGCCCA GGTGCCTCAGG
 |||| | |||||
 TCGGGT CTACGGAGTCC
 AAG_
 GAM2364 U5-116KD 3' CCTGCTCCCTACAGTGGGCTG 10437 C T CTC
 CAGCCAC GTGGGG GC AGG
 ||||| ||||| || |||
 GTCGGGTG CATCCC CG TCC
 A T ____
 GAM2364 LOC130074 3' CCCGAAGCATATGGTGGAGC 37471 _ GGG C A
 GC CCACCGT GTGC TC GG
 || ||||| ||| |||
 CG GGTGGTA TACG AG CC
 A ____ A C
 GAM2364 LOC146506 3' CCTGTGCCCCACAAGGAGCTG 38179 _ ACC TG CTC
 CAGC CC GTGGGG C AGG
 ||| | ||||| | |||
 GTCG GG CACCCC G TCC
 A AA_ GT_
 GAM2364 LOC147229 5' CTAAAGGCACCGCAAGCTG 38317 CCACCG G C_
 CAGC TG GGTGCCT AG
 ||| | ||||| |||
 GTCG AC CCACGGA TC
 A____ G AA
 GAM2364 LOC150244 5' CCTAAGGCACCTTCTGTGG 38920 CGT C
 CCAC GGGGTGCCT AGG
 ||| ||||| |||

			GGTG TTCCACGGA TCC		
			TC_ A		
GAM2364	LOC257426	3'	GTCCCCACGGTGA CTG 33099	CC	T
			CAG CACCGTGGGG GC		
			GTC GTGGCACCCC TG		
			A_ _		
GAM2364	LOC51608	3'	CTGAGGCTGGCGGTGG 31840	G GGT	
			CCACCGT G GCCTCAG		
			GGTGGCG T CGGAGTC		
			G _		
GAM2365	PKHD1	3'	TTCATTCATGTCTGGAGA 28946	C TATTTT	
			TCTCCAGACA GG TGAA		
			AGAGGTCTGT CT ACTT		
			A T _		
GAM2365	RAD17	5'	TTCAAAAGAATATCTGTCTG 28482	C _	
			CAGACA GGTATTT TTGAA		
			GTCTGT CTATAAG AACTT		
			_ AA		
GAM2365	SLC25A15	3'	AAATACTGTGTCTAAAGA 15524	CC	
			TCT AGACACGGTATTT		
			AGA TCTGTGTCATAAA		
			AA		
GAM2365	SLC38A2	3'	GTTCAAAATCAAGTGCCTAGGG 21050	C A GGTAT	
	A		TCTC AG CAC TTTTGAAC		
			AGGG TC GTG AAAACTTG		
			A C AACT_		
GAM2365	ARNTL2	3'	AAATACCATGTTTGAAGA 21410	C C	
			TCT CAGACA GGTATTT		
			AGA GTTTGT CCATAAA		
			A A		
GAM2365	C20orf7	3'	TTCAAAATCATTTGGAGA 23572	CAC ATT	
			TCTCCAGA GGT TTTGAA		
			AGAGGTTT CTA AACTT		
			A_ _		
GAM2365	CDA02	5'	CAAAAATACTGTCCTGG 33702	AC	
			CCAG ACGGTATTTTGT		
			GGTC TGT CATAAAAAC		
			C_		
GAM2365	DAPK2	3'	GTTCAAGAGAACCCACCCAGAG 15637	CAGACAC A	
	A		TCTC GGT TTTTGAAC		

AGAG CCA GAGAACTTG
 ACCCAC_ A
 GAM2365 DKFZP586I2223 3' TCATCACCCAGTCTGGAGA 17733 AC ATTTT
 TCTCCAGAC GGT TGA
 ||||| ||| |||
 AGAGGTCTG CCA ACT
 AC CT__
 GAM2365 FLJ10803 3' TTCAAAACCTTCTGGA 20157 CAC ATT
 TCCAGA GGT TTTGAA
 ||||| ||| |||||
 AGGTCT CCA AAACCTT
 T__ __
 GAM2365 FLJ13031 5' TTCAAAAAATATACCATTTGGAG 23998 ACAC ____
 A TCTCCAG GGTAT TTTTGAA
 ||||| ||||| |||||
 AGAGGTT CCATA AAAACCTT
 A__ TAA
 GAM2365 FLJ32762 3' TTCAAAAAATATACCATTTGGAG 29636 ACAC ____
 A TCTCCAG GGTAT TTTTGAA
 ||||| ||||| |||||
 AGAGGTT CCATA AAAACCTT
 A__ TAA
 GAM2365 KIAA1946 3' TCAAAAATACCTTCAGGA 40119 A CAC
 TCC GA GGTATTTTGA
 ||| || |||||
 AGG CT CCATAAAACT
 A T__
 GAM2365 MGC16142 3' GTTCTTGATACCATGTTTG 26508 C TTTT
 CAGACA GGTAT GAAC
 ||||| ||||| |||
 GTTTGT CCATA CTTG
 A TGTT
 GAM2365 NCOA2 3' TCAAAACACTTCCAGTCTGGAG 13297 AC TAT__
 A TCTCCAGAC GG TTTTGA
 ||||| || |||||
 AGAGGTCTG CC AAAACT
 A_ TTCAC
 GAM2365 SSR1 3' GTTCAAATAGTGCCTCGGA 9114 A CAC ____
 TCC GA GGTATT TTTGAAC
 ||| || ||||| |||||
 AGG CT CCGTGA AAACCTTG
 _ __ TT
 GAM2365 UNC5D 3' GTTCAAAAACACATGAAGTCA 28114 C ACACG A
 GA TCT CAG GT TTTTGAAC
 ||| ||| || |||||
 AGA GTC CA AAAAAGTTCG
 C AAGTA C
 GAM2365 LOC203369 3' GTTCAAAAGAGAGCTCCCTGGA 43033 ACAC A__
 TCCAG GGT TTTTGAAC
 ||||| ||| |||||

		AGGTC TCG GAAAACTTG CC__ AGA	
GAM2365	LOC206480 5'	TCTCTGACACCACTCTGGAGA 43614	CAC A TTT
		TCTCCAGA GGT TT GA AGAGGTCT CCA AG CT CA_ C TCT	
GAM2366	ABCC5 3'	CGGTGCCAGGTTTTCTGGGTG 12248	C G AA
		TACCCAGAAA AC CT CACCG GTGGGTCTTT TG GA GTGGC _ _ CC	
GAM2366	ADPRT 5'	GCGGCAAGCGTGTCTAGGT 7324	C AACA
		ACC AGAAACACGCT CCGC TGG TCTTTGTGCGA GGCG A AC__	
GAM2366	IRS2 3'	AGTGTTTTCTTTTTGGGTA 30029	C__
		TACCCAGAAA ACGCT ATGGGTTTTT TGTGA CTTT	
GAM2366	NPY2R 5'	GCGAGGGGGCGCCCCCTCTGGGT 6612	AACA AACAC
	A	TACCCAGA CGCT CGC ATGGGTCT GCGG GCG CCCC GGGA_	
GAM2366	PROML1 3'	CGGCACCATTGGTCTCTGGGTA 12635	A A CTAACA
		TACCCAGA AC CG CCG ATGGGTCT TG GT GGC C _ TACCAC	
GAM2366	TMEM2 3'	GCAGTGCCTGGGGGCCCTGTTTC 15042	C_ AA__ C
	TGGG	CCCAGAAACA GCT CAC GC GGGTCTTTGT CGG GTG CG CC GTCC A	
GAM2366	FLJ13491 3'	CGGTGTGCCAGCTTCTGGGT 23888	ACAC A__
		ACCCAGAA GCT ACACCG TGGGTCTT CGA TGTGGC __ CCG	
GAM2366	KIAA0125 3'	GCAGAGTCAGATGTTTCTGGGT 30347	CG A ACC
	A	TACCCAGAAACA CT AC GC ATGGGTCTTTGT GA TG CG A_ C AGA	
GAM2366	KIAA0125 5'	GCGGAGTCAGATGTTTCTGGG 16692	CG A A
		CCCAGAAACA CT AC CCGC 	

		GGGTCTTTGT GA TG GGCG	
		A_ C A	
GAM2366 KIAA0317	3'	GTGTCAGCATGTTTCTGG 16795	C A
		CCAGAAACA GCT ACAC	
		GGTCTTTGT CGA TGTG	
		A C	
GAM2366 KIAA0469	3'	CGTGTTAGTCTGAGGTA 16890	_ AAACAC C
		TACC CAG GCTAACAC G	
		ATGG GTC TGATTGTG C	
		A _____ A	
GAM2366 KIAA1005	3'	GTGCCAGGGTGTATCTGGGTA 35778	A G AA
		TACCCAGA ACAC CT CAC	
		ATGGGTCT TGTG GA GTG	
		A G CC	
GAM2366 PP1628	5'	GCGGCACTTGGGGTTTCTGGG 24858	ACG CA_
		CCCAGAAAC CTAA CCGC	
		GGGTCTTTG GGTT GGCG	
		G_ CAC	
GAM2366 THEA	3'	GCAGTATTTTGCCTCTCTGGGT 32952	AAC T_ C C
A		TACCCAGA ACGC AA AC GC	
		ATGGGTCT TGCG TT TG CG	
		C_ TT A A	
GAM2366 LOC128338	3'	GTGTTCTCATTTTTTCTGGGTA 36927	CACGCT_
		TACCCAGAAA AACAC	
		ATGGGTCTTT TTGTG	
		TTTACTC	
GAM2366 LOC146713	5'	GCATGTGGCGTGCTCTGGGTA 40714	AA A CC
		TACCCAGA CACGCTA CA GC	
		ATGGGTCT GTGCGGT GT CG	
		C_ _ A_	
GAM2366 LOC220070	3'	CGGTGAGAGAATGTTTCTG 29820	CG AA
		CAGAAACA CT CACCG	
		GTCTTTGT GA GTGGC	
		AA GA	
GAM2367 AKAP2	3'	ATCGTGTCTGCTTATAATA 14058	CAAT
		TATTATAAGCG TACGAT	
		ATAATATTCGT GTGCTA	
		CT_	
GAM2368 APOL6	5'	CGAAACCAGTTTTGCAATCAAT 24968	CAT TA_
TC		GAATTGAT CGAG GTTTCG	

		CTTAACTA GTTT CAAAGC		
		AC_ TGAC		
GAM2369	NUMB	3' AACACAATCATGCTTATGA 9831	T	A_
		TCATAGGCAT GGT TTGTT		
		AGTATTCGTA CTA AACAA		
		_ AC		
GAM2369	PCDHA1	3' AATCTTACTAACACCTATGAT 20860	CA	TT
		ATCATAGG TTGGTA GTT		
		TAGTATCC AATCAT TAA		
		AC TC		
GAM2369	PCDHA1	3' AATCTTACTAACACCTATGAT 25379	CA	TT
		ATCATAGG TTGGTA GTT		
		TAGTATCC AATCAT TAA		
		AC TC		
GAM2369	PCDHA10	3' AATCTTACTAACACCTATGAT 25611	CA	TT
		ATCATAGG TTGGTA GTT		
		TAGTATCC AATCAT TAA		
		AC TC		
GAM2369	PCDHA10	3' AATCTTACTAACACCTATGAT 20870	CA	TT
		ATCATAGG TTGGTA GTT		
		TAGTATCC AATCAT TAA		
		AC TC		
GAM2369	PCDHA11	3' AATCTTACTAACACCTATGAT 20880	CA	TT
		ATCATAGG TTGGTA GTT		
		TAGTATCC AATCAT TAA		
		AC TC		
GAM2369	PCDHA12	3' AATCTTACTAACACCTATGAT 20891	CA	TT
		ATCATAGG TTGGTA GTT		
		TAGTATCC AATCAT TAA		
		AC TC		
GAM2369	PCDHA13	3' AATCTTACTAACACCTATGAT 20901	CA	TT
		ATCATAGG TTGGTA GTT		
		TAGTATCC AATCAT TAA		
		AC TC		
GAM2369	PCDHA2	3' AATCTTACTAACACCTATGAT 20911	CA	TT
		ATCATAGG TTGGTA GTT		
		TAGTATCC AATCAT TAA		
		AC TC		
GAM2369	PCDHA3	3' AATCTTACTAACACCTATGAT 20921	CA	TT
		ATCATAGG TTGGTA GTT		

			TAGTATCC AATCAT TAA AC TC		
GAM2369	PCDHA4	3'	AATCTTACTAACACCTATGAT 20931 ATCATAGG TTGGTA GTT TAGTATCC AATCAT TAA AC TC	CA	TT
GAM2369	PCDHA5	3'	AATCTTACTAACACCTATGAT 20941 ATCATAGG TTGGTA GTT TAGTATCC AATCAT TAA AC TC	CA	TT
GAM2369	PCDHA6	3'	AATCTTACTAACACCTATGAT 20951 ATCATAGG TTGGTA GTT TAGTATCC AATCAT TAA AC TC	CA	TT
GAM2369	PCDHA6	3'	AATCTTACTAACACCTATGAT 25583 ATCATAGG TTGGTA GTT TAGTATCC AATCAT TAA AC TC	CA	TT
GAM2369	PCDHA7	3'	AATCTTACTAACACCTATGAT 20961 ATCATAGG TTGGTA GTT TAGTATCC AATCAT TAA AC TC	CA	TT
GAM2369	PCDHA8	3'	AATCTTACTAACACCTATGAT 20971 ATCATAGG TTGGTA GTT TAGTATCC AATCAT TAA AC TC	CA	TT
GAM2369	PCDHA9	3'	AATCTTACTAACACCTATGAT 25596 ATCATAGG TTGGTA GTT TAGTATCC AATCAT TAA AC TC	CA	TT
GAM2369	PCDHAC1	3'	AATCTTACTAACACCTATGAT 20840 ATCATAGG TTGGTA GTT TAGTATCC AATCAT TAA AC TC	CA	TT
GAM2369	PCDHAC2	3'	AATCTTACTAACACCTATGAT 20850 ATCATAGG TTGGTA GTT TAGTATCC AATCAT TAA AC TC	CA	TT
GAM2369	FHR5	3'	AACAAATCCAATCCCATGAT 25082 ATCAT GG ATTGG ATTGTT 	A C T	

TAGTA CC TAACC TAACAA
 C _ _
 GAM2369 FLJ10511 3' AACAAAAATCAAATGCCTAT 19897 _ A_
 ATAGGCATT GGT TTGTT
 ||||| ||| ||||
 TATCCGTAA CTA AACAA
 A AA
 GAM2369 FLJ13962 3' AATAACAATGCCAACATCC 24296 CA_
 GG TTGGTATTGTTATT
 || |||||
 CC AACCGTAACAATAA
 TAC
 GAM2369 LOC143785 3' AACATACCCACAAATGCCTATG 37631 ____ T
 AT ATCATAGGCATT GGTAT GTT
 ||||| ||| |||
 TAGTATCCGTAA CCATA CAA
 ACAC _
 GAM2369 LOC152215 3' AATAAGCAATCCTATGAT 39224 C G_
 ATCATAGG ATTG TATT
 ||||| ||| |||
 TAGTATCC TAAC ATAA
 _ GA
 GAM2370 COL4A1 3' TGAATGACTTGACTTC 7580 AATC G
 GAAGTCA GGTC ATTCA
 ||||| ||| ||||
 CTTCACT TCAG TAAGT
 _ _
 GAM2370 CTNNA2 3' ATGAATTGAACAATTTAACCTT 10617 A C CGG
 GA TCGA GT AAAT TCGATTCAT
 ||| || ||| |||||
 AGTT CA TTTA AGTTAAGTA
 C A ACA
 GAM2370 CTNND2 3' ATGAATCGCAAGTTAACTTGGA 7015 G CA CG T
 TC AAGT AAT G CGATTCAT
 || ||| ||| | |||||
 AG TTCA TTG C GCTAAGTA
 G A_ AA_
 GAM2370 FKSG28 3' ATGGGAGGCCTATTTGACT 25201 C GA
 AGTCAAAT GGTC TTCAT
 ||||| ||| ||||
 TCAGTTTA CCGG GGGTA
 T A_
 GAM2370 MARCKS 3' TTGACCAATTTGACTTAGA 8169 G C
 TC AAGTCAAAT GGTCGA
 || ||||| ||||
 AG TTCAGTTTA CCAGTT
 A A
 GAM2370 NPD009 5' TGGGAACTGATTTGACCTCGA 45565 A CGA
 TCGA GTCAAATCGGT TTCA
 ||| ||||| |||

AGCT CAGTTTAGTCA GGGT
 C A__
 GAM2371 B4GALT1 3' CGAAGTGTGTCATGTGCCG 7246 A AGAACG
 TG CACATGACACA TCG
 || ||||| |||
 GC GTGTACTGTGT AGC
 C GA____
 GAM2371 IRTA2 3' TCTCCTGCTCATGTGTCA 25299 _ CA
 TGACACATGA CA AGA
 ||||| || |||
 ACTGTGTACT GT TCT
 C CC
 GAM2371 KIAA1318 3' GCGTATCTTGCCATGTGTCA 33433 ACA _
 TGACACATG CAAGA ACGT
 ||||| |||| |||
 ACTGTGTAC GTTCT TGCG
 C__ A
 GAM2371 MOST2 5' GGCCCCTGTGTCATAGTCA 21554 AC A AAC
 TGAC ATGACACA G GTC
 ||| ||||| | |||
 ACTG TACTGTGT C CGG
 A__ _CC_
 GAM2371 LOC158364 5' GACTGAGTCATGTGCCA 39818 A A AGAAC
 TG CACATGAC CA GTC
 || ||||| || |||
 AC GTGTACTG GT CAG
 C A ____
 GAM2372 DMD 3' TCTTTTGGATTTTAAATC 5573 ACAGC
 GAT GAAATCAAAAAGA
 ||| |||||
 CTA TTTAGTTTTTCT
 AAT__
 GAM2372 DMD 3' TCTTTTGGATTTTAAATC 10156 ACAGC
 GAT GAAATCAAAAAGA
 ||| |||||
 CTA TTTAGTTTTTCT
 AAT__
 GAM2372 DMD 3' TCTTTTGGATTTTAAATC 10163 ACAGC
 GAT GAAATCAAAAAGA
 ||| |||||
 CTA TTTAGTTTTTCT
 AAT__
 GAM2372 DMD 3' TCTTTTGGATTTTAAATC 10209 ACAGC
 GAT GAAATCAAAAAGA
 ||| |||||
 CTA TTTAGTTTTTCT
 AAT__
 GAM2372 DMD 3' TCTTTTGGATTTTAAATC 10214 ACAGC
 GAT GAAATCAAAAAGA
 ||| |||||

			CTA TTTAGTTTTTCT		
			AAT__		
GAM2372	DMD	3'	TCTTTTTGATTTTTAAATC	10225	ACAGC
			GAT GAAATCAAAAAGA		
			CTA TTTAGTTTTTCT		
			AAT__		
GAM2372	DMD	3'	TCTTTTTGATTTTTAAATC	10169	ACAGC
			GAT GAAATCAAAAAGA		
			CTA TTTAGTTTTTCT		
			AAT__		
GAM2372	DMD	3'	TCTTTTTGATTTTTAAATC	10177	ACAGC
			GAT GAAATCAAAAAGA		
			CTA TTTAGTTTTTCT		
			AAT__		
GAM2372	DMD	3'	TCTTTTTGATTTTTAAATC	10182	ACAGC
			GAT GAAATCAAAAAGA		
			CTA TTTAGTTTTTCT		
			AAT__		
GAM2372	DMD	3'	TCTTTTTGATTTTTAAATC	10187	ACAGC
			GAT GAAATCAAAAAGA		
			CTA TTTAGTTTTTCT		
			AAT__		
GAM2372	DMD	3'	TCTTTTTGATTTTTAAATC	10198	ACAGC
			GAT GAAATCAAAAAGA		
			CTA TTTAGTTTTTCT		
			AAT__		
GAM2372	DMD	3'	TCTTTTTGATTTTTAAATC	10204	ACAGC
			GAT GAAATCAAAAAGA		
			CTA TTTAGTTTTTCT		
			AAT__		
GAM2372	DMD	3'	TCTTTTTGATTTTTAAATC	10237	ACAGC
			GAT GAAATCAAAAAGA		
			CTA TTTAGTTTTTCT		
			AAT__		
GAM2372	CAMK2	3'	TCTTTTTGACTTCCAAC	13315	C__ A
			GAG GAA TCAAAAAGA		
			GTC CTT AGTTTTTCT		
			AAC C		
GAM2372	DIO2	3'	TCTCCTTGATTTTTGGTAGTAT	6462	A __ AA
	C		GATAC GC GAAATCAA AGA		

			CTATG TG TTTTAGTT TCT		
			A GT CC		
GAM2372	DIO2	3'	TCTCCTTGATTTTTGGTAGTAT 15173	A _	AA
	C		GATAC GC GAAATCAA AGA		
			CTATG TG TTTTAGTT TCT		
			A GT CC		
GAM2372	DKFZP586A011	3'	TCTTTTCTGGGCTGTATT 17718	GAAA _	
			GATACAGC TCA AAAAGA		
			TTATGTCG GGT TTTTCT		
			_ C		
GAM2372	FLJ14906	3'	CTTTTTGATTATTGCATTGTA 26661	ACA _	
			TACGAT GCGA AATCAAAAAG		
			ATGTTA CGTT TTAGTTTTTC		
			_ A		
GAM2372	PRO1584	5'	TTGATTTCCTTTATCGTG 20662	CAGC	
			TACGATA GAAATCAA		
			GTGCTAT CTTTAGTT		
			TT_		
GAM2372	LOC203078	3'	TCTTTCCAGTCGCTGTATGTA 43006	G	AATCAA
			TAC ATACAGCGA AAAGA		
			ATG TATGTCGCT TTTCT		
			_ GACC_		
GAM2373	LIMK1	3'	GGACCGGGCAGGTGTCCAC 8127	_	GTTT
			GTG ACACC CTCGGTCC		
			CAC TGTGG GGGCCAGG		
			C AC_		
GAM2373	LIMK1	3'	GGACCGGGCAGGTGTCCAC 18804	_	GTTT
			GTG ACACC CTCGGTCC		
			CAC TGTGG GGGCCAGG		
			C AC_		
GAM2373	CDIPT	3'	GGACCGGGCAGTGTACAC 13010	C TTT	
			GTGACAC G CTCGGTCC		
			CACTGTG C GGGCCAGG		
			A _		
GAM2374	CASP10	3'	AAAATGTCAAGGAATGA 26832	AGACAA	
			TCAT CTTGACATTTT		
			AGTA GAACTGTAAAA		
			AG_		
GAM2374	CASP10	3'	AAAATGTCAAGGAATGA 26835	AGACAA	
			TCAT CTTGACATTTT		

			AGTA	GA	ACTGTAAAA	
			AG	_____		
GAM2374	CCR2	3'	AAGATGCATTATCTATGATA	6311	CAACT	A
			TATCATAGA	TG	CATTTT	
			ATAGTATCT	AC	GTAGAA	
			ATT	__ _		
GAM2374	PRKG1	3'	GAAAATGTCAAGCTGATTTA	12937	_	A
			TAGA	CA	CTTGACATTTTC	
			ATTT	GT	GA	ACTGTAAAAG
			A	C		
GAM2374	TRAF5	3'	AAAATGCCAAGTTGTCCTGA	10962	TA	A
			TCA	GACAACTTG	CATTTT	
			AGT	CTGTTGAAC	GTAAAA	
			C	_	C	
GAM2374	YWHAG	3'	GAAATGCACTTGCCTATGATA	14856	A	CT A
			TATCATAG	CAA	TG	CATTTT
			ATAGTATC	GTT	AC	GTAAAG
			C	C	_	_
GAM2374	FLJ10097	3'	AAAATCTCAGTTGTCTTTGA	33987	T	T C
			TCA	AGACAACT	GA	ATTTT
			AGT	TCTGTTGA	CT	TAAAA
			T	_	C	
GAM2374	KIAA0884	5'	GAAAATGTACAGACCATGATA	34777	AGACAACT	
			TATCAT	TG	CATTTTC	
			ATAGTA	ACTGTAAAAG		
			CCAGAC	_____		
GAM2374	KIAA1058	3'	AAAATGTCAAAATGATA	40011	AGACAAC	
			TATCAT	TTG	CATTTT	
			ATAGTA	AACTGTAAAA		
			A	_____		
GAM2374	LANO	3'	AAAATGTCAAATGCTTTGA	24803	T A	AC
			TCA	AG	CA	TTGACATTTT
			AGT	TC	GT	AACTGTAAAA
			T	_	A	_
GAM2374	PAIP1	3'	GAAAATGTCACATCTAT	33234	CAACT	
			ATAGA	TG	CATTTTC	
			TATCT	ACTGTAAAAG		
			AC	_____		
GAM2374	USP25	3'	GAAAATGTTTAAAGTCTTTGA	15047	T	AACTT
			TCA	AGAC	GACATTTTC	

			AGT TCTG TTGTAAG		
			T AAT__		
GAM2375	TIRAP	3'	ATTCTTTTTCTATTTA 27474	T	
			TAAATAGAAA AAAGAGT		
			ATTTATCTTT TTTCTTA		
			—		
GAM2375	CCR6	3'	ACATACTTTATTTCTTCTTA 10575	AT	A
			TAA AGAAATAAAG GTGT		
			ATT TCTTTATTTTCA TACA		
			CT A		
GAM2375	CCR6	3'	ACATACTTTATTTCTTCTTA 25367	AT	A
			TAA AGAAATAAAG GTGT		
			ATT TCTTTATTTTCA TACA		
			CT A		
GAM2375	SS18L1	3'	TTAGCCACTTCATTTCTATTTA 32565	AAA	—
			TAAATAGAAAT GAGTG TTAA		
			ATTTATCTTTA TTCAC GATT		
			C__ C		
GAM2375	ZIN	3'	ACTCTTTCCCTCTATTTA 15070	AAT	
			TAAATAGA AAAGAGT		
			ATTTATCT TTTCTCA		
			CCC		
GAM2375	LOC63928	3'	GTGCACTTTATTTCTATT 22638	A TG	
			AATAGAAATAAAG G T		
			TTATCTTTATTTTCA C G		
			A GT		
GAM2376	OPHN1	3'	CTTAAGAATGCCAAAGAATGAA 8404	C TGG__	
			TTCGTTCTT GGT TAAG		
			AAGTAAGAA CCG ATTC		
			A TAAGA		
GAM2376	XPNPEP2	3'	TACCAGAGGTTGGAGAAC 9435	—	
			GTTCTTCGG TTGGTA		
			CAAGAGGTT GACCAT		
			GGA		
GAM2376	ATIP1	3'	ATCTTAGAATAAAGAACGAG 21859	CG GG	
			TTCGTTCTT GTT TAAGAT		
			GAGCAAGAA TAA ATTCTA		
			A_ G_		
GAM2376	Cab45	3'	ATCTCACTTCTGAGAACGAA 18619	T TT A	
			TTCGTTCT CGG GGT AGAT		

			AAGCAAGA GTC TCA TCTA		
			_ T_ C		
GAM2376	Cab45	3'	ATCTCACTTCTGAGAACGAA 18276	T TT A	
			TTCGTTCT CGG GGT AGAT		
			AAGCAAGA GTC TCA TCTA		
			_ T_ C		
GAM2376	LOC147639	5'	ATCTCACCAACTGCAAAC 38344	CTT A	
			GTT CGGTTGGT AGAT		
			CAA GTCAACCA TCTA		
			AC_ C		
GAM2376	LOC151126	3'	ATCTTACCAACGGATCAC 39056	TCT G	
			GT TC GTTGGTAAGAT		
			CA AG CAACCATTCTA		
			CT_ G		
GAM2377	LOC151126	5'	CGTGAACGTGGACTGTAACCTT 39057	TCG T	
			AAG ACG TCCACGTTACAG		
			TTC TGT AGGTGCAAGTGC		
			CAA C		
GAM2377	LOC257407	5'	ATGTTGACATCGACTTT 46334	C CC	
			AAAGTCGA GTT ACGT		
			TTTCAGCT CAG TGTA		
			A T_		
GAM2377	LOC93626	3'	CGATGGAAGTCGACTTTT 36043	G _	
			AAAAGTCGAC TTCCA CG		
			TTTTCAGCTG AAGGT GC		
			_ A		
GAM2378	PSEN2	5'	GTCAGGAGAGTGATGTGA 6035	G TCTC	
			TCA ATC GCTCTCCTGAC		
			AGT TAG TGAGAGGACTG		
			G _		
GAM2378	PSEN2	5'	GTCAGGAGAGTGATGTGA 14865	G TCTC	
			TCA ATC GCTCTCCTGAC		
			AGT TAG TGAGAGGACTG		
			G _		
GAM2378	WNT5B	3'	ATGTCAGGAAAGCCCTAAACTG 25056	ATCTCTC C	
	A		TCAG GCT TCCTGACAT		
			AGTC CGA AGGACTGTA		
			AAATCC_ A		
GAM2378	WNT5B	3'	ATGTCAGGAAAGCCCTAAACTG 26358	ATCTCTC C	
	A		TCAG GCT TCCTGACAT		

		AGTC	CGA AGGACTGTA		
		AAATCC_	A		
GAM2378	BNIP-S	5'	TAGGAGGCAAGAGATCTGA	28693	C T
			TCAGATCTCT GC CTCCTG		
			AGTCTAGAGA CG GAGGAT		
			A _		
GAM2378	HT014	3'	ATGCCAGAATTTGGAGATTTGA	21635	CGCTCTC A
			TCAGATCTCT CTG CAT		
			AGTTTAGAGG GAC GTA		
			TTTAA_	C	
GAM2378	KIAA0433	3'	GTTAGGAGAAATCTGA	17549	CTCTCGC
			TCAGAT TCTCCTGAC		
			AGTCTA AGAGGATTG		
			A_____		
GAM2378	LOC149606	5'	TTAGGAGAGGAAGAAATC	38787	C CG
			GAT TCT CTCTCCTGA		
			CTA AGA GAGAGGATT		
			A AG		
GAM2378	LOC255967	5'	TGTCAGCAAGCAGATCTGA	45495	CTC CTC
			TCAGATCT GCT CTGACA		
			AGTCTAGA CGA GACTGT		
			___ AC_		
GAM2378	LOC84549	3'	GTCAGTGGGGCAAGAAATCTGG	26262	C C TC
			TCAGAT TCT GCTC CTGAC		
			GGTCTA AGA CGGG GACTG		
			A A GT		
GAM2379	ABCB11	3'	TCTGCTTTAGATGTGT	9830	AGGA _
			ACACA TC AAAGCAGA		
			TGTGT AG TTTCGTCT		
			___ A		
GAM2379	ARF1	3'	TCTGCTTTACTCTCATGTGG	34993	CAA TC
			CCACA GGA AAAGCAGA		
			GGTGT TCT TTTCGTCT		
			AC_ CA		
GAM2379	ARHGEF7	3'	CTGCCCTGGTTGTGTGG	9982	AGG AA
			CCACACA ATCA GCAG		
			GGTGTGT TGGT CGTC		
			___ CC		
GAM2379	ATP11A	3'	CTGCCCTGAGGTCCTTGTGTGG	37805	AAA_
			CCACACAAGGATC GCAG		

		GGTGTGTTCTGG	CGTC	
		AGTCC		
GAM2379	BCL2	3' TCTGCGAAGAACCTTGTGTG	6263	A AAA
		CACACAAGG TC GCAGA		
		GTGTGTTCC AG CGTCT		
		A AAG		
GAM2379	CXCL16	3' TCTGCTTTTCACACTGGGTG	22601	A CAAG TC
		TACC CA GA AAAGCAGA		
		GTGG GT CT TTTCGTCT		
		_ CACA _		
GAM2379	E2F3	3' TCTGCTTCCAGCTTTGTGT	7671	ATCA
		ACACAAGG AAGCAGA		
		TGTGTTTC TTCGTCT		
		GACC		
GAM2379	FZD4	3' TCTGCTTTGGCTTTGCCGG	14488	ACA A
		CC CAAGG TCAAAGCAGA		
		GG GTTTC GGTTTCGTCT		
		CC_ _		
GAM2379	HTR4	3' TCTGCTTTTGCCGCGTGGT	6545	ACAA ATC
		ACCAC GG AAAGCAGA		
		TGGTG CC TTTCGTCT		
		CG_ GT_		
GAM2379	ITGA6	3' TCTACTTCTGTAATTGTGTGG	5704	GG CA C
		CCACACAA AT AAG AGA		
		GGTGTGTT TG TTC TCT		
		AA TC A		
GAM2379	MAP2	3' TCTGCTCTGTTTTGCATGG	25582	CA AT A
		CCA CAAGG CA AGCAGA		
		GGT GTTTT GT TCGTCT		
		AC _ C		
GAM2379	MYCBP	3' TCTGCTCTTGTGTTGTGTG	14727	GAT _
		CACACAAG CAA AGCAGA		
		GTGTGTTT GTT TCGTCT		
		_ C		
GAM2379	RNGTT	3' TCTGCTTTACCTCAGTGGTA	9897	ACA ATC
		TACCAC AGG AAAGCAGA		
		ATGGTG TCC TTTCGTCT		
		AC_ A_		
GAM2379	SFRS1	3' TCTGCCCTGGTTTGTGTG	13802	AG AA
		CACACA GATCA GCAGA		

			GTGTGT TTGGT CGTCT		
			— CC		
GAM2379	SLC17A4	3'	TCTGCTTTTTGGCTTTGTG 12000	ATC_	
			CACAAGG AAAGCAGA		
			GTGTTT TTTCTCT		
			GGTT		
GAM2379	SLC21A3	5'	CTGCTTTGGCTTGCGCACGGTG 28674	ACACA_ A	
			TACC AGG TCAAAGCAG		
			GTGG TTC GGTTTCGTC		
			CACGCG _		
GAM2379	SOX13	3'	TCTGTGTGTCCTTGTGTG 12245	CAAA	
			CACACAAGGAT GCAGA		
			GTGTGTTCTG TGTCT		
			TG_		
GAM2379	AP4S1	3'	TCTACTTTGTATTCTTGTGAGG 13943	A _ C	
			CC CACAAGGAT CAAAG AGA		
			GG GTGTTCTTA GTTTC TCT		
			A T A		
GAM2379	C5orf5	3'	CTGCCCTTTTTGTGTGGT 18697	TCAA	
			ACCACACAAGGA GCAG		
			TGGTGTGTTTT CGTC		
			CC_		
GAM2379	CGGBP1	3'	TCTGCTTTGCCTCTGGTGGTA 9741	A _ AT	
			TACCAC CA AGG CAAAGCAGA		
			ATGGTG GT TCC GTTTCGTCT		
			_ C _		
GAM2379	CMG2	3'	CTGCTTTGATGTGAACTGGTA 27718	_ AGGA	
			TACCA CACA TCAAAGCAG		
			ATGGT GTGT AGTTTCGTC		
			CAA _		
GAM2379	DKFZP727C091	3'	CTGCTTTGGAGCTGTGT 32904	A GA	
			ACACA G TCAAAGCAG		
			TGTGT C GGTTTCGTC		
			_ GA		
GAM2379	ELKS	3'	CTGCTTTGGATGTGGT 17420	CAAGGA	
			ACCACA TCAAAGCAG		
			TGGTGT GGTTTCGTC		
			A_		
GAM2379	KIAA0179	3'	TCTGCTGAGGTCCTTGCGTGG 32367	A AA	
			CCAC CAAGGATC AGCAGA		

		GGTG GTTCCTGG TCGTCT		
		C AG		
GAM2379	KIAA0265	3' TCTGCTTTAATGTGCATGGTG 34629	___	AGGATC
		TACCA CACA AAAGCAGA		
		GTGGT GTGT TTTCGTCT		
		AC AA___		
GAM2379	KIAA0323	3' TCTGCTTTATGTGTGTGTGTA 31697	_	AGGATC
		TAC CACACA AAAGCAGA		
		ATG GTGTGT TTTCGTCT		
		T GTA___		
GAM2379	KIAA0352	3' TCTGCTTTTCTGATCTGTGAGT 16824	_	CAAG ___
	A	TAC CACA GATCA AAGCAGA		
		ATG GTGT CTAGT TTCGTCT		
		A ___ CTT		
GAM2379	KIAA1163	3' CTGCCAATTCTCAGTGTGGTA 38557	AA	TCAAA
		TACCACAC GGA GCAG		
		ATGGTGTG TCT CGTC		
		AC TAAC_		
GAM2379	MGC20235	3' TCTGCTTTGACCATGTG 29670	A A	
		CACA GG TCAAAGCAGA		
		GTGT CC AGTTTCGTCT		
		A _		
GAM2379	MGC4677	5' CTGTAAGTCCTTGTGTG 27451	CAAA	
		CACACAAGGAT GCAG		
		GTGTGTTCTG TGTC		
		AA___		
GAM2379	NECL1	3' CTGCTTTGGGTGCGGT 22166	A	AAGGA
		ACC CAC TCAAAGCAG		
		TGG GTG GGTTTCGTC		
		C ___		
GAM2379	PLAC3	5' TCTGCCCATCACTCTGGTGTGG 34368	A	ATCAAA_
	TA	TACCACAC AGG GCAGA		
		ATGGTGTG TCT CGTCT		
		G CACTACC		
GAM2379	LOC149603	3' CTGCAGCATCCTTGTGTG 34972	CAAA	
		CACACAAGGAT GCAG		
		GTGTGTTCTA CGTC		
		CGA_		
GAM2379	LOC152445	3' TCTGCTTCAAGATCTTTGCATG 41511	CA	A_
	G	CCA CAAGGATC AAGCAGA		

GGT GTTTCTAG TTCGTCT
AC AAC
GAM2379 LOC199992 5' CTGCTTCTGCTGTGTGGTG 42678 A_ TCAA
TACCACACA GGA AGCAG
||||||| ||| |||||
GTGGTGTGT TCT TCGTC
CG ____
GAM2379 LOC90462 3' TCTGCTCTGATCTTTTAGG 31504 ACAC A
CC AAGGATCA AGCAGA
|| ||||| |||||
GG TTTCTAGT TCGTCT
AT__ C
GAM2379 LOC91496 5' CTGCTTTGACTTCAGCCATGG 32916 CACAA _
CCA GGA TCAAAGCAG
||| ||| |||||
GGT CTT AGTTTCGTC
ACCGA C
GAM2380 DYRK2 3' AGATTAGGATAAGTAAGCT 9630 A GC
AGC TAT TATCCTAATCT
||| ||| |||||
TCG ATG ATAGGATTAGA
A A_
GAM2380 DYRK2 3' AGATTAGGATAAGTAAGCT 13206 A GC
AGC TAT TATCCTAATCT
||| ||| |||||
TCG ATG ATAGGATTAGA
A A_
GAM2380 CPSF2 3' TATAGATTAAGCCCTATAATGC 30865 AT____ ATCC
TA AGCAT GCT TAATCTATA
||||| ||| |||||
TCGTA CGA ATTAGATAT
ATATCC ____
GAM2380 MGC29891 3' TGGGAGGACAGGCATATGC 29439 A_ AA
GCATATGCT TCCT TCTA
||||||| ||| |||
CGTATACGG AGGA GGGT
AC ____
GAM2380 PRO1163 5' TATAGATTAGGAACAATGC 20654 A CTA
GCAT TG TCCTAATCTATA
||| ||| |||||
CGTA AC AGGATTAGATAT
_ A_
GAM2380 ZNF294 3' ATGGAAATAGCATATCTA 35056 C CCTAA
TAG ATATGCTAT TCTAT
||| ||||| |||||
ATC TATACGATA AGGTA
_ A____
GAM2381 CELSR1 3' TTACCAAAAAACAACGTCA 15520 CC_
TGACAGTTGTT TGGTAG
||||||| |||||

		ACTGTCAACAA ACCATT		
		AAA		
GAM2381	FLJ10815	3' CCCCACCATGAACCTGTCA	20170	TT C A
		TGACAG GTTC TGGT GGG		
		ACTGTC CAAG ACCA CCC		
		_ T C		
GAM2381	FLJ21290	3' AATTATTCCAGAAACAGCTGTC	24632	C TAGG
	A	TGACAGTTGTT CTGG GATT		
		ACTGTCGACAA GACC TTAA		
		A TTA_		
GAM2381	LOC122830	3' ATCAAGGAACAACACTATCA	36702	C _
		TGA AGTTGTTCTT GGT		
		ACT TCAACAAGGA CTA		
		A A		
GAM2382	PMX1	5' CGGAAGGCGGCTGGTGCACA	13780	AG _
		TGT ACCAGCCGCC CTG		
		ACA TGGTCGGCGG GGC		
		CG AA		
GAM2382	PMX1	5' CGGAAGGCGGCTGGTGCACA	22915	AG _
		TGT ACCAGCCGCC CTG		
		ACA TGGTCGGCGG GGC		
		CG AA		
GAM2382	C11orf21	3' CATCCCCGGACACCTGGTCTAC	15426	CCGCC TT
	A	TGTAGACCAG CTG GATG		
		ACATCTGGTC GGC CTAC		
		CACA_ CC		
GAM2383	FUT8	3' AAGATCGGAACAGCTCCTTA	10794	CG_ TTAT
		TAAGGAGC TCC TCTT		
		ATTCCTCG AGG AGAA		
		ACA CT_		
GAM2383	LZTR1	5' AAGAATAAAAACGACCTCTTTG	13634	C_ CC
		TAAGGAG CGT TTATTCTT		
		GTTTCTC GCA AATAAGAA		
		CA AA		
GAM2383	DKFZP434L187	3' AATAAGGAACACCTTATTA	34116	AGCCG
		TAATAAGG TCCTTATT		
		ATTATTCC AGGAATAA		
		ACA_		
GAM2383	FLJ13881	3' GGGAGTGGGACGGCTCCT	24069	T
		AGGAGCCGTCCT ATTCTT		

TCCTCGGCAGGG TGAGGG

GAM2383 KIAA0971 3' AAGAATAAAGACTCGAGGCTTC 17223 ____ C
T AGGAGCC GTC TTATTCTT

||||| ||| |||||
TCTTCGG CAG AATAAGAA
AGCT A

GAM2383 RBM7 3' AATAAGGATCCTTTTTA 18177 T GCCG
TAA AAGGA TCCTTATT

||| ||||| |||||
ATT TTCCT AGGAATAA
T ____

GAM2383 LOC151277 5' AAGAATAAGGATGATCTCCT 39093 C_
AGGAG CGTCCTTATTCTT

||||| |||||
TCCTC GTAGGAATAAGAA
TA

GAM2383 LOC159199 5' AATAAGGAGCCTTTATTA 39977 A CG
TAATAAGG GC TCCTTATT

||||| ||| |||||
ATTATTTC CG AGGAATAA

GAM2384 WISP1 3' GCCCCCAGTTAATACTCCAGAG 9963 C_ TCCAC
A TCTCTGGA ATTAAC GC

||||| ||||| |||
AGAGACCT TAATTGA CG
CA CCCC_

GAM2384 C20orf121 5' GGTAGCTAATGTCCGAAGA 23633 C A T
TCT TGGACATTA CT CC

||| ||||| |||
AGA GCCTGTAAT GA GG
A C T

GAM2384 KIAA0763 3' GCACTTTGTTAATCTCCAGAGA 16969 C TTCCAC
TCTCTGGA ATTAAC GC

||||| ||||| |||
AGAGACCT TAATTG CG
C TTTCA_

GAM2384 KIAA0820 3' TGGTAATGTCCATAGA 34222 C ACTT
TCT TGGACATTA CCA

||| ||||| |||
AGA ACCTGTAAT GGT
T ____

GAM2384 SEZ6 5' GGCGTGGAATCAAGGTCCAGA 36775 ATTAAC
TCTGGAC TTCCACGCC

||||| |||||
AGACCTG AAGGTGCGG
GAACTA

GAM2384 LOC152359 3' GACGTTAAGTCCAGAGA 41494 A T
TCTCTGGAC TTAAC TC

||||| ||||| |||

AGAGACCTG AATTG AG
 _ C
 GAM2384 LOC161829 5' GCGTGGAGCGTCCCGAGA 40038 T ATTAAC
 TCTC GGAC TTCCACGC
 |||| ||| |||||
 AGAG CCTG GAGGTGCG
 C C____
 GAM2384 LOC220739 3' GGCACAAAAGCCGGTGTCCAGG 44658 AA CCAC
 GA TCTCTGGACATT CTT GCC
 ||||| ||| |||
 AGGGACCTGTGG GAA CGG
 CC AACA
 GAM2385 DYRK2 3' AGATTAGGATAAGTAAGCT 9630 A GC
 AGC TAT TATCCTAATCT
 ||| ||| |||||
 TCG ATG ATAGGATTAGA
 A A_
 GAM2385 DYRK2 3' AGATTAGGATAAGTAAGCT 13206 A GC
 AGC TAT TATCCTAATCT
 ||| ||| |||||
 TCG ATG ATAGGATTAGA
 A A_
 GAM2385 CPSF2 3' TATAGATTAAGCCCTATAATGC 30865 AT____ ATCC
 TA AGCAT GCT TAATCTATA
 |||| ||| |||||
 TCGTA CGA ATTAGATAT
 ATATCC ____
 GAM2385 MGC29891 3' TGGGAGGACAGGCATATGC 29439 A_ AA
 GCATATGCT TCCT TCTA
 ||||| ||| |||
 CGTATACGG AGGA GGGT
 AC _
 GAM2385 PRO1163 5' TATAGATTAGGAACAATGC 20654 A CTA
 GCAT TG TCCTAATCTATA
 |||| ||| |||||
 CGTA AC AGGATTAGATAT
 _ A_
 GAM2385 ZNF294 3' ATGGA AATAGCATATCTA 35056 C CCTAA
 TAG ATATGCTAT TCTAT
 ||| ||||| |||||
 ATC TATACGATA AGGTA
 _ A____
 GAM2386 ARGBP2 5' AAACGGAGGGTGTGCA 9657 TTAAG _
 TGCAACG CC CCGTTT
 ||||| ||| |||||
 ACGTTGT GG GGCAAA
 G____ A
 GAM2386 FLJ00058 5' TAAACGGGCTGAGCGTTCCA 38511 C A C
 TG AACGTT AGCCC GTTTA
 || ||||| ||||| |||||

			AC TTGCGA TCGGG CAAAT		
			C G _		
GAM2386	IL22R	3'	AACTGCCTGACGTTGCA 22234	A CCC	
			TGCAACGTTA GC GTT		
			ACGTTGCAGT CG CAA		
			C T__		
GAM2386	KIAA0748	3'	TAAACAGGGCTTGAGCA 16704	AACG C	
			TGC TTAAGCCC GTTTA		
			ACG AGTTCGGG CAAAT		
			_____ A		
GAM2386	LOC147184	5'	TAAACGGGGTGAGGTCACA 29788	CA G AA	
			TG AC TT GCCCGTTTA		
			AC TG AG TGGGGCAAAT		
			AC G _		
GAM2387	ATP2A3	3'	TCAAGACTCACATCCCTTT 11673	TA AA C	
			AGAGGGAT GAG TC TGA		
			TTTCCTA CTC AG ACT		
			CA _ A		
GAM2387	OCRL	3'	AGCGTTTCCTAATCCCTC 5817	AG C	
			GAGGGATTAG AAT CT		
			CTCCCTAATC TTG GA		
			CT C		
GAM2387	OCRL	3'	AGCGTTTCCTAATCCCTC 7304	AG C	
			GAGGGATTAG AAT CT		
			CTCCCTAATC TTG GA		
			CT C		
GAM2387	TRRAP	3'	AAGCCAGGATTCTCCGGTCT 9587	TA A	
			GGAT GAGAATCCTG CTT		
			TCTG CTCTTAGGAC GAA		
			GC C		
GAM2387	ARHGEF9	5'	CAGCCCTTCTCTAACCACCCT 17538	A__ TC_	
			AGGG TTAGAGAA CTG		
			TCCC AATCTCTT GAC		
			ACC CCC		
GAM2387	NUDT12	3'	CAAGATTCTCTGCTTTT 25447	AT C	
			GAGGG TAGAGAATC TG		
			TTTTC GTCTCTTAG AC		
			_____ A		
GAM2387	UBE3B	3'	AAGCCAGGAAGGCCAGTCCCT 37772	AGAGAA A	
	C		GAGGGATT TCCTG CTT		

CTCCTGA AGGAC GAA
 CCCGA C
 GAM2387 LOC149506 3' AGGCTTTTAATCCCTTAATCCC 41002 _____ T
 TCT AGAGGGATTAG AGAA CCT
 ||||| ||| |||
 TCTCCCTAATT TTTT GGA
 CCCTAA C
 GAM2387 LOC153711 3' AGCCAGGATTTCCCTC 41666 TTAGAG A
 GAGGGA AATCCTG CT
 |||| | |||| ||
 CTCCCT TTAGGAC GA
 _____ C
 GAM2387 LOC253912 3' AAGTCAGGACCAGGGGTCGCC 46483 _ AGAGAA
 GG GATT TCCTGACTT
 || ||| |||||
 CC CTGG AGGACTGAA
 G GGACC_
 GAM2387 LOC255106 5' GCAGGATTCCTCTCT 45570 ATTAGA A
 AGAGGG GAATCCTG C
 |||| | ||||| |
 TCTCTC CTTAGGAC G
 _____ C
 GAM2387 LOC90917 3' AGCCAGGATCACTCACTCT 32163 ATTA A_ A
 AGGG GAG ATCCTG CT
 ||| || ||||| ||
 TCTC CTC TAGGAC GA
 A_ AC C
 GAM2388 SCD 3' GGTGCCTCAGTTTTCCTTCTGT 11492 _ _ G A
 TAAAA TTTAAC GAAG AGC TGA GCACC
 ||||| ||| ||| |||||
 AAATTG CTTC TTG ACT CGTGG
 T CTT _ C
 GAM2388 TRIM9 3' TGCTTCACATGGTTAAAA 27552 GAAGAGC
 TTTTAAC GTGAAGCA
 ||||| |||||
 AAAATTG CACTTCGT
 GTA_
 GAM2388 FLJ12604 3' GTGCCATCTCCGTTAAAA 32192 AA C AA
 TTTTAACG GAG GTG GCAC
 ||||| ||| ||| |||||
 AAAATTGC CTC TAC CGTG
 _ _ _
 GAM2388 FLJ13162 3' TGCTCTCACGCTTGTTAAAA 24574 GAA _
 TTTTAAC GAGCGTGA AGCA
 ||||| ||||| |||||
 AAAATTG TTCGCACT TCGT
 _____ C
 GAM2388 LOC145474 5' GTGCTTTGAGGCTTCTTC 37869 _ G_
 GAAGA GC TGAAGCAC
 ||||| || |||||

CTTCT CG GTTTCGTG
 T GA
 GAM2389 CLCN4 5' CTCCATTAGACCCTCAA 7572 T AC
 TTGA GG CTAATGGAG
 ||| || |||||
 AACT CC GATTACCTC
 _ CA
 GAM2389 CNR1 3' AACCCCATATTAGATCCATTA 18161 C _ A
 ATTTA TAAATTGATGGA CTA ATGG GTT
 ||||| ||| ||| |||
 ATTTAATTACCT GAT TACC CAA
 A TAA C
 GAM2389 MSL3L1 3' AACTCCATCAGATCTTCTCA 27810 T_ C A
 TGA GGA CT ATGGAGTT
 || ||| |||||
 ACT TCT GA TACCTCAA
 CT A C
 GAM2389 S100B 3' AACTCCATCAGAACTCGCAAT 12954 AT AC A
 ATTG GG CT ATGGAGTT
 ||| || |||||
 TAAC TC GA TACCTCAA
 GC AA C
 GAM2389 CNNM1 3' AACTTGGGGTCCATCA 21602 AATG
 TGATGGACCT GAGTT
 ||||| |||
 ACTACCTGGG TTCAA
 G_
 GAM2389 MGC16309 5' AACTCCAGACCCTTCACATCAA 27238 _ CCTAA_
 TTTA TAAATTGATG GA TGGAGTT
 ||||| || |||||
 ATTTAACTAC CT ACCTCAA
 A TCCCAG
 GAM2389 PURG 3' AACTCCATCAGGCCAAAATTTA 15005 GA GA A
 TAAATT TG CCT ATGGAGTT
 |||| || ||| |||||
 ATTTAA AC GGA TACCTCAA
 A_ _ C
 GAM2389 LOC137362 3' AACTCCATCTCAATCAAT 37104 G CCTA
 ATTGAT GA ATGGAGTT
 |||| || |||||
 TAACTA CT TACCTCAA
 A C_
 GAM2389 LOC203025 3' AACTCCATCTCAATCAAT 42999 G CCTA
 ATTGAT GA ATGGAGTT
 |||| || |||||
 TAACTA CT TACCTCAA
 A C_
 GAM2390 GAD1 3' AACCTAAGGCAACATTTCC 6478 CAGT A
 GG AATGTT CCTTAGGTT
 || |||| |||||

CC TTACAA GGAATCCAA
 T___ C
 GAM2390 GALGT 3' GAACCTAAGGTGGAAACACTGT 7211 AATG
 C GGCAGT TTACCTTAGGTT
 ||||| |||||
 CTGTCA GGTGGAATCCAAG
 CAAA
 GAM2390 DKFZp761H2121 5' AACCTAAGGTATGTGCC 28737 GTAATGT
 GGCA TACCTTAGGTT
 ||| |||||
 CCGT ATGGAATCCAA
 GT____
 GAM2390 EPHA7 3' AATCTGTAACATTACT 10723 CTT
 AGTAATGTTAC AGGTT
 ||||| ||||
 TCATTACAATG TCTAA

 GAM2390 KIAA1655 5' GACTGCAGCACATTACTGCC 33089 TAC TA
 GGCAGTAATGT CT GGTT
 ||||| || ||||
 CCGTCATTACA GA TCAG
 C__ CG
 GAM2390 MGC2541 3' GAATTAAGGTAACATCAATACC 27964 CAGTA G
 T AGG ATGTTACCTTAG TTC
 ||| ||||| ||||
 TCC TACAATGGAATT AAG
 ATAAC _
 GAM2390 RNF2 3' GAACCCAAGGCTCAAATTTACT 14076 ___ TTA A
 GTC GGCAGTAA TG CCTT GGTTG
 ||||| || |||||
 CTGTCATT AC GGAA CCAAG
 TAA TC_ C
 GAM2390 LOC139770 3' GAACCTAAATTTGACCATGCC 37145 GTAAT CC_
 GGCA GTTA TTAGGTTG
 ||| ||| |||||
 CCGT CAGT AATCCAAG
 AC___ TTA
 GAM2391 LOC91408 3' CAAGCTAGATATCTTTATTTGA 32790 C AAA
 TA TATCAAATAA GATATT CTTG
 ||||| |||| ||||
 ATAGTTTATT CTATAG GAAC
 T ATC
 GAM2392 GJA1 5' AACTTGCCTTTTCATTTTACTT 5675 AATATGT
 CA TGAAGTAAAT TAAGTT
 ||||| ||||
 ACTTCATTTA GTTCAA
 CTTTCC
 GAM2392 RB1 3' AACTTACTGATTATTTTCTTCA 43703 T ATGT
 TGAAG AAAATAAT TAAGTT
 |||| ||||| ||||

		ACTTC TTTTATTA ATTCAA	
		— GTC—	
GAM2392 RPE	3'	GATATATTATTTTATTCCA 31155 A	
		TG AGTAAAATAATATGTT	
		AC TTATTTTATTATATAG	
		C	
GAM2392 KIAA1078	3'	AGCTTCACATTATTTTACTT 32469	AT T
		AAGTAAAATA ATGT AAGTT	
		TTCATTTTAT TACA TTCGA	
		— C	
GAM2392 RYK	5'	GCTTTTTATTTTCTTCA 40205	T TGTT
		TGAAGTAAAA AATA AAGT	
		ACTTCATTTT TTAT TTCG	
		T TT—	
GAM2392 TBDN100	3'	AGCATCCATTTTACTTCA 24694	AAT
		TGAAGTAAAAT ATGTT	
		ACTTCATTTTA TACGA	
		CC—	
GAM2392 LOC157627	3'	GGCATATTTTCTTCA 39620	T
		TGAAGTAAAA AATATGTT	
		ACTTCATTTT TTATACGG	
		—	
GAM2393 ADAMTS5	3'	AAAGTAGGTCTGCAGCTATTTT 13917	A A
A		TGAAATA CTG TAGACCTACTTT	
		ACTTTAT GAC GTCTGGATGAAA	
		C —	
GAM2393 SSX3	3'	AAGTATTGTCAGTTACCTC 22002 AA	ACC
		GA TAACTGATAG TACTT	
		CT ATTGACTGTT ATGAA	
		CC —	
GAM2393 LOC144486	3'	AAAGTAGGCGGTCAGCCTTTCA 40416	TAA AGA
		TGAAA CTGAT CCTACTTT	
		ACTTT GACTG GGATGAAA	
		CC— GC—	
GAM2394 ANK1	5'	ACCAAGAGAGCAAACCAGAGA 21734	ATTAT G
		TCTCTG TT TTTTGGT	
		AGAGAC GA AGAACCA	
		CAAAC G	
GAM2394 ANK1	5'	ACCAAGAGAGCAAACCAGAGA 21732	ATTAT G
		TCTCTG TT TTTTGGT	

			AGAGAC GA AGAACCA		
			CAAAC G		
GAM2394	ANK1	5'	ACCAAGAGAGCAAACCAGAGA 21733	ATTAT	G
			TCTCTG TT TTTTGGT		
			AGAGAC GA AGAACCA		
			CAAAC G		
GAM2394	CEACAM5	3'	ACCAAGATCAAGCAGAGA 10571	ATTA	_
			TCTCTG TTTG TTTTGGT		
			AGAGAC GAAC AGAACCA		
			_____ T		
GAM2394	DMRT1	3'	ACTGAAATATAATCAGA 22479	TT	TG
			TCTGATTAT GTTT GT		
			AGACTAATA TAAA CA		
			_____ GT		
GAM2394	EXTL3	3'	ACCAAAACATGCCGCAGGGA 7165	ATTATT	
			TCTCTG TGTTTTGGT		
			AGGGAC ACAAACCA		
			GCCGT_		
GAM2394	ITGA6	3'	ACCAAAACAGTTAATCAGTGA 5700	T	T
			TC CTGATTA TTGTTTTGGT		
			AG GACTAAT GACAAAACCA		
			T T		
GAM2394	NEBL	3'	ACCAAAACGGGTTAATCA 13096	_	
			TGATTA TTTGTTTTGGT		
			ACTAAT GGGCAAAACCA		
			T		
GAM2394	TNFSF10	3'	TACCAAAACAAACAAACAGA 9900	A A	III
			TCTG TT TTTGTTTTGGT A		
			AGAC AA AAACAAAACCA T		
			A C III		
GAM2394	WASF3	3'	ACCAAAACAAATGGAGA 13439	GATT	
			TCTCT ATTTGTTTTGGT		
			AGAGG TAAACAAAACCA		

GAM2394	C15orf5	3'	ACCATCTGATAAGTCAGAGA 25212	_	TGTTT
			TCTCTGATT ATT TGGT		
			AGAGACTGA TAG ACCA		
			A TCT_		
GAM2394	CENTA2	3'	ACCATGAGGAAATAATCAGA 20441	G	_
			TCTGATTATTT TTT TGGT		

AGACTAATAAAA GAG ACCA
 G T
 GAM2394 FADS1 3' ACCAAAACAGATGGTAGAGA 15066 G
 TCTCT ATTATTTGTTTTGGT
 ||||| |||||
 AGAGA TGGTAGACAAAACCA
 —
 GAM2394 FLJ11088 3' ACCAAAACAATATTTAGA 20311 T T
 TCTGA TATT GTTTTGGT
 ||||| |||||
 AGATT ATAA CAAAACCA
 T —
 GAM2394 HSNV1 3' ACCAAAATAGAGCAGA 18963 ATTA
 TCTG TTTGTTTTGGT
 ||||| |||||
 AGAC AGATAAAACCA
 G—
 GAM2394 KCNH8 3' ACCACAAAAAATAATCTGAGA 29453 T G T
 TCTC GATTATTT TT TGGT
 ||||| ||||| |||||
 AGAG CTAATAAA AA ACCA
 T A C
 GAM2394 KIAA0087 3' ACCAAAACAAAATTAATGA 16555 TC AT
 TC TGATT TTGTTTTGGT
 || ||||| |||||
 AG ATTAA AACAAAACCA
 TA —
 GAM2394 KIAA0217 3' CAGTTGTAAATAATCAGA 33278 TT_
 TCTGATTATTTG TTG
 ||||| ||||| |||||
 AGACTAATAAAT GAC
 GTT
 GAM2394 KIAA0350 3' ACCAAAACCAAACAGAGA 30657 ATTA _
 TCTCTG TTTG TTTTGGT
 ||||| ||||| |||||
 AGAGAC AAAC AAAACCA
 — C
 GAM2394 KIAA1128 3' ATCTTGCAAATAATCAGA 33966 TTT
 TCTGATTATTTGT GGT
 ||||| ||||| |||||
 AGACTAATAAACG CTA
 TT_
 GAM2394 KLK7 3' ACCAAAACAAATAAAGA 11475 GA
 TCT TTATTTGTTTTGGT
 ||||| ||||| |||||
 AGA AATAAACAAAACCA
 —
 GAM2394 KLK7 3' ACCAAAACAAATAAAGA 29272 GA
 TCT TTATTTGTTTTGGT
 ||||| ||||| |||||

AGA AATAAACAAAACCA

GAM2394 MEGF11 3' ACTTTGGGCAATAATCAGA 26204 T T_
TCTGATTATT GTTT GGT
||||||| ||| |||
AGACTAATAA CGGG TCA
_ TT
GAM2394 MGC4827 3' ACCAGAGACAAATCAGA 23566 ATT _
TCTGATT TGTTT TGGT
||||| |||| ||||
AGACTAA ACAGA ACCA
_ G
GAM2394 MGC4832 3' ACCAAAACAAAATTTGAG 29698 T AT
CTC GATT TTGTTTTGGT
||| ||| |||||
GAG TTAA AACAAAACCA
T _
GAM2394 SNRK 3' CCAAAACAATAATCAAAGA 19308 C T
TCT TGATTATT GTTTTGG
||| ||||| |||||
AGA ACTAATAA CAAAACC
A _
GAM2394 LOC145842 5' ACCATGTGAATAATAGAGA 37995 A TG TT
TCTCTG TTATT T TGGT
||||| |||| | |||
AGAGAT AATAA G ACCA
_ GT T_
GAM2394 LOC149111 3' ACCATGCACATCATCAGAGA 38647 T T TT
TCTCTGAT AT TGT TGGT
||||||| || ||| |||
AGAGACTA TA ACG ACCA
C C T_
GAM2394 LOC155435 3' ACCAAAACAAACTGAAGAG 39566 GATTA
CTCT TTTGTTTTGGT
||| |||||
GAGA AAACAAAACCA
AGTC_
GAM2394 LOC201562 3' ACCAAAACAAACTTTTCAATGA 42882 TC TTA_
TC TGA TTTGTTTTGGT
|| ||| |||||
AG ACT AAACAAAACCA
TA TTTC
GAM2394 LOC219401 3' ACCACAATACATCAGAGA 44585 TATT T
TCTCTGAT TGTT TGGT
||||||| ||| |||
AGAGACTA ATAA ACCA
C_ C
GAM2394 LOC220766 5' ACCATCACAAATAACAGA 43646 A TT
TCTG TTATTTGT TGGT
||| ||||| |||

		AGAC AATAAACA ACCA		
		— CT		
GAM2394	LOC221495 3'	CCAGAACTATCAGAGA	45056	TATTT
		TCTCTGAT GTTTTGG		
		AGAGACTA CAAGACC		
		T_____		
GAM2394	LOC256112 3'	ACCTCATTAAACATCAGAGA	46102	TA TTTT
		TCTCTGAT TTTG GGT		
		AGAGACTA AAAT CCA		
		C_ TACT		
GAM2394	LOC256846 5'	ACCAAGCTACAATTAGAGA	45696	ATTT T
		TCTCTGATT GTTT GGT		
		AGAGATTAA CGAA CCA		
		CAT_ _		
GAM2394	LOC86651 3'	ACCAAAAGATCTGTGATCAGA	34096	TTG__
		TCTGATTAT TTTTGGT		
		AGACTAGTG AAAACCA		
		TCTAG		
GAM2395	MGC4832 3'	TTATTAGTGTTTCATTGATA	29702	AAA
		TATCAATGAAATA AATAA		
		ATAGTTACTTTGT TTATT		
		GA_		
GAM2395	PALMD 3'	ATTTTTTATTCTATTGATA	19320	A
		TATCAATG AATAAAAAAT		
		ATAGTTAT TTATTTTTTA		
		C		
GAM2395	LOC151647 3'	TTTATTTTCATTGAATTA	39160	A
		TAAT TCAATGAAATAAA		
		ATTA AGTTACTTTATTT		
		—		
GAM2396	ADAM17 3'	GGTGCAAAAGCAGAAAATA	9157	A A
		TATT TTCT CTTTTGCATT		
		ATAA AAGA GAAAACGTGG		
		_ C		
GAM2396	ADAM17 3'	GGTGCAAAAGCAGAAAATA	22410	A A
		TATT TTCT CTTTTGCATT		
		ATAA AAGA GAAAACGTGG		
		_ C		
GAM2396	13CDNA73 3'	GTCAGAAGTAGAATCATA	23323	T _
		TAT ATTCTACTTTTG C		

			ATA TAAGATGAAGAC G		
			C T		
GAM2396	DKFZP586D2223	5'	AATGACTGTGGAATAATA	20643	TTTTG
			TATTATTCTAC CATT		
			ATAATAAGGTG GTAA		
			TCA__		
GAM2396	FLJ20276	3'	AATCAAAAGGAGAATAATA	19325	A C
			TATTATTCT CTTTGT ATT		
			ATAATAAGA GAAAAC TAA		
			G _		
GAM2396	LOC150848	5'	TAATGCTTCAGTAGAATA	41255	TTT
			TATTCTACT GCATTA		
			ATAAGATGA CGTAAT		
			CTT		
GAM2396	LOC93206	3'	AGTGAGTAAAGTAGAATA	35516	TG_
			TATTCTACTTT CATT		
			ATAAGATGAAA GTGA		
			TGA		
GAM2397	COG3	3'	AGTGCTGACTGCAGAATGAAAT	25426	__ A TAAA
	A		TATTTCTG CT GT TCAGCACT		
			ATAAAGT GA CG AGTCGTGA		
			AA _ TC__		
GAM2397	CBX3	3'	AGTGTGTTTTAACTAGC	18659	TCA
			GCTAGTTAAA GCACT		
			CGATCAATTT TGTGA		
			TG_		
GAM2397	CBX3	3'	AGTGTGTTTTAACTAGC	14139	TCA
			GCTAGTTAAA GCACT		
			CGATCAATTT TGTGA		
			TG_		
GAM2397	MGC2629	5'	AGTGCCGACGGTAGCGAAA	26268	GTAAA A
			TTTCGCTA TC GCACT		
			AAAGCGAT AG CGTGA		
			GGC__ C		
GAM2398	FZD7	3'	CTAATACCCTGAAAAGAAGTGA	9598	CATG AA
	TG		TATCACTTCT AG TATTAG		
			GTAGTGAAGA TC ATAATC		
			AAAG CC		
GAM2398	LEC3	3'	CTAATATTTGTTGTAAAAGTGA	17567	CT_ TGA
			TCACTT CA GAATATTAG		

		AGTGAA GT TTTATAATC		
		AAT TG_		
GAM2399	ATP7A	3' TCAGTAATAAATACAAAAAAA 5495	C	TTG_
	A	TTTTTT TTGT ATTACTGA		
		AAAAAA AACA TAATGACT		
		A TAAA		
GAM2399	FOXF2	3' TCAGTAATCAGGGTGTGAAAAA 7187	TTG_	
	A	TTTTTTC TTTGATTACTGA		
		AAAAAAG GGACTAATGACT		
		TGTG		
GAM2399	FLJ12085	3' CAGTAATGAAATAAAAAATA 23033	TCT	G
		TATTTTT TGTTT ATTACTG		
		ATAAAAA ATAAA TAATGAC		
		— G		
GAM2399	FLJ20502	3' TCAGAGATAAACAAGAACAAT 19508	T	A A
	A	TATTT TTCTTGTTTG TT CTGA		
		ATAAA AAGAACAAT AG GACT		
		C _ A		
GAM2399	KIAA0826	3' CAGTATTTCAAAAAGAAA 40215	G	T_
		TTTCTT TTTGA TACTG		
		AAAGAA AACT ATGAC		
		_ TT		
GAM2399	KIAA0903	5' CAGTCTACAAAAAGAAAAATA 35369	G	ATT
		TATTTTTTCTT TTTG ACTG		
		ATAAAAAAGAA AAAC TGAC		
		_ ATC		
GAM2399	KIAA1729	5' AATGAACAAGAAAAAGTA 42945	G	
		TATTTTTTCTTGTTT ATT		
		ATGAAAAAGAACAAG TAA		
		—		
GAM2399	LNx	3' ATCAAACAAGAATAAATA 26338	T	
		TATTT TTCTTGTTTGAT		
		ATAAA AAGAACAACACTA		
		T		
GAM2399	PRO1866	5' TCAATATAAGGCAAGAAAAAAT 20582	GAT	C
		ATTTTTTCTTGTTT TA TGA		
		TAAAAAAGAACGGA AT ACT		
		AT_ A		
GAM2399	LOC122830	3' CAGCAAAATAAGAAAAAATA 36703	GATTA	
		TATTTTTTCTTGTTT CTG		

			ATAAAAAGAATAAA	GAC	
			AC__		
GAM2399	LOC170372	5'	CAGTAAGCCAAGAAAAA	37538	TTTGA
			TTTTTCTTG	TTACTG	
			AAAAAGAAC	AATGAC	
			CG__		
GAM2400	PDE4D	3'	CTTTTGTAAGTCTTTATTA	36429	T C
			TAATA	AGACTTATA GAAG	
			ATTAT	TCTGAATGT TTTC	
			T	T	
GAM2401	ATP5B	5'	GTTACTCTGTGTTTGCTG	30006	A__
			CAGCAAACACA	TAAC	
			GTCGTTTGTGT	ATTG	
			CTC		
GAM2401	CELSR3	3'	ACTTTTGCTATTTTGTCTGCTG	7102	A C A
			CAGCA	ACA AATA CAGAAGT	
			GTCGT	TGT TTAT GTTTTCA	
			C	T C	
GAM2401	EPS15	3'	ATACCTCTCAGTGTGTTTGCT	7711	ATAAC A
			AGCAAACACA	AGA GTAT	
			TCGTTTGTGT	TCT CATA	
			GAC__	C	
GAM2401	IL4R	3'	CTGTTATCTGTGTTTGCTG	6000	_
			CAGCAAACACA	ATAACAG	
			GTCGTTTGTGT	TATTGTC	
			C		
GAM2401	ITGAM	3'	CTCTTGTTATTGCATCTGCTG	6248	AACA GA
			CAGCA	CAATAACA AG	
			GTCGT	GTTATTGT TC	
			CTAC	TC	
GAM2401	SPS2	3'	ATACTTCTGTTTTCTCTTGC	14554	ACACAAT
			GCAA	AACAGAAGTAT	
			CGTT	TTGTCTTCATA	
			CTCTT__		
GAM2401	STC1	3'	GCTTCGTCTTGTGTTTGCTG	9135	TAACA
			CAGCAAACACAA	GAAGT	
			GTCGTTTGTGTT	CTTCG	
			CTG__		
GAM2401	TCTA	3'	ATACTTCTGTTTCCATCTGCTG	22729	AACACAAT
			CAGCA	AACAGAAGTAT	

			GTCGT	TTGTCTTCATA		
			CTACCT__			
GAM2401	TRDN	3'	TCTGTTATGTGTGTTTGCTG	12717		—
			CAGCAAACACA	ATAACAGA		
			GTCGTTTGTGT	TATTGTCT		
			G			
GAM2401	ACVR2	3'	ACTTGTTTTTATTGCATTTGCT	7320	CA	C _
	G		CAGCAA	CAATAA AG AAGT		
			GTCGTTT	GTTATT TT TTCA		
			AC	T G		
GAM2401	AKAP12	3'	TACTGGATTGTGTTTGT	11573	AACAGA	
			GCAAACACAAT	AGTA		
			TGTTTGTGTTA	TCAT		
			GG__			
GAM2401	AKAP12	3'	TACTGGATTGTGTTTGT	29314	AACAGA	
			GCAAACACAAT	AGTA		
			TGTTTGTGTTA	TCAT		
			GG__			
GAM2401	DKFZP761G1913	3'	ATACTTCTGCTATTAACGCT	25543	AAACAC	A
			AGC	AATA CAGAAGTAT		
			TCG	TTAT GTCTTCATA		
			CAA__	C		
GAM2401	FLJ20154	5'	GCTGCTGCTGTGTTTGC	36105	ATAA	A
			GCAAACACA	CAG AGT		
			CGTTTGTGT	GTC TCG		
			C__	G		
GAM2401	FLJ21616	3'	ATACTTCTTTGGGTGCTGTGCT	23794	AA_	AATAAC
			AGCA	CAC AGAAGTAT		
			TCGT	GTG TCTTCATA		
			GTC	GGTT__		
GAM2401	FLJ22009	3'	ACTGCTGCCATTGTAGTTTGCT	30242	_	AA A
	G		CAGCAAAC	ACAAT CAG AGT		
			GTCGTTTG	TGTTA GTC TCA		
			A	CC G		
GAM2401	GNB4	3'	GCTCGCCATTGTGTTTGC	22271	AACA	A
			GCAAACACAAT	GA GT		
			CGTTTGTGTTA	CT CG		
			CCG_ _			
GAM2401	KIAA0630	3'	TTTGTGTTATTGTGATTGCTG	43066	A	G
			CAGCAA	CACAATAACA AAG		

GTCGTT GTGTTATTGT TTT
 A G
 GAM2401 KIAA0680 3' ACTCTCTATTATTGTGTTGCT 16283 A C _
 AGCAA CACAATAA AGA AGT
 ||||| ||||| ||| |||
 TCGTT GTGTTATT TCT TCA
 _ A C
 GAM2401 KIAA0716 3' ATACTTCTTTAAGGTTGCTTTT 16246 CA AAC_
 GCTG CAGCAA CAAT AGAAGTAT
 ||||| ||| |||||
 GTCGTTT GTTG TCTTCATA
 TC GAATT
 GAM2401 KIAA0953 3' TCTGTTCTGTGTCTGCTG 33171 A AT
 CAGCA ACACA AACAGA
 ||||| ||||| |||||
 GTCGT TGTGT TTGTCT
 C C_
 GAM2401 KIAA1319 3' ATACCCTATGTTATTGTGCTCC 21866 CAAA GAA_
 CTG CAG CACAATAACA GTAT
 ||| ||||| |||||
 GTC GTGTTATTGT CATA
 CCTC ATCC
 GAM2401 KIAA1361 3' TCTGTTTTGTGTTTACT 31172 C T
 AG AAACACAA AACAGA
 || ||||| |||||
 TC TTTGTGTT TTGTCT
 A _
 GAM2401 KIAA1719 3' TCTGTTACCTGTTTGCTG 33825 CAA
 CAGCAAACA TAACAGA
 ||||| |||||
 GTCGTTTGT ATTGTCT
 CC_
 GAM2401 NCK1 3' ATACCAAGTATATTGTGTCTGC 12808 A _ AGAA
 GCA ACACAATA AC GTAT
 ||| ||||| || |||||
 CGT TGTGTTAT TG CATA
 C A AAC_
 GAM2401 PRO1866 5' ATACCTCTCAATGTGTTTGCT 20579 ATAAC A
 AGCAAACACA AGA GTAT
 ||||| ||| |||||
 TCGTTTGTGT TCT CATA
 AAC_ C
 GAM2401 LOC148697 3' TGCTTCTGTGCTTGCTG 38575 ACACAATA
 CAGCAA ACAGAAGTA
 ||||| |||||
 GTCGTT TGTCTTCGT
 CG_____
 GAM2401 LOC154215 3' TTCCATTACTGTGTTTGC 39465 A CA
 GCAAACACA TAA GAA
 ||||| ||| |||

CGTTTGTGT ATT CTT
C AC
GAM2401 LOC205418 5' CTGTTATTTTTGCTG 43597 CAC
CAGCAAA AATAACAG
||||| ||||||
GTCGTTT TTATTGTC

—
GAM2402 PCDH11X 3' AGAAATAAAGCTGTATCTGCCA 26787 A _ TTA
TT AATG CAGAT CA TTTATTTCT
||||| || |||||||
TTAC GTCTA GT AAATAAAGA
C T CG_

GAM2402 PCDH11X 3' AGAAATAAAGCTGTATCTGCCA 26802 A _ TTA
TT AATG CAGAT CA TTTATTTCT
||||| || |||||||
TTAC GTCTA GT AAATAAAGA
C T CG_

GAM2402 PCDH11Y 3' AGAAATAAACTGTATCTGACA 26821 A _ TTA
TT AATG CAGAT CA TTTATTTCT
||||| || |||||||
TTAC GTCTA GT AAATAAAGA
A T CA_

GAM2402 SLC25A15 3' AGAAATTTTCAGTGGTCTATCAT 15525 C ATTT
T AATGA AGATCATT ATTTCT
||||| ||||||| |||||
TTACT TCTGGTGA TAAAGA
A CTT_

GAM2402 BIRC5 3' AGAAATAAAAAGCCTGTCATT 6835 ATCA A
AATGACAG TT TTTATTTCT
||||| || |||||||
TTACTGTC AA AAATAAAGA
CG_ _

GAM2402 CHSY1 3' AAGTGAAATGAATCTGTCATT 17170 _ AT
AATGACAGAT CATT TTATTT
||||||||| ||| |||||
TTACTGTCTA GTAA AGTGAA
A _

GAM2402 DKFZP434P0721 3' AGAAATATTCATTATCTGTCAT 31868 C TATT
T AATGACAGAT AT TATTTCT
||||||||| || |||||
TTACTGTCTA TA ATAAAGA
T CTT_

GAM2402 KIAA1336 3' AAGTTTAAATGATCTGCCAT 35800 A TTT
ATG CAGATCATT ATTT
||| ||||||| |||
TAC GTCTAGTAAT TGAA
C TT_

GAM2402 PER3 5' GAAACCGGTGTCTGTCA 18821 T ATTAA
TGACAGA CATT TTTC
||||| ||| |||

		ACTGTCT GTGG AAAG	
		— CC—	
GAM2402	SS-56	3' AGAAATAAACGCATTCTGTC 29987	TCATTA
		GACAGA TTTATTTCT	
		CTGTCT AAATAAAGA	
		TACGC—	
GAM2402	LOC148195	5' AGAAATAATCTTGCTCTGTCA 40871	T TTAT
		TGACAGA CA TTATTTCT	
		ACTGTCT GT AATAAAGA	
		C TCT—	
GAM2402	LOC152503	5' AGAAATAGACAACGATCTG 41515	A A
		CAGATC TT TTTATTTCT	
		GTCTAG AA AGATAAAGA	
		C C	
GAM2402	LOC51580	3' GAGTGAATGATTGTCATT 18015	GATC
		AATGACA ATTATTTATTT	
		TTACTGT TAGTAAGTGAG	
		—	
GAM2402	LOC90906	3' AAATAAATATGTTTGTGTCAT 32146	T T
		ATGACAGA CAT ATTTATTT	
		TACTGTTT GTA TAAATAAA	
		— —	
GAM2403	SLC6A8	5' ACACACATGAGATTCTTCA 12145	A ACGTA
		TGAAGGATCT GTGT TGT	
		ACTTCTTAGA TACA ACA	
		G C—	
GAM2403	FLJ20291	3' GCGTACACCAGACCCTTCA 19341	A A
		TGAAGG TCT GTGTACGT	
		ACTTCC AGA CACATGCG	
		C C	
GAM2404	DDX20	3' AACATTTAAAAAGATGACA 14066	T
		TGTTATCTTTTTTAAAT GTT	
		ACAGTAGAAAAATTTA CAA	
		—	
GAM2404	TACC1	3' GAAGAATCTAAAAGATAACA 12965	TAA G
		TGTTATCTTTT ATT TTC	
		ACAATAGAAAA TAA AAG	
		TC_ G	
GAM2404	DNAJA2	3' TGGGAACAATGGAAAAAATTAC 30068	TATC AA
	A	TGT TTTT ATTGTTCCCA	

			ACA AAAAA TAACAAGGGT		
			TTA_ GG		
GAM2404	FLJ12888	3'	GGAACAATTA AAAACAACA 24496	ATC	A
			TGTT TTTTAA TTGTTCC		
			ACAA AAAAAATT AACAAGG		
			C_ _		
GAM2404	KIAA0205	3'	GAACATGTTTTAAAAAGATACA 17007	T	T_
			TGT ATCTTTTAA TGTTC		
			ACA TAGAAAAATTT ACAAG		
			_ TGT		
GAM2404	KIAA0332	3'	AGCCATTTAAAAAGTAACA 31415	T	T
			TGTTA CTTTTAAAT GTT		
			ACAAT GAAAAATTTA CGA		
			_ C		
GAM2404	NUDT11	3'	GAACAATTTTAAGAAAATAACA 30142	C	_
			TGTTAT TTTTAA TTGTTCC		
			ACAATA AAGAATTT AACAAG		
			A T		
GAM2404	PI4KII	3'	TGGGAACAATGTTTCGAGAGAAC 20483	A	TTAA
	A		TGTT TCTT ATTGTTCCCA		
			ACAA AGAG TAACAAGGGT		
			G CTTG_		
GAM2404	LOC152316	3'	TGGAAACAGATGAGAGACAACA 41456	A	TAAA C
			TGTT TCTTTT TTGTT CCA		
			ACAA AGAGAG GACAA GGT		
			C TA_ A		
GAM2404	LOC153259	5'	GACATTTTAAAAAGAAAACA 41602	A	T
			TGTT TCTTTTAA TGT		
			ACAA AGAAAAATTT ACAG		
			A T		
GAM2404	LOC90488	3'	GAGAAGTTTAAAAAGATAA 31558		G
			TTATCTTTTAAATT TTC		
			AATAGAAAAATTTGA GAG		
			A		
GAM2404	LOC90750	3'	GGGGACTCTTAAAAAGA 31968	ATT	
			TCTTTTAA GTTCCC		
			AGAAAAATT CAGGGG		
			CT_		
GAM2405	CARKL	3'	TCTGTGGGTCATCCTTTCCC 14939	A	AT_
			GG AAAGGATGATT GA		

			CC TTTCCTACTGG CT		
			C GTGT		
GAM2405	CDC25B	3'	TCATCCCATCATTTTCCA 22414	G	ATT
			TGGAAAA GATG ATGA		
			ACCTTTT CTAC TACT		
			A CC_		
GAM2405	CDC25B	3'	TCATCCCATCATTTTCCA 22418	G	ATT
			TGGAAAA GATG ATGA		
			ACCTTTT CTAC TACT		
			A CC_		
GAM2405	CYP19	3'	TCATCCCCTTATCCTTCTCC 25272	A	TT__
			GGA AAGGATGA ATGA		
			CCT TTCCTATT TACT		
			C CCCC		
GAM2405	CYP19	3'	TCATCCCCTTATCCTTCTCC 5562	A	TT__
			GGA AAGGATGA ATGA		
			CCT TTCCTATT TACT		
			C CCCC		
GAM2405	GLO1	3'	TATTTAGCTGTTCTTTTC 13531		TGATTA
			GAAAAGGA TGAAATA		
			CTTTTCCT ACTTTAT		
			TGTCG_		
GAM2405	KIF3B	3'	TCATTTGTCACCATCTTTTCC 11218	A__	T_
			GGAAAAGG TGAT ATGA		
			CCTTTTCT ACTG TACT		
			ACC TT		
GAM2405	MS4A4A	3'	TATTTTCATCTTCTTCCTTTCCC 23449	A	T TT
			GG AAAGGA GA ATGAAATA		
			CC TTTCCT CT TACTTTAT		
			C T TC		
GAM2405	MYCBP	3'	TATTTTCATATATTCTCTCC 14726	AA	AT
			GGA AGGATG TATGAAATA		
			CCT TCTTAT ATACTTTAT		
			C_ _		
GAM2405	PAICS	3'	TTCTCAATCCACCCTTTTCCA 13167	AT_	AT
			TGGAAAAGG GATT GAA		
			ACCTTTTCC CTAA CTT		
			CAC CT		
GAM2405	PRV1	3'	CATGAATCATCTTCCCCA 36397	AAA	_
			TGG AGGATGAT TATG		

ACC TTCTACTA GTAC
 CC_ A
 GAM2405 VSNL1 3' ATTTCATAAAAATCCCTCTTCC 9415 AA_ GA
 GGAA GGAT TTATGAAAT
 ||| ||| |||||
 CCTT CCTA AATACTTTA
 CTC AA
 GAM2405 XK 3' CATAATACCCTTTTCCA 22055 ATG
 TGGAAAAGG ATTATG
 ||||| |||||
 ACCTTTTCC TAATAC
 CA_
 GAM2405 ZNF202 3' TCTTACCCATTCCCTTTTCCA 9511 _ AT T
 TGGAAAAGGA TG TA GA
 ||||| || |||
 ACCTTTTCCT AC AT CT
 T CC T
 GAM2405 C21orf42 3' TTATTTTCATCTTCCCTATTCCA 27751 A AT TT
 TGGAA AGG GA ATGAAATAA
 |||| ||| || |||||
 ACCTT TCC CT TACTTTATT
 A _ TC
 GAM2405 CNM4 3' CATTGATCATCCCTTCTCA 21423 GA A _
 TG AA GGATGATTA TG
 || || ||||| ||
 AC TT CCTACTAGT AC
 TC C T
 GAM2405 CPEB1 5' TTCAACATCGTCTTCCA 24960 AAA TA
 TGGA GGATGAT TGAA
 ||| ||||| |||
 ACCT TCTGCTA ACTT
 _ CA
 GAM2405 DKFZP434G1415 3' TTATAAATCATCCTTCACCA 25316 AA _
 TGG AAGGATGATT ATGA
 || ||||| |||
 ACC TTCCTACTAA TATT
 AC A
 GAM2405 DKFZP564D0462 3' CATCAATCATCCCTGTCCA 34896 AAA _
 TGGA GGATGATT ATG
 ||| ||||| |||
 ACCT CCTACTAA TAC
 GTC C
 GAM2405 DKFZp761F2014 3' TATTTCTGACCTTTTCCA 21461 ATGA T
 TGGAAAAGG TTA GAAATA
 ||||| || |||||
 ACCTTTTTC AGT CTTTAT
 C_ _
 GAM2405 FLJ10830 3' TCACCTCACCCTTTTCCA 20183 A TTA
 TGGAAAAGG TGA TGA
 ||||| ||| |||

ACCTTTTCC ACT ACT
 C CC_
 GAM2405 FLJ14753 3' TTCTGCTCATCCTCCTCC 26286 AA T T
 GGA AGGATGA TA GAA
 ||| ||||| || |||
 CCT TCCTACT GT CTT
 CC C _
 GAM2405 FLJ20195 3' TGTTTTTCTCCCTTTTCCA 19282 AT TTAT
 TGGAAAAGG GA GAAATA
 ||||| || |||||
 ACCTTTTCC CT TTTTGT
 CT ____
 GAM2405 GABBR1 3' TCACAATCATCTTCTCC 7207 AA A
 GGA AGGATGATT TGA
 ||| ||||| |||
 CCT TTCTACTAA ACT
 C_ C
 GAM2405 GABBR1 3' TCACAATCATCTTCTCC 22425 AA A
 GGA AGGATGATT TGA
 ||| ||||| |||
 CCT TTCTACTAA ACT
 C_ C
 GAM2405 KIAA1829 3' CATCACCATCCTTTTCA 31030 ATT
 TGGAAAAGGATG ATG
 ||||| |||
 ACTTTTTCCTAC TAC
 CAC
 GAM2405 SDC3 3' TTATTTTCAGGGCCCTTTTC 16092 ATGATTA
 GAAAAGG TGAAATAA
 ||||| |||||
 CTTTTC ACTTTATT
 CGGG____
 GAM2405 ZNF297B 3' CATGTCATCTTTTCCA 15219 G T
 TGGAAAAG ATGAT ATG
 ||||| ||||| |||
 ACCTTTTC TACTG TAC
 - -
 GAM2405 LOC133418 3' TCAGTCTCCTTTTCTA 37042 T TA
 TGGAAAAGGA GAT TGA
 ||||| ||| |||
 ATCTTTTCCT CTG ACT
 - -
 GAM2405 LOC143173 5' TTATTTTCAGAGCCCATCCCCCA 30274 AAAA ATTA_
 TGG GGATG TGAAATAA
 ||| ||||| |||||
 ACC CCTAC ACTTTATT
 C__ CCGAG
 GAM2405 LOC148811 3' TTATTTCACTGCTTCACCTTCC 38601 AA A TTA_
 A TGGG AGG TGA TGAAATAA
 ||||| ||| ||| |||||

ACCT TCC ACT ACTTTATT
 — _ TCGTC
 GAM2405 LOC152018 3' TATTTTCATACTCCCCGCTTCCA 41422 AA AT T
 TGGAA GG GA TATGAAATA
 |||| | | |||||
 ACCTT CC CT ATACTTTAT
 CG C_ C
 GAM2405 LOC253639 3' TTATCTCCCATGCATCCTTTCT 45855 GA ATTAT A
 CA TG AAAGGATG GA ATAA
 || ||||| | ||||
 AC TTTCCTAC CT TATT
 TC GTACC C
 GAM2405 LOC91689 3' TTCAATCATCCCTATCCA 27158 AAA TA
 TGGA GGATGAT TGAA
 ||| ||||| |||
 ACCT CCTACTA ACTT
 ATC _
 GAM2406 DAAM2 3' TATTAAATTCATACCATCCCTA 44333 AAATAT
 TAGG TATGAATTTAATA
 ||| |||||
 ATCC ATACTTAAATTAT
 CTACC_
 GAM2406 LOC153711 3' ATTAAACTCATTATTTCTTAA 41667 TT A
 TTAGGAAATA ATGA TTTAAT
 ||||| ||| |||||
 AATTCTTTAT TACT AAATTA
 _ C
 GAM2406 LOC154442 3' ATTAAATTCACCTGTGGTTCC 41704 A TA
 GGAA TAT TGAATTTAAT
 ||| ||| |||||
 CCTT GTG ACTTAAATTA
 G TC
 GAM2407 DDX11 3' GAAGAAGATATTCCAGGAACCT 24985 A ATCT_
 AA TTAG TTC ATATCTTCTTC
 ||| ||| |||||
 AATC AAG TATAGAAGAAG
 C GACCT
 GAM2407 KIAA0836 3' AAGAAGATACAGATCTG 32243 TTCA A
 TAGA TCT TATCTTCTT
 ||| ||| |||||
 GTCT AGA ATAGAAGAA
 _ C
 GAM2407 MGC2574 3' GAAGCCCCAGAGAATCTAA 23537 A ATAT
 TTAGATTC TCT CTTC
 ||||| ||| |||
 AATCTAAG AGA GAAG
 _ CCCC
 GAM2407 LOC133362 5' GAAGAAACCTGGATGAACCTAA 37379 A TA_
 TTAG TTCATCTA TCTTC
 ||| ||||| |||

		AATC AAGTAGGT AGAAG	
		C CCAA	
GAM2407	LOC145078 5'	AAGAAGATACAGAAGAATATAA 30247	G A A
	T	ATTA ATTC TCT TATCTTCTT	
		TAAT TAAG AGA ATAGAAGAA	
		A A C	
GAM2407	LOC145676 5'	GAAGAAAGATGAATCTA 37920	ATA
		TAGATTCATCT TCTTC	
		ATCTAAGTAGA AGAAG	
		A _	
GAM2407	LOC90459 3'	GAAGAGGTAGCAGATGAATCT 31490	A_ T
		AGATTCATCT TATCT CTTC	
		TCTAAGTAGA ATGGA GAAG	
		CG _	
GAM2408	MYEOV 5'	ACGCTTAACACCTCTAACAA 28998	T AC
		TTGTTGG GGT GTTAAGCGT	
		AACAATC CCA CAATTCGCA	
		T _	
GAM2408	JDD1 3'	ACACTTAAAACCAACCA 31667	ACG C
		TTGGTGGT TTAAG GT	
		AACCACCA AATTC CA	
		A_ A	
GAM2409	TP53INP1 3'	CAAAACATTTTATAATATATAT 27105	A G
	C	GATATA AT ATAAAATGTTTTG	
		CTATAT TA TATTTTACAAAAC	
		A A	
GAM2409	TP53INP1 3'	CAAAACATTTTATAATATATAT 36116	A G
	C	GATATA AT ATAAAATGTTTTG	
		CTATAT TA TATTTTACAAAAC	
		A A	
GAM2409	LOC254251 3'	CAAAACATTTTCAGTTTATCA 45896	TAAA TA
		TGATA TGA AAATGTTTTG	
		ACTAT ACT TTTACAAAAC	
		TTG_ _	
GAM2410	SPF30 3'	CCTGCTAAAAGAGATCTT 12490	C _ T
		AAGATCTCT TT GT GG	
		TTCTAGAGA AA CG CC	
		A T T	
GAM2410	LOC153339 3'	TAATCTCCAAAATCTGAAATGC 41614	_ C TCTTG
	T	AG AT TC TTGGAGATTA	

TC TA AG AACCTCTAAT
 G A TCTAA
 GAM2410 LOC154739 5' AATCTGGGCAAGAGGA 41711 T GG
 TC CTCTTGTT AGATT
 || ||||| ||||
 AG GAGAACGG TCTAA
 _ G_
 GAM2410 LOC92573 5' CTCCAAAGGGAAATCTT 34596 C GT
 AAGAT TCTCTT TGGAG
 ||||| ||||| |||||
 TTCTA AGGGAA ACCTC
 A _
 GAM2411 RDX 3' AACTGTGGGATTCTGATTTGTA 8806 A ATG_
 TTA TAGTACAAATCA AAT T T GTT
 ||||| ||||| ||||| |||||
 ATTATGTTTAGT TTA G G CAA
 C G GT T
 GAM2411 XT3 3' ACTCCATTTTGATCTGTACTA 21440 A ATT
 TAGTACA ATCAAAAT GT
 ||||| ||||| ||
 ATCATGT TAGTTTCA CA
 C CCT
 GAM2411 FLJ10607 3' AACACAATACTTAATGTATTGT 37832 AT _ A
 ACTA TAGTACAA CA AA TATTGTGTT
 ||||| || ||||| |||||
 ATCATGTT GT TT ATAACACAA
 AT AA C
 GAM2411 KIAA1622 3' ACAGCATTATTTGTACTA 27762 CA A
 TAGTACAAAT AAAT TTGT
 ||||| ||||| |||||
 ATCATGTTTA TTTA GACA
 _ C
 GAM2411 LOC196812 3' AATATTTTGATTAATACTA 43131 CA
 TAGTA AATCAAAATATT
 ||||| ||||| |||||
 ATCAT TTAGTTTTATAA
 AA
 GAM2412 ATP11B 3' CAAAATCTTTGTAGTA 39145 TGGT
 TACTG TAAAGATTTTG
 ||||| ||||| |||||
 ATGAT GTTCTAAAAC
 _
 GAM2412 MAOB 3' TCAAAATCTTTAGAATAGTTA 30148 T GG
 A ACTGT TTAAAGATTTTGA
 | ||||| ||||| |||||
 A TGATA GATTTCTAAAAC
 T A_
 GAM2412 USH2A 3' TCAAAATCATTGCAGAGTATTA 13981 G GT A
 TAATACT TG TAA GATTTTGA
 ||||| || ||||| |||||

			ATTATGA AC GTT CTAAAACT	
			G _ A	
GAM2412	C3orf4	3'	AGTCAACCAGCAGTATTA 21280	_ AAA
			TAATACTG TGGTT GATT	
			ATTATGAC ACCAA CTGA	
			G _ _	
GAM2412	GMFB	3'	CTGGTAATCACAGTATTA 10328	A_
			TAATACTGTGGTTA AG	
			ATTATGACACTAAT TC	
			GG	
GAM2412	KIAA0410	3'	CAAAATCTTTAAAGTAACA 16616	GG_
			TGT TTAAAGATTTTG	
			ACA AATTTCTAAAAC	
			ATGA	
GAM2412	KIAA1493	3'	TCAAAATCTTCACCTTGAGTA 32093	GT_ TA
			TACT GGT AAGATTTTGA	
			ATGA CCA TTCTAAAACT	
			GTT C_	
GAM2412	NFX1	3'	TCAAAATCTTTAGGAGCA 8327	GG
			TGT TTAAAGATTTTGA	
			ACG GATTTCTAAAACT	
			AG	
GAM2412	LOC143425	3'	TCAGCTGTAACCACAG 42356	A ATT
			CTGTGGTTA AG TTGA	
			GACACCAAT TC GACT	
			G _ _	
GAM2412	LOC221540	3'	TCAAAATCTCCACAGTA 45046	TTAA
			TACTGTGG AGATTTTGA	
			ATGACACC TCTAAAACT	

GAM2412	LOC257545	3'	TCAAAATCTCCACAGTA 46694	TTAA
			TACTGTGG AGATTTTGA	
			ATGACACC TCTAAAACT	

GAM2412	LOC257598	3'	TCAAAATCTCCACAGTA 46751	TTAA
			TACTGTGG AGATTTTGA	
			ATGACACC TCTAAAACT	

GAM2413	KIAA1155	3'	TACTTTGTTTAAACTTTTTTAA 31197	T TT
	A		TTTAAAAAGTTTA ATA AGTA	

			AAATTTTTTCAAAT TGT TCAT		
			T T_		
GAM2414	MAN2C1	5'	GTGTACTGGTCCACTTCC 36101	A A T	
			GGAA TG ACC AGTACAT		
			CCTT AC TGG TCATGTG		
			C C _		
GAM2414	PCSK2	3'	CAGAGCACTAGGTTCAATTCC 8455	A	ACA
			GGAA TGAACCTAGT TTTG		
			CCTT ACTTGGATCA AGAC		
			A CG_		
GAM2414	PHKA2	3'	ATCATTTTCTAGGTTCAATTCT 5835		TACATT
			GGAAATGAACCTAG TGAT		
			TCTTTACTTGGATC ACTA		
			TTTT_		
GAM2414	KIAA1458	3'	TGAACATAAGTTCATTTCC 34208	C _ A	
			GGAAATGAAC TA GT CA		
			CCTTTACTTG AT CA GT		
			A A A		
GAM2414	Rabip4R	3'	ATCAAATGTATTTGCCTTACTT 19715	A	ACCT
	CC		GGAA TGA AGTACATTTGAT		
			CCTT ATT TTATGTAAACTA		
			C CCGT		
GAM2414	SULT4A1	3'	CAAATAAAAGTTCATTTCC 33974		CTAGTAC
			GGAAATGAAC ATTTG		
			CCTTTACTTG TAAAC		
			AAAA_		
GAM2414	LOC146958	5'	GTGACTAGACTCATTTCC 40773	AC	A
			GGAAATGA CTAGT CAT		
			CCTTTACT GATCA GTG		
			CA _		
GAM2414	LOC257443	3'	TGAACATAAGTTCATTTCC 45876	C _ A	
			GGAAATGAAC TA GT CA		
			CCTTTACTTG AT CA GT		
			A A A		
GAM2414	LOC90643	3'	TCAAAGCAGGTTATTTCC 31854	A A	ACA
			GGAAATGA CCT GT TTTGA		
			CCTTTATT GGA CG AAAC		
			_ _ A_		
GAM2415	LANCL2	3'	TATTAGTCTTTCTAAC 20779	A T	
			GTTAGAAA G ACTGATA		

CAATCTTT C TGATTAT

GAM2415 MKRN1 3' GTCATACTTTTCCACCGAA 15114 TTA C
TTCG GAAAAGTA TGAT
|||| ||||||| |||
AAGC CTTTTCAT ACTG
CAC _

GAM2415 RTP801 3' TATTTTTTACTTTTCTAAT 21140 CT_
GTTAGAAAAGTA GATA
||||||||| |||
TAATCTTTTCAT TTAT
TTT

GAM2415 LOC158450 5' TATTATTGGCACTCTCTAACTG 39843 _ AA A TG
AA TTC GTTAGA AGT C ATAATA
||| ||||| ||| | |||||
AAG CAATCT TCA G TATTAT
T C_ C GT

GAM2415 LOC158504 5' TATTATTGGCACTCTCTAACTG 39854 _ AA A TG
AA TTC GTTAGA AGT C ATAATA
||| ||||| ||| | |||||
AAG CAATCT TCA G TATTAT
T C_ C GT

GAM2415 LOC253613 3' ATGTCTTAATTCCCTAACGAA 46011 AA GTACT
TTCGTTAG AA GATAAT
||||||| || |||||
AAGCAATC TT CTGTTA
CC AATT_

GAM2416 CBFB 3' TTTGAAAAATGTATTTTATCAT 7509 _
TA TGATGATAAAATATATT TCAAA
||||||||||||| |||||
ATTACTATTTTATGTAA AGTTT
AA

GAM2416 CBFB 3' TTTGAAAAATGTATTTTATCAT 23150 _
TA TGATGATAAAATATATT TCAAA
||||||||||||| |||||
ATTACTATTTTATGTAA AGTTT
AA

GAM2416 IL18R1 3' TTGAAATATATTTTGCATTA 9953 A
TGATG TAAAATATATTTCAA
||||| |||||||||||
ATTAC GTTTTATATAAAGTT

GAM2416 SFRP1 3' AAATCTGTTTTTCTCATCAGA 8925 T_ T
TCTGATGA AAAATA ATTT
||||||| ||||| |||
AGACTACT TTTTGT TAAA
CT C

GAM2416 SYT4 3' TTTGATGCAATTTTATCATAAG 31294 G ATATT
A TCT ATGATAAAAT TCAAA
||| ||||||||| |||||

			AGA TACTATTTTA AGTTT	
			A ACGT_	
GAM2416 TRPC5	3'	TTGAAATATTTTATCAGA 14852	TAAAAT	
		TCTGATGA ATATTTCAA		
		AGACTATT TATAAAGTT		
		TT____		
GAM2416 MIG2	3'	TTGAAATTTATCATTATCAT 35864	AT____	
		ATGATAAAAT ATTTCAA		
		TACTATTTTA TAAAGTT		
		CTATT		
GAM2416 NUDT4	3'	TGTGGTTTATTTTGTGCATCAGA 21170	T TT	
		TCTGATGATAAAATA AT CA		
		AGACTACTGTTTTAT TG GT		
		T GT		
GAM2416 PRO2012	5'	TTGAAATATTTTATCATT 20682	AT	
		TGATGATAAAATAT TTCAA		
		ATTACTATTTTATA AAGTT		
		—		
GAM2416 SS18L1	3'	TTTGGGGGTTCATTTTGTGCATCA 32566	ATA TT	
GA		TCTGATGATAAAAT T CAAA		
		AGACTACTGTTTTA G GTTT		
		CTG GG		
GAM2416 STAM2	3'	TTTGAAGTCAATCTTTTCATCA 12461	TAAAATAT	
GA		TCTGATGA ATTTCAA		
		AGACTACT TGAAGTTT		
		TTTCTAAC		
GAM2416 LOC139221	3'	TTGAAATATATTTTGTGAGA 37334	G TG TA	
		TCT A A AAATATATTCAA		
		AGA T T TTTATATAAAGTT		
		G GT _		
GAM2416 LOC161734	3'	TTGGAACAGATTTTATCATCA 42111	ATA	
		TGATGATAAAAT TTTCAA		
		ACTACTATTTTA AAGTT		
		GAC		
GAM2417 CCND1	3'	GTAACCGGCATGTTTCCA 27601	AC T A	
		TG AAC AT CCGTTAC		
		AC TTG TA GGCCAATG		
		CT _ C		
GAM2417 CD164	3'	ACTGATGTAATTGTCATT 12629	C C	
		AATGACAA TATA CGGT		

		TTACTGTT ATGT GTCA	
		A A	
GAM2417 CRYZ	3'	TAACATGTTAGTTGTCATT 7618	TACCG
		AATGACAATA GTTA	
		TTACTGTTGAT CAAT	
		TGTA_	
GAM2417 FLJ12960	3'	TAGCCCTAGTTGTCAT 23919	TACC
		ATGACAATA GGTTA	
		TACTGTTGAT CCGAT	
		C__	
GAM2417 KIAA0478	3'	TAACCCCTTGTCAAGTTGTCA 16984	_ CC_
		TGACAATA ATA GGTTA	
		ACTGTTGA TGT CCAAT	
		C TCC	
GAM2417 KIAA1116	3'	ACCTTTTGTAAAGTTGTCAT 17040	A C__
		ATGACAATA TAC GGT	
		TACTGTTGA ATG CCA	
		A TTTT	
GAM2417 KIAA1559	3'	GTAATTGTTATTATTGTCATT 36165	CT C
		AATGACAA ATA CGGTAC	
		TTACTGTT TAT GTTAATG	
		AT T	
GAM2417 PB1	3'	GTAAGTGGGTGATTGCCATT 19981	A C A
		AATG CAA TAT CCGGTAC	
		TTAC GTT GTG GGTCAATG	
		C A _	
GAM2417 PRO0641	5'	GTGACAGTAGTTGTCA 15402	ACCG
		TGACAATA TAT GTTAC	
		ACTGTTGATG CAGTG	
		A__	
GAM2417 SH3BGRL2	3'	ACTGGTTAGTTGTCATT 25523	T
		AATGACAATA ACCGGT	
		TTACTGTTGAT TGGTCA	
		-	
GAM2417 SSR3	3'	GTGATAGCAGTTGTCATT 13972	ATACCG
		AATGACAATA GTTAC	
		TTACTGTTGA TAGTG	
		CGA__	
GAM2417 LOC144871	3'	GTAACCGGTTTTGTTGCA 40471	A TAT
		TG CAAC ACCGGTTAC	

		AC GTTG TGGCCAATG		
		— TTT		
GAM2417	LOC151473 3'	GTAAC TGGCACTGTCATT	39121	ACTATA
		AATGACA CCGGTTAC		
		TTACTGT GGTCAATG		
		CAC__		
GAM2417	LOC158428 5'	GTAACCGGAAGTGCTGTC	34922	__ ATA
		GACA ACT CCGGTTAC		
		CTGT TGA GGCCAATG		
		CG A__		
GAM2417	LOC197287 3'	GTATCCATAGTTGTCAT	30523	ACC T
		ATGACAACTAT GG TAC		
		TACTGTTGATA CC ATG		
		__ T		
GAM2417	LOC255265 5'	GGCCTACAGTTGTCGTT	45658	A CC
		AATGACAACT TA GGTT		
		TTGCTGTTGA AT CCGG		
		C __		
GAM2418	NTN4 3'	AGAATTTGTTATATTTTGT	31508	T C
		CAGAG TATAACAAAT CT		
		GTTTT ATATTGTTTA GA		
		T A		
GAM2419	CALB1 3'	ATTAAATTTAATATACTGCA	11369	GG C
		TGCAGTATAT TAA TTTAAT		
		ACGTCATATA ATT AAATTA		
		__ T		
GAM2419	FBXL2 3'	AAAGTGACTGTACTGCA	14453	AT A
		TGCAGTAT GGT ACTTT		
		ACGTCATG TCA TGAAA		
		__ G		
GAM2419	SMT3H1 3'	ATTAAAATGCTAAATATTGCA	30123	A AC
		TGCAGTAT TGGTA TTTAAT		
		ACGTTATA ATCGT AAATTA		
		A A_		
GAM2419	DKFZP434P0721 3'	TTAAAGTCACCTCTACTG	31873	TAT A
		CAGTA GGT ACTTTAA		
		GTCAT CCA TGAAATT		
		CT_ C		
GAM2419	KIAA1084 3'	ATTAAAGTTAGAAACGACTACA	17134	C ATATGG
	GA	TCTG AGT TAACTTTAAT		

		AGAC TCA ATTGAAATTA	
		A GCAAAG	
GAM2419	MGC10911	5' TTAAAGCTGCCACTGCAGA 26084	ATAT A
		TCTGCAGT GGTA CTTTAA	
		AGACGTCA CCGT GAAATT	
		_____ C	
GAM2419	SLC38A4	3' ATTAAAATTCATATATACTGCA 19758	GTAAC
	GG	TCTGCAGTATATG TTTAAT	
		GGACGTCATATAT AAATTA	
		ACTTA	
GAM2420	ANK2	3' AATCCATTGATCAGAAGAA 6819	A TTTGG
		TTCTTC TG TAATGGATT	
		AAGAAG AC GTTACCTAA	
		_ TA_	
GAM2420	ANK2	3' AATCCATTGATCAGAAGAA 21963	A TTTGG
		TTCTTC TG TAATGGATT	
		AAGAAG AC GTTACCTAA	
		_ TA_	
GAM2420	EIF1A	3' AAATACCCCAAACATGAA 42716	TAAT _
		TTCATGTTTGG GG ATTT	
		AAGTACAAACC CC TAAA	
		_____ A	
GAM2420	TEM8	3' AAATCCATTAAAGAACAGGAA 25915	A GG
		TTC TGTTT TAATGGATTT	
		AAG ACAAG ATTACCTAAA	
		G AA	
GAM2420	ZNF138	3' CCACAAATATGAAGAA 39507	GTAA
		TTCTTCATGTTTG TGG	
		AAGAAGTATAAAC ACC	

GAM2420	PB1	3' CCTTAGCCAAACAGGAAGAA 20306	A AAT
		TTCTTC TGTTTGGT GG	
		AAGAAG ACAAACCG CC	
		G ATT	
GAM2420	PRO2086	5' AAATCCATATACACCGTAGAA 15343	TC T GTA
		TTCT ATGT TG ATGGATTT	
		AAGA TGCA AC TACCTAAA	
		_ C ATA	
GAM2420	LOC154930	3' CCACAAATATGAAGAA 39504	GTAA
		TTCTTCATGTTTG TGG	

AAGAAGTATAAAC ACC

GAM2420 LOC199775 5' CCTACAAACGTGAAGAA 42614 GTAAT
TTCTTCATGTTTG GG
||||| ||
AAGAAGTGCAAAC CC

AT__

GAM2420 LOC51246 3' AAATCTCAAGCCAAACTCAAAG 18577 CAT AAT
AA TTCTT GTTTGGT GGATTT
|||| ||||| |||||
AAGAA CAAACCG TCTAAA
ACT AAC

GAM2420 LOC51652 3' AAATCCATCTGCTCATGAAG 18150 TTT _
CTTCATG GGTA ATGGATTT
||||| ||| |||||
GAAGTAC TCGT TACCTAAA
_ C

GAM2421 PIGH 3' ATGTTAACAAAGAATAAATAA 10911 C CC
TTATTTGTTCTT GT GACAT
||||| || |||||
AATAAATAAGAA CA TTGTA
A A_

GAM2421 DCTD 3' TGTGCTGGAAGGACAAATAA 7636 TCG A
TTATTTGTTCT TCCG CATA
||||| ||| |||||
AATAAACAGGA AGGT GTGT
_ C

GAM2421 FLJ14906 3' TTATGCCGGTATTTAGAAAAAA 26664 G TC _ A
TAA TTATTT TTCT GT CCG CATAA
||||| ||| || ||| |||||
AATAAA AAGA TA GGC GTATT
A TT T C

GAM2421 LOC138389 5' ATGTGGATGAAAAACAGA 37503 C G
TTTGTT TTCGTCC ACAT
||||| ||||| |||||
AGACAA AAGTAGG TGTA
A _

GAM2421 LOC145622 3' TTATGTCACAGAAGAAAAAACA 37916 ____ GTCC
AATAA TATTTGT TCTTC GACATAA
||||| ||||| |||||
ATAAACA AGAAG CTGTATT
AAAA ACA_

GAM2421 LOC54499 3' TTATGTAATGAAAAACAAATAG 34968 C CCG
TTATTTGTT TTCGT ACATAA
||||| ||||| |||||
GATAAACAA AAGTA TGTATT
A A_

GAM2422 NAPB 3' AAATGTGTTGCCAGACTTAA 34765 A _
TTAA TCTGGCAA ATGTTT
||| ||||| |||||

			AATT AGACCGTT TGTA	
			C G	
GAM2422	NCKAP1	3'	AAACATTTGCCAACTAAAT 15094	AATC
			GTTTA TGGCAAATGTTT	
			TAAAT ACCGTTTACAAA	
			CAA_	
GAM2422	ATP10D	3'	AAACATTTGCCAAATCCAACT 36199	TAA C
			AGTT AT TGGCAAATGTTT	
			TCAA TA ACCGTTTACAAA	
			CC_ A	
GAM2422	FLJ12085	3'	AAACATTCACCTTTGTTTAAGCT 23031	CT CA
			TA TAAGTTTAAAT GG AATGTTT	
			ATTCGAATTTG TC TTACAAA	
			TT AC	
GAM2422	SCLY	3'	AAACACTTGCCAGAACTAAAT 18587	AA_ A
			T AGTTTA TCTGGCAA TGTTT	
			TTAAAT AGACCGTT ACAA	
			CAA C	
GAM2422	LOC143879	3'	AAACATTTCAGGATTTAAATT 37657	GGC
			AGTTTAAATCT AAATGTTT	
			TTAAATTTAGG TTTACAAA	
			AC_	
GAM2423	IL17	3'	TAAACCCTTATAATAAAATCCT 7947	TA_
			TCT AGAAGGATTTTGTTAT GGTTTA	
			TCTTCCTAAAATAATA CCAAAT	
			TTC	
GAM2423	FKBP5	3'	TGATAACTAAAATCCCTCT 10326	A _
			AGA GGATTTT GTTATTA	
			TCT CCTAAAA CAATAGT	
			C T	
GAM2423	KIAA1383	3'	TAAACCTGCAGAAAATCCTT 34584	GTTAT
			AAGGATTTT TAGGTTTA	
			TTCTAAAA GTCCAAAT	
			GAC_	
GAM2423	PLA2G3	3'	TAAACCTAAATTCAAATCTCCT 17929	T_ TTA
			AGGA TTTG TTAGGTTTA	
			TCCT AAAC AATCCAAAT	
			CT TTA	
GAM2423	LOC120103	3'	TAAACCTATGAAAAATCCTTGC 36618	_ GTTAT
			T AG AAGGATTTT TAGGTTTA	

		TC TTCCTAAAA ATCCAAAT	
		G AGT__	
GAM2424	EXT2	3' TTGGTGGGATTTGATAAA 5977	AT
		TTTATCAAATTC CCAA	
		AAATAGTTTAGG GGTT	
		GT	
GAM2424	FLJ23047	3' GGAATGAAATTTGATAAA 23761	- -
		TTTATCAAATT CAT CC	
		AAATAGTTTAA GTA GG	
		A A	
GAM2424	HERC3	3' AAGTATTTATGAACTGTGATAA 15970	AA_ CC
	A	TTTATCA TTCAT AAATACTT	
		AAATAGT AAGTA TTTATGAA	
		GTC _	
GAM2424	LOC200933	3' AAGTATTTATTGTGATTTTGAT 43361	T CC_
	A	TATCAAAT CAT AAATACTT	
		ATAGTTTA GTG TTTATGAA	
		T TTA	
GAM2425	CA3	3' TCATTTTCCCACTGAGCAA 11679	C AAAATTT
		TTGCTCAG TGT AGTGA	
		AACGAGTC ACA TTACT	
		_ CCTT_	
GAM2425	FADD	3' CACTATGACACTGAGCAA 9917	C AAAATT
		TTGCTCAG TGT TAGTG	
		AACGAGTC ACA ATCAC	
		_ GT_	
GAM2425	DKFZP547E2110	3' TCATTATTCTTGCAGCTAAGCA 43732	C AATT
	A	TTGCT AGCTGTAA TAGTGA	
		AACGA TCGACGTT ATTACT	
		A CTT_	
GAM2425	KIAA0767	3' CTATTTTACAGCGAGCAA 30409	A TT
		TTGCTC GCTGTAAAA TAG	
		AACGAG CGACATTTT ATC	
		_ TT	
GAM2425	KIAA1464	3' TCACTGGGCCCCACAGCTGGGCA 33886	AAAA
	A	TTGCTCAGCTGT TTAGTGA	
		AACGGGTCGACA GGGTCACT	
		CCC_	
GAM2425	LOC122830	3' TCACTTGGCTACAAGTGAAGCA 36709	C AAATTT
		TTGCTCAG TGTA AGTGA	

		AACGAGTC ACAT	TCACT	
		A CGGT__		
GAM2425	LOC144481	3' CACTGTACCACAGCCTGAGCAA	40419	_ AAAATT
		TTGCTCAG CTGT	TAGTG	
		AACGAGTC GACA	GTCAC	
		C CCAT__		
GAM2425	LOC144501	3' ACCAGAAGCTGAGCAA	40421	GTAAAA A
		TTGCTCAGCT	TTT GT	
		AACGAGTCGA	AGA CA	
		_____ C		
GAM2425	LOC168667	3' CACAGGCTACAGCTGAGCAA	44564	AAA A
		TTGCTCAGCTGTA	TTT GTG	
		AACGAGTCGACAT	GGA CAC	
		C__ _		
GAM2425	LOC254045	3' CACTGTACCACAGCCTGAGCAA	46161	_ AAAATT
		TTGCTCAG CTGT	TAGTG	
		AACGAGTC GACA	GTCAC	
		C CCAT__		
GAM2425	LOC51068	3' CACTAAATAAAGAGATTGAGCA	18058	_ GTAAA
	A	TTGCTCAG CT	ATTTAGTG	
		AACGAGTT GA	TAAATCAC	
		A GAAA_		
GAM2426	ARCNI	3' ATCTGTTTACAGGCATTA	7366	ATAC T
		TAATGCCT	GAAC GAT	
		ATTACGGA	TTTG CTA	
		CA__ T		
GAM2426	RB1	3' ATGGGTTAGGCATTAA	43704	TACGA G
		TTAATGCCTA	ACT AT	
		AATTACGGAT	TGG TA	
		_____ G		
GAM2426	MCJ	5' ATCAGTTCGCAGGGCTTAA	14898	T ATA
		TTAA GCCT	CGAACTGAT	
		AATT CGGG	GCTTGACTA	
		_ AC_		
GAM2426	PLU-1	3' CAATTTGGAAGGCATTGA	42251	ATA C
		TTAATGCCT	CGAA TG	
		AGTTACGGA	GTTT AC	
		AG_ A		
GAM2426	PLU-1	3' CAATTTGGAAGGCATTGA	13402	ATA C
		TTAATGCCT	CGAA TG	

AGTTACGGA GTTT AC
 AG_ A
 GAM2426 TRIM4 3' ATCCCGCAGTATAGGCTTAA 26901 T GAACT
 TTAA GCCTATAC GAT
 ||| ||||| ||
 AATT CGGATATG CTA
 _ ACGCC
 GAM2427 ABCD2 3' CTATTTTTCCTACTTTGCTTTT 11658 A ____
 GA TCAAGA GCAAA AAAAATAG
 ||||| ||||| |||||
 AGTTTT CGTTT TTTTATC
 _ CATCC
 GAM2427 NQO1 3' CTGGTGGTTTTTGCTCTCGACA 6606 A A AAA_
 TGTC AGA GCAAAAA TAG
 ||| ||| ||||| |||
 ACAG TCT CGTTTTT GTC
 C _ GGTG
 GAM2427 RAB18 3' TGCTATTCTTTTTGCTTAAATA 22224 CAAG A
 C GT AAGCAAAAA AATAGCA
 || ||||| |||||
 CA TTCGTTTTT TTATCGT
 TAAA C
 GAM2427 RAD23B 3' TGCTATTTTAAATTTCTTGAT 8785 CAAAA
 GTCAAGAAG AAAATAGCA
 ||||| |||||
 TAGTTCTTT TTTTATCGT
 AAAA_
 GAM2427 REV3L 3' TGCTATTTTTTTTCAGTGCTT 8816 ____
 AAGCA AAAAAAATAGCA
 |||| |||||
 TTCGT TTTTTTTATCGT
 GAC
 GAM2427 TNFRSF9 3' TTTTTTTTTTTTTTGACA 7291 C
 TGTCAAGAAG AAAAAAAA
 ||||| |||||
 ACAGTTTTTT TTTTTTT
 T
 GAM2427 ACVR2 3' TGCTATTTTTTTTAAATC 7322 AGC
 GA AAAAAAATAGCA
 || |||||
 CT TTTTTTTATCGT
 AAA
 GAM2427 C9orf14 5' TGCCATTCTCTGTGCCCTTTT 41913 A_ AAAA_ A
 GACA TGTCAAGA GCA AAAT GCA
 ||||| ||| ||| |||
 ACAGTTTT CGT TTTA CGT
 CC GTCTC C
 GAM2427 DKFZP586M0622 5' TGTTTTCTTTGCTTCTCAACA 17850 CA A
 TGT AGAAGCAAA AAAATA
 ||| ||||| |||||

		ACA TCTTCGTTT TTTTGT		
		AC C		
GAM2427	FLJ10697	3' TATTTCTCTGGCTCTTGACA 20017	A	AAAAA
		TGTCAAGA GC AAATA		
		ACAGTTCT CG TTTAT		
		_ GTCTC		
GAM2427	FLJ13057	3' TGCTATTTTTTTTAATTTGAC 45778	AAGC	
		GTCAAG AAAAAAATAGCA		
		CAGTTT TTTTTTTTATCGT		
		AA__		
GAM2427	KIAA0121	3' TGCTTTTTCCTTTGCTTCTTGA 35973	AA	T
		TCAAGAAGCAAA AAA AGCA		
		AGTTCTTCGTTT TTT TCGT		
		CC T		
GAM2427	KIAA0265	3' ATTTCTTTGGCTCTTGACA 34622	A A A	
		TGTCAAGA GC AAA AAAT		
		ACAGTTCT CG TTT TTTA		
		_ G C		
GAM2427	KIAA1948	3' TGCTGAACCCTGTCTTCTTGAC 40084	_	AAAAAAA
A		TGTCAAGAAG CA TAGCA		
		ACAGTTCTTC GT GTCGT		
		T CCCAA__		
GAM2427	KIAA1950	3' TGCCGGAATTTTGCTTCCTGCA 44491	T A	AAAATA
		TG CA GAAGCAAAA GCA		
		AC GT CTTCTGTTTT CGT		
		_ C AGGC__		
GAM2427	KIAA1979	3' TGCTTGACTCTGCTTCTTGCCA 42592	T	AAAAAAAT
		TG CAAGAAGCA AGCA		
		AC GTTCTTCGT TCGT		
		C CTCAGT__		
GAM2427	NYD-SP15	3' TGCCATTTTTTTTCTTCTGTAC 25178	CA C A	
A		TGT AGAAG AAAAAAAT GCA		
		ACA TCTTC TTTTTTTTA CGT		
		TG _ C		
GAM2427	PTPNS1	3' TGCTGAGGGCTGCCTCTTGACA 28059	A	AAAAAAA
		TGTCAAGA GCA TAGCA		
		ACAGTTCT CGT GTCGT		
		C CGGGA__		
GAM2427	SMAP-5	3' TGCTATTTCTTTCTGGTTCCTG 25100	T A G _ A	
CA		TG CA GAA CA AAA AAATAGCA		

			AC GT CTT GT TTT TTTATCGT		
			_ C G C C		
GAM2427	LOC112609	3'	TGCTATTTTTTTTAAAGCTC 36059	A	___
			GA GC AAAAAAATAGCA		
			CT CG TTTTTTTTATCGT		
			_ AAA		
GAM2427	LOC219540	5'	TTTTCCTGCCTCTTGATA 44960	A	AA
			TGTCAAGA GCA AAAA		
			ATAGTTCT CGT TTTT		
			C CC		
GAM2427	LOC254485	5'	ATGCTATTTCTTTTTTTTTTCT 45550	A C	_____
			CTTGAC GA G AAAAAA ATAGCA T		
			CT C TTTTTT TATCGT A		
			_ T TTCTT		
GAM2427	LOC256940	3'	TATTTTTTTACTTCTTGCA 46156	T	CA
			TG CAAGAAG AAAAAAATA		
			AC GTTCTTC TTTTTTAT		
			_ A_		
GAM2428	ADAR	3'	GCCAGCTGCCTCTTCTTTA 6774	A	ATGA
			TAAAGAAGAG CG CTGGC		
			ATTTCTTCTC GT GACCG		
			C C___		
GAM2428	ADAR	3'	GCCAGCTGCCTCTTCTTTA 17967	A	ATGA
			TAAAGAAGAG CG CTGGC		
			ATTTCTTCTC GT GACCG		
			C C___		
GAM2428	ADAR	3'	GCCAGCTGCCTCTTCTTTA 17960	A	ATGA
			TAAAGAAGAG CG CTGGC		
			ATTTCTTCTC GT GACCG		
			C C___		
GAM2428	CLASP2	3'	CCAGCACCTTTTCTTTA 32268	ACGA	A
			TAAAGAAGAG TG CTGG		
			ATTTCTTTTC AC GACC		
			C___ _		
GAM2428	MMP19	3'	GTCATCTCTTCTCTGGA 23082	A	CGA
			TCTA AGAAGAGA TGAC		
			AGGT TCTTCTCT ACTG		
			C ___		
GAM2428	MMP19	3'	GTCATCTCTTCTCTGGA 23077	A	CGA
			TCTA AGAAGAGA TGAC		

			AGGT TCTTCTCT ACTG			
			C _			
GAM2428	MMP19	3'	GTCATCTCTTCTCTGGA	23079	A	CGA
			TCTA AGAAGAGA TGAC			
			AGGT TCTTCTCT ACTG			
			C _			
GAM2428	MMP19	3'	GTCATCTCTTCTCTGGA	8269	A	CGA
			TCTA AGAAGAGA TGAC			
			AGGT TCTTCTCT ACTG			
			C _			
GAM2428	FLJ12598	3'	CCACATTATCTCTTTTCAGA	24096	AA	CG AC
			TCT AGAAGAGA ATG TGG			
			AGA TTTTCTCT TAC ACC			
			C_ AT _			
GAM2428	FLJ12704	3'	GCCAATCATCCTTACTTCCTTA	24565	A A C C	
			TAA GAAG GA GATGA TGGC			
			ATT CTTC TT CTA CT ACT ACCG			
			C A C A			
GAM2428	H326	3'	CCAGTTCCTTCTTTA	17938	A	CGATG
			TAAAGAAG GA ACTGG			
			ATTTCTTC CT TGACC			
			C _			
GAM2428	KIAA0594	3'	CCAGTCATCTTATTTCT	32387	A C	
			AGAAG GA GATGACTGG			
			TCTTT TT CTA CT GACC			
			A _			
GAM2428	KIAA1634	3'	CATCAGTCTCTTCTCCAGA	31750	AA	_
			TCT AGAAGAGAC GATG			
			AGA TCTTCTCTG CTAC			
			CC A			
GAM2428	KIAA1831	3'	GCCCTCCACCTTTTCTTTAGA	31905		ACGAT CT
			TCTAAAGAAGAG GA GGC			
			AGATTTCTTTTC CT CCG			
			CACC_ C_			
GAM2428	P2RXL1	3'	GCCTGGCACCTACTCTTTAGA	11932	AG	ACGA ACT
			TCTAAAGA AG TG GGC			
			AGATTTCT TC AC CCG			
			CA C_ GGT			
GAM2428	PRPF8	3'	CCCCATCCGTCTCTTCTGCAGA	30680	AA	_ ACT
			TCT AGAAGAGACG ATG GG			

AGA TCTTCTCTGC TAC CC
 CG C C__
 GAM2428 LOC120534 3' CCAGTCATGTTATTTCTTT 36626 A G
 AAAGAAG GAC ATGACTGG
 ||||| ||| |||||
 TTTCTTT TTG TACTGACC
 A _
 GAM2428 LOC131870 3' CGGTGTCTCTCCTCTAGA 37016 A A GATG TG
 TCTA AG AGAGAC AC G
 ||| || ||||| || |
 AGAT TC TCTCTG TG C
 C C ____ GT
 GAM2428 LOC144866 5' CCAGTTATCCTCTCCTCT 40476 A C
 AGA GAGA GATGACTGG
 || ||| |||||
 TCT CTCT CTATTGACC
 C C
 GAM2428 LOC146774 3' GCCAGCCACCGTGTGAACTCTT 38234 AGAG__ A A
 TGGA TCTAAAGA ACG TG CTGGC
 ||||| ||| || |||||
 AGGTTTCT TGC AC GACCG
 CAAGTG C C
 GAM2428 LOC150848 5' GCCAGTCACTTTTCCCTCTTAG 41254 A__ ACGA
 A TCTAA GAAGAG TGA CTGGC
 |||| ||||| |||||
 AGATT CTTTTC ACTGACCG
 CTCC ____
 GAM2428 LOC151610 3' CCAGACCTCTTTTTTCAGA 39134 A ACGATGA
 TCT AAGAAGAG CTGG
 || ||||| |||
 AGA TTTTCTC GACC
 C CA____
 GAM2428 LOC152317 5' GCCAGTCAAGACCTTTCTCCAG 41467 AA A ACGA
 A TCT AGA GAG TGA CTGGC
 || ||| ||| |||||
 AGA TCT TTC ACTGACCG
 CC _ CAGA
 GAM2428 LOC203378 5' TCTCACCTCTTCTTCAGG 43558 A AC T
 TCT AAGAAGAG GA GA
 || ||||| || ||
 GGA TTCTTCTC CT CT
 C CA _
 GAM2428 LOC219347 3' CATTGTCTCCTCCTTAGA 44678 A A
 TCTAA GA GAGACGATG
 |||| || |||||
 AGATT CT CTCTGTTAC
 C C
 GAM2428 LOC91561 5' GCCAGTCACCTCCCTTTTTTA 33021 A CGA
 TAAAGAAG GA TGA CTGGC
 ||||| || |||||

ATTTTTTC CT ACTGACCG
 C CC_
 GAM2429 APXL 3' TCTGTATCTAGTTGTATTA 7356 TAAA
 TAATACAATA ATATGGA
 ||||| |||||
 ATTATGTTGAT TATGTCT
 C__
 GAM2429 EIF2S3 3' CCATATTTTATGTTGCTTTA 7110 TA T
 TAA CAAC ATAAAATATGG
 || ||| |||||
 ATT GTTG TATTTTATACC
 TC _
 GAM2429 LUM 3' TCCATATTTTATTACTGT 8145 ACT
 ACA ATAAAATATGGA
 || |||||
 TGT TATTTTATACCT
 CAT
 GAM2429 ERp44 3' TCTTGTTATAGTTGTAT 39726 AATAT
 ATACAATAATAA GGA
 ||||| |||
 TATGTTGATATT TCT
 GT__
 GAM2429 PNPASE 3' CCATATTTGTTTAATTGTATT 35102 C TA_
 AATACAA TA AAATATGG
 ||||| || |||||
 TTATGTT AT TTTATACC
 A TTG
 GAM2429 LOC115648 3' TCCATATTTAGTTGT 29829 TAA
 ACAACTA AATATGGA
 ||||| |||||
 TGTTGAT TTATACCT

 GAM2429 LOC255308 3' CCATATTTTATGTTGCTTTA 45353 TA T
 TAA CAAC ATAAAATATGG
 || ||| |||||
 ATT GTTG TATTTTATACC
 TC _
 GAM2430 CLN5 3' TCTTAGGATTTAGGATTGCTGT 13230 A GTC
 A TATA CAATCCTAAATT GAGA
 ||| ||||| |||
 ATGT GTTAGGATTTAG TTCT
 C GA_
 GAM2430 DKFZP434I0714 3' CAGTTTAGGATTGTTATA 41529
 TATAACAATCCTAAATTG
 |||||
 ATATTGTTAGGATTTGAC

 GAM2430 DKFZP564F013 3' CTTGATTTTAAGTTGTTATA 45200 CC TT
 TATAACAAT TAAA GTCGAG
 ||||| ||| |||||

		ATATTGTTG ATTT TAGTTC	
		A_ _	
GAM2430	KIAA1674	3' CTACAAATTTAGGATTGTT 34111	GTCG
		AACAATCCTAAATT AG	
		TTGTTAGGATTTAA TC	
		ACA_	
GAM2430	LOC145773	3' TCGCTGCATTCAGGATTGTT 37984	AAAT _
		AACAATCCT TGT CGA	
		TTGTTAGGA ACG GCT	
		CTT_ TC	
GAM2431	CCNF	3' CATGATCTCAACTCTCAACTCA 7524	AAAT TAT
		TGAGTT GTT AGATCATG	
		ACTCAA CAA TCTAGTAC	
		CTCT C_	
GAM2431	MAP3K1	3' CATGATCTGTACCTAAGCTCA 33681	AAA TT
		TGAGTT TG TATAGATCATG	
		ACTCGA AT ATGTCTAGTAC	
		_ CC	
GAM2431	C6.1A	3' ATCTTATATAAAATTTAACTCA 23639	GTT_ _
		TGAGTTAAAT TATA GAT	
		ACTCAATTTA ATAT CTA	
		AAAT T	
GAM2431	KIAA1715	3' CATGATCTACAAACATGGTCT 33791	TTAA A
		AG ATGTTT TAGATCATG	
		TC TACAAA ATCTAGTAC	
		TGG_ C	
GAM2431	LOC146839	5' CATGGTAAACATTTAAC 40752	ATAG
		GTAAATGTTT ATCATG	
		CAATTTACAAA TGGTAC	
		A_	
GAM2431	LOC200609	5' ATGATCTACAAGAGACTCA 43324	AAA TTAT
		TGAGTT TGT AGATCAT	
		ACTCAG ACA TCTAGTA	
		AGA _	
GAM2432	CRYZ	3' AATCTCATTGGATGTG 7616	CTAC
		CACATTC AATGAGATT	
		GTGTAGG TTA CTCTAA	
		T_	
GAM2432	EPHA3	3' AATCAAGCCATGTATAAATGTG 11738	CC A A_
	ATA	TATCACATT TACA TG GATT	

		ATAGTGTA	ATGT AC	CTAA	
		AT	_ CGAA		
GAM2432	FLJ20686	5'	TAATCTCAAGAAG	AATGGTGAT 19595	_ CTACAA
		A	TATCAC ATTC	TGAGATTA	
			ATAGTG TAAG	ACTCTAAT	
			G AAGA	_	
GAM2432	KIAA0089	3'	TAATCTCATCACGG	AATATGT 34669	_ TACA
			ACAT TCC	ATGAGATTA	
			TGTA AGG	TACTCTAAT	
			T CAC	_	
GAM2432	KIAA0429	3'	CAATGTAGAAAGA	AATGTGA 16465	___ A
			TCACATTC	CTACA TG	
			AGTGTAAG	GATGT AC	
			AAA	A	
GAM2432	SEC15L	3'	CTCAGTAAGA	AATGTGA 35764	C AA
			TCACATTC TAC	TGAG	
			AGTGTAAG	ATG ACTC	
			A	_	
GAM2432	LOC147341	3'	AATTCGCGAGA	AATGTGATA 40825	CTACAA
			TATCACATTC	TGAGATT	
			ATAGTGTAAG	GCTTTAA	
			AC	___	
GAM2432	LOC256277	5'	ATCTTGCAAGG	ATGTGATA 45425	T ACAA
			TATCACAT CCT	TGAGAT	
			ATAGTGTA GGA	GTTCTA	
			_ AC	_	
GAM2432	LOC86651	3'	CAATGTAGACA	AATGTGATA 34097	C_ A
			TATCACATT	CTACA TG	
			ATAGTGTA	GATGT AC	
			CA	A	
GAM2433	BCL11B	3'	GATGTCAGTA	AACATTCCA 23164	ACAAAT
			TGGAATGTTA	ATATC	
			ACCTTACAAT	TGTAG	
			GAC	___	
GAM2433	CFTR	3'	TGTTTGCTAAG	CATTCCA 6104	AA_
			TGGAATGTT	CAAATA	
			ACCTTACGA	GTTTGT	
			ATC		
GAM2433	COX15	3'	TGATAAGGCTG	TTAACATTACA 27790	G AATA
			TG AATGTTAACA	TATCA	

			AC TTACAATTGT ATAGT		
			A CGGA		
GAM2433	RPA3	5'	TGATATCATTAACATTTCA 8858	CAAAT	
			TGGAATGTAA ATATCA		
			ACTTTACAATT TATAGT		
			AC__		
GAM2433	SCN3A	3'	ATATATTTTCTACCATTCCA 13798	T AC	
			TGGAATG TA AAATATAT		
			ACCTTAC AT TTTATATA		
			C CT		
GAM2433	FLJ23151	3'	ATATATTTGAGCAGTCC 24135	A AA	
			GGA TGTT CAAATATAT		
			CCT ACGA GTTTATATA		
			G _		
GAM2433	KIAA1468	5'	TGATGTAGGATTAAACATTCCA 44102	AACAAA	
			TGGAATGTT TATATCA		
			ACCTTACAA ATGTAGT		
			ATTAGG		
GAM2433	LRP15	5'	TGATTATGCTGACATTCCA 27510	A AATAT	
			TGGAATGTTA CA ATCA		
			ACCTTACAGT GT TAGT		
			C AT__		
GAM2433	LOC121536	3'	TGATACTGTTAACACACCA 36666	AA AATA	
			TGG TGTTAACA TATCA		
			ACC ACAATTGT ATAGT		
			AC C__		
GAM2433	LOC254251	3'	ATATATTTGCTGCTGTGACATT 45895	A_____	
			TCA TGGAATGTTA CAAATATAT		
			ACTTTACAGT GTTTATATA		
			GTCGTC		
GAM2433	LOC51301	5'	TGATTTTCTGTTAATATTCCA 18674	AATAT	
			TGGAATGTTAACA ATCA		
			ACCTTATAATTGT TAGT		
			CTTT_		
GAM2434	A1BG	3'	TCTACCTCCTGGGTTCAA 28279	A CAA	
			TTGAACCTA GAG TGGA		
			AACTTGGGT CTC ATCT		
			C C__		
GAM2434	A1BG	3'	TGGTCTTGAACCTCTGGGCTCA 28280	A CAAT	
			A TTGA CCTAAGAG GGACCA		

			AACT GGGTTCTC TCTGGT		
			C AAGT		
GAM2434	AHR	3'	TCTACCTCCTGGGTTCAA 7336	A	CAA
			TTGAACCTA GAG TGGA		
			AACTTGGGT CTC ATCT		
			C C__		
GAM2434	APAF1	3'	TCAGACTCCTGGGTTCAA 6830	A	CAA
			TTGAACCTA GAG TGG		
			AACTTGGGT CTC ACT		
			C AG_		
GAM2434	APAF1	3'	TCGCTGCCTCCTGGGTTCAA 6831	A	_ A
			TTGAACCTA GAG CA TGG		
			AACTTGGGT CTC GT GCT		
			C C C		
GAM2434	APAF1	3'	TCAGACTCCTGGGTTCAA 14869	A	CAA
			TTGAACCTA GAG TGG		
			AACTTGGGT CTC ACT		
			C AG_		
GAM2434	APAF1	3'	TCGCTGCCTCCTGGGTTCAA 14870	A	_ A
			TTGAACCTA GAG CA TGG		
			AACTTGGGT CTC GT GCT		
			C C C		
GAM2434	APM1	3'	CCTTTGCCTCCCAGGTTTAA 11209	AA	_ T
			TTGAACCT GAG CAA GG		
			AATTTGGA CTC GTT CC		
			CC C T		
GAM2434	AQP6	3'	TCTACCTCCTGGGTTCAA 7361	A	CAA
			TTGAACCTA GAG TGGA		
			AACTTGGGT CTC ATCT		
			C C__		
GAM2434	AQP6	3'	TCTACCTCCTGGGTTCAA 27619	A	CAA
			TTGAACCTA GAG TGGA		
			AACTTGGGT CTC ATCT		
			C C__		
GAM2434	ARCN1	3'	TCCGCCTCCTGGGTTCAA 7370	A	CAA
			TTGAACCTA GAG TGGA		
			AACTTGGGT CTC GCCT		
			C C__		
GAM2434	ATP1B2	3'	TCCGCATCCCAGGTTCAA 7393	AA	_ AAT
			TTGAACCT GA GC GGA		

			AACTTGGA CT CG CCT		
			CC A _		
GAM2434	ATP8B2	3'	TCCACCTCCTGGGTTCAA 32517	A	CAA
			TTGAACCTA GAG TGGA		
			AACTTGGGT CTC ACCT		
			C C_		
GAM2434	BRIP1	3'	TTCACCTCCAGGTTCAA 25757	AA	CAA
			TTGAACCT GAG TGGA		
			AACTTGGA CTC ACTT		
			C_ C_		
GAM2434	C20orf1	3'	TGGGACCTGCTCTTAACCTCAA 14428	ACC	AT A_
			TTGA TAAGAGCA GG CCA		
			AACT ATTCTCGT CC GGT		
			CCA _ AG		
GAM2434	CIAS1	5'	TCCACCTCCCGGGTTCAA 11322	AA	CAA
			TTGAACCT GAG TGGA		
			AACTTGGG CTC ACCT		
			CC C_		
GAM2434	COX15	3'	TCCAATTCCCAGGTTCAA 27789	AA	CAA
			TTGAACCT GAG TGGA		
			AACTTGGA CTT ACCT		
			CC C_		
GAM2434	CRTAP	3'	TCCGCCTCTTGGGTTCAA 13063		CAA
			TTGAACCTAAGAG TGGA		
			AACTTGGGTCTC GCCT		
			C_		
GAM2434	CXCL16	3'	CCATCTCCCAGGTTCAA 22598	AA	CA
			TTGAACCT GAG ATGG		
			AACTTGGA CTC TACC		
			CC _		
GAM2434	CYP1A2	3'	TCCACCTCGCAGGTTCAA 6413	AA	CAA
			TTGAACCT GAG TGGA		
			AACTTGGA CTC ACCT		
			CG C_		
GAM2434	CYP1A2	3'	CCTCTGCCTCCCAGGTTCAA 6411	AA	_ AT
			TTGAACCT GAG CA GG		
			AACTTGGA CTC GT CC		
			CC C CT		
GAM2434	CYP1A2	3'	CCTCTGCCTCCCAGGTTCAA 34255	AA	_ AT
			TTGAACCT GAG CA GG		

			AACTTGGA CTC GT CC		
			CC C CT		
GAM2434	CYP1A2	3'	TCCACCTCGCAGGTTCAA 34257	AA	CAA
			TTGAACCT GAG TGGA		
			AACTTGGA CTC ACCT		
			CG C__		
GAM2434	CYP8B1	3'	CCTCTGCCTCCCGGGTTCAA 10624	AA	_ AT
			TTGAACCT GAG CA GG		
			AACTTGGG CTC GT CC		
			CC C CT		
GAM2434	DFFB	3'	TCCGCCTCTCAGGTTCAA 42246	A	CAA
			TTGAACCT AGAG TGGA		
			AACTTGGA TCTC GCCT		
			C C__		
GAM2434	DISC1	3'	TCTACCTCCCAGGTTCAA 20740	AA	CAA
			TTGAACCT GAG TGGA		
			AACTTGGA CTC ATCT		
			CC C__		
GAM2434	DSCR3	3'	TCCACCTCCCAGGTTCAA 12688	AA	CAA
			TTGAACCT GAG TGGA		
			AACTTGGA CTC ACCT		
			CC C__		
GAM2434	EPB72	3'	TCCGCCTCCTGGGTTCAA 10307	A	CAA
			TTGAACCTA GAG TGGA		
			AACTTGGGT CTC GCCT		
			C C__		
GAM2434	EVC	3'	TCCATCTCCCGGGTTCAA 15895	AA	CA
			TTGAACCT GAG ATGGA		
			AACTTGGG CTC TACCT		
			CC _		
GAM2434	FEZ1	3'	TCCACCTCCCAGGTTCAA 22879	AA	CAA
			TTGAACCT GAG TGGA		
			AACTTGGA CTC ACCT		
			CC C__		
GAM2434	FZD4	3'	CCTCTGCCTCCTGGGTTCAA 14484	A	_ AT
			TTGAACCTA GAG CA GG		
			AACTTGGGT CTC GT CC		
			C C CT		
GAM2434	GM2A	3'	TCCGCCTCCTGGGTTCAA 33662	A	CAA
			TTGAACCTA GAG TGGA		

			AACTTGGGT CTC GCCT	
			C C__	
GAM2434	GPR56	5'	TCCACCTCCCGGGTTCAA 12239	AA CAA
			TTGAACCT GAG TGGA	
			AACTTGGG CTC ACCT	
			CC C__	
GAM2434	GPR81	3'	CCTCTGCCTCCCGGGTTCAA 26281	AA _ AT
			TTGAACCT GAG CA GG	
			AACTTGGG CTC GT CC	
			CC C CT	
GAM2434	GRAF	3'	TCCGCCTCCCGGGTTCAA 17445	AA CAA
			TTGAACCT GAG TGGA	
			AACTTGGG CTC GCCT	
			CC C__	
GAM2434	HCS	3'	TCCGCCTTCCAGGTTCOA 21016	AA CAA
			TTGAACCT GAG TGGA	
			AACTTGGA TTC GCCT	
			CC C__	
GAM2434	HMG20A	3'	TCCAACCTCTTGGGCTCAA 20074	A CAA
			TTGA CCTAAGAG TGGA	
			AACT GGGTTCTC ACCT	
			C A__	
GAM2434	IDH3A	3'	CAGTGGCTCTTGGGTTCAA 12051	AA_
			TTGAACCTAAGAGC TG	
			AACTTGGGTTCTCG AC	
			GTG	
GAM2434	ITGAM	3'	TCCGCCTCCCGGGTTCAA 35565	AA CAA
			TTGAACCT GAG TGGA	
			AACTTGGG CTC GCCT	
			CC C__	
GAM2434	LZTS1	3'	CCATTGCTCTTAGTCCCAA 22007	AAC
			TTG CTAAGAGCAATGG	
			AAC GATTCTCGTTACC	
			CCT	
GAM2434	MAK	3'	TCCACCTCCTGGGTTCAA 12531	A CAA
			TTGAACCTA GAG TGGA	
			AACTTGGGT CTC ACCT	
			C C__	
GAM2434	MEF2A	5'	TCCGCCTCCAGGTTCOA 12118	AA CAA
			TTGAACCT GAG TGGA	

			AACTTGGA CTC GCCT		
			C_ C__		
GAM2434	MEFV	3'	TCCGCCTCCCAGGTTCAA 5772	AA	CAA
			TTGAACCT GAG TGGA		
			AACTTGGA CTC GCCT		
			CC C__		
GAM2434	MEFV	3'	TCCACCTCCCAGGTTCAA 5771	AA	CAA
			TTGAACCT GAG TGGA		
			AACTTGGA CTC ACCT		
			CC C__		
GAM2434	MHC2TA	3'	TCCGCCTCTTGGGTTCAA 5783		CAA
			TTGAACCTAAGAG TGGA		
			AACTTGGGTTCTC GCCT		
			C__		
GAM2434	MICB	3'	CCTCTGCCTCCCAGGTTCAA 12564	AA	_ AT
			TTGAACCT GAG CA GG		
			AACTTGGA CTC GT CC		
			CC C CT		
GAM2434	MLANA	3'	TCCGCCTCCCAGGTTCAA 12028	AA	CAA
			TTGAACCT GAG TGGA		
			AACTTGGA CTC GCCT		
			CC C__		
GAM2434	MPL	3'	CCTCTGCCTCCCGGGTTCAA 11848	AA	_ AT
			TTGAACCT GAG CA GG		
			AACTTGGG CTC GT CC		
			CC C CT		
GAM2434	MYCL2	3'	CCTCTGCCTCCCGGGTTCAA 11855	AA	_ AT
			TTGAACCT GAG CA GG		
			AACTTGGG CTC GT CC		
			CC C CT		
GAM2434	NCOA6	5'	TCCGTCTCCCAGGTTCAA 15293	AA	CA
			TTGAACCT GAG ATGGA		
			AACTTGGA CTC TGCCT		
			CC _		
GAM2434	NONO	3'	TCTCTGCCTCCCGGGTTCAA 39899	AA	_ AT
			TTGAACCT GAG CA GGA		
			AACTTGGG CTC GT TCT		
			CC C C_		
GAM2434	PCDHB9	3'	TCCGCCTCCCAGGTTCAA 21206	AA	CAA
			TTGAACCT GAG TGGA		

			AACTTGGA CTC GCCT CC C__	
GAM2434	PDCL	3'	TCCACCTCCTGGGTTCAA 11866 TTGAACCTA GAG TGGA AACTTGGGT CTC ACCT C C__	A CAA
GAM2434	PDE6B	3'	TCCACCTCCCAGGTTCAA 5830 TTGAACCT GAG TGGA AACTTGGA CTC ACCT CC C__	AA CAA
GAM2434	PER2	3'	CCTCTGCCTCCCAGGTTCAA 23090 TTGAACCT GAG CA GG AACTTGGA CTC GT CC CC C CT	AA _ AT
GAM2434	PIK3CD	3'	TCCGCCTCCCAGGTTCAA 11465 TTGAACCT GAG TGGA AACTTGGA CTC GCCT CC C__	AA CAA
GAM2434	PLOD	5'	GTTCTCACTCTTAGGTTCA 5845 TGAACCTAAGAG GGAC ACTTGATTCTC CTTG ACT_	CAAT
GAM2434	PTGES	3'	TCCGCCTCCCGGGTTCAA 11313 TTGAACCT GAG TGGA AACTTGGG CTC GCCT CC C__	AA CAA
GAM2434	RBM8A	3'	TTCAAACCTCTTGGGCTCAA 11582 TTGA CCTAAGAG TGGA AACT GGGTTCTC ACTT C AA_	A CAA
GAM2434	RHD	3'	TCCGCCTCCCAGGTTCAA 18338 TTGAACCT GAG TGGA AACTTGGA CTC GCCT CC C__	AA CAA
GAM2434	RHD	3'	TCTACCTCCTGGGTTCAA 18339 TTGAACCTA GAG TGGA AACTTGGGT CTC ATCT C C__	A CAA
GAM2434	RHD	3'	TCCGCCTCCCAGGTTCAA 18218 TTGAACCT GAG TGGA 	AA CAA

			AACTTGGA CTC GCCT		
			CC C__		
GAM2434	RHD	3'	TCTACCTCCTGGGTTCAA 18219	A	CAA
			TTGAACCTA GAG TGGA		
			AACTTGGGT CTC ATCT		
			C C__		
GAM2434	SAS	3'	CCTCTGCCTCCCGGGTTCAA 12604	AA	_ AT
			TTGAACCT GAG CA GG		
			AACTTGGG CTC GT CC		
			CC C CT		
GAM2434	SEDL	3'	TCCACCTCCCGGGTTCAA 15911	AA	CAA
			TTGAACCT GAG TGGA		
			AACTTGGG CTC ACCT		
			CC C__		
GAM2434	SEDL	3'	TCCACCTCCTGGGTTCAA 15912	A	CAA
			TTGAACCTA GAG TGGA		
			AACTTGGGT CTC ACCT		
			C C__		
GAM2434	SEDL	3'	TCCGCCTCCCAGGTTTCAG 15913	AA	CAA
			TTGAACCT GAG TGGA		
			GACTTGGA CTC GCCT		
			CC C__		
GAM2434	SEPN1	3'	TCCACCTCCCAGGTTCAA 32991	AA	CAA
			TTGAACCT GAG TGGA		
			AACTTGGA CTC ACCT		
			CC C__		
GAM2434	SHC1	3'	CCATCTCTTAGGTCTAA 8969	A	CA
			TTG ACCTAAGAG ATGG		
			AAT TGGATTCTC TACC		
			C _		
GAM2434	SIL	3'	CCTCTGCCTCCTGGGTTCAA 8984	A	_ AT
			TTGAACCTA GAG CA GG		
			AACTTGGGT CTC GT CC		
			C C CT		
GAM2434	SLC14A2	5'	TCCACCTCCCAGGTTCAA 14012	AA	CAA
			TTGAACCT GAG TGGA		
			AACTTGGA CTC ACCT		
			CC C__		
GAM2434	SLC15A1	3'	TCCGCCTCCCAGGTTCAA 11522	AA	CAA
			TTGAACCT GAG TGGA		

			AACTTGGA CTC GCCT		
			CC C__		
GAM2434	SMAC	5'	CCTCTGCCTCCCAGGTTCAA 29049	AA _ AT	
			TTGAACCT GAG CA GG		
			AACTTGGA CTC GT CC		
			CC C CT		
GAM2434	SNX15	3'	TCCACCTCCCAGGTTCAA 36506	AA CAA	
			TTGAACCT GAG TGGA		
			AACTTGGA CTC ACCT		
			CC C__		
GAM2434	SS18	3'	TCCGCCTCCCAGGTTCAA 12165	AA CAA	
			TTGAACCT GAG TGGA		
			AACTTGGA CTC GCCT		
			CC C__		
GAM2434	SULT2B1	5'	TCCGCCTCCTGGGTTCAA 10949	A CAA	
			TTGAACCTA GAG TGGA		
			AACTTGGGT CTC GCCT		
			C C__		
GAM2434	TAPBP	3'	TCCGCCTCCTGGGTTCAA 9183	A CAA	
			TTGAACCTA GAG TGGA		
			AACTTGGGT CTC GCCT		
			C C__		
GAM2434	TAT	3'	TCCACCTCCTGGGTTCAA 5914	A CAA	
			TTGAACCTA GAG TGGA		
			AACTTGGGT CTC ACCT		
			C C__		
GAM2434	TBXA2R	3'	TCCACCTCCCGGGTTCAA 6729	AA CAA	
			TTGAACCT GAG TGGA		
			AACTTGGG CTC ACCT		
			CC C__		
GAM2434	TBXA2R	3'	TCCGCCTCCCGGGTTCAA 6730	AA CAA	
			TTGAACCT GAG TGGA		
			AACTTGGG CTC GCCT		
			CC C__		
GAM2434	TMC1	5'	TCCGCCTCCCAGGTTCAA 28935	AA CAA	
			TTGAACCT GAG TGGA		
			AACTTGGA CTC GCCT		
			CC C__		
GAM2434	TNFRSF10B	3'	TCCGCCTCCTGGGTTCAA 9940	A CAA	
			TTGAACCTA GAG TGGA		

			AACTTGGGT CTC GCCT	
			C C__	
GAM2434	TNFRSF9	3'	TGGTCTCAAACCTCCTAGGTTCA 7289	A CAAT
			TGAACCTA GAG GGACCA	
			ACTTGGAT CTC TCTGGT	
			C AAAC	
GAM2434	TRIM9	5'	TCCGCCTCCCAGGTTCAA 17519	AA CAA
			TTGAACCT GAG TGGA	
			AACTTGGA CTC GCCT	
			CC C__	
GAM2434	TRPV1	3'	CCTCTGCCTCCCGGGTTCAA 20814	AA _ AT
			TTGAACCT GAG CA GG	
			AACTTGGG CTC GT CC	
			CC C CT	
GAM2434	TRPV1	3'	CCTCTGCCTCCCGGGTTCAA 27994	AA _ AT
			TTGAACCT GAG CA GG	
			AACTTGGG CTC GT CC	
			CC C CT	
GAM2434	TRPV1	3'	CCTCTGCCTCCCGGGTTCAA 28002	AA _ AT
			TTGAACCT GAG CA GG	
			AACTTGGG CTC GT CC	
			CC C CT	
GAM2434	TRPV1	3'	CCTCTGCCTCCCGGGTTCAA 28010	AA _ AT
			TTGAACCT GAG CA GG	
			AACTTGGG CTC GT CC	
			CC C CT	
GAM2434	VENTX2	3'	TCCGCCTCCTGGGTTCAA 15817	A CAA
			TTGAACCTA GAG TGGA	
			AACTTGGGT CTC GCCT	
			C C__	
GAM2434	XRCC2	3'	CCTCTGCCTCTTGGGTTCAA 11901	_ AT
			TTGAACCTAAGAG CA GG	
			AACTTGGGTTCTC GT CC	
			C CT	
GAM2434	ZNF22	3'	TGGTTTATCACTCTAGATTCAA 43971	C A CA
			TTGAA CTA GAG ATGGACCA	
			AACTT GAT CTC TATTTGGT	
			A _ AC	
GAM2434	ZNF264	3'	CCTCTGCCTCCCGGGTTCAA 9455	AA _ AT
			TTGAACCT GAG CA GG	

		AACTTGGG CTC GT CC	
		CC C CT	
GAM2434	ZNF264	3' TCCGCCTCCTGGGTTCAA 9460	A CAA
		TTGAACCTA GAG TGGA	
		AACTTGGGT CTC GCCT	
		C C__	
GAM2434	ARPP-19	3' CCTCTGCCTCCTGGGTTCAA 13419	A _ AT
		TTGAACCTA GAG CA GG	
		AACTTGGGT CTC GT CC	
		C C CT	
GAM2434	ASB16	5' TCCGCCTCCCGGGTTCAA 34655	AA CAA
		TTGAACCT GAG TGGA	
		AACTTGGG CTC GCCT	
		CC C__	
GAM2434	BA108L7.2	3' CCTCTGCCTCCTGGGTTCAA 25237	A _ AT
		TTGAACCTA GAG CA GG	
		AACTTGGGT CTC GT CC	
		C C CT	
GAM2434	BAG5	3' TCCACCTCCCAGGTTCAA 11309	AA CAA
		TTGAACCT GAG TGGA	
		AACTTGGA CTC ACCT	
		CC C__	
GAM2434	BTN3A1	3' TCCACCTCCTGGGTTCAA 13921	A CAA
		TTGAACCTA GAG TGGA	
		AACTTGGGT CTC ACCT	
		C C__	
GAM2434	C1QTNF6	3' CCTCTGCCTCCCGGGTTCAA 25656	AA _ AT
		TTGAACCT GAG CA GG	
		AACTTGGG CTC GT CC	
		CC C CT	
GAM2434	C3F	3' TCCACCTCCTGGGTTCAA 12331	A CAA
		TTGAACCTA GAG TGGA	
		AACTTGGGT CTC ACCT	
		C C__	
GAM2434	C6orf5	3' CCTGCGCCTCCTGGGTTCAA 17780	A _ AAT
		TTGAACCTA GAG C GG	
		AACTTGGGT CTC G CC	
		C C CGT	
GAM2434	C9orf9	3' TCCACCTCCAGGTTCAA 21029	AA CAA
		TTGAACCT GAG TGGA	

			AACTTGGA CTC ACCT		
			C_ C__		
GAM2434	CDC14B	3'	TCCTTCTCCCAGGTTCAA 27174	AA	C T
			TTGAACCT GAG AA GGA		
			AACTTGGA CTC TT CCT		
			CC _ _		
GAM2434	CECR1	3'	TCCACTCCCGGGTTCAA 18884	AA	CAA
			TTGAACCT GAG TGGA		
			AACTTGGG CTC ACCT		
			CC ____		
GAM2434	CHRA1	3'	TCCGCCTCCCAGGTTCAA 18908	AA	CAA
			TTGAACCT GAG TGGA		
			AACTTGGA CTC GCCT		
			CC C__		
GAM2434	CIP29	3'	CCTCTGTCTCCCGGGTTCAA 26148	AA	_ AT
			TTGAACCT GAG CA GG		
			AACTTGGG CTC GT CC		
			CC T CT		
GAM2434	CPSF2	3'	CCTCTGCCTCCTGGGTTCAA 30862	A	_ AT
			TTGAACCTA GAG CA GG		
			AACTTGGGT CTC GT CC		
			C C CT		
GAM2434	CYLC2	3'	TCCACCTTCAGGTTCAA 7020	AA	CAA
			TTGAACCT GAG TGGA		
			AACTTGGA TTC ACCT		
			C_ C__		
GAM2434	DKFZP434D146	3'	CCTCTGCTTCCTAGGTTCAA 17871	A_	AT
			TTGAACCTA GAGCA GG		
			AACTTGGAT TTCGT CC		
			CC CT		
GAM2434	DKFZp434E2220	5'	TCCGCCTCCCGGGTTCAA 19111	AA	CAA
			TTGAACCT GAG TGGA		
			AACTTGGG CTC GCCT		
			CC C__		
GAM2434	DKFZP434F0318	3'	TCCGACTCCTGGGTTCAA 25143	A	CAA
			TTGAACCTA GAG TGGA		
			AACTTGGGT CTC GCCT		
			C A__		
GAM2434	DKFZP434J037	3'	TCCGCCTCCCGGGTTCAA 25220	AA	CAA
			TTGAACCT GAG TGGA		

		AACTTGGG CTC GCCT		
		CC C__		
GAM2434	DKFZp547H025 3'	TCCACCTCCTGGGTTCAA	21375	A CAA
		TTGAACCTA GAG TGGA		
		AACTTGGGT CTC ACCT		
		C C__		
GAM2434	DKFZP564O0523 3'	TCCACCTCCCGGGTTCAA	25805	AA CAA
		TTGAACCT GAG TGGA		
		AACTTGGG CTC ACCT		
		CC C__		
GAM2434	DKFZp762L0311 3'	CCTTTGCCTCCTAGGTTCAA	20799	A _ T
		TTGAACCTA GAG CAA GG		
		AACTTGGAT CTC GTT CC		
		C C T		
GAM2434	EVI5 3'	TCCGCTTCCAGGTTCAA	12215	AA_ AAT
		TTGAACCT GAGC GGA		
		AACTTGGA TTCG CCT		
		CCC ____		
GAM2434	FER1L4 3'	TCCACCTCCTGGGTTCAA	24875	A CAA
		TTGAACCTA GAG TGGA		
		AACTTGGGT CTC ACCT		
		C C__		
GAM2434	FER1L4 3'	TCCACCTCCTGGGTTCAA	24876	A CAA
		TTGAACCTA GAG TGGA		
		AACTTGGGT CTC ACCT		
		C C__		
GAM2434	FLJ00024 5'	CCTCTGCCTCCCAGGTTCAA	31888	AA _ AT
		TTGAACCT GAG CA GG		
		AACTTGGA CTC GT CC		
		CC C CT		
GAM2434	FLJ10232 3'	TCCGCCTCCCGGGTTCAA	19774	AA CAA
		TTGAACCT GAG TGGA		
		AACTTGGG CTC GCCT		
		CC C__		
GAM2434	FLJ10298 3'	TCCGTCTCCTGGGTTCAA	19809	A CA
		TTGAACCTA GAG ATGGA		
		AACTTGGGT CTC TGCCT		
		C _		
GAM2434	FLJ10535 3'	CCTCTGCCTCCCAGGTTCAA	19917	AA _ AT
		TTGAACCT GAG CA GG		

		AACTTGGA CTC GT CC		
		CC C CT		
GAM2434	FLJ10713	3' TCCGCCTCCTGGGTTCAA 20043	A	CAA
		TTGAACCTA GAG TGGA		
		AACTTGGGT CTC GCCT		
		C C__		
GAM2434	FLJ10901	3' CCGTCTCCCGGGTTCAA 20229	AA	CA
		TTGAACCT GAG ATGG		
		AACTTGGG CTC TGCC		
		CC _		
GAM2434	FLJ11004	5' TCTACCTCCTGGGTTCAA 20289	A	CAA
		TTGAACCTA GAG TGGA		
		AACTTGGGT CTC ATCT		
		C C__		
GAM2434	FLJ11710	3' GGCATGCTCTTAGGCCAG 24275	AA	A GA
		TTG CCTAAGAGCA TG CC		
		GAC GGATTCTCGT AC GG		
		CC _ _		
GAM2434	FLJ12572	5' CCTCTGCCTCCCAGGTTCAA 23197	AA	_ AT
		TTGAACCT GAG CA GG		
		AACTTGGA CTC GT CC		
		CC C CT		
GAM2434	FLJ12586	3' CCTCTGCCTCCCAGGTTCAA 23883	AA	_ AT
		TTGAACCT GAG CA GG		
		AACTTGGA CTC GT CC		
		CC C CT		
GAM2434	FLJ12687	3' TCCGCCTCCCGGGTTCAA 24447	AA	CAA
		TTGAACCT GAG TGGA		
		AACTTGGG CTC GCCT		
		CC C__		
GAM2434	FLJ12903	3' TCCGCCTCCTGGGTTCAA 22983	A	CAA
		TTGAACCTA GAG TGGA		
		AACTTGGGT CTC GCCT		
		C C__		
GAM2434	FLJ12973	3' TCCGCCTCCCAGGTTCAA 24408	AA	CAA
		TTGAACCT GAG TGGA		
		AACTTGGA CTC GCCT		
		CC C__		
GAM2434	FLJ13193	3' TCCATCTCCCAGGTTCAA 25891	AA	CA
		TTGAACCT GAG ATGGA		

		AACTTGGA CTC TACCT	
		CC _	
GAM2434	FLJ14950	3' TCCACCTCCCAGGTTCAA 26675	AA CAA
		TTGAACCT GAG TGGA	
		AACTTGGA CTC ACCT	
		CC C_	
GAM2434	FLJ20034	3' CCTCTGCCTCCCGGGTTCAA 19132	AA _ AT
		TTGAACCT GAG CA GG	
		AACTTGGG CTC GT CC	
		CC C CT	
GAM2434	FLJ20136	3' TCTCTGCCTCTCGGGTTCAA 19232	TA _ AT
		TTGAACC AGAG CA GGA	
		AACTTGG TCTC GT TCT	
		GC C C_	
GAM2434	FLJ20342	3' CCTCTGCCTCCTGGGTTCAA 19398	A _ AT
		TTGAACCTA GAG CA GG	
		AACTTGGGT CTC GT CC	
		C C CT	
GAM2434	FLJ20344	3' TCCGCCTCTTGGGTTCAA 19405	CAA
		TTGAACCTAAGAG TGGA	
		AACTTGGGTCTC GCCT	
		C_	
GAM2434	FLJ20507	3' CCTCTGCCTCCTGGGTTCAA 19510	A _ AT
		TTGAACCTA GAG CA GG	
		AACTTGGGT CTC GT CC	
		C C CT	
GAM2434	FLJ20507	3' CCTCTGCCTCCTGGGTTCAA 30218	A _ AT
		TTGAACCTA GAG CA GG	
		AACTTGGGT CTC GT CC	
		C C CT	
GAM2434	FLJ21302	3' TCCGCCTCCTGGGTTCAA 23186	A CAA
		TTGAACCTA GAG TGGA	
		AACTTGGGT CTC GCCT	
		C C_	
GAM2434	FLJ22002	3' TCCGCCTCCCAGGTTCAA 24249	AA CAA
		TTGAACCT GAG TGGA	
		AACTTGGA CTC GCCT	
		CC C_	
GAM2434	FLJ22531	5' TCCACCTCCCAGGTTCAA 23946	AA CAA
		TTGAACCT GAG TGGA	

		AACTTGGA CTC ACCT	
		CC C__	
GAM2434	FLJ22794	3' TCCACCTCCCAGGTTCAA 44037	AA CAA
		TTGAACCT GAG TGGA	
		AACTTGGA CTC ACCT	
		CC C__	
GAM2434	FLJ23024	3' CCTCTGCCTCCCAGGTTCAA 24472	AA _ AT
		TTGAACCT GAG CA GG	
		AACTTGGG CTC GT CC	
		CC C CT	
GAM2434	FLJ23356	3' CCTCTGCCTCCCAGGTTCAA 25958	AA _ AT
		TTGAACCT GAG CA GG	
		AACTTGGA CTC GT CC	
		CC C CT	
GAM2434	FLJ23392	3' CCTCTGCCTCCCAGGTTCAA 24160	AA _ AT
		TTGAACCT GAG CA GG	
		AACTTGGA CTC GT CC	
		CC C CT	
GAM2434	FLJ23563	3' CCTCTGCCTCCCAGGTTCAA 33562	AA _ AT
		TTGAACCT GAG CA GG	
		AACTTGGA CTC GT CC	
		CC C CT	
GAM2434	FLJ25416	5' TCCGCATCCTAGGTTCAA 29627	A _ AAT
		TTGAACCTA GA GC GGA	
		AACTTGGAT CT CG CCT	
		C A ____	
GAM2434	FLJ30532	3' CCTCTGCCTCCTGGGTTCAA 29549	A _ AT
		TTGAACCTA GAG CA GG	
		AACTTGGGT CTC GT CC	
		C C CT	
GAM2434	FLJ32865	3' CCTCTGCCTCCCAGGTTCAA 29426	AA _ AT
		TTGAACCT GAG CA GG	
		AACTTGGG CTC GT CC	
		CC C CT	
GAM2434	GAL3ST-4	3' CCTCTGCCTCCCAGGTTCAA 23910	AA _ AT
		TTGAACCT GAG CA GG	
		AACTTGGA CTC GT CC	
		CC C CT	
GAM2434	GMPPB	5' TCCACCTCCCAGGTTCAA 45819	AA CAA
		TTGAACCT GAG TGGA	

			AACTTGGG CTC ACCT		
			CC C__		
GAM2434	GNG4	3'	TCCACCTCCTGGGTTCAA 10813	A	CAA
			TTGAACCTA GAG TGGA		
			AACTTGGGT CTC ACCT		
			C C__		
GAM2434	GP5	3'	TCCGCCCTCCAGGTTCAA 10819	AA	CAA
			TTGAACCT GAG TGGA		
			AACTTGGA CTC GCCT		
			C_ CC_		
GAM2434	GREB1	3'	CCTCTGCCTCCTGGGTTCAA 16124	A	_ AT
			TTGAACCTA GAG CA GG		
			AACTTGGGT CTC GT CC		
			C C CT		
GAM2434	GTF2E1	3'	CCTCTGCCTCCTGGGTTCAA 12036	A	_ AT
			TTGAACCTA GAG CA GG		
			AACTTGGGT CTC GT CC		
			C C CT		
GAM2434	GTPBG3	3'	TCCACCTCCCGGGTTCAA 26335	AA	CAA
			TTGAACCT GAG TGGA		
			AACTTGGG CTC ACCT		
			CC C__		
GAM2434	H-plk	5'	TCCACCTCCCAGGTTTCAG 17986	AA	CAA
			TTGAACCT GAG TGGA		
			GACTTGGA CTC ACCT		
			CC C__		
GAM2434	HRH4	3'	CCTCTGCCTCCTGGGTTCAA 22258	A	_ AT
			TTGAACCTA GAG CA GG		
			AACTTGGGT CTC GT CC		
			C C CT		
GAM2434	ICK	3'	CCTCTGCCTCCCAGGTTCAA 17196	AA	_ AT
			TTGAACCT GAG CA GG		
			AACTTGGA CTC GT CC		
			CC C CT		
GAM2434	JAM1	3'	TCCGCCTCCCGGGTTCAA 29331	AA	CAA
			TTGAACCT GAG TGGA		
			AACTTGGG CTC GCCT		
			CC C__		
GAM2434	JAM1	3'	TCCGCCTCCCGGGTTCAA 29342	AA	CAA
			TTGAACCT GAG TGGA		

			AACTTGGG CTC GCCT		
			CC C__		
GAM2434	JAM1	3'	TCCGCCTCCCGGGTTCAA 29352	AA	CAA
			TTGAACCT GAG TGGA		
			AACTTGGG CTC GCCT		
			CC C__		
GAM2434	JAM1	3'	TCCGCCTCCCGGGTTCAA 18864	AA	CAA
			TTGAACCT GAG TGGA		
			AACTTGGG CTC GCCT		
			CC C__		
GAM2434	KIAA0265	3'	CATTACTTTAGGTTCAA 34624	A	C
			TTGAACCTA GAG AATG		
			AACTTGGAT TTC TTAC		
			_ A		
GAM2434	KIAA0391	3'	CCTCTGCCTCCTGGGTTCAA 16136	A	_ AT
			TTGAACCTA GAG CA GG		
			AACTTGGGT CTC GT CC		
			C C CT		
GAM2434	KIAA0426	3'	TCCGCCTCCCAGGTTCAA 16312	AA	CAA
			TTGAACCT GAG TGGA		
			AACTTGGA CTC GCCT		
			CC C__		
GAM2434	KIAA0459	3'	TCCACCTCCCGGGTTCAA 30578	AA	CAA
			TTGAACCT GAG TGGA		
			AACTTGGG CTC ACCT		
			CC C__		
GAM2434	KIAA0475	3'	TCCGTCTCCCAGGTTCAA 16951	AA	CA
			TTGAACCT GAG ATGGA		
			AACTTGGA CTC TGCCT		
			CC _		
GAM2434	KIAA0495	3'	TCCGTCTCCCAGGTTCAA 31364	AA	CA
			TTGAACCT GAG ATGGA		
			AACTTGGA CTC TGCCT		
			CC _		
GAM2434	KIAA0513	3'	TCCACCTCCCGGGTTCAA 16361	AA	CAA
			TTGAACCT GAG TGGA		
			AACTTGGG CTC ACCT		
			CC C__		
GAM2434	KIAA0544	3'	TCCGCCTCCCGGGTTCAA 35117	AA	CAA
			TTGAACCT GAG TGGA		

	AACTTGGG CTC GCCT	
	CC C__	
GAM2434 KIAA0557	3' TCCACCTCCCAGGTTCAA 38212	AA CAA
	TTGAACCT GAG TGGA	
	AACTTGGA CTC ACCT	
	CC C__	
GAM2434 KIAA0563	5' CCTCTGCCTCCCGGGTTCAA 16841	AA _ AT
	TTGAACCT GAG CA GG	
	AACTTGGG CTC GT CC	
	CC C CT	
GAM2434 KIAA0594	3' TCCGCCTCCCGGGTTCAA 32390	AA CAA
	TTGAACCT GAG TGGA	
	AACTTGGG CTC GCCT	
	CC C__	
GAM2434 KIAA0599	3' TCCGCCTCCCAGGTTCAA 37859	AA CAA
	TTGAACCT GAG TGGA	
	AACTTGGA CTC GCCT	
	CC C__	
GAM2434 KIAA0650	3' GTCTTGAACCTCCTGGGTTCAA 42571	A CAAT
	TTGAACCTA GAG GGAC	
	AACTTGGGT CTC TCTG	
	C AAGT	
GAM2434 KIAA0663	5' TCCGCCTCCCGGGTTCAA 16814	AA CAA
	TTGAACCT GAG TGGA	
	AACTTGGG CTC GCCT	
	CC C__	
GAM2434 KIAA0676	3' GTCTGCCCTTGGGTTCAA 17395	A ATG
	TTGAACCTAAG GCA GAC	
	AACTTGGGTTC CGT CTG	
	C ____	
GAM2434 KIAA0720	3' CCTCTGCCTCCCGGGTTCAA 31232	AA _ AT
	TTGAACCT GAG CA GG	
	AACTTGGG CTC GT CC	
	CC C CT	
GAM2434 KIAA0841	3' TCCGCCTCCCAGGTTCAA 35363	AA CAA
	TTGAACCT GAG TGGA	
	AACTTGGA CTC GCCT	
	CC C__	
GAM2434 KIAA0889	3' TCCGCCTCCTGGGTTCAA 17680	A CAA
	TTGAACCTA GAG TGGA	

		AACTTGGGT CTC GCCT		
		C C__		
GAM2434	KIAA0924	3' TCCAACCTCTTGGGTTCAA 17067	CAA	
		TTGAACCTAAGAG TGGA		
		AACTTGGGTTCTC ACCT		
		A__		
GAM2434	KIAA1028	3' TCCACCTTCCAGGTTCAA 44164	AA CAA	
		TTGAACCT GAG TGGA		
		AACTTGGA TTC ACCT		
		CC C__		
GAM2434	KIAA1041	3' TCCGCCTCCCGGGTTCAA 17266	AA CAA	
		TTGAACCT GAG TGGA		
		AACTTGGG CTC GCCT		
		CC C__		
GAM2434	KIAA1054	3' TCCGCCTCCCAGGTTCAA 33957	AA CAA	
		TTGAACCT GAG TGGA		
		AACTTGGA CTC GCCT		
		CC C__		
GAM2434	KIAA1165	3' GTTTCTGGCTCTTAGACTCA 33478	AC AAT	
		TGA CTAAGAGC GGAC		
		ACT GATTCTCG TTTG		
		CA GTC		
GAM2434	KIAA1170	3' TCCGCCTCCCGGGTTCAA 34613	AA CAA	
		TTGAACCT GAG TGGA		
		AACTTGGG CTC GCCT		
		CC C__		
GAM2434	KIAA1185	3' CCTGTGTCTCCTGGGTTCAA 31369	A _ AT	
		TTGAACCTA GAG CA GG		
		AACTTGGGT CTC GT CC		
		C T GT		
GAM2434	KIAA1198	3' TCCAACCTCTCAGGTTCAA 31716	A CAA	
		TTGAACCT AGAG TGGA		
		AACTTGGA TCTT ACCT		
		C C__		
GAM2434	KIAA1198	3' TCTCTGCCTCCCAGGTTCAA 31718	AA _ AT	
		TTGAACCT GAG CA GGA		
		AACTTGGA CTC GT TCT		
		CC C C__		
GAM2434	KIAA1257	3' TCCGCCTCCCGGGTTCAA 31439	AA CAA	
		TTGAACCT GAG TGGA		

		AACTTGGG CTC GCCT CC C__	
GAM2434 KIAA1320	5'	CCTCTGCCTCCTGGGTTCAA 34356	A _ AT
		TTGAACCTA GAG CA GG 	
		AACTTGGGT CTC GT CC C C CT	
GAM2434 KIAA1373	3'	TCCACCTCCCAGGTTCAA 35128	AA CAA
		TTGAACCT GAG TGGA 	
		AACTTGGA CTC ACCT CC C__	
GAM2434 KIAA1467	3'	CCTTCGCCTCCTGGGTTCAA 35454	A _ AAT
		TTGAACCTA GAG C GG 	
		AACTTGGGT CTC G CC C C CTT	
GAM2434 KIAA1497	5'	CCTCTGCCTCCCAGGTTCAA 33527	AA _ AT
		TTGAACCT GAG CA GG 	
		AACTTGGA CTC GT CC CC C CT	
GAM2434 KIAA1571	3'	TCCACCTCCCGGGTTCAA 30566	AA CAA
		TTGAACCT GAG TGGA 	
		AACTTGGG CTC ACCT CC C__	
GAM2434 KIAA1615	3'	CCTCTGCCTCCCAGGTTCA 34082	AA _ AT
		TTGAACCT GAG CA GG 	
		GACTTGGA CTC GT CC CC C CT	
GAM2434 KIAA1615	3'	TCCACCTCCCAGGTTCAA 34088	AA CAA
		TTGAACCT GAG TGGA 	
		AACTTGGA CTC ACCT CC C__	
GAM2434 KIAA1655	3'	TCCGCCTCCCAGGTTCAA 33091	AA CAA
		TTGAACCT GAG TGGA 	
		AACTTGGA CTC GCCT CC C__	
GAM2434 KIAA1737	3'	TCCGCCTCCTGGGTTCAA 33448	A CAA
		TTGAACCTA GAG TGGA 	
		AACTTGGGT CTC GCCT C C__	
GAM2434 KIAA1784	3'	TCCGCCTCCCGGGTTCAA 32486	AA CAA
		TTGAACCT GAG TGGA 	

		AACTTGGG CTC GCCT		
		CC C__		
GAM2434	KIAA1829	3' CCTCTGCCTCCTGGGTTCAA 31031	A _ AT	
		TTGAACCTA GAG CA GG		
		AACTTGGGT CTC GT CC		
		C C CT		
GAM2434	KIAA1854	3' TGGAAGACTCTTGGGTCCAA 35537	A CAATGGA	
		TTG ACCTAAGAG CCA		
		AAC TGGGTTCTC GGT		
		C AGAA__		
GAM2434	KIAA1922	5' TCCGCCTCCCAGGTTCAA 36460	AA CAA	
		TTGAACCT GAG TGGA		
		AACTTGGA CTC GCCT		
		CC C__		
GAM2434	KIAA1971	3' TCCACCTCCCAGGTTCAA 36731	AA CAA	
		TTGAACCT GAG TGGA		
		AACTTGGA CTC ACCT		
		CC C__		
GAM2434	KIAA1987	5' TCCGCCTCCCAGGTTCAA 42500	AA CAA	
		TTGAACCT GAG TGGA		
		AACTTGGA CTC GCCT		
		CC C__		
GAM2434	KLK7	3' TCCGCCTCCTGGGTTCAA 29274	A CAA	
		TTGAACCTA GAG TGGA		
		AACTTGGGT CTC GCCT		
		C C__		
GAM2434	KLK7	3' TCCGCCTCCTGGGTTCAA 11477	A CAA	
		TTGAACCTA GAG TGGA		
		AACTTGGGT CTC GCCT		
		C C__		
GAM2434	LAMP3	3' TCCGCCTCCCGGGTTCAA 29920	AA CAA	
		TTGAACCT GAG TGGA		
		AACTTGGG CTC GCCT		
		CC C__		
GAM2434	LIECG3	3' TCCGACTCCTGGGTTCAA 42248	A CAA	
		TTGAACCTA GAG TGGA		
		AACTTGGGT CTC GCCT		
		C A__		
GAM2434	LY75	3' TCCGCCTCCCAGGTTCAA 8151	AA CAA	
		TTGAACCT GAG TGGA		

			AACTTGGA CTC GCCT		
			CC C__		
GAM2434	MCLC	3'	TCCACCTCCCAGGTTCAA 17493	AA	CAA
			TTGAACCT GAG TGGA		
			AACTTGGA CTC ACCT		
			CC C__		
GAM2434	MGC1842	3'	TCCGCCTCCTGGGTTCAA 32689	A	CAA
			TTGAACCTA GAG TGGA		
			AACTTGGGT CTC GCCT		
			C C__		
GAM2434	MGC4638	3'	TCCGTCTCCTGGGTTCAA 25559	A	CA
			TTGAACCTA GAG ATGGA		
			AACTTGGGT CTC TGCCT		
			C _		
GAM2434	MGC5149	3'	CCTCTGCCTCCCAGGTTCAA 35783	AA	_ AT
			TTGAACCT GAG CA GG		
			AACTTGGA CTC GT CC		
			CC C CT		
GAM2434	MLZE	5'	CCTCTGCCTCCCGGGTTCAA 25394	AA	_ AT
			TTGAACCT GAG CA GG		
			AACTTGGG CTC GT CC		
			CC C CT		
GAM2434	MMPL1	3'	GTCTTGAACCTTTGGGCTCAA 10349	A	CAAT
			TTGA CCTAAGAG GGAC		
			AACT GGGTTCTC TCTG		
			C AAGT		
GAM2434	MOCS3	3'	TCCGCCTCCCAGGTTCAA 15831	AA	CAA
			TTGAACCT GAG TGGA		
			AACTTGGA CTC GCCT		
			CC C__		
GAM2434	MRPL44	3'	TCCACCTCACAGGTTCAA 23227	AA	CAA
			TTGAACCT GAG TGGA		
			AACTTGGA CTC ACCT		
			CA C__		
GAM2434	MRPS27	3'	TCCGACTCCCAGGTTCAA 17476	AA	CAA
			TTGAACCT GAG TGGA		
			AACTTGGA CTC GCCT		
			CC A__		
GAM2434	NDP52	3'	CCTCTGCCTCCCAGGTTCAA 12443	AA	_ AT
			TTGAACCT GAG CA GG		

			AACTTGGA CTC GT CC		
			CC C CT		
GAM2434	NDUFC2	3'	TCCACCTCCTGGGTTCAA 10895	A	CAA
			TTGAACCTA GAG TGGA		
			AACTTGGGT CTC ACCT		
			C C__		
GAM2434	NINJ2	3'	TCCGCCTCCCAGGTTCAA 18605	AA	CAA
			TTGAACCT GAG TGGA		
			AACTTGGA CTC GCCT		
			CC C__		
GAM2434	Nup43	3'	TCCACCTCCCGGGTTCAA 23936	AA	CAA
			TTGAACCT GAG TGGA		
			AACTTGGG CTC ACCT		
			CC C__		
GAM2434	OSBPL2	3'	TCCGCCTCCCGGGTTCAA 16852	AA	CAA
			TTGAACCT GAG TGGA		
			AACTTGGG CTC GCCT		
			CC C__		
GAM2434	OSBPL2	3'	TCCGCCTCCCGGGTTCAA 29320	AA	CAA
			TTGAACCT GAG TGGA		
			AACTTGGG CTC GCCT		
			CC C__		
GAM2434	PELI1	5'	CCTCTGCCTCCAGGTTCAA 21816	A_	A AT
			TTGAACCT AG GCA GG		
			AACTTGGA TC CGT CC		
			CC _ CT		
GAM2434	PRO0365	5'	CCTCTGTCTCCCAGGTTCAAG 15386	AA	_ AT
			TTGAACCT GAG CA GG		
			GACTTGGA CTC GT CC		
			CC T CT		
GAM2434	PRO1992	5'	CCTCTGCCTCCTGGGTTCAA 15333	A	_ AT
			TTGAACCTA GAG CA GG		
			AACTTGGGT CTC GT CC		
			C C CT		
GAM2434	PRO2955	3'	CCTCTGCCTCCCGGGTTCAA 20621	AA	_ AT
			TTGAACCT GAG CA GG		
			AACTTGGG CTC GT CC		
			CC C CT		
GAM2434	PSTPIP2	3'	CCTCTGCCTCCCGGGTTCAA 23680	AA	_ AT
			TTGAACCT GAG CA GG		

			AACTTGGG CTC GT CC		
			CC C CT		
GAM2434	RAB33B	3'	TCCGCCTCCCAGGTTCAA	25331	AA CAA
			TTGAACCT GAG TGGA		
			AACTTGGA CTC GCCT		
			CC C__		
GAM2434	RAI	5'	TCCGCCTCCTGGGTTCAA	13472	A CAA
			TTGAACCTA GAG TGGA		
			AACTTGGGT CTC GCCT		
			C C__		
GAM2434	RES4-25	3'	TCCACCTCCTGGGTTCAA	32287	A CAA
			TTGAACCTA GAG TGGA		
			AACTTGGGT CTC ACCT		
			C C__		
GAM2434	SEC24A	3'	TTCTTGTTCTTAAATTCAA	40235	CC T
			TTGAA TAAGAGCAA GGA		
			AACTT ATTCTTGTT CTT		
			AA _		
GAM2434	SERF1B	3'	CCTCTGCCTCCTGGGTTCAA	23258	A _ AT
			TTGAACCTA GAG CA GG		
			AACTTGGGT CTC GT CC		
			C C CT		
GAM2434	SERF1B	3'	TCCGCCTCCCGGGTTCAA	23259	AA CAA
			TTGAACCT GAG TGGA		
			AACTTGGG CTC GCCT		
			CC C__		
GAM2434	SLC16A4	3'	TCCGCCTCCTGGGTTCAA	11047	A CAA
			TTGAACCTA GAG TGGA		
			AACTTGGGT CTC GCCT		
			C C__		
GAM2434	STAF65(gamma)	3'	CCTCTGCCTCCCAGGTTCAA	16923	AA _ AT
			TTGAACCT GAG CA GG		
			AACTTGGA CTC GT CC		
			CC C CT		
GAM2434	TRIM6	3'	CCTCTGCCTCCTGGGTTCAA	27712	A _ AT
			TTGAACCTA GAG CA GG		
			AACTTGGGT CTC GT CC		
			C C CT		
GAM2434	TU12B1-TY	3'	CCTCTGCCTCCCGGGTTCAA	18646	AA _ AT
			TTGAACCT GAG CA GG		

		AACTTGGG CTC GT CC	
		CC C CT	
GAM2434	TU12B1-TY 3'	CTCTTGCCCTCCCAGGTTCAA 18647	AA _ T
		TTGAACCT GAG CAA GG	
		AACTTGGA CTC GTT TC	
		CC C C	
GAM2434	TU12B1-TY 3'	TCCGCCTCCTGGGTTCAA 18651	A CAA
		TTGAACCTA GAG TGGA	
		AACTTGGGT CTC GCCT	
		C C__	
GAM2434	USP22 3'	TCCACCTCCTGGGTTCAA 33754	A CAA
		TTGAACCTA GAG TGGA	
		AACTTGGGT CTC ACCT	
		C C__	
GAM2434	VDU1 3'	TCCACCTCCTGGGTTCAA 17382	A CAA
		TTGAACCTA GAG TGGA	
		AACTTGGGT CTC ACCT	
		C C__	
GAM2434	VPS33A 3'	TCCACCTCCTAGGTTCAA 23232	A CAA
		TTGAACCTA GAG TGGA	
		AACTTGGAT CTC ACCT	
		C C__	
GAM2434	WBSCR20A 5'	CCTCTGCCTCCTGGGTTCAA 25859	A _ AT
		TTGAACCTA GAG CA GG	
		AACTTGGGT CTC GT CC	
		C C CT	
GAM2434	WBSCR23 3'	TCCGCCTCTCAGGTTCAA 24641	A CAA
		TTGAACCT AGAG TGGA	
		AACTTGGA TCTC GCCT	
		C C__	
GAM2434	ZNF185 3'	TCCTCTGCTCAGGTTTCAG 14004	AA AT
		TTGAACCT GAGCA GGA	
		GACTTGGA CTCGT CCT	
		_ CT	
GAM2434	ZNF338 3'	GTCCGCCTCCCAGGTTCAA 22633	AA CAA
		TTGAACCT GAG TGGAC	
		AACTTGGA CTC GCCTG	
		CC C__	
GAM2434	ZTL1 3'	CCTCTGCCTCCCGGTTCAA 23491	AA _ AT
		TTGAACCT GAG CA GG	

	AACTTGGG CTC GT CC	
	CC C CT	
GAM2434 LOC112817 3'	TGATCTCGCCTCCTGGGTTCAA 28782	A CAAT C
	TTGAACCTA GAG GGA CA	
	AACTTGGGT CTC TCT GT	
	C CGC_ A	
GAM2434 LOC113675 5'	TCCGCCTCCCGGGTTCAA 28797	AA CAA
	TTGAACCT GAG TGGA	
	AACTTGGG CTC GCCT	
	CC C__	
GAM2434 LOC115219 5'	TCCGCCTCCTGGGTTCAA 36282	A CAA
	TTGAACCTA GAG TGGA	
	AACTTGGGT CTC GCCT	
	C C__	
GAM2434 LOC120114 3'	TCCACCTCCTGGGTTCAA 37213	A CAA
	TTGAACCTA GAG TGGA	
	AACTTGGGT CTC ACCT	
	C C__	
GAM2434 LOC126364 3'	TCCGCCTCCTGGGTTCAA 37273	A CAA
	TTGAACCTA GAG TGGA	
	AACTTGGGT CTC GCCT	
	C C__	
GAM2434 LOC126661 3'	TCCGCCTCCCAGGTTCAA 36856	AA CAA
	TTGAACCT GAG TGGA	
	AACTTGA CTC GCCT	
	CC C__	
GAM2434 LOC126669 3'	CATCTGACTCCTGGGTTCAA 37157	A _ _
	TTGAACCTA GAG CA ATG	
	AACTTGGGT CTC GT TAC	
	C A C	
GAM2434 LOC132625 3'	TCCACCTCCCGGGTTCAA 37374	AA CAA
	TTGAACCT GAG TGGA	
	AACTTGGG CTC ACCT	
	CC C__	
GAM2434 LOC133686 3'	TCCATCTCCCAGGTTCAA 37054	AA CA
	TTGAACCT GAG ATGGA	
	AACTTGA CTC TACCT	
	CC _	
GAM2434 LOC135293 3'	CCTCTGCCTCCCAGGTTCAA 37492	AA _ AT
	TTGAACCT GAG CA GG	

	AACTTGGA CTC GT CC	
	CC C CT	
GAM2434 LOC135763 3'	TCCGCCTCCTGGGTTCAA 28884	A CAA
	TTGAACCTA GAG TGGA	
	AACTTGGGT CTC GCCT	
	C C__	
GAM2434 LOC135818 3'	TCCGCCTCCCAGGTTCAA 37095	AA CAA
	TTGAACCT GAG TGGA	
	AACTTGGA CTC GCCT	
	CC C__	
GAM2434 LOC143241 5'	CCTCTGCCTCCCGGGTTCAA 29035	AA _ AT
	TTGAACCT GAG CA GG	
	AACTTGGG CTC GT CC	
	CC C CT	
GAM2434 LOC145757 5'	CCTCTGCCTCCCAGGTTCAA 37973	AA _ AT
	TTGAACCT GAG CA GG	
	AACTTGGA CTC GT CC	
	CC C CT	
GAM2434 LOC146229 3'	TCCACCTCCCGGGTTCAA 38116	AA CAA
	TTGAACCT GAG TGGA	
	AACTTGGG CTC ACCT	
	CC C__	
GAM2434 LOC146336 3'	TGGCCTTGAACCTTTGGGCTCA 38133	A _ T A
A	TTGA CCTAAGAG CAA GG CCA	
	AACT GGGTTCTC GTT CC GGT	
	C AA _ _	
GAM2434 LOC146346 5'	CTTCTGCCTCCTAGGTTCAA 38136	A _ AT
	TTGAACCTA GAG CA GG	
	AACTTGGAT CTC GT TC	
	C C CT	
GAM2434 LOC146455 3'	TCTCTGCCTCTCGGGTTCAA 38159	TA _ AT
	TTGAACC AGAG CA GGA	
	AACTTGG TCTC GT TCT	
	GC C C__	
GAM2434 LOC146784 5'	TCCACCTCCCAGGTTCAA 38240	AA CAA
	TTGAACCT GAG TGGA	
	AACTTGGA CTC ACCT	
	CC C__	
GAM2434 LOC146895 5'	TGGCCCAGCTCTTAGGCCAA 40760	AA AA A
	TTG CCTAAGAGC TGG CCA	

		AAC GGATTCTCG ACC GGT	
		C_ _ C	
GAM2434	LOC146909 3'	TCCGCCTCCTGGGTTCAA 38268	A CAA
		TTGAACCTA GAG TGGA	
		AACTTGGGT CTC GCCT	
		C C_	
GAM2434	LOC146952 5'	TCCACCTCTCAGGTTCAA 40769	A CAA
		TTGAACCT AGAG TGGA	
		AACTTGGA TCTC ACCT	
		C C_	
GAM2434	LOC147071 5'	CCTCTGCCTCCCAGGTTCAA 36135	AA _ AT
		TTGAACCT GAG CA GG	
		AACTTGGA CTC GT CC	
		CC C CT	
GAM2434	LOC147093 3'	TGGTTTTCTCTTAGGTCCAA 40806	A CAAT
		TTG ACCTAAGAG GGACCA	
		AAC TGGATTCTC TTTGGT	
		C T_	
GAM2434	LOC147429 5'	TCCATCTCCCGGGTTCAA 38338	AA CA
		TTGAACCT GAG ATGGA	
		AACTTGGG CTC TACCT	
		CC _	
GAM2434	LOC147660 3'	TCCGCCTCCTGGGTTCAA 38350	A CAA
		TTGAACCTA GAG TGGA	
		AACTTGGGT CTC GCCT	
		C C_	
GAM2434	LOC147817 3'	TCCACCTCCCAGGTTCAA 38389	AA CAA
		TTGAACCT GAG TGGA	
		AACTTGGA CTC ACCT	
		CC C_	
GAM2434	LOC148137 3'	TCCACCTCCCGGGTTCAA 29519	AA CAA
		TTGAACCT GAG TGGA	
		AACTTGGG CTC ACCT	
		CC C_	
GAM2434	LOC148189 5'	TCCACCTCCTGGGTTCAA 38486	A CAA
		TTGAACCTA GAG TGGA	
		AACTTGGGT CTC ACCT	
		C C_	
GAM2434	LOC149506 3'	CCTCTGCCTCCTGGGTTCAA 41006	A _ AT
		TTGAACCTA GAG CA GG	

	AACTTGGGT CTC GT CC	
	C C CT	
GAM2434 LOC149577 3'	TCCACCTCCCAGGTTCAA 41025	AA CAA
	TTGAACCT GAG TGGA	
	AACTTGGA CTC ACCT	
	CC C__	
GAM2434 LOC149703 5'	TCTACCTCCCAGGTTCAA 41064	AA CAA
	TTGAACCT GAG TGGA	
	AACTTGGA CTC ATCT	
	CC C__	
GAM2434 LOC150397 3'	TCCGCCTCCCGGGTTCAA 38962	AA CAA
	TTGAACCT GAG TGGA	
	AACTTGGG CTC GCCT	
	CC C__	
GAM2434 LOC150960 3'	TCCGCCTCCCAGGTTCAA 39031	AA CAA
	TTGAACCT GAG TGGA	
	AACTTGGA CTC GCCT	
	CC C__	
GAM2434 LOC151057 3'	CCTCTGCCTCCTGGGTTCAA 41293	A _ AT
	TTGAACCTA GAG CA GG	
	AACTTGGGT CTC GT CC	
	C C CT	
GAM2434 LOC151475 5'	CCTCTGCCTCCTGGGTTCAA 41354	A _ AT
	TTGAACCTA GAG CA GG	
	AACTTGGGT CTC GT CC	
	C C CT	
GAM2434 LOC151475 5'	TCCACCTCCCAGGTTCAA 41360	AA CAA
	TTGAACCT GAG TGGA	
	AACTTGGA CTC ACCT	
	CC C__	
GAM2434 LOC151701 3'	CCATGCTCAGGTTTAA 41385	AA A
	TTGAACCT GAGCA TGG	
	AATTTGGA CTCGT ACC	
	— —	
GAM2434 LOC151826 3'	TCCGCCTCCTGAGGTTCAA 39166	AA_ CAA
	TTGAACCT GAG TGGA	
	AACTTGGA CTC GCCT	
	GTC C__	
GAM2434 LOC152343 3'	TCCGCCTCCCAGGTTCAA 39264	AA CAA
	TTGAACCT GAG TGGA	

	AACTTGGA CTC GCCT CC C__	
GAM2434 LOC152445 3'	CCTCTGCCTCCTGGGTTCAA 41509 TTGAACCTA GAG CA GG AACTTGGGT CTC GT CC C C CT	A _ AT
GAM2434 LOC152445 3'	TGGTCTTGAACCTCTTGGGCTCA 41513 A TTGA CCTAAGAG GGACCA AACT GGGTTCTC TCTGGT C AAGT	A CAAT
GAM2434 LOC152719 5'	CCTCTGCCTCCCGGGTTCAA 41543 TTGAACCT GAG CA GG AACTTGGG CTC GT CC CC C CT	AA _ AT
GAM2434 LOC152794 5'	TCTACCTCCCAGGTTCAA 39321 TTGAACCT GAG TGGA AACTTGGA CTC ATCT CC C__	AA CAA
GAM2434 LOC152925 3'	CCTCTGCCTCCCAGGTTCAA 39331 TTGAACCT GAG CA GG AACTTGGA CTC GT CC CC C CT	AA _ AT
GAM2434 LOC153077 3'	TCCGCCTCCTGGGTTCAA 41570 TTGAACCTA GAG TGGA AACTTGGGT CTC GCCT C C__	A CAA
GAM2434 LOC153883 5'	TCCACCCTGCAGGTTCAA 39431 TTGAACCT GCA TGGA AACTTGGA CGT ACCT ____ CCC	AAGA A__
GAM2434 LOC154282 5'	TCCACCTCCCAGGTTCAA 41701 TTGAACCT GAG TGGA AACTTGGA CTC ACCT CC C__	AA CAA
GAM2434 LOC154726 5'	TCCGCCTCCCAGGTTCAA 39478 TTGAACCT GAG TGGA AACTTGGA CTC GCCT CC C__	AA CAA
GAM2434 LOC154877 3'	TCTACCTCCTGGGTTCAA 41746 TTGAACCTA GAG TGGA 	A CAA

	AACTTGGGT CTC ATCT	
	C C__	
GAM2434 LOC154930 3'	CCTCTGCCTTCCAGGTTCAA 39505	__ A AT
	TTGAACCT AAG GCA GG	
	AACTTGGA TTC CGT CC	
	CC _ CT	
GAM2434 LOC157798 5'	TCCGCCTCCCAGGTTCAA 41852	AA CAA
	TTGAACCT GAG TGGA	
	AACTTGGA CTC GCCT	
	CC C__	
GAM2434 LOC158549 5'	TCCGCCTCCTGGGTTCAA 42011	A CAA
	TTGAACCTA GAG TGGA	
	AACTTGGGT CTC GCCT	
	C C__	
GAM2434 LOC158668 3'	CCTCTGCCTCCCGGGTTCAA 34379	AA _ AT
	TTGAACCT GAG CA GG	
	AACTTGGG CTC GT CC	
	CC C CT	
GAM2434 LOC158865 5'	CCTCTGCCTCCTGGGTTCAA 42038	A _ AT
	TTGAACCTA GAG CA GG	
	AACTTGGGT CTC GT CC	
	C C CT	
GAM2434 LOC160646 3'	TCCGCCTCCCAGGTTCAA 40005	AA CAA
	TTGAACCT GAG TGGA	
	AACTTGGA CTC GCCT	
	CC C__	
GAM2434 LOC161829 3'	TCCGCCTCCCGGGTTCAA 40040	AA CAA
	TTGAACCT GAG TGGA	
	AACTTGGG CTC GCCT	
	CC C__	
GAM2434 LOC169611 3'	TCCGCCTCCCGGGTTCAA 40287	AA CAA
	TTGAACCT GAG TGGA	
	AACTTGGG CTC GCCT	
	CC C__	
GAM2434 LOC196047 5'	TCCGCCTCCCAGGTTCAA 43147	AA CAA
	TTGAACCT GAG TGGA	
	AACTTGGA CTC GCCT	
	CC C__	
GAM2434 LOC196264 3'	CCTCTGCCTCCTGGGTTCAA 42334	A _ AT
	TTGAACCTA GAG CA GG	

	AACTTGGGT CTC GT CC	
	C C CT	
GAM2434 LOC196411 3'	TCCGCCTCCCGGGTTCAA 42366	AA CAA
	TTGAACCT GAG TGGA	
	AACTTGGG CTC GCCT	
	CC C__	
GAM2434 LOC196529 3'	TCCACCTCCCGGGTTCAA 42411	AA CAA
	TTGAACCT GAG TGGA	
	AACTTGGG CTC ACCT	
	CC C__	
GAM2434 LOC199786 3'	TCCGCCTCCCGGGTTCAA 42621	AA CAA
	TTGAACCT GAG TGGA	
	AACTTGGG CTC GCCT	
	CC C__	
GAM2434 LOC200169 5'	CCTCTGCCTCCTGGGTTCAA 43284	A _ AT
	TTGAACCTA GAG CA GG	
	AACTTGGGT CTC GT CC	
	C C CT	
GAM2434 LOC200310 3'	CCTCTGCCTCCCAGGTTTAA 32706	AA _ AT
	TTGAACCT GAG CA GG	
	AATTTGGA CTC GT CC	
	CC C CT	
GAM2434 LOC200314 3'	TCCACCTCCCGGGTTCAA 43295	AA CAA
	TTGAACCT GAG TGGA	
	AACTTGGG CTC ACCT	
	CC C__	
GAM2434 LOC200845 5'	TCCGCCTCTCGGGTTCAA 42864	TA CAA
	TTGAACC AGAG TGGA	
	AACTTGG TCTC GCCT	
	GC C__	
GAM2434 LOC200860 3'	TCCACCTCCCAGGTTCAA 43357	AA CAA
	TTGAACCT GAG TGGA	
	AACTTGGA CTC ACCT	
	CC C__	
GAM2434 LOC201173 5'	CCTCTGCCTCCCAGGTTCAA 42214	AA _ AT
	TTGAACCT GAG CA GG	
	AACTTGGA CTC GT CC	
	CC C CT	
GAM2434 LOC201220 5'	CCTCTGCCTCCCAGGTTCAA 42221	AA _ AT
	TTGAACCT GAG CA GG	

	AACTTGGA CTC GT CC	
	CC C CT	
GAM2434 LOC201294 3'	TCCGCCTCCTGGGTTCAA 42569	A CAA
	TTGAACCTA GAG TGGA	
	AACTTGGGT CTC GCCT	
	C C__	
GAM2434 LOC201411 3'	CCTCTGCCTCCCAGGTTCAA 31527	AA _ AT
	TTGAACCT GAG CA GG	
	AACTTGGA CTC GT CC	
	CC C CT	
GAM2434 LOC201696 3'	CCACTGCCTCCCAGGTTCAA 31621	AA _ A
	TTGAACCT GAG CA TGG	
	AACTTGGA CTC GT ACC	
	CC C C	
GAM2434 LOC201702 5'	CCTCTGACTCCTGGGTTCAA 42900	A _ AT
	TTGAACCTA GAG CA GG	
	AACTTGGGT CTC GT CC	
	C A CT	
GAM2434 LOC202025 3'	TCCGCCTCCCAGGTTCAA 43405	AA CAA
	TTGAACCT GAG TGGA	
	AACTTGGA CTC GCCT	
	CC C__	
GAM2434 LOC202934 3'	CCTCTGCCTCCCAGGTTCAA 43456	AA _ AT
	TTGAACCT GAG CA GG	
	AACTTGGA CTC GT CC	
	CC C CT	
GAM2434 LOC203297 5'	CCTCTGCCTCCCAGGTTCAA 37135	AA _ AT
	TTGAACCT GAG CA GG	
	AACTTGGA CTC GT CC	
	CC C CT	
GAM2434 LOC203339 3'	CCACTGCCTCCCAGGTTCAA 43524	AA _ A
	TTGAACCT GAG CA TGG	
	AACTTGGA CTC GT ACC	
	CC C C	
GAM2434 LOC203350 3'	TCCGCCTCCCAGGTTCAA 43538	AA CAA
	TTGAACCT GAG TGGA	
	AACTTGGA CTC GCCT	
	CC C__	
GAM2434 LOC203378 3'	CCTCTGCCTCCCGGTTCAA 43551	AA _ AT
	TTGAACCT GAG CA GG	

	AACTTGGG CTC GT CC	
	CC C CT	
GAM2434 LOC219673 5'	CCTCTGCCTCCCAGGTTCAA 44692	AA _ AT
	TTGAACCT GAG CA GG	
	AACTTGGA CTC GT CC	
	CC C CT	
GAM2434 LOC220662 3'	TCCACTTCCTAGGTTCAA 43825	A CAA
	TTGAACCTA GAG TGGA	
	AACTTGAT CTT ACCT	
	C C__	
GAM2434 LOC221296 3'	TCCACCTCCCGGGTTCAA 44171	AA CAA
	TTGAACCT GAG TGGA	
	AACTTGGG CTC ACCT	
	CC C__	
GAM2434 LOC221773 3'	TCCGCCTCCTGGGTTCAA 43767	A CAA
	TTGAACCTA GAG TGGA	
	AACTTGGGT CTC GCCT	
	C C__	
GAM2434 LOC222031 3'	TCCGCCTCCTGGGTTCAA 45137	A CAA
	TTGAACCTA GAG TGGA	
	AACTTGGGT CTC GCCT	
	C C__	
GAM2434 LOC222070 5'	CCTCTGCCTCCCAGGTTCAA 45180	AA _ AT
	TTGAACCT GAG CA GG	
	AACTTGGA CTC GT CC	
	CC C CT	
GAM2434 LOC245771 5'	CCGTCTCCCGGGTTCAA 44634	AA CA
	TTGAACCT GAG ATGG	
	AACTTGGG CTC TGCC	
	CC _	
GAM2434 LOC253664 3'	CCTCTGCCTCCCGGGTTCAA 45448	AA _ AT
	TTGAACCT GAG CA GG	
	AACTTGGG CTC GT CC	
	CC C CT	
GAM2434 LOC253666 5'	TCCGCCTCCCAGGTTCAA 45569	AA CAA
	TTGAACCT GAG TGGA	
	AACTTGGA CTC GCCT	
	CC C__	
GAM2434 LOC254778 3'	TGGTCTCAAACCTCCTGGGTTCA 45979	A CAAT
A	TTGAACCTA GAG GGACCA	

	AACTTGGGT CTC TCTGGT	
	C AAAC	
GAM2434 LOC255177 3'	TCCACCTCCCAGGTTCAA 46203	AA CAA
	TTGAACCT GAG TGGA	
	AACTTGGA CTC ACCT	
	CC C__	
GAM2434 LOC255308 3'	TCTCTGCCTCCCAGGTTCAA 45357	AA _ AT
	TTGAACCT GAG CA GGA	
	AACTTGGA CTC GT TCT	
	CC C C_	
GAM2434 LOC255919 3'	CCTCTGCCTCCCAGGTTCAA 45555	AA _ AT
	TTGAACCT GAG CA GG	
	AACTTGGA CTC GT CC	
	CC C CT	
GAM2434 LOC256360 5'	TCCGCCTCCCAGGTTCAA 46176	AA CAA
	TTGAACCT GAG TGGA	
	AACTTGGA CTC GCCT	
	CC C__	
GAM2434 LOC257463 3'	TGGTCTTGAACCTCCTGGGTTCA 35212	A CAAT
A	TTGAACCTA GAG GGACCA	
	AACTTGGGT CTC TCTGGT	
	C AAGT	
GAM2434 LOC51200 3'	CCTCTGCCTCCTGGGTTCAA 18481	A _ AT
	TTGAACCTA GAG CA GG	
	AACTTGGGT CTC GT CC	
	C C CT	
GAM2434 LOC57107 3'	TCCGCCTCCTGGGTTCAA 21653	A CAA
	TTGAACCTA GAG TGGA	
	AACTTGGGT CTC GCCT	
	C C__	
GAM2434 LOC57146 3'	TCCAACCTCCCAGGTTCAA 21680	AA CAA
	TTGAACCT GAG TGGA	
	AACTTGGA CTC ACCT	
	CC A__	
GAM2434 LOC63929 3'	GGCCCACATGCACCTCAGGTTC 22640	A A_ A_ A
AA	TTGAACCT AG GCA TGG CC	
	AACTTGGA TC CGT ACC GG	
	C CA AC C	
GAM2434 LOC89932 3'	TCCACCTCCTGGGTTCAA 30494	A CAA
	TTGAACCTA GAG TGGA	

	AACTTGGGT CTC ACCT	
	C C__	
GAM2434 LOC90288 3'	TCCACCTCCCGGGTTCAA 31116	AA CAA
	TTGAACCT GAG TGGA	
	AACTTGGG CTC ACCT	
	CC C__	
GAM2434 LOC90333 5'	TCCACTTCCCAGGTTCAA 31226	AA CAA
	TTGAACCT GAG TGGA	
	AACTTGGA CTT ACCT	
	CC C__	
GAM2434 LOC90371 5'	TCCACCTCCCAGGTTCAA 31323	AA CAA
	TTGAACCT GAG TGGA	
	AACTTGGA CTC ACCT	
	CC C__	
GAM2434 LOC90408 5'	TCTACCTCCTGGGTTCAA 31399	A CAA
	TTGAACCTA GAG TGGA	
	AACTTGGGT CTC ATCT	
	C C__	
GAM2434 LOC90485 3'	TCCGCCTCCCGGGTTCAA 31555	AA CAA
	TTGAACCT GAG TGGA	
	AACTTGGG CTC GCCT	
	CC C__	
GAM2434 LOC91115 3'	TCCGCCTCCCAGGTTCAA 32402	AA CAA
	TTGAACCT GAG TGGA	
	AACTTGGA CTC GCCT	
	CC C__	
GAM2434 LOC91308 3'	TCCACCTCCCGGGTTCAA 32658	AA CAA
	TTGAACCT GAG TGGA	
	AACTTGGG CTC ACCT	
	CC C__	
GAM2434 LOC92267 3'	TCCACCTCCCGGGTTCAA 34058	AA CAA
	TTGAACCT GAG TGGA	
	AACTTGGG CTC ACCT	
	CC C__	
GAM2434 LOC92303 3'	CCTCTGCCCTCCAGGTTCAA 34136	A_ A AT
	TTGAACCT AG GCA GG	
	AACTTGGA TC CGT CC	
	CC C CT	
GAM2434 LOC92689 3'	TCCGCCTCCTGGGTTCAA 34784	A CAA
	TTGAACCTA GAG TGGA	

		AACTTGGGT CTC GCCT	
		C C__	
GAM2434	LOC92697 5'	TCCGCCTCCCGGGTTCAA 34805	AA CAA
		TTGAACCT GAG TGA	
		AACTTGGG CTC GCCT	
		CC C__	
GAM2434	LOC93132 5'	TCCGCCTCCCGGGTTCAA 35410	AA CAA
		TTGAACCT GAG TGA	
		AACTTGGG CTC GCCT	
		CC C__	
GAM2435	PARK2 3'	ACCACTATCTTTTGTCTA 15150	TGAC A
		TGGAACAAA GATA TGGT	
		ATCTTGTTT CTAT ACCA	
		T__ C	
GAM2435	PARK2 3'	ACCACTATCTTTTGTCTA 10903	TGAC A
		TGGAACAAA GATA TGGT	
		ATCTTGTTT CTAT ACCA	
		T__ C	
GAM2435	PARK2 3'	ACCACTATCTTTTGTCTA 15157	TGAC A
		TGGAACAAA GATA TGGT	
		ATCTTGTTT CTAT ACCA	
		T__ C	
GAM2435	XT3 3'	ACCATTCCCATTGTTCTATT 21438	A ACGAT
		AATGGAAC AATG AATGGT	
		TTATCTTG TTAC TTACCA	
		C CC__	
GAM2435	DKFZP564G092 5'	ACCATTATCTCCTATTCC 17875	CAAAT C
		GGAA GA GATAATGGT	
		CCTT CT CTATTACCA	
		ATC__ _	
GAM2435	KIAA1271 3'	CCACCCATCTGTTCCGTT 34467	A ACGATAA
		AATGGAACA ATG TGG	
		TTGCCTTGT TAC ACC	
		C CC__	
GAM2435	LOC150333 5'	ACCATTATTCTCATCACCAT 41195	AACAA C
		ATGG ATGA GATAATGGT	
		TACC TACT TTATTACCA	
		AC__ C	
GAM2435	LOC254778 3'	TGTCATCATCAATTCCATT 45980	CAA C
		AATGGAA ATGA GATA	

		TTACCTT TACT CTGT	
		AAC A	
GAM2436 GRM1	3'	TCTGCTATTTGCTGTTGTGTAA 6499	T TAT A
		TTGCACAACA GT ATA CAGA	
		AATGTGTTGT CG TAT GTCT	
		_ TT_ C	
GAM2436 IHPK3	5'	TCTGCCGCCATGGTTGTGCAA 27660	_ TTATATAA
		TTGCACAAC ATG CAGA	
		AACGTGTTG TAC GTCT	
		G CGCC__	
GAM2436 PITX2	3'	CTGTGTATAACATTTTCGTACAA 5868	C AAC A
		TTG AC ATGTTATATA CAG	
		AAC TG TACAATATGT GTC	
		A CTT _	
GAM2436 CEP3	3'	CTGTTATGCCCTGTTTGCAA 13157	C TGTTA
		TTGCA AACA TATAACAG	
		AACGT TTGT GTATTGTC	
		_ CCC__	
GAM2436 CNOT7	3'	ATATAGCACGTTGTGCAA 15000	A
		TTGCACAAC TGTTATAT	
		AACGTGTTG ACGATATA	
		C	
GAM2436 FLJ14440	3'	ATATAACATGTTTGCAA 26531	C
		TTGCA AACATGTTATAT	
		AACGT TTGTACAATATA	
		_	
GAM2436 GT650	3'	TCTGTTATCAGCAATGTGCAA 27432	ACA AT
		TTGCACA TGTT ATAACAGA	
		AACGTGT ACGA TATTGTCT	
		A_ C_	
GAM2436 KIAA0332	3'	TCTGTCATTGTTTTATATTGTG 31422	C TT TA_
TAA		TTGCACAA ATG ATA ACAGA	
		AATGTGTT TAT TGT TGTCT	
		A TT TAC	
GAM2436 KIAA1458	3'	CTGTTATATACTCAGTGCAA 34205	AACA T_
		TTGCAC TG TATATAACAG	
		AACGTG AC ATATATTGTC	
		__ TC	
GAM2436 KIAA1813	5'	TCTGCCACCATGGCCATTGTGC 34814	CAT ATAA_
AG		TTGCACAA GTTAT CAGA	

			GACGTGTT CGGTA GTCT		
			AC_ CCACC		
GAM2436	MGC16703	3'	CTGCTGCATGTTGTACAG 36180	C	TATATAA
			TTG ACAACATGT CAG		
			GAC TGTTGTACG GTC		
			A TC_____		
GAM2436	PRO0255	3'	CTGCTATGTTTTGTATGCAG 15383	C	TGTT A
			TTGCA AACA ATATA CAG		
			GACGT TTGT TGTAT GTC		
			A TT_ C		
GAM2436	LOC162239	3'	TCTGTTACCAAAATATTGTGTA 40054	C	GTTATA
	A		TTGCACAA AT TAACAGA		
			AATGTGTT TA ATTGTCT		
			A AAACC_		
GAM2436	LOC254848	5'	TCTGTTCTAAACAGATTGTGCA 46383	CA	A T
	A		TTGCACAA TGTT TA AACAGA		
			AACGTGTT ACAA AT TTGTCT		
			AG _ C		
GAM2436	LOC257443	3'	CTGTTATATACTCAGTGCAA 45873	AACA	T_
			TTGCAC TG TATATAACAG		
			AACGTG AC ATATATTGTC		
			_____ TC		
GAM2437	FLJ23189	3'	TATGCTTATTTGGTACTTTCAC 24658	T TT	A
			GTGA AAGT CCAAATAA CATA		
			CACT TTCA GGTTTATT GTAT		
			_ T_ C		
GAM2437	PC4	3'	TATGCTTATTTGGAAAGTCA 13540	AAG	A
			TGAT TTTCCAAATAA CATA		
			ACTG AAAGGTTTATT GTAT		
			_____ C		
GAM2438	CACNA1C	5'	CCAATGAGACTACACAATTGA 6379	GCAC	G
			TCAATTG AGTT TATTGG		
			AGTTAAC TCAG GTAACC		
			ACA_ A		
GAM2438	CRI1	3'	CCAATACAAAAGCCCACTGA 15648	ATT	ACAG
			TCA GGC TTGTATTGG		
			AGT CCG AACATAACC		
			CAC AA_		
GAM2438	FGF7	3'	CCACATATTCTTGCCAATT 7749	C TT	_
			AATTGGCA AG GTAT TGG		

			TTAACCGT TC TATA ACC		
			_ T _ C		
GAM2438	SCD	3'	CCAACCACTGTGCCACTGA 11488	AT	T AT
			TCA TGGCACAGT GT TGG		
			AGT ACCGTGTCA CA ACC		
			C _ C _		
GAM2438	FLJ10508	5'	CCAAGCACTATGCAATTGA 19892		G C T A
			TCAATTG CA AGT GT TTGG		
			AGTTAAC GT TCA CG AACC		
			_ A _ _		
GAM2438	FLJ21106	5'	CGATATCATGCCAATTGA 24735		CAGTT TG
			TCAATTGGCA GTAT G		
			AGTTAACCGT TATA C		
			AC _ GT		
GAM2438	KIAA0918	3'	CCAATGCAACCCACCCAATTGA 36197		CACA
			TCAATTGG GTTGTATTGG		
			AGTTAACC CAACGTAACC		
			CACC		
GAM2438	KIAA1750	3'	CCAAGACACTATGCCAAT 33872		C T A
			ATTGGCA AGT GT TTGG		
			TAACCGT TCA CA AACC		
			A _ G		
GAM2438	PC326	5'	CCAACAGACAATGCCAATT 20513		CA GTA
			AATTGGCA GTT TTGG		
			TTAACCGT CAG AACC		
			AA AC _		
GAM2438	STAM2	3'	CCAAACAGTCATGCCAACTG 12458	A	CA A
			CA TTGGCA GTTGT TTGG		
			GT AACCGT TGACA AACC		
			C AC _		
GAM2438	LOC122830	3'	CCAACAAGATGTGCCAGTTGA 36704		G _ AT
			TCAATTGGCACA TTGT TGG		
			AGTTGACCGTGT AACA ACC		
			AG _		
GAM2438	LOC147649	3'	CCAACCTTTGTGCCAAT 38355		TT AT
			ATTGGCACAG GT TGG		
			TAACCGTGT CA ACC		
			TC _		
GAM2438	LOC158116	3'	CCACATATTCTTGCCAATT 30252		C TT _
			AATTGGCA AG GTAT TGG		

		TTAACCGT TC TATA ACC		
		_ T_ C		
GAM2438	LOC257464	3' CCAATACAAC TTTATTGA	43164	TGGCAC
		TCAAT AGTTGTATTGG		
		AGTTA TCAACATAACC		
		TT____		
GAM2438	LOC90092	5' CCAATAATACCGTCAATTGA	30785	ACA TG
		TCAATTGGC GT TATTGG		
		AGTTAACTG CA ATAACC		
		C__ TA		
GAM2439	FRAP1	3' GTGTAGCCATGTCTAGA	11405	AGTA
		TCTAGACAT GGTTGCAT		
		AGATCTGTA CCGATGTG		

GAM2439	MGAM	3' TATGCAATTTATATGCCAGATA	35826	AGA G
		TATCT CATA TAGGTTGCATA		
		ATAGA GTAT ATTTAACGTAT		
		CC_ _		
GAM2439	ORC4L	3' ACCTTTTCTATGTCTAAATA	31090	C T__
		TAT TAGACATAG AGGT		
		ATA ATCTGTATC TCCA		
		A TTT		
GAM2439	PFKFB4	3' ATGCAACACTGTGTCCAG	10908	A AG
		CT GACATAGT GTTGCAT		
		GA CTGTGTCA CAACGTA		
		C _		
GAM2439	RIG	3' CAGCCTACTATATCTACATA	13104	C C
		TAT TAGA ATAGTAGGTTG		
		ATA ATCT TATCATCCGAC		
		C A		
GAM2439	ABCC13	3' ATCTCTATATCTAGATA	28971	C T
		TATCTAGA ATAG AGGT		
		ATAGATCT TATC TCTA		
		A _		
GAM2439	PRO1048	3' TAGCCAAC TCCATCTAGATA	20560	CAT A
		TATCTAGA AGT GGTTG		
		ATAGATCT TCA CCGAT		
		ACC A		
GAM2439	LOC81537	3' TATGCAATTATATATCTGATA	25088	T C GTAG
		TATC AGA ATA GTTGCATA		

		ATAG TCT TAT TAACGTAT	
		_ A AT_	
GAM2440 KLF5	3'	ATAGTAAGTTTTTTTAGAAGAC 7461	AGAT_
		GT GAAAACTTACTAT	
		CA TTTTTTGAATGATA	
		GAAGAT	
GAM2440 MKNK1	3'	AGGCTTTTTCATCTACGA 9791	_
		TCGTAGATGAAAAA CTT	
		AGCATCTACTTTTT GGA	
		C	
GAM2440 MSC	3'	ATAGCAAGTGATCCTGCGATA 37534	AT AAA A
		TATCGTAG GA ACTT CTAT	
		ATAGCGTC CT TGAA GATA	
		_ AG_ C	
GAM2441 CRTAP	3'	AAAGAGACTTCCTCTTGCGTT 13058	_ AA
C		GAACG GGA AAGTCTCTTT	
		CTTGC TCT TTCAGAGAAA	
		GGT CC	
GAM2441 HPCAL1	3'	GGCTGCCCCCCCCGTTTCATTT 28636	AAAA_
		AAATGAACGGG AGTC	
		TTTACTTGCCC TCGG	
		CCCCG	
GAM2441 HPCAL1	3'	GGCTGCCCCCCCCGTTTCATTT 7929	AAAA_
		AAATGAACGGG AGTC	
		TTTACTTGCCC TCGG	
		CCCCG	
GAM2441 LOXL2	3'	AAAGGGACCCTCCCATCATT 8130	AC AAAA
		AATGA GGGA GTCTCTTT	
		TTACT CCCT CAGGGAAA	
		A_ CC_	
GAM2441 NPEPPS	3'	GGCTTCTCCCGGTTTCATTT 13000	_ AA
		AAATGAAC GGGA AAGTC	
		TTTACTTG CCCT TTCGG	
		G C_	
GAM2441 PCDH9	5'	AAAGAGAGGTCCCATTTTCATTT 40292	C_ AAAAG
		AAATGAA GGGA TCTCTTT	
		TTTACTT CCCT AGAGAAA	
		TA GG_	
GAM2441 SIM1	5'	AAAGAACATATTTTCCGTTCA 11506	AA_ C
		TGAACGGGAAA GT TCTTT	

		ACTTGCCTTTT CA AGAAA		
		ATA _		
GAM2441	TGFA	3' AAAGAGACGGACTCCTGTTCA 9228	AAAA	
		TGAACGGGA GTCTCTTT		
		ACTTGCCT CAGAGAAA		
		CAGG		
GAM2441	ZNF265	3' AAAGTCATTATTTTCTTATTC 11938	CG	GTCT__
	ATTT	AAATGAA GGAAAAA CTTT		
		TTTACTT CCTTTT GAAA		
		AT ATTACT		
GAM2441	FLJ11618	3' AAAGTGCCCCCTCCCGTTCA 22789	AAAA	CT
		TGAACGGGA GT CTTT		
		ACTTGCCCT CG GAAA		
		CCCC T_		
GAM2441	FLJ20651	3' AAAGAGACTTTCTCTTTCAT 19572	C	AA
		ATGAA GGGAA AGTCTCTTT		
		TACTT CTCTT TCAGAGAAA		
		T _		
GAM2441	KIAA0379	3' AAAGAGACCTGAGGTTTCATCC 33809	A	GGGAAAAA
		A ATGAAC GTCTCTTT		
		C TACTTG CAGAGAAA		
		C GAGTC__		
GAM2441	KIAA1610	3' GCTTCTTCCAGTTCATTT 33341	G	A
		AAATGAAC GGAA AAGT		
		TTTACTTG CCTT TTCG		
		A C		
GAM2441	PRO1048	3' AAGAGACTTAAGATCATTT 20555	ACGGGAAA	
		AAATGA AAGTCTCTT		
		TTTACT TTCAGAGAA		
		AGAA__		
GAM2441	LOC197319	3' AAAGTTTAGTTTTTCCCATTTCG 42473	C	GTCT_
		TGAA GGGAAAAA CTTT		
		GCTT CCCTTTTT GAAA		
		A GATTT		
GAM2441	LOC90591	3' AGGCCTCTCTCCCGTTCATTT 31757	AAAAA__	
		AAATGAACGGG GTCT		
		TTTACTTGCCC CGGA		
		CTCTCTC		
GAM2442	DKFZp434A2417	3' CAAACGATAACATTTTAAGGAC 32861	ATCAT	C
	TA	TAGT AAATGT ATCGTTTG		

			ATCA	TTTACA TAGCAAAC		
			GGAAT	A		
GAM2442	MacGAP	3'	CAAACGGTGTTCATGATACT	27287	AAATGT	
			AGTATCAT	CATCGTTTG		
			TCATAGTA	GTGGCAAAC		
			CTT__			
GAM2442	PYGO1	5'	CATTTGATGACAACATAATAC	40022	C AA	TT
	TA		TAGTAT ATA	TGTCATCG TG		
			ATCATA TAT	ACAGTAGT AC		
			A CA	TT		
GAM2443	EGFL5	5'	CAGCAGCAGCAACAGCAGC	41880	A_ AC	
			GT CT	TGCTGCTGCTG		
			CG GA	ACGACGACGAC		
			AC CA			
GAM2443	EIF2C1	3'	CAGCAGCAGCAGCAGCAC	14501	A A	
			GT CT	CTGCTGCTGCTG		
			CA GA	GACGACGACGAC		
			C C			
GAM2443	IRS2	5'	CAGCAGCAGCAGCAACACCA	30030	ACTA	
			TGGT	CTGCTGCTGCTG		
			ACCA	GACGACGACGAC		
			CAAC			
GAM2443	KCNJ6	3'	CAGCATGTACAAAAGTACCATA	8022	AC C	_
			TATGGTACT	TG TGC TGCTG		
			ATACCATGA	AC ATG ACGAC		
			AA _	T		
GAM2443	MAP3K7IP2	3'	CAGCAACAGCAGCAGTACC	17484	A	C
			GGTACT	CTGCTG TGCTG		
			CCATGA	GACGAC ACGAC		
			C	A		
GAM2443	RAI3	3'	CTCAGCAGCTCCCCAGCACCA	10112	A	ACTGCT
			TGGT CT	GCTGCTGAG		
			ACCA GA	CGACGACTC		
			C	CCCCT_		
GAM2443	STC1	3'	CAGCAGCAGCAGCAGCAC	9132	A A	
			GT CT	CTGCTGCTGCTG		
			CA GA	GACGACGACGAC		
			C C			
GAM2443	AMOT	5'	CAGCAGCAGCAGCACCAT	28408	ACTA	
			ATGGT	CTGCTGCTGCTG		

TACCA GACGACGACGAC
 C____
 GAM2443 AMOT 5' CAGCAGCAGCAGCAGCCA 28409 ACTA
 TGGT CTGCTGCTGCTG
 ||| |||||
 ACCG GACGACGACGAC
 AC____
 GAM2443 BIKE 3' CAGCAGCAGCAGCACCACCA 19039 ACTA
 TGGT CTGCTGCTGCTG
 ||| |||||
 ACCA GACGACGACGAC
 CCAC
 GAM2443 DKFZP434J046 5' CGGCAGCAGCAGCAGCAC 35151 A A
 GT CT CTGCTGCTGCTG
 || || |||||
 CA GA GACGACGACGGC
 C C
 GAM2443 FLJ12505 5' CAGCAGCAGCAGCAGCCCC 24092 TA A
 GG CT CTGCTGCTGCTG
 || || |||||
 CC GA GACGACGACGAC
 CC C
 GAM2443 KIAA0182 3' CTCAAAGAACACAGTAGCACC 35644 A CTG_ GC
 GGT CTACTG CT TGAG
 ||| ||||| || |||
 CCA GATGAC GA ACTC
 C ACAA A_
 GAM2443 KIAA1028 3' CTCAGCAGAGCTCACAGTACCA 44159 ACT_ G
 TGGTACT GCT CTGCTGAG
 ||||| ||| |||||
 ACCATGA CGA GACGACTC
 CACT _
 GAM2443 KIAA1416 5' CAGCAGCAGCAGCCA 41800 TACTA
 TGG CTGCTGCTGCTG
 ||| |||||
 ACC GACGACGACGAC

 GAM2443 MAPKAPK2 3' CTCAGGGAACAGCAGCAGTGCC 11149 ACT _____
 ATA ATGGT ACTGCTGCTG CTGAG
 ||||| ||||| |||||
 TACCG TGACGACGAC GACTC
 _____ AAGG
 GAM2443 SP329 5' CAGCTGCAGCAGCACCA 25095 ACTA T
 TGGT CTGCTGC GCTG
 ||| ||||| |||
 ACCA GACGACG CGAC
 C____ T
 GAM2443 TREX1 5' CTCAGCAGCAGGTACGTACC 27337 _ TG
 GGTAC TAC CTGCTGCTGAG
 ||||| ||| |||||

CCATG ATG GACGACGACTC
 C _
 GAM2443 TREX1 5' CTCAGCAGCAGGTACGTACC 27346 _ TG
 GGTAC TAC CTGCTGCTGAG
 ||||| ||| |||||
 CCATG ATG GACGACGACTC
 C _
 GAM2443 LOC144473 3' CAGCACTAGCAGTACCA 40412 ACT C
 TGGT ACTGCTG TGCTG
 |||| | ||||| |||||
 ACCA TGACGAT ACGAC
 _ C
 GAM2443 LOC150197 3' CAGCAGCAGCAGGAGCCCATG 38865 TA A
 TATGG CT CTGCTGCTGCTG
 |||| | |||||
 GTACC GA GACGACGACGAC
 C_ G
 GAM2443 LOC219894 3' CAGCAACAAGGTACCAT 44795 AC C
 ATGGTACT TG TGCTG
 ||||| || |||||
 TACCATGG AC ACGAC
 A_ A
 GAM2443 LOC222484 3' CAGCAGCAGCCAGCACCA 45298 A ACT
 TGGT CT GCTGCTGCTG
 |||| | |||||
 ACCA GA CGACGACGAC
 C C_
 GAM2444 DUSP1 3' ACCAATATATAGTGGGTACATC 10681 CAC TGTG_
 A TGA ACCC ATATTGGT
 ||| |||| | |||||
 ACT TGGG TATAACCA
 ACA TGATA
 GAM2444 DKFZP572C163 5' ACCAATATGAGGAATGTGCA 30656 A C_ GTG
 TG CACA CCT ATATTGGT
 || |||| | |||||
 AC GTGT GGA TATAACCA
 _ AA G_
 GAM2444 EFA6R 3' ACCAATATGGCCCATGTGTCAG 17620 CCCT G
 A TCTGACACA GT ATATTGGT
 ||||| || |||||
 AGACTGTGT CG TATAACCA
 ACC_ G
 GAM2444 ERAP140 3' ACCAATATTATTGATTACCAGA 37081 ACACACCCT
 TCTG GTGATATTGGT
 |||| | |||||
 AGAC TATTATAACCA
 CATTAGT_
 GAM2444 FLJ20413 3' ACCAACTTCACAGGGTGTTCAG 19450 C TA
 A TCTGA ACACCCTGTGA TTGGT
 |||| | ||||| |||||

AGACT TGTGGGACACT AACCA
 _ TC
 GAM2444 LOC160156 5' ACCAATATCTTGGCACATGGCA 39989 A CAC_ TGT
 GA TCTG CA CC GATATTGGT
 ||| || || |||||
 AGAC GT GG CTATAACCA
 G ACAC TT_
 GAM2444 LOC169966 3' ACCAATATTACCTGAAGTGTCA 40164 ACCCT
 GA TCTGACAC GTGATATTGGT
 ||||| |||||
 AGACTGTG CATTATAACCA
 AAGTC
 GAM2445 RAP1A 3' AAAAAAATTGCTCTGTGTATA 8791 _ TTGGT
 TATAC CAGAGT ATTTTTT
 ||| ||| |||||
 ATATG GTCTCG TAAAAAA
 T T____
 GAM2445 KIAA1033 3' AAAAAAATACCACTGTG 32228 G TT
 CA AGT GGTATTTTTTT
 || ||| |||||
 GT TCA CCATAAAAAA
 G ____
 GAM2445 PPP1R16B 3' AAAAAAATTAAACTCTGTATA 30762 C GGT
 TATAC AGAGTTT ATTTTTT
 ||| ||||| |||||
 ATATG TCTCAA TAAAAAA
 _ AT_
 GAM2446 CNTNAP2 3' ATGGACACCCCTTAATTTTA 15416 TTAAC A
 TGAAATT AG GTGTCCAT
 ||||| || |||||
 ATTTTAA TC CACAGGTA
 T____ C
 GAM2446 DKFZP566B183 3' GGACATGTATAAAATTCCA 17768 A GAG
 TG AATTTTAACA TGTCC
 || ||||| |||||
 AC TTAAAATTGT ACAGG
 C ____
 GAM2446 FLJ10511 3' CATGGGTCCACTGTAAAA 19898 AGTG
 TTTTAACAG TCCATG
 ||||| |||||
 AAAATTGTC GGGTAC
 ACCT
 GAM2446 FLJ13842 3' TATTCTGTAAATCCTCA 23929 AAT
 TGA TTAAACAGAGTG
 || |||||
 ACT AAATTGTCTTAT
 CCT
 GAM2446 RBBP7 3' CACACTGCTAAGATTTC 30150 A A
 TGAAATTTTA CAG GTG
 ||||| ||| |||

ACTTTAGAAT GTC CAC
 C A
 GAM2446 LOC219654 3' CATAGATGTTAAAATTTC 43872 GA_
 GAAATTTTAACA GTG
 ||||| ||
 CTTTAAAATTGT TAC
 AGA
 GAM2446 LOC221271 3' GGGCATTGTAAAGTTCCA 44126 A GA
 TG AATTTTAACA GTGTCC
 || ||||| ||||
 AC TTGAAATTGT TACGGG
 C _
 GAM2447 EPHB2 3' ACGTTTGACTGGTGTGCTG 10730 TC A
 CAGTA CCA TCAAACGT
 |||| || |||||
 GTCGT GGT AGTTTGCA
 GT C
 GAM2447 GPR23 3' TGTTTGAAGGTATACTGTA 30364 C AA
 TACAGTAT CC TCAAACG
 ||||| || |||||
 ATGTCATA GG AGTTTGT
 T A_
 GAM2447 KIAA1209 3' ACATTTTCATTGTGATACTGTA 30469 C C C
 TACAGTATC CAAT AAA GT
 ||||| |||| || ||
 ATGTCATAG GTTA TTT CA
 T C A
 GAM2448 MAPK4 3' CCTCAGCACTCCCTATGCA 8621 T C GATC
 TG CATAGGGAG GT GAGG
 || ||||| || ||||
 AC GTATCCCTC CG CTCC
 _ A A_
 GAM2448 FLJ10008 3' CCAAACCATGCTCCCATGACA 19691 A ATCGA
 TGT CAT GGGAGCGTG GG
 ||||| ||||| ||
 ACAGTA CCCTCGTAC CC
 C CAAA_
 GAM2449 EGFL5 3' ACTCATCTCTCCAAGCAGG 41878 _ _ CTAAA
 CC GC GGA AGATGAGT
 || || || |||||
 GG CG CCT TCTACTCA
 A AA C_
 GAM2449 NPR1 5' ACCCACCTGCTCCGCGGCG 42232 CTAAA A A
 CGCCGCGGA AG TG GT
 ||||| || ||
 GCGGCGCCT TC AC CA
 CG_ C C
 GAM2449 ZNF80 5' ACTCACCACAAGGGTCCGCGGC 13985 AAAAGA_
 GCCGCGGACT TGAGT
 ||||| ||||

CGGCGCCTGG ACTCA
 GAACACC
 GAM2449 13CDNA73 5' ATCCCTTAGCCCCGCGGCG 23320 A_ AA
 CGCCGCGG CTAA GAT
 ||||| ||| ||
 GCGGCGCC GATT CTA
 CC CC
 GAM2449 ARTN 5' ACTCATCTCTTAATTTGC 10109 C A
 GCGGA TAA AGATGAGT
 |||| || |||||
 CGTTT ATT TCTACTCA
 A C
 GAM2449 CBX6 3' ACTCATCTCTTGCTGACGGT 15573 _ AC A
 GCCG CGG TAA AGATGAGT
 ||| || || |||||
 TGGC GTC GTT TCTACTCA
 A _ C
 GAM2449 GNB4 3' ACTCATCTTTCAGAAGTTTG 22268 A____
 CGGACT AAAGATGAGT
 |||| |||||
 GTTTGA TTTCTACTCA
 AGAC
 GAM2449 MADHIP 3' ACTCATCTTTTATATTCTG 14242 C____
 CGGA TAAAAGATGAGT
 ||| |||||
 GTCT ATTTTCTACTCA
 TAT
 GAM2449 SFRS12 3' ACTCATCTTCTAAATCTGTG 29174 C__ A
 CGCGGA TA AAGATGAGT
 |||| || |||||
 GTGTCT AT TTCTACTCA
 AAA C
 GAM2449 SPEC1 3' ACTCATCTTAAGCCCGAGC 21508 _ C A AA
 GC CG GG CT AAGATGAGT
 || || || |||||
 CG GC CC GA TTCTACTCA
 A _ _ A_
 GAM2449 TTTY9 5' ACTCATCTTTTAAATATCC 25675 C____
 GGA TAAAAGATGAGT
 || |||||
 CCT ATTTTCTACTCA
 ATAA
 GAM2449 LOC126432 5' ACTCATCTGGAGCCCGG 36839 C A AAA
 CCG GG CT AGATGAGT
 || || || |||||
 GGC CC GA TCTACTCA
 _ _ GG_
 GAM2449 LOC257239 5' ACTCACGCGAGGGTCCGCGGC 46373 AAAAGA_
 GCCGCGGACT TGAGT
 ||||| |||

CGGCGCCTGG ACTCA
 GAGCGCC
 GAM2450 C20orf162 5' CCACCCCATCTGAGAAAC 27914 CG TATT
 GT TCTT ATGGGGTGG
 || ||| |||||
 CA AGAG TACCCACC
 A_ TC_

GAM2450 HRIHFB2436 5' CCACCGGCCTAAAGACGACG 15666 TTAT _
 CGTCGTCTTTA GG GGTGG
 ||||| || |||
 GCAGCAGAAAT CC CCACC
 _ GG

GAM2450 LOC145988 5' CCACCCACAATGGCAGAAGA 38036 G _ A
 TC TCT TTATT TGGGGTGG
 || ||| |||||
 AG AGA GGTA ACCCCACC
 A C C

GAM2450 LOC220110 5' CCATGTGGAATAAAACGACGAG 44893 C ATGGG
 CTCGTCGT TTTATT GTGG
 ||||| ||||| |||
 GAGCAGCA AAATAA TACC
 _ GGTG_

GAM2450 LOC221943 5' CCACCTCAAAAAACAAC 45116 C C ATTA
 GT GT TTT TGGGGTGG
 || ||| |||||
 CA CA AAA ACTCCACC
 A A A_

GAM2451 KIAA1384 3' CGATCGTTATTCCCCCAATTCA 32258 CGAGC _
 TCA TGATGAAT GGAG GATCG
 ||||| ||| ||||
 ACTACTTA CCTT CTAGC
 ACCC_ ATTG

GAM2452 FMO4 5' GCACAGCAAAGATCTGCCA 7768 CT GGA
 TGGCAGATCTT TGT TGC
 ||||| ||| |||
 ACCGTCTAGAA ACG ACG
 _ AC_

GAM2452 JRK 3' GCATACAAGAAACTGCCA 41836 ATC GG
 TGGCAG TTCTTGT ATGC
 |||| ||||| |||
 ACCGTC AAGAACA TACG
 AA_ _

GAM2452 MAGEA3 5' GCACTGAAGGAGAAGATCTGCC 11839 G_ A
 A TGGCAGATCTTCTT TGG TGC
 ||||| ||| |||
 ACCGTCTAGAAGAG GTC ACG
 GAA _

GAM2452 C5orf4 3' TCTACAAGAAAATCCACA 26185 GCA C
 TG GAT TTCTTGTGGA
 || ||| |||||

		AC CTA AAGAACATCT		
		AC_ A		
GAM2452	CPSF2	3' TACAAAAAGAATCTGCCA	30864	_ C
		TGGCAGAT CTT TTGTG		
		ACCGTCTA GAA AACAT		
		A A		
GAM2452	KIAA1024	3' CGCACCACTAATATCTGCCA	34234	CTTCTT A
		TGGCAGAT GTGG TGCG		
		ACCGTCTA CACC ACGC		
		TAAT__ _		
GAM2452	MAGE-E1	3' CTACAAGAAGATCCCCA	25106	CA
		TGG GATCTTCTTGTGG		
		ACC CTAGAAGAACATC		
		C_		
GAM2452	LOC128259	5' CGTGTCCAAGAAGTTCCACCA	36920	CA T TG
		TGG GA CTTCT TGGATGCG		
		ACC CT GAAGA ACCTGTGC		
		AC T _		
GAM2452	LOC155036	5' CATCCAGTAAGAAGACCTGCC	41752	A _
		GGCAG TCTTCTTG TGGATG		
		CCGTC AGAAGAAT ACCTAC		
		C G		
GAM2452	LOC158510	5' GCACTGAAGGAGAAGATCTGCC	39858	G_ A
	A	TGGCAGATCTTCTT TGG TGC		
		ACCGTCTAGAAGAG GTC ACG		
		GAA _		
GAM2452	LOC199991	5' GCAGTATCAAGAAGATCTCCA	43275	C TGGA
		TGG AGATCTTCTTG TGC		
		ACC TCTAGAAGAAC ACG		
		_ TATG		
GAM2452	LOC201229	3' CACACCCAGCAGTCTGCCA	42541	T T _
		TGGCAGA CT CT TGTG		
		ACCGTCT GA GA ACAC		
		_ C CCC		
GAM2452	LOC222681	5' GTATCAAGAAGGCCTGCCA	44617	AT GTG
		TGGCAG CTTCTT GATGC		
		ACCGTC GAAGAA CTATG		
		CG _		
GAM2452	LOC257507	5' GTATCAAGAAGGCCTGCCA	46683	AT GTG
		TGGCAG CTTCTT GATGC		

		ACCGTC GAAGAA CTATG		
		CG ____		
GAM2452	LOC257625 5'	GTATCAAGAAGGCCTGCCA 46739	AT	GTG
		TGGCAG CTTCTT GATGC		
		ACCGTC GAAGAA CTATG		
		CG ____		
GAM2453	C20orf44 3'	CTGCCGAGTCCGGTCGGTGACC 20208	T	GTT TC A
		GGT CACCGAC A CG CAG		
		CCA GTGGCTG T GC GTC		
		_ GCC GA C		
GAM2454	ACTN2 5'	CCCTCGCGCCCCGCCGCAGC 6756	AT	A A
		GCTGCGGCGG CG CGA GG		
		CGACGCCGCC GC GCT CC		
		CC _ C		
GAM2454	ARHGEF7 3'	TCCTCCACCATTTGGCCGTAGC 9985	G	CGAC A
		GCTGCGGC GAT GA GGA		
		CGATGCCG TTA CT CCT		
		G CCAC _		
GAM2454	BAI2 5'	CCTCCGCGCGGCTGCAGCTA 7426	GGAT	A A
		TAGCTGCGGC CG CG AGG		
		ATCGACGTCG GC GC TCC		
		GC__ _ C		
GAM2454	CBFA2T3 3'	CCCATCGCCCCACCGCAGCTA 11687	C AT	CGAA
		TAGCTGCGG GG CGA GG		
		ATCGACGCC CC GCT CC		
		A CC AC__		
GAM2454	FLNA 5'	CCCTCGCCGAGGCTGCAGC 7192	GGA	A A
		GCTGCGGC TCG CGA GG		
		CGACGTCG AGC GCT CC		
		G__ C C		
GAM2454	MAF 5'	CTTCGCCGCCGCAGC 11836	ATCGA	
		GCTGCGGCGG CGAAG		
		CGACGCCGCC GCTTC		

GAM2454	MAZ 5'	CCCCCGCCTCCGCCGCACTA 36324	CT	TCGA AA
		TAG GCGGCGGA CG GG		
		ATC CGCCGCCT GC CC		
		AC CC__ CC		
GAM2454	RIMS1 5'	CCTCCTGCCGCCGCCGCTA 35956	T	ATCGAC A
		TAGC GCGGCGG GA GG		

		ATCG CGCCGCC	CT CC	
		C GTC__ _		
GAM2454	CPLX1	5' CCTTCAGCCGCCGCCGAGCT	13448	ATCGAC
		AGCTGCGGCGG	GAAGG	
		TCGACGCCGCC	CTTCC	
		GCCGA_		
GAM2454	GC20	5' TCCTCCCGGCTTCCGCCGCCGC	34167	T TCGA A_
		GC GCGGCGGA	CG AGGA	
		CG CGCCGCCT	GC TCCT	
		C TCG_ CC		
GAM2454	MGC14386	5' CCCCCGGGCCGCCGCAGC	27306	AT GA AA
		GCTGCGGCGG	C CG GG	
		CGACGCCGCC	G GC CC	
		CG__ CC		
GAM2454	PRO1048	3' TCCTTCTCGGCCCGCGCCGCAG	20563	__ AT C
	C	GCTGCGGC	GG CGA GAAGGA	
		CGACGCCG	CC GCT CTCCT	
		CG CG _		
GAM2454	RGS19	3' CCCTCATCGGCCCGCAGCTG	12491	CGGA C A
		TAGTGCGG	TCGA GA GG	
		GTCGACGCC	GGCT CT CC	
		C__ A C		
GAM2454	SCYD1	3' CCTTTGTCCCCACCGCAG	43709	C ATC
		CTGCGG	GG GACGAAGG	
		GACGCC	CC CTGTTTCC	
		A C__		
GAM2454	LOC128977	5' CCTCCGCGCGCGCCGCAGC	36949	GAT A A
		GCTGCGGCG	CG CG AGG	
		CGACGCCGC	GC GC TCC	
		GC_ _ C		
GAM2455	DKFZP434J214	3' GCTTCCACACACTTATTTA	30549	A AT
		TGAATAA	TGTGTG AAGT	
		ATTTATT	ACACAC TTCG	
		C C_		
GAM2455	KIAA1708	3' TTAACATTCATGTAGTTTAT	33274	_ TG TA_
	TCA	TGAATAAA	TG TGA AGTTAA	
		ACTTATTT	AT ACT TCAATT	
		G GT	TAC	
GAM2455	MGC20235	3' GTTAACTTCATACACACA	29669	_ _
		TGTGTG	AT AAGTTAAC	

ACACAC TA TTCAATTG
 A C
 GAM2455 LOC147949 3' TTAAAGCACACATTCTTCA 38423 TA ATAAG
 TGAA AATGTGTG TTAA
 ||| ||||| |||
 ACTT TTACACAC AATT
 C_ GA__
 GAM2455 LOC147990 3' TTAACCTATTCCATTTATTTA 40864 TGT
 TGAATAAATG GATAAGTTAA
 ||||| |||||
 ATTTATTTAC TTATTCAATT
 C_
 GAM2455 LOC163115 3' TTATTCAACATTTATTCA 40089 GT
 TGAATAAATGT GATAA
 ||||| |||
 ACTTATTTACA TTATT
 AC
 GAM2455 LOC92697 5' AACTTGATTTTACATTTATTTA 34799 T _
 TGAATAAATGTG GAT AAGTT
 ||||| ||| |||
 ATTTATTTACAT TTA TTCAA
 T G
 GAM2456 CARD4 3' CAACGGGAGCGAGTTGGTCACC 12739 T _
 GC GCGGT GG AACTCGCTCCCGTTG
 ||| || |||||
 CGCCA CT TTGAGCGAGGGCAAC
 _ GG
 GAM2457 APM1 3' GACGGGGTTTCACCACATTCGT 11210 CC_ ACC
 C GACGAG GG GAAACCCCGTC
 ||| || |||||
 CTGCTT CC CTTTGGGGCAG
 ACA A_
 GAM2457 ATP8A2 3' ACAAGGCTTCAGGTTTCGTC 44913 GGACC A CC
 GACGAGCC GAA CC GT
 ||||| ||| |||
 CTGCTTGG CTT GG CA
 A_ C AA
 GAM2457 C14orf1 3' GACGGGGTTTCACTCTGTC 14029 GC CC
 GA CGGA GAAACCCCGTC
 || ||| |||||
 CT GTCT CTTTGGGGCAG
 _ CA
 GAM2457 EPHA8 3' ACAGGGTTCCCGGTCAGTCCGG 21741 C _ C
 CT AGCCGGAC GA AACCC GT
 ||||| || ||| |||
 TCGGCCTG CT TTGGG CA
 A GGCCC A
 GAM2457 EVC 3' GACGGGGTTTCACCATACTGGC 15884 ACC_
 GCCGG GAAACCCCGTC
 ||| |||||

		CGGTC CTTTGGGGCAG	
		ATACCA	
GAM2457 FANCF	3'	GACGGGGTTTCACCATGCTGGC 22923	ACC___
		GCCGG GAAACCCCGTC	
		CGGTC CTTTGGGGCAG	
		GTACCA	
GAM2457 IMPDH1	5'	GACGGGGTTCTTTCCAGTCC 6579	C_ _
		GGAC GAA ACCCCGTC	
		CCTG CTT TGGGGCAG	
		AC TCT	
GAM2457 TRIM9	5'	GACGGGGTTTCACCATACTGGC 17517	ACC___
		GCCGG GAAACCCCGTC	
		CGGTC CTTTGGGGCAG	
		ATACCA	
GAM2457 ASB16	5'	GACGGGGTCTCACTCTGTCTG 34653	GC CC A
		CGA CGGA GA ACCCCGTC	
		GCT GTCT CT TGGGGCAG	
		_ CA C	
GAM2457 FLJ20897	5'	GACGGGGTTTCAACGTGTTGGC 26173	_ C_
		GCCGG AC GAAACCCCGTC	
		CGGTT TG CTTTGGGGCAG	
		G CAA	
GAM2457 KIAA0441	3'	GACGGGGTCTCACTGTATC 16710	GC ACC A
		GA CGG GA ACCCCGTC	
		CT GTC CT TGGGGCAG	
		AT A_ C	
GAM2457 MGC14697	5'	GACCGGACCTCGACCGGCTCGT 26484	AC AAC C
	C	GACGAGCCGG CGA CC GTC	
		CTGCTCGGCC GCT GG CAG	
		A_ CCA C	
GAM2457 SFXN2	3'	GACGGGGTTTCACCATGCTGGC 36603	ACC___
		GCCGG GAAACCCCGTC	
		CGGTC CTTTGGGGCAG	
		GTACCA	
GAM2457 SKRP1	5'	ACGGAGCTGGACGACTCAGTC 28120	_ C GA AAACC
		GAC GAG CG CCG CCGT	
		CTG CTC GC GGT GGCA	
		A A A_ CGA_	
GAM2457 STX4A	5'	GACGGAGCCTCTGGCGGCTCGT 10947	GA _ AACC
		ACGAGCCG CC GA CCGTC	

TGCTCGGC GG CT GGCAG
 ___ T CCGA
 GAM2457 VPS4A 3' GACAGGGGCTCCAGGGCTTGTC 14906 ___ CCGAAA C
 GACGAGCC GGA CCC GTC
 ||||| || ||| ||
 CTGTTTCGG CCT GGG CAG
 GA C___ A
 GAM2457 LOC160646 3' GACGGAGTCTCGGTCTGTC 40002 GC A C
 GA CGGACCGA AC CCGTC
 || ||||| || ||||
 CT GTCTGGCT TG GGCAG
 ___ C A
 GAM2457 LOC221296 3' GACGGGGTTTCACCATGCTGGC 44169 ACC___
 GCCGG GAAACCCCGTC
 |||| |||||
 CGGTC CTTTGGGGCAG
 GTACCA
 GAM2457 LOC255308 3' GACGGGGTTTCGGCATGTTGGC 45355 A___
 GCCGG CCGAAACCCCGTC
 |||| |||||
 CGGTT GGCTTTGGGGCAG
 GTAC
 GAM2457 LOC56963 5' GACGGAGCCTCCCGGCTCG 35399 ACC AACC
 CGAGCCGG GA CCGTC
 ||||| || ||||
 GCTCGGCC CT GGCAG
 ___ CCGA
 GAM2458 MAK 3' CACTGACTCAGCTCTGACCTTC 12528 A CCTA
 GAA GTC TTGAGTCAGTG
 ||| || |||||
 CTT CAG GACTCAGTCAC
 C TCTC
 GAM2458 PROML1 3' CTGGGTCTACAAGGACTTTCCA 12636 CTATT G
 TGGAAAGTCC GA TCAG
 ||||| || ||||
 ACCTTTCAGG CT GGTC
 AACAT G
 GAM2458 RAD9 3' GCCAATCAGGACTTTCCA 10931 CT A
 TGGAAAGTCC ATTG GT
 ||||| |||| ||
 ACCTTTCAGG TAAC CG
 AC _
 GAM2458 DKFZp434J0617 3' CACTGTACTTAATAGGAAGCTT 25981 A C_ _
 CCA TGGAA GT CCTATTGAGT CAGTG
 |||| || ||||| ||||
 ACCTT CG GGATAATTCA GTCAC
 _ AA T
 GAM2458 HT012 5' CACTAACTTCTGGACTTTCCA 20540 CTATT C
 TGGAAAGTCC GAGT AGTG
 ||||| |||| ||||

			ACCTTTCAGG	TTCA TCAC		
			TC__	A		
GAM2458	KIAA0945	5'	ACCTAACAGGGACTTCCCA	17288	A	A A
			TGG AAGTCCCT TTG GT			
			ACC TTCAGGGA AAT CA			
			C	C C		
GAM2458	SIRPB1	3'	CACTGACTCATGGCACCTCC	12707	AA C	TAT
			GGA GT CC TGAGTCAGTG			
			CCT CA GG ACTCAGTCAC			
			C_ C T__			
GAM2458	LOC154834	3'	CACCGACCGGTCAGCTTTCCA	41731	CCCT	A A
			TGAAAAGT ATTG GTC GTG			
			ACCTTTCG TGGC CAG CAC			
			AC__ _ C			
GAM2458	LOC51094	3'	CACTGGGCAATAAACTTTCCA	18089	CCC	AG
			TGAAAAGT TATTG TCAGTG			
			ACCTTTCA ATAAC GGTCAC			
			A__ G_			
GAM2459	GGT2	5'	CCGCGGCTGGCTGACACCT	36489	CC	TGTT
			AGG GTCAGCC GCCGCGG			
			TCC CAGTCGG CGGCGCC			
			A_ T__			
GAM2459	IRAK4	3'	CAGCCTGGGCTGACACCT	30692	CC	__
			AGG GTCAGCCT GTTG			
			TCC CAGTCGGG CGAC			
			A_ TC			
GAM2459	KCNN4	5'	GCCAGCAGAGCAGGCTGACGAC	8038	C	GCC _
	CT		AGG CGTCAGCCTGTT GC GGC			
			TCC GCAGTCGGACGA CG CCG			
			A GA_ A			
GAM2459	PAX7	5'	GCCACTCTGAGGCTGGCGGCCT	8446		GTTGCCGC
			AGGCCGTCAGCCT GGC			
			TCCGGCGGTCGGA CCG			
			GTCTCA__			
GAM2459	PAX7	5'	GCCACTCTGAGGCTGGCGGCCT	15134		GTTGCCGC
			AGGCCGTCAGCCT GGC			
			TCCGGCGGTCGGA CCG			
			GTCTCA__			
GAM2459	POU4F1	5'	GCCGCGACCGCCGCGGCTGCAG	12900	C T	T T __
	CCT		AGGC G CAGCC GT GC CGCGGC			

TCCG C GTCGG CG CG GCGCCG
 A _ _ C CCA
 GAM2459 RPS6KA1 5' GCCGCGGCGGCGGCGGCGGACG 29836 A _
 GCC GGCCGTC GCC TGTGCGCGGC
 ||||| || |||||
 CCGGCAG CGG GCGGCGGCGCCG
 G CG
 GAM2459 ARS2 5' GCCGCGGCCGCACCAAGGCC 18045 GTCAGCC T
 GGCC TGT GCCGCGGC
 ||| || |||||
 CCGG ACG CGGCGCCG
 AACC _ C
 GAM2459 CBLN1 5' GCCGCGGCACCCCTGAGGCC 10557 G CCT T
 GGCC TCAG GT GCCGCGGC
 ||| ||| || |||||
 CCGG AGTC CA CGGCGCCG
 _ CC _
 GAM2459 DKFZP566F2124 5' CCGCGGCAAGGACATGCCT 17887 CGTCAG GT
 AGGC CCT TGCCGCGG
 ||| || |||||
 TCCG GGA ACGGCGCC
 TACA _ _
 GAM2459 FLJ11712 5' GCCGCGAGGGAGAGGCCGCGGC 23796 CA G GC_
 C GGCCGT GCCT TT CGCGGC
 ||||| ||| || |||||
 CCGGCG CGGA AG GCGCCG
 C _ G GGA
 GAM2459 FLJ32468 5' CCGCGGATAGCACTGGCGACC 29721 C CC _
 GG CGTCAG TGTTG CCGCGG
 || ||||| ||||| |||||
 CC GCGGTC ACGAT GGCGCC
 A _ A
 GAM2459 KIAA0469 5' GCCGCGGCGTCCTCGACAACCT 16893 CC _ CCTGT
 AGG GTC AG TGCCGCGGC
 ||| ||| || |||||
 TCC CAG TC GCGGCGCCG
 AA C CT_
 GAM2459 KIAA0662 3' GCCACAGGCTGGCAGCCT 39803 C T
 AGGC GTCAGCCTGT GC
 |||| ||||| ||
 TCCG CGGTCGGACA CG
 A C
 GAM2459 KIAA1530 5' GCCGAGTGACAGGCCGAGCC 33733 C CA TG CG
 GGC GT GCCTGT C CGGC
 ||| || ||||| | |||
 CCG CG CGGACA G GCCG
 A C _ GT A_
 GAM2459 LOC161635 5' GCCCTTCACAACTGCGGCCT 46184 T CC TGCCGC
 AGGCCG CAG TGT GGC
 ||||| ||| ||| |||

		TCCGGC GTC ACA CCG		
		_ AA CTTC__		
GAM2459	LOC254057	5' GCCGCGGGCTCAGGCTGAGGCC 46347	G	TTG
		T AGGCC TCAGCCTG CCGCGGC		
		TCCGG AGTCGGAC GGCGCCG		
		_ TCG		
GAM2459	LOC83693	5' GCCACATACTGCTGACGGCC 25495	CT	TGCCGC
		GGCCGTCAGC GT GGC		
		CCGGCAGTCG CA CCG		
		T_ TACA__		
GAM2459	LOC90288	5' CCACGGCAACAGGTTGC 31105	T	C
		G CAGCCTGTTGCCG GG		
		C GTTGGACAACGGC CC		
		_ A		
GAM2460	CAP350	5' CCGAGGGCGGAGGCGACACTCT 16771	C	TGGATA
		AGA TGTCGCCTCC TCGG		
		TCT ACAGCGGAGG AGCC		
		C CGGG__		
GAM2460	KIAA0350	3' CGTGACCAGGAGGAACAGCCT 30663	A	CG A T
		AG CTGT CCTCCTGG TA CG		
		TC GACA GGAGGACC GT GC		
		C A_ A_		
GAM2460	KIAA1944	3' GTCCAGGAAAGAACAGCCT 37229	A	_ GCC
		AG CTGT C TCCTGGAT		
		TC GACA G AGGACCTG		
		C A AA_		
GAM2460	LOC152579	3' TCCTGAAGGCGACAGTCT 39290		CCT
		AGACTGTCGCCT GGA		
		TCTGACAGCGGA CCT		
		AGT		
GAM2460	LOC158654	3' CCAAGAGAGGCGACAGCT 39876	A	_ _
		AG CTGTCGCCTC CT GG		
		TC GACAGCGGAG GA CC		
		_ A A		
GAM2460	LOC200448	5' CCAATATCCAGAAAACATTCT 42816	C	CGCCTC C
		AGA TGT CTGGATAT GG		
		TCT ACA GACCTATA CC		
		T AAA__ A		
GAM2460	LOC222166	3' CCAGACAGAAAGCTGACAGTCT 45150	_ C_ _	
		AGACTGTC GC TC CTGG		

			TCTGACAG CG AG GACC		
			T AA ACA		
GAM2461	CDK2	3'	AGCCTTCCTACACGTTA 7552	TATT	A
			TAGCGTGT AGGAAG CT		
			ATTGCACA TCCTTC GA		
			_____ C		
GAM2461	CYP8B1	3'	GGAAGCCTTCCTGGATTTCACG 10625	TT _	A _
	C		GCGTG ATT AGGAAG CT CC		
			CGCAC TAG TCCTTC GA GG		
			TT G C A		
GAM2461	HMG2	3'	AGTTGTAAACAACATGCTA 12040	ATTAG	A
			TAGCGTGTT GA GACT		
			ATCGTACAA TT TTGA		
			CAAA_ G		
GAM2461	RAD1	5'	GGGAGTCTCCCTATGTTGC 28500	TGTTAT	A
			GCG TAGG AGACTCCC		
			CGT ATCC TCTGAGGG		
			TGT___ C		
GAM2461	RNMT	3'	GGAAGTCTTCCTGTACAT 9888	TAT	_
			GTGT TAGGAAGACT CC		
			TACA GTCCTTCTGA GG		
			CT_ A		
GAM2461	WW45	3'	GGAAGTCTTCAGAAATAC 22397	ATTA	_
			GTGTT GGAAGACT CC		
			CATAA CCTTCTGA GG		
			GA_ A		
GAM2461	CXYorf1	3'	GGGGTCTAATAACAACTA 39910	CG	AGGA
			TAG TGTTATT AGACTCC		
			ATC ACAATAA TCTGGGG		
			AA _____		
GAM2461	KIAA1393	3'	AGTTGTAAACAACATGCTA 35684	ATTAG	A
			TAGCGTGTT GA GACT		
			ATCGTACAA TT TTGA		
			CAAA_ G		
GAM2461	PRO0902	5'	AGTCTTCCAGTCACGC 27606	TT	A
			GCGTG ATT GGAAGACT		
			CGCAC TGA CCTTCTGA		

GAM2461	TU3A	5'	GGAACCCAGCAACACGCT 14034	A A	AAGAC
			AGCGTGTT TT GG TCC		

			TCGCACAA GA CC AGG		
			C C A_____		
GAM2461	LOC152267	3'	AGTTGTAAACAACATGCTA 30294	ATTAG A	
			TAGCGTGTT GA GACT		
			ATCGTACAA TT TTGA		
			CAAA_ G		
GAM2461	LOC200093	3'	GGGGTCTAATAACAACTA 31602	CG AGGA	
			TAG TGTTATT AGACTCC		
			ATC ACAATAA TCTGGGG		
			AA _____		
GAM2461	LOC204084	3'	GGAAATCTCCTTCACACAGCTA 43086	_ TATT A C_	
			TAGC GTGT AGGA GA TCC		
			ATCG CACA TCCT CT AGG		
			A CT_ _ AA		
GAM2461	LOC221463	3'	GGGAGTCTCCCCAGGACGGC 44202	G ATTA A	
			GC TGTT GGA GACTCCC		
			CG GCAG CCT CTGAGGG		
			_ GACC _		
GAM2461	LOC91040	3'	GGGGTCTAATAACAACTA 32319	CG AGGA	
			TAG TGTTATT AGACTCC		
			ATC ACAATAA TCTGGGG		
			AA _____		
GAM2462	CARPX	5'	TCCTGGATCTTCCCA 21397	TGGC	
			TGGGAAGATTC GGGA		
			ACCCTTCTAGG TCCT		

GAM2462	NRL	3'	GAAGTCCCCAAGACAATCTCGC 12837	GA _ GGC A	
	CA		TGG AGAT TCT GGGA CTTC		
			ACC TCTA AGA CCCT GAAG		
			GC AC AC_ _		
GAM2462	RARB	5'	AAGGGGGGACCAGAATTCCCCA 18235	AA CGGGAA	
			TGGG GATTCTGG CTT		
			ACCC TTAAGACC GAA		
			C_ AGGGGG		
GAM2462	RARB	5'	AAGGGGGGACCAGAATTCCCCA 6691	AA CGGGAA	
			TGGG GATTCTGG CTT		
			ACCC TTAAGACC GAA		
			C_ AGGGGG		
GAM2462	SEZ6L	5'	AAGGTCCTAAATCTCCCCA 22092	A CTGGC A	
			TGGG AGATT GGGA CTT		

ACCC TCTAA TCCT GAA
 C A___ G
 GAM2462 TEM7 3' GAAGTTCTGCAAACCTCCCC 21673 A ATTCTG G
 GGG AG GCGG AACTTC
 ||| || ||| |||||
 CCC TC CGTC TTGAAG
 C CAAA___ _
 GAM2462 KIAA1340 3' TCTGAACCAAAATCTTCCCA 34299 C ___
 TGGGAAGATT TGG CGGG
 ||||| ||| |||
 ACCCTTCTAA ACC GTCT
 A AA
 GAM2462 PRO1331 5' AAGTCTTCTGCAGAATCTCCCA 25066 A G _
 TGGGA GATTCTG CGGGA ACTT
 |||| ||||| |||| |||
 ACCCT CTAAGAC GTCTT TGAA
 _ _ C
 GAM2462 LOC201696 3' GAAGTTTAAATTTCCCCA 31625 A CTGGCG
 TGGG AGATT GGA ACTTC
 ||| |||| |||||
 ACCC TTAA TTTTGAAG
 C AAA___
 GAM2462 LOC221092 5' AGGTAACCCAGAATCTCCCA 44774 A CG GA
 TGGGA GATTCTGG G ACTT
 |||| ||||| | |||
 ACCCT CTAAGACC C TGGA
 _ _ AA
 GAM2463 ABR 3' GCTTCTCTCTTGGCCCTGCT 6750 A AG C
 GGCAG GG GA AGAGAAGC
 |||| || |||||
 TCGTC CC TT TCTCTTCG
 _ GG C
 GAM2463 ABR 3' GCTTCTCTCTTGGCCCTGCT 22495 A AG C
 GGCAG GG GA AGAGAAGC
 |||| || |||||
 TCGTC CC TT TCTCTTCG
 _ GG C
 GAM2463 AES 3' CTTCCCTCCTCCTCCCCT 6804 CA CA A
 AGG GAGGAGGA G GAAG
 || ||||| | |||
 TCC CTCCTCCT C CTTC
 C_ _ C
 GAM2463 ARF3 3' CTCCCTCTCCTCTCCTCT 7379 C ACA
 AGAGG AGAGGAGG GAG
 |||| ||||| |||
 TCTCC TCTCCTCT CTC
 _ CC_
 GAM2463 ASGR2 5' GCCCCTCCTCCACTCTCCTCT 6852 C GA CA AA
 AGAGG AGAG GGA GAG GC
 |||| ||| ||| ||| ||

			TCTCC TCTC CCT CTC CG		
			_ A_ C_ CC		
GAM2463	ASGR2	5'	GCCCCCTCCTCCACTCTCCTCT 28132	C	GA CA AA
			AGAGG AGAG GGA GAG GC		
			TCTCC TCTC CCT CTC CG		
			_ A_ C_ CC		
GAM2463	ASGR2	5'	GCCCCCTCCTCCACTCTCCTCT 28131	C	GA CA AA
			AGAGG AGAG GGA GAG GC		
			TCTCC TCTC CCT CTC CG		
			_ A_ C_ CC		
GAM2463	BAZ1B	3'	CTCTGCTTCCTCCGTCCTC 26193	_ A	A
			GAGG C GAGGAGG CAGAG		
			CTCC G CTCCTTC GTCTC		
			T C _		
GAM2463	BCL9	3'	GCTTCTCTGTCTTTTTTCCCC 10523	CA	
			GG GAGGAGGACAGAGAAGC		
			CC TTTTCTGTCTCTTCG		
			CC		
GAM2463	BRIP1	3'	GTGATCTGCCCTTCTCTGCCTC 25755	A	GAA
			GAGGCAGAGGAGG CAGA GC		
			CTCCGTCTCTTCC GTCT TG		
			C AG_		
GAM2463	CACNG7	3'	GCCCCCTCGGAGCTCCCCCTGCC 25639	A_	GACA AA
	TC		GAGGCAG GGAG GAG GC		
			CTCCGTC CCTC CTC CG		
			CC GAGG CC		
GAM2463	CACNG7	3'	GCTCCCCCTGCCTCCTCCTCCT 25640	CA	A AGA_
	C		GAGG GAGGAGG CAG AGC		
			CTCC CTCCTCC GTC TCG		
			TC _ CCCC		
GAM2463	CGTHBA	5'	CTCCGTCCTCCTCTGGCC 14357	_	A
			GGC AGAGGAGGAC GAG		
			CCG TCTCCTCCTG CTC		
			G C		
GAM2463	CHRNA5	5'	GCCCCCTGTGTGCGTCTGCCCT 30058	A	GGA A AA
			AG GGCAGA GG CAGAG GC		
			TC CCGTCT TC GTCTC CG		
			_ GCG _ CC		
GAM2463	CHRNA1	3'	CTATCCTTCTCTGCCTCT 30359	C	
			AGAGGCAGAGGAGGA AG		

			TCTCCGTCTCTTCCT TC			
			A			
GAM2463	CLN6	3'	CTGCCCTCCTCTGCACCT 19550	AG	A	
			AG GCAGAGGAGG CAG			
			TC CGTCTCCTCC GTC			
			CA C			
GAM2463	COL1A1	3'	CTTCTCAGGCCTCTGCTCT 5538	G	AGGACA	
			AGAG CAGAGG GAGAAG			
			TCTC GTCTCC CTCTTC			
			— GGA—			
GAM2463	CRHR2	3'	CGCTCCCCTGTCCTCCTCCACC 7612	CA	AGA	
	TT		GAGG GAGGAGGACAG AGC G			
			TTCC CTCCTCCTGTC TCG C			
			AC CCC			
GAM2463	CYB561	5'	CTCCTCTGAGCTCTGCTCT 7630	G	GAGGA A	
			AGA GCAGAG CAGAG AG			
			TCT CGTCTC GTCTC TC			
			— GA— C			
GAM2463	DDB1	3'	CTGCTGCCCTCCCCCTCCTCT 7639	C A_ A _		
			AGAGG AG GGAGG CAG AG			
			TCTCC TC CCTCC GTC TC			
			_ CC C G			
GAM2463	DLST	3'	CTTCAAGATGCCTCTTCTACCT 7643	C	A GA_	
	CT		AGAGG AGAGGAGG CA GAAG			
			TCTCC TCTTCTCC GT CTTC			
			A _ AGAA			
GAM2463	ED1	5'	CTCCCCTCTCTCCCGCCCCT 7097	A A_ _ ACA		
			AG GGC GAG GAGG GAG			
			TC CCG CTC CTCC CTC			
			C CC T C_			
GAM2463	EHD3	3'	CTGTCCCTGCTCTGCCTC 15957	G _		
			GAGGCAGAG AGG ACAG			
			CTCCGTCTC TCC TGTC			
			G C			
GAM2463	EMX2	5'	GCCTCTCCCTCTCCCTCCCCC 42316	A CA AG CA A		
	T		AG GG GAGG GA GAGA GC			
			TC CC CTCC CT CTCT CG			
			_ CC CT CC C			
GAM2463	EYA4	5'	GCTCCTCTTCCTTTCTCCTC 10309	C AG C A		
			GAGG AG GAGGA AGAG AGC			

CTCC TC TTCCT TCTC TCG
 _ CT _ C
 GAM2463 FANCC 3' CTCTTCCTCCTCCCCT 34906 CA C
 AGG GAGGAGGA AGAG
 ||| ||||| |||
 TCC CTCCTCCT TCTC
 C_ _
 GAM2463 FBXL4 5' GCTCCTCGCGGCTCCGCGTCT 14459 G AGA ACA_ A
 AGA GC GGAGG GAG AGC
 ||| || ||||| ||| |||
 TCT CG CCTCC CTC TCG
 G _ _ GGCG C
 GAM2463 FHIT 5' CTCCCTCCCTCTGCCTTT 7753 _ ACA
 AGAGGCAGAGG AGG GAG
 ||||| ||| |||
 TTTCCGTCTCC TCC CTC
 C _ _
 GAM2463 FKBP1A 3' CTCTGTTTCCTCTTCCCCT 6474 A C G
 AG GG AGAGGAG ACAGAG
 || || ||||| |||||
 TC CC TCTCCTT TGTCTC
 C T _
 GAM2463 FN1 5' CTTCTCTGGTCCTCTGCATC 7779 G GGA
 GA GCAGAGGA CAGAGAAG
 || ||||| |||||
 CT CGTCTCCT GTCTCTTC
 A G_
 GAM2463 FN1 5' CTTCTCTGGTCCTCTGCATC 27645 G GGA
 GA GCAGAGGA CAGAGAAG
 || ||||| |||||
 CT CGTCTCCT GTCTCTTC
 A G_
 GAM2463 FRG1 5' GCTTCTGTTCCCTCCGCGCC 10793 AGA CAG
 GGC GGAGGA AGAAGC
 ||| ||||| |||||
 CCG CCTCCT TCTTCG
 CG_ TG_
 GAM2463 FXD6 3' GCTTCTCTGCCTACGTCCCCT 22552 CAGAGG A
 AGG AGG CAGAGAAGC
 ||| ||| |||||
 TCC TCC GTCTCTTCG
 CCTGCA _
 GAM2463 FZD7 3' TCTCTCCTCCCCTGCC 9600 A CA
 GGCAG GGAGGA GAGA
 ||||| ||||| |||
 CCGTC CCTCCT CTCT
 C _ _
 GAM2463 GALNT2 3' CTGCCCTCCCCCTCCTCT 10799 C A_ A
 AGAGG AG GGAGG CAG
 ||||| || ||||| |||

TCTCC TC CCTCC GTC
 _ CC C
 GAM2463 GALNT7 3' CTCTATTCCCCCTGCCCT 27651 A A A C_
 AG GGCAG GG GGA AGAG
 || |||| || ||| ||||
 TC CCGTC CC CCT TCTC
 _ _ _ TA
 GAM2463 GFAP 3' GCTCCCCTCCCTCCTCTGTCCC 7815 A ACA A_
 T AG GGCAGAGGAGG GAG AGC
 || ||||| ||| |||
 TC CTGTCTCCTCC CTC TCG
 C _ _ CCC
 GAM2463 GNA11 5' GCTTCTCTGGGCTGTGCCTC 37454 G GAGGA
 GAGGCA AG CAGAGAAGC
 ||||| || |||||
 CTCCGT TC GTCTCTTCG
 G GG_
 GAM2463 GNAO1 3' GCCCCTCCCCACCCCTGCCTTT 43721 A A ACA AA
 AGAGGCAG GG GG GAG GC
 ||||| || || ||| ||
 TTTCCGTC CC CC CTC CG
 C A C_ CC
 GAM2463 GNAS 5' CTCAGTCTCCTCTGTCCTCT 18679 _ G A
 AGAGG CAGAGGAG AC GAG
 |||| ||||| || |||
 TCTCC GTCTCCTC TG CTC
 T _ A
 GAM2463 GRM4 3' CTCTGTCTGTCTCCAGCCCT 6504 A A_ GA
 AG GGC GAG GGACAGAG
 || ||| || |||||
 TC CCG CTC TCTGTCTC
 _ AC TG
 GAM2463 GRM6 5' CTCCCCGCCCCTCTGTCTC 6508 A ACA_
 GAGGCAGAGG GG GAG
 ||||| || |||
 CTCTGTCTCC CC CTC
 _ GCCC
 GAM2463 GTF2IRD1 5' GCCGTCCTCGCCTCCCTCTGCC 18452 _ AC A A_
 TCT AGAGGCAGAGG AGG AG GA GC
 ||||| ||| || ||| ||
 TCTCCGTCTCC TCC TC CT CG
 C GC _ GC
 GAM2463 HAP1 3' GCTTGGGGACCCCTCCCTGCC 10076 A A ACAGAG_
 CT AG GGCAG GGAGG AAGC
 || |||| |||| |||
 TC CCGTC CCTCC TTCG
 C _ CCAGGGG
 GAM2463 HCFC1 3' CTCTTCTACCCTCCCCCTCT 35157 CA A_ C
 AGAGG GAGG GGA AGAG
 |||| ||| ||| |||

			TCTCC CTCC TCT TCTC			
			CC CA _			
GAM2463	HMGA2	5'	TCCTCTCCTCCTCCTCCTC	9572	CA	C A
			GAGG GAGGAGGA AG GA			
			CTCC CTCCTCCT TC CT			
			TC C _			
GAM2463	HTRA3	3'	CTTCCCGCCTCTGCCCT	42940	A	A ACAGA
			AG GGCAGAGG GG GAAG			
			TC CCGTCTCC CC CTTC			
			C G _			
GAM2463	ITPKB	3'	GCTTCCCTGCCATCTGGCCCT	7982	A	AG GA A A
			AG GGC AG GG CAG GAAGC			
			TC CCG TC CC GTC CTTCG			
			_ G_ TA _ C			
GAM2463	KCNAB2	3'	CTGGGGGTCTTCTCCACCTC	9707	CA	AGAGA
			GAGG GAGGAGGAC AG			
			CTCC CTCCTTCTG TC			
			AC GGGG_			
GAM2463	KCNAB2	3'	GCCCCTCTGTCTGGCCACCCCT	9708	CAGA A_	AA
	C		GAGG GG GGACAGAG GC			
			CTCC CC TCTGTCTC CG			
			CCA_ GG CC			
GAM2463	LDOC1	3'	CTCCGAGTGTCTCCCTGCC	14692	A	_
			GGCAG GGAGGACA GAG			
			CCGTC CCTCCTGT CTC			
			C GAGC			
GAM2463	LIMK1	3'	CTCCTCATGCCCTCTGTCCTC	18801	_	A A _ A
	T		AGAGG CAGAGG GG CA GAG AG			
			TCTCC GTCTCC CC GT CTC TC			
			T _ _ A C			
GAM2463	LIMK1	3'	GCTCCCTGCCCTCCTCATGCC	18803	A _	A_ A A
	CCT		AG GGCA GAGGAGG CAG GA GC			
			TC CCGT CTCCTCC GTC CT CG			
			C A CC C _			
GAM2463	LIMK1	3'	CTCCTCATGCCCTCTGTCCTC	8125	_	A A _ A
	T		AGAGG CAGAGG GG CA GAG AG			
			TCTCC GTCTCC CC GT CTC TC			
			T _ _ A C			
GAM2463	LIMK1	3'	GCTCCCTGCCCTCCTCATGCC	8126	A _	A_ A A
	CCT		AG GGCA GAGGAGG CAG GA GC			

			TC CCGT CTCCTCC GTC CT CG	
			C A CC C _	
GAM2463 LZTS1	3'	GCTTCTCTCCTTGCCCCCGCC 22008	A AGA A AC___	
CT		AG GGC GG GG AGAGAAGC		
		TC CCG CC CC TCTCTTCG		
		_ CC_ _ GTTCC		
GAM2463 MAF	5'	GCTTGGCTCCCCCTCCCCCT 11837	A CA A CA AG	
		AG GG GAGG GGA G AAGC		
		TC CC CTCC CCT C TTCG		
		_ CC C _ GG		
GAM2463 MARK3	5'	CTTCCTTCACATCCTCCTCCGC 8190	A C___ A	
CTC		GAGGC GAGGAGGA AG GAAG		
		CTCCG CTCCTCCT TC CTTC		
		C AACT _		
GAM2463 MN1	5'	CTATTGATCCCCCTCTGCC 8273	A _ _	
		GGCAGAGG GGA CAG AG		
		CCGTCTCC CCT GTT TC		
		C A A		
GAM2463 MNT	3'	CTCCAGCCCCTTTGCCTCT 21563	A ACA	
		AGAGGCAGAGG GG GAG		
		TCTCCGTTTCC CC CTC		
		_ GAC		
GAM2463 NESH	5'	CTGGCTTCCCCCTTCCTCT 18548	C A_ A	
		AGAGG AG GGAGG CAG		
		TCTCC TC CCTTC GTC		
		T CC G		
GAM2463 NOS1	3'	CTGTGGCCCTCGCTCTGCCTC 6231	_ A_ G	
		GAGGCAGAG GAGG CA AG		
		CTCCGTCTC CTCC GT TC		
		G CG G		
GAM2463 NRXN1	5'	CTCCCCTGCGCCCTCTCCTCT 28996	C ____ ACA	
		AGAGG AGAGG AGG GAG		
		TCTCC TCTCC TCC CTC		
		_ CGCG C_		
GAM2463 OCLN	5'	CTCTCCCTCCCTGCTTC 8381	A AC	
		GAGGCAG GGAGG AGAG		
		CTTCGTC CCTCC TCTC		
		_ C_		
GAM2463 PAX2	5'	CTCCCGCTCCTCTGCCTC 10138	GACA	
		GAGGCAGAGGAG GAG		

			CTCCGTCTCCTC CTC		
			GCC_		
GAM2463	PAX2	3'	GCCCCTCTCTCCCTCTGCCCCT 10140	A	AG CA AA
			AG GGCAGAGG GA GAG GC		
			TC CCGTCTCC CT CTC CG		
			C CT _ CC		
GAM2463	PAX2	3'	GCTTCTCTCCCCCTCTGTCTCT 10141	A	CA
			AGAGGCAGAGG GGA GAGAAGC		
			TCTCTGTCTCC CCT CTCTTCG		
			C _		
GAM2463	PAX2	5'	CTCCCGCTCCTCTGCCTC 10144		GACA
			GAGGCAGAGGAG GAG		
			CTCCGTCTCCTC CTC		
			GCC_		
GAM2463	PAX2	3'	GCCCCTCTCTCCCTCTGCCCCT 10146	A	AG CA AA
			AG GGCAGAGG GA GAG GC		
			TC CCGTCTCC CT CTC CG		
			C CT _ CC		
GAM2463	PAX2	3'	GCTTCTCTCCCCCTCTGTCTCT 10147	A	CA
			AGAGGCAGAGG GGA GAGAAGC		
			TCTCTGTCTCC CCT CTCTTCG		
			C _		
GAM2463	PGR	5'	CTTTCTCCTCCCTCTGCCCCT 6636	A	_ C
			AG GGCAGAGG AGGA AGAG		
			TC CCGTCTCC TCCT TTTC		
			C C C		
GAM2463	PKD2L1	5'	CTCTGCTCCCTCTTCCTCT 18192	C	AG A
			AGAGG AGAGG G CAGAG		
			TCTCC TCTCC C GTCTC		
			T CT _		
GAM2463	PLEK	3'	TCCTGCATTCTCCTCCCTC 8534	CA	_ _ A
			GAGG GAGGAGGA CAG GA		
			CTCC CTCCTCCT GTC CT		
			C _ TAC _		
GAM2463	PMX1	5'	CTCCCCCGCCCTGCTGGCCTC 22916	_ _	A _ ACA
			GAGGC AG AGG GG GAG		
			CTCCG TC TCC CC CTC		
			G G CG CC _		
GAM2463	PMX1	5'	CTCCCCCGCCCTGCTGGCCTC 13781	_ _	A _ ACA
			GAGGC AG AGG GG GAG		

CTCCG TC TCC CC CTC
 G G CG CC_
 GAM2463 PPFIA3 3' GCTTCCCCTTCTCCTCTGGCTC 30583 G CAGA
 GAG CAGAGGAGGA GAAGC
 ||| ||||| ||||
 CTC GTCTCCTCTT CTTCG
 G CCC_
 GAM2463 PPP2R4 3' GCCCCTCCCCATCCCCTCCCTC 30376 CA A CA__ AA
 T AGAGG GAGG GGA GAG GC
 |||| ||| ||| || ||
 TCTCC CTCC CCT CTC CG
 __ _ ACCC CC
 GAM2463 PRX 3' CTAATTCCACCCTCTGCCCCT 21935 A A_ CAG
 AG GGCAGAGG GGA AG
 || ||||| ||| ||
 TC CCGTCTCC CCT TC
 C CA TAA
 GAM2463 PRX 3' GCCTCCCACTGTCCCACCGCCT 21940 AGA A_ A__ A
 C GAGGC GG GGACAG GA GC
 |||| || ||||| |||
 CTCCG CC CCTGTC CT CG
 __ AC ACC C
 GAM2463 PTGS1 3' CTTCTAACCCCTCTGCTCT 27894 G A ACAG
 AGAG CAGAGG GG AGAAG
 ||| ||||| || ||||
 TCTC GTCTCC CC TCTTC
 _ _ CAA_
 GAM2463 PTGS1 3' CTTCTAACCCCTCTGCTCT 6673 G A ACAG
 AGAG CAGAGG GG AGAAG
 ||| ||||| || ||||
 TCTC GTCTCC CC TCTTC
 _ _ CAA_
 GAM2463 PTPRS 5' GCTCCATGTGACCCTCCCTCTG 8744 _ _ GA A
 CCTC GAGGCAGAGG AGG ACA GA GC
 ||||| ||| ||| || ||
 CTCCGTCTCC TCC TGT CT CG
 C CAG AC _
 GAM2463 PTPRS 5' GCTCCATGTGACCCTCCCTCTG 28392 _ _ GA A
 CCTC GAGGCAGAGG AGG ACA GA GC
 ||||| ||| ||| || ||
 CTCCGTCTCC TCC TGT CT CG
 C CAG AC _
 GAM2463 PTPRS 5' GCTCCATGTGACCCTCCCTCTG 28390 _ _ GA A
 CCTC GAGGCAGAGG AGG ACA GA GC
 ||||| ||| ||| || ||
 CTCCGTCTCC TCC TGT CT CG
 C CAG AC _
 GAM2463 PTPRS 5' GCTCCATGTGACCCTCCCTCTG 28391 _ _ GA A
 CCTC GAGGCAGAGG AGG ACA GA GC
 ||||| ||| ||| || ||

			CTCCGTCTCC TCC TGT CT CG	
			C CAG AC _	
GAM2463	PYGB	3'	CTGCCCCCTGCCCTCT 8767 _ A A A	
			AGAGG CAG GG GG CAG	
			TCTCC GTC CC CC GTC	
			C _ _ _	
GAM2463	PYGM	5'	TCTCCCTCCCCTCTCCTCT 12130 C A CA	
			AGAGG AGAGG GGA GAGA	
			TCTCC TCTCC CCT CTCT	
			_ _ CC	
GAM2463	REQ	3'	CTTCTCTGTGTTCTGCCTC 12951 GGA G	
			GAGGCAGA G ACAGAGAAG	
			CTCCGTCT T TGTCTCTTC	
			_ _ G	
GAM2463	RFNG	3'	GCCGTCATCTCCCCTCTGCCTC 42558 A CA _ A_	
			GAGGCAGAGG GGA GA GA GC	
			CTCCGTCTCC CCT CT CT CG	
			_ _ A GC	
GAM2463	RFP	3'	GCTTCTCTGTGGGTACGTGCCC 13260 A GAGGAGG	
	CT		AG GGCA ACAGAGAAGC	
			TC CCGT TGTCTCTTCG	
			C GCATGGG	
GAM2463	RS1	3'	GCTTCTCACCCTCCACCCTCT 5878 CAGA ACA	
			AGAGG GGAGG GAGAAGC	
			TCTCC CCTCC CTCTTCG	
			CA_ CA_	
GAM2463	RXRA	3'	CTGTTTTCTCTCTGCCTT 8869 _	
			GAGGCAGAG GAGGACAG	
			TTCCGTCTC CTTTTGTC	
			T	
GAM2463	SDC4	3'	GCTGGGTCCTCTTCTGCC 8891 AGAGA	
			GGCAGAGGAGGAC AGC	
			CCGTCTTCTCCTG TCG	
			GG_	
GAM2463	SET7	5'	CTCCTCTTCCTCCTCCTCCTC 24981 CA C A	
			GAGG GAGGAGGA AGAG AG	
			CTCC CTCCTCCT TCTC TC	
			TC _ C	
GAM2463	SET7	5'	CTGCTCCTCCTCTTCCTC 24982 C _	
			GAGG AGAGGAGGA CAG	

CTCC TCTCCTCCT GTC
 T C
 GAM2463 SIGLEC11 3' GCAATCTGCCCGCCTCTGCCTC 27464 A A GAA
 GAGGCAGAGG GG CAGA GC
 ||||| || ||| ||
 CTCCGTCTCC CC GTCT CG
 G C AA_
 GAM2463 SIX3 5' GCCCCTCTCTCCTCTTCCTC 11882 C GAC AA
 GAGG AGAGGAG AGAG GC
 ||| ||||| ||| ||
 CTCC TCTCCTC TCTC CG
 T ____ CC
 GAM2463 SLC16A2 3' CTCTCTCCTCACTCTGCCTCT 13269 _ C
 AGAGGCAGAG GAGGA AGAG
 ||||| ||||| ||||
 TCTCCGTCTC CTCCT TCTC
 A C
 GAM2463 SLC6A8 3' CTTACCCCTCTGCCCT 12150 A A ACA
 AG GGCAGAGG GG GAG
 || ||||| || |||
 TC CCGTCTCC CC TTC
 C _ A_
 GAM2463 SLC9A5 3' TCCCTGCTCCTAACCCCTGCC 10936 A _ _ A
 GGCAG GG AGGA CAG GA
 |||| || ||| ||| ||
 CCGTC CC TCCT GTC CT
 C AA C C
 GAM2463 SLC9A5 3' TCCCTGCTCCTAACCCCTGCC 30065 A _ _ A
 GGCAG GG AGGA CAG GA
 |||| || ||| ||| ||
 CCGTC CC TCCT GTC CT
 C AA C C
 GAM2463 SOX9 5' GCTCTTTTTCCTCCCCTCCTC 5901 C A C A
 GAGG AG GGAGGA AGAGA GC
 ||| || ||||| ||||| ||
 CTCC TC CCTCCT TTTCT CG
 _ C T _
 GAM2463 STC1 3' CTTCTCTTTCCCCCACCCT 9134 CAGA A C
 AGG GG GGA AGAGAAG
 || | || |||||
 TCC CC CCT TCTCTTC
 CAC_ _ T
 GAM2463 STK13 5' CTCTCCGCACCCTCTGTCTC 9139 A_ CA
 GAGGCAGAGG GGA GAG
 ||||| ||| |||
 CTCTGTCTCC CCT CTC
 CACG _
 GAM2463 SUFU 3' GCTCCTCATTGCTCCCATCTGC 18257 _ GACA A
 CTCT AGAGGCAGA GGAG GAG AGC
 ||||| ||| ||| |||

TCTCCGTCT CCTC CTC TCG
 AC GTTA C
 GAM2463 SUPT6H 3' CTCCCTCCCTGCCCT 30292 A A ACA
 AG GGCAG GGAGG GAG
 || |||| |||| ||
 TC CCGTC CCTCC CTC
 C _ _ _
 GAM2463 TACC1 3' CTTTCTCCCCCTCTGCCTTT 12964 A C
 AGAGGCAGAGG GGA AGAG
 ||||| |||| ||||
 TTTCCGTCTCC CCT TTTC
 C C
 GAM2463 TAZ 3' CTTCTCCATCCTTTCTGCCTCT 5585 G CA
 AGAGGCAGAG AGGA GAGAAG
 ||||| |||| ||||
 TCTCCGTCTT TCCT CTCTTC
 _ AC
 GAM2463 TERF2 3' CTGTCCCCTGCCTCT 12189 GA A
 AGAGGCA GG GGACAG
 ||||| || |||||
 TCTCCGT CC CCTGTC
 _ _
 GAM2463 TIRAP 3' CTCAGGAAGTCCTCCCCTACAT 27477 GGC A A____
 CT AGA AG GGAGGAC GAG
 || || ||||| ||
 TCT TC CCTCCTG CTC
 ACA C AAGGA
 GAM2463 TPMT 3' GCTTCTCTGAGACCTGCTC 5939 G A__
 GAG AGG CAGAGAAGC
 ||| || |||||
 CTC TCC GTCTCTTCG
 G AGA
 GAM2463 UNC5C 5' GTCTCTCTGTCCCCCTCCCCTC 9819 CA A AG
 GAGG GAGG GGACAGAGA C
 |||| |||| ||||| |
 CTCC CTCC CCTGTCTCT G
 C_ C CT
 GAM2463 VASP 3' CTCCCCTTCCCTCTGGCTC 9397 G _ ACA
 GAG CAGAGG AGG GAG
 ||| ||||| ||| ||
 CTC GTCTCC TCC CTC
 G CT C__
 GAM2463 WNT1 3' TCTCTGCCTCTCTTCTTC 11897 C G A
 GAGG AGAG AGG CAGAGA
 |||| |||| || |||||
 CTTC TCTC TCC GTCTCT
 T _ _
 GAM2463 WNT5B 3' CTCCCGGCCCCCTGCACTCT 26360 _ A A ACA_
 AGAG GCAG GG GG GAG
 |||| |||| || |||

		TCTC CGTC CC CC CTC		
		A _ C GGCC		
GAM2463	WNT5B	3' CTCCCGGCCCCCTGCACTCT 25058	_	A A ACA_
		AGAG GCAG GG GG GAG		
		TCTC CGTC CC CC CTC		
		A _ C GGCC		
GAM2463	ZFP36L1	3' CTTATTCTCCTCCCCTCT 11364	CA	CA
		AGAGG GAGGAGGA GAG		
		TCTCC CTCCTCCT TTC		
		C_ TA		
GAM2463	AKAP11	3' TCTCTTCCCCCTCCCCCT 18375	A CA	A C
		AG GG GAGG GGA AGAGA		
		TC CC CTCC CCT TCTCT		
		_ CC C _		
GAM2463	AMOT	5' TCCTCCATCTCCGCTCTCT 28419	_ _ _	
		AGAG GC AGA GGAGGA		
		TCTC CG TCT CCTCCT		
		T CC A		
GAM2463	BA108L7.2	3' CTCCATTTCCCCTCCTCCTCT 25238	CA	A CA_
		AGAGG GAGG GGA GAG		
		TCTCC CTCC CCT CTC		
		TC _ TTAC		
GAM2463	BFAR	5' GCCTCTCCCTCTTCCTCTGCT 30479	CA	A
		GGCAGAGGAGGA GAGA GC		
		TCGTCTCCTTCT CTCT CG		
		CC C		
GAM2463	C11orf11	3' GCCTCTCATGCTGCCTCCTCTG 44787	A_ _	A
	CC	GGCAGAGGAGG CA GAGA GC		
		CCGTCTCCTCC GT CTCT CG		
		GTC A C		
GAM2463	C17orf31	5' CTCCTTAGCTCCCCTCTCCTCT 19004	C	A CA_ A
		AGAGG AGAGG GGA GAG AG		
		TCTCC TCTCC CCT TTC TC		
		_ _ CGA C		
GAM2463	C1QTNF2	3' CTCACCTCCTCCGCCTCT 25651	A	ACA
		AGAGGC GAGGAGG GAG		
		TCTCCG CTCCTCC CTC		
		C A_		
GAM2463	C20orf142	3' CTTAGCCCCCTTGCCCTCT 36930	A A	ACAGAG
		AGAGGCAG GG GG AAG		

TCTCCGTT CC CC TTC
 C _ GA____
 GAM2463 C22orf4 3' CTCCTCCTCCTGCCGCCTC 30422 AG_ CA
 GAGGC AGGAGGA GAG
 |||| ||||| ||
 CTCCG TCCTCCT CTC
 CCG C_
 GAM2463 C22orf4 3' CTTCCCAGACTCTCCTGTGTCC 30423 A ACAGA_
 CT AG GGCAGAGGAGG GAAG
 || ||||| ||||
 TC CTGTCTCCTCT CTTC
 C CAGACC
 GAM2463 C9orf7 3' GCCCCTCCCTCCCTGTC 19035 A ACA AA
 GGCAG GGAGG GAG GC
 |||| |||| || ||
 CTGTC CCTCC CTC CG
 _ _ CC
 GAM2463 CAMKK2 3' CTTCCCATTTCCTCTGCCCT 13311 A ACAGA
 AG GGCAGAGGAGG GAAG
 || ||||| ||||
 TC CCGTCTCCTTT CTTC
 _ ACC_
 GAM2463 CDIPT 3' GCTCCTCTGTCCTGCCTACCCT 13009 CAG _ A
 AGG AGG AGGACAGAG AGC
 || || ||||| ||||
 TCC TCC TCCTGTCTC TCG
 CA_ G C
 GAM2463 CECR6 3' CTGACTCCTCTCCTCT 25637 C GA
 AGAGG AGAGGAG CAG
 |||| ||||| ||
 TCTCC TCTCCTC GTC
 _ A_
 GAM2463 CHK 3' CTCTCCTGCCCTCTGCTCT 6945 G _ CA
 AGAG CAGAGG AGGA GAG
 |||| |||| |||| ||
 TCTC GTCTCC TCCT CTC
 _ CG _
 GAM2463 CLSTN3 5' TCTCTGCCCCCTCCCTCT 16274 CA A A
 AGAGG GAGG GG CAGAGA
 |||| |||| || ||||
 TCTCC CTCC CC GTCTCT
 _ C _
 GAM2463 CLSTN3 5' TTCCTGCCCTCTCTGCC 16275 GA A A
 GGCAGAG GG CAG GAA
 |||| || |||| ||
 CCGTCTC CC GTC CTT
 TC C _
 GAM2463 CMRF-35H 3' CTCTTTCCCCTTTGCCCT 34860 A A C
 AG GGCAGAGG GGA AGAG
 || ||||| || ||||

			TC CCGTTTCC CCT TCTC		
			C _ T		
GAM2463	CNNM3	3'	CTTCTCTGCCCACCTGCT 19124	GA A A	
			GGCA GG GG CAGAGAAG		
			TCGT CC CC GTCTCTTC		
			_ A C		
GAM2463	DCNP1	3'	CTTCTCCAGCTCTGCTCT 28384	G GA CAGA	
			AGAG CAGAG GGA GAAG		
			TCTC GTCTC CCT CTTC		
			_ GA _		
GAM2463	DGKD	3'	CCCTCTGTCCCCTCTGC 29880	A AA	
			GCAGAGG GGACAGAG G		
			CGTCTCC CCTGTCTC C		
			_ CC		
GAM2463	DGKD	3'	CTGCCCCTGCCCTGCCTCT 29882	A _ A_	
			AGAGGCAG GG AGG CAG		
			TCTCCGTC CC TCC GTC		
			_ G CC		
GAM2463	DJ37E16.5	3'	GCTTCTAGAGCTCTCTGCCC 21577	A GA ACAG	
	CT		AG GGCAGAG GG AGAAGC		
			TC CCGTCTC TC TCTTCG		
			C TC GAGA		
GAM2463	DKFZP434N178	5'	CTCTCTGCCCTGCTTCT 35596	AGGA A A	
			AGAGGCAG GG CAGAGA G		
			TCTTCGTC CC GTCTCT C		
			_ _ C		
GAM2463	DKFZp547I094	5'	CTTCTTCCCTTCCTCCTCAGCC 25856	A CA_	
			GGC GAGGAGGA GAGAAG		
			CCG CTCCTCCT TTCTTC		
			A TCCC		
GAM2463	DKFZp547M072	3'	GCCTCTCAGTGCCCCTGCCCT 30617	A A AGG A A	
			AG GGCAG GG AC GAGA GC		
			TC CCGTC CC TG CTCT CG		
			_ _ CG_ A C		
GAM2463	DKFZp547M072	3'	TCCTGCCCTCCTCTTCCTC 30618	C A A	
			GAGG AGAGGAGG CAG GA		
			CTCC TCTCCTCC GTC CT		
			T C _		
GAM2463	DKFZP586C1619	3'	GCTGTTTCCTCCTCCTCCCC 31020	CA CA _	
			GG GAGGAGGA GAGA AGC		

CC CTCCTCCT CTTT TCG
 CC C_ G
 GAM2463 DKFZP586M1120 3' CTATGGCCTCACTCTACCTCT 25321 C _ A G
 AGAGG AGAG GAGG CA AG
 |||| |||| |||| || ||
 TCTCC TCTC CTCC GT TC
 A A G A
 GAM2463 DKFZp762A227 5' GCTTGATATTCCTCCTCTACC 15319 C CAGAG
 GG AGAGGAGGA AAGC
 || |||| |||| ||
 CC TCTCCTCCT TTCG
 A TATAG
 GAM2463 EFS2 3' CTCCCTGACTCTGCTTCT 12477 G_ ACA
 AGAGGCAGAG AGG GAG
 |||| |||| || ||
 TCTTCGTCTC TCC CTC
 AG ____
 GAM2463 ERF 3' CTGGAAGCCCCCTCTGCCTC 13235 A A____
 GAGGCAGAGG GG CAG
 |||| || || ||
 CTCCGTCTCC CC GTC
 C GAAG
 GAM2463 FEM1B 5' CTCGGCCTCCTCTGCGTCT 17641 G ACA
 AGA GCAGAGGAGG GAG
 || |||| || ||
 TCT CGTCTCCTCC CTC
 G GG_
 GAM2463 FHX 5' CTCCTTCTCCTCCCCCTC 20458 CA CA
 GAGG GAGGAGGA GAG
 || |||| || ||
 CTCC CTCCTCTT CTC
 CC C_
 GAM2463 FLJ00024 3' CTCTGGTCTCCTTGCCCTCT 31890 G GA
 AGAGGCA AGGAG CAGAG
 |||| |||| ||||
 TCTCCGT TCCTC GTCTC
 _ TG
 GAM2463 FLJ00058 5' CTCCGCCTCCCCTGCCCTC 38510 _ A ACA
 GAGG CAG GGAGG GAG
 || || |||| ||
 CTCC GTC CCTCC CTC
 C C GC_
 GAM2463 FLJ10276 3' CTTCTCCGCCTCAGCCCT 19792 A A A CAGA
 AG GGC GAGG GGA GAAG
 || || || || ||
 TC CCG CTCC CCT CTTC
 _ A G ____
 GAM2463 FLJ10769 3' CTTTCGTTCTCCTCTGCTTC 20113 CAGA
 GAGGCAGAGGAGGA GAAG
 |||| |||| || ||

		CTTCGTCTCCTCCT CTTC		
		TG__		
GAM2463	FLJ11807	3' GCTGTCTCCCTCCTCTGCC 24512	ACA	_
		GGCAGAGGAGG GAGA AGC		
		CCGTCTCCTCC CTCT TCG		
		__ G		
GAM2463	FLJ13114	3' TCCCTTAGCCCCCCTCCTCT 23752	C A A AC_	A
		AGAGG AG GG GG AG GA		
		TCTCC TC CC CC TC CT		
		_ C C GAT C		
GAM2463	FLJ13154	3' TCCTGTCTCTCCTCCCCTCCTC 23844	CA__	_ A
	T	AGAGG GAGGAG GACAG GA		
		TCTCC CTCCTC CTGTC CT		
		TCCC T _		
GAM2463	FLJ13158	3' CTTCTCTGTTTTTCTCTCCC 24410	C	
		GG AGAGGAGGACAGAGAAG		
		CC TCTCTTTTTGTCTCTTC		
		C		
GAM2463	FLJ13189	5' GCTCCTCTTCTCCCCTCCTCCT 24332	CA A C_	A
	C	GAGG GAGG GGA AGAG AGC		
		CTCC CTCC CCT TCTC TCG		
		TC _ CT C		
GAM2463	FLJ13193	3' TCTGCCACCTCTGCCTC 25892	A A	
		GAGGCAGAGG GG CAGA		
		CTCCGTCTCC CC GTCT		
		A C		
GAM2463	FLJ13612	3' CTCTGCTCCTCTGCCCT 24861	A	GA
		AG GGCAGAGGAG CAGAG		
		TC CCGTCTCCTC GTCTC		
		_ _		
GAM2463	FLJ13612	3' CTCTGTCTCCTGCCTCT 24862	GA	G
		AGAGGCA GGAG ACAGAG		
		TCTCCGT CCTC TGTCTC		
		_ _		
GAM2463	FLJ13852	3' CTCTGTGCCCTGCCTCT 23340	A AGG	
		AGAGGCAG GG ACAGAG		
		TCTCCGTC CC TGTCTC		
		_ CG_		
GAM2463	FLJ14154	3' CTCCCCTCCCTGCTTCT 24271	A	ACA
		AGAGGCAG GGAGG GAG		

TCTTCGTC CCTCC CTC
 _ C_
 GAM2463 FLJ14249 3' CTCTATCCCTCCTCTGCCTCT 28170 AC_
 AGAGGCAGAGGAGG AGAG
 ||||| |||
 TCTCCGTCTCCTCC TCTC
 CTA
 GAM2463 FLJ14249 3' CTCTATCCCTCCTCTGCCTCT 22800 AC_
 AGAGGCAGAGGAGG AGAG
 ||||| |||
 TCTCCGTCTCCTCC TCTC
 CTA
 GAM2463 FLJ14251 3' CTTCTCTCTTCTCCTTTGCCTC 24324 C
 GAGGCAGAGGAGGA AGAGAAG
 ||||| |||||
 CTCCGTTTCCTCTT TCTCTTC
 C
 GAM2463 FLJ14442 3' CTTCTTTTCCCTCCTC 26537 C A A C
 GAGG AG GG GGA AGAGAAG
 ||| || || |||||
 CTCC TC CC CCT TTTCTTC
 _ _ _ T
 GAM2463 FLJ20378 3' CTCTCCTCCTCTCCTC 19436 C CA
 GAGG AGAGGAGGA GAG
 ||| ||||| |||
 CTCC TCTCCTCCT CTC
 _ _
 GAM2463 FLJ20651 3' GCTTCTGAACTCTTCCTCTGCC 19575 CAG_
 TCT AGAGGCAGAGGAGGA AGAAGC
 ||||| |||||
 TCTCCGTCTCCTTCT TCTTCG
 CAAG
 GAM2463 FLJ20694 3' CTCTTCACCTCCTCTGCCCT 19608 A AC_
 AG GGCAGAGGAGG AGAG
 || ||||| |||
 TC CCGTCTCCTCC TCTC
 ACT
 GAM2463 FLJ21596 3' CTTCTCTGTATCTGCCTTT 24212 GGAGG
 AGAGGCAGA ACAGAGAAG
 ||||| |||||
 TTTCCGTCT TGTCTCTTC
 A_
 GAM2463 FLJ22551 5' GCCTCCCTGCACCTCTGCC 24027 AGGA A A
 GGCAGAGG CAG GA GC
 ||||| ||| |||
 CCGTCTCC GTC CT CG
 AC_ C C
 GAM2463 FLJ22679 3' GCCCCTCTTCCCCTACCCCT 25951 CAG A C AA
 AGG AGG GGA AGAG GC
 ||| ||| ||| ||| ||

TCC TCC CCT TCTC CG
CCA _ _ CC
GAM2463 FLJ22679 3' GCCCCTCTTCCCCTACCCCT 19264 CAG A C AA
AGG AGG GGA AGAG GC
||| ||| ||| ||| ||
TCC TCC CCT TCTC CG
CCA _ _ CC
GAM2463 FLJ23441 5' GCTTCTGTTCCCTCCGCC 23989 AGA CAG
GGC GGAGGA AGAAGC
||| ||||| |||||
CCG CCTCCT TCTTCG
____ TG_
GAM2463 FLJ23537 3' TCTCCGCTCACTCTCTTCCTC 24364 C AG CA_
GAGG AGAGG GA GAGA
||| ||||| || |||
CTCC TCTCT CT CTCT
T CA CGC
GAM2463 FLJ23563 5' GCTCCTCATGTCCTCGCCTCT 33564 AGAG _ A
AGAGGC GAGGACA GAG AGC
||||| ||||| ||| |||
TCTCCG CTCCTGT CTC TCG
____ A C
GAM2463 FLJ31952 3' CTCCCCCATTTCTGGCTCT 29499 G A ACA
AGAG CAGAGG GG GAG
||| ||||| || |||
TCTC GTCTTT CC CTC
G A CC_
GAM2463 FLJ32389 3' CTTAAGACCCCTCCTCTACTTC 29434 C ACAGAG
GAGG AGAGGAGG AAG
||||| ||||| |||
CTTC TCTCCTCC TTC
A CCAGAA
GAM2463 FLJ32884 5' CTTCGTCCCCTCCGCCTCT 29527 A A AG
AGAGGC GAGG GGAC AG
||||| ||| ||| ||| ||
TCTCCG CTCC CCTG TC
C _ CT
GAM2463 FREQ 3' CTTTTCCCTGCTGCCTCT 15563 A A C
AGAGGCAG GG GGA AGAG
||||| || ||| |||
TCTCCGTC TC CCT TTTC
G _ _
GAM2463 GABARAPL3 5' CTGGCTCTCCTCTACCTC 26299 C A_
GAGG AGAGGAGG CAG
||| ||||| |||
CTCC TCTCCTCT GTC
A CG
GAM2463 GABBR1 3' CTGCAGCTCCTCTGCCTTT 7205 GA_
AGAGGCAGAGGAG CAG
||||| ||||| |||

			TTTCCGTCTCCTC	GTC		
			GAC			
GAM2463	GABBR1	3'	CTGCAGCTCCTCTGCCTTT	22422	GA_	
			AGAGGCAGAGGAG	CAG		
			TTTCCGTCTCCTC	GTC		
			GAC			
GAM2463	GBTS1	3'	GCTTTTCTTCCTCCCCTGCTCT	29731	_ A C	
	CT		AGAG GCAG GGAGGA AGAGAAGC			
			TCTC CGTC CCTCCT TCTTTTCG			
			T C _			
GAM2463	GPS2	3'	CTTCCCTGCTTCTGCCT	42148	AGGA A	
			AGGCAGAGG CAG GAAG			
			TCCGTCTTC GTC CTTC			
			_ C			
GAM2463	GPS2	5'	CTTCCCTGCTTCTGCCT	10826	AGGA A	
			AGGCAGAGG CAG GAAG			
			TCCGTCTTC GTC CTTC			
			_ C			
GAM2463	GPT2	3'	GCTTCTCTGCCATTAGCAGCCC	28524	A AGAG _ A	
	T		AG GGC GA GG CAGAGAAGC			
			TC CCG TT CC GTCTCTTCG			
			_ ACGA A _			
GAM2463	GS3955	5'	CTCTTCTGTCCCCTCCCCTCT	22302	CA A GA	
			AGAGG GAGG GGACAGA AG			
			TCTCC CTCC CCTGTCT TC			
			C _ _ TC			
GAM2463	HARS2	3'	GCTTCTCTATCCCCCTTCTGCC	28079	_ A C	
			GGCAGA GG GGA AGAGAAGC			
			CCGTCT CC CCT TCTCTTCG			
			T C A			
GAM2463	HCRTR1	5'	CTCCCTCCTCTCCCTCT	7263	C ACA	
			AGAGG AGAGGAGG GAG			
			TCTCC TCTCCTCC CTC			
			C _			
GAM2463	HERC3	3'	CTCCCTTCCTCTCCTCT	15972	C ACA	
			AGAGG AGAGGAGG GAG			
			TCTCC TCTCCTTC CTC			
			_ C _			
GAM2463	HEYL	3'	CTCCTCCTCCTCCTCCTCT	15930	CA CA A	
			AGAGG GAGGAGGA GAG AG			

TCTCC CTCCTCCT CTC TC
 TC C_ C
 GAM2463 HNT 5' GCTTTTCTCCTCCCCGCGCCTC 18594 AGA_ CA
 GAGGC GGAGGA GAGAAGC
 |||| ||||| |||||
 CTCCG CCTCCT CTTTTCG
 CGCC _
 GAM2463 HRIHFB2122 3' CTGGTCCCCCTCTGTCTC 13900 A AG
 GAGGCAGAGG GGAC AG
 ||||| ||| ||
 CTCTGTCTCC CCTG TC
 C G_
 GAM2463 ITGA10 3' CTCCCACCCTCTGCTTC 29862 A_ ACA
 GAGGCAGAGG GG GAG
 ||||| || |||
 CTTCGTCTCC CC CTC
 CA _
 GAM2463 KIAA0152 3' GCTTCCCTGTCCCTTCCCTC 16336 CA A A
 GAGG GAGG GGACAG GAAGC
 ||| ||| ||||| |||||
 CTCC CTTC CCTGTC CTTCG
 _ _ C
 GAM2463 KIAA0237 3' GCTTCCCTGCCTCCTCCTACCT 16451 CA_ A A
 TT AGAGG GAGGAGG CAG GAAGC
 |||| ||||| || |||||
 TTTCC CTCCTCC GTC CTTCG
 ATC _ C
 GAM2463 KIAA0247 3' GCTCCCCTCTCGTCTCCTCCCC 16377 CA G _ A_
 TC GAGG GAGGAG AC AGAG AGC
 ||| ||||| || ||| |||
 CTCC CTCCTC TG TCTC TCG
 C_ _ C CCC
 GAM2463 KIAA0256 3' CTCCACCTCCTCTACTCT 32185 GC ACA
 AGAG AGAGGAGG GAG
 ||| ||||| |||
 TCTC TCTCCTCC CTC
 A_ AC_
 GAM2463 KIAA0284 3' GCTCCTTTGTTCTCCCCCTC 31619 CAGA _ A
 GAGG GGAGGA CAGAG AGC
 ||| ||||| ||||| |||
 CTCC CCTCCT GTTTC TCG
 C__ T C
 GAM2463 KIAA0321 5' CTCACCTCCTCTGCCTT 31267 ACA
 GAGGCAGAGGAGG GAG
 ||||| ||| |||
 TTCCGTCTCCTCC CTC
 A_
 GAM2463 KIAA0321 3' CTTCTCTGGCTCTGCCCT 31268 A GAGGA
 AG GGCAGAG CAGAGAAG
 || ||||| |||||

TC CCGTCTC GTCTCTTC
 — G —
 GAM2463 KIAA0429 5' GCTTCTCTCATCCTCCCTCT 16472 CAGA C_
 AGAGG GGAGGA AGAGAAGC
 |||| |||| |||||
 TCTCC CCTCCT TCTCTTCG
 — AC
 GAM2463 KIAA0450 3' CTCTCTCCCTGCCTC 16031 A GAC
 GAGGCAG GGAG AGAG
 ||||| ||| |||
 CTCCGTC CCTC TCTC
 — —
 GAM2463 KIAA0451 3' CTCCCCTCCTCTCCTC 16805 C ACA
 GAGG AGAGGAGG GAG
 ||| ||||| |||
 CTCC TCTCCTCC CTC
 — C —
 GAM2463 KIAA0451 3' TCTCCCCACCCTCCCCTCCTCT 16810 C A ACA_
 AGAGG AG GGAGG GAGA
 |||| || |||| |||
 TCTCC TC CCTCC CTCT
 — C CACCC
 GAM2463 KIAA0644 3' CTTCTCTGTGTCAGGGTTGCTCCT 16783 AG AGGAG
 AG GCAG GACAGAGAAG
 || ||| |||||
 TC CGTT CTGTCTCTTC
 CT GGGA_
 GAM2463 KIAA0720 3' TTCCGCCCGCCTCTGCCTC 31238 A ACA
 GAGGCAGAGG GG GAG
 ||||| || |||
 CTCCGTCTCC CC CTT
 G CGC
 GAM2463 KIAA0775 3' TCTCCCTCTGCCTTT 16322 AGGACA
 AGAGGCAGAGG GAGA
 ||||| |||
 TTTCCGTCTCC CTCT
 — —
 GAM2463 KIAA0794 3' CTCCGTACCCTTCTGCCTC 39180 A _ A
 GAGGCAGAGG GG AC GAG
 ||||| || |||
 CTCCGTCTTC CC TG CTC
 — A C
 GAM2463 KIAA0889 3' GCTTCTCCCTGTCTTCCTCTCC 17679 C _
 TCT AGAGG AGAGGAGGACA GAGAAGC
 |||| ||||| |||||
 TCTCC TCTCCTTCTGT CTCTTCG
 — CC
 GAM2463 KIAA0937 3' GCTTCTCTGGGCCCTCCTCTCC 44017 C A_
 TC GAGG AGAGGAGG CAGAGAAGC
 ||| ||||| |||||

CTCC TCTCCTCC GTCTCTTCG
 _ CGG
 GAM2463 KIAA0939 3' CTCCCTCCTCTACTCT 31062 GC ACA
 AGAG AGAGGAGG GAG
 |||| ||||| ||
 TCTC TCTCCTCC CTC
 A_ _
 GAM2463 KIAA1042 3' CTCCCTCCCTCTGCCCT 17351 A _ ACA
 AG GGCAGAGG AGG GAG
 || ||||| ||| ||
 TC CCGTCTCC TCC CTC
 _ C _
 GAM2463 KIAA1076 3' CTTCTCTCTCTCCGTCTCT 32640 AGA AC
 AGAGGC GGAGG AGAGAAG
 ||||| |||| |||||
 TCTCTG CCTCT TCTCTC
 _ C _
 GAM2463 KIAA1138 3' CTCCGCCGGTCCCCACCCTCTG 31127 A_ A_
 CC GGCAGAGG GGAC GAG
 ||||| |||| ||
 CCGTCTCC CCTG CTC
 CACC GCCGC
 GAM2463 KIAA1172 5' CTCTCCGCCTCTGCCTC 35077 A CA
 GAGGCAGAGG GGA GAG
 ||||| |||| ||
 CTCCGTCTCC CCT CTC
 G _
 GAM2463 KIAA1185 3' TCTGTCCACCTCTGCCCCT 31371 A A
 AG GGCAGAGG GGACAGA
 || ||||| |||||
 TC CCGTCTCC CCTGTCT
 C A
 GAM2463 KIAA1193 3' CTTTACACCCCCACCTGCCTCT 33582 A_ A AC_
 AGAGGCAG GG GG AGAG
 ||||| || || ||
 TCTCCGTC CC CC TTTC
 CA C ACA
 GAM2463 KIAA1434 3' GCTTCCTGCCACCCACCCACCT 34489 CAGA_ A A A
 CT AGAGG GG GG CAG GAAGC
 |||| || || || ||||
 TCTCC CC CC GTC CTTCG
 ACCCAC A _ _
 GAM2463 KIAA1538 5' CTCTCCCCCTGCTTCT 35426 A A CA
 AGAGGCAG GG GGA GAG
 ||||| || || ||
 TCTTCGTC CC CCT CTC
 _ _ _
 GAM2463 KIAA1538 5' CTCTTCCTCCTCCTCCTCT 35427 CA C
 AGAGG GAGGAGGA AGAG
 |||| ||||| ||||

TCTCC CTCCTCCT TCTC
 TC _
 GAM2463 KIAA1538 3' CTTCAATTCCTCCTCTGTCTCT 35428 CAGA
 AGAGGCAGAGGAGGA GAAG
 ||||| ||||
 TCTCTGTCTCCTCCT CTC
 TA_
 GAM2463 KIAA1644 5' CTCTCAGAGCCTCTGCTTCT 41201 AGGAC
 AGAGGCAGAGG AGAG
 ||||| ||||
 TCTTCGTCTCC TCTC
 GAGAC
 GAM2463 KIAA1656 3' CTCATCCTCCTCCGCCT 32730 A CA
 AGGC GAGGAGGA GAG
 ||| ||||| |||
 TCCG CTCCTCCT CTC
 C A_
 GAM2463 KIAA1656 3' CTCCCTTCCCTGCCTCT 32731 A ACA
 AGAGGCAG GGAGG GAG
 ||||| ||||| |||
 TCTCCGTC CCTTC CTC
 _ C_
 GAM2463 KIAA1706 3' CTCTCTGTCTATCTCCCCT 44577 CA AG A
 AGG GAGG GACAGAGA G
 ||| ||| ||||| |
 TCC CTCT CTGTCTCT C
 C_ A_ C
 GAM2463 KIAA1775 3' CTCCCCTTCCCTCTGCTCCT 26944 AG ACA
 AG GCAGAGGAGG GAG
 || ||||| |||
 TC CGTCTCCTTC CTC
 CT CC_
 GAM2463 KIAA1831 5' CTCCCCCACCTTTCTCT 31904 C A ACA
 AGAGG AGAGG GG GAG
 ||||| ||||| |||
 TCTCC TTTCC CC CTC
 _ A CC_
 GAM2463 KIAA1855 3' TCTCTGTCCTTCCCT 44361 CAGA
 AGG GGAGGACAGAGA
 ||| ||||| |||||
 TCC CTCCTGTCTCT

 GAM2463 KIAA1862 3' GCCTCCTGTCCCTCTGTC 34175 AG A A
 GGCAGAGG GACAG GA GC
 ||||| ||||| |||
 CTGTCTCC CTGTC CT CG
 _ _ C
 GAM2463 KIAA1904 3' GCTCCTCCTTCCCTCTGCCCCT 36381 A ACA A
 AG GGCAGAGGAGG GAG AGC
 || ||||| ||| |||

			TC CCGTCTCCTTC CTC TCG			
			C _ C			
GAM2463	KIAA1938	3'	GCTTCCTGGCCCCCTCCCCC 44280	CA	A A A	
			GG GAGG GG CAG GAAGC			
			CC CTCC CC GTC CTTCG			
			CC C G _			
GAM2463	KIAA1949	5'	GCCTCTTTCCCTCCTCCTCTCC 46669	C	C_	A
		CTC	GAGG AGAGGAGGA AGAGA GC			
			CTCC TCTCCTCCT TTTCT CG			
			C CCC C			
GAM2463	KIAA1949	5'	GCCTCTTTCCCTCCTCCTCTCC 46714	C	C_	A
		CTC	GAGG AGAGGAGGA AGAGA GC			
			CTCC TCTCCTCCT TTTCT CG			
			C CCC C			
GAM2463	KIAA1949	5'	GCCTCTTTCCCTCCTCCTCTCC 44210	C	C_	A
		CTC	GAGG AGAGGAGGA AGAGA GC			
			CTCC TCTCCTCCT TTTCT CG			
			C CCC C			
GAM2463	LASP1	3'	CCCTCTGTTCTCTCCCT 12793	CA G	AA	
			AGG GAG AGGACAGAG G			
			TCC CTC TCTTGTCTC C			
			C_ _ CC			
GAM2463	LGI2	3'	CTTCCCTGCCAGCCCACCTGCC 20001	A_	A_ A A	
			GGCAG GG GG CAG GAAG			
			CCGTC CC CC GTC CTTC			
			CAC GA _ C			
GAM2463	LHPP	3'	CTCCCCTCCACCCCTGCCTCT 22675	A A	CA_	
			AGAGGCAG GG GGA GAG			
			TCTCCGTC CC CCT CTC			
			C A CCC			
GAM2463	LHPP	3'	CTCCTCCACCCCTGCCTCT 22676	A A	CA	
			AGAGGCAG GG GGA GAG			
			TCTCCGTC CC CCT CTC			
			C A C_			
GAM2463	LHPP	3'	CTCCTCCACCCCTGCCTCT 22677	A A	CA	
			AGAGGCAG GG GGA GAG			
			TCTCCGTC CC CCT CTC			
			C A C_			
GAM2463	LHPP	3'	GCCTCTCCTCCACCCCTGCCTC 22679	A A	CA A	
			GAGGCAG GG GGA GAGA GC			

CTCCGTC CC CCT CTCT CG
 C A C_ C
 GAM2463 LY6G5B 5' CTCCATCCCTCCTTCTGCCTC 22201 _ ACA_
 GAGGCAGA GGAGG GAG
 ||||| |||| ||
 CTCCGTCT CCTCC CTC
 T CTAC
 GAM2463 MGC10812 3' GCTTCTCCCTGACCCCGCCCT 25414 A AGA A A _
 AG GGC GG GG CA GAGAAGC
 || || || || |||||
 TC CCG CC CC GT CTCTTCG
 _ C_ _ A CC
 GAM2463 MGC10986 3' CTCCCCTATCTAGGTGCCTTT 24951 G_ _ ACA
 AGAGGCA AGG AGG GAG
 ||||| ||| ||| ||
 TTTCCGT TCT TCC CTC
 GGA A C_
 GAM2463 MGC15854 5' CTTCCCCATCTTCTCCTCT 29643 C _ ACAGA
 AGAGG AGAGGA GG GAAG
 |||| ||||| || |||
 TCTCC TCTTCT CC CTTC
 _ A C_
 GAM2463 MGC16824 5' CTTCTTCCACGTCCTCCTCCTC 21572 CA A_
 CTC GAGG GAGGAGGAC GAGAAG
 ||| ||||| |||||
 CTCC CTCCTCCTG TTCTTC
 TC CACC
 GAM2463 MGC20255 3' TCTCTAGGCCTCTGCTCT 27429 G AGGAC
 AGAG CAGAGG AGAGA
 ||| ||||| |||||
 TCTC GTCTCC TCTCT
 _ GGA_
 GAM2463 MGC21621 3' CTAGCCACCTCTGCCTCT 29621 A AC
 AGAGGCAGAGG GG AG
 ||||| || ||
 TCTCCGTCTCC CC TC
 A GA
 GAM2463 MGC2574 3' CTCCACACCCCACTGCCTCT 23536 A A ACA_
 AGAGGCAG GG GG GAG
 ||||| || || |||
 TCTCCGTC CC CC CTC
 A _ ACAC
 GAM2463 MGC2817 5' CTTCTCCTCCTCCTCCTCT 34763 CA CA
 AGAGG GAGGAGGA GAG
 |||| ||||| |||
 TCTCC CTCCTCCT TTC
 TC CC
 GAM2463 MGC4342 3' CTTTTCCTCCTCTGCGTCT 23624 G C
 AGA GCAGAGGAGGA AGAG
 || ||||| ||||| |||

TCT CGTCTCCTCCT TTTC
 G _
 GAM2463 NBL1 3' CTCTTCCTCCCCTCT 29839 CAGA C
 AGAGG GGAGGA AGAG
 |||| ||||| ||||
 TCTCC CCTCCT TCTC

 GAM2463 NFASC 3' GCTCCTCATTCCTCCCCTGCCC 34831 A A CA A
 T AG GGCAG GGAGGA GAG AGC
 || ||||| ||||| ||| |||
 TC CCGTC CCTCCT CTC TCG
 _ C TA C
 GAM2463 NFAT5 5' CTCCCTCCTCTTCCTC 28954 C ACA
 GAGG AGAGGAGG GAG
 ||| ||||| |||
 CTCC TCTCCTCC CTC
 T _
 GAM2463 NFAT5 5' GCTTCTCTCGGCTCTGTCTC 28958 GA GAC
 GAGGCAGAG G AGAGAAGC
 ||||| | |||||
 CTCTGTCTC C TCTCTTCG
 GG _
 GAM2463 NR4A3 5' GCTCCTGCTCCTCCTCCGCT 13845 A _ A A
 GGC GAGGAGGA CAG GA GC
 ||| ||||| ||| |||
 TCG CTCCTCCT GTC CT CG
 C C _ _
 GAM2463 NTT73 5' GCTTCTCTGCCAACAGCTCCTC 19825 C AGGA_ A
 T AGAGG AG GG CAGAGAAGC
 |||| || || |||||
 TCTCC TC CC GTCTCTTCG
 _ GACAA _
 GAM2463 NXN 3' CTTCTCCTCCTCCCCCTC 22809 CA CAGA
 GAGG GAGGAGGA GAAG
 ||| ||||| |||
 CTCC CTCCTCCT CTTC
 CC _
 GAM2463 OAZ3 5' CCCTCTGTCTACTCCCT 18280 CA GA AA
 AGG GAG GGACAGAG G
 ||| ||| ||||| |
 TCC CTC TCTGTCTC C
 _ A_ CC
 GAM2463 PFDN1 3' GCCTCTCTGGGAAGCTCTTCCT 8483 C GAGGA A
 C GAGG AGAG CAGAGA GC
 |||| ||| ||||| |||
 CTCC TCTC GTCTCT CG
 T GAAGG C
 GAM2463 PIF1 3' CTCCCCGTCCTCCTGCTCCCT 30586 C _ A_
 AGG AG AGGAGGAC GAG
 ||| || ||||| |||

			TCC TC TCCTCCTG CTC		
			C G CCC		
GAM2463	PLA2G3	5'	CTCTTTCTCCTCCTC 17928	CAG	C
			GAGG AGGAGGA AGAG		
			CTCC TCCTCCT TCTC		
			____ T		
GAM2463	POLD3	3'	TTCTGTCCCCTAACCTC 44056	CAG	A
			GAGG AGG GGACAGAG		
			CTCC TCC CCTGTCTT		
			AA_ _		
GAM2463	PP3501	3'	GCTTCTGTCTCCCCCTGCCCCT 22332	A	A AG GA
			AG GGCAG GG GACAGA AGC		
			TC CCGTC CC CTGTCT TCG		
			C C CT ____		
GAM2463	PRDM11	5'	GCTTCACACTGCTCTGCCTCT 21501		G GACAGA
			AGAGGCAGAG AG GAAGC		
			TCTCCGTCTC TC CTTCG		
			G ACA____		
GAM2463	PRDM7	3'	CTTGGCTCCCCCTGTCTC 27569	A A	CA_
			GAGGCAG GG GGA GAG		
			CTCTGTC CC CCT TTC		
			_ _ CGG		
GAM2463	PRO0233	3'	CTTCTTGCTCTCCTCTCCTC 15373	C	GA G
			GAGG AGAGGAG CA AGAAG		
			CTCC TCTCCTC GT TCTTC		
			_ TC _		
GAM2463	PRO1048	3'	CTGTGTCCACCCCTGCCTCT 20557	A A	G
			AGAGGCAG GG GGACA AG		
			TCTCCGTC CC CCTGT TC		
			C A G		
GAM2463	PTPN3	3'	TCTCTGCCCTCCCTCCCTTT 8706	C A	A
			AGAGG AG GGAGG CAGAGA		
			TTTCC TC CCTCC GTCTCT		
			C _ C		
GAM2463	RAB40C	3'	GCTCCTCCACCCAGTGCTTCTG 22147	A____	ACA A
	CC		GGCAGAGG GG GAG AGC		
			CCGTCTTC CC CTC TCG		
			GTGA CAC C		
GAM2463	RAB6B	5'	CTTCCTCCGCCTCCGCCTCT 18653	A	A CA
			AGAGGC GAGG GGA GAG		

			TCTCCG CTCC CCT TTC			
			C G CC			
GAM2463	RAB6B	5'	GCCTCTCTCTCCTCCTCCTCCT 18654	CA	C	A
		C	GAGG GAGGAGGA AGAGA GC			
			CTCC CTCCTCCT TCTCT CG			
			TC C C			
GAM2463	RBPM5	5'	CGCTCCTCCGCCCGCTCCTCC 13737	CA_____	A	III
		TCCTCCTCT	GAGGAGGA GAG AGC G			
			CTCCTCCT CTC TCG C			
			CGCCCCGC C III			
GAM2463	RBPM5	5'	GCTCCTCCTCCTCCTCTTCCTC 13738	C	CA	A
			GAGG AGAGGAGGA GAG AGC			
			CTCC TCTCCTCCT CTC TCG			
			T C_ C			
GAM2463	RFX3	5'	TCTCCTCCTCCTCCTCCTCT 8824	CA	CA	
			AGAGG GAGGAGGA GAGA			
			TCTCC CTCCTCCT CTCT			
			TC C_			
GAM2463	RFX3	5'	TCTCCTCCTCCTCCTCCTCT 28671	CA	CA	
			AGAGG GAGGAGGA GAGA			
			TCTCC CTCCTCCT CTCT			
			TC C_			
GAM2463	SAE1	3'	CTTCCAAGCACCCCTCTGCCCT 12004	A	A	ACAGA_
			AG GGCAGAGG GG GAAG			
			TC CCGTCTCC CC CTC			
			_ _ ACGAAC			
GAM2463	SARM	3'	CTCTCTCAGGACCTCTCCTCT 17458	C	AG_	C
			AGAGG AGAGG GA AGAG			
			TCTCC TCTCC CT TCTC			
			_ AGGA C			
GAM2463	SCAMP5	3'	GCCCCTCTGCCTATGTCCCTCT 29075	_____	A	AA
		GCCTC	AGGCAGAGG AGG CAGAG GC			
			TCCGTCTCC TCC GTCTC CG			
			CTGTA _ CC			
GAM2463	SCYA22	3'	CTCTAACCCATCCTCTGCCTC 43715	_	AC_	
			GAGGCAGAGGA GG AGAG			
			CTCCGTCTCCT CC TCTC			
			A CAA			
GAM2463	SLC38A5	5'	GCCTCTCTGCCTGAATCTGCCT 27298	GG_	A	A
		CT	AGAGGCAGA AGG CAGAGA GC			

TCTCCGTCT TCC GTCTCT CG
 AAG _ C
 GAM2463 SNPH 3' CTAAACCTCTCTGCCTCT 16294 G ACA
 AGAGGCAGAG AGG GAG
 ||||| ||| |||
 TCTCCGTCTC TCC TTC
 _ AAA
 GAM2463 SNPH 3' GCCCCTCTGTCCCCTTGGCTCT 16297 G G A AA
 AGAG CA AGG GGACAGAG GC
 ||| || ||| ||||| ||
 TCTC GT TCC CCTGTCTC CG
 G _ _ CC
 GAM2463 SNPH 3' GCTTCAGGCCCTCTGCTCCT 16298 AG A ACAGA
 AG GCAGAGG GG GAAGC
 || ||||| || |||||
 TC CGTCTCC CC CTTCG
 CT _ GGA_
 GAM2463 SNTA1 5' GCCCCGCTGCCCTCTGCCCT 9068 A AG A AGAA_
 AG GGCAGAGG G CAG GC
 || ||||| || ||| ||
 TC CCGTCTCC C GTC CG
 _ _ _ GCCCC
 GAM2463 SPBPBP 5' CTTCCCCCTTCCCTACCTCT 13510 C A ACAGA
 AGAGG AG GGAGG GAAG
 |||| || |||| ||||
 TCTCC TC CCTTC CTTTC
 A _ CCC_
 GAM2463 SPEC1 3' TCCCTGCCCTTCTCCTC 21516 C A A A
 GAGG AGAGG GG CAG GA
 |||| |||| || ||| ||
 CTCC TCTTC CC GTC CT
 _ _ _ C
 GAM2463 SPINT1 3' CGCCTCTCTATCCTCTCTTCCT 31392 C G C A III
 CT GAGG AGAG AGGA AGAGA GC G
 |||| |||| |||| ||| ||
 CTCC TCTC TCCT TCTCT CG C
 T _ A C III
 GAM2463 SSH2 3' CTCTCTCTCTCTCCTCT 31182 _ C A
 AGAGGAG GA AGAGA G
 ||||| || ||||| ||
 TCTCCTC CT TCTCT C
 T C C
 GAM2463 TCF-3 3' CTTCTCTCTCTTACCTCT 25306 _ C
 AGAGG AGGA AGAGAAG
 |||| |||| |||||
 TCTCC TTCT TCTCTC
 A C
 GAM2463 TLOC1 5' CTTCTCTGCTTCCTCCACGTC 9273 A_ A
 GGC GAGGAGG CAGAGAAG
 ||| ||||| |||||

			CTG CTCCTTC GTCTCTTC		
			CAC _		
GAM2463	TNKS1BP1	5'	CTCATACCTCTCTGCCTC 27224	G	ACA
			GAGGCAGAG AGG GAG		
			CTCCGTCTC TCC CTC		
			_ ATA		
GAM2463	TNRC4	3'	GCCCCCTCCCACCCCCCTGCCTC 14041	A A	ACA AA
	T		AGAGGCAG GG GG GAG GC		
			TCTCCGTC CC CC CTC CG		
			_ C ACC CC		
GAM2463	TOLLIP	3'	CTCCCCCTCCTCTCCTCT 21092	C	ACA
			AGAGG AGAGGAGG GAG		
			TCTCC TCTCCTCC CTC		
			_ CC_		
GAM2463	TOM1	3'	CTCCCTCCCTCCTCT 11986	C A	ACA
			AGAGG AG GGAGG GAG		
			TCTCC TC CCTCC CTC		
			_ _ _		
GAM2463	TOR2A	3'	GCCTCTCTGAGCCTCTGTCTCT 28221	AGGA	A
			AGAGGCAGAGG CAGAGA GC		
			TCTCTGTCTCC GTCTCT CG		
			GA__ C		
GAM2463	TSC22	3'	CTCTCTCCTCTCCTC 12640	C	GAC
			GAGG AGAGGAG AGAG		
			CTCC TCTCCTC TCTC		
			_ _		
GAM2463	TTYH2	3'	CTCTGTCCTCGTTCCCT 26378	CA	G
			AGG GA GAGGACAGAG		
			TCC TT CTCCTGTCTC		
			C_ G		
GAM2463	TUSP	3'	CTCTACTCTCTCTGCCCCT 21528	A	_ GAC
			AG GGCAGAG GAG AGAG		
			TC CCGTCTC CTC TCTC		
			C T A__		
GAM2463	VAV3	3'	GCTTCTCTCAGAGTCTCCCCCT 12760	CA	AGGAC
	CT		AGAGG GAGG AGAGAAGC		
			TCTCC CTCT TCTCTTCG		
			CC GAGAC		
GAM2463	ZFP95	3'	CTTCTCTGTGAAACACTCTACC 15921	C	GAGG__
	TT		GAGG AGAG ACAGAGAAG		

			TTCC TCTC	TGTCTCTTC		
			A	ACAAAG		
GAM2463	ZFP95	3'	CTTCTCTGTGAAACACTCTACC	29711	C	GAGG__
		TT	GAGG AGAG	ACAGAGAAG		
			TTCC TCTC	TGTCTCTTC		
			A	ACAAAG		
GAM2463	ZNF384	5'	CTCCTCCTCCTCCATCTCT	28545	CA	CA
			AGAGG GAGGAGGA	GAG		
			TCTCT CTCCTCCT	CTC		
			AC	C_		
GAM2463	LOC115509	3'	CTTCCCCTACTCTGCCTCT	36363	G	ACAGA
			AGAGGCAGAG AGG	GAAG		
			TCTCCGTCTC TCC	CTTC		
			A	C_		
GAM2463	LOC123242	5'	GCTTCTCTGGGTCCCACTCTCT	37244	C	GA _
			GG AGAG GGAC	AGAGAAGC		
			TC TCTC CCTG	TCTCTTCG		
			_ AC	GG		
GAM2463	LOC124753	5'	GCGATTCCCTCCTCTACTC	36761	GC	ACA AA
			GAG AGAGGAGG	GAG GC		
			CTC TCTCCTCC	CTT CG		
			A_	__ AG		
GAM2463	LOC126208	3'	CTCCCCGCCCTCCTCTGTCCCT	36815	A	ACA__
			AG GGCAGAGGAGG	GAG		
			TC CTGTCTCCTCC	CTC		
			C	CGCCC		
GAM2463	LOC127703	3'	CTTCCCTGTCTCTGCCTCT	36907	GGAG	A
			AGAGGCAGA	GACAG GAAG		
			TCTCCGTCT	CTGTC CTTC		
			__	C		
GAM2463	LOC128077	3'	CTTATTCCTTCTCTGCCTC	36918	CA	
			GAGGCAGAGGAGGA	GAG		
			CTCCGTCTCTTCCT	TTC		
			TA			
GAM2463	LOC132671	3'	GCTTCTCTAAAGCATCTTACCC	29777	CAG	GGAC__
		CT	AGG AGGA	AGAGAAGC		
			TCC TTCT	TCTCTTCG		
			CCA	ACGAAA		
GAM2463	LOC136288	3'	CTCTGGTACCCTCTGCCCT	37099	A	AGGA
			AG GGCAGAGG	CAGAG		

				TC CCGTCTCC	GTCTC				
				—	CATG				
GAM2463	LOC145371	3'	CTTCTCTTTCTCTGACCCCT	37846	A	—	GGAC		
			AG GG CAGAGGA	AGAGAAG					
			TC CC GTCTCTT	TCTCTTC					
			C A	—					
GAM2463	LOC145988	5'	TCTCCCCCAAGTCCTCCTCCGC	38042	A		A	—	
		CTC	GAGGC GAGGAGGAC	GAGA					
			CTCCG CTCCTCCTG	CTCT					
			C	AACCC					
GAM2463	LOC146237	3'	CTCTCCCTGCTGCCTCT	40666	A	A	CA		
			AGAGGCAG GG GGA	GAG					
			TCTCCGTC TC CCT	CTC					
			G	—					
GAM2463	LOC146488	3'	CTTACCCCTCTGCCCCT	35046	A		A	ACA	
			AG GGCAGAGG GG	GAG					
			TC CCGTCTCC CC	TTC					
			C	— A					
GAM2463	LOC146780	5'	CTGAGATCCTCCTCTGCCCT	40741	A		—		
			AG GGCAGAGGAGGA	CAG					
			TC CCGTCTCCTCCT	GTC					
			—	AGA					
GAM2463	LOC146957	3'	CTCAGCCTCTCCTGCCTCT	38278		AG	ACA		
			AGAGGCAG GAGG	GAG					
			TCTCCGTC CTCC	CTC					
			CT	GA					
GAM2463	LOC146957	3'	GCCTCTCTGCCCAGGCTCTCCT	38279		C	GA	A	A
		C	GAGG AGAG	GG CAGAGA GC					
			CTCC TCTC	CC GTCTCT CG					
			—	GGA C C					
GAM2463	LOC148195	5'	GCTTCCCTTTTCTCCTCTCCTC	40878		C		C	A
		T	AGAGG AGAGGAGGA	AG GAAGC					
			TCTCC TCTCCTCTT	TC CTTCG					
			—	T C					
GAM2463	LOC148946	3'	CTCATGTATCCTCCTCTATC	40939		GC	—	—	
			G AGAGGAGGA	CA GAG					
			C TCTCCTCCT	GT CTC					
			TA	ACT A					
GAM2463	LOC149684	5'	CTTCTCTCCCTGCCTCT	41048		A	GAC	A	
			AGAGGCAG GGAG	AG GAAG					

		TCTCCGTC CCTC TC CTTC		
		C _ _ _		
GAM2463	LOC149912 5'	CTCCCCATACCTCTGTCTCT 41086	A_	ACA
		AGAGGCAGAGG GG GAG		
		TCTCTGTCTCC CC CTC		
		ATA C_		
GAM2463	LOC151174 5'	GCTTCTCTGCTGGCCCCGCGCC 41312	AGA A A_	
	T	AGGC GG GG CAGAGAAGC		
		TCCG CC CC GTCTCTTCG		
		CG_ _ GGTC		
GAM2463	LOC151201 3'	TTTGCCCGCCTCTGCCTC 41328	A A	
		GAGGCAGAGG GG CAGA		
		CTCCGTCTCC CC GTTT		
		G C		
GAM2463	LOC151473 3'	CTCCCTCCTCTATCTCT 39119	GC	ACA
		AGAG AGAGGAGG GAG		
		TCTC TCTCCTCC CTC		
		TA _		
GAM2463	LOC151516 5'	CTGGAACCCTCCTCTGCCTC 39128	A_	
		GAGGCAGAGGAGG CAG		
		CTCCGTCTCCTCC GTC		
		CAAG		
GAM2463	LOC151657 3'	CTCCCTCTCGCTTCTGCCTC 41382	A_	CA
		GAGGCAGAGG GGA GAG		
		CTCCGTCTTC TCT CTC		
		GC CC		
GAM2463	LOC151904 5'	GCTTCTCTGTTGCGCTTGCCCC 39173	A	G GAG
	T	AG GGCA AG GACAGAGAAGC		
		TC CCGT TC TTGTCTCTTCG		
		C _ GCG		
GAM2463	LOC153688 3'	CTCCCGGCCCTCTGCCCCT 41659	A	A ACA_
		AG GGCAGAGG GG GAG		
		TC CCGTCTCC CC CTC		
		C _ GGCC		
GAM2463	LOC154877 3'	GCTTCTCTGCCCTAGTTTGGCC 41743	G_	A
	TT	GAGGCAGAG AGG CAGAGAAGC		
		TTCCGTTTT TCC GTCTCTTCG		
		GA C		
GAM2463	LOC157349 3'	CTCTGCCCTGCGCCCCT 39593	A AG	A A
		AG GGC AGG GG CAGAG		

		TC CCG TCC CC GTCTC		
		C CG _ _		
GAM2463	LOC157349 3'	CTGCGCCCCCTCCTGCCTCT	39595	_ A A_
		AGAGGCAG AGG GG CAG		
		TCTCCGTC TCC CC GTC		
		C _ GC		
GAM2463	LOC157531 5'	GCTTTCTATTCCCCCCTGCCTC	41817	A A CAG _
	T	AGAGGCAG GG GGA AGAA GC		
		TCTCCGTC CC CCT TCTT CG		
		_ C TA_ T		
GAM2463	LOC157918 3'	CTCTCCTGCCCTGCCTT	41896	A _ CA
		GAGGCAG GG AGGA GAG		
		TTCCGTC CC TCCT CTC		
		_ G _		
GAM2463	LOC157919 5'	CTCTCCTGCCCTGCCTT	39683	A _ CA
		GAGGCAG GG AGGA GAG		
		TTCCGTC CC TCCT CTC		
		_ G _		
GAM2463	LOC158187 3'	CTTCTCCTTCCCTTCCCCT	41923	CA A CA
		AGG GAGG GGA GAGAAG		
		TCC CTTC CCT CTCTTC		
		C_ _ TC		
GAM2463	LOC158235 5'	CTTCCTGTGTCCCCTCTGCC	41924	A G _
		GGCAGAGG GGACA AG AAG		
		CCGTCTCC CCTGT TC TTC		
		_ G C		
GAM2463	LOC158288 5'	CTCACCTCTCTGCCTCT	41929	G ACA
		AGAGGCAGAG AGG GAG		
		TCTCCGTCTC TCC CTC		
		_ A_		
GAM2463	LOC165721 5'	CTCCACGTTCCCTCTCCTCT	40191	C A A_
		AGAGG AGAGG GGAC GAG		
		TCTCC TCTCC CTTG CTC		
		_ _ CAC		
GAM2463	LOC165741 3'	GCCTCTCTGAGCCCTGGCTC	42191	G A AGGA A
		GAG CAG GG CAGAGA GC		
		CTC GTC CC GTCTCT CG		
		G _ GA_ C		
GAM2463	LOC196463 3'	GCTCCTCCCAGCTCTGGCCCCT	42374	A _ GA ACA A
		AG GGC AGAG GG GAG AGC		

TC CCG TCTC CC CTC TCG
 C G GA _ C
 GAM2463 LOC196955 5' GCTTCTCTGGGTCCCACTCTCT 37936 C GA _
 GG AGAG GGAC AGAGAAGC
 || ||| ||| |||||
 TC TCTC CCTG TCTCTTCG
 _ AC GG
 GAM2463 LOC200010 3' CTTCTCTGTCCTTCTCCCT 43278 CA
 AGG GAGGAGGACAGAGAAG
 ||| |||||
 TCC CTCTTCCTGTCTCTTC
 _
 GAM2463 LOC200269 3' CTTCCCTTTCTCTACCTT 42760 C ACAGA
 GAGG AGAGGAGG GAAG
 ||| ||||| |||
 TTCC TCTCTTTC CTTC
 A C_
 GAM2463 LOC201245 5' CTCGTGGCCCTGCTCTGCCTCT 42230 G A_ _
 AGAGGCAGAG AGG CA GAG
 ||||| ||| |||
 TCTCCGTCTC TCC GT CTC
 G CG G
 GAM2463 LOC201294 3' GCCTCCCTGCCTGCTCCTCTGC 42567 _ A A A
 C GGCAGAGGA GG CAG GA GC
 ||||| ||| |||
 CCGTCTCCT CC GTC CT CG
 CGT _ C C
 GAM2463 LOC201562 3' GCCTTTTTTCTCCTCCCCATCCC 42883 A CAGA_ C A
 CT AG GG GGAGGA AGAGA GC
 || || |||| ||||
 TC CC CCTCCT TTTT CG
 C TACCC _ C
 GAM2463 LOC201702 5' CTCCCTCCCTCTGCCTT 42901 _ ACA
 AGAGGCAGAGG AGG GAG
 ||||| ||| |||
 TTTCCGTCTCC TCC CTC
 C _
 GAM2463 LOC203248 3' TCTCTGACTTCTCTTCCTC 43020 C GA
 GAGG AGAGGAG CAGAGA
 ||| ||||| |||||
 CTCC TCTCTTC GTCTCT
 T A_
 GAM2463 LOC203504 3' CTTCTCTACCTCCCCTC 43571 CAGA AC
 GAGG GGAGG AGAGAAG
 ||| ||||| |||||
 CTCC CCTCC TCTCTTC
 _ A_
 GAM2463 LOC219540 3' CTTCTTTGTTCTCTGCCCC 44958 A GA
 T AG GGCAGAG GGACAGAGAAG
 || ||||| |||||

		TC CCGTCTC CTTGTTTCTTC		
		C TC		
GAM2463	LOC219654 3'	CTTTCCTTCCCCTCTGCCTC 43875	A C AG	
		GAGGCAGAGG GGA AG AAG		
		CTCCGTCTCC CCT TC TTC		
		— — CT		
GAM2463	LOC219654 3'	TCTCTGTCCCTTGCC 43877	GA A	
		GGCA GG GGACAGAGA		
		CCGT TC CCTGTCTCT		
		— —		
GAM2463	LOC219688 5'	CTCCTCCTCCTCTTCCTC 44698	C CA	
		GAGG AGAGGAGGA GAG		
		CTCC TCTCCTCCT CTC		
		T C_		
GAM2463	LOC219688 5'	GCCCCGCTGCCCCCTCCTCCT 44699	CA A A AGAA	
	C	GAGG GAGG GG CAG GC		
		CTCC CTCC CC GTC CG		
		TC C C GCCC		
GAM2463	LOC219848 3'	CTCTCCTCTCTCCTC 43984	C G CA	
		GAGG AGAG AGGA GAG		
		CTCC TCTC TCCT CTC		
		— — —		
GAM2463	LOC220565 5'	CTCCTCCTCCTCCTCCTCCTC 43634	CA CA A	
		GAGG GAGGAGGA GAG AG		
		CTCC CTCCTCCT CTC TC		
		TC C_ C		
GAM2463	LOC221042 3'	GCCTCTCTACGGCTCTGCTTC 44756	GAGGAC A	
		GAGGCAGAG AGAGA GC		
		CTTCGTCTC TCTCT CG		
		GGCA_ C		
GAM2463	LOC221474 5'	GCTGGGTGATTCTCCCCTGCCT 44380	A _ GAGA	
	CT	AGAGGCAG GGAGGA CA AGC		
		TCTCCGTC CCTCTT GT TCG		
		C A GGG_		
GAM2463	LOC221683 5'	GCTTCTCCCATCCCTGCCTT 45004	A _ ACA	
		GAGGCAG GGA GG GAGAAGC		
		TTCCGTC CCT CC CTCTTCG		
		_ A _		
GAM2463	LOC221922 5'	CTCCCCTTCCTCCTCTGCC 44534	CA_	
		GGCAGAGGAGGA GAG		

		CCGTCTCCTCCT CTC			
		TCCC			
GAM2463	LOC253216 3'	CTTCTCTCCCTCCTCCTC 45520	CAG	AC	
		GAGG AGGAGG AGAGAAG			
		CTCC TCCTCC TCTCTTC			
		___ C_			
GAM2463	LOC253609 5'	CTCCCTCCCTGTCTCT 46259	A	ACA	
		AGAGGCAG GGAGG GAG			
		TCTCTGTC CCTCC CTC			

GAM2463	LOC253715 5'	CTCTTGTCTCCTCTGCCTC 46311	GA	_	
		GAGGCA GGAGGACA GAG			
		CTCCGT CCTCCTGT CTC			
		___ T			
GAM2463	LOC253805 5'	GCTGAGGTCTCCTCTGCCTC 46136		G AGAGA	
		GAGGCAGAGGAG AC AGC			
		CTCCGTCTCCTC TG TCG			
		_ GAG_			
GAM2463	LOC254057 3'	GCTCCCCTGTCCCCTGCTCTTC 46348	C _ A	AGA	
	T	AGAGG AG AGG GGACAG AGC			
		TCTTC TC TCC CCTGTC TCG			
		_ G _ CCC			
GAM2463	LOC254532 5'	CTTCTCCCGTCCTCCCCTCCCC 46210	A C A	A_	
	T	AG GG AG GGAGGAC GAGAAG			
		TC CC TC CCTCCTG CTCTTC			
		_ C C CC			
GAM2463	LOC255040 3'	CTCCAAATTCCTCCTCTGCGTC 46109	G	CA__	
		GA GCAGAGGAGGA GAG			
		CT CGTCTCCTCCT CTC			
		G TAAAC			
GAM2463	LOC255041 3'	CTCCAAATTCCTCCTCTGCGTC 46112	G	CA__	
		GA GCAGAGGAGGA GAG			
		CT CGTCTCCTCCT CTC			
		G TAAAC			
GAM2463	LOC256267 3'	TCTGCCCACCTCTGCCTC 46278	A A		
		GAGGCAGAGG GG CAGA			
		CTCCGTCTCC CC GTCT			
		A C			
GAM2463	LOC256846 5'	CTTTCCTCTCTGCCTCT 45697	G C		
		AGAGGCAGAG AGGA AG			

TCTCCGTCTC TCCT TC
 _ T
 GAM2463 LOC257106 3' CTCCCCACCCTCTGCCTC 45677 A_ ACA
 GAGGCAGAGG GG GAG
 ||||| || |||
 CTCCGTCTCC CC CTC
 CA C_
 GAM2463 LOC51236 3' GCTTCTCCCCAGCCACCCTCT 18572 A A_ ACA_
 GCCCCCT G GGCAGAGG GG GAGAAGC
 | ||||| || |||||
 C CCGTCTCC CC CTCTTCG
 C CA GACCCC
 GAM2463 LOC51337 3' CTCCTCCTCCTCCTCTACCTC 18763 C CA A
 GAGG AGAGGAGGA GAG AG
 ||| ||||| ||| ||
 CTCC TCTCCTCCT CTC TC
 A C_ C
 GAM2463 LOC57105 3' GCTCCCTGTCTCTTCAATCC 21640 A CA_ AGA
 CT AG GG GAGGAGGACAG AGC
 || || ||||| |||
 TC CC CTTCTCCTGTC TCG
 _ TAA CCC
 GAM2463 LOC57105 3' GCTTCTCCAGCTCCCCTGTCCT 21642 _ A GACA
 CT AGAGG CAG GGAG GAGAAGC
 |||| ||| ||| |||||
 TCTCC GTC CCTC CTCTTCG
 T C GAC_
 GAM2463 LOC57107 5' CTGTAAGTTCCTCCTCTGCCCC 21650 A _____
 T AG GGCAGAGGAGGA CAG
 || ||||| |||
 TC CCGTCTCCTCCT GTC
 C TGAAT
 GAM2463 LOC84548 3' TCTCTCCGCCTTCCTCTGCC 35299 _ AC_
 GGCAGAGGA GG AGAGA
 ||||| || |||||
 CCGTCTCCT CC TCTCT
 T GCC
 GAM2463 LOC90072 3' GCTTCTCCCTGTCTTCCTCTCC 30729 C ____
 TCT AGAGG AGAGGAGGACA GAGAAGC
 |||| ||||| |||||
 TCTCC TCTCCTTCTGT CTCTTCG
 CC
 GAM2463 LOC90288 3' TTTCCCTCCCCTGACCTCT 31118 _ A ACA
 AGAGG CAG GGAGG GAGA
 |||| ||| |||| |||
 TCTCC GTC CCTCC CTTT
 A C ____
 GAM2463 LOC90550 3' CTCCTGACCCTCCGCC 36178 AGA A_ A
 GGC GGAGG CAG GAAG
 ||| |||| ||| |||

CCG CCTCC GTC CTTC
 ____ CA _
 GAM2463 LOC90736 3' GCTTCCCTGTGTCCTCTCTCCC 31957 C G G ____
 TCT AGAGG AGAG AGGACA A GAAGC
 |||| |||| |||| | ||||
 TCTCC TCTC TCCTGT T CTTCG
 C _ G CC
 GAM2463 LOC90917 3' CTTCTCTGCACTGCCCCCTC 32166 CAGA _ GA
 GAGG GG AG CAGAGAAG
 ||| || |||||
 CTCC CC TC GTCTCTTC
 ____ G AC
 GAM2463 LOC91397 5' CCCTCCCCCCTTCCTCT 32780 C A A ACA AA
 AGAGG AG GG GG GAG G
 |||| || || || |
 TCTCC TC CC CC CTC C
 T _ _ C _ CC
 GAM2463 LOC91960 3' GCTCCCTGTTTTCTTCCTCT 33613 CAG AGA
 AGAGG AGGAGGACAG AGC
 |||| ||||| ||
 TCTCC TTCTTTTGTC TCG
 ____ CCC
 GAM2463 LOC92230 5' GCCCCTTGCCCACCTGCCTCT 34008 GA A ACA AA
 AGAGGCA GG GG GAG GC
 ||||| || || || ||
 TCTCCGT CC CC TTC CG
 _ A CG _ CC
 GAM2463 LOC92405 3' GCTTCCCTGTCTTGAGGGCGT 34304 G AGAG A
 CT AGA GC GAGGACAG GAAGC
 ||| || ||||| ||||
 TCT CG TTCCTGTC CTTCG
 G GGAG C
 GAM2463 LOC92466 3' TCTGCCACCTCTGCCTC 34397 A A
 GAGGCAGAGG GG CAGA
 ||||| || ||||
 CTCCGTCTCC CC GTCT
 A C
 GAM2463 LOC92710 5' CTCTTTGCTCTGCCTCT 34835 GAGGA A
 AGAGGCAGAG CAGAGA G
 ||||| |||| |
 TCTCCGTCTC GTTTCT C
 ____ C
 GAM2463 LOC95702 5' CTTCTCTCCCTCCTCCTC 31383 CAG AC
 GAGG AGGAGG AGAGAAG
 ||| |||| |||||
 CTCC TCCTCC TCTCTTC
 ____ C_
 GAM2464 BCL7A 3' AGGACTGGGCGTCTCCAAGCCC 21986 C _ GGA C
 A TGGGCT GG GACGC CG TCCT
 ||||| || |||| || ||||

		ACCCGA CC CTGCG GT AGGA		
		A T G_ C		
GAM2464	HERC2	3' AGAAGCGTCCGTCCTCGAGCC 11042	AC	C
		GGCTCGGG GCGGACGCT CT		
		CCGAGCTC TGCCTGCGA GA		
		C_ A		
GAM2464	ITM2B	5' AGCCCGCGCCCCGAGCCC 22538	A	AC
		GGGCTCGGG CGCGG GCT		
		CCCGAGCCC GCGCC CGA		
		C _		
GAM2464	DKFZp586l021	3' AGAAGCGTCCGTGGGAACTCCA 26017	CTCGGGA	C
		TGGG CGCGGACGCT CT		
		ACCT GTGCCTGCGA GA		
		CAAGG_ A		
GAM2464	KIAA1649	3' GGACGGTATCCCGAGCCCA 26108	CG GGA	C
		TGGGCTCGGGA C CG TCC		
		ACCCGAGCCCT G GC AGG		
		AT _ _		
GAM2464	KIAA1856	3' GGAGCCGGCCCAAGCCCA 44525	C A CGGAC	
		TGGGCT GGG CG GCTCC		
		ACCCGA CCC GC CGAGG		
		A G _ _ _		
GAM2464	MCF2L	3' GGCCACGTGCCCCGAGCCCA 30508	A GAC	
		TGGGCTCGGG CGCG GCT		
		ACCCGAGCCC GTGC CGG		
		C ACC		
GAM2464	MGC20235	3' GTCCACATCCTGAGCCCA 29668	CGC	
		TGGGCTCGGGA GGAC		
		ACCCGAGTCCT CTG		
		ACA		
GAM2464	WIT-1	3' GGCCCGCGCCCCGAGCCC 17990	A AC	
		GGGCTCGGG CGCGG GCT		
		CCCGAGCCC GCGCC CGG		
		C _		
GAM2464	LOC143888	3' GAGCAAGCTGTCCTGAGCCCA 37670	_ GGAC	
		TGGGCTCGGGAC GC GCTC		
		ACCCGAGTCCTG CG CGAG		
		T AA_		
GAM2464	LOC147463	5' AGGACAAGGCGCCCCGGGCCCA 38340	A GGACGC	
		TGGGCTCGGG CGC TCCT		

ACCCGGGCCC GCG AGGA
 C GAAC__
 GAM2464 LOC91695 5' GGACGGTATCCCGAGCCCA 33252 CG GGA C
 TGGGCTCGGGA C CG TCC
 ||||| | ||||
 ACCCGAGCCCT G GC AGG
 AT__ _
 GAM2465 PRG1 3' ATACCTCATACTGCTTTAC 8590 C CGGC
 GTAAAGCAGTA GAGG AT
 ||||| |||| ||
 CATTTCGTCAT CTCC TA
 A A__
 GAM2465 BSPECV 5' ATGCCGCCTGTGTGCCGT 18747 A _
 GC GTACG AGGCGGCAT
 || |||| |||||
 TG CGTGT TCCGCCGTA
 C G
 GAM2466 ARHGAP6 3' CAAGAAAAAGGCAGTGCCTC 6842 CC__
 GAGGCACTGCT TTTTG
 ||||| ||||
 CTCCGTGACGG AGAAC
 AAAA
 GAM2466 ARHGAP6 3' CAAGAAAAAGGCAGTGCCTC 15084 CC__
 GAGGCACTGCT TTTTG
 ||||| ||||
 CTCCGTGACGG AGAAC
 AAAA
 GAM2466 CNTNAP2 3' CCGCCCAAGCTCTCAGTGCCT 15418 CTCCT A
 AGGCACTG TTTG GCGG
 ||||| |||| ||||
 TCCGTGAC GAAC CGCC
 TCTC_ C
 GAM2466 DDAH2 5' CGCTTAGACAATGCCCCG 15142 A C CTCCT
 CG GGCA TG TTTGAGCG
 || |||| || |||||
 GC CCGT AC AGATTCGC
 C A ____
 GAM2466 DGKG 5' CCGCGAAGAAGGAGCGCCCCG 7026 A ACT GA
 CG GGC GCTCCTTTT GCGG
 || |||| ||||| ||||
 GC CCG CGAGGAAGA CGCC
 C ____ AG
 GAM2466 HOXB3 5' CGCTTGGAACAGACCCCG 7921 A CA C TTTT
 CG GG CTG TCC GAGCG
 || || |||| ||||
 GC CC GAC AGG TTCGC
 _ CA A ____
 GAM2466 OXTR 5' CCGCTCATTTGCAGTGGCTC 6619 G TCCTTT
 GAG CACTGC TGAGCGG
 ||||| |||||

CTC GTGACG ACTCGCC
 G TTT___
 GAM2466 ENDO180 3' CAGGAGGAGCAGCACCCG 12675 A CA
 CG GG CTGCTCCTTTTG
 || || |||||
 GC CC GACGAGGAGGAC
 _ AC
 GAM2466 FLJ14490 3' CTGGAAAGGAGCAGTGCCT 26545 G
 AGGCACTGCTCCTTTT AG
 |||||
 TCCGTGACGAGGAAAG TC
 G
 GAM2466 FLJ20435 3' CCAGCGGAAGGAGCTGTGCCCC 19467 A T AGC
 G CG GGCAC GCTCCTTTTG GG
 || ||||| ||
 GC CCGTG CGAGGAAGGC CC
 C T GA_
 GAM2466 FLJ22202 3' CCGTAGGAGGGACAGTACCTC 24336 C C GA
 GAGG ACTG TCCTTTT GCGG
 ||||| |||||
 CTCC TGAC AGGGAGG TGCC
 A _ A_
 GAM2466 KIAA0555 5' CTGGAAAGGAACAAGTGCCTCG 30187 GC_ G
 CGAGGCACT TCCTTTT AG
 ||||| |||||
 GCTCCGTGA AGGAAAG TC
 ACA G
 GAM2466 MGC4766 5' CTTAAAAGAGCCAATGCC 25465 CT_ C
 GGCA GCTC TTTTGAG
 ||||| |||||
 CCGT CGAG AAAATTC
 AAC _
 GAM2466 NXN 3' CCAGCGGAAGGAGCTGTGCCCC 22805 A T AGC
 G CG GGCAC GCTCCTTTTG GG
 || ||||| ||
 GC CCGTG CGAGGAAGGC CC
 C T GA_
 GAM2466 LOC93349 3' CCGCCCAAAAACAAATCCTC 28768 CAC CTCC A
 GAGG TG TTTTG GCGG
 ||||| |||||
 CTCC AC AAAAC CGCC
 TAA A__ C
 GAM2467 LOC154043 5' CCGAGCGCGCACGCTCTG 39458 A ACCGA _ A
 TAGA CGTGC GCG TCG G
 ||||| |||||
 GTCT GCACG CGC AGC C
 C _ G C
 GAM2468 GARS 5' CCGCCGCCGCTCCCGG 7795 A AGTC A
 CCG GA GC GCGGCGG
 ||||| |||||

GGC CT CG CCGCCGCC
C C___ _
GAM2468 MARK3 5' CCCGCCGCCCGCAGGCTCGG 8188 AAGTC A
CCGAG GC GGCGGCGGG
||||| || |||||
GGCTC CG CCGCCGCC
GGA___ C
GAM2468 RFP2 5' CCCGCCGCCCGGCTCCTCTCGG 27399 ___ CA
CCGAGA AGTCG GGCGGCGGG
||||| ||||| |||||
GGCTCT TCGGC CCGCCGCC
CC ___
GAM2468 DKFZP434H204 5' CCCGCCGCCCGTGTCTCTCGG 33016 ___ GT A
CC GAGAA CGC GGCGGCGGG
|| ||||| || |||||
GG CTCTT GTG CCGCCGCC
TC ___ C
GAM2468 FBXO26 5' CCCGCCGCTGCCGCCTCCG 24405 A A C G
CG GA GT GCAG CGGCGGG
|| || ||||| |||||
GC CT CG CGTC GCCGCC
_ C C _
GAM2468 FLJ12089 5' CCGCCGCCGCCCTCGGTG 23771 AAGTC A
TACCGAG GC GGCGGCGG
||||| || |||||
GTGGCTC CG CCGCCGCC
C___ G
GAM2468 FLJ32919 5' CGGACCTGCGACTTCCG 29408 A CGG
CG GAAGTCGCAGG CG
|| ||||| ||
GC CTTCAGCGTCC GC
_ AG_
GAM2468 KIAA0963 5' CCCGCCGCCTGCTGCCCGG 17343 AGAA C
CCG GT GCAGGCGGCGGG
|| || |||||
GGC CG CGTCCGCCGCC
C___ T
GAM2468 UAP1 5' CCCGCCGCCCGCGGCCCGG 9087 AGAA A
CCG GTCGC GGCGGCGGG
|| ||||| |||||
GGC CGGCG CCGCCGCC
CCCC _
GAM2468 XPO5 5' CCCGCCGCCCGCCGCGGCCCGG 43840 AGAA A___
TA TACCG GTCGC GGCGGCGGG
||||| ||||| |||||
ATGGC CGGCG CCGCCGCC
C___ CCGC
GAM2468 LOC128402 3' CCTGGCCACACCTTCTCGG 37317 TCGCA GG
CCGAGAAAG GGC CGGG
||||| || |||||

		GGCTCTTC CCG GTCC	
		CACA_ _	
GAM2468	LOC146243 5'	CCCGCCGCCTGGAAGTTCT 40676	G_ G
		AGAA TC CAGGCGGCGGG	
		TCTT AG GTCCGCCGCC	
		GA _	
GAM2468	LOC153811 3'	CCCGCCGCCTGCGTTCTC 39414	GT
		GAGAA CGCAGGCGGCGGG	
		CTCTT GCGTCCGCCGCC	
		—	
GAM2468	LOC157226 5'	CCCGCCGCCCGGCCCTC 31975	AA T CA
		GAG G CG GGCGGCGGG	
		CTC C GC CCGCCGCC	
		C_ _ CC	
GAM2468	LOC222166 5'	CCCGCCGCCCGCGTCCCGG 45153	A AGT A_
		CCG GA CG GGCGGCGGG	
		GGC CT GCG CCGCCGCC	
		C _ _ CC	
GAM2468	LOC93017 5'	CCCGCCGCCAGCTACCCGG 35254	AGAA C A
		CCG GT GC GGCGGCGGG	
		GGC CA CG CCGCCGCC	
		C _ _ T A	
GAM2469	DIA1 5'	CAGTTGGGCCATATGGTGCT 14245	_____ T
		AGCACCAT CCGA CTG	
		TCGTGGTA GGTT GAC	
		TACCG _	
GAM2469	DLEC1 3'	ACAGTGTGCTCCAGATGGTGCT 14268	CGATCTG C
		AGCACCATC ACAC GT	
		TCGTGGTAG TGTG CA	
		ACCTCG_ A	
GAM2469	DLEC1 3'	ACAGTGTGCTCCAGATGGTGCT 14262	CGATCTG C
		AGCACCATC ACAC GT	
		TCGTGGTAG TGTG CA	
		ACCTCG_ A	
GAM2469	HAX1 5'	ACAGTGTCAGGATCGCGGGCTT 12764	A ATC _ C
		AAGC CC CGATC TGACAC GT	
		TTCG GG GCTAG ACTGTG CA	
		_ C_ G A	
GAM2469	NTSR1 3'	ACGGTGTCTCTCAGGATGGTGC 8365	GATCT
	T	AGCACCATCC GACACCGT	

TCGTGGTAGG CTGTGGCA
 ACTCT

GAM2469 GOLGA1 3' ACGGCCCTTTGAGATGGTGC 7858 _ TCTGACA
 GCACCATC CGA CCGT
 ||||| || ||||
 CGTGGTAG GTT GGCA
 A TCCC__

GAM2469 LOC149566 3' ACAGTATCAGATTGAGTGAGCT 41014 AC TC C C
 T AAGC CA CGATCTGA AC GT
 ||| || ||||| ||||
 TTCG GT GTTAGACT TG CA
 A_ GA A A

GAM2469 LOC150967 5' ACAGTGTGAGGGTTAGATG 39033 CG _ C
 CATC ATC TGACAC GT
 ||| || ||||| ||
 GTAG TGG ACTGTG CA
 AT G A

GAM2469 LOC151124 5' CAGAGACGGATGGTGTTT 41300 A_
 AAGCACCATCCG TCTG
 ||||| ||||
 TTTGTGGTAGGC AGAC
 AG

GAM2470 EMP1 3' ACGGCTGTCCCTCATGGAGACC 7130 T C__ G
 TC GAGGTCT CCA GGC AGCCGT
 ||||| || |||||
 CTCCAGA GGT CTG TCGGCA
 _ ACTCC _

GAM2471 NOVA1 3' TCATTTCTGTCAAAC 8349 C CT
 AGT TGACAGAA ATGA
 || ||||| ||||
 TCA ACTGTCTT TACT
 A _

GAM2471 NOVA1 3' TCATTTCTGTCAAAC 13218 C CT
 AGT TGACAGAA ATGA
 || ||||| ||||
 TCA ACTGTCTT TACT
 A _

GAM2471 BC022889 3' TAATCATACAAATCAGACTTTA 40686 CAGAAC
 TAAAGTCTGA TATGATTA
 ||||| |||||
 ATTCAGACT ATACTAAT
 AAAC__

GAM2471 KIAA0446 3' AATCCTGCTGTCAGAGCTCA 34144 A _ AACTAT
 A AG TCTGACAG GATT
 || ||||| ||||
 A TC AGACTGTC CTAA
 C G GTC__

GAM2472 ITGA11 3' TTCCCCCACCAGCTGCAGC 14515 ACGA T A
 GCTGCA CT GT GGGGGAA
 |||| || |||||

CGACGT GA CA CCCCCTT
C__ C _

GAM2472 SFTP2 3' TCCCCTTGCAAACCATCCCAGC 13809 CAACGAC
GCTG TTGTAGGGGGA
|||| |||||||
CGAC AACGTTCCCCT
CCTACCA

GAM2472 SRRM1 3' CCCCTGCAGCCATTGCAGC 12450 CGAC
GCTGCAA TTGTAGGGG
||||| |||||||
CGACGTT GACGTCCCC
ACC_

GAM2472 GREB1 3' CTGACAATCATTGCAGC 35853 C C A
GCTGCAA GA TTGT GG
||||| || ||| ||
CGACGTT CT AACA TC
A _ G

GAM2472 KIAA0537 5' TCCCCCTCCTGCGCTGCGAGC 16868 _ A ACTTGT
GCT GCA CG AGGGGGA
||| ||| || |||||||
CGA CGT GC TCCCCCT
G C GTCC__

GAM2472 MGC4504 3' ATTCCCCCAGTGCTGCTGC 23558 T A G TGTA
GC GCA C ACT GGGGGAAT
|| ||| ||| |||||||
CG CGT G TGA CCCCCTTA
T C _ C__

GAM2472 P2RX5 3' TCCCCTCTGCAAGTGCCACAGC 8410 CAACG _
GCTG ACTTGTA GGGGA
|||| ||||||| |||||
CGAC TGAACGTC CCCCT
ACCG_ T

GAM2472 LOC148918 5' TTCCCCTGAAGACGTTACAGC 38615 C A G
GCTG AACG CTT TAGGGGGA
|||| |||| ||| |||||||
CGAC TTGC GAA GTCCCCTT
A A _

GAM2473 CDKN1C 5' CGTCCGGACGAGACAGGCG 5521 A C TTTT
TG CC GTCTCGTCT ACG
|| || ||||||| |||
GC GG CAGAGCAGG TGC
_ A CC__

GAM2473 DTNA 3' GGGAGACGAGAGGGTCA 7083 G
TGACCC TCTCGTCTTT
||||| |||||||
ACTGGG AGAGCAGAGGG
_

GAM2473 DTNA 3' GGGAGACGAGAGGGTCA 26840 G
TGACCC TCTCGTCTTT
||||| |||||||

ACTGGG AGAGCAGAGGG

GAM2473 DTNA 3' GGGAGACGAGAGGGTCA 26845 G
TGACCC TCTCGTCTTT
||||| |||||||
ACTGGG AGAGCAGAGGG

GAM2473 DTNA 3' GGGAGACGAGAGGGTCA 26850 G
TGACCC TCTCGTCTTT
||||| |||||||
ACTGGG AGAGCAGAGGG

GAM2473 DKFZP564B1023 5' CGCAGTCCTGACGAGCGGGTCA 25342 T TTTT A
TGACCCG CTCGTC TT CG
||||| ||||| ||
ACTGGGC GAGCAG GA GC
TCCT C

GAM2473 NOL4 5' CGTAAAAAATACGAACGGATC 9875 C C C
GA CCGT TCGT TTTTACG
|| ||| ||| |||||||
CT GGCA AGCA AAAAAATGC
A _ T

GAM2473 SC65 3' AAAAAACAAGACGGGCCG 13173 A C C
TG CCCGTCT GT TTTTT
|| |||||| || |||||
GC GGGCAGA CA AAAAA
C A _

GAM2474 KIAA0475 5' ACCACCAGCTCTCCTT 16945 C ACA
AAGGAGAGC GGT GGT
||||||| ||| |||
TTCCTCTCG CCA CCA
A _

GAM2474 LOC257482 3' CAACCCTTCATGGCTCTCCTTC 45234 GTACA
AG TTGAAGGAGAGCCG GGTG
||||||| |||||
GACTTCCTCTCGGT CCAAC
ACTTC

GAM2475 AK1 3' ACTCAATGTCCCCCTCACC 6084 _ A CT
GG GAG GGGACATT GT
|| ||| |||||| ||
CC CTC CCCTGTAA CA
A C CT

GAM2475 CDK5R2 3' CACACCCCTCTCCCCT 10040 A ACATTC
AG GGGAGAGGG TGTG
|| |||||| |||
TC CCCTCTCCC ACAC
C _

GAM2475 EGR2 3' ACCCTTTCCTGTCCCTCTCTCC 5969 A TTCTGT
CT AG GGGAGAGGGACA GGT
|| ||||||| |||

			TC CTCTCTCCCTGT	CCA		
			C	CCTTTC		
GAM2475	FXR2	3'	ACAGGGTCATACCCCCTCCCTC	11269	A	AC__
	T		AGAGGGAG GGG	ATTCTGT		
			TCTCCCTC CCC	TGGGACA		
			C	ATAC		
GAM2475	ITGA3	3'	GGAATTCCTCCCCCTC	7967	A	C
			GAGGG GAGGGA	ATTCT		
			CTCCC CTCCCT	TAAGG		
			C	_		
GAM2475	ITGA3	3'	GGAATTCCTCCCCCTC	12010	A	C
			GAGGG GAGGGA	ATTCT		
			CTCCC CTCCCT	TAAGG		
			C	_		
GAM2475	MFGE8	3'	ACCACACAGTCACCCCTCCCTC	12556	A	AC C
			GAGGGAG GGG	ATT TGTGGT		
			CTCCCTC CCC	TGA ACACCA		
			_	AC C		
GAM2475	NYX	3'	ACCACAATCCTCCTCCTCCTCT	22886	GA	ACATTC
			AGAGG GAGGG	TGTGGT		
			TCTCC CTCCT	ACACCA		
			TC	CCTA__		
GAM2475	PACSIN1	3'	ACCGCAGATGCCCTCCTCCCTC	44311	_	A T
			GAGGGAG AGGG	CAT CTGTGGT		
			CTCCCTC TCCC	GTA GACGCCA		
			C	_ _		
GAM2475	PAK4	3'	CCCAGCCCCCTCTCCCCCT	12506	A	ACATT T
			AG GGGAGAGGG	CTG GG		
			TC CCCTCTCCC	GAC CC		
			C	CC__ _		
GAM2475	PPP2R5A	3'	GAATATCCCCCTTCCTCT	12911	A	C
			AGAGGGAG GGGA	ATTC		
			TCTCCTTC CCCT	TAAG		
			C	A		
GAM2475	PRKACA	3'	CCAGTGCCTCCCTCCCTC	8596	A	A TCTG
			GAGGGAG GGG	CAT TGG		
			CTCCCTC CTC	GTG ACC		
			C	C ____		
GAM2475	RUNX3	3'	CATCAATGTCCCTGTCCC	10547	G	CT
			GGGA AGGGACATT	GTG		

CCCT TCCCTGTAA TAC
 G C_
 GAM2475 SECTM1 3' ACCAGGACGCATGCCCCTCCCT 8909 A A ____ G
 CT AGAGGGAG GGG CAT TCT TGGT
 ||||| ||| ||| ||| ||||
 TCTCCCTC CCC GTA AGG ACCA
 _ _ CGC _
 GAM2475 SH3GL1 3' TCACATTCCCCTCCCTCT 8963 A CATTCT
 AGAGGGAG GGGA TGTGG
 ||||| ||| ||||
 TCTCCCTC CCCT ACACT
 _ T____
 GAM2475 SORCS1 3' CACTCCCCTCTCCCTCT 27482 ACATTCT
 AGAGGGAGAGGG GTG
 ||||| ||| |||
 TCTCCCTCTCCC CAC
 CT____
 GAM2475 SOX4 3' ACCCAGCGCACCCCTCCCCCCC 9071 A A ACATT T
 T AG GGG GAGGG CTG GGT
 || ||| |||| ||| |||
 TC CCC CTCCC GAC CCA
 C C CACGC _
 GAM2475 TAL1 3' CCCTAGCCCTCTCCCTCT 9168 ACATT T
 AGAGGGAGAGGG CTG GG
 ||||| ||| |||
 TCTCCCTCTCCC GAT CC
 ____ C
 GAM2475 20D7-FC4 3' ACCACGCCCCACCCCTCCCCTCT 30536 A ACATTCT
 AGAGGG GAGGG TGTGGT
 ||||| |||| |||||
 TCTCCC CTCCC GCACCA
 _ CACCC_
 GAM2475 C5orf5 3' ACCACAGACTGTCCTCTCCACC 18695 AG G T
 T AG GGAGAGG ACA TCTGTGGT
 || ||||| ||| |||||
 TC CCTCTCC TGT AGACACCA
 CA _ C
 GAM2475 dJ309H15.1 3' ACCTCTAGACACCCCTCTCC 28886 ACAT T_
 GGAGAGGG TCTG GGT
 ||||| ||| |||
 CCTCTCCC AGAT CCA
 CAC_ CT
 GAM2475 DKFZP566K1924 5' CCACCTCCCTCACCCCTC 36518 A CATTCT
 GAGGG GAGGGA GTGG
 |||| |||| |||
 CTCCC CTCCCT CACC
 A C____
 GAM2475 FLJ11767 3' ACCATAGTGTCCCCATCCC 23829 GA TT
 GGGA GGGACA CTGTGGT
 ||| ||||| |||||

			CCCT CCCTGT GATACCA			
			AC _			
GAM2475	FLJ14596	3'	CCAGGGCCCCCTCTCCCCT	26570	A	ACATT G
			AG GGGAGAGGG CT TGG			
			TC CCCTCTCCC GG ACC			
			_ C _ G			
GAM2475	FLJ20375	3'	ACCACACTGCCCTCTCCTCCT	19431	AG	A TTC
			AG GGAGAGGG CA TGTGGT			
			TC CCTCTCCC GT ACACCA			
			CT C C _			
GAM2475	KIAA0450	5'	ACCGAGTGATGCCCTCTCCCC	16026	A	A CTG
	T		AG GGGAGAGGG CATT TGGT			
			TC CCCTCTCCC GTAG GCCA			
			_ C TGA			
GAM2475	KIAA1030	3'	ACCAGCACTGTGTCCCTCCCCC	44817	A	TC _
	T		AGGG GAGGGACAT TG TGGT			
			TCCC CTCCCTGTG AC ACCA			
			C TC G			
GAM2475	KIAA1045	3'	ACAGTGACATCCTCTCCCTC	35191		ACATT
			GAGGGAGAGGG CTGT			
			CTCCCTCTCCT GACA			
			ACAGT			
GAM2475	KIAA1536	3'	CCAAGGCCCCCTCCCTCT	21922	A	ACAT G
			AGAGGGAG GGG TCT TGG			
			TCTCCCTC CCC GGA ACC			
			_ CC _ _			
GAM2475	KIAA1538	5'	ACCACAGCTGCCTCTTCCTC	35419		GA TT
			GAGGGAGAGG CA CTGTGGT			
			CTCCTTCTCC GT GACACCA			
			_ C _			
GAM2475	KIAA1600	3'	ACCTTTTCCCCCTCTCCCTC	35389		ACATTCTGT
	T		AGAGGGAGAGGG GGT			
			TCTCCCTCTCCC CCA			
			CCCTTTT_			
GAM2475	KIAA1643	3'	CCACTTCCCCTTCCCTCT	32239	A	CATTCT
			AGAGGGAG GGGA GTGG			
			TCTCCCTT CCCT CACC			
			C T _			
GAM2475	MOST2	5'	GCCACCTCCCTCTCCCTCT	21553		CATTCT
			AGAGGGAGAGGGA GTGGT			

TCTCCCTCTCCCT CACCG
 C_____
 GAM2475 PHYHIP 3' ACCACAGAATGCCCCCTCCCTG 16508 _ A A
 CT AG AGGGAG GGG CATTCTGTGGT
 || ||||| ||| |||||
 TC TCCCTC CCC GTAAGACACCA
 G C _
 GAM2475 PRDM8 5' CCGCACCCCTCTCCCTTT 21491 ACATTC
 AGAGGGAGAGGG TGTGG
 ||||| |||||
 TTTCCCTCTCCC ACGCC
 C_____
 GAM2475 SBB103 3' CTA CTGCCCCCCCCCTCT 12364 AGA A TTCT
 AGAGGG GGG CA GTGG
 ||||| ||| || |||||
 TCTCCC CCC GT CATC
 CCC C _____
 GAM2475 STMN3 3' CCA CTGCCCCATCTCCCTCT 18036 _ A TTCT
 AGAGGGAGA GGG CA GTGG
 ||||| ||| || |||||
 TCTCCCTCT CCC GT CACC
 A C _____
 GAM2475 TIGD1 5' ACCGTTCCCCATCTCTCTCCCT 42846 CATTCTG
 CT AGAGGGAGAGGGA TGGT
 ||||| |||||
 TCTCCCTCTCTCT GCCA
 ACCCCTT
 GAM2475 LOC143677 3' CCTCGCCCCCTGTCCCTCT 40373 G ACATTC T
 AGAGGGA AGGG TG GG
 ||||| ||||| |||||
 TCTCCCT TCCC GC CC
 G C_____ T
 GAM2475 LOC154222 3' ACCACAAAAAACCTCCATCC 41690 _ ACA C
 GGA GAGGG TT TGTGGT
 ||| ||||| || |||||
 CCT CTCCC AA ACACCA
 AC AA_ A
 GAM2475 LOC159090 5' ACCCTCTGTCCTCCTCCCTC 39938 AG TTCTGT
 GAGGGAG GGACA GGT
 ||||| ||||| |||||
 CTCCCTC CCTGT CCA
 CT CTC_____
 GAM2475 LOC221100 5' ACCAGCAGCCATCCCTTTCCCT 44776 CATT _
 CT AGAGGGAGAGGGA CTG TGGT
 ||||| ||||| |||||
 TCTCCCTTTCCCT GAC ACCA
 ACC_ G
 GAM2475 LOC221935 3' CAGGCCGTCCCCTCCCTCT 44498 A AT
 AGAGGGAG GGGAC TCTG
 ||||| ||||| |||||

TCTCCCTC CCCTG GGAC
 _ CC
 GAM2475 LOC256942 3' CTACTGCCCCCCCCCTCT 45363 AGA A TTCT
 AGAGGG GGG CA GTGG
 ||||| ||| || ||||
 TCTCCC CCC GT CATC
 CCC C ____
 GAM2475 LOC91397 5' CACTGCCCCCTCCCCCCT 32779 A A A TTCT
 AG GGG GAGGG CA GTG
 || ||| ||||| || |||
 TC CCC CTCCC GT CAC
 C C C ____
 GAM2476 PITX2 5' CGAGGGTTAGGCCAACAGGGA 5867 C CAA AG
 TCCC GT GCT GATTCTCG
 ||||| || ||| |||||
 AGGG CA CGG TTGGGAGC
 A AC_ A_
 GAM2476 FER1L4 3' CGAGAATCCACTCACCGGAGA 24874 C TCA CTA
 TC CCG AG GGATTCTCG
 || ||| || |||||
 AG GGC TC CCTAAGAGC
 A CAC A_
 GAM2476 KIAA0876 3' GCGACCCTCAGCCCGGCGGGGA 32297 AA _ ATTC
 TCCCCGTC GCT AGG TCGC
 ||||| ||| ||| ||||
 AGGGGCGG CGA TCC AGCG
 CC C C ____
 GAM2476 KIAA1608 5' GCGGGCCCCAGCCTGAGGG 24210 G A A ATT
 CCC TCA GCT GG CTCGC
 ||| ||| ||| || |||||
 GGG AGT CGA CC GGGCG
 _ C C C ____
 GAM2476 LOC151124 5' CGAGAATCTCATTTAACAGG 41302 C C CTA
 CC GT AAG GGATTCTCG
 || ||| ||| |||||
 GG CA TTT TCTAAGAGC
 A A AC_
 GAM2477 INPPL1 3' GTTTGCTTAGTTCTCACTGT 7296 AAA _
 ACAGTGAGAAT TAA CAAAC
 ||||| ||| |||||
 TGTCACTCTTG ATT GTTTG
 _ C
 GAM2477 JRKL 3' GGTTTATTATTATTCATC 9856 _ C
 GA GAATAAATAA AAACC
 || ||||| |||||
 CT CTTATTTATT TTTGG
 A A
 GAM2477 NRXN2 3' GGCTTGCTGTGTCTCACTGT 17470 ATAA A A
 ACAGTGAGA ATA CAA CC
 ||||| ||| ||| ||

			TGTCACTCT	TGT GTT GG		
			G__ C C			
GAM2477	NRXN2	3'	GGCTTGCTGTGTCTCACTGT	28986	ATAA	A A
			ACAGTGAGA	ATA CAA CC		
			TGTCACTCT	TGT GTT GG		
			G__ C C			
GAM2477	NRXN2	3'	GGCTTGCTGTGTCTCACTGT	28991	ATAA	A A
			ACAGTGAGA	ATA CAA CC		
			TGTCACTCT	TGT GTT GG		
			G__ C C			
GAM2477	PTGFR	3'	GGTTTGTTATAACAACCTCTGC	6663	_ AATAA_	
			GT GAG	ATAACAAACC		
			CG CTC	TATTGTTTGG		
			T CAACAA			
GAM2477	UC28	3'	GTTTGTTATTTATCCTAGTG	22280	G A A	
			CA TG GA	TAAATAACAAAC		
			GT AT CT	ATTTATTGTTTG		
			G C _			
GAM2477	C9orf5	3'	GTTTGTTTCCTTACTGTA	25716	AATAAAT	
			TACAGTGAG	AACAAAC		
			ATGTCATTC	TTGTTTG		
			CT_____			
GAM2477	FLJ12542	3'	GGTTTGTTATTTTAAAATCAC	24383	GAAT_	
			GTGA	AAATAACAAACC		
			CACT	TTTATTGTTTGG		
			AAAAT			
GAM2477	GOLPH2	3'	TGTTACCTGTTCTCACTG	18625	AA	
			CAGTGAGAATA	TAACA		
			GTCACTCTTGT	ATTGT		
			CC			
GAM2477	HTEX4	5'	GTTTTTATTCTCACTTA	46653	C	T
			A AGTGAGAATAAA	AAC		
			A TCACTCTTATTT	TTG		
			T			
GAM2477	HTEX4	5'	GTTTTTATTCTCACTTA	46722	C	T
			A AGTGAGAATAAA	AAC		
			A TCACTCTTATTT	TTG		
			T			
GAM2477	HTEX4	5'	GTTTTTATTCTCACTTA	44217	C	T
			A AGTGAGAATAAA	AAC		

A TCACTCTTATTT TTG
 T _
 GAM2477 KIAA0317 3' GTTTGTATTGGCACTG 16797 AGAATA
 CAGTG AATAACAAAC
 ||||| |||||
 GTCAC TTATTGTTG
 GG__
 GAM2477 KIAA0557 3' GTTTATTTTCCATCACTGTA 38209 ____
 TACAGTGA GAATAAAT
 ||||| |||||
 ATGTCAC TTTATTG
 ACCT
 GAM2477 KIAA0783 3' GGTTTGTTACTTGGACTAAC 16105 G AA A
 GT AG TAA TAACAAACC
 || || || |||||
 CA TC GTT ATTGTTTGG
 A AG C
 GAM2477 KIAA1143 3' GTTTGTGTTATTCACCACTGTA 34076 A_ ATA
 TACAGTG GAATAA ACAAAC
 ||||| ||||| |||||
 ATGTCAC CTTATT TGTTTG
 CA G__
 GAM2477 KIAA1432 5' GTTTATTAAGAGTGTACTCACT 33152 A AA__ C
 GTA TACAGTGAG ATA TAA AAAC
 ||||| || || |||||
 ATGTCAC TC TGT ATT TTTG
 A GAGA A
 GAM2477 PCDH20 3' GTTGTTATTTCACTG 23137 GAATA A
 CAGTGA AATAACAA C
 ||||| ||||| |
 GTCAC TTATTGTT G
 ____ C
 GAM2477 PRO2533 3' TTTGTCCAGTTCTCACTTA 20704 C AAATA
 A AGTGAGAAT ACAA
 | ||||| |||||
 A TCACTCTTG TGTT
 T ACC__
 GAM2477 LOC118851 3' GGTTCTACTTAACCTCACTGTA 37203 AA A ACA
 TACAGTGAG TAA TA AACC
 ||||| || || |||||
 ATGTCAC TC ATT AT TTGG
 CA C C__
 GAM2477 LOC127943 3' TGTTATTTACTACATTGTG 36914 _ AA
 TACAGTG AG TAAATAACA
 ||||| || |||||
 GTGTTAC TC ATTTATTGT
 A __
 GAM2477 LOC143154 3' TTTGCTATTTATTCTTGT 37590 TG A
 G AGAATAAATA CAAA
 | ||||| |||||

T TCTTATTTAT GTTT
 GT C
 GAM2477 LOC169966 3' TGTGCTTATCTTCACTGTA 40167 GA ATA
 TACAGTGA ATAA ACA
 ||||| ||| ||
 ATGTCACT TATT TGT
 TC CG_
 GAM2477 LOC219294 3' TTTGCTATTTATTCTTGT 44690 TG A
 G AGAATAAATA CAAA
 | ||||| |||
 T TCTTATTTAT GTTT
 GT C
 GAM2478 ARHH 5' TGTGCTGCAGCTGCCCAC 10516 A G
 GTG GCAG TGCAGCACG
 ||| ||| |||||
 CAC CGTC ACGTCGTGT
 C G
 GAM2478 MX1 5' CGCCCTTGCCGCCACCTGCTC 8293 _ A C A
 AC GTGAGCAGGT GC GCA GGGG CG
 ||||| || ||| ||| ||
 CACTCGTCCA CG CGT TCCC GC
 CC C _ _
 GAM2478 MYBL1 5' CGTCCCCGCCAGCCTGCTC 32043 GCAGCA
 GAGCAGGT CGGGGACG
 ||||| |||||
 CTCGTCCG GCCCCTGC
 ACCC_
 GAM2478 SYNGR3 3' CTTGGGCCACACCTGCTCAC 10408 CA A
 GTGAGCAGGTG GC CGGG
 ||||| || |||
 CACTCGTCCAC CG GTTC
 AC G
 GAM2478 CNM2 3' CTGGCTGCACCCGCCCA 19154 A A A
 TG GC GGTGCAGC CGG
 || || ||||| |||
 AC CG CCACGTCG GTC
 C C _
 GAM2478 FLJ10759 5' GTCCCCGCGCCCAGCCCTC 20102 CA GCA A
 GAG GGT GC CGGGGAC
 ||| ||| || |||||
 CTC CCG CG GCCCCTG
 _ ACC C
 GAM2478 FLJ20507 3' CGCCCCCAGGCCACCTGCTC 30219 CA AC A
 GAGCAGGTG GC GGGG CG
 ||||| || ||| ||
 CTCGTCCAC CG CCCC GC
 _ GA C
 GAM2478 FLJ20507 3' CGCCCCCAGGCCACCTGCTC 19511 CA AC A
 GAGCAGGTG GC GGGG CG
 ||||| || ||| ||

			CTCGTCCAC CG CCCC GC			
			__ GA C			
GAM2478	KHDRBS3	5'	GCCCCGTGCCGCCGCCGC 13325	A A	CA	A
			GTG GC GGTG GCACGGGG C			
			CGC CG CCGC CGTGCCCC G			
			__ _ __ C			
GAM2478	KIAA1656	3'	GGGACGCAACTGCTGCACCTGC 32734	A	_____	GGGA
	TC		AGCAGGTGCAGC CG C			
			TCGTCCACGTCG GC G			
			TCAAC AGGG			
GAM2478	KIAA1912	5'	CCCACTTGACCTGCCAC 36312	A	CAC	
			GTG GCAGGTGCAG GGG			
			CAC CGTCCACGTT CCC			
			__ CA__			
GAM2478	KIAA1940	5'	CGGCGCCGCACCTGCTGCAC 39006	_	A A_	
			GTG AGCAGGTGC GC CG			
			CAC TCGTCCACG CG GC			
			G C CG			
GAM2478	MGC4309	3'	CGCATCCTGCACCTGCCAC 23568	A	CA_____	
			GTG GCAGGTGCAG CG			
			CAC CGTCCACGTC GC			
			__ CTAC			
GAM2478	MKNK1	3'	CTGGGCTCCACCTGCTCAC 9793	C A		
			GTGAGCAGGTG AGC CGG			
			CACTCGTCCAC TCG GTC			
			C G			
GAM2478	PABPC5	5'	CGTCAGAGCTGACCCACTCAC 28097	CA G	ACGGG	
			GTGAG GGT CAGC GACG			
			CACTC CCA GTCG CTGC			
			AC _ AGA__			
GAM2478	PIP5K2B	3'	CTGTGTGTGCACCTGCTCAC 9612	_		
			GTGAGCAGGTGCA GCACGG			
			CACTCGTCCACGT TGTGTC			
			G			
GAM2478	SCYD1	3'	CTGTGCTGCCCTGCCAC 43710	A T		
			GTG GCAGG GCAGCACGG			
			CAC CGTCC CGTCGTGTC			
			C _			
GAM2478	SEC14L1	3'	GGGACGCAGCAGCTGCACCCGC 8904	A A	AC_____	GGGA
	CCAC		GC GGTGCAGC G C			

		CG CCACGTCG	C G		
		C C	ACGACIIIG AGGG		
GAM2478	SMURF2	5'	CGCCCCCGTGCCGCCGCCGC	22946	A A T A A
			GTG GC GG GC GCACGGGG CG		
			CGC CG CC CG CGTGCCCC GC		
			_ _ _ C C		
GAM2478	LOC115704	3'	CGTCCCCGCTTCCTAGCTGCCC	36402	A G CAGCA
	AC		GTG GCAG TG CGGGGACG		
			CAC CGTC AT GCCCCTGC		
			C G CCTTC		
GAM2478	LOC124602	3'	TCCCGACACCTGCTCAC	36760	CAGCA
			GTGAGCAGGTG CGGGG		
			CACTCGTCCAC GCCCT		
			A _ _ _		
GAM2478	LOC147299	3'	CGCCATGGCCTCACCTGCTCAC	38332	CA A G A
			GTGAGCAGGTG GC CG GG CG		
			CACTCGTCCAC CG GT CC GC		
			TC _ A _		
GAM2478	LOC149194	5'	GTCCCCGTA CTGGCTCA	38671	AGGTG C
			TGAGC CAG ACGGGGAC		
			ACTCG GTC TGCCCCTG		
			_ _ _ A		
GAM2478	LOC151521	3'	CCCCACACTTCCACTCCACCTC	41367	CA _ C _ CAC
	AC		GTGAG GGTG AG GGGG		
			CACTC TCAC TC CCCC		
			CACC CT ACA		
GAM2478	LOC157349	5'	CCCCTGCACCTGCCAC	39590	A CAC
			GTG GCAGGTGCAG GGG		
			CAC CGTCCACGTC CCC		
			_ _ _		
GAM2478	LOC157349	5'	CCCCTGCACCTGCCAC	39591	A CAC
			GTG GCAGGTGCAG GGG		
			CAC CGTCCACGTC CCC		
			_ _ _		
GAM2478	LOC157349	5'	CCCCTGCACCTGCCAC	39592	A CAC
			GTG GCAGGTGCAG GGG		
			CAC CGTCCACGTC CCC		
			_ _ _		
GAM2478	LOC203397	3'	TCCCGACACCTGCTCAC	43040	CAGCA
			GTGAGCAGGTG CGGGG		

	CACTCGTCCAC	GCCCT		
	A_____			
GAM2478	LOC220110	5' CGTCCCCGCCAACCTGCTCGC 44894		TGCAGCA
	GTGAGCAGG	CGGGGACG		
	CGCTCGTCC	GCCCCTGC		
	CAACC__			
GAM2478	LOC222031	3' CGCACTGCCACACTGCTCAC 45133	- -	CA_____
	GTGAGCAG	GTG CAG CG		
	CACTCGTC	CAC GTC GC		
	A C	ACIII		
GAM2478	LOC92578	5' CGCATCCTGCACCTCCTCAC 34607	C	CA_____
	GTGAG	AGGTGCAG CG		
	CACTC	TCCACGTC GC		
	C	CTACIII		
GAM2479	VIPR1	3' GGTCACCAGCACCAACACCA 10994	A G	CGG
	TG TGT	GGTGCTGG GGCT		
	AC ACA	CCACGACC CTGG		
	C A	A__		
GAM2479	DKFZp762E1511	3' CAGCCCCACCAGGCCTCA 29931	T G C	
	G GGGT	CTGG GGGGCTG		
	A TCCG	GACC CCCCAC		
	C _	A		
GAM2479	LOC123242	5' TACAGCCCCACAAGGTCAGCAT 37245	_____	
	CCACATCA	GGGTGCTGGC GGGGCTGT A		
	CCTACGACTG	CCCCGACA T		
	GAACA			
GAM2479	LOC139248	5' GGCTGCCATCAACACCCACATC 37337	C GC _	
	A	TGATGTGGGTG TG GG GGCT		
	ACTACACCCAC	AC CC TCGG		
	A TA	G		
GAM2479	LOC196955	5' TACAGCCCCACAAGGTCAGCAT 37937	_____	
	CCACATCA	GGGTGCTGGC GGGGCTGT A		
	CCTACGACTG	CCCCGACA T		
	GAACA			
GAM2479	LOC253216	3' ACAGCCCCGCCAACAGCCACA 45516	G C	
	TGTGG	TG TGGCGGGGCTGT		
	ACACC	AC ACCGCCCCGACA		
	G A			
GAM2480	LOC155376	5' ACAGAGAAGAGGAGACCCCAAC 39563	C	GG G C
	A	TGT GGGGTCTC TC TCTC GT		

		ACA CCCCAGAG AG AGAG CA			
		A G_ A A			
GAM2480	LOC219513 3'	ACAGAGTGCAGAGACCCCGGCA 45289		GT T C	
		TGTCGGGGTCTC G CG CTC GT			
		ACGGCCCCAGAG C GT GAG CA			
		A _ _ A			
GAM2480	LOC222233 5'	ACAGAGACGAAGAGACCCCAAC 45241	C	GG C	
	A	TGT GGGGTCTC TCGTCTC GT			
		ACA CCCCAGAG AGCAGAG CA			
		A A_ A			
GAM2480	LOC253532 5'	ACAGAGAAGAGGAGACCCCAAC 45949	C	GG G C	
	A	TGT GGGGTCTC TC TCTC GT			
		ACA CCCCAGAG AG AGAG CA			
		A G_ A A			
GAM2480	LOC254875 5'	ACAGAGAAGAGGAGACCCCAAC 45953	C	GG G C	
	A	TGT GGGGTCTC TC TCTC GT			
		ACA CCCCAGAG AG AGAG CA			
		A G_ A A			
GAM2481	EHD2 3'	CCCTCAACCGGCTCCATCA 15961		TCA C A	
		TGGTGGAGC CGGT GA GG			
		ACTACCTCG GCCA CT CC			
		_ A C			
GAM2481	NORE1 3'	CGCCCCCAGGCTGTGCCCCACC 25442	A TC	GAA_	
	A	TGGTGG GC ACGGTC GGCG			
		ACCACC CG TGTCGG CCGC			
		C _ ACCC			
GAM2481	NR5A2 3'	ACCCAGTGGTAGCTCCACCA 9913	_ _		
		TGGTGGAGCT CAC GGT			
		ACCACCTCGA GTG CCA			
		TG AC			
GAM2481	DKFZP566H073 5'	CCTCCTTGAGCTCCGCCA 17796		C TCGA	
		TGGTGGAGCTCA GG AGG			
		ACCGCCTCGAGT CC TCC			
		T _ _ _			
GAM2481	FLJ20514 5'	CGCCCACGAGCTCCACCA 19533	AC T		
		TGGTGGAGCTC GG CG			
		ACCACCTCGAG CC GC			
		CA C			
GAM2481	KIAA1879 3'	CCTCCAGCACAGCTTCACCA 36413		CACG CGA	
		TGGTGGAGCT GT AGG			

		ACCACTTCGA CG TCC	
		CA__ ACC	
GAM2481	PTPNS1 3'	CCTCCCCTGACCTCCACCA 28053	C C TC A
		TGGTGGAG TCA GG GA GG	
		ACCACCTC AGT CC CT CC	
		C _ C_ _	
GAM2481	LOC124930 5'	CCTCCAACCTCCGCTTCCACCA 36768	_ TCAC CGA
		TGGTGGGA GC GGT AGG	
		ACCACCT CG CCA TCC	
		T CCT_ ACC	
GAM2481	LOC147160 5'	CGCGGGGTGCCGCAGCTCCACC 40808	CA CGAAG
	A	TGGTGGAGCT CGGT GCG	
		ACCACCTCGA GCCG CGC	
		C_ TGGGG	
GAM2481	LOC147669 5'	CGCCTCCTGGGCAAGCTCCCCA 40854	T CA__ TCGA
		TGG GGAGCT CGG AGGCG	
		ACC CCTCGA GTC TCCGC	
		_ ACGG C__	
GAM2481	LOC163682 3'	GCCCCCAGGAGCTCCACC 42094	AC TCGAA
		GGTGGAGCTC GG GGC	
		CCACCTCGAG CC CCG	
		GA C__	
GAM2481	LOC90342 5'	CCTTCAATAAGCCCCACTA 31250	A CACG C
		TGGTGG GCT GT GAAGG	
		ATCACC CGA TA CTTCC	
		C A__ A	
GAM2482	DGCR2 3'	GCAGTCCCCAGTCTGACCA 11614	CGAA
		TGGTCAGAC GACTGC	
		ACCAGTCTG CTGACG	
		ACCC	
GAM2482	RNPEPL1 3'	GCAGCCCTATGGTGACCGCC 20161	AG A A_
		GGTGGTC ACCG AG CTGC	
		CCGCCAG TGGT TC GACG	
		_ A CC	
GAM2482	CNNM1 3'	GCAGTCTTCAATCGATCA 21608	A CC
		TGGTC GA GAAGACTGC	
		ACTAG CT CTTCTGACG	
		_ AA	
GAM2482	DKFZP564D166 3'	GCAGTCTTCAGCCTCCCCAGTA 24991	_ T TCAGACC
		TAC GG GG GAAGACTGC	

			ATG CC CC CTTCTGACG		
			A _ TCCGA__		
GAM2482	FLJ12057	3'	CAGCTGGTCTGACCACCGT 24125	GA A	
			ACGGTGGTCAGACC AG CTG		
			TGCCACCAGTCTGG TC GAC		
			— —		
GAM2482	SS-56	3'	CAGTCTTCAGGACACCATT 29989	CAGA _	
			GGTGGT CC GAAGACTG		
			TTACCA GG CTTCTGAC		
			CA__ A		
GAM2482	LOC147515	5'	CAATCCTCTGACCACTG 40842	CCGAA C	
			CGGTGGTCAGA GA TG		
			GTCACCAGTCT CT AC		
			C__ A		
GAM2482	LOC92841	5'	CAGCCCTTCTGACCACCG 35003	CCGA A_	
			CGGTGGTCAGA AG CTG		
			GCCACCAGTCT TC GAC		
			__ CC		
GAM2483	BTG2	3'	GCGCCGCCGTGCTCATGCTGC 13628	C ACA_	
			GCAGCA GAGCACGG GC		
			CGTCGT CTCGTGCC CG		
			A GCCG		
GAM2483	CDS2	3'	TGCCATCCATGTTTGTGCTGT 9911	C CA	
			GCAGCACGAGCA GGA GCA		
			TGTCGTGTTTGT CCT CGT		
			A AC		
GAM2483	FBLN1	3'	TGCTGTCCCCCTGCAGACTGC 13212	CACGA C__	
			GCAG GCA GGACAGCA		
			CGTC CGT CCTGTCGT		
			AGA__ CCC		
GAM2483	GARS	5'	GTGCTGCTTAGAGGTGCTCGCG 7797	A A ____ A	
			CCGCT GC GC CGAGCAC GG CAGCAC		
			CG CG GCTCGTG TC GTCGTG		
			C C GAGAT _		
GAM2483	GLO1	3'	TGCCAACCGTGCTTGTACTGCT 13532	C ACA	
			A TAGCAG ACGAGCACGG GCA		
			ATCGTC TGTTCTGTGCC CGT		
			A AAC		
GAM2483	MATN1	5'	GTGCCGGCTGCTGCCCCGTGCTG 8195	A _ ACA	
			C GCAGCACG GCA CGG GCAC		

CGTCGTGC CGT GTC CGTG
 C C GGC
 GAM2483 PRG1 3' GTGCTGTCAATACCTCATACTG 8591 CAC CACG_
 CT AGCAG GAG GACAGCAC
 |||| || |||||
 TCGTC CTC CTGTCGTG
 ATA CATAA
 GAM2483 PTTG1IP 3' GTTGACTGCTCGTGTGC 10536 G CGGA
 GCA CACGAGCA CAGC
 || ||||| |||
 CGT GTGCTCGT GTTG
 _ CA_
 GAM2483 WTAP 3' GCATTCGTACTCATGCTGTTA 11345 C C CA
 TAGCAGCA GAG ACGGA GC
 ||||| || |||| ||
 ATTGTCGT CTC TGCTT CG
 A A A_
 GAM2483 CST7 5' GCACTGGCCCGTGCTGC 9726 A A ACA
 GCAGCACG GC CGG GC
 ||||| || || ||
 CGTCGTGC CG GTC CG
 C _ A_
 GAM2483 CYP2S1 3' GCTCACTTGACTCATGCTGCTA 24965 C _ C AC
 TAGCAGCA GAG CA GG AGC
 ||||| || || || ||
 ATCGTCGT CTC GT TC TCG
 A A _ AC
 GAM2483 DKFZP564I0422 3' GTGCTGTCCTGACAACATGCT 25436 GCACGAG C
 AGCA CA GGACAGCAC
 || || |||||
 TCGT GT CCTGTCGTG
 ACAACA_ _
 GAM2483 DOCK3 3' GCTGTCCGGCAGTGCCAGC 33037 A_ GA A
 GC GCAC GC CGGACAGC
 || || || |||||
 CG CGTG CG GCCTGTGCG
 AC A_ _
 GAM2483 FLJ11259 3' GCACCTTTTGCTCTTGCTGCTA 20385 C C_ ACA
 TAGCAGCA GAGCA GG GC
 ||||| || || ||
 ATCGTCGT CTCGT CC CG
 T TTT A_
 GAM2483 FLJ13197 3' TGCCCACTCGTGCTGC 23874 CAC ACA
 GCAGCACGAG GG GCA
 ||||| || || ||
 CGTCGTGCTC CC CGT
 A_ _
 GAM2483 KIAA0226 3' GTGCCGCCCGTGCTCTGAACTG 31788 CAG C ACA
 TAG CA GAGCACGG GCAC
 || || ||||| |||

		GTC GT CTCGTGCC CGTG	
		AA_ _ CGC	
GAM2483 KIAA1432	5'	GCACTGGAGCCATGCTGCTA 33150	CGA A_ ACA
		TAGCAGCA GC CGG GC	
		ATCGTCGT CG GTC CG	
		AC_ AG A__	
GAM2483 KIAA1530	3'	GTACGGCCGCTCTGCTGCTA 33736	C A__ G
		TAGCAGCA GAGC CG AC	
		ATCGTCGT CTCG GC TG	
		_ CCG A	
GAM2483 MGC23445	5'	GTGCCGGAGCAGCTCGTGACGC 29420	A ACGGACA
	TA	TAGC GCACGAGC GCAC	
		ATCG CGTGCTCG CGTG	
		A ACGAGGC	
GAM2483 phospho1	3'	GTGCTGTCCACACTCTCTTGC 40064	CAC CAC
		GCAG GAG GGACAGCAC	
		CGTT CTC CCTGTCTGTG	
		CT_ ACA	
GAM2483 SARM	3'	TGCCAGCCCTCGTGCTGC 17464	CAC ACA
		GCAGCACGAG GG GCA	
		CGTCGTGCTC CC CGT	
		_ GAC	
GAM2483 SSB-4	3'	TGCTGCTGCTGCCTCCGCCGC 28106	A AC _ _ A
		GC GC GAG CA CGG CAGCA	
		CG CG CTC GT GTC GTCGT	
		C C_ C C _	
GAM2483 LOC145694	5'	TGCTGTCCGCGCTGCCCGC 40558	A_ CGA A
		GC GCA GC CGGACAGCA	
		CG CGT CG GCCTGTCGT	
		CC _ C	
GAM2483 LOC256158	5'	GCATCTACACTTGTGCTGCTA 46629	CAC CA
		TAGCAGCACGAG GGA GC	
		ATCGTCGTGTTC TCT CG	
		ACA A_	
GAM2483 LOC57106	3'	GTGCTGTCCGTGCCCCAGGCTG 32074	ACGA_
		CAGC GCACGGACAGCAC	
		GTCG CGTGCCTGTCGTG	
		GACCC	
GAM2483 LOC90133	3'	GTGCTGTCCATGGACAGCAGC 30869	A ACGAG C
		GC GC CA GGACAGCAC	

	CG CG	GT CCTGTCGTG		
	A	ACAG_ A		
GAM2483	LOC91689	3' GTGCTGTCCACTAAGCACTGC	27157	CACG_ CAC
		GCAG AG GGACAGCAC		
		CGTC TC CCTGTCGTG		
		ACGAA A__		
GAM2483	LOC91974	5' TGCTGCTGTCCAGCTGCTA	33655	ACGAGC A
		TAGCAGC ACGG CAGCA		
		ATCGTCG TGTC GTCGT		
		ACC__ _		
GAM2484	FLJ10565	5' CCCAGAGCCAAGTGCACCGA	19938	A AGCAA
		TC GTGTACTTGGC TGGG		
		AG CACGTGAACCG ACCC		
		C AG__		
GAM2484	NXPH3	3' ACCCATTGCTGATGGCACAC	32712	A TGG
		GTGT CT CAGCAATGGGT		
		CACA GG GTCGTTACCCA		
		C TA_		
GAM2485	ARHGDIA	3' AACCATGATGCCTTAACA	10513	C_ A T
		TGT AGG CATCATG GTT		
		ACA TCC GTAGTAC CAA		
		AT _ _		
GAM2485	SLC20A2	5' CAAATGAAGTGCCTGACA	13600	_ G
		TGTCAGGACA TCAT TG		
		ACAGTCCTGT AGTA AC		
		CA A		
GAM2485	CCR5	3' GTCAAAGACATTCTGACA	6185	CATCA G A
		TGTCAGGA TGT TTT AC		
		ACAGTCTT ACA AAA TG		
		_ _ G C		
GAM2485	FLJ10826	3' GTTAAACACCAGCCTGACA	20175	ACATCAT
		TGTCAGG GTGTTTAAC		
		ACAGTCC CACAAATTG		
		GAC__		
GAM2485	LOC142941	3' TTAAAATAGAAATCCTGACA	40324	CA A G
		TGTCAGGA TC TGT TTAA		
		ACAGTCCT AG ATA AAATT		
		AA _ _		
GAM2485	LOC150279	3' TTAAAGGCATATCCTGATA	38901	CATC G
		TGTCAGGA ATGT TTAA		

		ATAGTCCT TACG AAATT		
		A _ G		
GAM2485	LOC152992 3'	ACTCATAATTTCTGACA 39347	C C T	
		TGTCAGGA AT ATG GT		
		ACAGTCCT TA TAC CA		
		T A T		
GAM2485	LOC158863 3'	TTAAGCATAACATACTGACA 42036	GACATCA	
		TGTCAG TGTGTTTAA		
		ACAGTC ATACGAATT		
		ATACA _		
GAM2485	LOC221954 5'	AGCCAAGGACTCCTGACA 45121	CA A T	
		TGTCAGGA TC TG GTT		
		ACAGTCCT GG AC CGA		
		CA A _		
GAM2486	CYLN2 3'	AGAGCGTCTCCAGCCCCATCT 9420	AGA TT _	
		AGATGG TGGAG CTCT		
		TCTACC ACCTC GAGA		
		CCG TGC		
GAM2486	GALR1 5'	GCGGAGAGAAGGGTCTTTCCAC 7216	A T AG _	
	CT	AG TGGAGA GG TTCTCTCCGC		
		TC ACCTTT CT AAGAGAGGCG		
		C _ GGG		
GAM2486	HPSE 3'	CGGAGAGAGATTCCATCT 13477	_	
		AGATGGAGT TCTCTCCG		
		TCTACCTTA AGAGAGGC		
		G		
GAM2486	IL17R 3'	TGGTGAAACCCCATCTCCACT 15660	A A C T	
		AG TGGAGATGG GTT TC CCG		
		TC ACCTCTACC CAA AG GGT		
		_ C _ T		
GAM2486	OAS3 3'	GCAGAGAGTTCCCATCTCATCT 12862	G AGTT C	
		AGATG AGATGG CTCTC GC		
		TCTAC TCTACC GAGAG CG		
		_ CTT _ A		
GAM2486	PCDH11X 3'	CGGTGAAACCCCATCTCCACT 26781	A A C T	
		AG TGGAGATGG GTT TC CCG		
		TC ACCTCTACC CAA AG GGC		
		_ C _ T		
GAM2486	PCDH11Y 3'	TGGTGAAACCCCATCTCCACT 26814	A A C T	
		AG TGGAGATGG GTT TC CCG		

TC ACCTCTACC CAA AG GGT
 _ C _ T
 GAM2486 PCDH11Y 3' TGGTGAAACCCCATCTCCACT 26816 A A C T
 AG TGGAGATGG GTT TC CCG
 || ||||| || || ||
 TC ACCTCTACC CAA AG GGT
 _ C _ T
 GAM2486 SIM2 3' GCTGAAACCCCATCTCCACT 14312 A A CTC C
 AG TGGAGATGG GTT TC GC
 || ||||| || || ||
 TC ACCTCTACC CAA AG CG
 _ C _ T
 GAM2486 SLC2A6 3' CGAGAGTGAAACTCCGTCCCCA 19031 A _ T _
 TGG GATGGAGTT C CTC CG
 ||| ||||| | || ||
 ACC CTGCCTCAA G GAG GC
 C A T A
 GAM2486 SMG1 3' GGAACTCCATTCCACCT 17480 A A
 AG TGGAG TGGAGTTCT
 || |||| |||||
 TC ACCTT ACCTCAAGG
 C _
 GAM2486 SURF5 3' AGAGTCCATGTCCATCT 13604 G GTT
 AGATGGA ATGGA CTCT
 ||||| |||| ||||
 TCTACCT TACCT GAGA
 G _
 GAM2486 ARHGEF15 3' CGGAGAGAACAAAGCCCATT 17318 AGATGGA
 GATGG GTTCTCTCCG
 |||| |||||
 TTACC CAAGAGAGGC
 CGAAA_
 GAM2486 FIGN 3' AGAACCTCTCCATCTCCTC 45774 T TTC_
 GA GGAGATGGAG TCT
 || ||||| ||
 CT CCTCTACCTC AGA
 _ TCCA
 GAM2486 FLJ10738 3' GCAGAAAGAACCACAACTCCA 20070 A_ GA C C
 TCT AGATGGAG TG GTTCT TC GC
 ||||| || |||| || ||
 TCTACCTC AC CAAGA AG CG
 AA AC A A
 GAM2486 FLJ12443 5' AGAGACATCCCGATCT 24222 _ A GAGT
 AGAT GG GATG TCTCT
 ||| || |||| ||||
 TCTA CC CTAC AGAGA
 G _ _
 GAM2486 FLJ12684 5' AGAACTTCATCTCCATCT 23745
 AGATGGAGATGGAGTTCT
 ||||| |||||

TCTACCTCTACTTCAAGA

GAM2486 FLJ20139 3' TGGTGAAACCCCATCTCCA 19238 A C T
TGGAGATGG GTT TC CCG
||||||| ||| || |||
ACCTCTACC CAA AG GGT
C _ T

GAM2486 FLJ23042 3' CGGAGAGGATTTCCACCT 24796 A _
AG TGGAG TTCTCTCCG
|| ||||| |||||
TC ACCTT AGGAGAGGC
C T

GAM2486 FLJ23403 3' AGCGCTCCATCCCCACT 22612 A A T
AG TGG GATGGAGT CT
|| ||| ||||| ||
TC ACC CTACCTCG GA
_ C C

GAM2486 G2 5' AGAGAATCATGCCTCCCCATCT 33110 A T A____
AGATGG GA GG GTTCTCT
||||| || || |||||
TCTACC CT CC TAAGAGA
C _ GTAC

GAM2486 HOMER-2B 3' GAGAGAACAACATTCCTCT 11248 T A GA
AGA GGAG TG GTTCTCTC
||| |||| || |||||
TCT CCTT AC CAAGAGAG
_ _ AA

GAM2486 KIAA0889 3' GAGTGAGACTCCATCTCCA 17678 _ T
TGGAGATGGAGT TC CTC
||||||| || |||
ACCTCTACCTCA AG GAG
G T

GAM2486 KIAA1786 3' GCAGAAAGAATTTATTCTCCTC 32845 T TG C C
GA GGAGA GAGTTCT TC GC
|| ||||| ||||| || ||
CT CCTCT TTAAAGA AG CG
_ TA A A

GAM2486 TTTY2 5' AGAATGTGCTTCCAACCTCCATC 42068 A _____
GATGGAG TGGA GTTCT
||||||| |||| |||||
CTACCTC ACCT TAAGA
A TCGTG

GAM2486 ZNF384 5' AGACCCTCCTCCTCCTCCATCT 28543 AT TTC__
AGATGGAG GGAG TCT
||||||| |||| |||
TCTACCTC CCTC AGA
CT CTCCC

GAM2486 LOC126917 3' GGGTGCCCCGTCTCCATC 36873 A T
GATGGAGATGG GT CTC
||||||| || |||

CTACCTCTGCC CG GGG
 C T
 GAM2486 LOC145945 5' AGAAAATCATCATCCCATCT 40628 A__ AG
 AGATGG GATGG TTCT
 ||||| ||||| |||||
 TCTACC CTACT AAGA
 CTA AA
 GAM2486 LOC149320 3' CGGAGAGGACCTCCAACC 35001 AGA _
 GG TGGAG TTCTCTCCG
 || ||||| |||||
 CC ACCTC AGGAGAGGC
 A__ C
 GAM2486 LOC152926 5' AGACTTCTCCCTCTCCATCT 39339 T TTC
 AGATGGAGA GGAG TCT
 ||||| ||||| |||||
 TCTACCTCT CCTC AGA
 C TTC
 GAM2486 LOC159148 5' AGAATGTGCTTCCAACCTCCATC 42075 A _____
 GATGGAG TGA GTTCT
 ||||| ||||| |||||
 CTACCTC ACCT TAAGA
 A TCGTG
 GAM2486 LOC255196 5' CGAAGAAACCCTCATCTCTA 46412 _A C C
 TGGAGATG G GTT TCT CG
 ||||| | ||||| |||||
 ATCTCTAC C CAA AGA GC
 T C _ A
 GAM2486 LOC93613 3' TGGTGAAACCCCATCTCCA 35997 A C T
 TGGAGATGG GTT TC CCG
 ||||| ||||| ||||| |||||
 ACCTCTACC CAA AG GGT
 C _ T
 GAM2487 GAN 3' TATCTCTCATTCTCACCTCA 22564 T CCGT
 TGAG TGA GAATGAGAGATA
 ||||| ||||| ||||| |||||
 ACTC ACT CTTACTCTCTAT
 C _____
 GAM2487 FLJ20174 3' CTGCATCCAAGTCAACTCA 19269 CG A _
 TGAGTTGAC TG ATG AG
 ||||| ||||| ||||| |||||
 ACTCAACTG AC TAC TC
 A_ C G
 GAM2487 KIAA0286 3' ATCTCTCAGACCAATCTCA 33902 _ ACCGTGAA
 TGAG TTG TGAGAGAT
 ||||| ||||| ||||| |||||
 ACTC AAC ACTCTCTA
 T CAG_____
 GAM2487 KIAA0930 3' ATCTCTCAGACCAGCTCA 34911 ACCGTGAA
 TGAGTTG TGAGAGAT
 ||||| ||||| ||||| |||||

			ACTCGAC	ACTCTCTA		
			CAG_____			
GAM2487	MYO5C	3'	ATCTCTCACTCACAGTGAC	20817	G C A	
			GTT AC GTGA TGAGAGAT			
			CAG TG CACT ACTCTCTA			
			_ A C			
GAM2487	LOC144600	3'	ATCTCTCAGACCAGCTCA	40445	ACCGTGAA	
			TGAGTTG TGAGAGAT			
			ACTCGAC ACTCTCTA			
			CAG_____			
GAM2487	LOC90768	3'	TATCCCTCACTCATTTAGCCA	31987	A CC A A	
			TG GTTGA GTGA TGAG GATA			
			AC CGATT TACT ACTC CTAT			
			_ _ C C			
GAM2488	ABCB1	5'	AGCACAGCGCTTCGCTCT	6637	A AAGGC	
			AGAGC AGGCGCTG GCT			
			TCTCG TTCGCGAC CGA			
			C A_____			
GAM2488	ACN	5'	AGCGCCCCAGCGCCTCATCT	17362	GCA AA	
			AGA AGGCGCTG GGCGCT			
			TCT TCCGCGAC CCGCGA			
			AC_ C_			
GAM2488	ARHGAP6	5'	GAGCGCCTGACCTTCCTC	12767	C CGCTGA	
			GAG AAGG AGGCGCTC			
			CTC TTCC TCCGCGAG			
			C AG_____			
GAM2488	ARHGAP6	5'	GAGCGCCTGACCTTCCTC	6845	C CGCTGA	
			GAG AAGG AGGCGCTC			
			CTC TTCC TCCGCGAG			
			C AG_____			
GAM2488	BHMT2	3'	AGCGAGAGAGGCACCTTGTCT	19115	C GAAGG	
			AGAGCAAGG GCT CGCT			
			TCTTGTTCC CGG GCGA			
			A AGAGA			
GAM2488	DACH	5'	GAGCGCCTCTCGTGCTCGC	28039	AA T _	
			GC GGCGC GA AGGCGCTC			
			CG TCGTG CT TCCGCGAG			
			C_ _ C			
GAM2488	DLC1	5'	GAGCGAGGGCGCTTCGCTC	12743	A GAAGG	
			GAGC AGGCGCT CGCTC			

CTCG TTCGCGG GCGAG
C GA____

GAM2488 MCC 3' GCTTTCAGCACTCACTCT 8203 CA GC
AGAG AG GCTGAAGGC
|||| || |||||
TCTC TC CGACTTTCG
AC A_

GAM2488 PGAM1 3' GAGCACCTCCCTGCCCGTCTT 37518 GCAA CT A C
AAGA GGCG GA GG GCTC
|||| ||| || |||
TTCT CCGT CT CC CGAG
GC__ CC C A

GAM2488 PLA2G10 5' AGCGCCTTTTCCTCCCTT 9618 CA CGCT
GAG AGG GAAGGCGCT
||| ||| |||||
TTC TCC TTTCCGCGA
CC T__

GAM2488 PSD 5' AGCGCCTGGCCACACTCTT 8666 CAA GCTGA
AAGAG GGC AGGCGCT
|||| ||| |||||
TTCTC CCG TCCGCGA
ACA G____

GAM2488 SOX9 5' AGCGCCCCCACTTTTGCTCTT 5898 CGC AA
AAGAGCAAGG TG GGCGCT
||||||| || |||||
TTCTCGTTTT AC CCGCGA
C__ CC

GAM2488 TBXA2R 3' AGCGCCCCTCCCGCGCCTT 6724 T_ A_
AAGGCGC GA GGCGCT
||||| || |||||
TTCCGCG CT CCGCGA
CC CC

GAM2488 TCF1 3' GAGCGCCCTGCAGACCCTGCCC 6150 A A CG AA_
TT AAG GCA GG CTG GGCGCTC
||| ||| || |||||
TTC CGT CC GAC CCGCGAG
C _ CA GTC

GAM2488 TIMM23 3' GAGCGCCTCTGCCCGCCGC 30198 AA_ C T A
GC GG GC GA GGCGCTC
|| ||| || |||||
CG CC CG CT CCGCGAG
CCG C T _

GAM2488 DGKZ 3' GAGCGCCTTCCTTGCCACCTC 9723 CAA CT
GAG GGCG GAAGGCGCTC
||| ||| |||||
CTC CCGT CTTCCGCGAG
CAC TC

GAM2488 FLJ14009 5' AGCACTTCGCCTTGTCTT 24111 AG GCT GC
AG CAAGGC GAAG GCT
|| ||||| ||| |||

TC GTTCCG CTTC CGA
 CT ____ A_
 GAM2488 FLJ20085 3' ACGCCTCCATTGCTGCTT 19183 AG C A C
 GAGCA GCG TG AGGCG T
 |||| ||| || ||||| |
 TTCGT CGT AC TCCGC A
 ____ T C A
 GAM2488 FLJ20359 3' GAGCGCCTCCAGGGCCCCGC 19413 AA G A
 GC GGC CTG AGGCGCTC
 || ||| ||| |||||
 CG CCG GAC TCCGCGAG
 CC G C
 GAM2488 FLJ22056 5' GAGCGCCTCCAGGCCAGCATCT 22869 _ AA G A
 AGA GC GGC CTG AGGCGCTC
 ||| || ||| ||| |||||
 TCT CG CCG GAC TCCGCGAG
 A A_ _ C
 GAM2488 HCA4 5' AGCGCCTCCAGTACGTCTT 38019 ____ A
 AAGGCG CTG AGGCGCT
 ||||| ||| |||||
 TTCTGC GAC TCCGCGA
 AT C
 GAM2488 KIAA1576 3' AGCACCTTCTTTCCTGTCTCTT 32770 CA CGCT C
 AAGAG AGG GAAGG GCT
 ||||| ||| ||||| |||
 TTCTC TCC CTTCC CGA
 TG TTT_ A
 GAM2488 KIAA1727 3' GAGCACCTTCAGCATGAGTTGT 32034 GG ____ C
 T AGCAA C GCTGAAGG GCTC
 ||||| | ||||| |||||
 TTGTT G CGACTTCC CGAG
 GA TA A
 GAM2488 MGC11115 3' AGCACCTTCTGTGGCTC 26092 AAGG T C
 GAGC CGC GAAGG GCT
 |||| ||| ||||| |||
 CTCG GTG CTTCC CGA
 ____ T A
 GAM2488 MGC16703 5' GTCTCCAGCCCCCTGCCCT 36181 A A C A
 AG GCA GG GCTG AGGC
 || ||| || ||||| |||||
 TC CGT CC CGAC TCTG
 C C C C
 GAM2488 MGC3047 3' ATGCCAGCCCTTGCTC 26137 C GAA C
 GAGCAAGG GCT GGCG T
 ||||| ||| ||||| |
 CTCGTTCC CGA CCGT A
 _ ____ A
 GAM2488 PP1665 5' GAGCGCCTCTGGTTCTGCTC 25091 A C GA
 GAGCA GG GCT AGGCGCTC
 ||||| ||| ||||| |||||

CTCGT CC TGG TCCGCGAG
_ T TC

GAM2488 SAST 5' GAGCGCCTTACCAGCTGCCCT 31540 A AG GC_
AG GCA GC TGAAGGCGCTC
|| ||| || |||||
TC CGT CG ACTTCCGCGAG
C _ ACC

GAM2488 URG4 3' AGCAGAAAGTAGGCCTTGCTC 19578 G AAGGC
GAGCAAGGC CTG GCT
||||||| ||| |||
CTCGTTCCG GAT CGA
_ GAAGA

GAM2488 LOC124460 3' AGCACCCCTGGAGACTTTGCTC 37442 CG GA C_
GAGCAAGG CT AGG GCT
||||||| || ||| |||
CTCGTTTC GA TCC CGA
A_ GG CA

GAM2488 LOC144483 3' GAGCACCTCCCTGCCCGTCTT 30211 GCAA CT A C
AAGA GGCG GA GG GCTC
|||| ||| || |||
TTCT CCGT CT CC CGAG
GC_ CC C A

GAM2488 LOC145447 3' GCCAGTGCCTTGCTCTT 37862 GAA
AAGAGCAAGGCGCT GGC
||||||| |||
TTCTCGTTCCGTGA CCG

GAM2488 LOC149706 5' GAGCCAGGAGAGCGCCTTCTCT 41060 C GAAGGC
AGAG AAGGCGCT GCTC
|||| ||||| |||
TCTC TTCCGCGA CGAG
_ GAGGAC

GAM2488 LOC151178 5' AGATGGGGTCAAGCGCCTGCCCT 39069 A A AGG _
AG GCA GCGCTGA CG CT
|| ||| ||||| |||
TC CGT CCGCGACT GT GA
C _ GGG A

GAM2488 LOC155061 3' GAGCGCCTCCAGCCCCATAGC 39537 AA_ C A
GC GG GCTG AGGCGCTC
|| || ||| |||||
CG CC CGAC TCCGCGAG
ATA C C

GAM2488 LOC155340 5' GCCTCAGCCGCCTCACTC 36317 CA _ A
GAG AGGCG CTGA GGC
||| |||| ||| |||
CTC TCCGC GACT CCG
AC C _

GAM2488 LOC157349 5' GAACGCCTTCTTCAGGCCCTGT 39596 G A G _ C
CTT AAGA CA GGC CTGA AGGCG TC
|||| ||| ||| |||| ||

TTCT GT CCG GACT TCCGC AG
 _ C _ TCT A
 GAM2488 LOC196759 3' AGCACCTCTTCACCTTGCTC 42292 CGC _ C
 GAGCAAGG TGA AGG GCT
 ||||| ||| ||| |||
 CTCGTTCC ACT TCC CGA
 _ TC A
 GAM2488 LOC199899 5' CCTCAGCGCCCAGCCCTT 43257 A AA A
 AAG GC GCGCTGA GG
 ||| || ||||| ||
 TTC CG CCGCGACT CC
 C AC _
 GAM2488 LOC221495 3' TGTCAAGGCCTTGCTC 45062 G GAA
 GAGCAAGGC CT GGCG
 ||||| || |||
 CTCGTTCCG GA CTGT
 _ A _
 GAM2488 LOC256598 5' GCCTCAGCCGCTCACTC 46098 CA _ A
 GAG AGGCG CTGA GGC
 ||| |||| ||| |||
 CTC TCCGC GACT CCG
 AC C _
 GAM2488 LOC256867 5' GCCCCTCAGCACCCCTGCCTT 45474 A A C A C
 AAG GCA GG GCTGA GG GC
 ||| ||| || |||| || ||
 TTC CGT CC CGACT CC CG
 _ C A C _
 GAM2488 LOC257054 3' GAGGCCTTCAGCCCCTCGCTC 45781 A C G
 GAGC AGG GCTGAAGGC CTC
 |||| ||| ||||| |||
 CTCG TCC CGACTTCCG GAG
 C C _
 GAM2488 LOC64744 3' TCTTCAGCCCTCGCTCT 30953 A C
 AGAGC AGG GCTGAAGG
 |||| ||| |||||
 TCTCG TCC CGACTTCT
 C _
 GAM2488 LOC90288 5' GCCCTTCAGCACCCCCTC 31108 CAA C C
 GAG GG GCTGAAGG GC
 ||| || ||||| ||
 CTC CC CGACTTCC CG
 CC_ A _
 GAM2488 LOC92080 3' GAGCAGCCCCAGCGCCTCATCT 33759 GCA AA _
 AGA AGGCGCTG GGC GCTC
 ||| ||||| ||| |||
 TCT TCCGCGAC CCG CGAG
 AC_ C_ A
 GAM2489 CDH1 3' TTTCAACTTTTGACAATC 10567 CG T
 GAT GTT GAAGTTGAAA
 ||| ||| ||||| |||

			CTA CAG TTTCAACTTT		
			A_ T		
GAM2489	RBBP9	3'	GTTTCAACATTCAATCTAA 34744	CGGTT _	
			TTAGAT TGAA GTTGAAAC		
			AATCTA ACTT CAACTTTG		
			_____ A		
GAM2489	BCCIP	3'	AATTTCAAATGGATCCGATCTA 27785	_____	
	A		TTAGATCGG TTTGAAGTT		
			AATCTAGCC AAACTTTAA		
			TAGGT		
GAM2490	KRT16	5'	CACCATTGAGAATGCGCAGC 45629	CCC GC	
			GCTGCGCAT CTCGA GTG		
			CGACGCGTA GAGTT CAC		
			A_ AC		
GAM2490	NHLH1	3'	CACTCTGAAAATGTGCAGC 12124	CCCC G C	
			GCTGCGCAT TC AG GTG		
			CGACGTGTA AG TC CAC		
			AA_ _ T		
GAM2490	P2RY2	5'	CGAGAGGAGAAGCGCAGCG 8414	A _ _	
			CGCTGCGC TC CC CTCG		
			GCGACGCG AG GG GAGC		
			A A A		
GAM2490	PCSK2	3'	CACGTTTGAAGATGCGAGCG 8454	G CCC	
			CGCT CGCATC TCGAGCGTG		
			GCGA GCGTAG AGTTTGCAC		
			_ A_		
GAM2490	FLJ22009	3'	ACGCTTGTAATCGCAGC 30241	C CCCCT	
			GCTGCG AT CGAGCGT		
			CGACGC TA GTTCGCA		
			_ AT_		
GAM2490	IRF7	3'	CACCTAGAGGGCACGCAGCGT 10249	CATC G C	
			ACGCTGCG CCCTC AG GTG		
			TGCGACGC GGGAG TC CAC		
			AC_ A _		
GAM2490	NRF	3'	CACGGTTTGGATGTGCAGC 18985	CCTC G	
			GCTGCGCATCC GA CGTG		
			CGACGTGTAGG TT GCAC		
			T_ G		
GAM2490	LOC200317	3'	ACGCTTGTAATCGCAGC 42801	C CCCCT	
			GCTGCG AT CGAGCGT		

CGACGC TA GTTCGCA
 _ AT_
 GAM2490 LOC91408 5' CACTAAGAGGGATGCGCAAAGC 32791 _ C GAGC
 GCT GCGCATCCC TC GTG
 ||| ||||| || |||
 CGA CGCGTAGGG AG CAC
 AA _ AAT_
 GAM2491 COL6A2 3' ACCCCGAGACCGCGCTGG 27725 ACC TTGAA
 CCAGC GC CTCGGGGT
 |||| || |||||
 GGTCG CG GAGCCCCA
 _ CCA_
 GAM2491 G6PD 3' GACCCCGAGTCGGGAGG 5980 G A
 CC CTTGA CTCGGGGTC
 || |||| |||||
 GG GGGCT GAGCCCCAG
 A _
 GAM2491 DQX1 5' ACCCCACTGGAGTGGTGCTGG 28596 GAACTC
 CCAGCACCGCTT GGGGT
 ||||| ||||
 GGTCGTGGTGAG CCCCA
 GTCA_
 GAM2491 ETR101 3' GACCCCGAGCGGCGCTGCCGG 35830 A C TGAA
 CC GCA CGCT CTCGGGGTC
 || ||| |||| |||||
 GG CGT GCGG GAGCCCCAG
 C C C_
 GAM2491 FLJ14054 3' ACTTCCAAAAGGTGCTGG 23781 GC AACTC
 CCAGCACCTTG GGGGT
 ||||| || ||||
 GGTCGTGG AAC CTTCA
 AA _
 GAM2491 KIAA1884 3' GACCCCGAGTCCATTGGCCGC 36296 A_ CT A
 GC CCG TG ACTCGGGGTC
 || ||| |||||
 CG GGT AC TGAGCCCCAG
 CC T_ C
 GAM2491 SEC14L2 3' ACCCCGAGACAAAAATGCT 14804 CCGC AA
 AGCA TTG CTCGGGGT
 |||| || |||||
 TCGT AAC GAGCCCCA
 AAA_ A_
 GAM2491 LOC122769 5' GACCCCGATGGCGGCGCCGG 36695 A A TGAAC
 CC GC CCGCT TCGGGGTC
 || |||| |||||
 GG CG GGCGG AGCCCCAG
 C C T_
 GAM2491 LOC151124 5' ACCCCGAGATCAGTGC 41299 CGCT A
 GCAC TGA CTCGGGGT
 |||| || |||||

CGTG ACT GAGCCCCA
 _____ A
 GAM2491 LOC254016 5' GACCCCTAAGAGTTCAAGCCAT 46309 CC _____
 GCTGG CCAGCA GCTTGAAGTC GGGGTC
 ||||| ||||| |||||
 GGTCGT CGAACTTGAG CCCCAG
 AC AAT
 GAM2491 LOC58509 5' GACCCCGACAGAGGGCGACGGC 42612 AC_ GAAC
 GC CGCTT TCGGGGTC
 || ||||| |||||
 CG GCGGG AGCCCCAG
 GCA AGAC
 GAM2491 LOC64150 5' GACCCCGAGAGCGGCGGCGC 33411 A T AA
 GC CCGCT G CTCGGGGTC
 || ||||| |||||
 CG GGCGG C GAGCCCCAG
 C _GA
 GAM2492 AXL 3' ATGTTGCCCCCGTGAGCCA 7419 T AA C
 TGGCTCACG GG CA CGT
 ||||| || |||||
 ACCGAGTGC CC GT GTA
 _ CC T
 GAM2492 AXL 3' ATGTTGCCCCCGTGAGCCA 22440 T AA C
 TGGCTCACG GG CA CGT
 ||||| || |||||
 ACCGAGTGC CC GT GTA
 _ CC T
 GAM2492 HMG20A 3' ACACGGTGCTCAGTGGGTGCCA 20072 TCA TG A
 TGGC CG GA CACCGTGT
 |||| || || |||||
 ACCG GT CT GTGGCACA
 TGG GA C
 GAM2492 EMILIN-2 3' CACGGTGAACATGGCCA 25766 TCA GAA
 TGGC CGTG CACCGTG
 |||| |||| |||||
 ACCG GTAC GTGGCAC
 _ AA_
 GAM2492 FLJ21742 3' ACACGGCATTCCGTGTGTGACC 25912 CT_ CA
 A TGG CACGTGGAA CCGTGT
 ||| ||||| |||||
 ACC GTGTGCCTT GGCACA
 AGT AC
 GAM2492 RNF24 3' ACACGACGTCTGTGTGGAGCC 14083 _ TG ACAC
 GGCTC ACG GA CGTGT
 |||| || || |||||
 CCGAG TGT CT GCACA
 G GT GCA_
 GAM2492 LOC153577 5' ACACGGTGCCTGGAAGACCA 41641 _ CA T AA
 TGG CT CG GG CACCGTGT
 ||| || || |||||

		ACC GA GT CC GTGGCACA	
		A AG _ _	
GAM2492	LOC165140 5'	ACACGGTGTTCCTGGTCAGCC 40116	C GT
		GGCT AC GGAACACCGTGT	
		CCGA TG CCTTGTGGCACA	
		C GT	
GAM2493	ATRN 3'	ATAAAACACTATCTGATG 29297	A C
		CATCAGATAG GTT TGT	
		GTAGTCTATC CAA ATA	
		A A	
GAM2493	CYP3A43 3'	ACAAAACACTGTTATCTGATG 27662	_ C
		CATCAGATAG AGTT TGT	
		GTAGTCTATT TCAA ACA	
		G A	
GAM2493	KCND2 3'	TAGTGAACTTATCTGATG 14610	A CT T
		CATCAGAT GAGTT G CTG	
		GTAGTCTA TTCAA T GAT	
		_ AG _	
GAM2493	SLC22A5 3'	TACAGACAACCTTCATCT 9028	AG TC
		AGAT AGT TGTCTGTA	
		TCTA TCA ACAGACAT	
		CT _	
GAM2493	TCF12 3'	TTACATCGGACTCTATCTG 9203	T TC
		CAGATAGAGT CTG TGTA	
		GTCTATCTCA GGC ACATT	
		_ T _	
GAM2493	TP53 3'	CAGCCAAACCCTGTCTGA 6152	A C T
		TCAGATAG GTT TG CTG	
		AGTCTGTC CAA AC GAC	
		C _ C	
GAM2493	MGC4172 5'	TACAGATGTGACCTATC 23600	A CT
		GATAG GTT GTCTGTA	
		CTATC CAG TAGACAT	
		_ TG	
GAM2493	PDZD2 5'	ACAGACAGTGAACCTGACTG 39387	A A _
		CAG TAG GTTC TGTCTGT	
		GTC GTC CAAG ACAGACA	
		A _ TG	
GAM2493	RRN3 3'	TTACAGACAAAATGAAGACTAT 20491	AG _ _ _
	C	GATAG TTC TGTCTGTAA	

			CTATC AAG ACAGACATT		
			AG TAAA		
GAM2493	LOC150951	5'	ATGAAACCTATCTGATG 41276	A	CT
			CATCAGATAG GTT GT		
			GTAGTCTATC CAA TA		
			_ AG		
GAM2493	LOC152274	3'	TACAGACAGACGTCCTG 39233	ATA	GT
			CAG GA TCTGTCTGTA		
			GTC CT AGACAGACAT		
			___ GC		
GAM2494	ARAF1	5'	GCGGCTGTAGCGGCGTGACA 31981	GA	
			TGTCACGTTGT ACAGCCGC		
			ACAGTGCGGCG TGTCGGCG		
			A_		
GAM2494	CAMK4	3'	GCAAGTTAACACAACGTAACA 7481	C	___ A_
			TGT ACGTTGTG AAC GC		
			ACA TGCAACAC TTG CG		
			A AA AA		
GAM2494	CD34	3'	CGGCCATTTCAGCAAGACA 7535	ACG	_ CA
			TGTC TTG TGAA GCCG		
			ACAG AAC ACTT CGGC		
			___ G AC		
GAM2494	FGF2	5'	CGGCTGCCCGCGGTTGCA 7737	C	GT AA
			TGT AC TGTG CAGCCG		
			ACG TG GCGC GTCGGC		
			T ___ CC		
GAM2494	FZD4	3'	GCAACTGCTTTGCAATGACA 14486	CG	TG _ CC
			TGTCA TTG AA CAG GC		
			ACAGT AAC TT GTC CG		
			___ GT C AA		
GAM2494	MGAM	3'	GCAGCACTACAACGTGCA 35824	T	AACA C
			TG CACGTTGTG GC GC		
			AC GTGCAACAT CG CG		
			_ CA_ A		
GAM2494	SERPINB13	3'	GTTTTCCCAACGTGACA 14763	T	C
			TGTCACGTTG GAA AGC		
			ACAGTGCAAC CTT TTG		
			C _		
GAM2494	SGCG	3'	GCAGCTGCACATCGTGA 5742	T	AA C
			TCACG TGTG CAGC GC		

AGTGC ACAC GTCG CG
 T _ A
 GAM2494 VENTX2 3' GCGAGTGACAATGTGACA 15816 GA A_
 TGTCACGTTGT AC GC
 ||||| || ||
 ACAGTGTAACA TG CG
 G_ AG
 GAM2494 EML4 5' GCGGCTCTCAACGTGAC 21144 T ACA
 GTCACGTTG GA GCCGC
 ||||| || ||||
 CAGTGCAAC CT CGGCG
 T _ _
 GAM2494 FLJ10936 5' GCAGCTGTCGGGACGTGAC 20270 G A C
 GTCACGTT TGA CAGC GC
 ||||| || |||| ||
 CAGTGCAG GCT GTCG CG
 G _ A
 GAM2494 KIAA0763 3' GCTGGCAATGTGACA 16970 GAA
 TGTCACGTTGT CAGC
 ||||| ||||
 ACAGTGTAACG GTCG
 _
 GAM2494 KIAA1297 3' GCGGCTGTCCAGCCGAT 35716 AC T A
 GTC GTTG GA CAGCCGC
 || |||| || |||||
 TAG CGAC CT GTCGGCG
 C_ _ _
 GAM2494 KIAA1297 5' GCGGCTGTCCATTCCTGAC 35717 CGTT A
 GTCA GTG ACAGCCGC
 |||| || |||||
 CAGT TAC TGTCGGCG
 CCT_ C
 GAM2494 MGC14425 5' GCGGCTGTCCCTGTGTGACA 26725 TTGT A
 TGTCACG GA CAGCCGC
 ||||| || |||||
 ACAGTGT CT GTCGGCG
 GTCC _
 GAM2494 MGC2865 5' GCAACTGCGCGGACGTGAC 26167 _ AA CC
 GTCACGT TGTG CAG GC
 ||||| |||| || ||
 CAGTGCA GCGC GTC CG
 G _ AA
 GAM2494 MGC9753 5' GCGGCTGCCTCACGTGCG 27242 _ A_
 CGT TGTGA CAGCCGC
 || |||| |||||
 GCG GCACT GTCGGCG
 T CC
 GAM2494 MSRA 5' GCGGCCGCGTCGACGTGACA 14721 _ AACA
 TGTCACGTTG TG GCCGC
 ||||| || ||||

ACAGTGCAGC GC CGGCG
 T GC__
 GAM2494 NFAT5 5' GCGGCTGTCCGGGCGATGACA 28957 _ G A
 TGTCA CGTT TG ACAGCCGC
 ||||| ||| || |||||
 ACAGT GCGG GC TGTCGGCG
 A _ C
 GAM2494 PRDM13 5' GCAGCTGCTTCGCAGCGCAAC 22255 CA _ C
 GT CGTTGTGAA CAGC GC
 || ||||| ||| ||
 CA GCGACGCTT GTCG CG
 AC C A
 GAM2494 PSR 3' GCGGCTGTTACAGGGC 32501 ACG
 GTC TTGTGAACAGCCGC
 ||| |||||
 CGG GACACTTGTCGGCG

 GAM2494 LOC134689 5' GCGGCTGTTCGGCTGGCA 37383 C TGA
 TGTCA GTTG ACAGCCGC
 ||||| ||| |||||
 ACGGT CGGC TGTCGGCG

 GAM2494 LOC151507 3' GCAACTGTTCCACAGTGA 39126 GT CC
 TCAC TGTGAACAG GC
 ||||| ||||| ||
 AGTG ACACTTGTC CG
 _____ AA
 GAM2494 LOC164295 5' CGGCTGTTCCACCTGCCA 40142 T C T T
 TG CA GT G GAACAGCCG
 || ||| | |||||
 AC GT CA C CTTGTCGGC
 C C __
 GAM2494 LOC219513 3' GCGGCTGCTCACAGAGCAC 45295 CACG A
 GT TTGTGA CAGCCGC
 || ||||| |||||
 CA GACACT GTCGGCG
 CGA_ C
 GAM2494 LOC253737 5' GCTGGTCAAGCACGTGACA 46046 TG_ A
 TGTCACGT TGA CAGC
 ||||| ||| |||
 ACAGTGCA ACT GTCG
 CGA G
 GAM2494 LOC51631 3' GCTGTTTCAGGGTGACA 33768 G TG
 TGTCAC T TGAACAGC
 ||||| | |||||
 ACAGTG G ACTTGTCG
 G __
 GAM2494 LOC58509 5' GCGGCTGCTCACGGCGCACG 42613 CA A
 TGT CGTTGTGA CAGCCGC
 ||| ||||| |||||

GCA GCGGCACT GTCGGCG
 C_ C
 GAM2494 LOC93070 5' GCAGCTGTCGGGACGTGAC 35325 G A C
 GTCACGTT TGA CAGC GC
 ||||| ||| ||| ||
 CAGTGCAG GCT GTCG CG
 G _ A
 GAM2495 HRIHFB2436 5' CACCGCGGGGCCGACG 15665 A C G A
 CG TC GC TTCGCGGT G
 || || || ||||| |
 GC AG CG GGGCGCCA C
 _ C _ C
 GAM2495 MGC12921 3' GCCACCGCCCGTGGGCATCGAT 31899 C _ TTC A
 GA TCA CGAT CCGCG GCGGT GC
 ||| ||| |||| ||||| ||
 AGT GCTA GGTGC CGCCA CG
 A CG C_ C
 GAM2495 LOC153579 3' GCCACCGGGGAACGGGGATCGG 39405 G _ G A
 TGA TCACCGATCC CGTT C CGGT GC
 ||||| ||| | ||| ||
 AGTGGCTAGG GCAA G GCCA CG
 G G G C
 GAM2496 PODXL 3' CTCTTGTAATAACCCA 11874 CTCG TGGC
 TGGGTTAT ACG GGAG
 ||||| ||| |||
 ACCCAATA TGT TCTC
 AAA_ _
 GAM2496 ARTN 5' CCCCACAAAAGATAACTCA 10110 CGAC C
 TGGGTTATCT GTGG GG
 ||||| ||| ||
 ACTCAATAGA CACC CC
 AAA_ _
 GAM2496 FLJ23191 5' TCTTTGCTGAAACAACCCA 23804 ATC GACGT
 TGGGTT TC GGCGGAGA
 ||||| || |||||
 ACCCAA AG TCGTTTCT
 CAA _
 GAM2496 FLJ23323 3' TCCACGGCCACCATAGATAACC 23955 CGAC _
 CA TGGGTTATCT GTGGC GGA
 ||||| ||| |||
 ACCCAATAGA CACCG CCT
 TAC_ GCA
 GAM2496 NAV3 3' CTCCAAAATATTAATAAACC 17091 CTC CG GGC
 A TGGGTTAT GA T GGAG
 ||||| || | |||
 ACCCAATA TT A CCTC
 AAA AT AAA
 GAM2497 FANCA 3' CCAGCCCAGCTCCCGTGT 5629 CCC C
 GCACGGGAGT GGC GG
 ||||| ||| ||

			TGTGCCCTCG CCG CC		
			AC_ A		
GAM2497 MBP	5'	GCGTCTTTGGGGACCCCGTGC 43222	A	GGCC	
GA		TCGCACGGG GTCCC GGCGC			
		AGCGTGCCC CAGGG CTGCG			
		C GTTT			
GAM2497 MYO1D	5'	GCGCCGGCCGAGAAGGCGCCG 35549	GA	C__	
		CGG GTC CGGCCGGCGC			
		GCC CGG GCCGGCCGCG			
		G_ AAGA			
GAM2497 MGC2817	5'	GCGCCGGCCCCCTTCCCATGCGG 34764	C	TCCC	
		TCGCA GGGAG GGCCGGCGC			
		GGCGT CCCTT CCGGCCGCG			
		A CC__			
GAM2497 SEC24D	5'	CGCCGGCCGGGGAAGAGGCGCG 16799	ACGGGAG		
G		TCGC TCCCGGCCGGCG			
		GGCG GGGGCCGGCCGC			
		CGGAGAA			
GAM2497 USP2	5'	GCGCCAGCCGGGACTCACCCGC 10402	AC _	C	
		GC GG GAGTCCCGGC GGCGC			
		CG CC CTCAGGGCCG CCGCG			
		C_ A A			
GAM2497 XPO5	5'	GCGCCGGCTTCTTCCCAGCGCG 43841	AC_	TCCC	
A		TCGC GGGAG GGCCGGCGC			
		AGCG CCCTT TCGGCCGCG			
		CGA CT__			
GAM2497 LOC153603	5'	GCGCCGGCCGAGACCTG 39406	AG C		
		CGGG TC CGGCCGGCGC			
		GTCC AG GCCGGCCGCG			
		_ A			
GAM2497 LOC164714	3'	CGCCGGCGCCCCTGTGCGA 42178	A	CCCG	
		TCGCACGGG GT GCCGGCG			
		AGCGTGTCC CG CGGCCGC			
		C _			
GAM2498 CBLB	3'	GGACAATCCAAAGCATGGTTCT 10552	AAGAC_	CC	
TC		GGAGAACCG GGA GTCC			
		CTTCTTGGT CCT CAGG			
		ACGAAA AA			
GAM2498 CELSR1	3'	GACACAAAGGTCTTGTTCTCC 15515	G	GGACC_	
		GGAGAACC AAGAC GTC			

		CCTCTTGG TTCTG CAG	
		— GAAACA	
GAM2498 PRKCH	5'	GACGGGACTCCCGTTCTCC 12934	AAGAC —
		GGAGAACCG GGA CCGTC	
		CCTCTTGGC CCT GGCAG	
		— CAG	
GAM2498 RXRA	3'	GGACAGCCCTGACCTTCGGTTT 8870	A_ ACC_
TCC		GGAGAACCGAAG CGG GTCC	
		CCTTTTGGCTTC GTC CAGG	
		CA CCGA	
GAM2498 AKAP12	5'	GGCACCTCCGGTTCTCC 29313	AA C A_
		GGAGAACCG GA GG CC	
		CCTCTTGGC CT CC GG	
		— — AC	
GAM2498 KIAA0644	3'	GGACAAGGCCTCTGGTTCTCC 16784	GA C A —
		GGAGAACC AGA GG CC GTCC	
		CCTCTTGG TCT CC GG CAGG	
		— — — AA	
GAM2498 LOC152345	3'	GACAGAAGTTCCTGGTTCTCC 39266	AA GGACC
		GGAGAACCG GAC GTC	
		CCTCTTGGT TTG CAG	
		CC AAGA_	
GAM2499 GASC1	5'	GGAACAAGTCTCCCAAATTTCC 32124	C_ _ C CG
CA		TGGGAAGTT GA ACT GT TCC	
		ACCCTTTAA CT TGA CA AGG	
		ACC C A —	
GAM2499 INSM1	3'	GGCTGTAAATTGAAGTTCCCA 7951	— TC
		TGGGAAGTTCGA AC GTC	
		ACCCTTCAAGTT TG CGG	
		AAA T_	
GAM2499 C17orf26	3'	GGGACAACAAGCTTCTTTCTTC 29187	TTC _ C C
		GAAG GAA CT GT GTCCC	
		CTTC CTT GA CA CAGGG	
		TTT C A A	
GAM2499 KIAA0416	3'	GGAATTGACTGAAGTTCCCA 17836	AAC TCG
		TGGGAAGTTCG TCG TCC	
		ACCCTTCAAGT AGT AGG	
		C_ TA_	
GAM2499 LOC255082	5'	GGACAACAAGAACTTCCC 46119	CGAA C C
		GGGAAGTT CT GT GTCC	

CCCTTCAA GA CA CAGG
 A__ A A
 GAM2500 CXX1 5' GTGGACGAGAACACGTTCTCCA 10025 CAC TC C
 TGG GAAT GT CTCGTCCAC
 ||| ||| || |||||
 ACC CTTG CA GAGCAGGTG
 T__ CA A
 GAM2500 SLC25A15 3' TGAAGTCAAATTGTGCCA 15529 A TCCTC C
 TGGCACGA TTCG GT CA
 ||||| ||| |||
 ACCGTGTT AAGT CA GT
 A ____ A
 GAM2500 DKFZP564B147 5' GTGGACGAGAACACGTTCTCCA 39936 CAC TC C
 TGG GAAT GT CTCGTCCAC
 ||| ||| || |||||
 ACC CTTG CA GAGCAGGTG
 T__ CA A
 GAM2500 KIAA1856 3' TGGACGAAAATGACGTGC 44527 AAT CC
 GCACG TCGT TCGTCCA
 |||| ||| |||||
 CGTGC AGTA AGCAGGT
 ____ AA
 GAM2500 SGKL 3' TGAAGTCAAATTGTGCCA 14928 A TCCTC C
 TGGCACGA TTCG GT CA
 ||||| ||| |||
 ACCGTGTT AAGT CA GT
 A ____ A
 GAM2500 LOC165246 5' TGGGGAAAAACTCGTGCCA 40127 A CG
 TGGCACGA TT TCCTCG
 ||||| || |||||
 ACCGTGCT AA AGGGGT
 C AA
 GAM2500 LOC196337 5' ATGAACGAATTCATGCC 42357 C CC
 GGCA GAATTCGT TCGT
 ||| ||||| |||
 CCGT CTTAAGCA AGTA
 A ____
 GAM2501 B4GALT5 3' CGTACAGCCAGGCCCGTGTG 11168 C A AC__
 CAC CGG GT G TGTACG
 ||| ||| || | |||||
 GTG GCC CG C ACATGC
 T _ GAC G
 GAM2501 GRB10 5' GCGGTCCCTGCAGCCCCGGGTG 11787 A ACG ____
 CACCCGG GT TGT ACGCC
 ||||| || ||| |||||
 GTGGGCC CG ACG TGCGG
 C ____ TCCC
 GAM2501 LDB2 3' GCACAGTGGCTCCGTGTG 6970 C _ _
 CAC CGGAGT AC GTGT
 ||| ||||| || |||||

			GTG GCCTCG TG CACG		
			T G A		
GAM2501	PAPPA	5'	GCTGGCAGCTCCGGGTG 8442	ACG AC	
			CACCCGGAGT TGT GC		
			GTGGGCCTCG ACG CG		
			___ GT		
GAM2501	PCDH11X	3'	GCATACTGGTTTTCCAGGTG 26791	C T GT C	
			CACC GGAG AC GTA GC		
			GTGG CCTT TG CAT CG		
			A T GT A		
GAM2501	PCDH11X	3'	GCATACTGGTTTTCCAGGTG 26806	C T GT C	
			CACC GGAG AC GTA GC		
			GTGG CCTT TG CAT CG		
			A T GT A		
GAM2501	PCDH11Y	3'	GCATACTGGTTTTCCAGGTG 26824	C T GT C	
			CACC GGAG AC GTA GC		
			GTGG CCTT TG CAT CG		
			A T GT A		
GAM2501	RAX	5'	GCGTGCGCAGCCCGGG 15093	A AC	
			CCCGG GT GTGTACGC		
			GGGCC CG CGCGTGCG		
			_ A _		
GAM2501	SHOX	3'	GGCCACCGTGCTCCGGG 6056	T AC	
			CCCGGAGTACG GT GCC		
			GGGCCTCGTGCA CGG		
			_ C _		
GAM2501	SLC6A3	3'	GCGTGTACTACCCAGG 6710	C A C	
			CC GG GTA GTGTACGC		
			GG CC CAT CATGTGCG		
			A C _		
GAM2501	SLC6A3	3'	GCGTGTACTACCCAGG 6709	C A C	
			CC GG GTA GTGTACGC		
			GG CC CAT CATGTGCG		
			A C _		
GAM2501	SLC6A3	3'	GCGTGTACTACCCAGG 6708	C A C	
			CC GG GTA GTGTACGC		
			GG CC CAT CATGTGCG		
			A C _		
GAM2501	SLC6A3	3'	GCGTGTACTACCCAGG 6711	C A C	
			CC GG GTA GTGTACGC		

			GG CC CAT CATGTGCG		
			A C _		
GAM2501	SLC6A3	3'	GCGTGTACTACCCCAGG	6707	C A C
			CC GG GTA GTGTACGC		
			GG CC CAT CATGTGCG		
			A C _		
GAM2501	SMAC	5'	GCGTGCCACCACTCCGGG	29052	AC _
			CCCGGAGT GTG TACGC		
			GGGCCTCA CAC GTGCG		
			C_ C		
GAM2501	C17orf31	5'	GCACACAGTTGACCGGTGTG	19005	_ AGT _ AC
			CAC CCGG AC GTGT GC		
			GTG GGCC TG CACA CG		
			T AGT A _		
GAM2501	FRAT1	5'	GCCCGCACAGCTCCGGGTG	11981	AC AC
			CACCCGGAGT GTGT GC		
			GTGGGCCTCG CACG CG		
			A_ CC		
GAM2501	KIAA0153	3'	GGCGCCACACTCCGGG	17499	AC TA
			CCCGGAGT GTG CGCC		
			GGGCCTCA CAC GCGG		
			_ C_		
GAM2501	KIAA0469	3'	GCTGCCGTACTCCAGG	16894	C T C
			CC GGAGTACG GTA GC		
			GG CCTCATGC CGT CG		
			A _ _		
GAM2501	KIAA1363	3'	GGCGTACACTGGCACCTGGTG	34334	C A AC
			CACC GG GT GTGTACGCC		
			GTGG CC CG CACATGCGG		
			T A GT		
GAM2501	KIAA1951	3'	GGCACATGCCTGTAATCCGAGT	36512	C G T C_
	G		CAC CGGA TACG GTA GCC		
			GTG GCCT ATGT CGT CGG		
			A A C ACA		
GAM2501	PEG10	3'	GCACACAGTATTCCCAGTG	17430	CC _ AC
			CAC GGAGTAC GTGT GC		
			GTG CCTTATG CACA CG		
			AC A _		
GAM2501	LOC128989	3'	GGCACACACATACACTCCTGCG	36944	C _ AC_ AC
	TG		CAC C GGAGT GTGT GCC		

GTG G CCTCA CACA CGG
 C T CATA CA
 GAM2501 LOC137964 3' GTGTGTTTCGTACTCCAGG 37112 C TG
 CC GGAGTACG TACGC
 || ||||| ||||
 GG CCTCATGC GTGTG
 A TT
 GAM2501 LOC148397 3' GGCACACACGTGTTATGACCG 38529 ____ AC
 CGG AGTACGTGT GCC
 ||| ||||| |||
 GCC TTGTGCACA CGG
 AGTA CA
 GAM2501 LOC149127 3' ACACGAGCACTCTGGGTG 40948 A__
 CACCCGGAGT CGTGT
 ||||| ||||
 GTGGGTCTCA GCACA
 CGA
 GAM2501 LOC152860 5' GGCCTTCGCGCTCCGGGTG 39324 TA TAC
 CACCCGGAG CGTG GCC
 ||||| ||| |||
 GTGGGCCTC GCGC CGG
 __ TTC
 GAM2501 LOC197408 5' GGCCTACACACACGGG 43207 GA AC
 CCGG GT GTGTACGCC
 ||| || |||||
 GGGC CA CACATGCGG
 A_ __
 GAM2501 LOC205095 3' GGCCTACACGTAGAGGCATGTG 43604 ____ GGAG
 CAC CC TACGTGTACGCC
 ||| || |||||
 GTG GG ATGCACATGCGG
 TAC AG__
 GAM2501 LOC219688 5' GCGCACGATCTCCGGGT 44700 TA TA
 ACCCGGAG CGTG CGC
 ||||| ||| |||
 TGGGCCTC GCAC GCG
 TA __
 GAM2501 LOC253897 3' GTGTGTTTCGTACTCCAGG 45968 C TG
 CC GGAGTACG TACGC
 || ||||| ||||
 GG CCTCATGC GTGTG
 A TT
 GAM2501 LOC255423 5' GGCTCTGCACACTCAGGT 46594 CG AC C_
 ACC GAGT GTGTA GCC
 ||| ||| |||| |||
 TGG CTCA CACGT CGG
 A_ __ CT
 GAM2501 LOC256222 5' GCGTATGTGCCCTGGGT 46427 A GT
 ACCCGG GTAC GTACGC
 ||||| ||| |||||

TGGGTC CGTG TATGCG
 C _
 GAM2502 DUSP7 5' CGGGGCGGGCGCGGCGA 32614 ATGG
 TCGCCGCG CGCCCCG
 ||||| |||||
 AGCGGCGC GCGGGGC
 GG_
 GAM2502 MLLT2 5' ATCGGGGCGCCGCGCCGGGA 12567 G _ A
 TC CCG CG TGGCGCCCCGAT
 || ||| || |||||
 AG GGC GC GCCGCGGGGCTA
 _ C _
 GAM2502 FLJ12132 5' GGTACCGGGGTGGGGCGCGGCG 24541 ATGG A
 CGCCGCG CGCCCCG TACC
 ||||| ||||| |||
 GCGGCGC GTGGGGC ATGG
 GGG_ C
 GAM2502 FLJ20306 3' ATCGAGGCTGCGGTGA 19367 ATGGC C
 TCGCCGCG GCC CGAT
 ||||| ||| |||
 AGTGGCGT CGG GCTA
 _ A
 GAM2503 CELL 3' GCGGAGCCTGAGAACCAACT 7558 C _
 AG TGGTTCTCGG CCGT
 || ||||| |||
 TC ACCAAGAGTC GGCG
 A CGA
 GAM2503 LMNA 5' GCAAGCCGAGAGCCAGC 12099 CG
 GCTGGTTCTCGGC TGT
 ||||| |||
 CGACCGAGAGCCG ACG
 A_
 GAM2503 NHP2L1 3' GGTGGACACTTGGCACCAGCT 11444 TCTCG _
 AGCTGGT GCC GTGTCCACC
 ||||| ||| |||||
 TCGACCA CGG CACAGGTGG
 _ TT
 GAM2503 RANBP3 3' GCATGGCCAAGAGCCAGCT 9689 C
 AGCTGGTTCT GGCCGTGT
 ||||| |||||
 TCGACCGAGA CCGGTACG
 A
 GAM2503 USH3A 5' GTGAACGAGTGCAGGAACCAGC 27564 CG CG_ C
 T AGCTGGTTCT GC TGT CAC
 ||||| || ||| |||
 TCGACCAAGG CG GCA GTG
 A_ TGA A
 GAM2503 C20orf121 5' GTGACTCTCTGAGAACCAGC 23634 CCGT C
 GCTGGTTCTCGG GTC AC
 ||||| ||| ||

CGACCAAGAGTC CAG TG
 TCT_ _
 GAM2503 DKFZP434K028 3' GACCAGCCACAGAACCAGCT 44772 C_ CGT
 AGCTGGTTCT GGC GTC
 ||||| ||| |||
 TCGACCAAGA CCG CAG
 CA AC_
 GAM2503 FLJ10847 3' GACATACCGAGGACCAACT 20202 C CC
 AG TGGTTCTCGG GTGTC
 || ||||| |||||
 TC ACCAGGAGCC TACAG
 A A_
 GAM2503 FLJ13490 3' GTAAACATCAGAACTAGC 24487 C GCC CC
 GCTGGTTCT G GTGT AC
 ||||| | ||| ||
 CGATCAAGA C TACA TG
 _ _ _ AA
 GAM2503 MDS006 3' GATTCAGCCAAGAACAGCT 21503 G C CGT
 AGCTG TTCT GGC GTC
 |||| ||| ||| |||
 TCGAC AAGA CCG TAG
 _ A ACT
 GAM2503 MGC15873 3' GGCAGAGGCCTCAGGAACCAGC 26743 C_ G_
 GCTGGTTCT GGCC TGTC
 ||||| ||| |||||
 CGACCAAGG CCGG ACGG
 ACT AG
 GAM2503 SCAM-1 3' GGTTCTCTAACCAGAACCAGC 12351 C CCGTGTCC
 T AGCTGGTTCT GG ACC
 ||||| || |||
 TCGACCAAGA CC TGG
 _ AATCTCCT
 GAM2503 SMOC2 3' TGGAGCCACAGAACCAGCT 35837 C_ CGTG
 AGCTGGTTCT GGC TCCA
 ||||| ||| |||||
 TCGACCAAGA CCG AGGT
 CA _ _
 GAM2503 TLK2 5' GCGCGCCAGGAACCAGC 38275 TC C
 GCTGGTTC GGC GTGT
 ||||| ||| |||||
 CGACCAAG CCG CGCG
 GA _
 GAM2503 LOC144587 5' GACAGCGGTAGCAACCAGCT 33270 CTCG _
 AGCTGGTT GCCG TGTC
 ||||| ||| |||||
 TCGACCAA TGGC ACAG
 CGA_ G
 GAM2503 LOC146802 3' GTGGACACTTTGAACCACT 38247 C TCGGCC
 AG TGGTTC GTGTCCAC
 || ||||| |||||

			TC ACCAAG	CACAGGTG		
			— TTT—			
GAM2503	LOC147841	5'	GACGGTGCCGAGAAGCAGCT	38398	G	CG
			AGCTG TTCTCGGC TGTC			
			TCGAC AAGAGCCG GCAG			
			G TG			
GAM2503	LOC202986	5'	GGAAGCCAAGGACCAGCT	43471	C	CGTG
			AGCTGGTTCT GGC TCC			
			TCGACCAGGA CCG AGG			
			A A—			
GAM2503	LOC221474	5'	ACAGAAAGCCTGAGAACCAGCT	44377	—	CG—
			AGCTGGTTCTC GGC TGT			
			TCGACCAAGAG CCG ACA			
			T AAAG			
GAM2504	ATP7A	3'	TTACAGGTGTGAGCCTCCATG	5500	—	TG
			CATGGAGGC CGC CTGTAA			
			GTACCTCCG GTG GACATT			
			A TG			
GAM2504	DPP6	3'	ACTCACGGCCTCCATG	28283	C	CT
			CATGGAGGCCG TG GT			
			GTACCTCCGGC AC CA			
			— T—			
GAM2504	EPHA8	3'	GCCTGGGGCCTCCACGTCA	21748	A	G —
			TGAC TGGAGGCC CT GC			
			ACTG ACCTCCGG GG CG			
			C — TC			
GAM2504	HD	3'	ACAGCAGCCTCCCTGTCA	7890	T	CGC
			TGACA GGAGGC TGCTGT			
			ACTGT CCTCCG ACGACA			
			C —			
GAM2504	MXI1	3'	ACAGCAGCATT TTTATTTC	12583	C	CC
			TGA ATGGAGG GCTGCTGT			
			ACT TATTTT CGACGACA			
			T A—			
GAM2504	MXI1	3'	ACAGCAGCATT TTTATTTC	28193	C	CC
			TGA ATGGAGG GCTGCTGT			
			ACT TATTTT CGACGACA			
			T A—			
GAM2504	PPP2R5E	3'	TTACAGCAGCACTGTAT	12925	G	GCC
			ATG AG GCTGCTGTAA			

			TAT TC CGACGACATT		
			G A__		
GAM2504	ACTR1A	3'	ACAGCAGCAGGTATGTGT 31530	GGAG	_
			ACAT GCC GCTGCTGT		
			TGTG TGG CGACGACA		
			TA__ A		
GAM2504	CCR8	3'	TACAGCAGCACGCATTCA 11701	G C_	
			TGGA GC GCTGCTGTA		
			ACTT CG CGACGACAT		
			A CA		
GAM2504	CIZ1	5'	GTTACAGCAGCAGCAGCTCCA 14442	_ C	
			TGGAG GC GCTGCTGTAAC		
			ACCTC CG CGACGACATTG		
			GA A		
GAM2504	DOCK3	3'	GTTACAGCAGCCCTCACCTCA 33040	CATG	CC
			TGA GAGG GCTGCTGTAAC		
			ACT CTCC CGACGACATTG		
			CCA_ _		
GAM2504	KIAA0894	3'	ACAAAGCCCCCATGTCA 17053	A CC	GC
			TGACATGG GG GCT TGT		
			ACTGTACC CC CGA ACA		
			_ _ A_		
GAM2504	KIAA1364	3'	ACCTCAGCCCTCATGTCA 31811	G CC	CT
			TGACATG AGG GCTG GT		
			ACTGTAC TCC CGAC CA		
			_ _ TC		
GAM2504	KIAA1416	3'	GCTGTGGCCTCCACGTCA 41809	A	T
			TGAC TGGAGGCCGC GC		
			ACTG ACCTCCGGTG CG		
			C T		
GAM2504	MGC21675	3'	GCTTCATGCGACTCCATGTCA 27445	GC	_ CT
			TGACATGGAG CGC TG GT		
			ACTGTACCTC GCG AC CG		
			A_ T TT		
GAM2504	PIPPIN	3'	GCCCTGCGGCCTCCACGTCA 38910	A	T_
			TGAC TGGAGGCCGC GC		
			ACTG ACCTCCGGCG CG		
			C TCC		
GAM2504	LOC150685	5'	ACAGCAGCAGCCCCGCTTC 42154	CA A	C
			GA TGG GGC GCTGCTGT		

		CT GCC CCG CGACGACA		
		TC C A		
GAM2504	LOC201522 3'	ACAGCTGTCGGCCTCCATG	42584	_ T
		CATGGAGGCCG C GCTGT		
		GTACCTCCGGC G CGACA		
		TT		
GAM2504	LOC221398 3'	ACAGCAGCACCTCCTCCATGCA	43748	A CC__
		TG CATGGAGG GCTGCTGT		
		AC GTACCTCC CGACGACA		
		— TCCA		
GAM2504	LOC256250 5'	GCCCACGGCCTCCAGTCA	46424	A CT_
		TGAC TGGAGGCCG GC		
		ACTG ACCTCCGGC CG		
		— ACC		
GAM2504	LOC91040 5'	CAGCTTGCCTGACCCCATGTC	32313	A CC__ T_
	A	TGACATGG GG GC GCTG		
		ACTGTACC CC CG CGAC		
		C AGTC TT		
GAM2505	ADRBK1 3'	GCCTCCACTCCCACTTCC	7329	A
		GGAGGTGG AGTGGAGGT		
		CCTTCACC TCACCTCCG		
		C		
GAM2505	ARHC 5'	GACCCACCACCACCTCC	11662	AA AG
		GGAGGTGG GTGG GTC		
		CCTCCACC CACC CAG		
		AC —		
GAM2505	ATP1A2 3'	CCATTTCCCACTTCCACCCCC	6364	A AG TC
		GG GGTGGAAGTGG G GG		
		CC CCACCTTCACC T CC		
		C CT TA		
GAM2505	ATP8B2 3'	CCTGCAACCTCCACCTCC	32513	AGT AG T C
		GGAGGTGGA GG G CGG G		
		CCTCCACCT CC C GTC C		
		— AA _ A		
GAM2505	BSG 3'	CGCCCCACCTCCACCCTC	33668	TGGAA C__
		GAGG GTGGAGGT GGCG		
		CTCC CACCTCCA CCGC		
		— CCC		
GAM2505	BSG 3'	CGCCCCACCTCCACCCTC	7457	TGGAA C__
		GAGG GTGGAGGT GGCG		

CTCC CACCTCCA CCGC
 _____ CCC
 GAM2505 CA3 5' GCCCACCTCCGCCCC 11678 T AA C
 GG GG GTGGAGGT GGC
 || || ||||| ||
 CC CC CGCCTCCA CCG
 _ _ C
 GAM2505 CACNA2D2 3' CCTGCCCCACCCACCTCC 12652 AA A C
 GGAGGTGG GTGG GGT GG
 ||||| ||| || ||
 CCTCCACC CACC CCG CC
 C _ _ T
 GAM2505 CACNA2D2 3' CCACCCACCTCCACTCCC 12649 AG A A C
 GG GTGA GTGG GGT GG
 || |||| ||| || ||
 CC CACCT CACC CCA CC
 CT C _ _
 GAM2505 CACNA2D2 3' CCACCTCCACTCCCACCTC 12650 A C
 GAGGTGG AGTGGAGGT GG
 ||||| ||||| ||
 CTCCACC TCACCTCCA CC
 C _
 GAM2505 CALM3 3' CCACCCACCCCCACCCC 11683 A AA_ A C
 GG GGTGG GTGG GGT GG
 || |||| ||| || ||
 CC CCACC CACC CCA CC
 _ CCC _ _
 GAM2505 CDH5 3' CCACCTCCACCCACCCC 7546 A AA C
 GG GGTGG GTGGAGGT GG
 || |||| ||||| ||
 CC CCACC CACCTCCA CC
 _ CA _
 GAM2505 CEBPA 3' CGCCTCTCCACCTCC 10572 AAGT T
 GGAGGTGG GGAGG CG
 ||||| |||| ||
 CCTCCACC TCTCC GC
 C _ _
 GAM2505 CLECSF12 3' CCCGCAACCTCCGCCCC 37684 T AA _ C
 GG GG GTGGAGGT CGG G
 || || ||||| ||| |
 CC CC CGCCTCCA GCC C
 _ _ AC A
 GAM2505 COL5A3 3' GACCCCTACCCCAACCC 17933 A AA A
 GG GGTGG GTGG GGTG
 || |||| ||| |||
 CC CCACC CATC CCAG
 _ CC C
 GAM2505 CSNK2A2 5' CCTGCAACCTCCACCTCC 7623 AGT AG T C
 GGAGGTGGA GG G CGG G
 ||||| || | ||| |

			CCTCCACCT CC C GTC C		
			___ AA _ A		
GAM2505	CYP2B6	3'	TGCAACCTCCACCCCC 6416	T AA	CG
			GG GG GTGGAGGT GCG		
			CC CC CACCTCCA CGT		
			_ _ _ A _		
GAM2505	DLEC1	3'	CGCCAATGCACCCCCAACCTCC 14265	_ AA	GAG C
			GGAGGT GG GTG GT GGCG		
			CCTCCA CC CAC TA CCGC		
			A CC G _ A		
GAM2505	DLEC1	3'	CGCCAATGCACCCCCAACCTCC 14272	_ AA	GAG C
			GGAGGT GG GTG GT GGCG		
			CCTCCA CC CAC TA CCGC		
			A CC G _ A		
GAM2505	DSCR3	3'	CCTGCAACCTCCACCTCC 12684	AGT AG T	C
			GGAGGTGGA GG G CGG G		
			CCTCCACCT CC C GTC C		
			___ AA _ A		
GAM2505	DYT1	3'	CCACACTTCCACCCCGAGCTCC 5578	G AA	C _
			GGAG TGG GTGGAGGT GG		
			CCTC ACC CACCTTCA CC		
			G CC CA		
GAM2505	DYT1	3'	GTCTTCCACACTTCCACCCC 5579	A	GA TC
			GG GGTGGAAGTG GG GGC		
			CC CCACCTTCACT CT CTG		
			_ AC TC		
GAM2505	EHD2	3'	CCTGCAACCTCCACCTCC 15962	AGT AG T	C
			GGAGGTGGA GG G CGG G		
			CCTCCACCT CC C GTC C		
			___ AA _ A		
GAM2505	ELK1	5'	CCACCACCACTCCACCGCC 11730	A A A	C
			GG GGTGGA GTGG GGT GG		
			CC CCACCT CACC CCA CC		
			G C A _		
GAM2505	ELK1	5'	CCACCGCCACCACCACCTCC 11731	AA A	C
			GGAGGTGG GTGG GGT GG		
			CCTCCACC CACC CCA CC		
			AC G _		
GAM2505	EN1	3'	CCACCTCTTCTCCCCACCTCC 7138	A _ T	C
			GGAGGTGG AG GGAGGT GG		

			CCTCCACC TC TCTCCA CC		
			CCC T _		
GAM2505 FEZ1	3'	CCTGCAACCTCCACCTCC	22876	AGT AG T C	
		GGAGGTGGA GG G CGG G			
		CCTCCACCT CC C GTC C			
		_ _ AA _ A			
GAM2505 FGFR1	3'	CCCTCTCCCTCCACCTCC	23369	A T TC C	
		GGAGGTGGA G GGAGG GG G			
		CCTCCACCT C CCTCT CC C			
		_ _ _ A			
GAM2505 FGFR1	3'	CCCTCTCCCTCCACCTCC	17975	A T TC C	
		GGAGGTGGA G GGAGG GG G			
		CCTCCACCT C CCTCT CC C			
		_ _ _ A			
GAM2505 FGFR1	3'	CCCTCTCCCTCCACCTCC	6204	A T TC C	
		GGAGGTGGA G GGAGG GG G			
		CCTCCACCT C CCTCT CC C			
		_ _ _ A			
GAM2505 G6PD	3'	GGCACCCACCTCCACCCC	5981	A A AG	
		GG GGTGGA GTGG GTC			
		CC CCACCT CACC CGG			
		_ C CA			
GAM2505 HIF1A	5'	CCGCCTCGCACCCCCACCTCT	7265	AA _ T	
		GGAGGTGG GTG GAGG CGG			
		TCTCCACC CAC CTCC GCC			
		CC G _			
GAM2505 HMGA2	5'	ACCTCCACCTCCACCGCC	9562	A A	
		GG GGTGGA GTGGAGGT			
		CC CCACCT CACCTCCA			
		G C			
GAM2505 HMGA2	5'	CCACCGCCACCTCCACCTCC	9564	A A C	
		GGAGGTGGA GTGG GGT GG			
		CCTCCACCT CACC CCA CC			
		C G _			
GAM2505 HMGA2	5'	CCACCTCCACCGCCACCTCC	9565	AA C	
		GGAGGTGG GTGGAGGT GG			
		CCTCCACC CACCTCCA CC			
		GC _			
GAM2505 HOXC13	3'	CCATCCCCAGCCTCCACCCC	30013	A A _ A TC	
		GG GGTGGA G TGG GG GG			

		CC CCACCT C ACC CC CC		
		— C G — TA		
GAM2505 HS3ST4	3'	GCCCCACCACCACCTCC 36370	AA	A
		GGAGGTGG GTGG GGT		
		CCTCCACC CACC CCG		
		AC —		
GAM2505 HUNK	3'	TCACCAACCCCTTCCACTTCC 15953	GT A	C C
		GGAGGTGGAA GG GGT GG GA		
		CCTTCACCTT CC CCA CC CT		
		— — A A		
GAM2505 HYOU1	3'	ACCCACACCCACCTCT 30001	AA	A
		GGAGGTGG GTGG GGT		
		TCTCCACC CACC CCA		
		CC —		
GAM2505 KCNE1L	3'	CCACCTTCCACCCCAACTCC 14613	G AA	TC
		GGAG TGG GTGGAGG GG		
		CCTC ACC CACCTTC CC		
		A CC CA		
GAM2505 LAG3	5'	ACCCCCGCCCCACCTCC 8066	AA	A
		GGAGGTGG GTGG GGT		
		CCTCCACC CGCC CCA		
		CC C		
GAM2505 LFG	3'	CCACCCTCCTCCACCTCC 37692	AGT	TC
		GGAGGTGGA GGAGG GG		
		CCTCCACCT CCTCC CC		
		— CA		
GAM2505 LRP1	5'	CGCCCCCACCCCCCTCC 8136	T AA	A TC
		GGAGG GG GTGG GG GGCG		
		CCTCC CC CACC CC CCGC		
		— CC — —		
GAM2505 LYZ	3'	CCTGCAACCTCCACCTCC 5757	AGT AG T	C
		GGAGGTGGA GG G CGG G		
		CCTCCACCT CC C GTC C		
		— AA — A		
GAM2505 MEFV	3'	CCTGCAACCTCCACCTCC 5768	AGT AG T	C
		GGAGGTGGA GG G CGG G		
		CCTCCACCT CC C GTC C		
		— AA — A		
GAM2505 MMP15	3'	GCCCCAGCTCCACCTCC 8264	A —	A
		GGAGGTGG AG TGG GGT		

			CCTCCACC TC ACC CCG		
			C G C		
GAM2505	MPL	3'	CCTGCAACCTCCACCTCC 11849	AGT AG T C	
			GGAGGTGGA GG G CGG G		
			CCTCCACCT CC C GTC C		
			___ AA _ A		
GAM2505	MPP3	5'	CCCACCTCCACCCCCT 7642	T AA C	
			AGG GG GTGGAGGT GG		
			TCC CC CACCTCCA CC		
			_ _ C		
GAM2505	NIPSNAP1	3'	GCCTACACCTCCACCTCC 9702	A G	
			GGAGGTGGA GTG AGGT		
			CCTCCACCT CAC TCCG		
			C A		
GAM2505	NOTCH3	3'	CCTCCCCACCCACCTCC 6017	AA A TC	
			GGAGGTGG GTGG GG GG		
			CCTCCACC CACC CC CC		
			C_ _ T_		
GAM2505	PCDHB11	3'	CCAGCCCACCTCCGCCTCC 21001	A AG C	
			GGAGGTGGA GTGG GT GG		
			CCTCCGCCT CACC CG CC		
			C _ A		
GAM2505	PDCL	3'	CCTGCAACCTCCACCTCC 11865	AGT AG T C	
			GGAGGTGGA GG G CGG G		
			CCTCCACCT CC C GTC C		
			___ AA _ A		
GAM2505	PDE6B	3'	CCTGCAACCTCCACCTCC 5827	AGT AG T C	
			GGAGGTGGA GG G CGG G		
			CCTCCACCT CC C GTC C		
			___ AA _ A		
GAM2505	PLXNA1	3'	CCACCGACTCCCACCTCC 35791	A _ A	
			GGAGGTGG AGT GG GG		
			CCTCCACC TCA CC CC		
			C G A		
GAM2505	PTGIS	3'	TCACCACAACCTCCACCTCC 6670	AGT AG C C	
			GGAGGTGGA GG GT GG GA		
			CCTCCACCT CC CA CC CT		
			___ AA _ A		
GAM2505	PTPN7	3'	GCCCACACCTCCACCTCC 8710	A GA	
			GGAGGTGGA GTG GGT		

			CCTCCACCT CAC CCG		
			C AC		
GAM2505	PTPN7	3'	CCCCACACCTCCACCTCC 27888	A GA	
			GGAGGTGGA GTG GGT		
			CCTCCACCT CAC CCG		
			C AC		
GAM2505	PTPN7	3'	CCCCACACCTCCACCTCC 27891	A GA	
			GGAGGTGGA GTG GGT		
			CCTCCACCT CAC CCG		
			C AC		
GAM2505	RAB5C	3'	CCTCCCCGCTCCACCTCC 30086	A A TC	
			GGAGGTGG AGTGG GG GG		
			CCTCCACC TCGCC CC CC		
			C _ T_		
GAM2505	RARB	5'	CCATCTCCACTTCCTCCCC 18237	A T C	
			GG GG GGAAGTGGAGGT GG		
			CC CC CCTTCACCTCTA CC		
			_ T _		
GAM2505	RPH3AL	3'	CCTGCAACCTCCACCTCC 13848	AGT AG T C	
			GGAGGTGGA GG G CGG G		
			CCTCCACCT CC C GTC C		
			_ AA _ A		
GAM2505	SED1	3'	CCTGCAACCTCCACCTCC 15907	AGT AG T C	
			GGAGGTGGA GG G CGG G		
			CCTCCACCT CC C GTC C		
			_ AA _ A		
GAM2505	SED1	3'	CCTGCAACCTCCACCTCC 15908	AGT AG T C	
			GGAGGTGGA GG G CGG G		
			CCTCCACCT CC C GTC C		
			_ AA _ A		
GAM2505	SEPN1	3'	CCTGCAACCTCCACCTCC 32988	AGT AG T C	
			GGAGGTGGA GG G CGG G		
			CCTCCACCT CC C GTC C		
			_ AA _ A		
GAM2505	SLC14A2	5'	CCTGCAACCTCCACCTCC 14008	AGT AG T C	
			GGAGGTGGA GG G CGG G		
			CCTCCACCT CC C GTC C		
			_ AA _ A		
GAM2505	SNX15	3'	CCTGCAACCTCCACCTCC 36504	AGT AG T C	
			GGAGGTGGA GG G CGG G		

			CCTCCACCT CC C GTC C		
			___ AA _ A		
GAM2505 SP4	5'	CCGCCTCGCCCCACCCC	9082	A	AA G T
		GG GGTGG GTG AGG CGG			
		CC CCACC CGC TCC GCC			
		_ CC _ _			
GAM2505 SP4	5'	TCGCCCCCACCCCCACCCACC	9083	AA	A C__
		GGTGG GTGG GGT GGCGA			
		CCACC CACC CCA CCGCT			
		_ C CCC			
GAM2505 STAU	5'	CCTGCAACCTCCACCTCC	10940	AGT	AG T C
		GGAGGTGGA GG G CGG G			
		CCTCCACCT CC C GTC C			
		___ AA _ A			
GAM2505 TAT	3'	CCTGCAACCTCCACCTCC	5913	AGT	AG T C
		GGAGGTGGA GG G CGG G			
		CCTCCACCT CC C GTC C			
		___ AA _ A			
GAM2505 TBXA2R	3'	CCTGCAACCTCCACCTCC	6725	AGT	AG T C
		GGAGGTGGA GG G CGG G			
		CCTCCACCT CC C GTC C			
		___ AA _ A			
GAM2505 TNFSF9	3'	TCATCCCCAGCCTCCACCTCC	9903	A _	A TC
		GGAGGTGGA G TGG GG GG			
		CCTCCACCT C ACC CC CT			
		C G _ TA			
GAM2505 TNS	5'	CCGAGTGTCCAGCCCCACCTCC	22900	AAG	G _
		GGAGGTGG TGGA G TCGG			
		CCTCCACC ACCT T AGCC			
		CCG G G			
GAM2505 TZFP	5'	ATCTTCACCCCCACCTCC	15719	AA	
		GGAGGTGG GTGGAGGT			
		CCTCCACC CACTTCTA			
		CC			
GAM2505 ZNF133	5'	TGCAACCTCCACCCCC	9486	T AA	CG
		GG GG GTGGAGGT GCG			
		CC CC CACCTCCA CGT			
		_ _ A _			
GAM2505 ZNF42	5'	TGTTGGCTCCACCTCCAGCCTC	9469	_ A	G
C		GGAGG TGGA GTGGAG TCGGCG			

			CCTCC ACCT CACCTC GGTTGT		
			G C _		
GAM2505	AGPAT1	5'	CCAACCTCCCACTCCCACCTCC 13115	A _ C	
			GGAGGTGG AGTGG AGGT GG		
			CCTCCACC TCACC TCCA CC		
			C C A		
GAM2505	AK5	3'	CCACCAACCACCACCTCC 14393	AAG A_ C	
			GGAGGTGG TGG GGT GG		
			CCTCCACC ACC CCA CC		
			_ _ AA _		
GAM2505	APCL	3'	CCGCCTCCCACCCCCACCCC 12498	A AA _ T	
			GG GGTGG GTGG AGG CGG		
			CC CCACC CACC TCC GCC		
			_ CC C _		
GAM2505	ARHGAP5	5'	CCCACAACCCCCACCTCC 37816	AAGT AG C C	
			GGAGGTGG GG GT GG G		
			CCTCCACC CC CA CC C		
			C_ AA _ A		
GAM2505	ATP1B4	3'	CCTGCAACCTCCACCTCC 14323	AGT AG T C	
			GGAGGTGGA GG G CGG G		
			CCTCCACCT CC C GTC C		
			_ AA _ A		
GAM2505	BA108L7.2	3'	CTGTCCCCACCTCCACCCTCC 25239	_ A A T	
			GGAGG TGGA GTGG GG CGG		
			CCTCC ACCT CACC CC GTC		
			C C _ T		
GAM2505	BAG5	3'	CCTGCAACCTCCACCTCC 11302	AGT AG T C	
			GGAGGTGGA GG G CGG G		
			CCTCCACCT CC C GTC C		
			_ AA _ A		
GAM2505	BMF	3'	CCGACCTCCACCCCC 27276	T AA	
			GG GG GTGGAGGTCGG		
			CC CC CACCTCCAGCC		
			_ _		
GAM2505	BMF	3'	GACTCCATCCCCCACCACCCC 27280	A AA_ G	
			GG GGTGG GTGGAG TC		
			CC CCACC TACCTC AG		
			_ CCC _		
GAM2505	C3F	3'	TCACCGCAACCTCCACCTCC 12330	AGT AG T C	
			GGAGGTGGA GG G CGG GA		

			CCTCCACCT CC C GCC CT		
			___ AA _ A		
GAM2505	C9orf9	3'	CCTGCAACCTCCACCTCC 21026	AGT AG T C	
			GGAGGTGGA GG G CGG G		
			CCTCCACCT CC C GTC C		
			___ AA _ A		
GAM2505	CENTA1	3'	CCGCCCTCCCCCACCTCC 13739	AAGT T	
			GGAGGTGG GGAGG CGG		
			CCTCCACC CCTCC GCC		
			CC__ C		
GAM2505	CLDN6	3'	GACCCCCGCCCCACCTCC 22171	AA A	
			GGAGGTGG GTGG GGTC		
			CCTCCACC CGCC CCAG		
			CC C		
GAM2505	CSEN	3'	CCACAGCCACCTCCACCCCC 15087	A A AG C	
			GG GGTGGA GTGG GT GG		
			CC CCACCT CACC CA CC		
			C C GA _		
GAM2505	DGKZ	3'	CGCTCCTGCCCCACCCACCTC 9721	AA A C__	
	C		GGAGGTGG GTGG GGT GGCG		
			CCTCCACC CACC CCG TCGC		
			C_ _ TCC		
GAM2505	DKFZp434A2417	3'	ACTGCAACTTCCACCTCC 32860	GGA	
			GGAGGTGGAAGT GGT		
			CCTCCACCTTCA TCA		
			ACG		
GAM2505	DKFZP434C212	3'	CCTGCAACCTCCACCTCC 34168	AGT AG T C	
			GGAGGTGGA GG G CGG G		
			CCTCCACCT CC C GTC C		
			___ AA _ A		
GAM2505	DKFZp434J0226	5'	CGCCAGCTCCACTCCCACCTTC 35805	A GTC	
			GGAGGTGG AGTGGAG GGCG		
			CTTCCACC TCACCTC CCGC		
			C GA_		
GAM2505	DKFZP434L187	5'	TCACCATTTACACCCACCTCC 34123	AA _ C C	
			GGAGGTGG GTG GAGGT GG GA		
			CCTCCACC CAC CTTTA CC CT		
			_ A _ A		
GAM2505	DKFZp547H025	3'	CCTGCAACCTCCACCTCC 21369	AGT AG T C	
			GGAGGTGGA GG G CGG G		

			CCTCCACCT CC C GTC C		
			___ AA _ A		
GAM2505	DKFZP564O0523	3'	CCTGCAACCTCCACCTCC	25804	AGT AG T C
			GGAGGTGGA GG G CGG G		
			CCTCCACCT CC C GTC C		
			___ AA _ A		
GAM2505	DMWD	3'	CGCCACCCTCCACCCCC	30531	T AA TC
			GG GG GTGGAGG GGCG		
			CC CC CACCTCC CCGC		
			— — CA		
GAM2505	FBP17	3'	CCTACAACCTCCACCTCC	36048	AGT AG C C
			GGAGGTGGA GG GT GG G		
			CCTCCACCT CC CA TC C		
			___ AA _ A		
GAM2505	FLJ00007	3'	TCGCCCTTATTTCCACCCTCAC	35313	AA C__
			CTCC GGAGGTGG GTGGAGGT GGCGA		
			CCTCCACT CACCTTTA CCGCT		
			CC TTC		
GAM2505	FLJ10748	3'	CCTCCCCCACCCTCATCTCC	20085	AA A TC
			GGAGGTGG GTGG GG GG		
			CCTCTACC CACC CC CC		
			CC C CT		
GAM2505	FLJ12363	3'	CCTGCAACCTCCACCTCC	25866	AGT AG T C
			GGAGGTGGA GG G CGG G		
			CCTCCACCT CC C GTC C		
			___ AA _ A		
GAM2505	FLJ12529	3'	CCAACCCCATCCCCACCTCC	24191	AA A C
			GGAGGTGG GTGG GGT GG		
			CCTCCACC TACC CCA CC		
			CC _ A		
GAM2505	FLJ12903	3'	CCCACAACCTCCGCCTCC	22978	AGT AG C C
			GGAGGTGGA GG GT GG G		
			CCTCCGCCT CC CA CC C		
			___ AA _ A		
GAM2505	FLJ12973	3'	CCCGCAACCTCCGCCTCC	24406	AGT AG T C
			GGAGGTGGA GG G CGG G		
			CCTCCGCCT CC C GCC C		
			___ AA _ A		
GAM2505	FLJ14950	3'	CCTGCAACCTCCACCTCC	26672	AGT AG T C
			GGAGGTGGA GG G CGG G		

		CCTCCACCT CC C GTC C	
		___ AA _ A	
GAM2505	FLJ20079 3'	TCACCGCAACCTCCACCTCC 19176	AGT AG T C
		GGAGGTGGA GG G CGG GA	
		CCTCCACCT CC C GCC CT	
		___ AA _ A	
GAM2505	FLJ20113 3'	TCATAGGCCCCACCTCCACGTC 19211	G A A GGC
	C	GGA GTGGA GTGG GGTC GA	
		CCT CACCT CACC CCGG CT	
		G C _ ATA	
GAM2505	FLJ21709 3'	CCACCTCGGTACCTCCACCTC 38167	A ___ C
		GAGGTGGA GTG GAGGT GG	
		CTCCACCT CAC CTCCA CC	
		C TGG _	
GAM2505	FLJ22002 3'	ATTTCCACTCCCACACCC 24245	AG A
		GG GTGG AGTGGAGGT	
		CC CACC TCACCTTTA	
		CA C	
GAM2505	FLJ22531 5'	CCTGCAACCTCCACCTCC 23944	AGT AG T C
		GGAGGTGGA GG G CGG G	
		CCTCCACCT CC C GTC C	
		___ AA _ A	
GAM2505	FLJ22794 3'	ACTGCAACTTCCACCTCC 44023	GGA
		GGAGGTGGAAGT GGT	
		CCTCCACCTTCA TCA	
		ACG	
GAM2505	GMPPB 5'	CCTGCAACCTCCACCTCC 45812	AGT AG T C
		GGAGGTGGA GG G CGG G	
		CCTCCACCT CC C GTC C	
		___ AA _ A	
GAM2505	H-plk 5'	CCTGCAACCTCCACCTCC 17984	AGT AG T C
		GGAGGTGGA GG G CGG G	
		CCTCCACCT CC C GTC C	
		___ AA _ A	
GAM2505	ICK 3'	CCACCCTCCTCCACCTCC 17195	AGT TC
		GGAGGTGGA GGAGG GG	
		CCTCCACCT CCTCC CC	
		___ CA	
GAM2505	KIAA0063 3'	CCTGCAACCTCCACCTCC 17016	AGT AG T C
		GGAGGTGGA GG G CGG G	

			CCTCCACCT CC C GTC C		
			___ AA _ A		
GAM2505	KIAA0429	5'	CCTTCCCCACTCCCATCCC 16471	A A A TC	
			GG GGTGG AGTGG GG GG		
			CC CTACC TCACC CC CC		
			_ C _ TT		
GAM2505	KIAA0450	3'	CCATCCCATTCCCACCTCC 16028	A A C	
			GGAGGTGG AGTGG GGT GG		
			CCTCCACC TTACC CTA CC		
			C _ _		
GAM2505	KIAA0459	3'	CCTGCAACCTCCACCTCC 30574	AGT AG T C	
			GGAGGTGGA GG G CGG G		
			CCTCCACCT CC C GTC C		
			___ AA _ A		
GAM2505	KIAA0513	3'	CCTGCAACCTCCACCTCC 16354	AGT AG T C	
			GGAGGTGGA GG G CGG G		
			CCTCCACCT CC C GTC C		
			___ AA _ A		
GAM2505	KIAA0532	3'	CCTCCCACCTCCACCTCC 35024	A _	
			GGAGGTGGA GTGG AGG		
			CCTCCACCT CACC TCC		
			C C		
GAM2505	KIAA0557	3'	TCACCACAACCTCCACCTCC 38211	AGT AG C C	
			GGAGGTGGA GG GT GG GA		
			CCTCCACCT CC CA CC CT		
			___ AA _ A		
GAM2505	KIAA0562	3'	CCACCCACCTCCGCCTCC 16242	A A_	
			GGAGGTGGA GTGG GG		
			CCTCCGCCT CACC CC		
			C CA		
GAM2505	KIAA0841	3'	TCACCCCAACACCTCACCTCC 35362	AA GA TC C	
			GGAGGTGG GTG GG GG GA		
			CCTCCACT CAC CC CC CT		
			C_ AA _ A		
GAM2505	KIAA1196	3'	CCAGTTCTCCATCCCCACCCC 30816	A AA_ TC_	
			GG GGTGG GTGGAGG GG		
			CC CCACC TACCTCT CC		
			_ CCC TGA		
GAM2505	KIAA1198	3'	CCCGCAACCTCCGCCTCC 31706	AGT AG T C	
			GGAGGTGGA GG G CGG G		

		CCTCCGCCT CC C GCC C		
		___ AA _ A		
GAM2505	KIAA1257	3' CCCGCAACCTCCGCCTCC 31431	AGT	AG T C
		GGAGGTGGA GG G CGG G		
		CCTCCGCCT CC C GCC C		
		___ AA _ A		
GAM2505	KIAA1373	3' CCTGCAACCTCCACCTCC 35126	AGT	AG T C
		GGAGGTGGA GG G CGG G		
		CCTCCACCT CC C GTC C		
		___ AA _ A		
GAM2505	KIAA1416	5' CCAGTCTTCACCTCCACACCC 41802	AG	A TC
		GG GTGGA GTGGAGG GG		
		CC CACCT CACTTCT CC		
		CA C GA		
GAM2505	KIAA1554	3' TCACCAACCCTGACCTTCCCCC 45614	T	T__ A C C
	TCC	GGAGG GGAAG GG GGT GG GA		
		CCTCC CCTTC TC CCA CC CT		
		C CAG _ A A		
GAM2505	KIAA1571	3' TCACCGCAACCTCCACCTCC 30565	AGT	AG T C
		GGAGGTGGA GG G CGG GA		
		CCTCCACCT CC C GCC CT		
		___ AA _ A		
GAM2505	KIAA1610	3' CCGCCTCATTCCCACCCC 33338	A	A G T
		GG GGTGG AGTG AGG CGG		
		CC CCACC TTAC TCC GCC		
		_ C _ _		
GAM2505	KIAA1615	3' CCTGCAACCTCCACCTCC 34083	AGT	AG T C
		GGAGGTGGA GG G CGG G		
		CCTCCACCT CC C GTC C		
		___ AA _ A		
GAM2505	KIAA1719	3' GGCACCCACTCCACCTCC 33821	A	AG
		GGAGGTGG AGTGG GTC		
		CCTCCACC TCACC CGG		
		C CA		
GAM2505	KIAA1904	3' CCTGCCCCACACCCACCTCC 36375	AA	A C
		GGAGGTGG GTGG GGT GG		
		CCTCCACC CACC CCG CC		
		CA _ T		
GAM2505	KIAA1910	3' CCACCCTCTACCCACCCCC 36286	A	AA TC
		GG GGTGG GTGGAGG GG		

CC CCACC CATCTCC CC
 C C_ CA
 GAM2505 KIAA1938 3' CCTTTTCTCCACTCCCAGCCCC 44277 A _ A TC_
 GG GG TGG AGTGGAGG GG
 || ||| ||||| ||
 CC CC ACC TCACCTCT CC
 _ G C TTT
 GAM2505 KPNA6 3' CTGCCCCACCCCCACCTCC 14687 AA A T
 GGAGGTGG GTGG GG CGG
 ||||| ||| |||
 CCTCCACC CACC CC GTC
 CC _ _
 GAM2505 MCLC 3' CCTGCAACCTCCACCTCC 17490 AGT AG T C
 GGAGGTGGA GG G CGG G
 ||||| || | |||
 CCTCCACCT CC C GTC C
 _ AA _ A
 GAM2505 MEIS3 3' TCACCCTCCTGTCCCCCCCACC 38311 AAGT _ TC C
 TCC GGAGGTGG GGA GG GG GA
 ||||| ||| || |||
 CCTCCACC CCT CC CC CT
 CCC_ GT TC A
 GAM2505 MGC10924 3' CCACCCCCACCCCCACCCCC 24945 A AA A C
 GG GGTGG GTGG GGT GG
 || |||| ||| ||| ||
 CC CCACC CACC CCA CC
 C CC C _
 GAM2505 MGC14376 3' CCGCCCTACTTCCACCTCC 26722 A T
 GGAGGTGGAAGTGG GG CGG
 ||||| ||||| ||| |||
 CCTCCACCTTCATC CC GCC
 _ _
 GAM2505 MGC15730 5' CCGCCACCGCCTCCACCCC 26700 A A A T
 GG GGTGGA GTGG GG CGG
 || ||||| |||| ||| |||
 CC CCACCT CGCC CC GCC
 _ C A _
 GAM2505 MGC16703 3' CCATACCCCCACATCCACCTCC 36179 A A C_
 GGAGGTGGA GTGG GGT GG
 ||||| |||| ||| ||
 CCTCCACCT CACC CCA CC
 A C TA
 GAM2505 MGC2474 3' ACTGCAACTTCCACCTCC 23414 GGA
 GGAGGTGGAAGT GGT
 ||||| ||||| |||
 CCTCCACCTTCA TCA
 ACG
 GAM2505 MGC9912 3' CCTGCAACCTCCACCTCC 27951 AGT AG T C
 GGAGGTGGA GG G CGG G
 ||||| || | ||| |

			CCTCCACCT CC C GTC C		
			___ AA _ A		
GAM2505	NDUFC2	3'	CCTGCAACCTCCACCTCC 10894	AGT AG T C	
			GGAGGTGGA GG G CGG G		
			CCTCCACCT CC C GTC C		
			___ AA _ A		
GAM2505	Nup43	3'	CCTGCAACCTCCACCTCC 23934	AGT AG T C	
			GGAGGTGGA GG G CGG G		
			CCTCCACCT CC C GTC C		
			___ AA _ A		
GAM2505	OBTP	3'	GCCCCTACCCCCACCTCC 19079	AA A	
			GGAGGTGG GTGG GGT		
			CCTCCACC CATC CCG		
			CC C		
GAM2505	OSBPL2	3'	CCCGCAACCTCCGCCTCC 29318	AGT AG T C	
			GGAGGTGGA GG G CGG G		
			CCTCCGCCT CC C GCC C		
			___ AA _ A		
GAM2505	OSBPL2	3'	CCCGCAACCTCCGCCTCC 16850	AGT AG T C	
			GGAGGTGGA GG G CGG G		
			CCTCCGCCT CC C GCC C		
			___ AA _ A		
GAM2505	P5-1	3'	CCACATCCACTTCCACCCC 13498	A G C	
			GG GGTGGAAGTGGA GT GG		
			CC CCACCTTCACCT CA CC		
			A _		
GAM2505	PDGFC	5'	TCGCCTTCACCCCCACCCC 18302	A AA T	
			GG GGTGG GTGGAGG CGG		
			CC CCACC CACTTCC GCT		
			CC		
GAM2505	PIP5K1C	3'	CCAATGCCCACTTCCCCTCC 35016	T AG C	
			GGAGG GGAAGTGG GT GG		
			CCTCC CCTTCACC TA CC		
			CG A		
GAM2505	PLAGL2	3'	CTGTGCCCCCACCCTCC 34877	AA A _	
			GGAGGTGG GTGG GGT CGG		
			CCTCCGCC CACC CCG GTC		
			CC C T		
GAM2505	PP3501	3'	CGCTGACCACTCCCTCCTCC 22331	T A GGA	
			GGAGG GG AGT GGTGGCG		

CCTCC CC TCA CCAGTCGC
 T C ____
 GAM2505 PPP1R16B 3' CCTGCCTCCACCTCCCACCCC 30773 A AA_ C
 GG GGTGG GTGGAGGT GG
 || |||| ||||| ||
 CC CCACC CACCTCCG CC
 _ CTC T
 GAM2505 PPP1R16B 3' CCACCCCCTTCCACCTCC 30769 T A C
 GGAGGTGGAAG GG GGT GG
 ||||| || || ||
 CCTCCACCTTC CC CCA CC

 GAM2505 PRO0365 5' CCTGCAACCTCCACCTCC 15387 AGT AG T C
 GGAGGTGGA GG G CGG G
 ||||| || | || |
 CCTCCACCT CC C GTC C
 _ AA _ A
 GAM2505 RASD2 3' CCACTTAGACCACGCCACCTC 15600 AA _ C
 C GGAGGTGG GTGG AGGT GG
 ||||| || || ||
 CCTCCACC CACC TTCA CC
 CG AGA _
 GAM2505 RNF8 3' CCTGCAACCTCCACCTCC 10095 AGT AG T C
 GGAGGTGGA GG G CGG G
 ||||| || | || |
 CCTCCACCT CC C GTC C
 _ AA _ A
 GAM2505 SCAMP5 3' GCCCCACCCCCACCCTCC 29074 _ AA A
 GGAGG TGG GTGG GGT
 |||| || || ||
 CCTCC ACC CACC CCG
 C CC C
 GAM2505 SEMA4G 3' TCACCCAACCTCTCCACCTCC 19564 AAGT C_ C
 GGAGGTGG GGAGGT GG GA
 ||||| |||| || ||
 CCTCCACC TCTCCA CC CT
 C_ AC A
 GAM2505 SEMA4G 3' TCACCCAACCTCTCCACCTCC 45413 AAGT C_ C
 GGAGGTGG GGAGGT GG GA
 ||||| |||| || ||
 CCTCCACC TCTCCA CC CT
 C_ AC A
 GAM2505 TCEA3 3' CTTACCCCACCCCCACCTCC 42677 AA A C
 GGAGGTGG GTGG GGT GG
 ||||| |||| || ||
 CCTCCACC CACC CCA TC
 CC _ T
 GAM2505 TNRC4 3' CCGGCCCTCCCACCCC 14040 A AAGT A
 GG GGTGG GG GGTCGG
 || |||| || ||||

		CC CCACC CC CCGGCC		
		CT__		
GAM2505 TUB	3'	CCTCCCCACTTCCCCC	9323	A T A TC
		GG GG GGAAGTGG GG GG		
		CC CC CCTTCACC CC CC		
		__ _ T_		
GAM2505 USP22	3'	CCTGCAACCTCCACCTCC	33751	AGT AG T C
		GGAGGTGGA GG G CGG G		
		CCTCCACCT CC C GTC C		
		__ AA _ A		
GAM2505 VPS33A	3'	CCTGCAACCTCCACCTCC	23231	AGT AG T C
		GGAGGTGGA GG G CGG G		
		CCTCCACCT CC C GTC C		
		__ AA _ A		
GAM2505 WBSCR23	3'	CCGTGCACCTCCACCTCC	24637	A GAGGT
		GGAGGTGGA GTG CGG		
		CCTCCACCT CAC GCC		
		C GT__		
GAM2505 LOC112724	5'	CCTGCAACCTCCACCTCC	28777	AGT AG T C
		GGAGGTGGA GG G CGG G		
		CCTCCACCT CC C GTC C		
		__ AA _ A		
GAM2505 LOC115399	3'	CCGCCAGCACTTCCACCCC	36346	A GA T
		GG GGTGGAAGTG GG CGG		
		CC CCACCTTCAC CC GCC		
		GA _		
GAM2505 LOC116113	3'	CCAGGCCTCCACCCCCACCCC	44284	A AA _
		GG GGTGG GTGGAGGTC GG		
		CC CCACC CACCTCCGG CC		
		_ CC A		
GAM2505 LOC116411	5'	CGCTACAACCTCCACCTCC	36568	AGT AG C
		GGAGGTGGA GG GT GGCG		
		CCTCCACCT CC CA TCGC		
		__ AA _		
GAM2505 LOC124976	3'	CCAGCCTCCACCCCCACTCC	36783	G AA C
		GGAG TGG GTGGAGGT GG		
		CCTC ACC CACCTCCG CC		
		_ CC A		
GAM2505 LOC130813	3'	CCCGCAACCTCCGCCTCC	37310	AGT AG T C
		GGAGGTGGA GG G CGG G		

	CCTCCGCCT CC C GCC C	
	___ AA _ A	
GAM2505 LOC132625 3'	CCTGCAACCTCCACCTCC 37373	AGT AG T C
	GGAGGTGGA GG G CGG G	
	CCTCCACCT CC C GTC C	
	___ AA _ A	
GAM2505 LOC135818 3'	CCCACAACCTCCGCCTCC 37093	AGT AG C C
	GGAGGTGGA GG GT GG G	
	CCTCCGCCT CC CA CC C	
	___ AA _ A	
GAM2505 LOC143187 3'	CCTGCAACCTCCACCTCC 29744	AGT AG T C
	GGAGGTGGA GG G CGG G	
	CCTCCACCT CC C GTC C	
	___ AA _ A	
GAM2505 LOC144248 5'	CCTGCAACCTCCACCTCC 37700	AGT AG T C
	GGAGGTGGA GG G CGG G	
	CCTCCACCT CC C GTC C	
	___ AA _ A	
GAM2505 LOC144524 5'	CCTGCAACCTCCACCTCC 40433	AGT AG T C
	GGAGGTGGA GG G CGG G	
	CCTCCACCT CC C GTC C	
	___ AA _ A	
GAM2505 LOC145468 3'	CCACCTCCACCTCCACCTCC 36545	A C
	GGAGGTGGA GTGGAGGT GG	
	CCTCCACCT CACCTCCA CC	
	C _	
GAM2505 LOC145468 3'	CCGATTCCACCTCCACCTCC 36546	A G
	GGAGGTGGA GTGGAG TCGG	
	CCTCCACCT CACCTT AGCC	
	C _	
GAM2505 LOC145693 5'	CGCCACCTCCACCCCA 37923	AA C
	TGG GTGGAGGT GGCG	
	ACC CACCTCCA CCGC	
	C _ C	
GAM2505 LOC145693 5'	TGTACCCACGCCCACCTCC 37924	AA A _
	GGAGGTGG GTGG GGT CG	
	CCTCCACC CACC CCA GT	
	CG _ T	
GAM2505 LOC145978 3'	CCACCTCCCACCTCCACCCC 38031	A A _ C
	GG GGTGGA GTGG AGGT GG	

	CC CCACCT CACC TCCA CC	
	— C C —	
GAM2505 LOC146229 3'	CCTGCAACCTCCACCTCC 38109	AGT AG T C
	GGAGGTGGA GG G CGG G	
	CCTCCACCT CC C GTC C	
	— AA _ A	
GAM2505 LOC146733 5'	CCTTCCCCACTTCACCTCC 40729	G A TC
	GGAGGTG AAGTGG GG GG	
	CCTCCAC TTCACC CC CC	
	— _ TT	
GAM2505 LOC146784 5'	CCTGCAACCTCCACCTCC 38237	AGT AG T C
	GGAGGTGGA GG G CGG G	
	CCTCCACCT CC C GTC C	
	— AA _ A	
GAM2505 LOC146839 3'	CCCACAACCTCCGCCTCC 40753	AGT AG C C
	GGAGGTGGA GG GT GG G	
	CCTCCGCCT CC CA CC C	
	— AA _ A	
GAM2505 LOC146957 3'	TTGCCACCTCCACTTCC 38284	C
	GGAAGTGGAGGT GGCGA	
	CCTTCACCTCCA CCGTT	
	C	
GAM2505 LOC147817 3'	CCTGCAACCTCCACCTCC 38384	AGT AG T C
	GGAGGTGGA GG G CGG G	
	CCTCCACCT CC C GTC C	
	— AA _ A	
GAM2505 LOC147958 3'	CGCCGGGACCCACCTCTACCT 42152	A A _
CC	GGAGGTGGA GTGG GGTC GGCG	
	CCTCCATCT CACC CCAG CCGC	
	C _ GG	
GAM2505 LOC148137 3'	CACGGCAACCTCCACCTCC 29514	AGT AG GC
	GGAGGTGGA GG GTCG G	
	CCTCCACCT CC CGGC C	
	— AA A_	
GAM2505 LOC148137 3'	CCACCCTTGACCCCCAGCCTC 29515	_ AA _ TC
C	GGAGG TGG GTG GAGG GG	
	CCTCC ACC CAC TTCC CC	
	G CC G CA	
GAM2505 LOC148189 5'	CCTGCAACCTCCACCTCC 38484	AGT AG T C
	GGAGGTGGA GG G CGG G	

	CCTCCACCT CC C GTC C	
	___ AA _ A	
GAM2505 LOC149506 3'	ACTGCAACTTCCACCTCC 41000	GGA
	GGAGGTGGAAGT GGT	
	CCTCCACCTTCA TCA	
	ACG	
GAM2505 LOC149577 3'	TCACCACAACCTCCACCTCC 41024	AGT AG C C
	GGAGGTGGA GG GT GG GA	
	CCTCCACCT CC CA CC CT	
	___ AA _ A	
GAM2505 LOC150155 3'	CCACCTCCGCCTCCACCTCC 35086	A C
	GGAGGTGGA GTGGAGGT GG	
	CCTCCACCT CGCCTCCA CC	
	C _	
GAM2505 LOC150155 3'	CCGATTCCACCTCCGCCTCC 35087	A G
	GGAGGTGGA GTGGAG TCGG	
	CCTCCGCCT CACCTT AGCC	
	C _	
GAM2505 LOC150378 5'	CCAGTCCTCCCCACCTCC 38922	AAGT TC_
	GGAGGTGG GGAGG GG	
	CCTCCACC CCTCC CC	
	C___ TGA	
GAM2505 LOC151201 3'	CCTGCAACCTCCACCTCC 41321	AGT AG T C
	GGAGGTGGA GG G CGG G	
	CCTCCACCT CC C GTC C	
	___ AA _ A	
GAM2505 LOC151475 5'	CCTGCAACCTCCACCTCC 41355	AGT AG T C
	GGAGGTGGA GG G CGG G	
	CCTCCACCT CC C GTC C	
	___ AA _ A	
GAM2505 LOC153525 5'	CCACCCCCACCCCCACCCC 41638	A AA A C
	GG GGTGG GTGG GGT GG	
	CC CCACC CACC CCA CC	
	C CC C _	
GAM2505 LOC153688 3'	CCTGCAACCTCCACCTCC 41658	AGT AG T C
	GGAGGTGGA GG G CGG G	
	CCTCCACCT CC C GTC C	
	___ AA _ A	
GAM2505 LOC154282 5'	CCTGCAACCTCCACCTCC 41698	AGT AG T C
	GGAGGTGGA GG G CGG G	

	CCTCCACCT CC C GTC C		
	___ AA _ A		
GAM2505 LOC154726 5'	CCCACAACCTCCGCCTCC 39477	AGT AG C C	
	GGAGGTGGA GG GT GG G		
	CCTCCGCCT CC CA CC C		
	___ AA _ A		
GAM2505 LOC155006 3'	CCATCTTCACCCCCACCTC 39523	AA C	
	GAGGTGG GTGGAGGT GG		
	CTCCACC CACTTCTA CC		
	CC _		
GAM2505 LOC157247 5'	TGCAACCTCCACCCCC 39576	T AA CG	
	GG GG GTGGAGGT GCG		
	CC CC CACCTCCA CGT		
	_ _ A _		
GAM2505 LOC195977 3'	CCACCTCCACTCCCGCCTCC 42300	A C	
	GGAGGTGG AGTGGAGGT GG		
	CCTCCGCC TCACCTCCA CC		
	C _		
GAM2505 LOC200014 3'	CGCTGCAACCCCCACCTCC 42689	AAGT AG T	
	GGAGGTGG GG G CGGCG		
	CCTCCACC CC C GTCGC		
	C ___ AA _		
GAM2505 LOC200314 3'	CCTGCAACCTCCACCTCC 43293	AGT AG T C	
	GGAGGTGGA GG G CGG G		
	CCTCCACCT CC C GTC C		
	___ AA _ A		
GAM2505 LOC200860 3'	CCTGCAACCTCCACCTCC 43353	AGT AG T C	
	GGAGGTGGA GG G CGG G		
	CCTCCACCT CC C GTC C		
	___ AA _ A		
GAM2505 LOC204804 3'	ACTGCCACCTCCACCTCC 43097	A A	
	GGAGGTGGA GTGG GGT		
	CCTCCACCT CACC TCA		
	C G		
GAM2505 LOC219653 3'	TCACCAACCTGGCTCTCCACC 43869	A TGG_ C C	
TCC	GGAGGTGG AG AGGT GG GA		
	CCTCCACC TC TCCA CC CT		
	C TCGG A A		
GAM2505 LOC219920 5'	CCACCTCAGTCCCACCTCC 44804	A G C	
	GGAGGTGG AGT GAGGT GG		

	CCTCCACC TCG CTCCA CC	
	C A _	
GAM2505 LOC220662 3'	CCTGCAACCTCCACCTCC 43822	AGT AG T C
	GGAGGTGGA GG G CGG G	
	CCTCCACCT CC C GTC C	
	_ AA _ A	
GAM2505 LOC221250 5'	CCACCATCAGCACCACTCC 44117	AAG GA C
	GGAGGTGG TG GGT GG	
	CCTCCACC AC CCA CC	
	ACG TA _	
GAM2505 LOC221296 3'	CCTGCAACCTCCACCTCC 44167	AGT AG T C
	GGAGGTGGA GG G CGG G	
	CCTCCACCT CC C GTC C	
	_ AA _ A	
GAM2505 LOC221336 5'	CCTCCACCTCCACCTCC 44319	AA_
	GGAGGTGG GTGGAGG	
	CCTCCACC CACCTCC	
	CTC	
GAM2505 LOC221424 5'	CGCCACAGCCGCCGCTCCACC 44978	A A A C_
CC	GG GGTGGA GTGG GGT GGCG	
	CC CCACCT CGCC CCG CCGC	
	_ C G ACA	
GAM2505 LOC221663 5'	CCTGCAACCTCCACCTCC 45039	AGT AG T C
	GGAGGTGGA GG G CGG G	
	CCTCCACCT CC C GTC C	
	_ AA _ A	
GAM2505 LOC253092 5'	CTGTCTCCATCTCCACCTCC 46549	AG T
	GGAGGTGGA TGGAGG CGG	
	CCTCCACCT ACCTCT GTC	
	CT _	
GAM2505 LOC254428 3'	CCACCCACACTCCACCTCT 45716	A GA TC
	GGAGGTGG AGTG GG GG	
	TCTCCACC TCAC CC CC	
	C AC CA	
GAM2505 LOC255177 3'	CCCGCATCCTCCACCTCC 46201	AGT G T C
	GGAGGTGGA GGA G CGG G	
	CCTCCACCT CCT C GCC C	
	_ A _ A	
GAM2505 LOC256306 3'	CCTGCAACCTCCACCTCC 46236	AGT AG T C
	GGAGGTGGA GG G CGG G	

	CCTCCACCT CC C GTC C	
	___ AA _ A	
GAM2505 LOC257468 3'	TCACCCTCCTGTCCCCCCCACC 45626	AAGT ___ TC C
TCC	GGAGGTGG GGA GG GG GA	
	CCTCCACC CCT CC CC CT	
	CCC_ GT TC A	
GAM2505 LOC51193 5'	CCCACAACCTCCGCCTCC 18455	AGT AG C C
	GGAGGTGGA GG GT GG G	
	CCTCCGCCT CC CA CC C	
	___ AA _ A	
GAM2505 LOC51219 5'	CCCGCAACCTCCGCCTCC 18544	AGT AG T C
	GGAGGTGGA GG G CGG G	
	CCTCCGCCT CC C GCC C	
	___ AA _ A	
GAM2505 LOC81034 3'	CCTGCAACCTCCACCTCC 25069	AGT AG T C
	GGAGGTGGA GG G CGG G	
	CCTCCACCT CC C GTC C	
	___ AA _ A	
GAM2505 LOC89932 3'	CCTGCAACCTCCACCTCC 30488	AGT AG T C
	GGAGGTGGA GG G CGG G	
	CCTCCACCT CC C GTC C	
	___ AA _ A	
GAM2505 LOC90288 3'	CCTGCAACCTCCACCTCC 31106	AGT AG T C
	GGAGGTGGA GG G CGG G	
	CCTCCACCT CC C GTC C	
	___ AA _ A	
GAM2505 LOC90371 5'	CCTGCAACCTCCACCTCC 31320	AGT AG T C
	GGAGGTGGA GG G CGG G	
	CCTCCACCT CC C GTC C	
	___ AA _ A	
GAM2505 LOC90591 3'	ACTGCCACCTCCACCTCC 31756	A A
	GGAGGTGGA GTGG GGT	
	CCTCCACCT CACC TCA	
	C G	
GAM2505 LOC91115 3'	CCTGCAACCTCCACCTCC 32394	AGT AG T C
	GGAGGTGGA GG G CGG G	
	CCTCCACCT CC C GTC C	
	___ AA _ A	
GAM2505 LOC91252 3'	CCGCCCTGTCACCTTCACCTCC 32552	A _ T
	GGAGGTGGA GTGG AGG CGG	

		CCTCCACTT CACT TCC GCC		
		C G C		
GAM2505	LOC92267	3' CCTGCAACCTCCACCTCC 34054	AGT	AG T C
		GGAGGTGGA GG G CGG G		
		CCTCCACCT CC C GTC C		
		___ AA _ A		
GAM2505	LOC92697	5' CCCGCAACCTCCGCCTCC 34800	AGT	AG T C
		GGAGGTGGA GG G CGG G		
		CCTCCGCCT CC C GCC C		
		___ AA _ A		
GAM2505	LOC92697	5' CGCTACAACCTCCACCTCC 34801	AGT	AG C
		GGAGGTGGA GG GT GGCG		
		CCTCCACCT CC CA TCGC		
		___ AA _		
GAM2506	HMGA2	3' AATGGAACAGTAAGAACATCA 9558	ATA	G TG
		TGAT CTTACTGTT T TT		
		ACTA GAATGACAA G AA		
		CAA _ GT		
GAM2506	PCDH11X	3' AATAACAACAAGAATATCA 26785	A	TAC
		TGATAT CT TGTTGTTGTT		
		ACTATA GA ACAACAATAA		
		A _		
GAM2506	PCDH11X	3' AATAACAACAAGAATATCA 26800	A	TAC
		TGATAT CT TGTTGTTGTT		
		ACTATA GA ACAACAATAA		
		A _		
GAM2506	PCDH11Y	3' AATAACAACAAGAATATCA 26819	A	TAC
		TGATAT CT TGTTGTTGTT		
		ACTATA GA ACAACAATAA		
		A _		
GAM2506	LOC124602	3' GGGTAGCAACAAGTACATCA 36759	A	TAC TT
		TGAT TACT TGTTGTTG C		
		ACTA ATGA ACAACGAT G		
		C _ GG		
GAM2506	LOC201229	3' CAATGAAGTAAATATATCA 42540	C	G TG
		TGATATA TTACT T TTG		
		ACTATAT AATGA A AAC		
		A _ GT		
GAM2506	LOC203397	3' GGGTAGCAACAAGTACATCA 43039	A	TAC TT
		TGAT TACT TGTTGTTG C		

ACTA ATGA ACAACGAT G
 C ____ GG
 GAM2507 BCL2L2 3' ATGCTGGGCTGCCTGG 10258 A TGAT
 CCGG GT GCCCAGCAT
 ||| || |||||
 GGTC CG CGGGTCGTA
 _ T____
 GAM2507 SLC16A2 3' CATGCTGGGCATCCTAGGCC 13268 AGTT_
 GG GATGCCCAGCATG
 || |||||
 CC CTACGGGTCGTAC
 GGATC
 GAM2507 FLJ14525 3' CATGCTGGCTGTGACCCCGG 26548 A GAT C
 CCGG GTT GCC AGCATG
 ||| ||| || |||||
 GGCC CAG CGG TCGTAC
 C TGT _
 GAM2507 FLJ20378 5' CATGCTGGGCCTTTCCAGT 19435 C TTGAT
 AC GGAG GCCCAGCATG
 || ||| |||||
 TG CCTT CGGGTCGTAC
 A TC____
 GAM2507 TRIP13 3' CATGCTGGACATCCCTT 10434 TT C
 GAG GATG CCAGCATG
 ||| ||| |||||
 TTC CTAC GGTCGTAC
 C_ A
 GAM2507 LOC120939 5' GCTGGAGTACTCTGGTGA 37513 TGAT _
 TCACCGGAGT GC CCAGC
 ||||| || |||||
 AGTGGTCTCA TG GGTCG
 ____ A
 GAM2507 LOC152200 3' ATGCTGGGACCTACGGTGA 41438 G TTGATG
 TCACCG AG CCCAGCAT
 |||| || |||||
 AGTGGC TC GGGTCGTA
 A CA____
 GAM2507 LOC203276 3' GCTGGGCACTCAGGGA 43488 A G TGAT
 TC CC GAGT GCCCAGC
 || ||| |||||
 AG GG CTCA CGGGTCG
 _ A ____
 GAM2507 LOC203305 3' GCTGGGCACTCAGGGA 43512 A G TGAT
 TC CC GAGT GCCCAGC
 || ||| |||||
 AG GG CTCA CGGGTCG
 _ A ____
 GAM2507 LOC255696 5' CATGCTGGGACATGCCCCCG 46567 AGTTG _
 CGG ATG CCCAGCATG
 || ||| |||||

GCC TAC GGGTCGTAC
 CCCCCG A
 GAM2507 LOC90019 3' CATGCTGGCCACCCCGGCGG 28870 A A TGAT C
 TC CCGG GT GCC AGCATG
 || ||| || ||| |||||
 GG GGCC CA CGG TCGTAC
 C C CC__ _
 GAM2508 ALX3 3' CGGAGGAAGCACCTCTGCCTCC 13222 A CG G GG
 GGAGGCAGA G GCT CT CG
 ||||| || ||| ||
 CCTCCGTCT C CGA GG GC
 _CA A AG
 GAM2508 APBA2 3' GCAGCCGTCACCCCTGCCTCC 12018 AA__
 GGAGGCAG GCGGCTGC
 ||||| |||||
 CCTCCGTC TGCCGACG
 CCCAC
 GAM2508 BMP1 3' CCAGGCCACCCTGCCTCC 12768 AAGC TG
 GGAGGCAG GGC CTGG
 ||||| ||| |||
 CCTCCGTC CCG GACC
 CCA_ _
 GAM2508 CBFA2T1 5' CGCCCAGCACCTGCCTCC 10543 AAGC C _
 GGAGGCAG GG TGCTGG CG
 ||||| || ||||| ||
 CCTCCGTC CC ACGACC GC
 _ _ C
 GAM2508 CDC25B 3' CGCCAGTCCTGCTACCTCC 22417 CAGA CT
 GGAGG AGCGG GCTGGCG
 |||| |||| |||||
 CCTCC TCGTC TGACCGC
 A_ _ C_
 GAM2508 CDC25B 3' CGCCAGTCCTGCTACCTCC 22413 CAGA CT
 GGAGG AGCGG GCTGGCG
 |||| |||| |||||
 CCTCC TCGTC TGACCGC
 A_ _ C_
 GAM2508 CHST2 5' CGCCAGCAGCCAGCCC 31414 CAGAA _
 GG GC GGCTGCTGGCG
 || || |||||
 CC CG CCGACGACCGC
 _ A
 GAM2508 EPB72 3' CCACCCACCTCTGCCTCC 10304 AGC C C_
 GGAGGCAGA GG TG TGG
 ||||| || |||
 CCTCCGTCT CC AC ACC
 _ _ CC
 GAM2508 EPM2A 3' GTCAGCCTGCTTCTGCCCC 12227 A CT
 GG GGCAGAAAGCGG GCTGGC
 || ||||| |||||

CC CCGTCTTCGTC CGACTG

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GAM2508 FNTB  3' GCACCAGGAGGTGCCTCTGCCT 7781      A G G C
      CT      GGAGGCAGA GCG CT CTGG GC
                ||||| ||| || ||| ||
                TCTCCGTCT CGT GA GACC CG
                  C G G A
GAM2508 GRF2  3' GCCAGCCGCTTCCTGCCTCC 11790      _ GCT
                GGAGGCAG AAGCGGCT GGC
                ||||| ||||| |||
                CCTCCGTC TTCGCCGA CCG
                  C
GAM2508 HPN   5' CGCCACCGCCTCTGCCTCC 7932      A CTGC
                GGAGGCAGA GCGG TGGCG
                ||||| ||| |||
                CCTCCGTCT CGCC ACCGC
                  C
GAM2508 ITM2B 5' CAGTAGCCGCCTCTGCCGCC 22539 A A
                GG GGCAGA GCGGCTGCTG
                || |||| |||||
                CC CCGTCT CGCCGATGAC
                  G C
GAM2508 MPP2  3' GCAGCTGCTTCTGCCCC 30083 A
                GG GGCAGAAGCGGCTGC
                || |||||
                CC CCGTCTTCGTCGACG
                  -
GAM2508 MUCDHL 3' GCACCCCCCGGCCCTGCCTCC 25283      AAGC CT_ C
                GGAGGCAG GGCTG GG GC
                ||||| ||| |||
                CCTCCGTC CCGGC CC CG
                  CCC A
GAM2508 NCOR2  3' GCACCTCCACGCCACTGCCTCC 13003      AAGC _ CT C
                GGAGGCAG GGC TG GG GC
                ||||| ||| |||
                CCTCCGTC CCG AC CC CG
                  A_ C CT A
GAM2508 NFIA  5' GCGCCGCAGCCGCCCCCTCC 34842      CAGAA T
                GGAGG GCGGCTGC GGCGC
                ||| ||||| |||
                CCTCC CGCCGACG CCGCG
                  CC_
GAM2508 NINJ1 3' CCCAGCGTCCCTGCCTCC 10351      AAGC C C
                GGAGGCAG GG TGCTGG G
                ||||| || |||||
                CCTCCGTC CC GCGACC C
                  T A
GAM2508 NPTX1 3' GCAGACCACCTTCTGCCCC 8355      A C_ _
                GG GGCAGAAG GG CTGC
                || ||||| || |||
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			CC CCGTCTTC CC GACG		
			— CA A		
GAM2508	PACE4	5'	GCGCCGCGGCGCCTCCTCCTC 8430	CA A	T
	C		GGAGG GA GCGGCTGC GGCGC		
			CCTCC CT CGCCGGCG CCGCG		
			TC C —		
GAM2508	PACE4	5'	GCGCCGCGGCGCCTCCTCCTC 28723	CA A	T
	C		GGAGG GA GCGGCTGC GGCGC		
			CCTCC CT CGCCGGCG CCGCG		
			TC C —		
GAM2508	PACE4	5'	GCGCCGCGGCGCCTCCTCCTC 28724	CA A	T
	C		GGAGG GA GCGGCTGC GGCGC		
			CCTCC CT CGCCGGCG CCGCG		
			TC C —		
GAM2508	PACE4	5'	GCGCCGCGGCGCCTCCTCCTC 28725	CA A	T
	C		GGAGG GA GCGGCTGC GGCGC		
			CCTCC CT CGCCGGCG CCGCG		
			TC C —		
GAM2508	PACE4	5'	GCGCCGCGGCGCCTCCTCCTC 28719	CA A	T
	C		GGAGG GA GCGGCTGC GGCGC		
			CCTCC CT CGCCGGCG CCGCG		
			TC C —		
GAM2508	PACE4	5'	GCGCCGCGGCGCCTCCTCCTC 28722	CA A	T
	C		GGAGG GA GCGGCTGC GGCGC		
			CCTCC CT CGCCGGCG CCGCG		
			TC C —		
GAM2508	PCDHB11	3'	CCAGCCCACCTCCGCTCC 21000	A AGC CT	
			GGAGGC GA GG GCTGG		
			CCTCCG CT CC CGACC		
			C CCA —		
GAM2508	PLXNB2	3'	GCACCAGCAGCCGCCTCCATGC 14777	— A	C
	C		GGCA GA GCGGCTGCTGG GC		
			CCGT CT CGCCGACGACC CG		
			AC C A		
GAM2508	RAI14	3'	CAACAGCCCCTTCTGCCCC 17845	A C C	
			GG GGCAGAAG GGCTG TG		
			CC CCGTCTTC CCGAC AC		
			— C A		
GAM2508	SIGLEC11	3'	GCAATCTGCCCGCCTCTGCCTC 27465	A _ TGCTG	
	C		GGAGGCAGA GCGG C GC		

CCTCCGTCT CGCC G CG
 C C TCTAA
 GAM2508 ZNF205 5' GCAGGTGCCCCCTCTGCCTCC 9513 A__ G
 GGAGGCAGA GCG CTGC
 ||||| |||||
 CCTCCGTCT CGT GACG
 CCCC G
 GAM2508 DKFZp434E2220 5' CCAGACCCACTCCTGCCTCC 19110 A C CTG
 GGAGGCAG AG GG CTGG
 ||||| || || |||||
 CCTCCGTC TC CC GACC
 C A CA_
 GAM2508 ERF 3' CTGGAAGCCCCCTCTGCCTCC 13236 AGC G TG
 GGAGGCAGA GGCT C G
 ||||| |||| | |
 CCTCCGTCT CCGA G C
 CCC A GT
 GAM2508 FER1L4 3' CCACCCACCTCTGCCTCC 24873 AGC C C_
 GGAGGCAGA GG TG TGG
 ||||| || || |||||
 CCTCCGTCT CC AC ACC
 _ _ CC
 GAM2508 FLJ10709 3' GCGGGTCGGCCGTTCTGCCCC 20038 A G _ G
 GG GGCAGAA CGGCTG CT GC
 || ||||| ||||| || ||
 CC CCGTCTT GCCGGC GG CG
 _ _ T G
 GAM2508 FLJ10743 3' GCAGCCCTCCTGCCCC 20078 A A C
 GG GGCAG AG GGCTGC
 || |||| || |||||
 CC CCGTC TC CCGACG
 _ C _
 GAM2508 FLJ12586 3' CAGCAACCTCTGCCTCC 23882 AGC C
 GGAGGCAGA GG TGCTG
 ||||| || |||||
 CCTCCGTCT CC ACGAC
 _ A
 GAM2508 FLJ13710 3' GTCACCACCCCTGCCTCC 24207 AAGC C C
 GGAGGCAG GG TG TGGC
 ||||| || || |||||
 CCTCCGTC CC AC ACTG
 _ C C
 GAM2508 FLJ14327 3' GCACCAGCATCAGTCCTGCCTC 24426 AA GGC C
 C GGAGGCAG GC TGCTGG GC
 ||||| || ||||| ||
 CCTCCGTC TG ACGACC CG
 C_ ACT A
 GAM2508 FLJ14351 3' CAGTTGCCGCTCTCCACC 24070 A C A T
 GG GG AGA GCGGC GCTG
 || || || ||||| |||||

CC CC TCT CGCCG TGAC
 A _ _ T
 GAM2508 FLJ20647 5' GCGCCCGTGGCCGCTGCCGCCT 19571 AGA TG T
 CC GGAGGC AGCGGC C GGCGC
 ||||| ||||| | |||||
 CCTCCG TCGCCG G CCGCG
 CCG GT C
 GAM2508 FLJ21736 3' GCACGGCAGCCCGCCTCTCCCC 24461 A C A _ _
 GG GG AGA GCGG CTGCTG GC
 || || || || || || || ||
 CC CC TCT CGCC GACGGC CG
 _ _ C C A
 GAM2508 FLJ32884 5' GCGACCGTTCTGCCTCC 29528 G C
 GGAGGCAGAA CGG TGC
 ||||| || || ||
 CCTCCGTCTT GCC GCG
 _ A
 GAM2508 FXYD3 3' GCACAGGCCCGCCCTCTGCCTC 22436 A_ CTG _
 C GGAGGCAGA GCGG CTG GC
 ||||| || || || ||
 CCTCCGTCT CGCC GAC CG
 CC CG_ A
 GAM2508 FXYD3 3' GCACAGGCCCGCCCTCTGCCTC 12593 A_ CTG _
 C GGAGGCAGA GCGG CTG GC
 ||||| || || || ||
 CCTCCGTCT CGCC GAC CG
 CC CG_ A
 GAM2508 KCND1 3' GCACCCCTTCTGCCCC 11425 A C C
 GG GGCAGAAG GG TGC
 || ||||| || || ||
 CC CCGTCTTC CC ACG
 _ _ C
 GAM2508 KIAA0481 3' CCAGCAGCTCCTGCCCC 35568 A AAGC
 GG GGCAG GGCTGCTGG
 || |||| |||||
 CC CCGTC TCGACGACC
 _ C__
 GAM2508 KIAA1026 3' GCACGGGCGCCTCTGCTCTCC 35275 _ A TG _
 GGAG GCAGA GCGGC CTG GC
 ||| |||| |||| || ||
 CCTC CGTCT CGCCG GGC CG
 T C _ A
 GAM2508 KIAA1126 3' CCAGCTCCCTGCCTCC 35607 AAGC CT
 GGAGGCAG GG GCTGG
 ||||| || ||||
 CCTCCGTC CC CGACC
 _ _ T_
 GAM2508 KIAA1344 5' GCACGGCCCCGTCTTCTGCCTC 35870 _ CT _
 C GGAGGCAGAAG CGG GCTG GC
 ||||| || || || ||

CCTCCGTCTTC GCC CGGC CG
 T C_ A
 GAM2508 KIAA1416 5' GCACCAGCAGCCCATCCACCCC 41808 A CA AGC C
 GG GG GA GGCTGCTGG GC
 || || || ||||| ||
 CC CC CT CCGACGACC CG
 _ AC AC_ A
 GAM2508 KIAA1538 5' CGCCTCAGCCCTGCCTCC 35424 AAGC CT
 GGAGGCAG GGCTG GGCG
 ||||| |||| ||||
 CCTCCGTC CCGAC CCGC
 _____ T_
 GAM2508 KIAA1854 3' GCACCCGCTTCTTCCCC 35533 A C C
 GG GG AGAAGCGG TGC
 || || ||||| ||||
 CC CC TCTTCGCC ACG
 _ T C
 GAM2508 KIAA1889 5' GCGCCACGGCCGCTGCTGCCTC 36388 A C
 C GGAGGCAG AGCGGCTG TGGCGC
 ||||| ||||| |||||
 CCTCCGTC TCGCCGGC ACCGCG
 G _
 GAM2508 MGC13057 5' CGCCAGCAAGCCCCCCTCC 26124 CAGAAGC _
 GGAGG GGCT GCTGGCG
 |||| |||| |||||
 CCTCC CCGA CGACCGC
 CC_____ A
 GAM2508 MGC21621 3' GCCTAGCCACCTCTGCCTCT 29622 AGC CT
 GGAGGCAGA GGCTG GGC
 ||||| |||| ||||
 TCTCCGTCT CCGAT CCG
 CCA _
 GAM2508 MGC2474 3' CCACCCACCTCTGCCTCC 23416 AGC C C_
 GGAGGCAGA GG TG TGG
 ||||| || ||||
 CCTCCGTCT CC AC ACC
 _____ CC
 GAM2508 MGC2555 5' CGCCAGCTCCTCCTCCTCC 26519 C AAGC CT
 GGAGG AG GG GCTGGCG
 |||| || || |||||
 CCTCC TC CC CGACCGC
 _ CT_ T_
 GAM2508 moblak 3' CCACACCTCTGTCTCC 28304 AGC C C
 GGAGGCAGA GG TG TGG
 ||||| || ||||
 CCTCTGTCT CC AC ACC
 _____ - - -
 GAM2508 QKI 5' GCGCCAGCAGCCCGCGCCCC 32618 A AGAA _
 GG GGC GCGG CTGCTGGCGC
 || ||| |||| |||||

			CC CCG CGCC GACGACCGCG		
			— C		
GAM2508	RoXaN	3'	CGCCTTCCTTCTGCCTCC 24602	C	CTGCT
			GGAGGCAGAAG GG GGCG		
			CCTCCGTCTTC CT CCGC		
			— T		
GAM2508	SES2	3'	GCACCCCACTCTCCTGCCTCC 25482	A	C C
			GGAGGCAG AG GG TGC		
			CCTCCGTC TC CC ACG		
			C TCAC C		
GAM2508	SRF	5'	GCGGCCAGCAGCCCTGCCCC 9099	A	AAGC
			GG GGCAG GGCTGCTGGC GC		
			CC CCGTC CCGACGACCG CG		
			— C G		
GAM2508	UBP1	5'	GCGCCAGCGGAGCTCCGGCTCC 15850	G	AGA GG
			GGAG C AGC CTGCTGGCGC		
			CCTC G TCG GGCGACCGCG		
			— GCC A		
GAM2508	ZNF145	5'	GCGCTCCCGGCCGCTCTCGCCT 12618	—	A CT
	CC		GGAGGC AGA GCGGCTG GGCGC		
			CCTCCG TCT CGCCGGC TCGCG		
			C — CC		
GAM2508	LOC124842	3'	CGCCATTACCCTCTTCTGCCCC 37260	A	C C C
			GG GGCAGAAG GG TG TGGCG		
			CC CCGTCTTC CC AT ACCGC		
			— T C T		
GAM2508	LOC145481	5'	CGCCAGAGTCCTCCTCCTCC 37889	C	A C G
			GGAGG AG AG GGCT CTGGCG		
			CCTCC TC TC CTGA GACCGC		
			— C —		
GAM2508	LOC147341	5'	GCGCTGTGACCCTTCTGCCTCC 40827	C	CT T
			GGAGGCAGAAG GG GC GGCGC		
			CCTCCGTCTTC CC TG TCGCG		
			— AG —		
GAM2508	LOC148809	3'	CTGGCAGTCCTGCCTCC 38594	AAGC	TG
			GGAGGCAG GGCTGC G		
			CCTCCGTC CTGACG C		
			— GT		
GAM2508	LOC150319	3'	CGCCCCCACTCTGCCTCC 38893	A	C CTGCT
			GGAGGCAGA G GG GGCG		

		CCTCCGTCT C CC CCGC		
		_ A C _		
GAM2508	LOC150319 3'	GCACCTGCCCCTCTGCCTCC 38896	A__ C	
		GGAGGCAGA GCGG TGC		
		CCTCCGTCT CGTC ACG		
		CCC C		
GAM2508	LOC150378 3'	GCGGCTGCCTCTGCCCC 38924	A A	
		GG GGCAGA GCGGCTGC		
		CC CCGTCT CGTCGGCG		
		_ C		
GAM2508	LOC157349 5'	CCAGCAGCCCCTGCCCC 39588	A AAGC	
		GG GGCAG GGCTGCTGG		
		CC CCGTC CCGACGACC		
		_ C _		
GAM2508	LOC157737 5'	GCACCTTGTTCACTCCTGCCT 41843	A C CT T_ C	
		CC GGAGGCAG AG GG GC GG GC		
		CCTCCGTC TC CT TG CC CG		
		C A T_ TT A		
GAM2508	LOC166879 5'	GCGGACCGCCCTCGCCTCC 42197	A A_ _	
		GGAGGC GA GCGG CTGC		
		CCTCCG CT CGCC GGCG		
		_ CC A		
GAM2508	LOC196746 3'	CGCCCGCAGCCCTGCCTCC 42288	AAGC T	
		GGAGGCAG GGCTGC GGCG		
		CCTCCGTC CCGACG CCGC		
		_ C		
GAM2508	LOC197196 3'	CCAGCAGCAGGGTTACCTCC 43201	C AAGCG	
		GGAGG AG GCTGCTGG		
		CCTCC TT CGACGACC		
		A GGGA_		
GAM2508	LOC199863 5'	GCACCTCCCTCCTGCCTCC 43256	A C C_	
		GGAGGCAG AG GG TGC		
		CCTCCGTC TC CC ACG		
		C _ TCC		
GAM2508	LOC203260 3'	CATAACCACTTCTGCCCC 43022	A C C C	
		GG GGCAGAAG GG TG TG		
		CC CCGTCTTC CC AT AC		
		_ A A _		
GAM2508	LOC203378 3'	CGGCAACCTCTGCCTCC 43552	AGC C	
		GGAGGCAGA GG TGCTG		

	CCTCCGTCT CC ACGGC		
	___ A		
GAM2508 LOC220021 3'	CGCCAATGCCCTGCCTCT 44850	AAGC	TGC
	GGAGGCAG GGC TGGCG		
	TCTCCGTC CCG ACCGC		
	C___ TA_		
GAM2508 LOC220776 3'	GCTCAGCCGCCCTGCCTCC 33934	AA	CT
	GGAGGCAG GCGGCTG GGC		
	CCTCCGTC CGCCGAC TCG		
	C_ _		
GAM2508 LOC254936 5'	CAGTACCATCTCTGCCTCC 45528	AGC	C
	GGAGGCAGA GG TGCTG		
	CCTCCGTCT CC ATGAC		
	CTA _		
GAM2508 LOC255271 5'	GCGCCCGCCTCGCCTCC 45727	A A	C
	GGAGGC GA GCGG TGC		
	CCTCCG CT CGCC GCG		
	_ C C		
GAM2508 LOC51008 5'	CAGCAACCTCTGCCTCC 18062	AGC	C
	GGAGGCAGA GG TGCTG		
	CCTCCGTCT CC ACGAC		
	___ A		
GAM2508 LOC81569 5'	GTCCCACCCACCTCTGCCTCC 31046	AGC	C CT
	GGAGGCAGA GG TG GGC		
	CCTCCGTCT CC AC CTG		
	CCA C C_		
GAM2508 LOC89919 5'	CCTGCACTTCTGCCTC 30462	CGGC	T
	GAGGCAGAAG TGC GG		
	CTCCGTCTTC ACG CC		
	___ T		
GAM2508 LOC90019 3'	GCACCACATGCCTCTGTCTCC 28873	AGC	_ C C
	GGAGGCAGA GGC TG TGG GC		
	CCTCTGTCT CCG AC ACC CG		
	___ T _ A		
GAM2508 LOC90355 5'	GCGCCTCTCCCGCCCCTGTCTC 27063	AA	CTGCT
C	GGAGGCAG GCGG GGCGC		
	CCTCTGTC CGCC CCGCG		
	CC CTCT_		
GAM2508 LOC91252 3'	GCACCAGCAGCTCTTGCCACC 32554	A	GA C C
	GG GGCA AG GGCTGCTGG GC		

			CC CCGT TC TCGACGACC CG	
			A _ _ A	
GAM2509	AMD1	3'	G TTCCTCTTAAC TACGGTGT 7347	GA CGC A
			ACACCG AG GGA GAAC	
			TGTGGC TC TCT CTTG	
			A_ AAT C	
GAM2509	BCL9	5'	G TTCCTTCCGTGTCCCGATGT 10524	C AA
			ACA CGG GCGCGGAAGAAC	
			TGT GCC TGTGCCTTCTTG	
			A C_	
GAM2509	CA3	3'	T TCCTTGCCTCCTTCTGGTG 11681	C_ _
			CACCGGAAG GC GGAA	
			GTGGTCTTC CG CCTT	
			CTC TT	
GAM2509	CAPZA1	3'	C TTCCAAGCACTTCTGGT 35950	C _
			ACCGGAAG GC GGAAG	
			TGGTCTTC CG CCTTC	
			A AA	
GAM2509	CARD15	3'	T CCTCCCAGGCTTCCGTGT 22718	C GC_ A
			ACAC GGAAGC GGA GA	
			TGTG CCTTCG CCT CT	
			_ GAC C	
GAM2509	CCR2	3'	G TTCCTTATGTTGCCAGTGT 6309	C AA _ G
			ACAC GG GCG CG AAGAAC	
			TGTG CC CGT GT TTCTTG	
			A _ T A	
GAM2509	CYP24	5'	C TTCCCGCGCTCCGGTGT 6425	A _
			ACACCGGA GCGCGG AAG	
			TGTGGCCT CGCGCC TTC	
			_ C	
GAM2509	DSG1	3'	T TCTTCTGATTCTAGTGT 7657	CG GCG
			ACAC GAA CGGAAGAA	
			TGTG CTT GTCTTCTT	
			AT A_	
GAM2509	EHF	3'	G TTCCTTTTTTGCTCCAAGTG 14452	C_ A CG
			CAC GGA GCG GAAGAAC	
			GTG CCT CGT TTTCTTG	
			AA _ TT	
GAM2509	ITGB1	3'	G TTCCTTCTTCTTGCCAGTGT 27395	C _ CGC
			ACAC GG AAG GGAAGAAC	

		TGTG CC TTC TCTTCTTG		
		A G T__		
GAM2509 MGEA5	5'	TCTCCGCTTATGCTTCTGG 14519	_____	A
		CCGGAAGC GCGGA GA		
		GGTCTTCG CGCCT CT		
		TATT _		
GAM2509 MTCP1	5'	TCTCCCTGGACCACTTCCGGT 15490	_____	C A
		ACCGGAAG CG GGA GA		
		TGGCCTTC GT CCT CT		
		ACCAG C _		
GAM2509 PABPN1	5'	TCCTCCCTGCTTTCTGGTG 11019	_	C A
		CACCGGAA GCG GGA GA		
		GTGGTCTT CGT CCT CT		
		T C C		
GAM2509 PSME3	5'	TCCACAGCGCCTCCGGTGT 12373	A	_____
		ACACCGGA GCGC GGA		
		TGTGGCCT CGCG CCT		
		C ACA		
GAM2509 SPG3A	3'	GTTCTTTTACTTCAGTGT 18047	CG	CGC
		ACAC GAAG GGAAGAAC		
		TGTG CTTC TTTTCTTG		
		A_ A__		
GAM2509 SSRP1	5'	TTCCGTACGGCTTCCGGTG 9116	_____	
		CACCGGAAGC GCGGAA		
		GTGGCCTTCG TGCCTT		
		GCA		
GAM2509 TBX3	3'	GTTCTTTCTCTTTCCTGT 18641	C	CGC
		AC GGAAG GGAAGAAC		
		TG CCTTT CTTTCTTG		
		T CT_		
GAM2509 TNFRSF1B	3'	TCCGCCTTCACTCCGGTGT 6735	_____	C
		ACACCGGA AG GCGGA		
		TGTGGCCT TC CGCCT		
		CACT _		
GAM2509 TRIM37	3'	TCTCCGTGTCTGATGT 17617	C	AA
		ACA CGG GCGCGGAAGA		
		TGT GTC TGTGCCTTCT		
		A _		
GAM2509 TSLP	5'	TCTTTCTCTCTCTGGTGT 28850	_	CGC
		ACACCGGA AG GGAAGA		

			TGTGGTCT TC CTTTCT		
			C T__		
GAM2509	AP4M1	5'	GTTCTTTTGTTCGG 11088	AGC	
			CCGGA GCGGAAGAAC		
			GGCCT TGTTTTCTTG		

GAM2509	ATP1B4	3'	TTCCTTGCTCTCTGGTGT 14328	_ C	
			ACACCGGA AGCG GGAA		
			TGTGGTCT TCGT CCTT		
			C T		
GAM2509	BHLHB2	3'	GTTCCCTGGGCTTCTGG 9756	G AA	
			CCGGAAGC CGG GAAC		
			GGTCTTCG GTC CTTG		
			G C_		
GAM2509	C7orf13	5'	GTTCTTCCTCCTCCGCGT 26343	_ A CGC	
			AC CGGA G GGAAGAAC		
			TG GCCT C CCTTCTTG		
			C _CT_		
GAM2509	DCOYM	3'	CTTCCAGGTGTTTTCCAGTG 25847	C _ _	
			CAC GGAAG CGC GGAAG		
			GTG CCTTT GTG CCTTC		
			A T GA		
GAM2509	DKFZp762A227	5'	TTCTTCCACCCCTTTCTGGT 15321	CGC__	
			ACCGGAAG GGAAGAA		
			TGGTCTTT CCTTCTT		
			CCCCA		
GAM2509	DMTF1	5'	GTTCTTCCAAAGTGCCCGG 22117	AA _	
			CCGG GCGC GGAAGAAC		
			GGCC CGTG CCTTCTTG		
			_ AAA		
GAM2509	ESPL1	5'	TCTGGGGCGCTCTCCGGTGT 14631	_ GGA	
			ACACCGGA AGCGC AGA		
			TGTGGCCT TCGCG TCT		
			C GGG		
GAM2509	FLJ00060	3'	TTCTTCCTCCTTCTGGT 30630	CGC	
			ACCGGAAG GGAAGAA		
			TGGTCTTC CCTTCTT		
			CT_		
GAM2509	FLJ12484	3'	CTGGCTGGGCTTCCGGTGT 34517	G A_	
			ACACCGGAAGC CGG AG		

TGTGGCCTTCG GTC TC
 G GG
 GAM2509 FLJ12484 3' CTGGCTGGGCTTCCGGTGT 23019 G A_
 ACACCGGAAGC CGG AG
 ||||| ||
 TGTGGCCTTCG GTC TC
 G GG
 GAM2509 FLJ12671 5' TCTTCCGCCTTCCATTGT 25244 CC C
 ACA GGAAG GCGGAAGA
 || |||| |||||
 TGT CCTTC CGCCTTCT
 TA _
 GAM2509 FLJ12875 3' TCTTCTGTTCCTGTGT 23756 C AGC
 ACAC GGA GCGGAAGA
 ||| || |||||
 TGTG CCT TGTCTTCT
 T _
 GAM2509 FLJ12975 3' TCCTCCCACCTCAGCCTCTGGT 34481 A GC_____ A
 GT ACACCGGA GC GGA GA
 ||||| || |||
 TGTGGTCT CG CCT CT
 C ACTCCAC C
 GAM2509 FLJ13081 3' GTTCTCTGTTTTCCAGTTC 24237 C C C A
 A AC GGAAG GCGGA GAAC
 | || |||| |||| ||||
 C TG CCTTT TGTCT CTTG
 T A T _
 GAM2509 HHGP 3' TCTTGATTGGAGCTTCCGGT 21435 G_ _
 ACCGGAAGC CGG AAGA
 ||||| || |||
 TGGCCTTCG GTT TTCT
 AG AG
 GAM2509 KIAA1204 5' GTTCTTCCATCTTCCGATG 34317 C CGC
 CA CGGAAG GGAAGAAC
 || |||| |||||
 GT GCCTTC CCTTCTTG
 A TA_
 GAM2509 KIAA1463 3' TCCTCTGTTCTTCCAGTTC 35772 C C C A
 A AC GGAAG GCGGA GA
 | || |||| |||| ||
 C TG CCTTC TGTCT CT
 T A T C
 GAM2509 KIAA1549 3' TTCTTCCTCCTTCTTCTGGTG 34371 CGC_
 CACCGGAAG GGAAGAA
 ||||| |||||
 GTGGTCTTC CCTTCTT
 TTCCT
 GAM2509 KIAA1576 3' TCTTCTGTGCCCCAGTG 32776 C AA
 CAC GG GCGCGGAAGA
 ||| || |||||

GTG CC CGTGTCTTCT
 A C_
 GAM2509 KIAA1908 3' TTCTTCTGCTCCATGT 36341 CC AGC
 ACA GGA GCGGAAGAA
 ||| ||| |||||
 TGT CCT CGTCTTCTT
 A_ _
 GAM2509 MGC22014 3' GTTCCTGAGCTTCCGG 32221 G AA
 CCGGAAGC CGG GAAC
 ||||| ||| |||
 GGCCTTCG GTC CTTG
 A _
 GAM2509 MGC32043 3' GTTCCTTTCAGGCTTCCGTG 29393 C GC _
 CAC GGAAGC GGAAG AAC
 ||| ||||| ||||| |||
 GTG CCTTCG CTTTC TTG
 _ GA C
 GAM2509 NPTXR 3' GTTCTTCCCCCTCCATGT 27735 CC A CGC
 ACA GGA G GGAAGAAC
 ||| ||| | |||||
 TGT CCT C CCTTCTTG
 A_ _CC_
 GAM2509 NPTXR 3' GTTCTTCCCCCTCCATGT 15587 CC A CGC
 ACA GGA G GGAAGAAC
 ||| ||| | |||||
 TGT CCT C CCTTCTTG
 A_ _CC_
 GAM2509 SEC14L1 3' GTTCTTCCCGTTTCCTTCCGTG 8905 C_ C
 CAC GGAAGCG GGAAGAAC
 ||| ||||| |||||
 GTG CCTTTGC CCTTCTTG
 CCTT _
 GAM2509 SMCR8 5' GTTCTTCTCCTCGGGTGT 29567 G A CGC
 ACACC GA G GGAAGAAC
 ||||| ||| |||||
 TGTGG CT C TCTTCTTG
 G _C_
 GAM2509 LOC126302 5' TTCTTGGGTTCCGCGTGT 36827 _ G G _
 ACAC CGGAA C CG GAA
 |||| ||||| | |||
 TGTG GCCTT G GT CTT
 C _G T
 GAM2509 LOC126353 3' TCCTCCACTTTCAGGTGT 36831 _ CGC A
 ACACC GGAAG GGA GA
 ||||| ||||| ||| ||
 TGTGG CTTTC CCT CT
 A A_ C
 GAM2509 LOC130535 3' TTCTTCCTTCAGGTGT 37477 G GCGC
 ACACC GAA GGAAGAA
 ||||| ||| |||||

	TGTGG CTT CTTCTT		
	A ____		
GAM2509 LOC144363 5'	CTTTTGC GGCTCCGGCGT 37730	A	AG
	AC CCGGA CGCGGAAG		
	TG GGCCT GCGTTTTC		
	C CG		
GAM2509 LOC146229 3'	GTTCTTCCCCTTCTGGTG 38113		CGC
	CACCGGAAG GGAAGAAC		
	GTGGTCTTC CTTCTTG		
	C__		
GAM2509 LOC147976 3'	TCCCTGTTCCCTCTGGTGT 38430	__	C
	ACACCGGA AGCG GGA		
	TGTGGTCT TTGT CCT		
	CCC C		
GAM2509 LOC150095 5'	TCTCTCCACGGCTTCCGG 41132	_C _	
	CCGGAAGC G GGA AGA		
	GGCCTTCG C CCT TCT		
	G A C		
GAM2509 LOC157753 3'	TCTGGTGTGCTTCCAGGT 39663	_	GA
	ACC GGAAGCGCG AGA		
	TGG CCTTCGTGT TCT		
	A GG		
GAM2509 LOC157858 5'	TCTCCTTGCGTTTCAGTG 41870	CG	__ A
	CAC GAAGCGC GGA GA		
	GTG CTTTGCG CCT CT		
	A_ TT _		
GAM2509 LOC163882 3'	TCCTGTGTAACCTCTGGTGT 39974	A__ _	
	ACACCGGA GCGC GGA		
	TGTGGTCT TGTG CCT		
	CCAA T		
GAM2509 LOC196205 3'	CTTTTGTCTGGTGT 42326		AGC
	ACACCGGA GCGGAAG		
	TGTGGTCT TGTTTTTC		
	__		
GAM2509 LOC200339 3'	TCTTCCACTTTTGGTGT 43300		CGC
	ACACCGGAAG GGAAGA		
	TGTGGTTTTTC CTTCT		
	A__		
GAM2509 LOC201245 5'	GTTCAGGCTGCTTCGGTGT 42231	AGC	AA_
	ACACCGGA GCGG GAAC		

TGTGGCTT CGTC CTTG
 ____ GGA
 GAM2509 LOC202934 3' GTTCTTTTGCTTCCCAATGT 43465 CC_ CG
 ACA GGAAGCG GAAGAAC
 ||| ||||| |||||
 TGT CCTTCGT TTTCTTG
 AAC ____
 GAM2509 LOC255465 3' GTTCTTTTCACTTCCCAATGT 46457 CC_ CGC
 ACA GGAAG GGAAGAAC
 ||| ||||| |||||
 TGT CCTTC CTTTCTTG
 AAC A____
 GAM2510 EFNB1 5' ACAGCGATCCCGGGACGGTCGA 10704 T C AAAC _
 TC ACCG CCCG GA CGTTGT
 || ||||| || |||||
 AG TGGC GGGC CT GCGACA
 C A C____ A
 GAM2510 CSTF1 5' ACGTGCGCTCGGAGCGGTAGA 7008 C AA _
 TCTACCGC CCGA CG ACGT
 ||||| ||||| || |||||
 AGATGGCG GGCT GC TGCA
 A C_ G
 GAM2510 FLJ22794 5' ACAACGTTTGGGAAAGTA 44022 CGC AACG
 TAC CCCGA ACGTTGT
 ||| ||||| |||||
 ATG GGGTT TGCAACA
 AAA ____
 GAM2510 KIAA1977 5' CAACGTCCAGGGTGGCAGA 36744 A CGAAAC
 TCT CCGCCC GACGTTG
 ||| ||||| |||||
 AGA GGTGGG CTGCAAC
 C AC____
 GAM2511 APACD 3' TGTCTATACATTGGTCACC 12363 C CGC A
 GG GATCG AT TATAGACA
 || ||||| || |||||
 CC CTGGT TA ATATCTGT
 A ____ C
 GAM2511 COPS7A 3' TCTATATATAATATGACGC 18437 A CGC_
 GCG TCG ATATATAGA
 ||| ||| |||||
 CGC AGT TATATATCT
 _ ATAA
 GAM2511 FLJ10702 3' GTGTCTATACATTGCTTTCCGC 20028 ATCGC TA_
 GCG GCA TATAGACAC
 ||| ||| |||||
 CGC CGT ATATCTGTG
 CTTT_ TAC
 GAM2511 SMPD2 5' GTGCCCACCTGTGCGCGCCGCC 9053 AT TATAGA
 GGCG CGCGCATA CAC
 |||| ||||| |||

CCGC GCGCGTGT GTG
 C_ CCACCC
 GAM2511 LOC254251 3' GTGTCTATATACACACGTGG 45898 CA__
 TCGCG TATATAGACAC
 |||| |||||
 GGTGC ATATATCTGTG
 ACAC
 GAM2512 ATP8A2 3' ACTGACACGTGCCAGC 44914 A TG
 GCT GTAT GTGTCAGT
 ||| ||| |||||
 CGA CGTG CACAGTCA
 C _
 GAM2512 DMC1 3' ACTGACATTACATAGCTA 13932 GTAT
 TAGCTA TGGTGTGTCAGT
 ||||| |||||
 ATCGAT ATTACAGTCA
 AC_
 GAM2512 GRM7 3' ACTGACATCAGCACTGC 6515 T A
 GC AGT TTGGTGTGTCAGT
 || ||| |||||
 CG TCA GACTACAGTCA
 _ C
 GAM2512 KCNJ1 5' TTGGTAAATATTAGCTA 5728 GG GT
 TAGCTAGTATT T CAG
 ||||| |||
 ATCGATTATAA A GTT
 _ TG
 GAM2512 SLC11A3 3' ACTCTTGTTCAAGACTAGCTA 15941 A TGTC_
 TAGCTAGT TTGG AGT
 ||||| ||| |||
 ATCGATCA AACT TCA
 G TGTTG
 GAM2512 DKFZP586F1318 3' ACTGACAGGATTTACTAGTTA 17903 TTGG_
 TAGCTAGTA TGTCAGT
 ||||| |||||
 ATTGATCAT ACAGTCA
 TTAGG
 GAM2512 DKFZp761N1114 3' TACTGACATTGACTAGC 38607 TA TG
 GCTAG T GTGTCAGTA
 |||| | |||||
 CGATC A TACAGTCAT
 _ GT
 GAM2512 FLJ32784 3' TACTGACGCGAGCAGC 29442 A AT G
 GCT GT T GTGTCAGTA
 ||| || | |||||
 CGA CG A CGCAGTCAT
 _ _ G
 GAM2512 INSM2 3' TACTAATTCCTACTAGC 26327 TT T C
 GCTAGTA GG GT AGTA
 ||||| || |||

		CGATCAT CC TA TCAT	
		C_ T A	
GAM2512 KIAA0332	3'	TACTAGTGAAGATACTAGT 31420	GG TC
		GCTAGTATT TG AGTA	
		TGATCATAG GT TCAT	
		AA GA	
GAM2512 KIAA0376	3'	ACCGACGCCATTAGCTA 32671	TAT A
		TAGCTAG TGGTGTC GT	
		ATCGATT ACCGCAG CA	
		_____ C	
GAM2512 KIAA0788	3'	ACTGAAATGTACTAGCTG 35343	TGGTG
		TAGCTAGTAT TCAGT	
		GTCGATCATG AGTCA	
		TAA_____	
GAM2512 ST7L	3'	TACTGACACCCCACTGGCTA 28978	ATT
		TAGCTAGT GGTGTCAGTA	
		ATCGGTCA CCACAGTCAT	
		CC_	
GAM2512 ST7L	3'	TACTGACACCCCACTGGCTA 29208	ATT
		TAGCTAGT GGTGTCAGTA	
		ATCGGTCA CCACAGTCAT	
		CC_	
GAM2512 ST7L	3'	TACTGACACCCCACTGGCTA 19336	ATT
		TAGCTAGT GGTGTCAGTA	
		ATCGGTCA CCACAGTCAT	
		CC_	
GAM2512 STAT5A	3'	ACTGACACCTTTGCAGGC 9125	A TT
		GCT GTA GGTGTCAGT	
		CGG CGT CCACAGTCA	
		A TT	
GAM2512 STK38L	3'	TACTGACAGGAGCAGCAGCTA 34292	A A_ GG
		TAGCT GT TT TGTCAGTA	
		ATCGA CG GA ACAGTCAT	
		_ AC GG	
GAM2512 SUCLG2	3'	ACTGAACATATTAGCTA 32677	TG G
		TAGCTAGTAT GT TCAGT	
		ATCGATTATA CA AGTCA	

GAM2512 TRIM2	3'	TACTGAGTACCTACTAGGTA 17602	G TT _
		TA CTAGTA GGTG TCAGTA	

AT GATCAT CCAT AGTCAT
 G _ G
 GAM2512 LOC149506 3' ACTGACACCAAGTGTGC 40999 TAG
 GC TATTGGTGTCACT
 || |||||
 CG GTGACCACAGTCA
 T__
 GAM2512 LOC153914 5' TACTGACACTGTCAGCT 39437 AG ATT
 AGCT T GGTGTCAGTA
 ||| | |||||
 TCGA G TCACAGTCAT
 CT__
 GAM2512 LOC153914 5' ACTGACAACACACTAGGC 39435 _ AT G
 GC TAGT TG TGTCAGT
 || ||| || |||||
 CG ATCA AC ACAGTCA
 G C_ A
 GAM2512 LOC221037 3' TACTGACACCACAGCAGT 44743 A AT
 GCT GT TGGTGTCACTA
 ||| || |||||
 TGA CG ACCACAGTCAT
 _ AC
 GAM2512 LOC222031 3' ACTGACACCATGGGCTG 45129 AGTAT
 TAGCT TGGTGTCACT
 |||| |||||
 GTCGG ACCACAGTCA
 GT__
 GAM2513 STIM1 3' CCCAGACACACCATCTC 30202 A ATAGGA
 GA ATGGTGTGT TGGG
 || ||||| |||
 CT TACCACACA ACCC
 C G____
 GAM2513 CAT56 3' ACCCATCCCATCCACCACTTC 24930 A TG ATA
 GAA TGGTG T GGATGGGT
 ||| |||| | |||||
 CTT ACCAC A CCTACCCA
 C CTC__
 GAM2513 FLJ23598 5' CCCATCCCAGACCCCTCA 24155 AAT G TATA
 TGA GGT TG GGATGGG
 ||| ||| || |||||
 ACT CCA AC CCTACCC
 CC_ G ____
 GAM2513 FLJ32332 3' CCTCAACACACATCCATCTCA 29469 A _ ATAG T
 TGA ATGG TGTGT GA GG
 ||| ||| |||| |||
 ACT TACC ACACA CT CC
 C T CAA_ _
 GAM2513 KIAA0022 3' TTTTACACACACCATTTTA 17029 A
 TGAAATGGTGTGT TAGGA
 ||||| |||||

		ATTTTACCACACA ATTTT		
		C		
GAM2513	KIAA1211	3' CCCACCCACACACCATTCA	34162	A ATA A
		TGAA TGGTGTGT GG TGGG		
		ACTT ACCACACA CC ACCC		
		— — C		
GAM2513	KIAA1522	3' ACCCATCCCAGAAACACAATCT	32414	A G GTATA
	CA	TGA AT GTGT GGATGGGT		
		ACT TA CACA CCTACCCA		
		C A AAGAC		
GAM2513	KIAA1866	3' ACCCATCCCCCTACCACTA	30552	T TA_
		TGGTG GTA GGATGGGT		
		ATCAC CAT CCTACCCA		
		— CCC		
GAM2513	P2RX1	3' ACCCAGTGACACACCA	33350	GGA
		TGGTGTGTATA TGGGT		
		ACCACACATGT ACCCA		
		G_		
GAM2513	PLAGL2	3' CCTCAGACACACCATTTC	34876	ATAG T
		TGAAATGGTGTGT GA GG		
		ACTTTACCACACA CT CC		
		GA_ _		
GAM2513	TRPV5	5' ACCTGCATGCACACACACCACC	21247	AA ATAGGAT_
	TCA	TGA TGGTGTGT GGGT		
		ACT ACCACACA TCCA		
		CC CACGTACG		
GAM2513	LOC219397	3' ACCGCGGACATCACACCATTCC	44897	A TATAGGA _
	A	TG AATGGTGTG TG GGT		
		AC TTACCACAC GC CCA		
		C TACAG_ G		
GAM2513	LOC221322	5' ACCCATCCCAGAACTACTCCA	44151	T _ ATA_
		TGG GT GT GGATGGGT		
		ACC CA CA CCTACCCA		
		T T AGAC		
GAM2513	LOC222060	5' ACCCTGAAACTACACACCATT	45158	TAGGAT
	C	GAAATGGTGTGTA GGGT		
		CTTTACCACACAT CCCA		
		CAAAGT		
GAM2514	AHR	5' GGCAGCTCACCTGTACTG	7332	C AA
		TAGTACAGG GA GTTGTT		

			GTCATGTCC CT CGACGG		
			A _		
GAM2514	EDAR	3'	TCAGATGCTCGCCTGTAC 22745	AA	TG
			GTACAGGCCGA GT TTGA		
			CATGTCCGCT CG GACT		
			_ TA		
GAM2514	FBLN5	3'	TGACTCTCACCTGTACTA 13026	C	A
			TAGTACAGG GA AGTTG		
			ATCATGTCC CT TCAGT		
			A C		
GAM2514	GABRE	3'	CATCTTTTCGTCTGCACTA 22528	A	T
			TAGT CAGGCGAAAG TG		
			ATCA GTCTGCTTTC AC		
			C T		
GAM2514	GABRE	3'	CATCTTTTCGTCTGCACTA 22513	A	T
			TAGT CAGGCGAAAG TG		
			ATCA GTCTGCTTTC AC		
			C T		
GAM2514	GABRE	3'	CATCTTTTCGTCTGCACTA 22509	A	T
			TAGT CAGGCGAAAG TG		
			ATCA GTCTGCTTTC AC		
			C T		
GAM2514	GABRE	3'	CATCTTTTCGTCTGCACTA 11407	A	T
			TAGT CAGGCGAAAG TG		
			ATCA GTCTGCTTTC AC		
			C T		
GAM2514	MAK	5'	TCAACAACCTTCTGCTGCATTA 12529	ACA	A
			TAGT GGCG AAGTTGTTGA		
			ATTA TCGT TTCAACAAC		
			CG_ C		
GAM2514	NPHP1	3'	CAACACTATCTGTACTA 31315	CGAA	T
			TAGTACAGG AGT GTTG		
			ATCATGTCT TCA CAAC		
			A_ _		
GAM2514	VANGL2	3'	CAACAACCTTTTGTATTACT 35477	CAG	
			AGTA GCGAAAGTTGTTG		
			TCAT TGTTTTCAACAAC		
			TA_		
GAM2514	CHFR	3'	TGGCTTCCGCCTGTGCTA 20149	A	
			TAGTACAGGCG AAGTTG		

ATCGTGTCCGC TTCGGT
 C
 GAM2514 DKFZp586l021 3' CAGCCTTCCACCTGTGCTA 26020 C_ A
 TAGTACAGG GAA GTTG
 ||||| |||||
 ATCGTGTCC CTT CGAC
 AC C
 GAM2514 DKFZP761l2123 3' CAACAACCTCCACTG 25463 AC CGAA
 TAGT AGG AGTTGTTG
 ||| || |||||
 GTCA TCC TCAACAAC
 CC ____
 GAM2514 FLJ14855 3' TAACCCTGCCTGTACTA 27060 AAA
 TAGTACAGGCG GTTG
 ||||| |||||
 ATCATGTCCGT CAAT
 CC_
 GAM2514 FLJ20069 3' TCAACAACACCAGCCTGAC 19157 A GAAA
 GT CAGGC GTTGTGTA
 || ||||| |||||
 CA GTCCG CAACAAC
 _ ACCA
 GAM2514 FLJ21140 3' CAACAACCTGACTTACTA 24140 C GCGAA
 TAGTA AG AGTTGTTG
 ||||| || |||||
 ATCAT TC TCAACAAC
 _ AG____
 GAM2514 PNPASE 3' CAACAACCTTACTTGCCT 35101 ____
 AGGCGA AAGTTGTTG
 ||||| |||||
 TCCGTT TTCAACAAC
 CAT
 GAM2514 PRO1914 5' CAACGCACATCCGCCTGTAT 15328 AAA _
 GTACAGGCG GT TGTG
 ||||| || |||||
 TATGTCCGC CA GCAAC
 CTA C
 GAM2514 TERA 3' TGATGATTCACACCTGTACTA 22206 CGAA TG
 TAGTACAGG AGT TTG
 ||||| || |||||
 ATCATGTCC TTA AGT
 ACAC GT
 GAM2514 LOC196283 3' TCAACAAAAGTAAGCTGTACT 42340 G GAAAG____
 A TAGTACAG C TTGTTGA
 ||||| | |||||
 ATCATGTC G AACAACT
 _ AATGAAA
 GAM2514 LOC202451 5' CAACAACCTGTTTCGTACTG 43436 AG GAA
 TAGTAC GC AGTTGTTG
 ||||| || |||||

GTCATG TG TCAACAAC
 CT ____
 GAM2515 PTPN1 3' GTGCCAGGCTGTAAGCATTCTG 8703 TC CGTG T_
 A TCAGA GC AC CCTGGCAC
 |||| || || |||||
 AGTCT CG TG GGACCGTG
 TA AA__ TC
 GAM2515 ZNF2 5' TGCCAGGAATCAGTGACATTC 22070 ____ CG C
 GA TCGC TGA TCCTGGCA
 || |||| || |||||
 CT AGTG ACT AGGACCGT
 TAC __ A
 GAM2515 D2S448 3' TGCCAGGAGCCGGCAGACCTG 36396 A _ TGA
 CAG TC GCCG CTCCTGGCA
 ||| || |||| |||||
 GTC AG CGGC GAGGACCGT
 C A C__
 GAM2515 FLJ13102 3' TGCCAGACACGGCGATT 24345 ACTC
 GATCGCCGTG CTGGCA
 ||||| |||||
 TTAGCGGCAC GACCGT
 A__
 GAM2515 KIAA0418 3' TGCCAGGAGCCAACCTGG 15998 ATCGCCG A
 TCAG TG CTCCTGGCA
 ||| || |||||
 GGTC AC GAGGACCGT
 CA____ C
 GAM2515 MAGE-E1 3' GCACCCATTCTCGGCGATCTG 25107 T_ CTCCTG
 A TCAGATCGCCG GA GC
 ||||| || ||
 AGTCTAGCGGC CT CG
 TC TACCCA
 GAM2515 MAGEE1 5' GTGCCAGGAGTCAAGGCCTG 18377 ATC G
 CAG GCC TGA CTCCTGGCAC
 ||| || |||||
 GTC CGG ACTGAGGACCGTG
 __ A
 GAM2515 MESDC1 5' GGGGTCACGGCGCCTGA 22884 AT
 TCAG CGCCGTGACTCC
 ||| |||||
 AGTC GCGGCACTGGGG
 C_
 GAM2515 MGC11335 5' GTGCCAGGAGCCATGTCTGA 25148 TCGC A
 TCAGA CGTG CTCCTGGCAC
 |||| |||| |||||
 AGTCT GTAC GAGGACCGTG
 __ C
 GAM2515 OS4 3' TGCCAGGAATCTGCCTACCTG 12291 ATC_ CGT C
 CAG GC GA TCCTGGCA
 ||| || || |||||

GTC CG CT AGGACCGT
 CATC T__ A
 GAM2515 PP1665 3' GCCAGGAGGCACCTGA 25092 ATCGCC A
 TCAG GTG CTCCTGGC
 |||| ||| |||||
 AGTC CAC GAGGACCG
 _____ G
 GAM2515 PPP1R16B 3' TGCCAGGAGCCAGCTGTGTGA 30778 G C CG A
 TCA AT GC TG CTCCTGGCA
 ||| || || |||||
 AGT TG CG AC GAGGACCGT
 G T __ C
 GAM2516 FLJ14442 3' CACCAGCCAACTGCAACTTA 26534 A A ATA
 TAA TTGCAGTTG GC GGTG
 ||| ||||| || |||
 ATT AACGTCAAC CG CCAC
 C _ A__
 GAM2516 ISL2 3' TCACCCATGCTCAGGCCATT 35081 T AG A
 AAT GC TTGAGCAT GGTGA
 ||| || ||||| ||||
 TTA CG GACTCGTA CCACT
 C __ C
 GAM2516 KIAA1915 3' TCACCTATACTCTACCAAT 36273 CA T C
 ATTG GT GAG ATAGGTGA
 |||| || || |||||
 TAAC CA CTC TATCCACT
 __ T A
 GAM2516 PLPL 3' TCACCTATGCCTGAAAGCA 21400 AG GA
 TGC TT GCATAGGTGA
 ||| || |||||
 ACG AG CGTATCCACT
 AA TC
 GAM2516 LOC256639 5' TCACCTATCTGAGCCACAA 46029 CA G C
 TTG GTT AG ATAGGTGA
 ||| ||| || |||||
 AAC CGA TC TATCCACT
 AC G _
 GAM2517 C5R1 3' CATATGGCAATAGGTGTG 7472 C TAAAT
 CAC CCTATTGCC TATG
 ||| ||||| |||
 GTG GGATAACGG ATAC
 T T____
 GAM2517 PCK1 3' CCATAAGGTGCAGTAGG 30117 _ AAAA
 CCTATTGC CT TTATGG
 ||||| || |||||
 GGATGACG GG AATACC
 T ____
 GAM2517 HHLA2 3' CCACAATTCCAGGCAATGG 13936 AA A
 CTATTGCCT AATT TGG
 ||||| ||| |||

GGTAACGGA TTAA ACC
CC C
GAM2517 KIAA1559 3' CCATAATTCCAGAAAGCAAAAG 36161 A ____ AA
G CCT TTGC CT AATTATGG
||| ||| || |||||
GGA AACG GA TTAATACC
A AAA CC
GAM2517 RASGRF2 3' CCAGTCTTTAGGCAATGGG 30598 ATTA
CCTATTGCCTAAA TGG
||||||| |||
GGGTAACGGATTT ACC
CTG_
GAM2517 LOC124460 3' ATTTTAGGCAAAGAGGT 37443 C A
ACC CT TTGCCTAAAAT
||| || |||||
TGG GA AACGGATTTTA
A _
GAM2517 LOC147817 5' CCATACGGTGAGGCAATGAGG 38383 C AAAAT
CC TATTGCCT TATGG
|| ||||| ||||
GG GTAACGGA ATACC
A GTGGC
GAM2517 LOC164397 5' CTGTGGACCTAGACAATGGGG 40152 C AAA
CCCTATTG CTA TTATGG
||||| ||| |||||
GGGGTAAC GAT GGTGTC
A CCA
GAM2517 LOC201294 3' CCAGCATGCCAGGCAACAGGCG 42566 _ A AAAATTA
GTG CACC CCT TTGCCT TGG
|||| ||| ||||| |||
GTGG GGA AACGGA ACC
C C CCGTACG
GAM2517 LOC245728 5' AGTTTCAGGCAATGAAGTG 43801 CCC A
CAC TATTGCCT AAATT
||| ||||| |||||
GTG GTAACGGA TTTGA
AA_ C
GAM2517 LOC253038 5' CCATAATTTTCAGGCTAAAG 46595 ATT A
CT GCCT AAATTATGG
|| ||| |||||
GA CGGA TTTAATACC
AAT C
GAM2517 LOC253776 3' CCAGGCACTAGGCAACCAGGGG 46525 A_ AAATTA
T ACCCCT TTGCCTA TGG
||||| ||||| |||
TGGGGA AACGGAT ACC
CC CACGG_
GAM2518 KAL1 3' GTCTTGATATTCTGTGACTCA 5718 CAAACACG T
TGAGTCAC ATCG GAC
||||| ||| |||

		ACTCAGTG	TAGT CTG		
		TCTTA__	T		
GAM2518	BIVM	5'	CATGGAGTTGTCCAGTGA	19251	CAA _ GA
			CTCA		
			TCGTG		
		ACTCAGTG	TGT G GGTAC		
		ACC	T A_		
GAM2518	BOP	5'	GCCATTGATTTTGGTGACCCA	41208	A CA C
			ATG		
		AC	CAGTGGTTT GTTA CG		
		C	TA C		
GAM2518	KIAA1458	3'	TCAGATGTGTTTGGTAATCA	34207	GTC G G
			TGA		
		ACT	TGGTTTGTG TAG ACT		
		AA_	_ _		
GAM2518	KIAA1829	3'	TCATTTGTCACAGTGA	31035	CAAAC TC
			CTCA		
		ACTCAGTG	TGTT TACT		
		ACAC_	_		
GAM2518	MGC11082	5'	GTTACAATCACACCAAGTGA	26412	CAAACAC C
		CA			
			CTCA		
		ACTCAGTG	CTA CATTG		
		AACCACA	A		
GAM2518	MGC4663	3'	GTCAGTCCCAACTTGGTGACTC	23718	ACACGATC
		A			
			CTCA		
		ACTCAGTGGTT	CACTG		
		CAACCGT_			
GAM2518	PDE4DIP	3'	CACTGAGGTCATGGTGACTCA	16050	AAC GA _
			CTCA		
		ACTCAGTGGT	TG AG CAC		
		AC_	G_ T		
GAM2518	LOC120227	5'	GTCAGTCCCAACTTGGTGACTC	36620	ACACGATC
		A			
			CTCA		
		ACTCAGTGGTT	CACTG		
		CAACCGT_			
GAM2518	LOC158318	5'	GTCATGGTCGCCTAGCGCTCA	41957	CACCAAACA
			CTCA		
		ACTCG	GCTGGTACTG		
		CGATCC_			
GAM2518	LOC158857	5'	GTCATAGTCACTATGGTGACTC	42031	AACAC CG
		A			
			CTCA		

		ACTCAGTGGT CTG ACTG		
		ATCA_ AT		
GAM2518	LOC159049 5'	GTCATAGTCACTATGGTGA	42057	AACAC CG
	A	TCAGTCACCA GAT TGAC		
		ACTCAGTGGT CTG ACTG		
		ATCA_ AT		
GAM2518	LOC200310 3'	GCCAGAGTGCTTGTGACTCA	32710	C A GATC
		TGAGTCAC AA CAC GT		
		ACTCAGTG TT GTG CG		
		_ C AGAC		
GAM2518	LOC257443 3'	TCAGATGTGTTTGGTAATCA	45875	GTC G G
		TGA ACCAAACAC ATC TGA		
		ACT TGGTTTGTG TAG ACT		
		AA_ _ _		
GAM2519	KIAA0356 3'	CGATCCCCGTGCGCTCCTCA	32892	C CACTC
		TGA GGAGCGCACG ATCG		
		ACT CCTCGCGTGC TAGC		
		_ CCC_		
GAM2519	LOC150295 3'	ATGAATGCACGGCCGTCGCTCC	41178	C _ _ _ C
	GTC	GACGGAGCG AC GCA TCAT		
		CTGCCTCGC TG CGT AGTA		
		_ CCGGCA A		
GAM2519	LOC219513 3'	CGAGACCTGCGCGCGCTCCGCG	45292	A A CTCA
		TG CGGAGCGC CGCA TCG		
		GC GCCTCGCG GCGT AGC		
		_ C CCAG		
GAM2520	BRCA1 3'	TCAAGAACCGGTTTCC	14171	AGACGT C
		GGAAATCGG TTCT GA		
		CCTTTGGCC AAGA CT		
		_ A		
GAM2520	BRCA1 3'	TCAAGAACCGGTTTCC	14177	AGACGT C
		GGAAATCGG TTCT GA		
		CCTTTGGCC AAGA CT		
		_ A		
GAM2520	BRCA1 3'	TCAAGAACCGGTTTCC	14184	AGACGT C
		GGAAATCGG TTCT GA		
		CCTTTGGCC AAGA CT		
		_ A		
GAM2520	BRCA1 3'	TCAAGAACCGGTTTCC	14190	AGACGT C
		GGAAATCGG TTCT GA		

			CCTTTGGCC	AAGA CT		
			_____ A			
GAM2520	BRCA1	3'	TCAAGAACCGGTTTCC	14196	AGACGT	C
			GGAAATCGG	TTCT GA		
			CCTTTGGCC	AAGA CT		
			_____ A			
GAM2520	BRCA1	3'	TCAAGAACCGGTTTCC	14204	AGACGT	C
			GGAAATCGG	TTCT GA		
			CCTTTGGCC	AAGA CT		
			_____ A			
GAM2520	BRCA1	3'	TCAAGAACCGGTTTCC	14210	AGACGT	C
			GGAAATCGG	TTCT GA		
			CCTTTGGCC	AAGA CT		
			_____ A			
GAM2520	BRCA1	3'	TCAAGAACCGGTTTCC	14216	AGACGT	C
			GGAAATCGG	TTCT GA		
			CCTTTGGCC	AAGA CT		
			_____ A			
GAM2520	BRCA1	3'	TCAAGAACCGGTTTCC	14222	AGACGT	C
			GGAAATCGG	TTCT GA		
			CCTTTGGCC	AAGA CT		
			_____ A			
GAM2520	BRCA1	3'	TCAAGAACCGGTTTCC	14165	AGACGT	C
			GGAAATCGG	TTCT GA		
			CCTTTGGCC	AAGA CT		
			_____ A			
GAM2520	FTL	5'	CGACCGCCCTCCGATTTC	5644	A_ TTTC	
			GGAAATCGGAG CG	TCG		
			CCTTTAGCCTC GC	AGC		
			CC C_			
GAM2520	HSPA4	5'	TTTCGAGATCTTCTCCGCCCC	42978	AAAT	CGTT
			GG CGGAGA	TCTCGAAA		
			CC GCCTCT	AGAGCTTT		
			CC_ TCT_			
GAM2520	RFX5	3'	AGAAACACTGATTTTC	6044	AGAC	
			GGAAATCGG	GTTTCT		
			CTTTTAGTC	CAAAGA		
			A_			
GAM2520	RTN3	3'	CGAGATTCAAATCTCCGATTCC	36585	A	CGTT_
			GGAA TCGGAGA	TCTCG		

			CCTT AGCCTCT	AGAGC		
			—	AAACTT		
GAM2520	SLC7A5	3'	TCGAACCCACTCCGGTTCC	9578	A	AC_ TTC
			GGAA TCGGAG	GT TCGA		
			CCTT GGCCTC	CA AGCT		
			—	ACC —		
GAM2520	MAP2K5	5'	CGGGAGACACCTCAGACCCC	8638	AAA G	AC
			GG TC GAG	GTTTCTCG		
			CC AG CTC	CAGAGGGC		
			CC_ A	CA		
GAM2520	LOC132001	5'	TCGATCCAGTCTCCGACTTCC	29030	A	GTTTC
			GGAA TCGGAGAC	TCGA		
			CCTT AGCCTCTG	AGCT		
			C	ACCT_		
GAM2520	LOC138050	5'	TCGAGAAACTGATCGCC	37116	AA	GAGAC
			GG ATCG	GTTTCTCGA		
			CC TAGT	CAAAGAGCT		
			GC	—		
GAM2520	LOC146901	5'	CGTGGTGTCTCTGATCTCC	40762	A	TT T
			GGA ATCGGAGACG	TC CG		
			CCT TAGTCTCTGT	GG GC		
			C	— T		
GAM2520	LOC151516	5'	TTCGAGAGGCCCGTTTTC	39130	T	AGAC
			GGAAA CGG	GTTTCTCGAA		
			CCTTT GCC	CGGAGAGCTT		
			T C_	—		
GAM2520	LOC165741	3'	AGAGGCGTCCCGACTCC	42190	AA	A
			GGA TCGG GACGTTTCT			
			CCT AGCC	CTGCGGAGA		
			C_	—		
GAM2520	LOC222008	3'	CGCGGCCGTCCCGATTTC	45124	A	TT T
			GGAAATCGG GACG	TC CG		
			CCTTTAGCC	CTGC GG GC		
			—	C_ C		
GAM2520	LOC253461	3'	TTTCAAAAAGGTCTCCGACTCC	46074	AA	G CTC
			GGA TCGGAGAC	TTT GAAA		
			CCT AGCCTCTG	AAA CTTT		
			C_	G AA_		
GAM2521	SEC22L1	3'	AAGAAAAGAGATGCCCTGAA	11319	AC	GTGCG
			TTCA GGCATCTC	TCTT		

AAGT CCGTAGAG AGAA
 C_ AAA_
 GAM2521 KIAA0189 3' AAGTCTCGAGATGCCAGTGAA 16315 AC TCGGT
 TTCA GGCATCTCG CTT
 ||| ||||| |||
 AAGT CCGTAGAGC GAA
 GA TCT_
 GAM2521 PRO1598 5' TAAGATGAGAACTAAAATGCCG 20570 CTCGTG_
 TTGAA TTCAACGGCAT CGTCTTA
 ||||| |||||
 AAGTTGCCGTA GTAGAAT
 AAATCAAGA
 GAM2522 CUL4B 3' TGAGCTCAGCTGACAAGCA 9641 C C
 TGCT GTCGGC GAGCTCA
 ||| ||||| |||||
 ACGA CAGTCG CTCGAGT
 A A
 GAM2522 PTPN9 3' TGAAC TCACTGAGCAGC 8711 GTC CC C
 GCTGCTC GG GAG TCA
 ||||| || ||| |||
 CGACGAG TC CTC AGT
 _ A_ A
 GAM2522 SNAP29 3' ATGAACCCGGGATGCAGAGCAG 11184 GT G_ AGC
 CT AGCTGCTC CG CCG TCAT
 ||||| || ||| |||
 TCGACGAG GT GGC AGTA
 AC AG CCA
 GAM2522 LOC254559 5' GAACTCGCCAGCAGCTA 46196 CGTC C C
 TAGCTGCT GGC GAG TC
 ||||| || ||| |||
 ATCGACGA CCG CTC AG
 _ _ A
 GAM2523 PRG2 5' CCCACTGCCCCCAACTACAGC 8593 TCCTCG C
 A TGTTGTAGTTGG AG GGG
 ||||| || |||
 ACGACATCAACC TC CCC
 CCCC_ A
 GAM2524 COL19A1 3' GCTTGGTGGTGAAGCCAC 7597 G
 GTGGCTTCACCA CAGGT
 ||||| |||||
 CACCGAAGTGGT GTTCG
 G
 GAM2524 ENG 3' GGAGCCCAGTGAAGCCTCTGA 5595 T CAGCA
 TCAG GGCTTCAC GGTTC
 ||| ||||| |||||
 AGTC CCGAAGTG CCGAGG
 T AC_
 GAM2524 HMGN2 3' GGACTTTCAGTGATGCCACTG 12041 T CAGC
 A TCAGTGGC TCAC AGGTTC
 ||||| ||| |||||

AGTCACCG AGTG TTCAGG
 T ACCT
 GAM2524 IL1F5 3' GATCTCAGCAAAGCCACTGA 14601 CACCA ____
 TCAGTGGCTT GC AGGTT
 ||||| || ||||
 AGTCACCGAA CG TCTAG
 A____ AC
 GAM2524 IL1F5 3' GATCTCAGCAAAGCCACTGA 14602 CACCA ____
 TCAGTGGCTT GC AGGTT
 ||||| || ||||
 AGTCACCGAA CG TCTAG
 A____ AC
 GAM2524 INPP5D 3' GGAACGGCGTGAAGCCACTGG 40305 CA AG
 TCAGTGGCTTCAC GC GTTCC
 ||||| || ||||
 GGTCACCGAAGTG CG CAAGG
 ____ G____
 GAM2524 ABT1 3' GAATCAGTGTAAGCCACT 15030 _ CAGCA
 AGTGGCTT CAC GGTT
 ||||| || ||||
 TCACCGAA GTG CTAAG
 T A____
 GAM2524 DKFZP434K1421 3' GGAACCTGCTGCGTAAAACCAT 25823 C C _
 GTGG TT AC CAGCAGGTTCC
 ||| || |||||
 TACC AA TG GTCGTCCAAGG
 A A C
 GAM2524 DKFZP761F241 3' GGAACCTGCTGGCACCTCACTG 25477 CTTCA
 G TCAGTGG CCAGCAGGTTCC
 ||||| |||||
 GGTCAC T GGTCGTCCAAGG
 CCAC_
 GAM2524 FLJ12903 3' GAACATGCGAAGCCAC 22980 ACCA G
 GTGGCTTC GCA GTTC
 ||||| || ||||
 CACCGAAG CGT CAAG
 ____ A
 GAM2524 KIAA0430 3' AACCCCCCGAAGCCATTGA 21149 ACCAGCA
 TCAGTGGCTTC GGTT
 ||||| ||||
 AGTTACCGAAG CCAA
 CCCC____
 GAM2524 KIAA0676 3' GAACCTGCTGGTGCAAGCT 17393 _
 GGCTT CACCAGCAGGTTCC
 |||| |||||
 TCGAA GTGGTCGTCCAAG
 C
 GAM2524 KIAA1036 3' TGCAGTGCAGCCACTGA 17132 T CA
 TCAGTGGCT CAC GCA
 ||||| || |||

AGTCACCGA GTG CGT
 C A_
 GAM2524 KIAA1393 3' GGACTTTCCAGTGATGCCACTG 35688 T CAGC
 A TCAGTGGC TCAC AGGTTC
 ||||| ||| |||||
 AGTCACCG AGTG TTCAGG
 T ACCT
 GAM2524 PMS2L3 5' GAACCTGCTAAGGCCAT 35342 CACC
 GTGGCTT AGCAGGTTC
 ||||| |||||
 TACCGGA TCGTCCAAG
 A_
 GAM2524 UST 3' GGAACCTGCCGAGTGAGCACTG 12271 G T CA_
 A TCAGTG CT CAC GCAGGTTCC
 ||||| ||| |||||
 AGTCAC GA GTG CGTCCAAGG
 _ _ AGC
 GAM2524 LOC115343 5' GAACCTGCTAAGGCCAT 35667 CACC
 GTGGCTT AGCAGGTTC
 ||||| |||||
 TACCGGA TCGTCCAAG
 A_
 GAM2524 LOC145268 5' AACTAACTGATGCAGCCACTGA 37811 T C CA
 TCAGTGGCT CA CAG GGTT
 ||||| ||| |||
 AGTCACCGA GT GTC TCAA
 C A AA
 GAM2524 LOC152212 3' GGACTTTCCAGTGATGCCACTG 40308 T CAGC
 A TCAGTGGC TCAC AGGTTC
 ||||| ||| |||||
 AGTCACCG AGTG TTCAGG
 T ACCT
 GAM2524 LOC152267 3' GGACTTTCCAGTGATGCCACTG 30295 T CAGC
 A TCAGTGGC TCAC AGGTTC
 ||||| ||| |||||
 AGTCACCG AGTG TTCAGG
 T ACCT
 GAM2524 LOC158382 3' AATCTAGGTGGAAGCCAC 41963 _ AGC
 GTGGCTTC ACC AGGTT
 ||||| ||| |||||
 CACCGAAG TGG TCTAA
 G A_
 GAM2524 LOC220926 5' GGAACCTGCCTGAAGCCAC 43917 CCA
 GTGGCTTCA GCAGGTTCC
 ||||| |||||
 CACCGAAGT CGTCCAAGG
 C_
 GAM2524 LOC222189 5' GAACCTGCTAAGGCCAT 45188 CACC
 GTGGCTT AGCAGGTTC
 ||||| |||||

TACCGGA TCGTCCAAG
 A____
 GAM2524 LOC90371 3' GGAAGCAGTAGGAAGCCACTGA 31322 ACCA_ AGG
 TCAGTGGCTTC GC TTCC
 ||||| || |||
 AGTCACCGAAG CG AAGG
 GATGA ____
 GAM2525 DAG1 3' CACCTGACCTAGCACACA 10631 C TCGA A
 TGT GTGCTAGGTT AG TG
 || ||||| || ||
 ACA CACGATCCAG TC AC
 _ ____ C
 GAM2525 DGKD 3' ACATCTTCACACGGCACGACA 29876 AG TTC
 TGTCGTGCT GT GAAGATGT
 ||||| || |||||
 ACAGCACGG CA CTTCTACA
 CA ____
 GAM2525 KIAA0746 5' ACATCTTCACACCAGCAGGACA 34413 G A TTC
 TGTC TGCT GGT GAAGATGT
 ||| ||| ||| |||||
 ACAG ACGA CCA CTTCTACA
 G _ CA_
 GAM2526 MLLT2 3' AGGGCAGTCACTGTTGAC 12566 AA CA
 GTCAACAG AC TGTTCT
 ||||| || |||||
 CAGTTGTC TG ACGGGA
 AC ____
 GAM2526 SH3GL1 3' ACAGAGAACATGGTCTCCTG 8959 AA_ C
 CAG ACCATGTTCTC GT
 || ||||| || ||
 GTC TGGTACAAGAG CA
 CTC A
 GAM2526 FLJ13576 5' ACGGAGAAAGTTTACGCCGAC 22860 AACAG CATG
 GTC AAAC TTCTCCGT
 || ||| |||||
 CAG TTTG AAGAGGCA
 CCGCA A____
 GAM2526 FLJ13769 3' GAAAATGTGGTTTCTGCTG 24594 A C
 CA CAGAAACCATGTT TC
 || ||||| || ||
 GT GTCTTTGGTGTAAG
 C A
 GAM2526 PRO2964 3' ACGGAGAAGTGTCTTCT 20629 AC G
 AGAA CAT TTCTCCGT
 ||| || |||||
 TCTT GTG AAGAGGCA
 CT _
 GAM2526 LOC145368 3' AACATAGCTTCTGTTGAC 37825 ACC
 GTCAACAGAA ATGTT
 ||||| |||||

	CAGTTGTCTT TACAA		
	CGA		
GAM2526 LOC150423 3'	AACATAGCTTCTGTTGAC 38966	ACC	
	GTCAACAGAA ATGTT		
	CAGTTGTCTT TACAA		
	CGA		
GAM2526 LOC158055 3'	ACAGCGGCTTCTGTTGGC 39701	A A_	
	GTCAACAGAA CC TGT		
	CGGTTGTCTT GG ACA		
	C CG		
GAM2526 LOC197117 3'	ACAGAGAATGTGTCCTCTGCTG 43191	A AAC C	
GC	GTCA CAGA CATGTTCTC GT		
	CGGT GTCT GTGTAAGAG CA		
	C CCT A		
GAM2526 LOC220164 3'	CGAGAGCCGCTGTTGAC 44108	AAACCAT C	
	GTCAACAG GTTCTC G		
	CAGTTGTC CGAGAG C		
	GC_____ A		
GAM2526 LOC255481 3'	GGAGAAACGATTTCTGTTGAC 45331	CCATG	
	GTCAACAGAAA TTCTCC		
	CAGTTGTCTTT AAGAGG		
	AGCA_		
GAM2527 LZTR1 3'	CGGGAAGAAGCCAGCAA 13638	ATTGATG	
	TTGCTG TTCTTCCCG		
	AACGAC AAGAAGGGC		
	CG_____		
GAM2527 KIAA1643 3'	GTCGGGTTTACCAATCAGC 32241	AT TCTT	
	GCTGATTG GT CCCGAC		
	CGACTAAC CA GGGCTG		
	__ TTT_		
GAM2527 LOC164395 5'	AGAACTAATCATTAGCAA 40144	T _	
	TTGCTGA TGAT GTTCT		
	AACGACT ACTA CAAGA		
	T AT		
GAM2527 LOC255177 3'	AGAAAATTTCAGATCAGCAA 46200	_ TG_	
	TTGCTGAT TGA TTCT		
	AACGACTA ACT AAGA		
	G TAA		
GAM2528 CLCN6 3'	CCTAAACTGACTGGACGGCTG 6960	AATT__	
	CAGCCGTC GTTTAGG		

			GTCGGCAG	CAAATCC	
			GTCAGT		
GAM2528	CLCN6	3'	CCTAAACTGACTGGACGGCTG	22342	AATT__
			CAGCCGTC	GTTTAGG	
			GTCGGCAG	CAAATCC	
			GTCAGT		
GAM2528	CLCN6	3'	CCTAAACTGACTGGACGGCTG	22337	AATT__
			CAGCCGTC	GTTTAGG	
			GTCGGCAG	CAAATCC	
			GTCAGT		
GAM2528	ATP1B4	3'	CCTAGACAACCAAGACCGCT	14322	C AA__
			AGC GTC	TTGTTTAGG	
			TCG CAG	AACAGATCC	
			C AACC		
GAM2528	KIAA0319	3'	CCTAAACAATATCCTGTTG	16761	CCGTCA
			TAACAG	ATTGTTTAGG	
			GTTGTC	TAACAAATCC	
			CTA__		
GAM2528	RAB40A	5'	CCTTTATCCTAACGGCTGTTCA	39930	T CAATT TT
			A AACAGCCGT	GT AGG	
			A TTGTCGGCA	TA TCC	
			C ATCC_	TT	
GAM2528	LOC123264	5'	CTAAGTGACAGCTGTTA	36723	C ATTG
			TAACAGC	GTCA TTTAG	
			ATTGTCG	CAGT GAATC	
			A	_____	
GAM2529	SPAP1	3'	CGACTTGAGTGTAACATA	25048	C GA
			TATGTT	AT TCAAGTCG	
			ATACAA	TG AGTTCAGC	
			A TG		
GAM2530	BCL9	3'	TCTGTCTTTTTTCCCCCT	10525	TGCA
			AGG	AAGAAAGACAGA	
			TCC	TTTTTTCTGTCT	
			CCC_		
GAM2530	CAPN10	3'	TTCTGTCTTCCTTCATT	23359	CA A
			GGTG	AAG AAGACAGAA	
			TTAC	TTC TTCTGTCTT	
			__	C	
GAM2530	CPO	3'	TTGGGATTCTCTGCACTTTTGA	5557	A AGA
			TCAAAGGTGCA	AGAA CAG	

AGTTTTACGT TCTT GTT
 C AGG
 GAM2530 CTF1 3' TTCCGTCTCTCCTTCCGCTTCT 7013 T A_ AA_ A
 TTG CAAAGG GC AAG AGAC GAA
 ||||| || ||| |||||
 GTTTCT CG TTC TCTG CTT
 T CC CTC C
 GAM2530 CTH 5' TTCTGTCTCTCCCAACCCCGGA 7626 AAA GCAAA A
 TC GGT GA AGACAGAA
 || ||| || |||||
 AG CCA CT TCTGTCTT
 GCC ACC_ C
 GAM2530 DIAPH2 3' TTCTGCCCCTTTTATGACACCT 13562 _ AA A_
 TTGA TCAAAGGTG CA GAAAG CAGAA
 ||||| || ||||| |||||
 AGTTCCAC GT TTTTC GTCTT
 A A_ CCC
 GAM2530 DNASE1 5' CTCCATTTGCACCTTTGG 11713 GAA
 TCAAAGGTGCAAA AG
 ||||| ||
 GGTTCCACGTTT TC
 ACC
 GAM2530 FACL5 3' CTGTCTTTCCCATCTTCGA 32107 A CAAA
 TC AAGGTG GAAAGACAG
 || ||||| |||||
 AG TTCTAC CTTTCTGTC
 C C_
 GAM2530 FEN1 3' TTCTGTCTTGTTCAGCCTTGA 10321 A GCAAAGA
 TCAA GGT AAGACAGAA
 ||| ||| |||||
 AGTT CCG TTCTGTCTT
 _ ACTTG_
 GAM2530 FNTB 3' TTCTATCTTTCTTCCACC 7784 CA C
 GGTG AAGAAAGA AGAA
 ||| ||||| |||
 CCAC TTCTTTCT TCTT
 C_ A
 GAM2530 GLRA3 5' TTCTGTCTTTCTGGTTCC 30169 T AA
 GG GC AGAAAGACAGAA
 || || |||||
 CC TG TCTTTCTGTCTT
 T G_
 GAM2530 GSBS 3' TTCTGTCTTTCTGTTCTCAC 43787 CAA_
 GTG AGAAAGACAGAA
 ||| |||||
 CAC TCTTTCTGTCTT
 TCTTG
 GAM2530 HAP1 3' TTCTGCCCTTTCCCACACCTTT 10077 CAAA A_
 G CAAAGGTG GAAAG CAGAA
 ||||| ||||| |||||

			GTTTCCAC	CTTTC	GTCTT		
			ACC_	CC			
GAM2530	HNRPD	3'	CTGAGATTTCTACCACACCTTT	11953		CAA_	GA_
			GA				
			TCAAAGGTG	AGAAA	CAG		
			AGTTTCCAC	TCTTT	GTC		
			ACCA	AGA			
GAM2530	NAB1	3'	TTTTTCTACACCTTTGA	12588		CAA	
			TCAAAGGTG	AGAAAGA			
			AGTTTCCAC	TCTTTT			
			A_				
GAM2530	OTP	3'	CTGTCTTTCTTTCT	25802	TGC		
			AGG	AAAGAAAGACAG			
			TCC	TTTCTTTCTGTC			

GAM2530	P53AIP1	3'	TGTCCTTTGCACCACTGA	22660	AA	AAA	
			TCA	GGTGCAAAG	GACA		
			AGT	CCACGTTTC	CTGT		
			CA	_____			
GAM2530	PIK3R2	3'	TCTGTCTTTCTTGCCCCT	11467	T	A	
			AGG	GC AAGAAAGACAGA			
			TCC	CG TTCTTTCTGTCT			
			C	G			
GAM2530	PPP1R12B	3'	TCTACATTTTCTCTGCACTTT	25798	A	AC_	
			AAGGTGCA	AGAAAG	AGA		
			TTTCACGT	TCTTTT	TCT		
			C	ACA			
GAM2530	RIG	3'	TCTGTCAATCTCTTTGCACCT	13109	AA_		
			AGGTGCAAAGA	GACAGA			
			TCCACGTTTCT	CTGTCT			
			CTAA				
GAM2530	SIX2	3'	TTCTGTCTTTCTCCCTCTCCTT	18851	TGCAA_		
			AAGG	AGAAAGACAGAA			
			TTCC	TCTTTCTGTCTT			
			TCTCCC				
GAM2530	SOX13	3'	TTCTGTCTCTCTCTGTCCT	12246	T	A	A
			AGG	GCA AGA AGACAGAA			
			TCC	TGT TCT TCTGTCTT			
			_	C	C		
GAM2530	TAGLN2	3'	TTCTGTCTCTCCTTCTTCCCC	9621	TGCA	_____	
			T	AGG	AAGAA	AGACAGAA	

			TCC TTCTT TCTGTCTT		
			CCC_ CCTC		
GAM2530	TAP2	3'	TTCTGCCTTCCCCAACACCTTT 6144	CAAAGA	A
	G		CAAAGGTG AAG CAGAA		
			GTTTCCAC TTC GTCTT		
			AACCCC C		
GAM2530	TGFBR3	3'	CTGTCTAATTTGCACCTTTG 9250	GAA	
			CAAAGGTGCAAA AGACAG		
			GTTTCCACGTTT TCTGTC		
			AA_		
GAM2530	WNT1	3'	TCTGCCTCTCTTCTTCCCCTTT 11898	TGCA_	A A
	G		CAAAGG AAGA AG CAGA		
			GTTTCC TTCT TC GTCT		
			CCTTC C C		
GAM2530	ZNF137	3'	TCTGTCTTTCCCTGTGTGTGA 9494	AAG TG	AA
			TCA G CA GAAAGACAGA		
			AGT T GT CTTTCTGTCT		
			G_ GT CC		
GAM2530	ALOXE3	3'	TTGTCCCTAGCACCTTT 22266	AA	AAA
			AAAGGTGC AG GACAGA		
			TTTCCACG TC CTGTTT		
			A_ C_		
GAM2530	C11orf25	3'	TTGTCCCTTTGCACCTTGA 25402	A	AAA
			TCAA GGTGCAAAG GACAG		
			AGTT CCACGTTTC CTGTT		
			_ C_		
GAM2530	DKFZp434K2435	3'	CTGCCCTTCACCTTTGG 25999	CAAAGA	A_
			TCAAAGGTG AAG CAG		
			GGTTTCCAC TTC GTC		
			_____ CC		
GAM2530	DKFZp761D0614	3'	TTCTGTCTCAAAACACTTTGA 42312	_	GCAAAGAA
			TCAAAG GT AGACAGAA		
			AGTTTC CA TCTGTCTT		
			A AAAC_		
GAM2530	DNM1L	3'	TTCTGAGCTTCTTTGCAGCCTT 14318	_	AGA
	TGA		TCAAAGG TGCAAAGAA CAGAA		
			AGTTTCC ACGTTTCTT GTCTT		
			G CGA		
GAM2530	FLJ10482	3'	TTCCATCTTCCTTTGTATACTT 19877	AG	A CA
	G		CAA GTGCAAAG AAGA GAA		

GTT TATGTTTC TTCT CTT
 CA C AC
 GAM2530 FLJ11142 3' TTCTGTCTCCTCATCACCT 20345 CAA AA
 AGGTG AG AGACAGAA
 |||| || |||||
 TCCAC TC TCTGTCTT
 TAC C_
 GAM2530 FLJ11722 3' CTGTCTTTCTGGTTGACCCTT 24520 TG _
 AAGG CAA AGAAAGACAG
 ||| ||| |||||
 TTCC GTT TCTTTCTGTC
 CA GG
 GAM2530 FLJ23322 3' TTCTGTCTCCCTGCCCTCTG 42800 A T AA AA
 CA AGG GCA G AGACAGAA
 || ||| ||| |||||
 GT TCC CGT C TCTGTCTT
 C _ _ CC
 GAM2530 FLJ32356 3' TTCTGTCTCTGGAGACCCTTGA 29494 A GCAA AA
 TCAA GGT AGA GACAGAA
 ||| ||| ||| |||||
 AGTT CCA TCT CTGTCTT
 C GAGG _
 GAM2530 FOXO3A 5' TTCTGTCTTTCTTTATTTTTT 7191 TGCAAA
 GG TCAAAGG GAAAGACAGAA
 ||||| |||||
 GGTTTT CTTTCTGTCTT
 TATTC
 GAM2530 GREB1 3' TCTGTAAATCCACCTTTGA 35854 CAAA AAG
 TCAAAGGTG GA ACAGA
 ||||| || |||||
 AGTTTCCAC CT TGTCT
 _ AAA
 GAM2530 H11 5' TTCTGTCTCTCTGAGCCTCTG 15694 A GCAA A
 CA AGGT AGA AGACAGAA
 || ||| ||| |||||
 GT TCCG TCT TCTGTCTT
 C AG_ C
 GAM2530 HHLA2 3' TTGTAATTCTCCCCACCCTTGA 13940 A CAA AG
 TCAA GGTG AGAA ACAG
 ||| ||| ||| |||
 AGTT CCAC TCTT TGTT
 C CCC AA
 GAM2530 HSGP25L2G 3' TTCTGTCTTCCTTTGCTAACTT 31136 GT_ A
 AAG GCAAAG AAGACAGAA
 || |||| |||||
 TTC CGTTTC TTCTGTCTT
 AAT C
 GAM2530 KCNS1 3' TCCATCTTTCTTCTGCCCT 8046 T _ CA
 AGG GCA AAGAAAGA GA
 ||| ||| ||||| ||

TCC CGT TTCTTTCT CT
 _ C AC
 GAM2530 KIAA0747 3' TCTGTCTTCCTGCCTT 17613 GCAA A
 AAGGT AG AAGACAGA
 |||| |||||||
 TTCCG TC TTCTGTCT
 ____ C
 GAM2530 KIAA1190 3' TCTTCCTTGCACTCCTTGA 35225 A_ A A
 TCAA GGTGCAA GAA GA
 ||| ||||| ||| ||
 AGTT TCACGTT CTT CT
 CC C _
 GAM2530 KIAA1456 3' TCTGTCTTTTAAGTGACC 33265 G AA_
 GGT CA GAAAGACAGA
 ||| || |||||||
 CCA GT TTTTCTGTCT
 _ GAA
 GAM2530 KIAA1813 5' CTGTCTTTCTCTGAGCCT 34812 G A
 AAGT CA AGAAAGACAG
 ||| || |||||||
 TCCG GT TCTTTCTGTC
 A C
 GAM2530 MGC20255 3' TTCTGTCTCTCTCCCTACC 27431 CAA A
 GGTG AGA AGACAGAA
 ||| || |||||||
 CCA TCT TCTGTCTT
 CCC C
 GAM2530 MGC20255 3' TCTGTCTTTCTTGGTGTCT 27430 TG A
 AGG C AAGAAAGACAGA
 ||| | |||||||
 TCT G TTCTTTCTGTCT
 GT G
 GAM2530 MGC27044 3' CTGTCTTTCCCTTCTGA 29587 A TGCAAA
 TCA AGG GAAAGACAG
 ||| || |||||||
 AGT TTC CTTTCTGTC
 C _____
 GAM2530 MGC5590 5' TCTGCCTTCCTTCTGCTTTTG 23496 T _ A A
 G TCAAAGG GCA AAG AAG CAGA
 ||||| ||| ||| ||| |||
 GGTTTTT CGT TTC TTC GTCT
 _ C C C
 GAM2530 NK4 5' TCTGTCTCTCTCGGGCCTT 10418 GCAA A
 AAGGT AGA AGACAGA
 |||| ||| |||||||
 TTCCG TCT TCTGTCT
 GGC_ C
 GAM2530 PB1 3' CTGTCTTTCTTATATGACCCT 19979 TG ____
 AGG CA AAGAAAGACAG
 ||| || |||||||

TCC GT TTCTTTCTGTC
 CA ATA
 GAM2530 PP3501 3' TTCTGTCTCCCCCTGCCCTTC 22334 A T AAGAA
 GA TC AAGG GCA AGACAGAA
 || ||| ||| |||||
 AG TTCC CGT TCTGTCTT
 C C CCCCC
 GAM2530 PRO0659 3' CTGTGCTTTTGCACCATTTGA 15406 A GAA _
 TCAA GGTGCAAA AG ACAG
 ||| ||||| || |||
 AGTT CCACGTTT TC TGTC
 A _ G
 GAM2530 R3HDM 3' CTGCCCTCTCCCATCTTTGA 17661 CAA AAGA
 TCAAAGGTG AGA CAG
 ||||| ||| |||
 AGTTTCTAC TCT GTC
 CC_ CCC_
 GAM2530 RBT1 3' TCTGCCTCTTGCACCTTGA 15013 A A AA A
 TCAA GGTGCAA GA G CAGA
 ||| ||||| || | |||
 AGTT CCACGTT CT C GTCT
 _ _ _ C
 GAM2530 RoXaN 3' CTGCCTTTCTCTGTCTTTT 24604 T A A
 AAAGG GCA AGAAAG CAG
 |||| ||| ||||| |||
 TTTTC TGT TCTTTC GTC
 _ C C
 GAM2530 U5-100K 3' TTCTGCCCTTCTTTGCTTTGG 30012 GGT AGA
 TCAAA GCAAAGAA CAGAA
 |||| ||||| |||||
 GGTTT CGTTTCTT GTCTT
 _ CCC
 GAM2530 ZAK 3' CTGTCTTTCCAGCATGCCCT 28607 T AA_
 AGG GCA GAAAGACAG
 ||| ||| |||||
 TCC CGT CTTTCTGTC
 _ ACGAC
 GAM2530 ZER6 3' TCTAGTTTGCACCTTGA 31745 A GAA
 TCAA GGTGCAAA AGA
 ||| ||||| |||
 AGTT CCACGTTT TCT
 _ GA_
 GAM2530 LOC138389 5' TCTGTCCCTTGCTCTCCTT 37508 T_ A AAA
 AAGG GCAA G GACAGA
 ||| ||| | |||||
 TTCC CGTT C CTGTCT
 TCT _ C_
 GAM2530 LOC145900 5' TCTGTCTTCCTCTTCCTAC 38014 CA _
 GTG AAGA AAGACAGA
 ||| ||| |||||

	CAT TTCT TTCTGTCT	
	CC CC	
GAM2530 LOC148137 3'	TTCTGTCTTTCCCTTCCACC 29520	C A_
	GGTG AA GAAAGACAGAA	
	CCAC TT CTTTCTGTCTT	
	C CC	
GAM2530 LOC148508 3'	TCTGTCTTTCCCATGAGCCT 40885	G AA_
	AGGT CA GAAAGACAGA	
	TCCG GT CTTTCTGTCT	
	A ACC	
GAM2530 LOC148534 3'	TTCTGCCTTTCTTTTGCCTT 38551	C A
	AAGGTG AAAGAAAG CAGAA	
	TTCCGT TTTCTTTC GTCTT	
	- C	
GAM2530 LOC148930 3'	TCTGTCTTGCCACCTTT 38620	CAAAGA
	AAAGGTG AAGACAGA	
	TTCCAC TTCTGTCT	
	CG__	
GAM2530 LOC149721 3'	TCTGTCCACGTGCACCTTT 38814	AAGAAA
	AAAGGTGCA GACAGA	
	TTCCACGT CTGTCT	
	GCAC__	
GAM2530 LOC150157 3'	CTGCTCCCTTCACCTTTGA 41143	CA AA A
	TCAAAGGTG AAG AG CAG	
	AGTTCCAC TTC TC GTC	
	- CC -	
GAM2530 LOC152972 5'	TCTGTCTTTCTTTATACC 39346	C
	GGTG AAAGAAAGACAGA	
	CCAT TTTCTTTCTGTCT	
	A	
GAM2530 LOC196890 3'	CTGCTCCCTTCACCTTTGA 43155	CA AA A
	TCAAAGGTG AAG AG CAG	
	AGTTCCAC TTC TC GTC	
	- CC -	
GAM2530 LOC200014 3'	TCTTGTGCTTTGCACCCCTG 42696	AA A__
	CA GGTGCAAAG AAGA	
	GT CCACGTTTC TTCT	
	CC GTG	
GAM2530 LOC200853 3'	TCTGCCCTTCTTTTGCA 42869	- A_
	TGCAAAGA AAG CAGA	

ACGTTTTT TTC GTCT
 C CC
 GAM2530 LOC253805 3' TTCTGTCTCCCATGTCCCTGCG 46139 AA TG AAGAA
 A TC AGG CA AGACAGAA
 || ||| || |||||
 AG TCC GT TCTGTCTT
 CG CT ACCC_
 GAM2530 LOC90593 3' TCTGCCTCACACCTTTGA 31767 CAAAGAA A
 TCAAAGGTG AG CAGA
 ||||| || |||
 AGTTTCCAC TC GTCT
 AC____ C
 GAM2530 LOC91516 5' TCTGCCTTTCTTTATGCCCTTG 32957 A GC A
 G TCAA GGT AAAGAAAG CAGA
 ||| ||| ||||| |||
 GGTT CCG TTTCTTTC GTCT
 C TA C
 GAM2530 LOC92539 5' TTCTACCTTCCTTGTGCCTT 34506 TG A A AC
 AAGG CAA GAA G AGAA
 ||| ||| ||| |||
 TTCC GTT CTT C TCTT
 GT C _CA
 GAM2531 DGAT2 3' ATCTGGGTGGCTCAGCTAACCT 26288 TCC ATG TT
 CT AGAGGTTA GA G TAGAT
 ||||| || | |||||
 TCTCCAAT CT T GTCTA
 CGA CGG GG
 GAM2531 HLA-DQA1 3' CTAATTCCTCAGTAACCTC 46725 CC AT T_
 GAGGTTAT GA GG TTAG
 ||||| || || |||
 CTCCAATG CT CC AATC
 A_ __ TT
 GAM2531 FLJ00001 3' TCTTCACTCGGATACCTCT 39788 T A TTT
 AGAGGT ATCCGA TGG AGA
 ||||| ||||| ||| |||
 TCTCCA TAGGCT ACT TCT
 _ C _
 GAM2531 LOC255042 3' AGGCCACTCAGATAACCTT 45647 C A
 GAGGTTATC GA TGGTTT
 ||||| || |||||
 TTCCAATAG CT ACCGGA
 A C
 GAM2532 BRAG 3' CACTCTTGTTGCGATCG 16939 AATTG
 TGATCG GCAAGAGTG
 ||||| |||||
 GCTAGC TGTTCTCAC
 GT____
 GAM2533 CRACC 3' AGTGTCTGGAGTTTCATTCCA 22153 CA G A T
 TGGAA AAA TCCA AT CT
 |||| ||| ||| ||| ||

			ACCTT TTT AGGT TG GA		
			AC G C T		
GAM2533	ITPR3	3'	CTAGAGACCTTTGTTCC 7997	A	CAAAT
			GGAACAAA GTC TCTAG		
			CCTTGTTT CAG AGATC		
			C _____		
GAM2533	LAMC1	3'	TCTAGAATGACACTCTGTTT 8079	AA	CCAA
			GAACA AGT ATTCTAGA		
			CTTGT TCA TAAGATCT		
			C_ CAG_		
GAM2533	LFG	3'	ATTTGAAGTTTTGTTCCA 37688	GTC	
			TGGAACAAAA CAAAT		
			ACCTTGTTTT GTTTA		
			GAA		
GAM2533	PTPRN	3'	TCTAGAAAAAACTACTTTTGTA 8734	A	CCAAA_
	CCA		TGG ACAAAGT TTCTAGA		
			ACC TGTTTTCA AAGATCT		
			A TCAAAA		
GAM2533	RBBP9	3'	AATTTGGATTTTGTTC 34741	G	
			TGGAACAAAA TCCAAATT		
			ACCTTGTTTT AGGTTTAA		
			—		
GAM2533	TBL1X	3'	CTAGAATCTTCTTTGTTT 12182	A	TCCAA
			GAACAAA G ATTCTAG		
			CTTGTTT C TAAGATC		
			TTC		
GAM2533	TERF1	3'	AATTTGACTTTTGTTC 18951	C	
			TGGAACAAAAGTC AAATT		
			ACCTTGTTTT CAG TTAA		
			—		
GAM2533	TRPS1	3'	TCTAGAATTTGAAAGGGTTT 15360	AAAAGTC	
			GAAC CAAATTCTAGA		
			TTTG GTTTAAGATCT		
			GGAAA_		
GAM2533	WBSCR1	3'	TCTAGAATCTGGCACTTT 22724	_	A
			AAAGT CCA ATTCTAGA		
			TTTCA GGT TAAGATCT		
			C C		
GAM2533	WBSCR1	3'	TCTAGAATCTGGCACTTT 25707	_	A
			AAAGT CCA ATTCTAGA		

			TTTCA GGT TAAGATCT		
			C C		
GAM2533	ASAH	3'	TCTAGAATTCAGTGGTTCCT 10519	G	CA__
			TTCA TGGAAACAAA TC AATTCTAGA		
			ACTTTGTTTT AG TTAAGATCT		
			G TCAC		
GAM2533	CKAP2	3'	TCTAGAGAGTAGGACTTTTATT 20089	C	AAA_
			CC GGAA AAAAGTCC TTCTAGA		
			CCTT TTTTCAGG GAGATCT		
			A ATGA		
GAM2533	DIO2	3'	GAATCTGGACATTTGTTCCA 15169	A	A
			TGGAACAAA GTCCA ATTC		
			ACCTTGTTT CAGGT TAAG		
			A C		
GAM2533	DIO2	3'	GAATCTGGACATTTGTTCCA 6458	A	A
			TGGAACAAA GTCCA ATTC		
			ACCTTGTTT CAGGT TAAG		
			A C		
GAM2533	FLJ10450	3'	TCTAGAATTCAGGATGTTCC 19864	AAAG	A_
			GGAACA TCC AATTCTAGA		
			CCTTGT AGG TTAAGATCT		
			___ AC		
GAM2533	FLJ10702	3'	CTAGAATTATTGTCCGTTCC 20026	AAA_	CCA
			GGAAC AGT AATTCTAG		
			CCTTG TTA TTAAGATC		
			CCTG ___		
GAM2533	FLJ11117	3'	CTGGTATCTGACTTTTGCTCCA 20326	A	CAAATT
			TGGA CAAAAGTC CTAG		
			ACCT GTTTTCAG GGTC		
			C TCTAT_		
GAM2533	KIAA0295	3'	CTAGAATGCTCTGATCCA 33781	A AA	CCAA
			TGGA CA AGT ATTCTAG		
			ACCT GT TCG TAAGATC		
			A C_ ___		
GAM2533	KIAA0836	3'	TCTAGAATTTTGTTATTTTATT 32249	C	GTCC
			CA TGGAA AAAA AAATTCTAGA		
			ACTTT TTTT TTTAAGATCT		
			A ATGT		
GAM2533	LRRFIP2	3'	CTAGAGGGGACTGACTTTTGTTCC 19314	A	CAAA_
			A TGGA CAAAAGTC TTCTAG		

			ACCT GTTTTCAG	GAGATC		
			— TCAGG			
GAM2533	PGS1	5'	TCCAGAAATTTGGAGTCTCCA	23658	— AAAAG	A
			TGGA AC TCCAAATTCT GA			
			ACCT TG AGGTTTAAGA CT			
			C ——— C			
GAM2533	STMN3	3'	TCTAGATGCAACTTTTGTTC	18040		CCAAAT
			GGAACAAAAGT TCTAGA			
			CCTTGTTTTCA AGATCT			
			ACGT—			
GAM2533	TACTILE	3'	TCTGTGTGGACTTTAGTCCCA	12415	A A	AATTC
			TGG AC AAAGTCCA TAGA			
			ACC TG TTTCAGGT GTCT			
			C A GT—			
GAM2533	TCL6	5'	TCTGGAATCTGGATTTTATTCC	21777	CA	A
	A		TGGAA AAAGTCCA ATTCTAGA			
			ACCTT TTTTAGGT TAAGGTCT			
			A_ C			
GAM2533	TCL6	5'	TCTGGAATCTGGATTTTATTCC	21779	CA	A
	A		TGGAA AAAGTCCA ATTCTAGA			
			ACCTT TTTTAGGT TAAGGTCT			
			A_ C			
GAM2533	TUSP	5'	CTAAAATTTGGACTCTTGTCT	21527	A A	C
			GGA CAA AGTCCAAATT TAG			
			TCT GTT TCAGGTTTAA ATC			
			— C A			
GAM2533	LOC152620	3'	AATTTGACTTTTGTTC	30171		C
			TGGAACAAAAGTC AAATT			
			ACCTTGTTTTTCAG TTAA			
			—			
GAM2533	LOC158668	3'	AATTTGACTTTTGTTC	34376		C
			TGGAACAAAAGTC AAATT			
			ACCTTGTTTTTCAG TTAA			
			—			
GAM2534	B3GALT3	3'	AAAGAAATTAATAGGACCA	9866		GAGGA
			TGGTCC GATTTCTTT			
			ACCAGG TTAAAGAAA			
			ATAA_			
GAM2534	B3GALT3	3'	AAAGAAATTAATAGGACCA	27015		GAGGA
			TGGTCC GATTTCTTT			

ACCAGG TTAAAGAAA
 ATAA_
 GAM2534 B3GALT3 3' AAAGAAATTAATAGGACCA 27018 GAGGA
 TGGTCC GATTTCTTT
 ||||| |||||
 ACCAGG TTAAAGAAA
 ATAA_
 GAM2534 C1orf1 3' AAGAAACCTAGACCAGAGA 6872 A CG AGA
 TC CTGGTC AGG TTTCTT
 || ||||| || |||||
 AG GACCAG TCC AAAGAA
 A A_ ____
 GAM2534 FGF1 3' AAAGAAATCCCCCCTTCAGAAC 26988 G C A____
 AG CTG TC GAGG GATTTCTTT
 ||| || ||||| |||||
 GAC AG CTTC CTAAAGAAA
 A A CCCC
 GAM2534 FGF1 3' AAAGAAATCCCCCCTTCAGAAC 26986 G C A____
 AG CTG TC GAGG GATTTCTTT
 ||| || ||||| |||||
 GAC AG CTTC CTAAAGAAA
 A A CCCC
 GAM2534 FGF1 3' AAAGAAATCCCCCCTTCAGAAC 6469 G C A____
 AG CTG TC GAGG GATTTCTTT
 ||| || ||||| |||||
 GAC AG CTTC CTAAAGAAA
 A A CCCC
 GAM2534 AP1GBP1 3' AAAGACACGATTCCTCAGACCA 14114 C ATT____
 GTGA TCACTGGTC GAGGAG TCTTT
 ||||| ||||| |||||
 AGTGACCAG CTCCTT AGAAA
 A AGCAC
 GAM2534 AP1GBP1 3' AAAGACACGATTCCTCAGACCA 27869 C ATT____
 GTGA TCACTGGTC GAGGAG TCTTT
 ||||| ||||| |||||
 AGTGACCAG CTCCTT AGAAA
 A AGCAC
 GAM2534 AP1GBP1 3' AAAGACACGATTCCTCAGACCA 27875 C ATT____
 GTGA TCACTGGTC GAGGAG TCTTT
 ||||| ||||| |||||
 AGTGACCAG CTCCTT AGAAA
 A AGCAC
 GAM2534 FLJ14107 3' AGATTTCTTTAACTCTCGGACC 24616 _____ ATTT
 AGTGA CTGGTCCGAG GAG CT
 ||||| ||| ||
 GACCAGGCTC TTC GA
 TCAAIIT TTTA
 GAM2534 KIAA0843 3' AGTCTCCCCAAATCAGTGA 17259 CCGA
 TCACTGGT GGAGATT
 ||||| |||||

AGTGA CTA CCTCTGA
 AACC
 GAM2534 KIAA1260 3' AAAGAAAGTCTCCAGACCAGGA 30155 A CGA _
 TC CTGGTC GGAGATTT CTTT
 || ||||| ||||| |||||
 AG GACCAG CCTCTGAA GAAA
 _ A_ A
 GAM2534 STIM2 3' AAATCTCTGCAAGTGA 21913 G CCGA
 TCACT GT GGAGATTT
 ||||| || |||||
 AGTGA CG TCTCTAAA
 A _
 GAM2534 LOC130752 3' AAATTGAACTGAGACCAGTGA 37005 CG GA_
 TCACTGGTC AG GATTT
 ||||| || |||||
 AGTGACCAG TC TTAAG
 AG AAG
 GAM2534 LOC157869 3' AAAGAAATGTTGACACCAGTGA 39674 CCGAG G
 TCACTGGT GA ATTTCTTT
 ||||| || |||||
 AGTGACCA TT TAAAGAAA
 CAG_ G
 GAM2535 CASP10 3' TATTGCCTCTTTCACATTG 26833 _ A
 CAATG GAAA AGGCAATA
 ||||| ||||| |||||
 GTTAC CTTT TCCGTTAT
 A C
 GAM2535 CASP10 3' TATTGCCTCTTTCACATTG 26836 _ A
 CAATG GAAA AGGCAATA
 ||||| ||||| |||||
 GTTAC CTTT TCCGTTAT
 A C
 GAM2535 FBLN5 5' ATTCCTCCTCCAATTGGTTTAA 13022 _ AAA C
 TTAAACCAAT GGA AGG AAT
 ||||| ||||| |||||
 AATTTGGTTA CCT TCC TTA
 A CC_ _
 GAM2535 CPEB1 3' TGCCTTTCCATTATTTAA 24959 CC AA
 TTAAA AATGGAA AGGCA
 ||||| ||||| |||||
 AATTT TTACCTT TCCGT
 AT _
 GAM2535 FAM8A1 3' TTGCTCCCACTGGTTTAA 18384 A AAAAA
 TTAAACCA TGG GGCAA
 ||||| ||||| |||||
 AATTTGGT ACC TCGTT
 C C_
 GAM2535 FLJ20280 5' TATTACCTTTTCTGGTT 19332 ATG C
 AACCA GAAAAAGG AATA
 ||||| ||||| |||||

			TTGGT CTTTTTCC TTAT		
			— A		
GAM2535	KIAA0350	3'	CTTTTTCCATTATTTAA 30668	CC	
			TTAAA AATGGAAAAAG		
			AATTT TTACCTTTTTC		
			AT		
GAM2535	KIAA0469	3'	TATTGCCTTTTCTAGTG 16895	A A	
			CA TGGAAAA GGCAATA		
			GT ATCTTTT CCGTTAT		
			G —		
GAM2535	KIAA1117	3'	ATTTTTTTTTTCCATTGGTTT 30633		C
			AAACCAATGGAAAAAGG AAT		
			TTTGGTTACCTTTTTTT TTA		
			T		
GAM2535	KIAA1128	3'	TATTGTTTTTCCCATTG 33972	AA	
			CAATGG AAAGGCAATA		
			GTTACC TTTTGTTAT		
			C_		
GAM2535	MACF1	3'	CTTTTTCCATTGTTTAA 14378		C
			TTAAAC AATGGAAAAAG		
			AATTTG TTACCTTTTTC		
			—		
GAM2535	LOC157273	3'	CTTTTTCCATTGGTCTAA 41784	A	
			TTA ACCAATGGAAAAAG		
			AAT TGGTTACCTTTTTC		
			C		
GAM2535	LOC202020	3'	TATTGCCTTTGCCTTTG 42955	T AA	
			CAA GG AAAGGCAATA		
			GTT CC TTTCCGTTAT		
			T G_		
GAM2535	LOC253250	3'	TCTAAATTCATTGGTTTAA 45427		AAA
			TTAAACCAATGGA AGG		
			AATTTGGTTACTT TCT		
			AAA		
GAM2535	LOC257106	3'	TGCCTTGGTTGGTTTA 45680	G AAAA	
			TAAACCAAT G AGGCA		
			ATTTGGTTG T TCCGT		
			G —		
GAM2535	LOC257463	3'	TATTTCTTTTCTTCCATTG 35211	— C	
			CAATGGAA AAAGG AATA		

			GTTACCTT TTTTC TTAT		
			C T		
GAM2535	LOC57826	3'	ATTGCCTTCCATGTTGTTTA 22160	CA_	AAA
			TAAAC ATGGA AGGCAAT		
			ATTTG TACCT TCCGTTA		
			TTG _		
GAM2536	GALNT1	3'	TATTATTTGGGTATTTGGAGAT 21725	TAAAA_	
	AATA		TATTATCTCCA AAATAATA		
			ATAATAGAGGT TTTATTAT		
			TTATGGG		
GAM2536	FLJ12787	3'	TATTATTTTTTTATAAAGAGA 25890	C_	
			TCTC ATAAAAAATAATA		
			AGAG TATTTTTTTATTAT		
			AAA		
GAM2536	SV2B	3'	ATTATTCCTTAATGGGATAATA 16880	T A A	
			TATTATC CCAT AAA AATAAT		
			ATAATAG GGTA TTT TTATTA		
			_ A C		
GAM2536	TA-PP2C	3'	TATTTTTTTATGGAAATAATA 29284	C	
			TATTAT TCCATAAAAAAATA		
			ATAATA AGGTATTTTTTTAT		
			A		
GAM2537	AGRN	3'	CTTCCCCACCCCCATCCCA 38535	AAA AATT T	
			TGG GA GG TGGGGAAG		
			ACC CT CC ACCCCTTC		
			_ ACC_ C		
GAM2537	ANK1	3'	CCCTCCCCAACCCACATACCTC 30281	AAGAAATT	A
	CA		TGGA GGTTGGGGA GG		
			ACCT CCAACCCCT CC		
			CCATACAC C		
GAM2537	ANK1	3'	CCCTCCCCAACCCACATACCTC 5477	AAGAAATT	A
	CA		TGGA GGTTGGGGA GG		
			ACCT CCAACCCCT CC		
			CCATACAC C		
GAM2537	ANK1	3'	CCCTCCCCAACCCACATACCTC 21730	AAGAAATT	A
	CA		TGGA GGTTGGGGA GG		
			ACCT CCAACCCCT CC		
			CCATACAC C		
GAM2537	ANXA8	3'	CTCTTCCCAACTTCCTCCA 7340	AA AATT	_
			TGGA GA GGTTGGGGA AG		

ACCT CT TCAACCCTT TC
 C_ _ _ C
 GAM2537 AR 5' CCTCCCCCGTCTTCTCTCC 5486 A AATT T A
 GGA AGA GG TGGGG AGG
 ||| ||| || ||||| |||
 CCT TCT TC GCCCC TCC
 C _ _ T C
 GAM2537 ATP1B2 3' CCCACCAACTTCTCCCA 7390 AA A T
 TGG AGAA TTGGT GGG
 ||| |||| ||||| |||
 ACC TCTT AACCA CCC
 C_ C _
 GAM2537 ATP1B2 3' CCTTCCCCCATTGCGCTTCCCA 7391 A AAATT T
 TGG AAG GGT GGGGAAGG
 ||| ||| ||| ||||| |||
 ACC TTC TTA CCCCTTCC
 C CGC_ C
 GAM2537 BAZ2A 3' CCTTCCCCACCTCCTTCCCA 15118 A AAATT T
 TGG AAG GGT GGGGAAGG
 ||| ||| ||| ||||| |||
 ACC TTC CCA CCCCTTCC
 C CT_ _
 GAM2537 BCL11B 3' CCTTCCCCTGCGTTTCCTCTCC 23160 AA_ TG T
 A TGGG A GAAAT GT GGGGAAGG
 |||| |||| || ||||| |||
 ACCT CTTTG CG CCCCTTCC
 CTC _ T
 GAM2537 BCL6 5' CCTTCCCCACTTCCTTCCCTCC 29056 AA ATT T
 A TGGG A GAA GGT GGGGAAGG
 |||| ||| ||| ||||| |||
 ACCT CTT TCA CCCCTTCC
 CC CCT _
 GAM2537 BCR 5' CCTCCCCCGGCCCTCCCTTCC 22237 A_ AATT A_
 GGAA GA GGTTGGGG AGG
 |||| || ||||| |||
 CCTT CT CCGGCCCC TCC
 CC C_ CC
 GAM2537 BTG2 3' CTTCCCAGACCTGCTTCCA 13626 A AAATT G
 TGGAA G GGTT GGGGAAG
 ||||| | ||| |||||
 ACCTT C CCAG CCCTTC
 GT A
 GAM2537 C5R1 3' CCCCCCCCACACACCATCTTTC 7474 AAT _ AA
 CA TGGAAAGA TGGT TGGGG GG
 ||||| ||| |||| |||
 ACCTTTCT ACCA ACCCC CC
 _ CAC CC
 GAM2537 CD8A 3' CCTTCCCTTTTCATTTTTTCCA 7529 AT TT
 TGGAAAGAA TGG GGGGAAGG
 ||||| ||| ||||| |||

ACCTTTTTT ACT TCCCTTCC
 _ T_
 GAM2537 CDKN1A 3' CCTCCCCCTTGTCTTTCC 27780 AAATT TT A
 GGAAAG GG GGGGA GG
 ||||| || |||||
 CCTTTC TC CCCCT CC
 CTGT_ _ _
 GAM2537 CLOCK 3' CCTCCCCCAACCCCTCTCC 11333 A AAATT A
 GGA AG GGTGGGG AGG
 ||| || ||||| |||
 CCT TC CCAACCCC TCC
 C C_ C
 GAM2537 CORO2B 3' CCTTCCCACATGATTCTCTACA 32255 GAA ATTGGT
 TG AGAA TGGGGAAGG
 || ||| |||||
 AC TCTT ACCCCTTCC
 ATC AGT_
 GAM2537 CRHR2 3' CCCTCCCCAGCCATCCTCCCC 7611 AA AAAT A
 GG AG TGGTTGGGGA GG
 || || ||||| ||
 CC TC ACCGACCCCT CC
 CC CT_ C
 GAM2537 CSK 5' CCTTCCCCCGCCTTTCTTCCC 10608 A TT T
 GG AAGAAA GGT GGGGAAGG
 || ||||| || |||||
 CC TTCTTT CCG CCCCTTCC
 C _ C
 GAM2537 DBN1 3' CTCCCCAACTCCTTCC 10639 A AATTG A
 GGAA GA GTTGGGGA G
 |||| || ||||| |
 CCTT CT CAACCCCT C
 C _ C
 GAM2537 DBN1 3' CTCCCCAACTCCTTCC 28122 A AATTG A
 GGAA GA GTTGGGGA G
 |||| || ||||| |
 CCTT CT CAACCCCT C
 C _ C
 GAM2537 DDX11 3' CTTCCCCTCCTCCTTCC 24984 A AATT TT
 GGAA GA GG GGGGAAG
 |||| || || |||||
 CCTT CT CC CCCCTTC
 C _ T_
 GAM2537 DDX11 3' CTTCCCCTCCTCCTTCC 10652 A AATT TT
 GGAA GA GG GGGGAAG
 |||| || || |||||
 CCTT CT CC CCCCTTC
 C _ T_
 GAM2537 DIAPH2 3' CTTTCCACTCTCTTTCCA 13561 AATT TG
 TGGAAAGA GGT GGGAAG
 ||||| || |||||

ACCTTTCT TCA CCTTTC
 C___ __
 GAM2537 DIRC1 3' CCTCCCCTCTTGCACTTTCTCT 27507 A T GTT__ A
 CCA TGGA AGAAA TG GGGGA GG
 |||| |||| || |||| ||
 ACCT TCTTT AC CCCCT CC
 C C GTTCT _
 GAM2537 DMRT2 3' CTTCCCTCTACCTCCCCCA 13323 AAA AATT T_
 TGG GA GGT GGGGAAG
 ||| || ||| |||||
 ACC CT CCA TCCCTTC
 CC_ ____ TC
 GAM2537 DUSP4 5' CTCCCCAACCTCCTCCA 27667 AA AATT A
 TGGA GA GGTTGGGGA G
 |||| || ||||| |
 ACCT CT CCAACCCCT C
 C_ ____ C
 GAM2537 ELK1 3' CCTCCCCAACCTTTCTCTC 11732 A TT A
 GA AGAAA GGTTGGGG AGG
 || |||| ||||| |||
 CT TCTTT CCAACCCC TCC
 C _ C
 GAM2537 ESRRG 3' CTTCCCCCTTTCTTTCC 32998 AAATT TT
 GGAAAG GG GGGGAAG
 ||||| || |||||
 CCTTTC TC CCCCTTC
 CTT__ __
 GAM2537 FGF12 3' CTTTCCCCTTCCCTTCCTTCC 22019 A ATT TT
 GGAA GAA GG GGGGAAGG
 |||| ||| || |||||
 CCTT CTT CC CCCCTTCC
 C C_ TT
 GAM2537 FXYD6 3' CCTTCGGTGGTTAATTTCTTCC 22550 A TT G
 CA TGG AAGAAATTGG G GGAAGG
 ||| ||||| ||| |||||
 ACC TTCTTTAATT T CCTTCC
 C GG G
 GAM2537 GABRE 5' CCTTCCCTTCATCCCCTTCC 22529 AGAAAT TT
 GGAA TGG GGGGAAGG
 |||| ||| |||||
 CCTT ACT TCCCTTCC
 CCCCT_ __
 GAM2537 GALNS 3' CTCCCCCAACCCTGCCCA 6124 AA AAATT A
 TGG AG GGTTGGGG AG
 ||| || ||||| ||
 ACC TC CCAACCCC TC
 CG ____ C
 GAM2537 GLP1R 3' CCCTCCCCAAAACCTTTCC 7822 AAATTGG A
 GGAAAG TTGGGGA GG
 ||||| ||||| ||

CCTTTC AACCCCT CC
 CAA_____ C
 GAM2537 GLP1R 3' CCCTCCCCTGTCTTCTCTC 7823 A ATT TT A
 GA AGAA GG GGGGA GG
 || ||| || ||||| ||
 CT TCTT CT CCCCT CC
 C _ GT C
 GAM2537 GLTSCR1 3' CCTTCCCCGTCCCCTCCTCC 17927 AA AATT T
 GGA GA GG TGGGGAAGG
 ||| || || ||||| |||
 CCT CT CC GCCCCTTCC
 C_ CC_ T
 GAM2537 GPR45 5' CCTTCCCGGCCATTTCTGTCC 14094 A T G
 GGA AGAAAT GGTGGAAGG
 ||| ||||| ||||| |||
 CCT TCTTTA CCGGCCC TTCC
 G _ _
 GAM2537 HDGF 3' CCTTCCCCATCGTTGCCCCCA 10832 AAAGAAAT T
 TGG TGGT GGGGAAGG
 ||| ||| ||||| |||
 ACC GCTA CCCCTTCC
 CCCGTT_ _
 GAM2537 HPCAL1 3' CCCCGTTCAATTTCTCCA 7927 AA T GT
 TGGA GAAA TG TGGGG
 ||| ||| || |||
 ACCT CTTT AC GCCCC
 _ T TT
 GAM2537 HPCAL1 5' CTTCTGCAGCCCCTCCCCA 28635 AA AAATT G
 TGG AG GGTG GGAAG
 ||| || |||| |||||
 ACC TC CCGAC TCTTC
 CC C_ G
 GAM2537 HPCAL1 3' CCCCGTTCAATTTCTCCA 28634 AA T GT
 TGGA GAAA TG TGGGG
 ||| ||| || |||
 ACCT CTTT AC GCCCC
 _ T TT
 GAM2537 IER5 3' CCCTCCCCACCTTTCTCTCC 18612 A TT T A
 GGA AGAAA GGT GGGGA GG
 ||| ||||| ||| ||||| ||
 CCT TCTTT CCA CCCCT CC
 C _ _ C
 GAM2537 IGFBP4 3' CCTTCCCCTACACCTCCCTCC 7275 AA AATTG T
 GGA GA GT GGGGAAGG
 ||| || || ||||| |||
 CCT CT CA CCCCTTCC
 CC CCA_ T
 GAM2537 IL8RA 3' CTCCCCAAATGCTTTCCA 6266 AAATTGG A
 TGGAAG TTGGGGA G
 ||||| ||||| |

ACCTTTC AACCCT C
 GTA_____ C
 GAM2537 KCNE1L 3' CCTTCCACCCCAACTCCCTTC 14614 A_ AA TT _
 CA TGGAA GA TTGG GG GGAAGG
 |||| | ||| | |||||
 ACCTT CT AACC CC CCTTCC
 CC C_ C_ A
 GAM2537 KCNK4 3' CTTCCCTCACTTCCATCCA 18716 AA AATT T
 TGG A GA GGT GGGGAAG
 |||| | ||| |||||
 ACCT CT TCA TCCCTTC
 AC _____ C
 GAM2537 L1CAM 3' CTCCCCCAGCCACTCCCCA 23429 AA AAAT A
 TGG AG TGGTTGGGG AG
 ||| | ||||| |||
 ACC TC ACCGACCCC TC
 CC _____ C
 GAM2537 L1CAM 3' CTCCCCCAGCCACTCCCCA 6001 AA AAAT A
 TGG AG TGGTTGGGG AG
 ||| | ||||| |||
 ACC TC ACCGACCCC TC
 CC _____ C
 GAM2537 LAD1 3' CCTTCCCCACAAGCCCCCTCCA 12086 AAGAAA GT
 TGG A TTG TGGGGAAGG
 |||| ||| |||||
 ACCT AAC ACCCCTTCC
 CCCCCG _
 GAM2537 MNT 3' CCCTCCCCGTCCCTGTCC 21560 A AAATT T A
 GGA AG GG TGGGGA GG
 ||| | || ||||| |||
 CCT TC CC GCCCCT CC
 G _____ T C
 GAM2537 MTMR3 3' TCCCTACCTTTTCCA 22072 AAATT T
 TGGAAG GGT GGGGA
 ||||| ||| |||||
 ACCTTTT CCA TCCCT

 GAM2537 NHLH1 3' CTTCTCAACTCCCTCCA 12125 AA AATTG
 TGG A GA GTTGGGGAAG
 |||| | |||||
 ACCT CT CAACTCCTTC
 CC _____
 GAM2537 PAFAH1B1 5' CCTCCCCCTCCTTCCCTCC 6010 AA ATT TT A
 GGA GAA GG GGGG AGG
 ||| ||| | ||| |||
 CCT CTT CC CCCC TCC
 CC ____ TC C
 GAM2537 PAX5 3' CTTCCCTCCTCTCTCCA 18790 A AATT TT
 TGG A AGA GG GGGGAAG
 |||| | ||| |||||

ACCT TCT CC CCCCTTC
 C ____ T_
 GAM2537 PDE4A 3' CCCTCCCCTCACCTTCCCCCA 12874 AAA ATT T_ A
 TGG GAA GGT GGGGA GG
 ||| ||| ||| ||||| ||
 ACC CTT CCA CCCCT CC
 CC_ ____ CT C
 GAM2537 PEX14 3' CCCTCCCCAGCCCCCTCTCC 31827 A AAATT A
 GGA AG GGTG GGGGA GG
 ||| || ||||| ||
 CCT TC CCGACCCCT CC
 C CC_ ____ C
 GAM2537 PIGR 3' CCTTCCCCTCTTCTTCTTTCC 35938 ATT TT
 GGAAAGAA GG GGGGAAGG
 ||||| || |||||
 CCTTTCTT TC CCCCTTCC
 CT_ T_
 GAM2537 PIK3CD 3' CCTCCCGAGGGAACCTTCTTCC 11463 A ATT ____ G A
 CA GG AAGAA GGT T GGA GG
 || |||| || | ||| ||
 CC TTCTT CCA A CCCT CC
 C ____ AGGG G _
 GAM2537 PLOD 3' CTTCCCCACCTCTTCCA 5844 A AATT T
 TGGAA GA GGT GGGGAAG
 |||| || ||| |||||
 ACCTT CT CCA CCCCTTC
 _ ____ C
 GAM2537 PNUTL2 3' CTCCCCAACCAAGTCCA 27837 AAGAAA A
 TGGA TTGGTTGGGGA G
 |||| ||||| |||
 ACCT AACCAACCCCT C
 G_ ____ C
 GAM2537 POLH 5' CCTTCCATTTTCTTCCA 13250 A T TT
 TGGAA GAAA TGG GGG
 |||| |||| ||| |||
 ACCTT CTTT ACC TCC
 C T T_
 GAM2537 PROK1 3' CTAAACAACCTCTTTCCA 26200 AAATT GGG
 TGGAAG GGTG AAG
 ||||| |||| |||
 ACCTTTC TCAAC TTC
 C_ ____ AAA
 GAM2537 RABL2A 3' CCTTCCCCACCCCTCCCCCA 15079 AAA AATT T
 TGG GA GG TGGGAAGG
 ||| || || |||||
 ACC CT CC ACCCCTTCC
 CCC CC_ ____ C
 GAM2537 RABL2B 3' CCTTCCCCACCCCTCCCC 13946 AA AAATT T
 GG AG GG TGGGAAGG
 || || || |||||

CC TC CC ACCCCTTCC
 CC C___ C
 GAM2537 RNMT 3' CCCCCGTCAGATTCCCTTCCA 9884 A_ A TT
 TGGAA GAA TTGG GGGG
 |||| ||| |||| ||||
 ACCTT CTT GACT CCCC
 CC A GC
 GAM2537 SCG3 5' CTTCTCACTTCCTCTCCA 14901 A AAATT T
 TGGAA AG GGT GGGGAAG
 |||| || ||| |||||
 ACCT TC TCA CTCCTTC
 C CT___ _
 GAM2537 SDC4 3' CCTCCCCCAGTGGCCTTCCTCC 8890 AA ATT ___ A
 GGA GAA GGT TGGGG AGG
 ||| ||| ||| ||||| |||
 CCT CTT CCG ACCCC TCC
 C_ ___ GTG C
 GAM2537 SELPLG 3' CCTTCCCCTGTGGCCACTTTCC 30017 AAAT ___
 A TGGAAAG TGGTT GGGGAAGG
 ||||| ||||| |||||
 ACCTTTC ACCGG CCCCTTCC
 ___ TGT
 GAM2537 SFRS2IP 3' CCTTCCCCTCCACCCTCCCCCA 11087 AAA AAT TT
 TGG GA TGG GGGGAAGG
 ||| || ||| |||||
 ACC CT ACC CCCCTTCC
 CC_ CCC T_
 GAM2537 SH3GL1 3' CCGCTCCCCAACTTCTCGCC 8962 AA AATT A_
 GG AGA GGTG GGGGA GG
 || ||| ||||| |||
 CC TCT TCAACCCCT CC
 GC ___ CG
 GAM2537 SHC1 3' CCCTCCAATCCTTTCCA 8970 AA TT
 TGGAAAG ATTGG GGG
 ||||| ||||| |||
 ACCTTTC TAACC CCC
 C_ T_
 GAM2537 SIGLEC6 5' CCTTCCCCTCCACTCCCTTCC 30108 A_ AAT TT
 GGAA GA TGG GGGGAAGG
 |||| || ||| |||||
 CCTT CT ACC CCCCTTCC
 CC C_ T_
 GAM2537 SLC9A5 3' CCTTCCCTGCCCAACTCCCTC 30064 AA AATT TT
 C GGA GA GG GGGGAAGG
 ||| || ||| |||||
 CCT CT CC TCCCTTCC
 CC CAAC CG
 GAM2537 SLC9A5 3' CTGCCCCAATCCTCCCCA 10935 AA AAATT A
 TGG AG GGTG GGGG AG
 ||| || ||||| |||

ACC TC CTAACCCC TC
 CC _____ G
 GAM2537 SNL 3' CTTCCCCGCCCCCTGCCCA 9061 AA AAATT T
 TGG AG GG TGGGGAAG
 ||| || || |||||
 ACC TC CC GCCCCTTC
 CG _____ C
 GAM2537 SNTB1 5' CCTCCCCCGGCCACCCTTCCC 22011 A AAAT A_
 GG AAG TGGTTGGGG AGG
 || ||| ||||| |||
 CC TTC ACCGGCCCC TCC
 C CC_____ CC
 GAM2537 SOX13 3' CCCTCCCCTTCACTCCCTCC 12242 AA AAT TT A
 GGA GA TGG GGGGA GG
 ||| || ||| ||||| ||
 CCT CT ACT CCCCT CC
 CC C_____ T_____ C
 GAM2537 TAF4 3' CCCTCCCCTCCCCTCCCTTCC 9162 A_ AATT TT A
 GGAA GA GG GGGGA GG
 |||| || || ||||| ||
 CCTT CT CC CCCCT CC
 CC C_____ CT C
 GAM2537 TAPBP 3' CCCTCCAATCTCTCTCCA 9179 A A TT
 TGGA AGA ATTGG GGG
 |||| ||| ||||| |||
 ACCT TCT TAACC CCC
 C C T_____
 GAM2537 TCF1 3' CTGCCCCAACTCCTTCCA 6146 A AATTG A
 TGGA GA GTTGGGG AGG
 ||||| || ||||| |||
 ACCTT CT CAACCCC TCC
 C _____ G
 GAM2537 TCF7L2 5' CCTTCCCCTCCCCTCCTCC 25040 AA AATT TT
 GGA GA GG GGGGAAGG
 ||| || || |||||
 CCT CT CC CCCCTTCC
 C_____ CT
 GAM2537 TEAD3 5' CCTCCCCACGACCCCCCTTCCC 9211 A AAATT _ A
 GG AAG GGTG GGG AGG
 || ||| ||||| ||| |||
 CC TTC CCAGC CCC TCC
 C CCC_____ A C
 GAM2537 TERF2 3' CTTTCCCAATTCCCTTCC 12190 A_ AATTG
 GGAA GA GTTGGGGAAGG
 |||| || ||||| |||||
 CCTT CT TAACCCTTTTC
 CC _____
 GAM2537 TIAL1 3' CCTCCCCCTGTAATACCTCCTC 22741 A_ AA GTT A
 C GGA AG ATTG GGGG AGG
 ||| || |||| ||||| |||

			CCT TC TAAT CCCC TCC		
			CC CA GT_ C		
GAM2537	TNFSF4	3'	CCTCACTCCACCTTCCTTCCA 9330	A AT T_	
			TGGAA GAA TGG TGGGG		
			ACCTT CTT ACC ACTCC		
			C CC TC		
GAM2537	TNFSF5	3'	CCTCCCCCAGTCTCTCTTCTCA 5518	GA AATT GT A	
			TG AAGA G TGGGG AGG		
			AC TTCT C ACCCC TCC		
			TC CT__TG C		
GAM2537	YWHAE	3'	CCTCCCCCTACCTCCTTCC 13613	A AATT T A	
			GGAA GA GGT GGGG AGG		
			CCTT CT CCA CCCC TCC		
			C ____ T C		
GAM2537	ZNF278	3'	CCCCACTCCAACCTCCTTCTCCA 15625	_ AAA T_	
			TGGA AAG TTGG TGGGG		
			ACCT TTC AACC ACCCC		
			C CTC TC		
GAM2537	ZNF278	3'	CCCCACTCCAACCTCCTTCTCCA 25774	_ AAA T_	
			TGGA AAG TTGG TGGGG		
			ACCT TTC AACC ACCCC		
			C CTC TC		
GAM2537	ZNF278	3'	CCTTCCCCTGGCATCACTTCCC 25777	A AAATTG _	
	A		TGG AAG GTT GGGGAAGG		
			ACC TTC CGG CCCCTTCC		
			C ACTA__ T		
GAM2537	ZNF278	3'	CCCCACTCCAACCTCCTTCTCCA 25784	_ AAA T_	
			TGGA AAG TTGG TGGGG		
			ACCT TTC AACC ACCCC		
			C CTC TC		
GAM2537	AP1GBP1	3'	CCTTCCCTTCACTTCTGTCCA 14117	A AT TT	
			TGGA AGAA TGG GGGGAAGG		
			ACCT TCTT ACT TCCCTTCC		
			G C_ _		
GAM2537	AP1GBP1	3'	CCTTCCCTTCACTTCTGTCCA 27872	A AT TT	
			TGGA AGAA TGG GGGGAAGG		
			ACCT TCTT ACT TCCCTTCC		
			G C_ _		
GAM2537	API5	3'	CTTCCCCTTCCCTTTCC 13362	AAATT TT	
			GGAAAG GG GGGGAAG		

CCTTTC CC CCCCTTC
 _____ TT
 GAM2537 ARHGAP5 3' CCTTCCCCCAAACCTTATCTCCA 37817 AA AATT ____
 TGA GA GGTT GGGGAAGG
 ||| || ||| |||||
 ACCT CT TCAA CCCCTTCC
 ____ AT__ AC
 GAM2537 C14orf4 3' CCCTAGACCAGCTCCTCTCCA 33444 A AAA _
 TGA AG TTGGT TGGGG
 ||| || ||| |||
 ACCT TC GACCA ATCCC
 C CTC G
 GAM2537 C17orf31 5' CCCCAAGGAAACCAATTTCTT 19000 A ____
 CTA TGGAA GAAATTGGT TGGGG
 ||| ||||| |||
 ATCTT CTTTAACCA ACCCC
 C AAGGA
 GAM2537 C1orf25 5' CCCTCCCCACTTGCTTCCC 35910 A AAATT T A
 GG AAG GGT GGGGA GG
 || ||| ||| ||| ||
 CC TTC TCA CCCCT CC
 C GT__ _ C
 GAM2537 CDC14B 3' CCCTCCTAGGCCCACTTCCTCC 27167 AA ATT TG A
 GGA GAA GGT GGGGA GG
 ||| ||| ||| ||| ||
 CCT CTT CCG TCCT CC
 C_ CAC GA C
 GAM2537 CLSTN3 3' CCCTCCTTTCCAACCTTCCTTCC 16272 A A TT A
 GGAA GAA TTGG GGGGA GG
 ||| ||| ||| ||| ||
 CCTT CTT AACC TTCCT CC
 C C T_ C
 GAM2537 COPS7B 3' CCTTCCCCAGTTGTTCCCTTCA 22933 AA AT GG
 TGA GAA T TTGGGGAAGG
 ||| ||| | |||||
 ACTT CTT G GACCCCTTCC
 CC __ TT
 GAM2537 DDX12 3' CTTCCCCTCCTCCTTCC 30022 A AATT TT
 GGAA GA GG GGGGAAG
 ||| || ||| |||
 CCTT CT CC CCCCTTC
 C ____ T_
 GAM2537 DEFCAP 5' CCTCCCCTGGCTTTTCTACCA 17201 AAA TT TG A
 TGG GAAA GGT GGG AGG
 || ||| ||| ||| |||
 ACC CTTT TCG CCC TCC
 ATC __ GT C
 GAM2537 DIO2 5' CCTTCCCCCTTACCTCCCCCA 15167 AAA AATT T__
 TGG GA GGT GGGGAAGG
 || || ||| |||||

ACC CT CCA CCCCTTCC
 CC_ ____ TTC
 GAM2537 DKFZp434J0617 3' CCCTCCCCATCCTCTTTCC 25982 AATT T A
 GGAAAGA GG TGGGGA GG
 ||||| || ||||| ||
 CCTTTCT CC ACCCCT CC
 ____ T C
 GAM2537 DKFZP434N014 3' CCCTGGTCCCAGTCCCTTTCCA 30389 AA ____ TG
 TGGAAG ATTGG T GGG
 ||||| |||| | ||
 ACCTTTC TGACC G CCC
 CC CT GT
 GAM2537 DKFZp434P0531 3' CCCCCTCCGTTTTTTCCA 44281 AT TT
 TGGAAGAA TGG GGGG
 ||||| || ||||
 ACCTTTTTT GCC CCCC
 ____ TC
 GAM2537 DKFZP586N0721 5' CCCTCCCCACCTCGCTTCTTCC 17708 A ATT_ T A
 CA TGG AAGAA GGT GGGGA GG
 || |||| || |||| ||
 ACC TTCTT CCA CCCCT CC
 C CGCT _ C
 GAM2537 DKFZp761G2113 3' CCTCCCCCTGCCTCTCCTCC 34641 A_ AATT T A
 GGA AGA GGT GGGG AGG
 || || || |||| ||
 CCT TCT CCG CCCC TCC
 CC ____ T C
 GAM2537 EZF-2 3' CCTTCCCCCTCTTCTCTCTCC 20340 A _ TT TT
 GGA AGA AA GG GGGGAAGG
 || || || || |||||
 CCT TCT TT CC CCCCTTCC
 C C CT _
 GAM2537 FBXO27 3' CCCTCCCCTCTCTTCTCCTCC 36834 A_ ATT TT A
 GGA AGAA GG GGGGA GG
 || || || |||| ||
 CCT TCTT CT CCCCT CC
 CC ____ CT C
 GAM2537 FHX 5' CCTCCCCCTCCCCCTCCTCCA 20457 AA AATT TT A
 TGGA GA GG GGGG AGG
 ||| || || |||| ||
 ACCT CT CC CCCC TCC
 C_ CC_ CT C
 GAM2537 FLJ10074 5' CCCTCCCCACCCCTTTCCTTCT 19720 A TT T A
 A TGGA GAAA GGT GGGGA GG
 |||| ||| || |||| ||
 ATCTT CTTT CCA CCCCT CC
 C CC _ C
 GAM2537 FLJ10704 3' CCTTCCCCAGGCTCTGCTTCCA 20032 A AAATT _
 TGGA G GGT TGGGGAAGG
 |||| | || |||||

		ACCTT C	TCG ACCCCTTCC		
		_ GTC_	G		
GAM2537	FLJ11286	3'	CTTCCCTATCTCCTTACCA	20415	A AAATT T
			TGG AAG	GG TGGGGAAG	
			ACC TTC	TC ATCCCTTC	
			A C_	T	
GAM2537	FLJ11939	3'	CCTTCCCCTTTCTCTGTCTCCA	23991	AA AATT TT
			TGGA GA	GG GGGGAAGG	
			ACCT CT	CT CCCCTTCC	
			_ GTCT	TT	
GAM2537	FLJ12541	3'	CCCTCCCCGGCTCTCCTCCCA	22757	AAA AATT A
			TGG GA	GGTTGGGGA GG	
			ACC CT	TCGGCCCCT CC	
			CTC C_	C	
GAM2537	FLJ12816	3'	CCTTCCTTGCCCCATCTTCC	22603	A AATT TT
			GGAA GA	GG GGGGAAGG	
			CCTT CT	CC TTCCTTCC	
			_ AC_	CG	
GAM2537	FLJ12921	3'	CCTTCCCCCACCTTCCTCC	24309	AA ATT T
			GGA GAA	GGT GGGGAAGG	
			CCT CTT	CCA CCCCTTCC	
			C_ _	C	
GAM2537	FLJ14721	3'	CCCAGACCAACTCCTTTCC	26604	AAA G
			GGAAAG	TTGGTT GGG	
			CCTTTC	AACCAG CCC	
			CTC	A	
GAM2537	FLJ14950	3'	CCTCCCCCAACCCACGCTCCA	26671	AAGAAATT A
			TGGA	GGTTGGGG AGG	
			ACCT	CCAACCCC TCC	
			CGCAC_	C	
GAM2537	FLJ22596	5'	CCCTGCCACCTTCTCTCCA	24703	A AT T
			TGGA AGAA	TGGT GGG	
			ACCT TCTT	ACCG CCC	
			C CC	T	
GAM2537	FLJ23537	3'	CCTTCCCCAACATCCTTCCCA	24362	A AAATTG
			TGG AAG	GTTGGGGAAGG	
			ACC TTC	CAACCCCTTCC	
			C CTA_		
GAM2537	FLJ23537	3'	CCTTCCCCAACACCTCCTTCC	24359	A AATTG
			GGAA GA	GTTGGGGAAGG	

	CCTT CT CAACCCCTTCC	
	C CCA__	
GAM2537 FLJ23537 3'	CCTTCCCCAACACCTCCTTCC 24360	A AATTG
	GGAA GA GTTGGGGAAGG	
	CCTT CT CAACCCCTTCC	
	C CCA__	
GAM2537 FLJ23537 3'	CCTTCCCCAACACTTCCTTCC 24361	A ATTG
	GGAA GAA GTTGGGGAAGG	
	CCTT CTT CAACCCCTTCC	
	C CA__	
GAM2537 FLJ23537 3'	CCTTCCCCAACACCTCCTTCC 24347	A AATTG G
	GGAA GA GTT GGGAAGG	
	CCTT CT CAA CCCTTCC	
	C CCA__ A	
GAM2537 FLJ23537 3'	CCTTCCCCAACACCTCCTTCC 24348	A AATTG G
	GGAA GA GTT GGGAAGG	
	CCTT CT CAA CCCTTCC	
	C CCA__ A	
GAM2537 FLJ23537 3'	CCTTCCCCAACACCTCTTTCC 24349	AATTG G
	GGAAAGA GTT GGGAAGG	
	CCTTTCT CAA CCCTTCC	
	CCA__ A	
GAM2537 FLJ23537 3'	CCTTCCCCAACCCCTTTCC 24350	AAATT G
	GGAAAG GGTT GGGAAGG	
	CCTTTC CCAA CCCTTCC	
	C__ A	
GAM2537 FLJ23537 3'	CCTTCCCAACACCGCCTTCCCA 24351	A AAAT TG_
	TGG AAG TGGT GGGAAGG	
	ACC TTC GCCA CCCTTCC	
	C C__ CAA	
GAM2537 FLJ23537 3'	CCTTCCCAACACCTCCTTCC 24352	A AATT TG_
	GGAA GA GGT GGGAAGG	
	CCTT CT CCA CCCTTCC	
	C__ CAA	
GAM2537 FLJ23537 3'	CCTTCCCAACACCTCCTTCC 24353	A AATT TG_
	GGAA GA GGT GGGAAGG	
	CCTT CT CCA CCCTTCC	
	C__ CAA	
GAM2537 FLJ23537 3'	CCTTCCCAACACCTCCTTCC 24354	A AATT TG_
	GGAA GA GGT GGGAAGG	

			CCTT CT CCA CCCTTCC		
			C ____ CAA		
GAM2537	FLJ23537	3'	CCTTCCCAACACCTCCTTCC 24355	A AATT TG_	
			GGAA GA GGT GGGAAGG		
			CCTT CT CCA CCCTTCC		
			C ____ CAA		
GAM2537	FLJ23537	3'	CCTTCCCAACACCTCCTTCC 24356	A AATT TG_	
			GGAA GA GGT GGGAAGG		
			CCTT CT CCA CCCTTCC		
			C ____ CAA		
GAM2537	FLJ23537	3'	CCTTCCCAGACACCTCCTTCC 24357	A AATTG G	
			GGAA GA GTT GGGAAGG		
			CCTT CT CAG CCCTTCC		
			C CCA__ A		
GAM2537	FLJ23537	3'	CCTTCCCCAACACCTCCTTCC 24358	A AATTG	
			GGAA GA GTTGGGGAAGG		
			CCTT CT CAACCCCTTCC		
			C CCA__		
GAM2537	FLJ31978	3'	CCTTCTGACCAACCTCTCCCA 29487	AA AATT _	
			TGG AGA GGTTGG GGAAGG		
			ACC TCT CCAACC TCTTCC		
			CC ____ AG		
GAM2537	FLJ32658	5'	TTTTCCCATCCCTCCCA 29508	AA AAATT T	
			TGG AG GG TGGGGAAG		
			ACC TC CC ACCCTTTT		
			CC ____ T		
GAM2537	GNG3	5'	CCCTCCCCAGGGGCCTCCTTTC 14508	AAATT ____ A	
	C		GGAAAG GGT TGGGGA GG		
			CCTTTC CCG ACCCCT CC		
			CT__ GGG C		
GAM2537	GPA33	3'	CTCCAGCTCCCACTCCCTTTC 12403	AAATT__	
	A		TGGAAAG GGTG GGG		
			ACCTTTC TCGACCTC		
			CCTCACCC		
GAM2537	GR6	3'	CCTCAAACAAGCCCTTCCA 14281	A AAA G_	
			TGG AAG TTG TTGGGG		
			ACC TTC AAC AACTCC		
			C CCG AA		
GAM2537	GTPBG3	3'	CCTTCCCCTACCCTTCCCTCC 26333	AA ATT T	
			GGA GAA GGT GGGAAGG		

CCT CTT CCA CCCCTTCC
 CC C__ T
 GAM2537 HIC2 3' CCCTCACCAACTTTCC 32526 AAA T
 GGAAAG TTGGT GGGG
 ||||| ||||| |||||
 CCTTTC AACCA TCCC
 ____ C
 GAM2537 HRMT1L3 3' CTTCCCCACCCCTTACCA 21258 A AAATT T
 TGG AAG GG TGGGGAAG
 ||| ||| || |||||
 ACC TTC CC ACCCCTTC
 A ____ C
 GAM2537 HTMP10 3' CCTTCCTCCTACCTCTTCCCA 27048 A AATT T _
 TGG AAGA GGT GG GGAAGG
 ||| ||| ||| || |||||
 ACC TTCT CCA CC CCTTCC
 C ____ T T
 GAM2537 IMP-2 3' CCCTCCCCTCCCCTTCTTCTCC 13304 _ ATT TT A
 A
 TGGA AAGAA GG GGGGA GG
 ||||| ||||| || ||||| ||
 ACCT TTCTT CC CCCCT CC
 C C__ CT C
 GAM2537 KALI 3' CCCTCTCCAACCCACTCTCCA 27488 A AAATT A
 TGGA AG GGTTGGGGA GG
 ||||| || ||||| || ||||| ||
 ACCT TC CCAACCTCT CC
 C AC__ C
 GAM2537 KIAA0121 5' CCCTCCCCTTTCTCTTTCTTTC 35968 TT TT A
 CA
 TGGAAAGAAA GG GGGGA GG
 ||||| ||||| || ||||| ||
 ACCTTTCTTT CT CCCCT CC
 CT TT C
 GAM2537 KIAA0205 3' CCCCCCAATCTCTTCCA 17006 A A TT
 TGGA GA ATTGG GGGG
 ||||| || ||||| |||||
 ACCTT CT TAACC CCCC
 _ C _
 GAM2537 KIAA0227 3' CCTTCTCCTCATCCCTCCCCA 30452 AA AAATT TT__
 TGG AG GG GGGGAAGG
 ||| || || |||||
 ACC TC CC CCTCTTCC
 CC ____ TACT
 GAM2537 KIAA0350 3' CTTCCACAACCTTTCCTCCA 30666 AA ATT G
 TGGA GAA GGTTG GGAAG
 ||||| || ||||| |||||
 ACCT CTT TCAAC CCTTC
 C_ ____ A
 GAM2537 KIAA0451 3' CCCTCCCCTATCCTCCTTCCC 16804 A AATT T A
 GG AAGA GG TGGGGA GG
 || ||||| || ||||| ||

CC TTCT CC ACCCCT CC
 C CCT_ T C
 GAM2537 KIAA0461 3' CCTCACCACCTTCCCTCCA 35074 AA AT T
 TGGA GAA TGGT GGGG
 |||| || |||| ||||
 ACCT CTT ACCA CTCC
 CC CC _
 GAM2537 KIAA0731 3' CCTTCCCCCTCCTCTCTCCA 33240 A AATT TT
 TGGA AGA GG GGGGAAGG
 |||| || || |||| ||||
 ACCT TCT CC CCCCTTCC
 C ____ TC
 GAM2537 KIAA0872 3' CCTCCCCACAGCCTCTTTTCT 17244 AA TT_ _ A
 CCA TGGA GAAA GGT TGGGG AGG
 |||| |||| || |||| ||||
 ACCT CTTT CCG ACCCC TCC
 _ TCT AC C
 GAM2537 KIAA1030 3' CCTCTTCCCAACTCCCTTCTCA 44820 A ATT _
 A AGAA GGTG GGGGA AGG
 | |||| |||| |||| ||||
 A TCTT TCAACCCTT TCC
 C CCC C
 GAM2537 KIAA1030 3' CTTCCCCAGCTCCCTCC 44821 AA AATTG
 GGA GA GTTGGGGAAG
 ||| || |||| |||| ||||
 CCT CT CGACCCCTTC
 CC ____
 GAM2537 KIAA1045 3' CCTGCCCCAACCCCCGTCCA 35194 AAGAAATT A
 TGGA GGTG GGGG AGG
 |||| |||| |||| ||||
 ACCT CCAACCCC TCC
 GCCC ____ G
 GAM2537 KIAA1205 3' CCTTCCCCCCAAGTCCCCC 34706 AAA AA TT
 GG GA TTGG GGGGAAGG
 || || |||| |||| ||||
 CC CT AACC CCCCTTCC
 CCC G_ _
 GAM2537 KIAA1465 3' CCTCCCCCTTACTACTCCCA 30501 AA AAAT T_ A
 TGG AG TGGT GGGG AGG
 ||| || |||| |||| ||||
 ACC TC ATCA CCCC TCC
 CC ____ TT C
 GAM2537 KIAA1538 3' CCTCCCCCAACTCTTCCTCCA 35423 AA ATT A
 TGGA GAA GGTG GGGG AGG
 |||| || |||| |||| ||||
 ACCT CTT TCAACCCC TCC
 C_ C_ C
 GAM2537 KIAA1750 3' CCTTCCCCTTCCTTCTTTCC 33875 ATT TT
 GGAAAGAA GG GGGGAAGG
 |||| || |||| |||| ||||

		CCTTTCTT CC CCCCTTCC		
		___ TT		
GAM2537	KIAA1817	3' CCTTCCCCAACCATGGCCCCA 33862	AAAGAAAT	
		TGG TGGTTGGGGAAGG		
		ACC ACCAACCCCTTCC		
		CCGGT___		
GAM2537	KIAA1819	5' CTCCCCCACAACCTTCTCCA 34533	AA A GT A	
		TGGA GAA TTG TGGGG AG		
		ACCT CTT AAC ACCCC TC		
		___ C ___ C		
GAM2537	KIAA1853	3' CCTCCCCCAACCACCTGCCCTC 34387	AAGAAAT A	
	C	GGA TGGTTGGGG AGG		
		CCT ACCAACCCC TCC		
		CCCGTCC C		
GAM2537	KIAA1853	3' CCCTACCCAATCTTTCC 34386	AA T	
		GGAAAGA TTGG TGGGG		
		CCTTTCT AACC ATCCC		
		___ C		
GAM2537	KIAA1855	3' CCTCCTCCGACCCCTTTCCA 44357	AAATT A	
		TGGAAAG GGTGAGG AGG		
		ACCTTTC CCAGCCTC TCC		
		C___ C		
GAM2537	KIAA1855	3' CCCTCCCCAAGCCCTTCCA 44355	A AAATT _ A	
		TGG AAG GGTGAGGGA GG		
		ACC TTC CCGA CCCCT CC		
		C ___ A C		
GAM2537	KIAA1870	3' CCCTCCCCAGCTTCTGCCCCA 25863	AA AAATT A	
		TGG AG GGTGAGGGA GG		
		ACC TC TCGACCCCT CC		
		CG CT___ C		
GAM2537	KIAA1884	3' CCTTCCCCCTTACACTCCTCTC 36295	A AAAT GTT_	
	C	GGA AG TG GGGGAAGG		
		CCT TC AC CCCCTTCC		
		C CTC_ ATTC		
GAM2537	KIAA1938	3' CCTCCCCCTCCCAATCTCCTTC 44276	A A TT A	
	CA	TGGAA GA ATTGG GGGG AGG		
		ACCTT CT TAACC CCCC TCC		
		C C CT C		
GAM2537	MAB21L2	3' CCCCCCCTTTTCTTCTTTCC 13150	ATT TT_ AA	
		GGAAAGAA GG GGGG GG		

CCTTTCTT CC CCCC CC
 ____ TTTT CC
 GAM2537 METL 3' CCTTAAACCACCAATTTATTTTC 20433 G T GG_
 CA TGGAAA AAATTGGT GG AAGG
 ||||| ||||| || ||||
 ACCTTT TTAAACCA CC TTCC
 A _ AAA
 GAM2537 MGC2714 5' CCTTCCCCGGCTCCCCTGCCCA 26079 AA AAATT
 TGG AG GGTG GGGGAAGG
 ||| || |||||
 ACC TC TCGGCCCTTCC
 CG CCC_
 GAM2537 MGC4737 3' CCTCCCCAGACCCCTCCCA 25506 AAA AATT _ A
 TGG GA GGT TGGGG AGG
 ||| || ||| |||||
 ACC CT CCA ACCCC TCC
 ____ CC_ G C
 GAM2537 MGC4796 3' CCTTCCCCAGAGGCCTACCCCC 30830 AAAGAAATT ____
 CA TGG GGT TGGGGAAGG
 ||| ||| |||||
 ACC CCG ACCCCTTCC
 CCCCAT_ GAG
 GAM2537 moblak 3' CTCCCCAATCTCTTCCA 28307 A AATT A
 TGGAA GA GGTG GGGGA G
 ||||| || ||||| |
 ACCTT CT CTAACCCCT C
 _ ____ C
 GAM2537 N4BP3 3' CCTTCCCTGCAGCCCCTCCCCA 32935 AA AAATT ____
 TGG AG GGTG GGGAAGG
 ||| || ||||| |||||
 ACC TC CCGAC CCCTTCC
 CC C_ GT
 GAM2537 NDST4 5' CCTTCCCATCTATTGCCTTCCA 22891 AGAAAT TTG
 TGGAA TGG GGGAAGG
 |||| ||| |||||
 ACCTT ATC CCCTTCC
 CCGTT_ TA_
 GAM2537 NXPH3 3' CCTTCCCCCCTTCCCTTCC 32718 AAATT TT
 GGAAAG GG GGGAAGG
 ||||| || |||||
 CCTTTC CC CCCCTTCC
 CCTT_ _
 GAM2537 P450RAI-2 3' CCTTCTGGCTCCAGCTTCCCTC 21268 AA A TTGG
 CA TGGG GAA TTGG GGAAGG
 |||| ||||| |||||
 ACCT CTT GACC TCTTCC
 CC C TCGG
 GAM2537 PPP1R10 3' CCTGTACCCCAAACCCCTTCC 8575 AAATT _ A_
 A TGGAAAG GGTG GGGG AGG
 ||||| ||||| |||

ACCTTTC CCAA CCCC TCC
 C____ A ATG
 GAM2537 PRKRI 5' CCTCCCCCTGTAACCTCTTCCC 12944 A AATT ____ A
 GG AAGA GGTT GGGG AGG
 || ||| ||| ||| |||
 CC TTCT CCAA CCCC TCC
 C ____ TGT C
 GAM2537 PTRF 3' CCTTCCCCTCAGCCTCTCCCCA 31782 AA AATT ____
 TGG AGA GGTT GGGGAAGG
 ||| ||| ||| ||| ||| |||
 ACC TCT CCGA CCCCTTCC
 CC ____ CT
 GAM2537 RAB35 3' CCCTCCCCGCGCCCTCCCCA 13732 AA AAATT _ A
 TGG AG GGT TGGGGA GG
 ||| || ||| ||| ||| |||
 ACC TC CCG GCCCCT CC
 CC C____ C C
 GAM2537 RAB3IL1 3' CCTCCCCCGCTTCTCCCTTCC 15062 A_ AATT T A
 GGAA GA GGT GGGGA GG
 ||| || ||| ||| ||| |||
 CCTT CT TCG CCCCT CC
 CC CCT_ C _
 GAM2537 RAI 3' CTGCCCCACCTCTCCCCA 13470 AA AATT T A
 TGG AGA GGT GGGG AG
 ||| ||| ||| ||| ||| |||
 ACC TCT CCA CCCC TC
 CC ____ _ G
 GAM2537 REV1L 5' CCTTCCCCCGGCCCTCCTCC 18435 AA AATT ____
 GGA GA GGTTGGGG AAGG
 ||| || ||| ||| ||| ||| |||
 CCT CT CCGGCCCC TTCC
 C_ C____ C
 GAM2537 SEMA6B 3' CCTCCCCCAGCCCCCTCCCCA 25799 AA AAATT A
 TGG AG GGTTGGGG AGG
 ||| || ||| ||| ||| ||| |||
 ACC TC CCGACCCC TCC
 CC CC____ C
 GAM2537 SMCR5 3' CCTTCCCTTCATCCCTTCCCA 29562 A AAAT TT
 TGG AAG TGG GGGGAAGG
 ||| ||| ||| ||| ||| ||| |||
 ACC TTC ACT TCCCTTCC
 C CCT_ ____
 GAM2537 SP192 5' CCTTCCCCTTTTCCCCTTTCC 22296 AAATT TT____
 GGAAAG GG GGGGAAGG
 ||| ||| ||| ||| ||| ||| |||
 CCTTTC CC CCCCTTCC
 C____ TTTT
 GAM2537 SSH2 3' CCTTCCCCATGCTGTTGTCCCC 31180 AAA AAT _
 A TGG GA TGGT TGGGAAGG
 ||| || ||| ||| ||| ||| |||

ACC CT GTCG ACCCCTTCC
 C__ GTT T
 GAM2537 STRN3 5' CTTCCCCGCCCCTCTCC 15935 A AAATT T
 GGA AG GG TGGGGAAG
 ||| || || |||||
 CCT TC CC GCCCCTTC
 C ____ C
 GAM2537 STX1B2 3' CCCCCCCCACCCTTCTCTCTCC 27454 A AATT T AA
 GGA AGA GG TGGGG GG
 ||| ||| || ||||| ||
 CCT TCT CC ACCCC CC
 C CTT_ C CC
 GAM2537 TRIP-Br2 3' CCTCCCCCAATTCCCCCCCCA 16486 AAAGA_ TT A
 TGG AATTGG GGGGA GG
 ||| ||||| ||||| ||
 ACC TTAACC CCCCT CC
 CCCCCC _ _
 GAM2537 TUSP 3' CCTCCCCCAAAGGCGCTTTCC 21524 AAATTGG A
 GGAAAG TTGGGG AGG
 ||||| ||||| |||
 CCTTTC AACCCC TCC
 GCGGA__ C
 GAM2537 ZDHC8 3' CCCTCCCCACCAACTTCTCTGC 31961 AA_ A T A
 C GG AGAA TTGGT GGGGA GG
 || |||| |||| |||| ||
 CC TCTT AACCA CCCCT CC
 GTC C _ C
 GAM2537 ZIN 3' CCCTCCCCAACGGCTGCCTTCC 15071 A AAATTG A
 C GG AAG GTTGGGGA GG
 || ||| ||||| ||
 CC TTC CAACCCCT CC
 C CGTCGG C
 GAM2537 LOC116411 5' CCCCCCCCGCTCTTTCCA 36565 AAT TT
 TGGAAAGA TGG GGGG
 ||||| ||| |||
 ACCTTTCT GCC CCCC
 C__ CC
 GAM2537 LOC120376 5' CCTGAACCAATTTCTTCCA 37413 A G
 TGGAA GAAATTGGTT GGG
 |||| ||||| |||
 ACCTT CTTTAACCAA TCC
 _ G
 GAM2537 LOC123096 3' CCTTCCCCAGGGCTCCTTCTCA 36720 A ATT _
 A AGAA GGT TGGGGAAGG
 | ||| ||| |||||
 A TCTT TCG ACCCCTTCC
 C CC_ GG
 GAM2537 LOC124446 5' CCCTCCCTTTAACCCCTTCCA 36750 AGAAATT _ A
 TGGAA GGTT GGGGA GG
 |||| ||| ||||| ||

ACCTT CCAA TCCCT CC
 CCC___ TT C
 GAM2537 LOC133308 5' CCTCCCCACAGCCCCTTTCC 37034 AAATT _ A
 GGAAAG GGT TGGGG AGG
 ||||| || ||||| ||
 CCTTTC CCG ACCCC TCC
 C___ AC C
 GAM2537 LOC142972 3' CTCTTCCCAACTTCCTCCA 32477 AA AATT _
 TGGA GA GGTTGGGGA AG
 ||| || ||||| ||
 ACCT CT TCAACCCTT TC
 C_ ___ C
 GAM2537 LOC143524 3' CCTTCCCAGTTTCTCCCCA 37628 AA TT
 TGG AGAAATTGG GGG
 || ||||| ||
 ACC TCTTTGACC TCC
 CC CT
 GAM2537 LOC143920 3' CCTTCTTGCAACCTCTTCCC 37639 A AATT _
 GG AAGA GGTTG GGGAAGG
 || ||| ||||| |||||
 CC TTCT CCAAC TTCTTCC
 C ___ G
 GAM2537 LOC144373 3' CTTCCCCTCCTCCTTCC 37727 A AATT TT
 GGAA GA GG GGGGAAG
 ||| || || |||||
 CCTT CT CC CCCCTTC
 C ___ T_
 GAM2537 LOC144501 3' CCTTCCCCTTCCTCCCTCCA 40424 AA AATT TT
 TGGA GA GG GGGGAAGG
 ||| || || |||||
 ACCT CT CC CCCCTTCC
 CC ___ TT
 GAM2537 LOC144559 3' CCTTCCCAGTTTCTCCCCA 37764 AA TT
 TGG AGAAATTGG GGG
 || ||||| ||
 ACC TCTTTGACC TCC
 CC CT
 GAM2537 LOC145255 3' CTCTCCCAACCCCTGCTCCA 40528 A_ AAATT GA
 TGGA AG GGTTGGG AG
 ||| || ||||| ||
 ACCT TC CCAACCC TC
 CG C___ TC
 GAM2537 LOC145719 5' CTCCCCTTTCCTTTCCA 40575 AAATT TT A
 TGGAAAG GG GGGGA G
 ||||| || |||||
 ACCTTTC CT CCCCT C
 ___ TT C
 GAM2537 LOC147057 3' CCTTCCCCTGTGCCCTTCGCCC 40783 AAA ATT T_
 CA TGG GAA GGT GGGGAAGG
 || ||| || |||||

	ACC CTT CCG CCCCTTCC		
	CCG C__ TGT		
GAM2537 LOC149478 5'	CCTCCACCCCAACCCCTTCTCA 38750	A ATT A__	
	A AGAA GGTG GGGG AGG		
	A TCTT CCAACCCC TCC		
	C CC_ ACC		
GAM2537 LOC150135 3'	CCTTCCCCCTTCCCTCCTTCC 38845	A AATT TT_	
	GGAA GA GG GGGGAAGG		
	CCTT CT CC CCCCTTCC		
	C C__ TTC		
GAM2537 LOC150498 3'	CCCTCCCACCTACCTCCTTCC 38984	A AATT TG_ A	
	GGAA GA GGT GGGGA GG		
	CCTT CT CCA CCCT CC		
	C ____ TCA C		
GAM2537 LOC152220 3'	CCTTCCCCCATTAACCTTCCCCC 41441	AAA A T	
C	GG GAA TTGGT GGGGAAGG		
	CC CTT AATTA CCCCTTCC		
	CCC C C		
GAM2537 LOC155006 3'	CCTCCCCGGCTCATCACTCCCC 39524	AA AA T A	
A	TGG AG AT GGTG GGGGA GG		
	ACC TC TA TCGGCCCT CC		
	CC AC C _		
GAM2537 LOC157848 3'	CTTCCCCTCCCCTTCCCCA 39673	AAA ATT TT	
	TGG GAA GG GGGGAAG		
	ACC CTT CC CCCCTTC		
	C_ C_ CT		
GAM2537 LOC167147 5'	CCCCAAGAGCCACTTCCCTTCC 40226	A_ AT _	
A	TGGAA GAA TGGT TGGGG		
	ACCTT CTT ACCG ACCCC		
	CC C_ AGA		
GAM2537 LOC199786 3'	CCTTTCCACCTATTTCCCTCCA 42619	AA T TG	
	TGGA GAAAT GGT GGGGAAGG		
	ACCT CTTTA CCA CCTTTCC		
	CC T _		
GAM2537 LOC201500 5'	CCCTCCCCTCTCTTTTCTTGCC 43223	A TT TT A	
A	TGG AAGAAA GG GGGGA GG		
	ACC TTCTTT TC CCCCT CC		
	G TC T_ C		
GAM2537 LOC202460 5'	CCTTCCCTGGTGATTCTTTCCA 42982	ATTG TT	
	TGGAAAGAA G GGGGAAGG		

ACCTTTCTT T TCCCTTCC
 AG__ GG
 GAM2537 LOC203248 3' CCCTCCCCGACTCCCCTTCCA 43018 AGAAATT A
 TGGAA GGTGGGGA GG
 |||| ||||| ||
 ACCTT TCAGCCCCT CC
 CACCC__ C
 GAM2537 LOC203504 3' CCCTCCCCACCTCTTCTCTCC 43568 A ATT T A
 GGA AGAA GGT GGGGA GG
 ||| ||| || ||||| ||
 CCT TCTT CCA CCCCT CC
 C CT_ _ C
 GAM2537 LOC203504 5' CTCCCCAGTCTTCTCCA 43569 AA ATT GT A
 TGGA GAA G TGGGGA G
 ||| || | ||||| |
 ACCT CTT C ACCCCT C
 _ _ TG C
 GAM2537 LOC220753 3' CCTCCCCCTTTCCTTCTCTCC 44661 A ATT TT_ A
 GGA AGAA GG GGGG AGG
 ||| ||| || ||||| ||
 CCT TCTT CC CCCC TCC
 C _ TTT C
 GAM2537 LOC221833 3' CCTCTCCCCGACCTCCTCCCA 44455 AAA AATT _
 TGG GA GGTGGGGA AGG
 ||| || ||||| |||
 ACC CT CCAGCCCCT TCC
 _ CCT_ C
 GAM2537 LOC221922 5' CCCTCCCCTTCCTCCTCTGCCA 44532 AA AATT TT A
 TGG AGA GG GGGGA GG
 ||| ||| || ||||| ||
 ACC TCT CC CCCCT CC
 G_ CCT_ TT C
 GAM2537 LOC221935 3' CTTTCCCCTCCTTCCTTTCC 44500 AAATT TT
 GGAAAG GG GGGGAAGG
 ||||| || ||||| ||
 CCTTTC CC CCCCTTCC
 CTT_ T_
 GAM2537 LOC222070 5' CCCTCCCCACCCCTTCTTCCC 45179 A ATT T A
 GG AAGAA GG TGGGGA GG
 || |||| || ||||| ||
 CC TTCTT CC ACCCCT CC
 C C_ C C
 GAM2537 LOC253143 5' CCTCCCCAGCCTCCAGCTCCTC 46315 A AAATT__ A
 TCCA TGGAGG GGTGGGGA GG
 ||| || ||||| ||
 ACCT TC CCGACCCCT CC
 C CTCGACCT _
 GAM2537 LOC254387 3' CTTCCCATCCGCTCTCCA 45488 A AAAT TTG
 TGGAGG TGG GGGGAAG
 ||| || || |||||

ACCT TC GCC CCCTTC
 C ____ TA_
 GAM2537 LOC255515 3' CCTTCCCAGTTTCTCCCCA 45960 AA TT
 TGG AGAAATTGG GGG
 ||| ||||| |||
 ACC TCTTTGACC TCC
 CC CT
 GAM2537 LOC257463 3' CCTGTGCTCCACCTCCCTCCA 35209 AA AATT T A_
 TGGA GA GGT GGGG AGG
 ||| || ||| ||| |||
 ACCT CT CCA CCTC TCC
 CC ____ _ GTG
 GAM2537 LOC56961 5' CCTTCCCCAAGCCAGCTGCCC 31506 AA AAA _
 GG AG TTGGTT GGGGAAGG
 || || ||||| |||||
 CC TC GACCGA CCCCTTCC
 CG ____ A
 GAM2537 LOC57105 3' CCTACCAATTTCTCTCC 21638 AA T
 GGA GAAATTGGT GGG
 ||| ||||| |||
 CCT CTTTAACCA TCC
 C_ _
 GAM2537 LOC90643 3' CCTTTCCCCAACCTCCTCCA 31853 AA AATT _
 TGGA GA GGTTGGGG AAGG
 ||| || ||||| |||
 ACCT CT CCAACCCC TTCC
 C_ ____ CT
 GAM2537 LOC90906 3' CCTTCTCAGTTTCTCCCCA 32149 AA TT
 TGG AGAAATTGG GGG
 ||| ||||| |||
 ACC TCTTTGACT TCC
 CC CT
 GAM2537 LOC91308 3' CCTTCCCTATCACCCCTCCCCC 32656 AAA AATT _
 A TGG GA GGT TGGGAAGG
 ||| || ||| |||||
 ACC CT CCA ATCCCTTCC
 CC_ CC_ CT
 GAM2537 LOC91397 5' CCTCCCCCCTTCTCTTGCCA 32781 A AATT TT A
 TGG AAGA GG GGGGA GG
 ||| ||| || ||||| ||
 ACC TTCT CC CCCCT CC
 G CCTT C_ _
 GAM2537 LOC91974 5' CCCTCCCCAGTGTCTTCCA 33652 A A TT
 TGG AAGA ATTGG GGGG
 ||| ||| ||||| |||
 ACC TTCT TGACC TCCC
 C G CC
 GAM2538 AQP6 5' GGACCTGGGAATGCAC 27615 AAT T G
 GTGCATTCC TAG GT CC
 ||||| ||| |||

CACGTAAGG GTC CA GG

GAM2538 F7 3' TGAACACACATGGATGCAC 5611 T ATTA CC
GTGCAT CCA GTGTG CA
||||| ||| ||||| ||
CACGTA GGT CACAC GT
_ A_ AA

GAM2538 F7 3' TGAACACACATGGATGCAC 21240 T ATTA CC
GTGCAT CCA GTGTG CA
||||| ||| ||||| ||
CACGTA GGT CACAC GT
_ A_ AA

GAM2538 TRPS1 3' CAAGCTACTGGATGCAC 15347 T AT G
GTGCAT CCA TAGT TG
||||| ||| ||||| ||
CACGTA GGT ATCG AC
_ C_ A

GAM2538 TSN 3' ATGGTTACACTAACC AAAAGAC 10983 CA CCAA C
AC
GTG TT TTAGTGTG CCAT
||| || ||||| |||||
CAC AA AATCACAT GGTA
AG AACC T

GAM2538 ARGBP2 5' TGGGCATGTTAGAATACA 9659 C CAAT TG
TG ATTC TAG TGCCCA
|| |||| ||| |||||
AC TAAG ATT ACGGGT
A _ GT

GAM2538 FLJ11800 3' ATGGGCACGTGCCCAGAACACA 24530 CA CAATTA
C
GTG TTC GTGTGCCCAT
||| ||| ||||| |||||
CAC AAG TGCACGGGTA
AC ACCCG_

GAM2538 FLJ12649 3' ATGGGCACACAGAAATGCAC 23833 CCAA A
GTGCATT TT GTGTGCCCAT
||||| || ||||| |||||
CACGTAA AG CACACGGGTA
_ A

GAM2538 GREB1 3' ATGGACACACTAACAGCAC 35851 ATTCCAA C
GTGC TTAGTGTG CCAT
||| ||||| ||||| |||||
CACG AATCACAC GGTA
AC_ A

GAM2538 MGC3329 3' GTTTCTAATTGGAATGC 23528 TGT
GCATTCCAATTAG GC
||||||| ||
CGTAAGGTTAATC TG
TT_

GAM2538 S164 3' ATGGAGTTTAAAATTGGAATGC 30482 AGTGT _
A
TGCATTCCAATT GC CCAT
||||||| || |||||

		ACGTAAGGTTAA	TG GGTA		
		AATT_ A			
GAM2538	TRAF3	3' ACTTAATTGGAAAACAC	30040 CA	T	
		GTG TTCCAATTAG GT			
		CAC AAGGTTAATT CA			
		AA _			
GAM2538	LOC220575	3' ATGGGCACGTGCCCAGAACACA	37528 CA	CAATTA	
	C	GTG TTC GTGTGCCCAT			
		CAC AAG TGCACGGGTA			
		AC ACCCG_			
GAM2538	LOC90593	3' GCACACATAAGAATGCAT	31765	CAA _	
		GTGCATTC TTA GTGTGC			
		TACGTAAG AAT CACACG			
		_ A			
GAM2539	ADAR	3' GCCCCCATGCCCTCTGAG	6775	GAACA A	
		CTCAGAGGGGT GG GC			
		GAGTCTCCCCG CC CG			
		TACC_ _			
GAM2539	ADAR	3' GCCCCCATGCCCTCTGAG	17961	GAACA A	
		CTCAGAGGGGT GG GC			
		GAGTCTCCCCG CC CG			
		TACC_ _			
GAM2539	ADAR	3' GCCCCCATGCCCTCTGAG	17968	GAACA A	
		CTCAGAGGGGT GG GC			
		GAGTCTCCCCG CC CG			
		TACC_ _			
GAM2539	RAB18	3' CTCCTATCATTTTCTGA	22221	G AC	
		TCAGAGGG TGA AGGAG			
		AGTCTTTT ACT TCCTC			
		_ A_			
GAM2539	CXYorf1	3' CTGCAGCCCCCTGAGATA	39907	A GAA	
		TATCTCAG GGGGT CAG			
		ATAGAGTC CCCCCG GTC			
		_ AC_			
GAM2539	EIF4G3	5' CCCTTATCCCTCTGGA	9841 T	ACA	
		TC CAGAGGGGTGA GG			
		AG GTCTCCCTATT CC			
		_ C_			
GAM2539	FLJ20584	3' CCCGAGACCCCTCTGAGA	19560	GAACA A	
		TCTCAGAGGGGT GG G			

		AGAGTCTCCCCA	CC C	
		GAG__ _		
GAM2539	FLJ22390	3' CCTGTTCATGAGGTA	22957	GAGGGG
		TATCTCA	TGAACAGG	
		ATGGAGT	ACTTGTCC	
GAM2539	KIAA1453	3' GCCCCCCCGAGCCCCTCTGAG	24714	GAACA_ A
	A	TCTCAGAGGGGT	GG GC	
		AGAGTCTCCCCG	CC CG	
		AGGCCC	C	
GAM2539	MGC14859	3' GCCCCTGTAGGTCCCTCTGGGA	31005	GA A
		TCTCAGAGGGGT	ACAGG GC	
		AGGGTCTCCCTG	TGTCC CG	
		GA	C	
GAM2539	PRO1048	3' GCTCCTGTCCAAGCATCTGAG	20559	GGGG A
		CTCAGA	TG ACAGGAGC	
		GAGTCT	AC TGTCTCG	
		ACGA	C	
GAM2539	RPH3A	3' GCTCCCACTGCCCCCTGAGATG	17306	A GAACA
		TATCTCAG	GGGGT GGAGC	
		GTAGAGTC	CCCCG CCTCG	
		_	TCAC_	
GAM2539	SNPH	3' CTCCTGTTCTGGCCTGAGA	16293	AGGGGT
		TCTCAG	GAACAGGAG	
		AGAGTC	CTTGTCTC	
		CGGT_		
GAM2539	SPEC1	3' GCTCCTGCCTGCTCTGAGA	21511	G TGAA
		TCTCAGAG	GG CAGGAGC	
		AGAGTCTC	TC GTCCTCG	
		G C_		
GAM2539	ZNF300	5' GCCCCACGTCCTCTGAAATA	27440	C _ AACA A
		TAT TCAGAGGG	GTG GG GC	
		ATA AGTCTCCT	CAC CC CG	
		A	G C_ _	
GAM2539	LOC146756	3' GCTCCTGCCAGGAGCTCTGAGA	40737	GGGTGAA
		TCTCAGAG	CAGGAGC	
		AGAGTCTC	GTCCTCG	
		GAGGACC		
GAM2539	LOC92661	3' GCCTTGCCACCCCTCTGAGG	34722	AA A
		TCTCAGAGGGGTG	CAGG GC	

GGAGTCTCCCCAC GTTC CG
C_ _
GAM2540 FLJ13659 5' GGAGATCTACAGCTAAGACG 24833 ACC A
TGT TAGCT TAGATCTCC
||| |||| |||||
GCA ATCGA ATCTAGAGG
GA_ C
GAM2541 SEL1L 3' AGTTTTGGAAACCCCTGCCAGT 11501 T CC T
GA TCACTGGC GGGGT CTG AGCT
||||| |||| ||| ||||
AGTGACCG CCCCCA GGT TTGA
T AA T
GAM2541 DKFZP434E2135 3' CTGCTACCCCAGCCAAAGA 25114 AC CCCT
TC TGGCTGGGGT GTAG
|| ||||| ||||
AG ACCGACCCCA CGTC
AA T__
GAM2541 FLJ20958 3' AGCCACCACACCCAGCCAGTGA 22646 _ CCCT A
TCACTGGCTGGG GT GT GCT
||||||| || |||
AGTGACCGACCC CA CA CGA
A C__ C
GAM2541 FLJ22833 3' CTACAAGGAACAGCTAGT 23121 GGG C
ACTGGCTG TCC TGTA
||||| ||| ||||
TGATCGAC AGG ACATC
A__ A
GAM2541 GRIN3A 3' AGCCACAGGGACCCAAGCAGTC 28528 _ G G A
GA TC ACTG CT GGGTCCCTGT GCT
|| |||| || ||||| ||||
AG TGAC GA CCCAGGGACA CGA
C _ A C
GAM2541 KIAA0240 3' AGCCACATGCCCCAGCCA 44405 CCC A
TGGCTGGGGT TGT GCT
||||||| ||| |||
ACCGACCCCG ACA CGA
T__ C
GAM2541 KIAA1247 3' AGTGTTCAAAACCCAGCCAAT 30987 C CCC TA_
GA TCA TGGCTGGGGT TG GCT
||| ||||| || |||
AGT ACCGACCCCA AC TGA
A AA_ TTG
GAM2541 KIAA1944 5' AGCCACAGGGACCCCAGGAAG 37225 GG A
CT CTGGGGTCCCTGT GCT
|| ||||| ||||| |||
GA GACCCCAGGGACA CGA
AG C
GAM2541 LBP-9 3' AGCTACAGAGCACCAACCAGCA 15874 G _ CC_
G CTG CTGG GGT CTGTAGCT
||| |||| ||| |||||

			GAC GACC CCA GACATCGA		
			_ AA CGA		
GAM2541	RAI	5'	AGCCACTCTGACTCAGCCA 13467	G CCT A	
			TGGCTGGG TC GT GCT		
			ACCGACTC AG CA CGA		
			_ TCT C		
GAM2541	RES4-25	3'	AGCCACAGCACCCAGCCA 32286	GTCC A	
			TGGCTGGG CTGT GCT		
			ACCGACCC GACA CGA		
			AC_ C		
GAM2541	SDC3	3'	AGCCACCAACCCCAGCCAGTG 16075	CCCT A	
			CACTGGCTGGGGT GT GCT		
			GTGACCGACCCCA CA CGA		
			AC_ C		
GAM2541	TP53INP1	3'	AGCTACAGAAGTTCAGCCATGA 27102	C GTCC	
			TCA TGGCTGGG CTGTAGCT		
			AGT ACCGACTT GACATCGA		
			_ GAA_		
GAM2541	TP53INP1	3'	AGCTACAGAAGTTCAGCCATGA 36113	C GTCC	
			TCA TGGCTGGG CTGTAGCT		
			AGT ACCGACTT GACATCGA		
			_ GAA_		
GAM2541	LOC127262	3'	AGCTACAGACAAAAGCCA 37457	GGG CC	
			TGGCT GTC TGTAGCT		
			ACCGA CAG ACATCGA		
			AAA _		
GAM2541	LOC144563	5'	GCAACCTCAGCCAATGA 37766	C CCC	
			TCA TGGCTGGGGT TGT		
			AGT ACCGACTCCA ACG		
			A _		
GAM2541	LOC146780	5'	GCTACAGGATGAACAGTGA 40742	GCTGGG C	
			TCACTG GTCC TGTAGC		
			AGTGAC TAGG ACATCG		
			AAG_ _		
GAM2541	LOC151632	5'	GCAACCTCAGCCAATGA 41381	C CCC	
			TCA TGGCTGGGGT TGT		
			AGT ACCGACTCCA ACG		
			A _		
GAM2541	LOC161829	5'	GCATGGACCCCAGCAGTGA 40037	G C	
			TCACTG CTGGGGTCC TGT		

AGTGAC GACCCCAGG ACG
 — T
 GAM2541 LOC164714 3' AGCCACAGGAACCGTGAGT 42173 G TGG C A
 ACT GC GGT CCTGT GCT
 ||| || ||| ||||| |||
 TGA TG CCA GGACA CGA
 G — A C
 GAM2541 LOC200904 5' GCAACCTCAGCCAATGA 43360 C CCC
 TCA TGGCTGGGGT TGT
 ||| ||||| |||
 AGT ACCGACTCCA ACG
 A —
 GAM2541 LOC201252 3' AGCTACAGGAATCCAAGAACCA 42555 — G C
 GTG CACTGG CT GGGT CCTGTAGCT
 ||||| || ||| ||||| |||
 GTGACC GA CCTA GGACATCGA
 AA A A
 GAM2541 LOC203083 5' GCAACCTCAGCCAATGA 43478 C CCC
 TCA TGGCTGGGGT TGT
 ||| ||||| |||
 AGT ACCGACTCCA ACG
 A —
 GAM2541 LOC219919 5' GCAACCTCAGCCAGTGA 44800 CCC
 TCACTGGCTGGGGT TGT
 ||||| |||
 AGTGACCGACTCCA ACG
 —
 GAM2541 LOC221795 5' GCAACCTCAGCCAATGA 44423 C CCC
 TCA TGGCTGGGGT TGT
 ||| ||||| |||
 AGT ACCGACTCCA ACG
 A —
 GAM2541 LOC221810 3' AGCTACAGAATTTTGCCAGATG 45081 — T CC
 A TCA CTGGC GGGGT CTGTAGCT
 ||| ||||| ||| ||||| |||
 AGT GACCG TTTTA GACATCGA
 A — A—
 GAM2541 LOC254176 5' GCAACCTCAGCCAATGA 46475 C CCC
 TCA TGGCTGGGGT TGT
 ||| ||||| |||
 AGT ACCGACTCCA ACG
 A —
 GAM2541 LOC256515 5' GCAACCTCAGCCAATGA 46144 C CCC
 TCA TGGCTGGGGT TGT
 ||| ||||| |||
 AGT ACCGACTCCA ACG
 A —
 GAM2541 LOC256594 5' GCAACCTCAGCCAATGA 46377 C CCC
 TCA TGGCTGGGGT TGT
 ||| ||||| |||

AGT ACCGACTCCA ACG
 A ____
 GAM2541 LOC57406 3' AGAAACCCCGAGCCATGA 21838 C CC
 TCA TGGCTGGGGT CT
 ||| ||||| ||
 AGT ACCGACCCCA GA
 _ AA
 GAM2541 LOC92578 5' AGCTACAGCTCTACAACCAG 34606 C GG TCC
 CTGG TG G CTGTAGCT
 ||| || | |||||
 GACC AC C GACATCGA
 A AT TC_
 GAM2542 ADRA2A 5' AGGCGGACGCCCAGGA 6336 A AGG
 TC CTGGGCGTCC GCTT
 || ||||| |||
 AG GACCCGCAGG CGGA
 _ _
 GAM2542 SMURF1 3' CTAGAAGCCCGTTCCCCAGTGG 44412 CGTCCA
 TCACTGGG GGGCTTCTAG
 ||||| |||||
 GGTGACCC CCCGAAGATC
 CTTG_
 GAM2542 BM039 5' AGACGCCGAAACCCAGTGA 20527 CG CAG T
 TCACTGGG TC GGC TCT
 ||||| || ||| |||
 AGTGACCC AG CCG AGA
 AA _ C
 GAM2542 DKFZP434A0131 3' GGCCCTGGACACCCAGTG 21063 C
 CACTGGG GTCCAGGGCT
 ||||| |||||
 GTGACCC CAGGTCCCGG
 A
 GAM2542 FLJ00001 3' AGTTGCCCTGGCCGCCAGTGA 39772 T TT
 TCACTGGGCG CCAGGGC CT
 ||||| ||||| ||
 AGTGACCCGC GGTCCCG GA
 C TT
 GAM2542 FLJ14249 3' AGAAGCCCGAGCCCAAGGA 22797 AC C CCA
 TC TGGG GT GGGCTTCT
 || ||| || |||||
 AG ACCC CG CCCGAAGA
 GA _ A_
 GAM2542 KCNJ9 5' GCCTAGGCGCCCAGCGA 11432 A T A
 TC CTGGGCG CC GGGC
 || ||||| || |||
 AG GACCCGC GG TCCG
 C _ A
 GAM2542 KIAA0789 5' AGAAACAAGGCCCCAGTGA 31843 C CAGGGC
 TCACTGGG GTC TTCT
 ||||| || |||

			AGTGACCC CGG	AAGA	
			C AACA__		
GAM2542	SYT12	3'	GTTCTGGAACCCAGTGA	45430	CG
			TCACTGGG TCCAGGGC		
			AGTGACCC AGGTCTTG		
			A_		
GAM2542	TED	3'	AAGCCCTGACCCAGGGA	17911	A C C
			TC CTGGG GTC AGGGCTT		
			AG GACCC CAG TCCCGAA		
			G _ _		
GAM2542	USP20	3'	AGAAGCCCTGGCCAGTGA	13501	GCGT
			TCACTGG CCAGGGCTTCT		
			AGTGACC GGTCCCGAAGA		

GAM2542	LOC135398	3'	AGAAGCCACTCCAGTGA	37384	C CCAG
			TCACTGGG GT GGCTTCT		
			AGTGACCT CA CCGAAGA		
			_ _____		
GAM2542	LOC164537	5'	AGAAGCCCTGTGGCAGCT	42171	_ _
			GGC GTC CAGGGCTTCT		
			TCG CGG GTCCCGAAGA		
			A T		
GAM2542	LOC169021	5'	AGAAGCCCATTCCCGCCCAGT	40256	TCCA_
			ACTGGGCG GGGCTTCT		
			TGACCCGC CCCGAAGA		
			CCTTA		
GAM2542	LOC205095	3'	AGAAGCCCCTCACAGCCCAGGA	43601	A _ CCA
			TC CTGGGC GT GGGCTTCT		
			AG GACCCG CA CCCGAAGA		
			_ A CTC		
GAM2542	LOC58525	5'	AAGCCCTGGCCAAGATGA	38454	_ G GTC
			TCA CT GGC CAGGGCTT		
			AGT GA CCG GTCCCGAA		
			A A ____		
GAM2542	LOC90246	3'	AGGAGCTGGACCCAGTGA	30998	C GG
			TCACTGGG GTCCA GCTTCT		
			AGTGACCC CAGGT CGAGGA		
			_ _____		
GAM2542	LOC92017	3'	GAGCTACTAAACGCTCAGTGA	33709	CC _
			TCACTGGGCGT AG GGCTT		

AGTGA~~CT~~CGCA TC TCGAG
 AA A
 GAM2542 LOC93166 3' AGCGGATGCCCAATGA 35458 C AGG
 TCA TGGGCGTCC GCT
 ||| ||||| |||
 AGT ACCCGTAGG CGA
 A ____
 GAM2543 EDN3 3' CCAGCTCAAGGCTATTAGG 5580 CACAT T C
 CCT TGGT CT GAGCTGG
 ||| |||| || |||||
 GGA ATCG GA CTCGACC
 TT____ _ A
 GAM2543 INPP5D 3' CCAGCTTCCTATGCAAGG 40304 CA T TTCTC
 CCT CAT GG GAGCTGG
 ||| ||| || |||||
 GGA GTA CC TTCGACC
 AC T ____
 GAM2543 LCP1 3' CCATTGTGAACCAATGCAAG 8083 CA T GC
 CT CATTGGTTC CGA TGG
 || ||||| ||| |||
 GA GTAACCAAG GTT ACC
 AC T ____
 GAM2543 DOCK3 3' CCCAGCTCAAGGAGCTTATGCA 33032 CA T C_
 GG CCT CAT GGTTCT GAGCTGGG
 ||| ||| ||||| |||||
 GGA GTA TCGAGG CTCGACCC
 C_ T AA
 GAM2543 FASTK 3' CCCAGCTCAAGAGCTACCTGAG 24727 CAT C
 G CCTCA TGGTTCT GAGCTGGG
 |||| ||||| |||||
 GGAGT ATCGAGA CTCGACCC
 CC_ A
 GAM2543 FLJ20004 5' CCCAGCTCAAGAAGGCGCTGCA 45643 _ CATTGG C
 GG CCT CA TTCT GAGCTGGG
 ||| || |||| |||||
 GGA GT AAGA CTCGACCC
 C CGCGG_ A
 GAM2543 KIAA0914 5' CCCAGCTTAGCCACTGTAAG 17035 C T CTC
 CT ACA TGGTT GAGCTGGG
 || ||| |||| |||||
 GA TGT ACCGA TTCGACCC
 A C ____
 GAM2543 KIAA1030 3' CCCAACTCCCTTCTCAACATGG 44819 CA TTCTC C
 GG CCTCA TTGG GAG TGGG
 |||| ||| || |||
 GGGGT AACT CTC ACCC
 AC CTTCC A
 GAM2543 L3MBTL2 5' CCCATCTTCAGAACCAATGGAG 42787 A C C
 G CCTC CATTGGTTCT GAG TGGG
 |||| ||||| ||| |||

			GGAG GTAACCAAGA TTC ACCC		
			— C T		
GAM2543	MGC15631	3'	CCCAACCCGAGAACCGGGG	26491	ACATT AGC
			CCTC GGTTCCTG TGGG		
			GGGG CCAAGAGC ACCC		
			— CCA		
GAM2543	SCAMP5	3'	CCCGGGGAGAGAACCAGTATGA	29073	C GAG
	G		CTCA ATTGGTTCTC CTGGG		
			GAGT TGACCAAGAG GGCCC		
			A AGG		
GAM2543	STATI2	3'	CCCGTTAATAAAAACCAATGTA	45370	C CTCG__ T
	GG		CCT ACATTGGTT AGC GGG		
			GGA TGTAACCAA TTG CCC		
			— AAATAA —		
GAM2543	STATI2	3'	CCCGTTAATAAAAACCAATGTA	9959	C CTCG__ T
	GG		CCT ACATTGGTT AGC GGG		
			GGA TGTAACCAA TTG CCC		
			— AAATAA —		
GAM2543	LOC158436	5'	CAGCTCGAGTTGTGGG	41992	TTGGTT
			CTCACA CTCGAGCTG		
			GGGTGT GAGCTCGAC		
			T__		
GAM2543	LOC196510	3'	CCATCAAACCAATGGAGG	42393	A CTC GC
			CCTC CATTGGTT GA TGG		
			GGAG GTAACCAA CT ACC		
			— A__ —		
GAM2543	LOC200093	3'	CCCAGCTCAAACCTGACAGGAG	31596	ACA TG CTC
			CTC T GTT GAGCTGGG		
			GAG A CAA CTCGACCC		
			GAC GT A__		
GAM2543	LOC200220	3'	CCATCAAACCAATGGAGG	42742	A CTC GC
			CCTC CATTGGTT GA TGG		
			GGAG GTAACCAA CT ACC		
			— A__ —		
GAM2543	LOC203536	3'	CCCAACTCATTGAATGTGA	43056	_TG TCTC C
			TCACA T GT GAG TGGG		
			AGTGT A TA CTC ACCC		
			A GT __ A		
GAM2543	LOC91149	3'	CCAGCTTTTCAATGTGA	32454	TTCTC
			TCACATTGG GAGCTGG		

		AGTGTA ACT TCGACC		
		T_____		
GAM2544 BPAG1	3'	CGTTAGGGATACCTCATGACA 17810	AC_	A_
		TGTCATGG ATC TAACG		
		ACAGTACT TAG ATTGC		
		CCA GG		
GAM2544 NOTCH2	3'	GTGCTGTGATGCCCATGACA 23650	A	A
		TGTCATGG CATCATA CGC		
		ACAGTACC GTAGTGT GTG		
		C C		
GAM2544 CHST3	3'	ACGCGTTAAAGGGCCATGACA 10475	ACATCA	
		TGTCATGG TAACGCGT		
		ACAGTACC ATTGCGCA		
		GGGAA_		
GAM2545 HSF2BP	5'	CCCGGCTAAGCCAGAAGAGCCA 13896	GA__	
		TGGCTCTTTTGGT CGGG		
		ACCGAGAAGACCG GCCC		
		AATCG		
GAM2545 MYD88	3'	AGTCCCATCACTGAGGGAGCC 8295	TG	C
		GGCTCTTT GTGA GGGACT		
		CCGAGGGA CACT CCCTGA		
		GT A		
GAM2545 PTPN7	3'	CCCCATCTCAGAGCTCAGA 8709	_	TTT AC
		TCTG GCTCT GGTG GGG		
		AGAC CGAGA CTAC CCC		
		T CT_ _		
GAM2545 PTPN7	3'	CCCCATCTCAGAGCTCAGA 27887	_	TTT AC
		TCTG GCTCT GGTG GGG		
		AGAC CGAGA CTAC CCC		
		T CT_ _		
GAM2545 PTPN7	3'	CCCCATCTCAGAGCTCAGA 27890	_	TTT AC
		TCTG GCTCT GGTG GGG		
		AGAC CGAGA CTAC CCC		
		T CT_ _		
GAM2545 SMARCA5	5'	GCCCGCGGAAGAGCAGA 9656	G	GTGA A
		TCTG CTCTTTTG CGGG C		
		AGAC GAGAAGGC GCCC G		
		_ _ _ C		
GAM2545 SNCAIP	5'	AGTGATGACCAAAAGAACCAGA 45903	C	GA GG
		TCTGG TCTTTTGGT CG ACT		

AGACC AGAAAACCA GT TGA
 A _ AG
 GAM2545 BTN2A2 3' AGTCCCACCATAAGAGCTA 13857 T GAC
 TGGCTCTT TGGT GGGACT
 ||||| ||| |||||
 ATCGAGAA ACCA CCCTGA
 T _
 GAM2545 DKFZP434A0131 3' AGCCCCGCCACCAACTAGGGCG 21061 G T_ A A
 AGA TCT GCTCT TTGGTG CGGG CT
 || |||| ||||| ||| ||
 AGA CGGGA AACCAC GCCC GA
 G TC C C
 GAM2545 FBXO27 3' CCCGTCTCTACTAAAAATCCA 36833 CTC _
 TGG TTTTGGT GACGGG
 || ||||| |||||
 ACC AAAATCA CTGCCC
 TA_ TCT
 GAM2545 FLJ31762 3' CCTCACAAAAGAGCCAGA 29417 G C
 TCTGGCTCTTTTG TGA GG
 ||||| ||| ||
 AGACCGAGAAAAC ACT CC
 _ _
 GAM2545 KIAA0057 3' GCCCGTCAGGGGCCA 14620 TTTGG A
 TGGCTCT TGACGGG C
 ||||| ||||| |
 ACCGGGG ACTGCCC G
 C
 GAM2545 PAXIP1L 3' AGCCTTCTTCCAAAAGAGCCAG 34738 T_ C A
 A TCTGGCTCTTTTG GA GGG CT
 ||||| || ||| ||
 AGACCGAGAAAACC CT TCC GA
 TT _ _
 GAM2545 PRO0456 3' CCCATCACTTTGGGAGGCCAGA 15394 _ TT C
 TCTGGC TCTT GGTGA GGG
 ||||| ||| ||||| ||
 AGACCG AGGG TCACT CCC
 G TT A
 GAM2545 PRO2964 3' AGCCTGGGCAAAAAGAGCCAGA 20630 G GA A
 TCTGGCTCTTTT GT CGGG CT
 ||||| || ||| ||
 AGACCGAGAAAA CG GTCC GA
 A G_ _
 GAM2545 SPTLC2 3' CCCGTCTCTACTAAAAAGACA 11276 G C _
 TG CT TTTTGGT GACGGG
 || || ||||| |||||
 AC GA AAAATCA CTGCCC
 A _ TCT
 GAM2545 SSR3 3' CCCGTCTCTACTAAAAATACCA 13970 CTC _
 TGG TTTTGGT GACGGG
 || ||||| |||||

ACC AAAATCA CTGCCC
 ATA TCT
 GAM2545 ZNF145 5' AGCCCCGCCACGCAGAGCCCAG 12617 _ TT_ AC A
 A TCTGG CTCT TGGTG GGG CT
 ||||| |||| |||| ||||
 AGACC GAGA ACCGC CCC GA
 C CGC _ _
 GAM2545 LOC115073 5' AGTCCCGGAGGAAAAAGAGCCA 36238 GGTGA
 G CTGGCTCTTTT CGGGACT
 ||||| |||||
 GACCGAGAAAA GCCCTGA
 AGGAG
 GAM2545 LOC145719 3' AGTCCCATCACCAGGCAGCCAT 40570 _ CT C
 GA TC TGGCT TTTGGTGA GGGACT
 || |||| ||||| |||||
 AG ACCGA GGACCACT CCCTGA
 T C_ A
 GAM2545 LOC145720 3' AGTCCCATCACCAGGCAGCCAT 40560 _ CT C
 GA TC TGGCT TTTGGTGA GGGACT
 || |||| ||||| |||||
 AG ACCGA GGACCACT CCCTGA
 T C_ A
 GAM2545 LOC197114 3' AGTCCCATCACCAGGGAGCCAT 43184 _ T C
 GA TC TGGCTCTTT GGTGA GGGACT
 || ||||| |||| |||||
 AG ACCGAGGGA CCACT CCCTGA
 T _ A
 GAM2545 LOC197117 3' AGTCCCATCACCAGGCAGCCAT 43193 _ CT C
 GA TC TGGCT TTTGGTGA GGGACT
 || |||| ||||| |||||
 AG ACCGA GGACCACT CCCTGA
 T C_ A
 GAM2545 LOC222252 5' TCCTAAGCCAAAAGAACA 45286 GC GAC
 TG TCTTTTGGT GGGA
 || ||||| ||||
 AC AGAAAACCG TCCT
 A_ AA_
 GAM2546 CGTHBA 3' CTGCAGAGCCCCGCTGTC 14358 A ACT
 GACA CGGGGCTCT CAG
 |||| ||||| ||||
 CTGT GCCCCGAGA GTC
 C C_
 GAM2546 COL11A2 3' CACTGAGTATGTTTCATTGCCA 27975 A CG TC
 TG CAA GGGC TACTCAGTG
 || |||| ||||| |||||
 AC GTT CTTG ATGAGTCAC
 C A_ T_
 GAM2546 COL11A2 3' CACTGAGTATGTTTCATTGCCA 27980 A CG TC
 TG CAA GGGC TACTCAGTG
 || |||| ||||| |||||

AC GTT CTTG ATGAGTCAC
 C A_ T_
 GAM2546 DKFZP434K028 3' TCACTGAGCAAAGGAGCAACTG 44773 ACGGG A____
 TC GACA GCTCT CTCAGTGA
 ||| |||| |||||
 CTGT CGAGG GAGTCACT
 CAA_ AAAC
 GAM2546 FLJ20464 5' CACCCTTCGGAGCCCCGCTTTC 19500 CAA ACTCA
 A TGA CGGGGCTCT GTG
 || ||||| ||
 ACT GCCCGAGG CAC
 TTC CTTCC
 GAM2546 KIAA0515 3' CACTCCCGAAAGCTCCGTTGTC 31920 CTACTC
 A TGACAACGGGGCT AGTG
 ||||| |||
 ACTGTTGCCTCGA TCAC
 AAGCCC
 GAM2546 KIAA0542 3' CACCAAGCAGAACCTCTGGTC 32857 AAC C A CA
 GAC GGGG TCT CT GTG
 || ||| || ||
 CTG CTCC AGA GA CAC
 GT_ A C AC
 GAM2546 VRP 5' TCACTGAGCAGGGACTGTCA 13926 ACGGGG A
 TGACA CTCT CTCAGTGA
 |||| ||| |||||
 ACTGT GGGA GAGTCACT
 CA____ C
 GAM2546 LOC148756 3' CACTGAGTACCTACCATGTGCC 40902 A ACG GCTC
 A TG CA GG TACTCAGTG
 || || || |||||
 AC GT CC ATGAGTCAC
 C GTA ATCC
 GAM2546 LOC254413 5' CACGGGGAGTCCCATTGCCA 46399 A C ACTCA
 TG CAA GGGGCTCT GTG
 || ||| ||||| ||
 AC GTT CCCTGAGG CAC
 C A GG____
 GAM2546 LOC255974 5' CACCAAGAGCCCTCTGTCA 46555 AC ACTCA
 TGACA GGGGCTCT GTG
 |||| ||||| ||
 ACTGT TCCCGAGA CAC
 C_ AC____
 GAM2546 LOC256306 3' CACCAGGCCCGTTGCA 46235 A T ACTCA
 TG CAACGGGGC CT GTG
 || ||||| || ||
 AC GTTGCCCCG GA CAC
 _ C____
 GAM2547 GUCY1A3 5' CAGCAGGGTAAGAGACACCA 31779 AC A
 TGGTGTTTT ACCCT CTG
 ||||| |||| ||

ACCACAGAG TGGGA GAC
 AA C
 GAM2547 BIRC8 5' GTGTATAAAACACAGTGC 27197 G ____
 GCACTG TGTTT TACAC
 ||||| ||||| |||||
 CGTGAC ACAA ATGTG
 _ AT
 GAM2547 CHST3 3' CAGTAGGGCCCCCAGCCAGCGC 10477 A GTTTTACA
 GC CTGGT CCCTACTG
 || ||||| |||||
 CG GACCG GGGATGAC
 C ACCCCC_
 GAM2547 FLJ10201 3' CAGCAGGGCATAGGGCACGCA 19761 _ CA A
 TG GTGTTTTA CCCT CTG
 || ||||| |||||
 AC CACGGGAT GGA GAC
 G AC C
 GAM2547 FLJ33069 3' TAGGCAAAACACCAATGC 29475 C ACAC
 GCA TGGTGTTTT CTA
 ||| ||||| |||||
 CGT ACCACAAAA GGAT
 A C_
 GAM2547 KIAA0478 5' AGAGCTAAACACCAAGTGC 16974 TACACC A
 GCACTGGTGTTT CT CT
 ||||| ||||| |||||
 CGTGACCACAAA GA GA
 TC_____
 GAM2547 KIAA0478 3' CAGAAGGCACAAACCCAGTGC 16975 T TACAC A
 GCACTGG GTTT CCT CTG
 ||||| ||||| |||||
 CGTGACC CAAA GGA GAC
 _ CAC__ A
 GAM2547 RNF2 3' TAGGGTGTAGACCTCCAGT 14077 TGT
 ACTGG TTTACACCCTA
 ||||| ||||| |||||
 TGACC AGATGTGGGAT
 TCC
 GAM2547 LOC130271 5' CAGCAGGGCATGTTACCA 36986 TTTT _ A
 TGGTG ACA CCCT CTG
 ||||| ||||| |||||
 ACCAT TGT GGA GAC
 _ AC C
 GAM2547 LOC143943 3' CAGTAGGGCATAATTCAGAGC 40382 A TGTT CA
 GC CTGG TTA CCCTACTG
 || ||||| |||||
 CG GACT AAT GGGATGAC
 A T__ AC
 GAM2548 DKFZP434P0721 5' ACAACATCAGTACACTC 31867 TG A C
 GAGT GTG TGA GTTGT
 ||||| ||||| |||||

CTCA CAT ACT CAACA
 _ G A
 GAM2548 LOC149386 5' ACAACGCCATCCGCTCC 40984 TGGT A
 GGAGT GATG CGTTGT
 |||| ||| |||||
 CCTCG CTAC GCAACA
 C_ C
 GAM2549 DDX6 5' GAGAGCAAGTTACTGCTGCT 10645 ACTA
 AGCAGCAGTAGCT TTCTC
 ||||| ||||
 TCGTCGTCATTGA GAGAG
 AC_
 GAM2549 IL16 5' GCGAGAGAGCTGCTGCCACTGC 10840 _ TA A
 TGCT AGCAGCAGT AGC CT TTCTCGC
 ||||| ||| || |||||
 TCGTCGTCA TCG GA GAGAGCG
 CCG TC _
 GAM2549 KIF5B 5' GCGGCGCAGCTGACTGCTGC 10850 _ ACTATTC
 GCAGCAGT AGCT TCGC
 ||||| ||| ||||
 CGTCGTCA TCGA GGCG
 G CGC_
 GAM2549 OSR1 3' AGAATAGTGGCTTACCGCT 11587 A _
 AGC GTA GCTACTATTCT
 ||| ||| |||||
 TCG CAT CGGTGATAAGA
 C T
 GAM2549 APEG1 3' GCGAGTGCATGTGCTACTGCTG 35694 T TATT_
 CT AGCAGCAGTAGC AC CTCGC
 ||||| ||| ||||
 TCGTCGTCATCG TG GAGCG
 _ TACGT
 GAM2549 DCAMKL1 5' GCGCTCCAGCAGCTGCTGCCGC 11115 A A ATTCT
 GC GCAGTAGCT CT CGC
 || ||||| || |||
 CG CGTCGTCA GA GCG
 C C CCTC_
 GAM2549 FLJ10853 3' AGGACAGCACTGCTGCT 20211 A ACTA
 AGCAGCAGT GCT TTCT
 ||||| ||| ||||
 TCGTCGTCA CGA AGGA
 _ C_
 GAM2549 KIAA0397 3' TGGGAGTAGCCCCACTGC 30896 A_ TAT
 GCAGT GCTAC TCTCG
 |||| |||| ||||
 CGTCA CGATG AGGGT
 CCC _
 GAM2549 KIAA1344 3' GCAAGTCTTCCAGCCCTGCTGC 35869 TA ACTATT C
 T AGCAGCAG GCT CT GC
 ||||| ||| || ||

		TCGTCGTC CGA GA CG		
		C_ CCTTCT A		
GAM2549 TED	3'	GCCGAATAGGCTACTGC 17919	TA	TC
		GCAGTAGC CTATTC GC		
		CGTCATCG GATAAG CG		
		_ C_		
GAM2549 LOC147229 5'		GCGAGGCCCCAGCTCTGCTGCT 38319	T	ACTAT
		AGCAGCAG AGCT TCTCGC		
		TCGTCGTC TCGA GGAGCG		
		_ CCCC_		
GAM2549 LOC219722 5'		GCGTCGTGGTAGCTACCACGCT 44710	AGCA	TCT
		AGC GTAGCTACTAT CGC		
		TCG CATCGATGGTG GCG		
		CAC_ CT_		
GAM2549 LOC253758 5'		GCGAGGAGAGGCAGCACTGCTG 46321	A	A_ A
	CT	AGCAGCAGT GCT CT TTCTCGC		
		TCGTCGTCA CGA GA AGGAGCG		
		_ CG G		
GAM2549 LOC253955 5'		GCGTGGTGCAGCTCTGCTGCT 45327	T	ACTAT T
		AGCAGCAG AGCT TC CGC		
		TCGTCGTC TCGA GG GCG		
		_ CGT_ T		
GAM2549 LOC51026 3'		GCAAGAATAGTATCTGCT 18140	C	C
		AGTAG TACTATTCT GC		
		TCGTC ATGATAAGA CG		
		T A		
GAM2549 LOC91574 3'		AGAATAATGGCTACTTCT 33047	C	C
		AG AGTAGCTA TATTCT		
		TC TCATCGGT ATAAGA		
		T A		
GAM2549 LOC92231 3'		CGAGCTGTAGCCACCCTGCT 34010	CA A	TATT
		AGCAG GT GCTAC CTCG		
		TCGTC CA CGATG GAGC		
		C_ C TC_		
GAM2550 CNGB3	3'	CATGAATTAGCTAGCATTAGCA 21176	CCTG	A
	TA	TATGCTAA AGC AATTCATG		
		ATACGATT TCG TTAAGTAC		
		ACGA A		
GAM2550 FKBP5	3'	TATGGATTGCCAAGTCAGCATA 10324	A C A	A
		TATGCT AC TG GCAA TTCATG		

			ATACGA TG AC CGTT AGGTAT		
			C A _ _		
GAM2550	KIAA0939	3'	GAGTCGCCCCAGGTTAGC	31065	A AA
			GCTAACCTG GC ATTC		
			CGATTGGAC CG TGAG		
			C C_		
GAM2550	LOC200010	3'	CATGAATTTACCCAGGAGAGT	43277	AA AGC
			GCT CCTG AAATTCATG		
			TGA GGAC TTAAAGTAC		
			GA CCA		
GAM2551	ARNT2	3'	GCAGATTTCTTCTTGAT	16936	C GATGGA
			ATCA AGAAGAAA TGC		
			TAGT TCTTCTTT ACG		
			_ AG_		
GAM2551	BAZ1B	3'	AGCACCCAAGCTCTTCTGT	26190	AAGA A
			ACAGAAGA TGG TGCT		
			TGTCTTCT ACC ACGA		
			CGA_ C		
GAM2551	C1orf6	3'	AGCATTTCGTTCTTCTGT	21327	AGAT
			ACAGAAGAA GGATGCT		
			TGTCTTCTT CTTACGA		
			GG_		
GAM2551	CENPF	3'	AGTGTTTATCTTTCTCT	18470	A
			AGA GAAAGATGGATGCT		
			TCT CTTTCTATTTGTGA		
			_		
GAM2551	CHS1	3'	AGCCGTCTGTCTCTCCCATATG	5523	CAGAA A _
	AT		ATCA GA AGATGGATG CT		
			TAGT CT TCTGTCTGC GA		
			ATACC C C		
GAM2551	CRTL1	5'	GCATCCGAACCTCCTGGAT	7615	A A AAAGA
			ATC CAG AG TGGATGC		
			TAG GTC TC GCCTACG		
			_ C AA_		
GAM2551	DAPK1	3'	AGCAAGTTTCTTCCATGAT	11386	CA ATGGA
			ATCA GAAGAAAG TGCT		
			TAGT CTTCTTTT ACGA		
			AC GA_		
GAM2551	HNRPD	3'	GGCTTCATCTTCTCCCTGT	11954	A_ A T
			ACAG AGAA GATGGA GCT		

			TGTC TCTT CTACTT CGG		
			CC _ _		
GAM2551	NPTX1	3'	GCATCCATCCCTGCTGT 8356	A AAA	
			ACAG AG GATGGATGC		
			TGTC TC CTACCTACG		
			G C__		
GAM2551	PLIN	3'	AGCACTGAACTCCTCTGTGAT 8535	A AAGAT A	
			ATCACAGA GA GG TGCT		
			TAGTGTCT CT TC ACGA		
			C CAAG_ _		
GAM2551	PPP1R12A	3'	CACTTGCTCTTCTGTGAT 8304	_ A	
			ATCACAGAAGA AAG TG		
			TAGTGTCTTCT TTC AC		
			CG _		
GAM2551	PTGFRN	3'	AGCACCATGTTTTTTCTATGA 33361	C G A	
			TCA AGAAGAAA ATGG TGCT		
			AGT TCTTTTTT TACC ACGA		
			A G _		
GAM2551	PXN	3'	TTGTCTTTGTTCTGTGAT 8759	G TG	
			ATCACAGAA AAAGA G		
			TAGTGTCTT TTTCT T		
			G GT		
GAM2551	SMURF1	3'	AGCATCCAGCTTCTGTG 44409	AAAGA	
			CACAGAAG TGGATGCT		
			GTGTCTTC ACCTACGA		
			G__		
GAM2551	STAC	3'	GGCTTCCTCTCTTTGTGAT 9119	A AA T T	
			ATCACAGA GA GA GGA GCT		
			TAGTGTTT CT CT CCT CGG		
			_ _ _ T		
GAM2551	TEM8	3'	CTTCTTCTTTCTGTGAT 25917	GA T	
			ATCACAGAA AAGA GG		
			TAGTGTCTT TTCT TC		
			TC T		
GAM2551	TNC	3'	AGCATGGGCCTCACCTCCTCTG 7934	A AA_ T _	
	TGAT		ATCACAGA GA GA GG ATGCT		
			TAGTGTCT CT CT CC TACGA		
			C CCA _ GGG		
GAM2551	TPM4	3'	AGCGTTTGCTTTCGCCTGT 9300	AA A GG	
			ACAG GAAAG T ATGCT		

		TGTC CTTTC G TGCGA		
		CG _ TT		
GAM2551	XPNPEP2	3' AGCTAGTCTCTTCTCTTCTGTG 9433	_ T AT_	
	AT	ATCACAGAAGA AAGA GG GCT		
		TAGTGTCTTCT TTCT CT CGA		
		C _ GAT		
GAM2551	BRAG	5' CCATCCATCTTCTGTGAT 16940	AA	
		ATCACAGAAGA GATGG		
		TAGTGTCTTCT CTACC		
		AC		
GAM2551	C20orf98	3' GGCGTCATCTCTTCTGT 35416	A G	
		ACAGAAGA AGATG ATGCT		
		TGTCTTCT TCTAC TGCGG		
		C _		
GAM2551	ENDO180	3' AGCATCCATCACTCCTGTG 12674	A AAA	
		CACAG AG GATGGATGCT		
		GTGTC TC CTACCTACGA		
		C A_		
GAM2551	FBXO4	3' ATTTATTTTCCCCTGTGAT 27262	AA A	
		ATCACAG GAA GATGGAT		
		TAGTGTC CTT TTATTTA		
		CC _		
GAM2551	FLJ10512	3' AGCATAAATCTCTTCTGT 19902	AA GG	
		ACAGAAGA GAT ATGCT		
		TGTCTTCT CTA TACGA		
		_ AA		
GAM2551	FLJ11457	3' AGCTATGTCTTTCTCCAGTGAT 24094	AGA GAT	
		ATCAC AGAAAGATG GCT		
		TAGTG TCTTTCTGT CGA		
		ACC AT_		
GAM2551	FLJ14146	3' AGCATCCTGTCTTCTTCTGTG 24029	A _	
		CACAGAAGAA GAT GGATGCT		
		GTGTCTTCTT CTG CCTACGA		
		_ T		
GAM2551	FLJ20034	3' AGCATCCACCAGATTCTATGG 19128	C GAAAGA	
		TCA AGAA TGGATGCT		
		GGT TCTT ACCTACGA		
		A AGACC_		
GAM2551	FLJ20094	3' CATCACAGTATTCTGTGAT 19208	GAAAGA _	
		ATCACAGAA TG GATG		

			TAGTGTCTT AC CTAC ATG___ A	
GAM2551	GBTS1	3'	AGCATGTTTGTTCCTCTGTG 29725 CACAGA GAAAG ATGCT GTGTCT CTTTT TACGA C GTTTG	A ATGG_
GAM2551	HCC-4	5'	AGCATCACATCTTCTGTG 28896 CACAGA AGATG GATGCT GTGTCT TCTAC CTACGA _____ A	AGAA _
GAM2551	HRIHFB2072	3'	GCATCCCTTTTGTGA 26271 TCACAGAAG GGATGC AGTGTTTTC CCTACG	AAAGAT
GAM2551	KIAA0255	3'	AGCATCCACTTGTCTGTG 16413 CACAGA AAG TGGATGCT GTGTCT TTC ACCTACGA G___ _	AGA A
GAM2551	KIAA1198	3'	AGCATCCACTCTCCTGCGGT 31702 ATC CAG AGA TGGATGCT TGG GTC TCT ACCTACGA C C C___	A A AAGA
GAM2551	KIAA1473	3'	AGCATTATGACCTCTTCTATG 34995 TCA AGAAGA ATGGATGCT AGT TCTTCT TATTACGA A CCAG	C AAG_
	A			
GAM2551	KIAA1538	3'	GGCCTCCCTGCTCTGTGAT 35431 ATCACAGA AG GGA GCT TAGTGTCT TC CCT CGG CG___ _ C	AGAA AT T
GAM2551	MGC15906	5'	GCATCCACCTCTGTGG 26707 TCACAGA G TGGATGC GGTGTCT C ACCTACG _____ C	AGAAA A
GAM2551	MGC22014	3'	CTATCTCCCTTCTGTGAT 32218 ATCACAGAAG AGATGG TAGTGTCTTT TCTATC CCC	AA_
GAM2551	MGC5466	5'	AGCGGTTTCTCTGTTCTGTGAT 36159 ATCACAGAA AGA TGCT 	GAA TGGA

			TAGTGTCTT TCT GCGA		
			GTC TTG_		
GAM2551	PELI1	3'	ATCTATTTTTCTCCCATGAT 21815	CAGA	
			ATCA AGAAAGATGGAT		
			TAGT TCTTTTATCTA		
			ACCC		
GAM2551	RAB3GAP	3'	GCATTCTCTTCTGTGA 33245	AAGAT	
			TCACAGAAGA GGATGC		
			AGTGTCTTCT CTTACG		

GAM2551	SEC31B-1	3'	CCATTCCTTCTGTGAT 17760	AAA	
			ATCACAGAAG GATGG		
			TAGTGTCTTC TTACC		
			C_		
GAM2551	SLC38A4	3'	AGCACCATTTTTTTCTTC 19756	__ A	
			GAAGAAA GATGG TGCT		
			CTTCTTT TTACC ACGA		
			TT _		
GAM2551	TBX4	3'	AGCATCCATCTTCTG 20544	AGAA	
			CAGA AGATGGATGCT		
			GTCT TCTACCTACGA		

GAM2551	TOB2	3'	AGCACCATCTGTTCCCCT 45762	AA _ A	
			AG GAA AGATGG TGCT		
			TC CTT TCTACC ACGA		
			CC G _		
GAM2551	ZNF221	5'	AGTTACCCTTTATTCTGTGAT 15008	G AT AT	
			ATCACAGAA AAAG GG GCT		
			TAGTGTCTT TTTC CC TGA		
			A _ AT		
GAM2551	LOC144395	3'	AGCATCTGTTCTTCTGAGA 37732	A AAA	
			TC CAGAAG GATGGATGCT		
			AG GTCTTC TTGTCTACGA		
			A C_		
GAM2551	LOC145719	5'	GCCCCCTTCTTCTGTGA 40577	AGAT AT	
			TCACAGAAGAA GG GC		
			AGTGTCTTCTT CC CG		
			_____ CC		
GAM2551	LOC145720	5'	GCCCCCTTCTTCTGTGA 40566	AGAT AT	
			TCACAGAAGAA GG GC		

	AGTGTCTTCTT CC CG	
	____ CC	
GAM2551 LOC146802 3'	AGCTGGAGTTTTCTTCTGTGA 38245	ATGGAT
	TCACAGAAGAAAG GCT	
	AGTGTCTTCTTTT CGA	
	GAGGT_	
GAM2551 LOC148198 3'	AGCATTTATGACCTCTTCTATG 34999	C AAG_
A	TCA AGAAGA ATGGATGCT	
	AGT TCTTCT TATTTACGA	
	A CCAG	
GAM2551 LOC150203 5'	GCAATACCTTCTGTGAT 30349	AAAG GGA
	ATCACAGAAG AT TGC	
	TAGTGTCTTC TA ACG	
	CA_ _	
GAM2551 LOC150350 3'	ATCTTTTCTTTCTTCCAGAT 38929	ACA T_
	ATC GAAGAAAGA GGAT	
	TAG CTTCTTTCT TCTA	
	AC_ TT	
GAM2551 LOC151647 3'	GTTTCCCTACTTCTGTGA 39156	AA AT T
	TCACAGAAG AG GGA GC	
	AGTGTCTTC TC CCT TG	
	A_ _ T	
GAM2551 LOC197114 5'	GCCCCCTTCTTCTGTGA 43189	AGAT AT
	TCACAGAAGAA GG GC	
	AGTGTCTTCTT CC CG	
	____ CC	
GAM2551 LOC197117 3'	GCCCCCTTCTTCTGTGA 43196	AGAT AT
	TCACAGAAGAA GG GC	
	AGTGTCTTCTT CC CG	
	____ CC	
GAM2551 LOC221178 3'	AGCTCTTACTCTCTTCTGT 44925	A AT T
	ACAGAAGA AG GGA GCT	
	TGTCTTCT TC TCT CGA	
	C AT _	
GAM2551 LOC221398 3'	AGCATTTGCTTTCCTCTGAGAT 43749	A A A GG
	ATC CAGA GAAAG T ATGCT	
	TAG GTCT CTTTC G TACGA	
	A C _ TT	
GAM2551 LOC221656 3'	AGCCATGTTTTTCTTCTGTGA 44292	GAT
	TCACAGAAGAAAGATG GCT	

		AGTGTCTTCTTTTGT CGA		
		AC_		
GAM2551	LOC254018 3'	AGCTACCTCCCTTCTGTG 46317	AAA T AT	
		CACAGAAG GA GG GCT		
		GTGTCTTC CT CC CGA		
		C_ _ AT		
GAM2551	LOC91012 3'	TATCTACTCTTCTGTGAT 32285	A_	
		ATCACAGAAGA AGATG		
		TAGTGTCTTCT TCTAT		
		CA		
GAM2552	OSBPL8 3'	TAATCGTTTATGCCATGA 21909	C TT	
		TCAT GCATGGAT GATTA		
		AGTA CGTATTTG CTAAT		
		C _		
GAM2553	CYP24 3'	GACCTACAACAGCTAAAT 6426	TAA	
		ATTTAGCTGTTGT TC		
		TAAATCGACAACA AG		
		TCC		
GAM2553	C1QTNF7 3'	GCTTACAGATAACAGCCAAA 25665	A AATC	
		TTT GCTGTTGTT GTAAGC		
		AAA CGACAATAG CATTG		
		C A_		
GAM2553	KIAA1274 3'	GCATTAAAAACAGCTAAAT 43910	G C	
		ATTTAGCTGTT TTAAT GT		
		TAAATCGACAA AATTA CG		
		A _		
GAM2553	RERG 5'	GCTTTAGTTTTAACAACAGT 26739	TCGT_	
		GCTGTTGTAA AAGC		
		TGACAACAATT TTCG		
		TTGAT		
GAM2553	LOC256940 5'	TATGGTAACAACAATAAAT 46155	GC A	
		ATTTA TGTTGTTA TCGTA		
		TAAAT ACAACAAT GGTAT		
		A_ _		
GAM2554	ABCD4 3'	TAAGAACCTTCTATTACATC 21592	A TA A	
		GAT TGGATGG AAG TTCTTA		
		CTA ACTTATC TTC AAGAAT		
		C _ C		
GAM2554	CNR1 3'	AAGAGACCACCCATATCA 18162	A AAAGA	
		TGATATGG TGGT TTCTT		

ACTATACC ACCA GAGAA
 C _____
 GAM2554 FCGR2A 3' AAGAATCTTCTGTTCCACATC 38697 A TGGTA
 GAT TGA AAGATTCTT
 ||| ||| |||||
 CTA ACCT TTCTAAGAA
 C TGTC_
 GAM2554 MAPK1 3' AAGAATCTTTATGAATATACA 8614 A GATG
 TG TATG GTAAAGATTCTT
 || ||| |||||
 AC ATAT TATTTCTAAGAA
 _ AAG_
 GAM2554 RP2 3' GAATCTGCCATCCACATCA 13792 A AA
 TGAT TGGATGGT AGATTG
 ||| ||||| |||||
 ACTA ACCTACCG TCTAAG
 C _
 GAM2554 DKFZP434C1715 3' AGTCTTATCATCCATATCA 41673 A
 TGATATGGATGGTAA GATT
 ||||| ||||| |||||
 ACTATACCTACTATT CTGA
 _
 GAM2554 KIAA1416 3' GAAATTTACCATACATATCA 41807 G GA
 TGATATG ATGGTAAA TTC
 ||||| ||||| |||
 ACTATAC TACCATTT AAG
 A A_
 GAM2554 MGC9912 3' TAAGAATCTTTACTTGATATA 27952 GAT
 TATG GGTAAGATTCTTA
 ||| |||||
 ATAT TCATTTCTAAGAAT
 AGT
 GAM2554 LOC154222 3' AAGAAAACCATCCATTCA 41689 T AAAGA
 TGA ATGGATGGT TTCTT
 ||| ||||| |||||
 ACT TACCTACCA AAGAA
 _ A_
 GAM2554 LOC222060 5' AATCCCTACTTTGTTCATATCA 45156 AT_ AA
 TGATATGG GGTA GATT
 ||||| ||| |||||
 ACTATACT TCAT CTAA
 GTT CC
 GAM2555 GM2A 3' CAGTGGTGCAATCTCACC 33659 CTA
 GGTGAGA CACCACTG
 ||||| |||||
 CCACTCT GTGGTGAC
 AAC
 GAM2555 HCS 3' CAGTGGTGCAATCTCACT 21014 CTA
 GGTGAGA CACCACTG
 ||||| |||||

			TC	ACTCT		GTGGTGAC		
				AAC				
GAM2555	WDR4	3'	CAGTGGTGTCTCTCACC		27391		CT	
			GGTGAGA	ACACCACTG				
			CCACTCT	TGTGGTGAC				
				C_				
GAM2555	WDR4	3'	CAGTGGTGTCTCTCACC		20744		CT	
			GGTGAGA	ACACCACTG				
			CCACTCT	TGTGGTGAC				
				C_				
GAM2555	CRTAM	3'	CAGTGAGTCAAGATCTCACCAC	21214		A		_ AC _
	TGAA		TTTA	TGGTGAGA		CT	AC	CACTG
			AAGT	ACCACTCT		GA	TG	GTGAC
				C		A	AC	A
GAM2555	KIAA1755	3'	CAGTGGTGCAATCATAGCCTTA	30748		T	GA_	CTA
	AA		TTTAA	GGT		GA		CACCACTG
			AAATT	CCG		CT		GTGGTGAC
				_		ATA		AAC
GAM2555	MRPL35	3'	CAGTGGTGCAATCATAGCTCAT	18735		_	GA_	CTA
	TGAA		TTTAATG	GT		GA		CACCACTG
			AAGTTAC	CG		CT		GTGGTGAC
				T		ATA		AAC
GAM2555	MRPS27	3'	CAGTGGTGTAATTTTATT	17475				C
			GGTGAGA	TACACCACTG				
			TTATTTT	ATGTGGTGAC				
				A				
GAM2555	RAP140	3'	CAGTGGTGCAATCTCACT	17554				CTA
			GGTGAGA	CACCACTG				
			TC	ACTCT		GTGGTGAC		
				AAC				
GAM2555	LOC152373	5'	CAGTGGTG	CAGCGGTCCAT	39270	A		A__
			GTG	GA		CT		CACCACTG
			TAC	CTGG		GTGGTGAC		
				_		CGAC		
GAM2555	LOC90155	3'	CAGTGGTGTAATCATGACTA	30899			GA_	C
			TGGT	GA		TACACCACTG		
			ATCA	CT		ATGTGGTGAC		
				GTA		A		
GAM2556	AHR	5'	AACAGGGGCAGCCGTGTAGCC	7330			AC	TG _
			GGT	A		TGG		TGCCCCTGTT

CCG T GCC ACGGGGACAA
 A_ GT G
 GAM2556 F8 3' AACAGGGGAAATTATATACCGT 5612 _ CA G_
 GA TCA GGTA TGTGGT CCCCTGTT
 ||| ||| ||||| |||||
 AGT CCAT ATATTA GGGGACAA
 G _ AA
 GAM2556 FLJ10697 3' CAGGGGACAGTTCCTGA 20015 T ATGTGG
 TCAGG AC TGCCCCTG
 ||||| || |||||
 AGTCC TG ACGGGGAC
 T _____
 GAM2556 LOC114971 3' AACAAAAATCTATTATGTACCT 36205 _ TGCCCC
 AGGTACATG TGG TGTT
 ||||| ||| |||
 TCCATGTAT ATC ACAA
 T TAAAA_
 GAM2556 LOC158158 3' AACAGGGGACACTGACACCT 39731 ACAT G
 AGGT GTG TGCCCCTGTT
 ||| ||| |||||
 TCCA CAC ACGGGGACAA
 CAGT _
 GAM2556 LOC257319 3' GACATAGTACATGTAC 45833 G CCCC
 GTACATGTG TG TGTT
 ||||| || |||
 CATGTACAT AT ACAG
 G _____
 GAM2557 KCND2 3' TATTTAGCAATATTTGATGA 14611 ATCC
 TCATCGAATAT CTAAATA
 ||||| || |||||
 AGTAGTTTATA GATTTAT
 AC_
 GAM2557 RASGRP1 3' ATTTAGGAATTCTCTTTGATGA 12301 TAT_ C
 TCATCGAA AT CCTAAAT
 ||||| || |||||
 AGTAGTTT TA GGATTTA
 CTCT A
 GAM2557 FLJ14166 3' TATTTAGGGATCTGCAGCGA 23793 AA_ T
 TCG TA ATCCCTAAATA
 || ||| |||||
 AGC GT TAGGGATTTAT
 GAC C
 GAM2557 FLJ33069 3' ATTTAGGAATGCCTTCGATGA 29473 TA C
 TCATCGAA TAT CCTAAAT
 ||||| ||| |||||
 AGTAGCTT GTA GGATTTA
 CC A
 GAM2557 KIAA0152 3' ATTTAGGCTTTGATGAGA 16331 TATATC
 TCTCATCGAA CCTAAAT
 ||||| || |||||

AGAGTAGTTT GGATTTA
 C____
 GAM2557 LOC148195 5' TATTTATAGATATATTCTATGA 40879 C CC
 GA TCTCAT GAATATATC TAAATA
 ||||| ||||| |||||
 AGAGTA CTTATATAG ATTTAT
 T AT
 GAM2557 LOC148562 3' ATTCAGGGATATTGGAGA 38565 ATCGAAT A
 TCTC ATATCCCT AAT
 ||| ||||| |||
 AGAG TATAGGGA TTA
 GT____ C
 GAM2558 DNAM-1 3' GCAGTGATTAACCAAGA 13338 G TGTT C
 TCTTGG TAA TTAC GC
 ||||| ||| ||| ||
 AGAACC ATT AGTG CG
 A ____ A
 GAM2559 DMWD 3' CCCACACCAGCGGCTGGAG 30529 ACT A_
 CTCCAGCCGCT GGT GGG
 ||||| ||| |||
 GAGGTCGGCGA CCA CCC
 ____ CA
 GAM2559 KIAA0450 3' CCCGCTGTGGCAGCGGCTGGAG 16029 A __ A
 CTCCAGCCGCT CT GGT GGG
 ||||| ||| ||| |||
 GAGGTCGGCGA GG TCG CCC
 C TG _
 GAM2559 KIAA0594 3' CCAAAATAGCAGCTGGTAGTAA 32386 _ C C_
 TTACT CCAGC GCTA TGG
 ||||| ||||| ||| |||
 AATGA GGTCTG CGAT ACC
 T A AAA
 GAM2559 KIAA1940 3' CCTACCCCGGCTGGAGTAG 39005 CTACT
 TTACTCCAGCCG GGTAGG
 ||||| ||||| |||||
 GATGAGGTCGGC CCATCC
 C____
 GAM2559 MGC11257 3' CCAGCAGGGCAGCGGCTGAG 26139 C A_ G A
 CTC AGCCGCT CT GT GG
 ||| ||||| || ||| ||
 GAG TCGGCGA GG CG CC
 _ CG A A
 GAM2559 LOC154739 5' CCCTAGAAGCAGAGCTGGAGTA 41717 CG A GG
 A TTACTCCAGC CT CT TAGGG
 ||||| ||| ||| |||||
 AATGAGGTCG GA GA ATCCC
 A_ C AG
 GAM2560 HUNK 5' CTGGTGTCTGAAAGGGG 15949 AAC
 CCCCTTTCA GCATTAG
 ||||| |||||

			GGGGAAAGT TGTGGTC		
			CC_		
GAM2560	IL1B	3'	GGTCTAATTTATTCAAAGGGG 6175	CAAACGC	
			CCCCTTT ATTAGACC		
			GGGGAAA TAATCTGG		
			CTTATT_		
GAM2560	MUC4	3'	GCTTGCCTTGAAGGGG 28711	AC TT A	
			CCCTTTCAA GCA AG C		
			GGGGAAGTT CGT TC G		
			C_ _ C		
GAM2560	PMP2	3'	GTCTCAGTTAAAAGGGGTA 8545	CA GCATT	
			TACCCCTTT AAC AGAC		
			ATGGGGAAA TTG TCTG		
			A_ AC_		
GAM2560	SWAP70	3'	TCTGATTTGAAAGGAGTA 35350	C ACGC	
			TAC CCTTTCAA ATTAGA		
			ATG GGAAAGTT TAGTCT		
			A _		
GAM2560	SULT4A1	3'	GTCTAATGCAGTCAGGAG 33976	AA _	
			TTTC AC GCATTAGAC		
			GAGG TG CGTAATCTG		
			AC A		
GAM2560	LOC202934	3'	GGTCTGATGGTTTTGAAAAGGG 43463	C _ G	
	TA		TACCC TTTCAA C CATTAGACC		
			ATGGG AAAGTTT G GTAGTCTGG		
			A T_		
GAM2560	LOC255465	3'	GGTCTGATGGTTTTGAAAAGGG 46455	C _ G	
	TA		TACCC TTTCAA C CATTAGACC		
			ATGGG AAAGTTT G GTAGTCTGG		
			A T_		
GAM2560	LOC54505	5'	TCTATTTTGAAAGTGGTA 33697	C CGCAT	
			TACC CTTTCAA TAGA		
			ATGG GAAAGTTT ATCT		
			T T_		
GAM2561	MTM1	3'	TATTTGTAAAAGCTAAGGCTCG 5791	_ _	
	A		TCG GTT GCTTTTACAAATA		
			AGC CGG CGAAAATGTTTAT		
			T AAT		
GAM2561	RECK	3'	TATTTGTAAAATGACAATC 22091	C_	
			GGTTG TTTTACAAATA		

		CTAAC AAAATGTTTAT	
		AGT	
GAM2561	KIAA1915	5' GTATTTGTGGAACCAATT 36270	C
		GGTTG TTTTACAAATAC	
		TTAAC AAGGTGTTTATG	
		C	
GAM2561	PRO1617	5' ATTTGTAAACTGCTACTGA 20664	T T_
		TCGGT GC TTTACAAAT	
		AGTCA CG AAATGTTTA	
		T TC	
GAM2561	SE70-2	3' TATTTGTAAAAACAATTTTTGG 22664	TC C
		TCAA GGTG TTTTACAAATA	
		GGTT TTAAC AAAATGTTTAT	
		T_ A	
GAM2561	SLC26A10	5' TATTTGTAACTTCCCAACTG 28561	CTT__
		CGGTTG TTACAAATA	
		GTCAAC AATGTTTAT	
		CCTTC	
GAM2561	LOC157273	3' GTATTTATAGAGCAACCG 41787	TAC
		CGGTTGCTTT AAATAC	
		GCCAACGAGA TTTATG	
		TA_	
GAM2562	AS3	3' GGCGATGAACAAATGTAAT 18050	GA TT
		ATTACATT TTCATT CC	
		TAATGTAA AAGTAG GG	
		AC C_	
GAM2562	CD164	3' GAAGTGACCAATGTAAT 12630	AT
		ATTACATTG TCATTTT	
		TAATGTAAC AGTGAAG	
		C_	
GAM2562	COVA1	3' AATAGTAATGAATCAATG 36265	TTC
		CATTGATTCATT CTATT	
		GTAAGTAAGTAA GATAA	
		T__	
GAM2562	FLJ11273	3' AATAGGAAAATGAAATTCAG 20392	__
		TTGA TTCATTTTCCTATT	
		GAAGTAAAGGATAA	
		TA	
GAM2562	KIAA0092	3' AATAGGAGGACATCAATGTA 16152	TCA
		TACATTGAT TTTTCCTATT	

			ATGTA ACTA AGGAGGATAA		
			C_		
GAM2562	LIN-28	3'	AATAGGAGACGAACGAATGTAA 23978	GA	AT
			TTACATT TTC TTTCCTATT		
			AATGTAA AAG AGAGGATAA		
			GC C_		
GAM2562	NUDT12	3'	GAAATGAATCAAAGTAAT 25448	A	
			ATTAC TTGATTCATTTT		
			TAATG AACTAAGTAAAG		
			A		
GAM2563	LOC222484	3'	AATCATAGCAGCAGCAGCCA 45297		
			TGGCTGCTGCTG ATGATT		
			ACCGACGACGAC TACTAA		
			GA		
GAM2564	ABR	3'	GCTATGGGAAGGCTGCAA 6749	CAC	
			TTGCAGCCTTTCC GC		
			AACGTCGGAAGGG CG		
			TAT		
GAM2564	ABR	3'	GCTATGGGAAGGCTGCAA 22494	CAC	
			TTGCAGCCTTTCC GC		
			AACGTCGGAAGGG CG		
			TAT		
GAM2564	CYP24	3'	TAAAATGCACAGAAATGCATGC 6429	_ C	CCAC
	AA		TTGCA GC TTTC GCATTTTA		
			AACGT CG AAAG CGTAAAAT		
			A T ACA_		
GAM2564	PFN2	3'	TAAAATTGTAAAAGGCTGC 8488	CC	CGC
			GCAGCCTTT CA ATTTTA		
			CGTCGGA AAA GT TAAAAT		
			AT _		
GAM2564	PFN2	3'	TAAAATTGTAAAAGGCTGC 27581	CC	CGC
			GCAGCCTTT CA ATTTTA		
			CGTCGGA AAA GT TAAAAT		
			AT _		
GAM2564	TACSTD2	3'	TAAAATATGGGAAAGGC 8160		CGC
			GCCTTTCCCA ATTTTA		
			CGGAAAGGGT TAAAAT		
			A_		
GAM2564	DKFZP434P211	3'	TAAAATGCTGGAAAAGTGTAA 15870	CC	CAC
			TTGCAG TTTCC GCATTTTA		

		AATGTC AAAGG CGTAAAAT		
		A_ T__		
GAM2564	DKFZP586F1318 5'	AGAAGCAAAAAAGGCTGC	17904	CCCAC A
		GCAGCCTTT GC TTTT		
		CGTCGGAAA CG AAGA		
		AAA__ _		
GAM2564	LOC145009 3'	AAAATGAAAAAGGTTGCAA	30261	CCCACG
		TTGCAGCCTTT CATT TT		
		AACGTTGGAAA GTAAAA		
		AA_____		
GAM2564	LOC150213 3'	TAAAATGCTGGAAAACTGTAA	36961	CC CAC
		TTGCAG TTTCC GCATTTTA		
		AATGTC AAAGG CGTAAAAT		
		A_ T__		
GAM2564	LOC255027 3'	TAAAATGCACAGAATTGCCTGC	45572	_CT CCAC
	AG	TTGCAG C TTC GCATTTTA		
		GACGTC G AAG CGTAAAAT		
		C TT ACA_		
GAM2565	EGLN1 5'	AATAGGTGAAAATCCTGAAAT	22578	_
		GTTTCAGGATTTT GCCTATT		
		TAAAGTCCTAAAA TGGATAA		
		G		
GAM2565	LAMP1 3'	AGGGAAAATCCTAAGACA	12089	C G
		TGTTT AGGATTTT CCT		
		ACAGA TCCTAAAA GGA		
		A G		
GAM2565	LIF 3'	ATAGCGCCCTGGAACA	8093	ATTTT _
		TGTTTCAGG GC CTAT		
		ACAAGGTCC CG GATA		
		_____ C		
GAM2565	SET 3'	AATAGGCAAAAAGTGTAAACA	8921	T GGA
		TGTT CA TTTTGCCTATT		
		ACAA GT AAAACGGATAA		
		T G__		
GAM2565	VPS41 3'	AATAGGCATTTAATGAAACA	15734	GGATT T
		TGTTTCA TGCCTATT		
		ACAAAGT ACGGATAA		
		AATTT_		
GAM2565	VPS41 3'	AATAGGCATTTAATGAAACA	27934	GGATT T
		TGTTTCA TGCCTATT		

		ACAAAGT	ACGGATAA		
		AATTT_			
GAM2565	CAMP-GEFII 3'	GCAAAAACACATCCTGAGACA	13881		_____
		TGTTTCAGGAT	TTTGC		
		ACAGAGTCCTA	AAACG		
		CACAA			
GAM2565	CDV-1 3'	AATAGTCAACCTGAAACA	25539	ATT C	
		TGTTTCAGG	TTG CTATT		
		ACAAAGTCC	AAC GATAA		
		____ T			
GAM2565	CSAD 3'	AATAGGCAATTTTAAACA	18082	C TT	
		TGTTT AGGAT	TGCCTATT		
		ACAAA TTTTA	ACGGATAA		
		A ____			
GAM2565	CSL4 3'	AATAGATGCCGATTCTGAAACA	18124	TT ____	
		TGTTTCAGGATT	GC CTATT		
		ACAAAGTCTTAG	CG GATAA		
		C_ TA			
GAM2565	ENDOFIN 3'	AATAAATGAAGCCTGAAACA	16367	A CC	
		TGTTTCAGG	TTTTG TATT		
		ACAAAGTCC	GAAGT ATAA		
		_ AA			
GAM2565	FLJ11160 3'	CAGAACACTCCTGAGACA	20351		_____
		TGTTTCAGGA	TTTTG		
		ACAGAGTCCT	AAGAC		
		CAC			
GAM2565	KIAA0527 3'	AATAGGCAATATTAATACA	45840	TTCAG T	
		TGT GAT	TTGCCTATT		
		ACA TTA	AACGGATAA		
		TAA_ T			
GAM2565	KIAA1900 3'	AATAGACATACACTGGAACA	36258	GATTT C	
		TGTTTCAG	TG CTATT		
		ACAAGGTC	AC GATAA		
		ACAT_ A			
GAM2565	MRPL35 3'	AGGTAAAAGCCTGAAACA	18732	A	
		TGTTTCAGG	TTTTGCCT		
		ACAAAGTCC	AAAATGGA		
		G			
GAM2565	PLSCR4 3'	AATAGGAGTTCATCCTGAAA	21620	TTTG_	
		TTTCAGGAT	CCTATT		

			AAAGTCCTA GGATAA		
			CTTGA		
GAM2565	PRDM8	5'	AATAGGCAAAAGGAAACA 21489	AGGA	
			TGTTTC TTTTGCCTATT		
			ACAAAG AAAACGGATAA		
			G__		
GAM2565	TRIM2	3'	AATAGGCAGCACTCTGAAA 17595	ATT	
			TTTCAGG TTGCCTATT		
			AAAGTCT GACGGATAA		
			CAC		
GAM2565	LOC118611	5'	AATAAGCGAAGCCCTGAAGCA 37185	AT C	
			TGTTTCAGG TTTGC TATT		
			ACGAAGTCC AAGCG ATAA		
			CG A		
GAM2565	LOC130026	3'	AATAGTATTCCTGAAATA 28817	TTTTGC	
			TGTTTCAGGA CTATT		
			ATAAAGTCCT GATAA		
			TAT__		
GAM2565	LOC153810	5'	AATAGGCAGAGGCTGGAACA 39410	GA	
			TGTTTCAG TTTTGCCTATT		
			ACAAGGTC GAGACGGATAA		
			G_		
GAM2565	LOC221312	3'	CAAAGTTACCCTGGAACA 44138	__	
			TGTTTCAGG ATTTTG		
			ACAAGGTCC TGAAAC		
			CAT		
GAM2565	LOC256080	5'	AGGCAGGATTGAAACA 46584	GG	
			TGTTTCA ATTTTGCCT		
			ACAAAGT TAGGACGGA		
			__		
GAM2566	UNC119	3'	CAATAAAGCAGACTATTCCTA 27647	C TTG C	
			TAG GAAT CT GCTTTATTG		
			ATC CTTA GA CGAAATAAC		
			_ TCA _		
GAM2567	ACCN1	3'	CACCATGAGGCCACCCTG 6752	AGCAT AA	
			TAGGGT GGTCTCAT TG		
			GTCCCA CCGGAGTA AC		
			__ CC		
GAM2567	PB1	3'	TGAGACCACGCCACTCTA 20308	A A	
			TAGGGT GC TGGTCTCA		

			ATCTCA CG ACCAGAGT		
			C C		
GAM2568	H2AFJ	3'	TTTATTTTTATTGGTTCCTGA 20239	AT	CT_
			TCA GAACCAATAA TGGA		
			AGT CTTGGTTATT ATTT		
			C_ TTT		
GAM2568	KIAA0061	3'	ATTCCAGTAATGTCATTGA 33892	ACCAATA	T
			TCAATGA ACT GGAAT		
			AGTTACT TGA CCTTA		
			GTAA_ _		
GAM2568	KIAA1655	3'	CATTCCGTTTTCTAGTTCATTG 33083	CAATAACT	
	A		TCAATGAAC TGGAATG		
			AGTTACTTG GCCTTAC		
			ATCTTTT_		
GAM2568	KLHL6	3'	TTCCTTTTATCGGTTTCATT 28215	A	CTT
			AATGAACC ATAA GGAA		
			TTACTTGG TATT CCTT		
			C TT_		
GAM2568	LOC147947	5'	CATTCCAAGATGTGGCCATTGA 38424	AA	ATAA
			TCAATG CCA CTTGGAATG		
			AGTTAC GGT GAACCTTAC		
			C_ GTA_		
GAM2569	CLCN3	3'	AGAAGGGAGTGTTTCTTGTGCC 7564	TGGG_	
			GGTACAAGAA CCCTTCT		
			CCGTGTTCTT GGGAAGA		
			TGTGA		
GAM2569	DUOX2	3'	AGAAACTCCCCTTGTACC 15306	AAT	CCC
			GGTACAAG GGG TTCT		
			CCATGTTC CCC AAGA		
			_ TCA		
GAM2569	FLT1	3'	AGAAAAGCCCATTTTCAACTG 7763	ACA	CC
			CGGT AGAATGGGC TTCT		
			GTCA TTTTACCCG AAGA		
			AC_ AA		
GAM2569	FOXE1	5'	GAAGGGCCGAGCGTCCGTT 10782	T	AAGAATG
			AACGG AC GGCCCTTC		
			TTGCC TG CCGGGAAG		
			_ CGAG_		
GAM2569	GALNT7	3'	AAGGATCCATTGTACCGTT 27649	AGA	GC
			AACGGTACA ATGG CCTT		

			TTGCCATGT TACC GGAA	
			____ TA	
GAM2569	NFATC1	3'	GGAACGGCCTGTACCGT 12815	AGAATG C
			ACGGTACA GGCC TTCT	
			TGCCATGT CCGG AAGG	
			_____ C	
GAM2569	PXF	3'	AGAAGGGCCCATCCTATTTCC 8748	TACA A
			GG AG ATGGGCCCTTCT	
			CC TC TACCCGGGAAGA	
			TTTA C	
GAM2569	VPS26	3'	AAGGGTCCATGTACC 11323	AGAA
			GGTACA TGGGCCCTT	
			CCATGT ACCTGGGAA	

GAM2569	AGMAT	3'	AAGGAGTACTTGTACTG 24104	AATGG _
			CGGTACAAG GC CCTT	
			GTCATGTTC TG GGAA	
			A____ A	
GAM2569	DKFZp761O17121	3'	AAGGGCCCATGCTGCAGCC 26044	ACA A
			GGT AG ATGGGCCCTT	
			CCG TC TACCCGGGAA	
			ACG G	
GAM2569	JAM1	3'	AGAAGGTACTTACTCTTGTACC 29335	AT_ GC
			GGTACAAGA GG CCTTCT	
			CCATGTTCT TC GGAAGA	
			CAT AT	
GAM2569	JAM1	3'	AGAAGGTACTTACTCTTGTACC 29346	AT_ GC
			GGTACAAGA GG CCTTCT	
			CCATGTTCT TC GGAAGA	
			CAT AT	
GAM2569	JAM1	3'	AGAAGGTACTTACTCTTGTACC 29326	AT_ GC
			GGTACAAGA GG CCTTCT	
			CCATGTTCT TC GGAAGA	
			CAT AT	
GAM2569	JAM1	3'	AGAAGGTACTTACTCTTGTACC 18859	AT_ GC
			GGTACAAGA GG CCTTCT	
			CCATGTTCT TC GGAAGA	
			CAT AT	
GAM2569	KIAA0767	3'	AGAAGGGCCCACCCCTCGCCTG 30406	CAA A____
	CC		GGTA GA TGGGCCCTTCT	

CCGT CT ACCCGGGAAGA
 CCG CCCC
 GAM2569 KIAA1573 3' AAGGCATTCTTGCACC 31412 A GGC
 GGT CAAGAATG CCTT
 ||| ||||| |||
 CCA GTTCTTAC GGAA
 C ____
 GAM2569 KIAA1750 3' AGAAGGACTGTATCTACACCTG 33871 TACA _ GC
 TT AACGG AGA ATGG CCTTCT
 |||| | ||| |||||
 TTGTC TCT TGTC GGAAGA
 CACA A A_
 GAM2569 MGC11034 3' AGAAGGTACATCCTGTCC 25469 T A A GGC
 GG ACA GA TG CCTTCT
 || ||| || |||||
 CC TGT CT AC GGAAGA
 _ C _ AT_
 GAM2569 NR6A1 3' AGAAGAATTTCTGTTCTCACAC 7231 ACA CC_
 C GGT AGAATGGG CTTCT
 || | ||||| |||||
 CCA TCTTGTCT GAAGA
 CAC TTAA
 GAM2569 NR6A1 3' AGAAGAATTTCTGTTCTCACAC 27179 ACA CC_
 C GGT AGAATGGG CTTCT
 || | ||||| |||||
 CCA TCTTGTCT GAAGA
 CAC TTAA
 GAM2569 NR6A1 3' AGAAGAATTTCTGTTCTCACAC 27185 ACA CC_
 C GGT AGAATGGG CTTCT
 || | ||||| |||||
 CCA TCTTGTCT GAAGA
 CAC TTAA
 GAM2569 PRO0159 5' AGAAAATTTCTGTTCTTGACACG 15371 GTA CCC_
 TT AACG CAAGAATGGG TTCT
 |||| | ||||| |||||
 TTGC GTTCTTGTCT AAGA
 AC_ TTAA
 GAM2569 ROBO4 3' GCACCATCCTCGTACTGTT 21134 A A _
 AACGGTAC AG ATGG GC
 ||||| || ||||| ||
 TTGTCATG TC TACC CG
 C C A
 GAM2569 LOC154860 5' AGAAGGGTATTTCTCCACCG 41733 ACA TGG
 CCGT AGAA GCCCTTCT
 |||| ||| |||||
 GCCA TCTT TGGAAGA
 CC_ TA_
 GAM2569 LOC220522 3' AGAAGGGCCTGACGTACC 30350 AAGAAT
 GGTAC GGGCCCTTCT
 |||| | ||||| |||||

CCATG TCCGGAAGA
 CAG____
 GAM2569 LOC253596 5' AGAAGATTATGTTCTTGAC 45721 GGCC
 GTACAAGAATG CTTCT
 ||||| ||||
 CATGTTCTTGT GAAGA
 ATTA
 GAM2569 LOC93268 5' GAAGGGCATCTTGAC 35587 ATGG
 GTACAAGA GCCCTTC
 ||||| |||||
 CATGTTCT CGGGAAG
 A____
 GAM2570 FGA 3' AATGCACAATTATAATTACAA 6119 GTG CA
 TA TGTGTAAT GGGT TGCATT
 ||||| ||| |||||
 ATAACATTA TTTA ACGTAA
 ATA AC
 GAM2570 XPO5 3' CATGCCTTCACATCACAAC 43839 A T
 GTTGT ATGTGGGG CATG
 |||| ||||| ||||
 CAACA TACACTTC GTAC
 C C
 GAM2570 LOC51333 3' AGTGCCACCCACATCACTAC 18750 T A CAT
 A TGT GT ATGTGGGGT GCATT
 ||| || ||||| ||||
 ACA CA TACACCCCA CGTGA
 T C CC_
 GAM2571 RNF6 3' AGTATCTTTTCATGAAA 12603 TTGGGC
 TTTCATGA AGATACT
 ||||| |||||
 AAAGTACT TCTATGA
 TT____
 GAM2571 BAG5 3' AGTATTTCCCAATCATGAAA 11301 C
 TTTCATGATTGGG AGATACT
 ||||| |||||
 AAAGTACTAACCC TTTATGA
 -
 GAM2571 LOC143425 3' AGCATCTGCCCTGGAAAT 42349 ATGATT A
 ATTTG GGGCAGAT CT
 |||| ||||| ||
 TAAAG CCCGTCTA GA
 GT____ C
 GAM2571 LOC220936 3' TAGTATCTGTTACGTCCAAAAT 43931 CAT TG
 A TATTT GAT GGCAGATACTA
 |||| || ||||| |||||
 ATAAA CTG TTGTCTATGAT
 AC_ CA
 GAM2572 LENG4 3' CCAGCTAAATACCCTGCCTG 23582 C
 CAGGTAGGGTATTTA CTGG
 ||||| ||||| ||||

			GTCCGTCCCATAAAT GACC		
			C		
GAM2572	MUC3B	3'	GCCCTAAATACCCCAGCTG 45255	GTA	CCT
			CAG GGGTATTTA GGC		
			GTC CCCATAAAT CCG		
			GAC C__		
GAM2572	PDE4D	3'	TCACCAAATGACCTTACCTGT 36435	ATTTACC	C
			ACAGGTAGGGT TGG GA		
			TGTCCATTCCA ACC CT		
			GTAA__ A		
GAM2572	RUNX1	3'	TCACCAGGCTGAGACCCTACC 7502	A _	C
			GGTAGGGT TTTA CCTGG GA		
			CCATCCCA GAGT GGACC CT		
			_ C A		
GAM2572	YWHAZ	3'	CCTTTAAAACCCTACCT 9444	A	CCT
			AGGTAGGGT TTTA GG		
			TCCATCCCA AAAT CC		
			_ TT_		
GAM2572	FEM-2	3'	TCACCACTAGCCCACCCTGCCC 16009	A	ATTTACC C
	GT		AC GGTAGGGT TGG GA		
			TG CCGTCCCA ACC CT		
			C CCGATC A		
GAM2572	FLJ20514	3'	AGACAAATACCACTACCTGT 19532	_	AC
			ACAGGTAG GGTATTT CT		
			TGTCCATC CCATAAA GA		
			A CA		
GAM2572	G4	5'	TCACCAGGCAAATACCTGTTCT 43735	TA	A C
	G		CAGG GGGTATTT CCTGG GA		
			GTCT TCCATAAA GGACC CT		
			TG C A		
GAM2572	KIAA1036	3'	CGCCAGGTACCATCGCCTCCTG 17125	T	GTATT_
			CAGG AGG TACCTGGCG		
			GTCC TCC ATGGACCGC		
			_ GCTACC		
GAM2572	KIAA1340	3'	TCACCAAATAATCTTACCT 34298	_	TACC C
			AGGTAGGGT ATT TGG GA		
			TCCATTCTA TAA ACC CT		
			A ____ A		
GAM2572	PTP4A1	3'	TCACCAATGAGTACCCGACCCG 9534	A A	CC C
	T		AC GGT GGGTATTTA TGG GA		

		TG CCA CCCATGAGT ACC CT		
		C G A_ A		
GAM2572	RNF8	3' TCGCCAAGCAGTATCTCCTG 10097	TA	TACC
		CAGG GGGTATT TGGCGA		
		GTCC TCTATGA ACGCT		
		___ CGA_		
GAM2572	LOC219376	5' TCGCCAGGTGACTGTCCCACC 45069	A _ T	
		GGT GGG TA TTACCTGGCGA		
		CCA CCC GT AGTGGACCGCT		
		_ T C		
GAM2572	LOC257554	5' TCACCAGGCAAATACCTGTTCT 46642	TA	A C
	G	CAGG GGGTATTT CCTGG GA		
		GTCT TCCATAAA GGACC CT		
		TG C A		
GAM2573	CNTN3	3' ACCATTGTTATTTCCACTTT 33132	CAAC	CT
		AAAGTGGAA GAC GTGGT		
		TTTCACCTT TTG TACCA		
		TA__ T_		
GAM2573	CRP	3' ACCACGCAGTCCCTCCACTTT 35463	ACAAC	C_
		AAAGTGGAA GAC TGTGGT		
		TTTCACCT CTG GCACCA		
		CC__ AC		
GAM2573	ENTPD6	3' CCTCATGTGTTCCACT 6919	A ACC	T
		AGTGAACA CG TG GG		
		TCACCTTGT GT AC CC		
		_ __ T		
GAM2573	MTR	3' ACCACAATGAGATTCCATTTT 5795	CAACGACC	
		AAAGTGGAA TGTGGT		
		TTTTACCTT ACACCA		
		AGAGTA_		
GAM2573	PCDH11X	3' CCTGTGGTACTCATGCTGTTCC 26780	A G_____	TGT
	ACT	GTGGAACA C ACC GG		
		CACCTTGT G TGG CC		
		C TACTCA TGT		
GAM2573	PCDH11Y	3' CCTGTGGTACTCATGCTGTTCC 26813	A G_____	TGT
	ACT	GTGGAACA C ACC GG		
		CACCTTGT G TGG CC		
		C TACTCA TGT		
GAM2573	PCDH11Y	3' CCTGTGGTACTCATGCTGTTCC 26815	A G_____	TGT
	ACT	GTGGAACA C ACC GG		

			CACCTTGT G	TGG CC	
			C TACTCAIII	TGT	
GAM2573	UBE2V1	3'	ACCACAGGCCCTTCCCCTTCC	22765	A T CAACGA
			A AAG GGAA	CCTGTGGT	
			C TTC CCTT	GGACACCA	
			C C CCC__		
GAM2573	UBE2V1	3'	ACCACAGGCCCTTCCCCTTCC	9366	A T CAACGA
			A AAG GGAA	CCTGTGGT	
			C TTC CCTT	GGACACCA	
			C C CCC__		
GAM2573	UBE2V1	3'	ACCACAGGCCCTTCCCCTTCC	22518	A T CAACGA
			A AAG GGAA	CCTGTGGT	
			C TTC CCTT	GGACACCA	
			C C CCC__		
GAM2573	ALDH9	5'	TGTGGTGTCTTGTTCAC	6362	C _TG
			GTGGAACAA GAC C TG		
			CACCTTGTT CTG G GT		
			_ T GT		
GAM2573	KIAA1765	3'	ACCATATGATATTCCACTT	34955	CAA ACC
			AAGTGGAA CG TGTGGT		
			TTCACCTT GT ATACCA		
			ATA __		
GAM2573	MGC12466	3'	CCACACCTGGCCCACTTTT	38609	AA ACGACC
			AAAAGTGG CA TGTGG		
			TTTTACAC GT ACACC		
			CG CC__		
GAM2573	OR7C1	3'	CCACAATTTGTTCACTTTT	18961	G CGACC
			AAAAGTG AACAA TGTGG		
			TTTTCAC TTGTT ACACC		
			_ TA__		
GAM2573	OSBPL6	3'	ACCACACGATTGTTCCACT	26269	_ ACC
			AGTGAACAA CG TGTGGT		
			TCACCTTGTT GC ACACCA		
			A __		
GAM2573	PCCX2	3'	ACCACAACGCAATTCCATTTT	32820	CAA ACC
			AAAGTGGAA CG TGTGGT		
			TTTTACCTT GC ACACCA		
			AAC A__		
GAM2573	TUSP	3'	ACAGCCTCATCATTCCACTTTT	21521	CAAC C_
			AAAAGTGGAA GA CTGT		

	TTTTCACCTT CT GACA	
	ACTA CC	
GAM2573 LOC118738 3'	ACCACCTCGCTGCTGTTCCACT 37192	A__ CCT
	AGTGGAACA CGA GTGGT	
	TCACCTTGT GCT CACCA	
	CGTC C__	
GAM2573 LOC158056 5'	ACCACAGGCCAAGGCCACTTT 39712	AACAACGA
	AAAGTGG CCTGTGGT	
	TTTCACC GGACACCA	
	GGAACC__	
GAM2573 LOC163231 5'	ACCACAGGGACAACATGTCCAC 40092	ACAACGA__
TTT	AAAGTGGA CCTGTGGT	
	TTTCACCT GGACACCA	
	GTACAACAG	
GAM2573 LOC205669 5'	CCACAGCAGCTCCACTTTT 43607	ACAACGAC
	AAAAGTGGA CTGTGG	
	TTTTCACCT GACACC	
	CGAC__	
GAM2573 LOC219738 3'	ACCACAGGTGTGTGTTCCCCT 29817	T CA _
TT	AAAG GGAA ACG ACCTGTGGT	
	TTTC CCTT TGT TGGACACCA	
	C TG G	
GAM2573 LOC253039 3'	ACCCAGAATCACCCTGCCACT 45991	AACAAC_ C_ T
TTT	AAAAGTGG GA CTG GGT	
	TTTTTACC CT GAC CCA	
	GTCACCA AA _	
GAM2573 LOC51337 3'	ACCACAGGCCGCTGTACCCCCT 18761	T_ A A A
T	AAG GG ACA CG CCTGTGGT	
	TTC CC TGT GC GGACACCA	
	CC A C C	
GAM2574 ALS2CR3 3'	AGATCCCAAATCTTATGTAA 17409	AAT A
	TTACATGA ATTTGG ATCT	
	AATGTATT TAAACC TAGA	
	C__ C	
GAM2574 KIAA0555 3'	ATTCCCTCATGTAATA 16681	AATATTT
	TATTACATGA GGAAT	
	ATAATGTACT CCTTA	
	C_____	
GAM2574 KIAA0979 3'	CTTAACATTTTCATGTAGTA 17388	A T
	TATTACATGAAAT TT GG	

			ATGATGTACTTTA AA TC	
			C T	
GAM2574	SBBI26	3'	AGATTCTATTTTCATG 20830	TATT
			CATGAAA TGAATCT	
			GTACTTT ATCTTAGA	
			T__	
GAM2574	LOC120892	3'	CCAAATACCTATGTAATA 36647	AAA
			TATTACATG TATTTGG	
			ATAATGTAT ATAAACC	
			CC_	
GAM2574	LOC149734	3'	TCCAACATTCATGTAATA 41055	ATAT
			TATTACATGAA TTGGA	
			ATAATGTACTT AACCT	
			AC_	
GAM2574	LOC152687	5'	AAATATTTCAATGTAATA 39301	_
			TATTACAT GAAATATTT	
			ATAATGTA CTTTATAAA	
			A	
GAM2574	LOC166793	5'	AGATCCTGGACTTCATGTA 29805	ATA TG A
			TACATGAA TT G ATCT	
			ATGTACTT AG C TAGA	
			C_ GT C	
GAM2574	LOC168391	5'	CCAAAACCTCATGTAATA 40242	AATA
			TATTACATGA TTTGG	
			ATAATGTACT AAACC	
			CCA_	
GAM2575	EVC	3'	TTTCCAGACCATCCCCTCTCAC 15897	A AACA T_
	CA		TGGT AGA GAT TTTGGAAA	
			ACCA TCT CTA AGACCTTT	
			C CCC_ CC	
GAM2575	HMGA2	3'	TTTCAGGAAATCTACTTCCTAC 9574	A AC TG
			GTA GAA AGATTTT GAAA	
			CAT CTT TCTAAAG CTTT	
			C CA GA	
GAM2575	ITGB1	3'	CCAAAAGTTTCTTACT 27393	AGAT
			GGTAAGAAAC TTTTGG	
			TCATTCTTTG AAAACC	

GAM2575	MASP1	3'	TTTCCAGGCCATGCTTCTTACC 29161	A GATT
			GGTAAGAA CA TTTGGAAA	

CCATTCTT GT GGACCTTT
 C ACC_
 GAM2575 MCL1 3' TTAGGAACCTGTTTCTTAC 22491 A
 GTAAGAAACAG TTTTGG
 ||||| |||||
 CATTCTTTGTC AAGGATT
 C
 GAM2575 SP3 3' TTTCCAAAAACCATGTCTCCCA 40137 TAA A GA_
 TGG GA ACA TTTTGGAAA
 || || || |||||
 ACC CT TGT AAAAACCTTT
 C ACC
 GAM2575 ZNF180 3' CTTGTAATCTGTTCTTAC 14925 A TTT
 GTAAG AACAGATT GG
 |||| ||||| ||
 CATTCTTGTCTAA TC
 C TGT
 GAM2575 ZNF192 3' TCCATCTGTTTCTTGCCA 12989 TTTT
 TGGTAAGAAACAGA TGGA
 ||||| ||||| ||||
 ACCGTTCTTTGTCT ACCT
 C
 GAM2575 C11orf11 3' CCAAGGATCCTCACCA 44783 A AAACA
 TGGT AG GATTTTGG
 |||| || |||||
 ACCA TC CTAGGAACC
 C
 GAM2575 C3IP1 3' TTTCCAGAATGTCTGTTTCTCA 22277 A _
 CTA TGGT AGAAACAGAT TTTTGGAAA
 |||| ||||| |||||
 ATCA TCTTTGTCTG AAGACCTTT
 C T
 GAM2575 C6orf33 3' CCATCTATTTTTTACCA 28492 C TTTT
 TGGTAAGAAA AGA TGG
 ||||| || ||||
 ACCATTTTTT TCT ACC
 A
 GAM2575 CDC14A 3' TTCCTGCTGTTTGCTACCA 9767 AG ATTTTT
 TGGTA AAACAG GGAA
 |||| |||| ||||
 ACCAT TTTGTC CCTT
 CG GT
 GAM2575 DKFZP434L187 5' TTCCTTGACTGCTCTTCACCA 34126 _ AA A TTT
 TGGT AAGA CAG TT GGAA
 |||| |||| |||| ||||
 ACCA TTCT GTC AG CCTT
 C C _ TT_
 GAM2575 FLJ00001 3' TCCAAAAACCTCACTCACCA 39786 A AAAC A
 TGGT AG AG TTTTGGGA
 |||| || || |||||

ACCA TC TC AAAAACCT
 C AC__ C
 GAM2575 FLJ13081 3' TTTCCAAAAATCTGGGGTACTA 24239 AGAAA
 TGGTA CAGATTTTTTGAAA
 |||| ||||||||
 ATCAT GTCTAAAAACCTTT
 GGG__
 GAM2575 FLJ13614 3' TTTCTTTCTGTTTCTTCCCA 29151 T TTTT
 TGG AAGAAACAGA GGAA
 || |||||||| ||
 ACC TTCTTTGTCT CTTT
 C TT__
 GAM2575 FLJ13693 3' CCGAGGAATCTGCCTCCCACC 24187 AA AA _
 GGT GA CAGATTT TTGG
 || || |||||| ||
 CCA CT GTCTAAG AGCC
 CC CC G
 GAM2575 FLJ20232 3' CCCCTGTCCTGTTTCTCACC 21082 A _ TTTT
 GGT AGAAACAG AT GG
 || |||||| ||
 CCA TCTTTGTC TG CC
 C C TCC_
 GAM2575 HEMK 3' TCCCAGAATCTGCCCTCACCA 18272 A AAA T
 TGGT AG CAGATTTT GGA
 |||| || |||||| ||
 ACCA TC GTCTAAGA CCT
 C CCC C
 GAM2575 HSA249128 3' TTCCAAATCACAATTTCTTAC 19029 CAGATT
 GTAAGAAA TTTGGAA
 |||||| ||||||
 CATTCTTT AAACCTT
 AACACT
 GAM2575 KIAA0172 5' TCCCTTTTCTTACCA 32412 C ATTTTT
 TGGTAAGAAA AG GGA
 |||||| || ||
 ACCATTCTTT TC CCT
 _ _
 GAM2575 KIAA0247 3' TTCCAAAGCAATTTCTTAACCA 16381 _ CAGAT
 TGGT AAGAAA TTTTGGAA
 |||| |||| ||||||
 ACCA TTCTTT GAAACCTT
 A AAC__
 GAM2575 KIAA1034 3' TTTCCAAATTGTCTTCTTAC 31314 AAC T_
 GTAAGA AGAT TTTGGAAA
 |||| || ||||||
 CATTCT TCTG AAACCTTT
 __ TT
 GAM2575 KIAA1061 3' TCCCAATCTCCCATTTTTACCA 35270 AC__ TTT
 TGGTAAGAA AGATT GGA
 |||||| |||| ||

ACCATTTTT TCTAA CCT
 ACCC C__
 GAM2575 KIAA1877 3' CCAGGTTCTGTCTCTTCCA 32881 T A TT
 TGG AAGA ACAGA TTTGG
 ||| ||| ||||| |||||
 ACC TTCT TGTCT GGACC
 _ C T_
 GAM2575 KIAA1946 3' TCCAAAAATGTTGCCTCTACCA 40120 A AA _
 TGGTA GA CAG ATTTTTGGA
 ||||| || ||| |||||
 ACCAT CT GTT TAAAAACCT
 _ CC G
 GAM2575 LIN-28 3' TCCAGATCTGTTCTTCACCA 23983 _ A TT
 TGGT AAGAA CAGATT TGGA
 ||| ||||| ||||| |||||
 ACCA TTCTT GTCTAG ACCT
 C _ _
 GAM2575 MRPS35 3' CCTGTCAGCTGTTTCTTACCA 22399 ATTTTT
 TGGTAAGAAACAG GG
 ||||| ||||| ||
 ACCATTCTTTGTC CC
 GACTGT
 GAM2575 PPP1R16B 3' TTTCTTGGAATCTGCCTCCC 30779 TAA AA _
 TCCA TGG GA CAGATTTTT GGAAA
 ||| || ||||| |||||
 ACC CT GTCTAAGGG CCTTT
 TCC CC TT
 GAM2575 PRO0097 5' TCCCCAAGTAAGGTTTTTACCA 15366 ACAG TT
 TGGTAAGAA ATTT GGA
 ||||| ||||| |||||
 ACCATTTTT TGAA CCT
 GGAA CC
 GAM2575 LOC144871 5' TTTAGGAGTCTATTTCTTACCA 40473 C
 TGGTAAGAAA AGATTTTTGGA
 ||||| ||||| |||||
 ACCATTCTTT TCTGAGGATTT
 A
 GAM2575 LOC147495 3' TTTCCAAACCAGGATTCCTTAC 40841 AAACAGATT
 TA TGGTAAG TTTGGAAA
 ||||| |||||
 ATCATTC AAACCTTT
 CTTAGGACC
 GAM2575 LOC149332 3' TTTCTGGCTTTGCCTCTTACCA 40982 AA TTT TG
 TGGTAAGA CAGA T GAAA
 ||||| ||||| |||||
 ACCATTCT GTTT G CTTT
 CC C__GT
 GAM2575 LOC149837 3' TCCCCTCTGTTTCCCCTA 41101 AA TTTTT
 TGGT GAAACAGA GGA
 ||| ||||| |||||

ATCA CTTTGTCT CCT
 CC CC___
 GAM2575 LOC153027 3' CCAAAGATCCTCTCACC 33490 A AACA
 GGT AGA GATTTTTGG
 ||| ||| |||||
 CCA TCT CTAGAAACC
 C C___
 GAM2575 LOC255862 3' TTCCCTTCTGTTTCTTAC 45342 TTTT
 GTAAGAAACAGA GGAA
 ||||| |||
 CATTCTTTGTCT CCTT
 TC___
 GAM2575 LOC257471 3' TTTCCAAAACCATGTCTCCCA 45789 TAA A GA_
 TGG GA ACA TTTTGGAAA
 ||| ||| |||||
 ACC CT TGT AAAAACCTTT
 ___ C ACC
 GAM2575 LOC51097 3' CCTAACCTGTTTCTTGCCA 18090 ATTTT
 TGGTAAGAAACAG GG
 ||||| ||
 ACCGTTCTTTGTC CC
 CAAT___
 GAM2575 LOC56965 5' TTTGTGGGAATCTGTTCTCAC 21455 A A TT G
 CA TGGT AG AACAGATT G AAA
 ||| || ||||| | |||
 ACCA TC TTGTCTAAG T TTT
 C C GG G
 GAM2575 LOC91397 5' TCCCGGTGTCCGTCTCTTCCA 32783 T A A T TT
 TGG AAGA AC GAT T GGA
 ||| ||| ||| | |||
 ACC TTCT TG CTG G CCT
 _ C C T GC
 GAM2576 COL19A1 3' CCCTCAGACTTTAAGA 7595 ATCCA T
 TCTTAA AGTCTGA GG
 ||||| ||||| ||
 AGAATT TCAGACT CC
 ___ C
 GAM2576 EIF1A 3' ACCAAACTCTGGATTTAA 42718 _ CTGA
 TTAAATCCA AGT TGGT
 ||||| ||| |||
 AATTTAGGT TCA ACCA
 C A___
 GAM2576 CRIPT 3' CAGTTGGATTTATGATA 36538 T GT
 TATC TAAATCCAA CTG
 ||| ||||| |||
 ATAG ATTTAGGTT GAC
 T ___
 GAM2576 H_GS165L15.1 3' ACCATCAGACCTGGCCTCCAAG 11337 AAAT_ A
 A TCTT CCA GTCTGATGGT
 ||| ||| |||||

AGAA GGT CAGACTACCA
 CCTCC C
 GAM2576 NS1-BP 5' CCATTAGAGCTTAAGA 35912 AATCCA _
 TCTTA AG TCTGATGG
 |||| | |||||
 AGAAT TC AGATTACC
 _____ G
 GAM2576 SFRS12 3' CGTTTACTTGAGTTTAAGATA 29176 TC CT
 TATCTTAAA CAAGT GATG
 ||||| |||| |||
 ATAGAATTT GTTCA TTGC
 GA T_
 GAM2577 DQX1 5' ATGACCTCTCAGCCTCTCA 28597 A AT A
 TGA AG TGAGAGG TAT
 ||| || ||||| |||
 ACT TC ACTCTCC GTA
 C CG A
 GAM2577 FLJ11608 3' CATGGATATCATGTATCCTTC 23777 A TGAGAG
 GAA GAT GATATCCATG
 ||| ||| |||||
 CTT CTA CTATAGGTAC
 C TGTA_
 GAM2577 FLJ13263 3' TATCCTCTCAAACCTTCCA 24769 A A
 TG AAG TTGAGAGGATA
 || ||| |||||
 AC TTC AACTCTCCTAT
 C A
 GAM2577 ICB-1 3' GGGTTCCTCTCAATCCTGCA 11259 AAA T
 TG GATTGAGAGGA ATCC
 || ||||| |||
 AC CTAACCTCTCCT TGGG
 GTC _
 GAM2577 TNFAIP3 3' CATGGTGCTATCCTCTGAACCC 12978 AAGA G T_
 CTCA TGA TT AGAGGATA CCATG
 ||| || ||||| |||||
 ACT AA TCTCCTAT GGTAC
 CCCC G CGT
 GAM2577 LOC130813 3' ATGGATTCAATTCTTTCA 37307 T GAGGAT
 TGAAAGA TGA ATCCAT
 ||||| ||| |||||
 ACTTTCT ACT TAGGTA
 T _____
 GAM2577 LOC145828 5' CATGAACCAGAGCCTCATCTTT 40611 TGA ATATC_
 CA TGAAAGAT GAGG CATG
 ||||| ||| |||
 ACTTTCTA CTCC GTAC
 _____ GAGACCAA
 GAM2577 LOC151996 3' CATGGACACAATTTCCACAACC 41412 A AGA TA_
 TTTCA AAAG TTG GGA TCCATG
 |||| ||| ||| |||||

TTTC AAC CCT AGGTAC
 C A__ TTAACAC
 GAM2578 CA12 3' ATATTCTTCCCCGAATCA 6878 A_
 TGATTCCG AAGAGTAT
 ||||| |||||
 ACTAAGCC TTCTTATA
 CC
 GAM2579 DXF68S1E 3' TCTTACCATTTCCTAACA 30152 T TTCG
 TGTTA GGA GATGGTAAGA
 ||||| |||||
 ACAAT CCT TTACCATTCT
 C ____
 GAM2579 JAM1 3' CTATTTGGAAATCCCTAACA 18862 T ____
 TGTTA GGA TTCGGATGG
 ||||| |||||
 ACAAT CCT AGGTTTATC
 C AA
 GAM2579 JAM1 3' CTATTTGGAAATCCCTAACA 29329 T ____
 TGTTA GGA TTCGGATGG
 ||||| |||||
 ACAAT CCT AGGTTTATC
 C AA
 GAM2579 JAM1 3' CTATTTGGAAATCCCTAACA 29340 T ____
 TGTTA GGA TTCGGATGG
 ||||| |||||
 ACAAT CCT AGGTTTATC
 C AA
 GAM2579 JAM1 3' CTATTTGGAAATCCCTAACA 29350 T ____
 TGTTA GGA TTCGGATGG
 ||||| |||||
 ACAAT CCT AGGTTTATC
 C AA
 GAM2579 LOC158263 3' ATCTCCTGACTCCAAATCCATA 39797 C T__ TA
 GCA TGTTATGGATT GGA GG AGAT
 ||||| || |||||
 ACGATACCTAA CCT CC TCTA
 A CAGT ____
 GAM2580 FLRT2 3' CATGACTTACCATTCCAG 14879 TCT AAA
 CTGGAATG AG TCATG
 ||||| || |||||
 GACCTTAC TC AGTAC
 CAT ____
 GAM2580 STS 3' CATAATTCCTTTAGTTCTAGT 5907 GTCTA C
 TA TAACTGGAAT GAAAT ATG
 ||||| |||||
 ATTGATCTTG CTTTA TAC
 ATTC A
 GAM2580 TRH 3' CATGACCTCTGTATTCTCTAGT 13979 AT C AA
 TA TAACTGGA GT TAGA TCATG
 ||||| || |||||

		ATTGATCT TA GTCT AGTAC	
		CT T CC	
GAM2580	LOC84549 3'	CATGAAACAGCAGAATTCCAG 26258	G AGAAA_
		CTGGAAT TCT TCATG	
		GACCTTA AGA AGTAC	
		_ CGACAA	
GAM2580	LOC90538 3'	CATAATTTTCCATTCCAGTT 31654	TCTA C
		AACTGGAATG GAAAT ATG	
		TTGACCTTAC TTTTA TAC	
		C__ A	
GAM2580	LOC92935 3'	CATGATTTTCTTTTGGTCAATC 35131	A T __
		GA TG CT AGAAATCATG	
		CT AC GG TCTTTAGTAC	
		A T TTT	
GAM2581	FACL4 3'	AGGTAAAAAGTTAACAGG 10760	CCA A
		CCTGTT GAT TTTTACCT	
		GGACAA TTG AAAATGGA	
		_ A	
GAM2581	FACL4 3'	AGGTAAAAAGTTAACAGG 23250	CCA A
		CCTGTT GAT TTTTACCT	
		GGACAA TTG AAAATGGA	
		_ A	
GAM2581	KHK 3'	GAGGTCCGATCTGGAACA 13215	ATTTT
		TGTTCCAGAT ACCTC	
		ACAAGGTCTA TGGAG	
		GCC__	
GAM2581	KHK 3'	GAGGTCCGATCTGGAACA 5730	ATTTT
		TGTTCCAGAT ACCTC	
		ACAAGGTCTA TGGAG	
		GCC__	
GAM2581	LDB3 3'	GAGACAGTGTCTGAAACAGG 37563	C TTAC
		CCTGTT CAGATATT CTC	
		GGACAA GTCTGTGA GAG	
		A CA__	
GAM2581	PIGA 3'	GAGATATCTGAAACCAGGTA 21709	_ C
		TACCTG TT CAGATATTTT	
		ATGGAC AA GTCTATAGAG	
		C A	
GAM2581	PIGA 3'	GAGATATCTGAAACCAGGTA 21716	_ C
		TACCTG TT CAGATATTTT	

			ATGGAC AA GTCTATAGAG		
			C A		
GAM2581	RXRA	3'	AAAGCATCTGGAAGGTA 8866	G	A
			TACCT TTCCAGAT TTTT		
			ATGGA AAGGTCTA GAAA		
			— C		
GAM2581	SCD	3'	AAAGCTTCTAAAGCAGGTA 11487	CC	TA
			TACCTGTT AGA TTTT		
			ATGGACGA TCT GAAA		
			AA TC		
GAM2581	SIAT1	3'	GAGGCAGACATCTGAACAGG 8975	C	AT A
			CCTGTTT AGAT TTT CCTC		
			GGACAAG TCTA AGA GGAG		
			— C_ C		
GAM2581	CLDN1	3'	AAAATATCTCTAAAATAGGTA 22078	CC	—
			TACCTGTT AGATATTTT		
			ATGGATAA TCTATAAAA		
			AATC		
GAM2581	KIAA0426	3'	AGGTGCTGGAACAGG 16306	ATATTT	
			CCTGTTCCAG TACCT		
			GGACAAGGTC GTGGA		
			—		
GAM2581	KIAA1255	5'	AGATAAAGGTTGGGGACAGG 33345	AGATA	C
			CCTGTTCC TTTTA CT		
			GGACAGGG GAAAT GA		
			GTTG_ A		
GAM2581	KIAA1712	3'	AGGTAAAATACTAGTCAG 33537	TTCC	A
			CTG AG TATTTTACCT		
			GAC TC ATAAAATGGA		
			TGA_ _		
GAM2581	MEGF10	3'	GGAATGACCTGGAACAGG 26213	A_	
			CCTGTTCCAG TATTTT		
			GGACAAGGTC GTAAGG		
			CA		
GAM2581	SCAND2	3'	GTAAAATATCTAACAGGTG 22576	CC	
			TACCTGTT AGATATTTTAC		
			GTGGACAA TCTATAAAATG		
			—		
GAM2581	TAF9L	3'	AGGTAATATAAAAACAGGTA 18071	CCAG	TT
			TACCTGTT ATAT TACCT		

		ATGGACAA TATA ATGGA		
		AAA_ _		
GAM2581	TOMM70A 3'	AGGTAAGATGAAACAG 16788	CCAGA	
		CTGTT TATTTTACCT		
		GACAA GTAGAATGGA		
		A_		
GAM2581	UQCR 3'	AAAATAAAAATGAACAGGTA 13708	CAGA_	
		TACCTGTTC TATTTT		
		ATGGACAAG ATAAAA		
		TAAAA		
GAM2581	LOC120939 5'	GAAGTAAAATATGGCACAG 37512	T GA C	
		CTGT CCA TATTTTAC TC		
		GACA GGT ATAAAATG AG		
		C _ A		
GAM2581	LOC128338 3'	AAAGTAGTCTTGAACAGGTA 36925	C _	
		TACCTGTTC AGAT ATTTT		
		ATGGACAAG TCTG TGAAA		
		T A		
GAM2581	LOC144845 5'	GAGGCTGACCTGAAAGCAGGTA 28822	C_ ATAT TA	
		TACCTGTT CAG TT CCTC		
		ATGGACGA GTC AG GGAG		
		AA C_ TC		
GAM2581	LOC146780 3'	GTAAAATCTGGAAAAGG 40744	G AT	
		CCT TTCCAGAT TTTAC		
		GGA AAGGTCTA AAATG		
		A _		
GAM2581	LOC147804 5'	AGGTGGGCCTGGGAACAGG 38381	AGATAT	
		CCTGTTCC TTTACCT		
		GGACAAGG GGGTGGA		
		GTCC_		
GAM2581	LOC150998 3'	AGGTAAAAGACTGGAACG 41285	ATA	
		TGTTCCAG TTTTACCT		
		GCAAGGTC AAAATGGA		
		AG_		
GAM2581	LOC151318 3'	AAGATAATTTGGAACAGG 39104	_	
		CCTGTTCCAGAT ATTTT		
		GGACAAGGTTTA TAGAA		
		A		
GAM2581	LOC255481 3'	AGGCAAGAATGGAACGG 45329	GATA A	
		CTGTTCCA TTTT CCT		

			GGCAAGGT AGAA GGA	
			A__ C	
GAM2582	DACH	3'	TCAGAAAAAATAAAGTCCTTT 28040	A TC C
	TA		TGAAAG A TTAT TTTTCTGA	
			I	
			ATTTTC T AATA AAAAAGACT	
			C GA A	
GAM2582	EIF3S10	3'	TCTTTTGAAGATAGATTCTTTC 35500	T TTCT
	A		TGAAAGAATCT ATCTTT GA	
			ACTTTCTTAGA TAGAAG CT	
			_ TTTT	
GAM2582	FUT9	3'	CAGAAAAATGATTGTTTCA 33699	G TTATC
			TGAAA AATC TTTTCTG	
			ACTTT TTAG AAAAAGAC	
			G T__	
GAM2582	LOH11CR2A	3'	CAGAAAAAGAAGTGCCTTT 15985	AAT TA
			AAAG CT TCTTTTCTG	
			TTTC GA AGAAAAAGAC	
			CGT _	
GAM2582	OPA1	3'	TCAGAAAAAGGCTTTCTTTCA 28331	TCTTA
			TGAAAGAA TCTTTTCTGA	
			ACTTTCTT GGAAAAAGACT	
			TC__	
GAM2582	OPA1	3'	TCAGAAAAAGGCTTTCTTTCA 28355	TCTTA
			TGAAAGAA TCTTTTCTGA	
			ACTTTCTT GGAAAAAGACT	
			TC__	
GAM2582	OPA1	3'	TCAGAAAAAGGCTTTCTTTCA 28339	TCTTA
			TGAAAGAA TCTTTTCTGA	
			ACTTTCTT GGAAAAAGACT	
			TC__	
GAM2582	OPA1	3'	TCAGAAAAAGGCTTTCTTTCA 28323	TCTTA
			TGAAAGAA TCTTTTCTGA	
			ACTTTCTT GGAAAAAGACT	
			TC__	
GAM2582	OPA1	3'	TCAGAAAAAGGCTTTCTTTCA 28347	TCTTA
			TGAAAGAA TCTTTTCTGA	
			ACTTTCTT GGAAAAAGACT	
			TC__	
GAM2582	SLC10A2	3'	GGAAAAACATAATTCTTTCA 6065	CT C
			TGAAAGAAT TAT TTTTCT	

			ACTTTCTTA ATA AAAAAGG		
			— C		
GAM2582	UBE4A	3'	CAGAATGTAAGATTCATTCA 11196	A	CTTT
			TGAA GAATCTTAT TTCTG		
			ACTT CTTAGAATG AAGAC		
			A T__		
GAM2582	FLJ10803	3'	TCAGAAAAAATAGATTTCTTTC 20156	TC	C
	A		TGAAAGAA TTAT TTTTCTGA		
			ACTTTCTT GATA AAAAAGACT		
			TA _		
GAM2582	KIAA0553	3'	CAGAAAAGAAGATCCTATCA 34633	A A	ATC
			TGA AG ATCTT TTTTCTG		
			ACT TC TAGAA GAAAAGAC		
			A C _		
GAM2582	KIAA0924	5'	AAAAGATAAGATGCTCCCA 17062	AA	A
			TG AG ATCTTATCTTTT		
			AC TC TAGAATAGAAAA		
			CC G		
GAM2582	KIAA1266	3'	CAGAAGGGGAAATGATTCCCTC 32867	AA	TTA
	A		TGA GAATC TCTTTTCTG		
			ACT CTTAG AGGGGAAGAC		
			CC TAA		
GAM2582	KIAA1328	3'	TCAGAAAGGCAGACTCTCTCA 30889	A A	TATC
			TGA AGA TCT TTTTCTGA		
			ACT TCT AGA GGAAAGACT		
			C C C__		
GAM2582	KIAA1554	3'	AAAAAGGAAAGGTTCTTCCA 45606	A	A
			TG AAGAATCTT TCTTTT		
			AC TTCTTGAA GGAAAAA		
			C A		
GAM2582	SKIP	5'	TCAGATTGAGATAAGATCCTTT 28263	A	TT
			AAAG ATCTTATCTT TCTGA		
			TTTC TAGAATAGAG AGACT		
			C TT		
GAM2582	LOC118668	5'	CAGGGGAGAACTAGATCCTTTC 37190	A	TA_ TTT
	A		TGAAAG ATCT TCT T CTG		
			ACTTTC TAGA AGA G GAC		
			C TCA _GG		
GAM2582	LOC151318	3'	TCAGAAAAAGAAAGTCCTTCA 39106	A AT	A
			TGAA GA CTT TCTTTTCTGA		

ACTT CT GAA AGAAAAAGACT
 C _ _
 GAM2582 LOC91115 3' TCAGAGGCACAAGATTCTCTC 32401 A ATCTT
 GA AGAATCTT TTTCTGA
 || ||||| |||||
 CT TCTTAGAA GGAGACT
 C CAC_
 GAM2583 CFTR 3' CAACTATCTCATTTCCA 6100 TATT
 TGGAAATGAGGT TTG
 ||||| |||
 ACCTTTACTCTA AAC
 TC_
 GAM2583 LDOC1 3' TTTCAAATTGCAGCAGTCCCA 14694 AAA AG T
 TGG TG GT ATTTTGAAA
 || || || |||||
 ACC AC CG TAAAACTTT
 CTG GA T
 GAM2583 POU4F1 3' TTTCAAATAAGCTTTTCC 12902 AT G
 GGAA GAG TTATTTTGAAA
 ||| || |||||
 CCTT TTC AATAAACTTT
 _ G
 GAM2583 SLC21A2 3' CAAAGCCACCTCATTTCCA 12157 TA
 TGGAAATGAGGT TTTTG
 ||||| |||||
 ACCTTTACTCCA GAAAC
 CC
 GAM2583 BICD2 3' TTCAAATAGCATTCCCCA 34853 AAAT _
 TGG GAG GTTATTTTGAA
 || || |||||
 ACC CTT CGATAAACTT
 C _ A
 GAM2583 FLJ11117 3' TCAAACCAAGACCTCATCTACA 20328 GAA AT_
 TA TATG ATGAGGTT TTTGA
 ||| ||||| |||||
 ATAC TACTCCAG AAAC
 ATC AACC
 GAM2583 FLJ20209 3' TTCACTGACCCCATCTCCA 41406 A A TTT
 TGGA ATG GGTGA TGAA
 ||| || |||| |||||
 ACCT TAC CCAGT ACTT
 C C C_
 GAM2583 KIAA0172 3' TTTCAAATAAAATTCCAT 32413 ATGAGG
 ATGGAA TTATTTTGAAA
 |||| |||||
 TACCTT AATAAACTTT
 AA_
 GAM2583 KIAA0564 3' TTTCAAATGTACCTTATTCCC 32901 A _
 A TGG AATGAGGT TATTTTGAAA
 || ||||| |||||

		ACC TTATTCCA GTAAACTTT		
		C T		
GAM2583	PEG10	3' TTCAAACCTCCATTTCCATG	17435	AG ATTT
		TATGGAAATG GTT TGAA		
		GTACCTTTAC CAA ACTT		
		CT ____		
GAM2583	XPO5	3' TCAAAGGCCATTTC	43842	GA TA
		TGGAAAT GGT TTTTGA		
		ACCTTTA CCG GAAACT		
		____ _		
GAM2583	LOC144558	3' TCAAAGACTACTCATTTC	40439	GTTA
		TGGAAATGAG TTTTGA		
		ACCTTTACTC GAAACT		
		ATCA		
GAM2583	LOC151623	3' TCAAGGACTACTCATTTC	41379	GTTA
		TGGAAATGAG TTTTGA		
		ACCTTTACTC GGAACT		
		ATCA		
GAM2583	LOC221962	3' TCAAAGACTACTCATTTC	44529	GTTA
		TGGAAATGAG TTTTGA		
		ACCTTTACTC GAAACT		
		ATCA		
GAM2584	KIAA0471	3' CACTAATAGGAATGCCATTCAA	16909	ACG ATA
		TTGAA GGCG CTATTAGTG		
		AACTT CCGT GATAATCAC		
		A__ AAG		
GAM2584	UBE2N	3' CACTAATAACATTGCTGTCAA	9363	AACG AC
		TTGA GGCGAT TATTAGTG		
		AACT TCGTTA ATAATCAC		
		G__ CA		
GAM2584	UBE2N	3' CACTAATAACATTGCTGTCAA	45358	AACG AC
		TTGA GGCGAT TATTAGTG		
		AACT TCGTTA ATAATCAC		
		G__ CA		
GAM2585	ARHGAP9	5' ACCCAGAAAGCCTCACAT	26247	TTCAT
		ATGTGAGGCTTTCT GGT		
		TACACTCCGAAAGA CCA		
		C__		
GAM2585	C22orf19	3' ACCATAAAGGTCTTCACATA	9773	CTT C
		TATGTGAGG TCTTT ATGGT		

	ATACACTTC GGAAA TACCA	
	T__ _	
GAM2585 KIAA1040 3'	TACCATGAGTTTAAAGCCTCAC 35743	TCT_
AT	ATGTGAGGCTT TTCATGGTA	
	TACACTCCGAA GAGTACCAT	
	TTTT	
GAM2585 KIAA1204 3'	ACCATAGATAAAAGCCTCATA 34312	CT TC
	TGTGAGGCTTT T ATGGT	
	ATACTCCGAAA A TACCA	
	AT GA	
GAM2585 LOC144871 3'	TACCATGAAAAAACTACATA 40472	A C C
	TGTG GG TTT TTTCATGGTA	
	ATAC TC AAA AAAGTACCAT	
	A _ _	
GAM2585 LOC145921 3'	TACCAATGAGAGCCTCACA 37426	TTTCA
	TGTGAGGCTTTC TGGTA	
	ACACTCCGAGAG ACCAT	
	TA__	
GAM2585 LOC150333 5'	ACCTGCGAAAGAAAGCCCACA 41196	A AT_
	TGTG GGCTTTTCTTTC GGT	
	ACAC CCGAAAGAAAG CCA	
	_ CGT	
GAM2585 LOC152190 5'	TACCATGAAAGAAAAGATCA 34525	GGC
	TGA TTTCTTTCATGGTA	
	ACT AAAGAAAGTACCAT	
	AGA	
GAM2586 GCK 5'	TTGGAACAAATCGCCCCT 27286	A A G
	AG GGC ATTTGTT CAG	
	TC CCG TAAACAA GTT	
	C C G	
GAM2586 IL1RAPL2 5'	CAGAGTCTGCACCTGCCGCCT 18873	AATTTGT
	AGGC TGCAGACTCTG	
	TCCG ACGTCTGAGAC	
	CCGTCC_	
GAM2586 FLJ10751 3'	CAGAGTCTGCATGGCACTC 20190	_ AATTTGT
	GAG GC TGCAGACTCTG	
	CTC CG ACGTCTGAGAC	
	A GT_____	
GAM2586 FLJ10751 3'	CAGAGTCTGCATGGCACTC 20091	_ AATTTGT
	GAG GC TGCAGACTCTG	

CTC CG ACGTCTGAGAC
 A GT_____
 GAM2586 GLTP 3' CAGAGTCTGCAGGGGACAGCCC 18555 A AA G
 T AG GGC TTT TTGCAGACTCTG
 || ||| ||| |||||
 TC CCG AGG GACGTCTGAGAC
 _ AC G
 GAM2586 KIAA0062 3' AGTCTGTTTAATTGCCT 34793 TGTT
 AGGCAATT GCAGACT
 ||||||| |||||
 TCCGTTAA TGTCTGA
 TT_____
 GAM2586 KIAA0237 3' AGAGTCTTATAACACCTC 16436 CAATT C_
 GAGG TGTTG AGACTCT
 ||| ||||| |||||
 CTCC ACAAT TCTGAGA

 AT
 GAM2586 LGALS8 3' CAGAGTCTACACAGACGCCT 13244 AA T C
 AGGC TTTGT G AGACTCTG
 ||| ||||| | |||||
 TCCG AGACA C TCTGAGAC
 C_ _A
 GAM2586 LOC158156 3' AGAACCTGCATTGCTTC 39735 TTTGT AC
 GAGGCAA TGCAG TCT
 ||||||| ||||| |||
 CTTCGTT ACGTC AGA

 CA
 GAM2587 COL19A1 3' TCTTTACGATTTAATTGA 7600 GAAT
 TCAGT GTCGTAAAGA
 ||||| |||||
 AGTTA TAGCATTCT
 ATT_____
 GAM2587 HTRA3 3' AGTTCTCCGGATATTCAC 42939 GTAA
 GTGAATGTC AGAACT
 ||||||| |||||
 CACTTATAG TCTTGA
 GCC_____
 GAM2587 IVD 3' TGAGTTCTCCACAACAGCTC 8003 A_ C AA
 GA TGT GT AGAACTCA
 || ||| || |||||
 CT ACA CA TCTTGAGT
 CG A CC
 GAM2587 KMO 3' TCTGTATTAATTCAGTGA 9781 GTC A
 TCAGTGAAT GTA AGA
 ||||||| ||| |||
 AGTCACTTA TAT TCT
 AT_ G
 GAM2587 SMURF1 3' TGAGCTCTTTACGGGAGCATCA 44416 A ____ A
 TGA TGT CGTAAAGA CTCA
 ||| ||| ||||| |||||

		ACT ACG GCATTTCT GAGT	
		_ AGG C	
GAM2587 SPS2	3'	TTCTTTATTCAATTTTACTGA 14556	TGTC_
		TCAGTGAA GTAAAGAA	
		AGTCATTT TATTTCTT	
		TAACT	
GAM2587 VAPA	3'	TGAGTCCTTTATGAAATTCAT 9626	G A
		GTGAAT TCGTAAAG ACTCA	
		TACTTA AGTATTTT TGAGT	
		A C	
GAM2587 C1QR1	3'	GAATTCTCCATATATTTCACT 14334	C AA C
		AGTGAATGT GT AGAA TC	
		TCACTTATA TA TCTT AG	
		_ CC A	
GAM2587 DKFZP434F091	3'	AGTTCTTTACCTCAACCTGA 17737	TGAA TC
		TCAG TG GTAAAGAACT	
		AGTC AC CATTTCTTGA	
		CA_ TC	
GAM2587 FLJ11413	3'	GAATTCTCTACGATGGCCAT 23773	AA A C
		GTG TGTCGTA AGAA TC	
		TAC GTAGCAT TCTT AG	
		CG C A	
GAM2587 KIAA1271	3'	GAGTCCTGGCATTAC 34468	GTAA A
		GTGAATGTC AG ACTC	
		CATTACGG TC TGAG	
		_ C	
GAM2587 LNX	5'	TTCTTTGTGATCTACTGA 26339	AAT
		TCAGTG GTCGTAAAGAA	
		AGTCAT TAGTGTTTCTT	
		C_	
GAM2587 PRO0246	5'	AGCTCTTTCTCTATTTACTGA 15379	TCGT A
		TCAGTGAATG AAAGA CT	
		AGTCATTTAT TTTCT GA	
		CTC_ C	
GAM2587 LOC143154	3'	TGAGCTCTCTATTCTGTTTCAT 37589	TGTC_ A A
	TGA	TCAGTGAA GTA AGA CTCA	
		AGTTACTT TAT TCT GAGT	
		TGTCT C C	
GAM2587 LOC204970	5'	TGAGTTCTCCGACGCCACATG 43075	_ AA TAA
	A	TCA GTG TGTCG AGAACTCA	

		AGT CAC GCAGC TCTTGAGT		
		A CC C__		
GAM2587	LOC219294 3'	GAGCTCTCTATTCTGTTTCATT 44687	TGTC_	A A
	GA	TCAGTGAA GTA AGA CTC		
		AGTTACTT TAT TCT GAG		
		TGTCT C C		
GAM2588	CLASP1 3'	ACGAAAGGTGATATATCTTTAA 32539	CCAA TG	_
		TTAAAG AT CCTT CGT		
		AATTTC TA GGAA GCA		
		TATA GT A		
GAM2588	FLJ21817 3'	TGAAGCAATTTGGATTAA 22784	G	C
		TTAAA CCAAATTGC TTCG		
		AATTT GGTTTAACG AAGT		
		A _		
GAM2588	KIAA1069 3'	ACGAAAGGGGGTGGCCTTGA 33722	A AA G	_
		TTAA GCCA TT CCTT CGT		
		AGTT CGGT GG GGAA GCA		
		C _ G A		
GAM2588	PHRET1 3'	TACGACTTCATTTGGCTTCGA 22176	TA	TGCCT
		T AAGCCAAAT TCGTA		
		A TTCGGTTTA AGCAT		
		GC CTC_		
GAM2588	PRO1600 3'	AAGGCTATCTGGCTTTAA 15313	A T	
		TTAAAGCCA AT GCCTT		
		AATTCGGT TA CGGAA		
		C T		
GAM2588	SMT3H2 3'	AGGGCAATCTGTCTTTAA 13819	C A	
		TTAAAG CA ATTGCCTT		
		AATTTC GT TAACGGGA		
		T C		
GAM2588	LOC143888 3'	TACAAGCTGCTTTTGGCTTT 37672	TT _	C
		AAAGCCAAA GC CTT GTA		
		TTTCGGTTT CG GAA CAT		
		T_ TC _		
GAM2588	LOC157695 5'	GGGACAATTTGGTTTTAA 41832	_	
		TTAAAGCCAAATTG CCT		
		AATTTTGGTTTAAC GGG		
		A		
GAM2588	LOC158997 3'	AGGGCAATCTGTCTTTAA 39933	C A	
		TTAAAG CA ATTGCCTT		

AAT TTC GT TAACGGGA
 T C
 GAM2589 ABCD3 3' CACAAAGTCCTTAACATGCCA 8752 T CGTTA
 TGGCATGTTA GGAT TGTG
 ||||| ||| |||
 ACCGTACAAT CCTG ACAC
 T AA__
 GAM2589 ESM1 3' ACAATCCATAACATCCA 13912 C C
 TGG ATGTTATGGAT GT
 || ||||| ||
 ACC TACAATACCTA CA
 _ A
 GAM2590 ANKTM1 3' TTCCTGCACTCATTCTC 14260 CG CA
 GAGAATGG GCA GGAA
 ||||| || |||
 CTCTTACT CGT CCTT
 CA _
 GAM2590 CACNA2D3 5' TTCCTGTGCCCTTCTC 20435 T C
 GAGAA GG GGCACAGGAA
 |||| || |||||
 CTCTT CC CCGTGTCTT
 _ _
 GAM2590 CELSR1 3' CCTCCTGCCAATTCTCT 15513 _ CAC
 AGAGAAT GGCGG AGG
 ||||| ||| |||
 TCTCTTA CCGTC TCC
 A C__
 GAM2590 DHCR7 3' CCTGTGAGCGCCACCTCTCG 7039 _ AAT_ G_
 AA TTC AGAG GGCG CACAGG
 || ||| ||| |||||
 AAG TCTC CCGC GTGTCC
 C CCAC GA
 GAM2590 MYBL1 3' TCCCTCTCCACTCCTGAA 32045 A A C CACA
 TTCAG GA TGG GG GGA
 |||| || ||| || |||
 AAGTC CT ACC CT CCT
 _ C T C__
 GAM2590 PDE4C 3' CCCACCATCTCTGAA 6634 A C CACA
 TTCAGAGA TGG GG GG
 ||||| ||| || ||
 AAGTCTCT ACC CC CC
 _ A _
 GAM2590 PMSCL1 5' TTTCCTGTGAACTTGTGTCTC 11474 AT__ CGG
 GAGA GG CACAGGAAA
 ||| || |||||
 CTCT TC GTGTCTTT
 GTGT AA_
 GAM2590 POU4F1 3' TTTCCTCCACCCATTCTCTGA 12903 C_ CAC
 TCAGAGAATGG GG AGGAAA
 ||||| || |||||

		AGTCTCTTACC CC TCCTTT	
		CA ____	
GAM2590	PRKCB1	3' TTTGGCACCACCTCTCTGAA 34904	A CG A
		TTCAGAGA TGG GC CAGG	
		AAGTCTCT ACC CG GTTT	
		C A_ _	
GAM2590	SH3BP2	3' TTCCTGTGGTTCCATCCGAA 8953	A GAA CGG
		TTC GA TGG CACAGGAA	
		AAG CT ACC GTGTCCTT	
		C ____ TTG	
GAM2590	SOX13	3' CCTGTGCCCTCTGGA 12243	AATGGC
		TTCAGAG GGCACAGG	
		AGGTCTC CCGTGTCC	

GAM2590	SP3	5' CCTGTCTCCCTCTCTGAA 40134	AT C C
		TTCAGAGA GG GG ACAGG	
		AAGTCTCT CC TC TGTCC	
		_ C _	
GAM2590	TIAL1	3' TTCCTGTGACACTCTGAA 22743	AATGGCGG
		TTCAGAG CACAGGAA	
		AAGTCTC GTGTCCTT	
		ACA_____	
GAM2590	TMC1	5' CCTGTGCTTCACATCTGAA 28932	GAA C
		TTCAGA TGG GGCACAGG	
		AAGTCT ACT TCGTGTCC	
		AC_ _	
GAM2590	TXNRD1	3' TCCAAGTCCACCAGTCTCTGAA 9337	A C C A_
		TTCAGAGA TGG GG AC GGA	
		AAGTCTCT ACC CC TG CCT	
		G A _ AA	
GAM2590	VANGL2	3' TCCCTGCCTGATTCTCTGAG 35486	_ CACA
		TTCAGAGAAT GGCGG GGA	
		GAGTCTCTTA CCGTC CCT	
		GT _____	
GAM2590	ABLIM	3' TCCTGTGTCCTCTGAA 8121	AATGGC
		TTCAGAG GGCACAGGA	
		AAGTCTC CTGTGTCCT	

GAM2590	ABLIM	3' TCCTGTGTCCTCTGAA 13554	AATGGC
		TTCAGAG GGCACAGGA	

AAGTCTC CTGTGTCCT

GAM2590 ARHGEF2 3' TCCTATCTCCACATCTCTGAA 11093 A_ C CAC
TTCAGAGA TGG GG AGGA
||||||| ||| || ||||
AAGTCTCT ACC CT TCCT
AC T A__

GAM2590 BPES 3' TCCTGTGCTCACCTCCCTGA 23326 A AT C_
TCAG GA GG G GCACAGGA
|||| || ||| |||||
AGTC CT CC C CGTGTCTCT
C __ A T

GAM2590 C11orf23 3' TTTCCCGGGTGAGCCCCTCTCT 20305 AT GG A__
GAA TTCAGAGA GGC CAC GGAAA
||||||| ||| ||| |||||
AAGTCTCT CCG GTG CCTTT
CC A_ GGC

GAM2590 C20orf108 3' CCTGGGCCATTCTCTGA 28083 GGCA
TCAGAGAATGGC CAGG
||||||| |||
AGTCTCTTACCG GTCC
G__

GAM2590 DOCK3 3' TCCCTTCCATTCTTGAA 33041 G C CACA
TTCA AGAATGG GG GGA
||| ||||| || |||
AAGT TCTTACC TC CCT
_ T ____

GAM2590 FLJ10702 3' TTTCTGTGTCATTAACCTCTG 20029 AATGGCG
CAGAG GCACAGGAAA
||||| |||||
GTCTC CGTGTCTCTT
CAATTA_

GAM2590 FLJ21438 5' CTGGCCACACTCTCTGAA 30846 A GC A
TTCAGAGA TG GGC CAG
||||||| || ||| |||
AAGTCTCT AC CCG GTC
C A_ _

GAM2590 HNRPA3 3' TCCTACGTTAGAAACCATTCTT 12325 C____ AC
GAGAATGG GGC AGGA
||||||| ||| |||||
TTCTTACC TTG TCCT
AAAGA CA

GAM2590 KIAA0133 3' TCCTGTGTTAGCTCTGTGAA 16610 G ATG_
TTCA AGA GC GGCACAGGA
||| ||| || |||||
AAGT TCT CG TTGTGTCCT
G __ A

GAM2590 KIAA0469 3' TCCTGTGTCTGTCCTCCGGA 16897 A AAT_
TTC GAG GGC GG CACAGGA
||| ||| ||||| |||||

AGG CTC CTGTC GTGTCCT
 C ____ T
 GAM2590 KIAA1023 3' TCCCGTGGCTCGGATTCTCTGA 19094 ____ GG A
 G TTCAGAGAAT GGC CAC GGA
 ||||| ||| ||| |||
 GAGTCTCTTA TCG GTG CCT
 GGC ____ C
 GAM2590 KIAA1069 3' TTCCTGTGCTCATCTCCGGA 33726 A A GC
 TTC GAGA TG GGCACAGGAA
 ||| ||| || |||||
 AGG CTCT AC TCGTGTCTT
 C _ _
 GAM2590 KIAA1203 3' TCCTATCTGAATCTCTGAA 35472 ATGG CAC
 TTCAGAGA CGG AGGA
 ||||| ||| |||
 AAGTCTCT GTC TCCT
 AA__ TA_
 GAM2590 KIAA1872 3' TTTCTGTGCTTTCCCTCCAG 31525 A_ AAT C_
 AA TTC GAG GG GGCACAGGAAA
 ||| ||| || |||||
 AAG CTC CC CCGTGTCTTT
 AC ____ TTT
 GAM2590 LHX6 3' TTCCTTGGAACCATCTCTGAA 15701 A CGG C
 TTCAGAGA TGG CA AGGAA
 ||||| ||| || |||
 AAGTCTCT ACC GT TCCTT
 _ AAG _
 GAM2590 LIPG 3' TCCCCAGCTCACTCTCTGAA 12656 A _ _ CACA
 TTCAGAGA TG GC GG GGA
 ||||| || ||| |||
 AAGTCTCT AC CG CC CCT
 C T A ____
 GAM2590 MGC15634 3' TTCCTGTAAGCTACCTGAA 26497 AGAA GGC
 TTCAG TGGC ACAGGAA
 |||| ||| |||||
 AAGTC ATCG TGTCTT
 C__ AA_
 GAM2590 MGC26684 3' TTCCTGTGTGCTCCCTGAG 29374 A ATG G
 TTCAG GA GCG CACAGGAA
 |||| || || |||||
 GAGTC CT CGT GTGTCCTT
 C ____ _
 GAM2590 NCUBE1 3' TTTCTATATTGCCCTTTGAA 18095 AAT CAC
 TTCAGAG GGCGG AGGAAA
 ||||| |||| |||||
 AAGTTTC CCGTT TCCTTT
 ____ ATA
 GAM2590 NMT1 3' TTCCCCACACATGCCTATTTCT 22052 AT GCACA_
 GAA TTCAGAGA GGCG GGAA
 ||||| ||| |||

		AAGTCTTT CCGT CCTT	
		AT ACACACC	
GAM2590	NYD-SP11	3' CCTCCTACAGTTTCTGAA 25689	A GC CAC
		TTCAGAGA TG GG AGG	
		AAGTCTTT AC CC TCC	
		G AT ____	
GAM2590	OSBPL3	3' TCCTGTGCTTGCCTTCTGAA 17817	AAT _
		TTCAGAG GGCG GCACAGGA	
		AAGTCTT CCGT CGTGCCT	
		____ T	
GAM2590	POU4F2	3' CCTTTTCCTTCTCTGAA 10920	T CG CAC
		TTCAGAGAA GG G AGG	
		AAGTCTCTT CC T TCC	
		_ TT ____	
GAM2590	PP1665	5' TCCCAGGTGACCATTCTCTG 25093	CG ACA
		CAGAGAATGG GC GGA	
		GTCTCTTACC TG CCT	
		AG GAC	
GAM2590	SNPH	3' TCCTGCCCTCAGCCTCTGAA 16301	AA C CA
		TTCAGAG TGG GGCA GGA	
		AAGTCTC ACT CCGT CCT	
		CG C ____	
GAM2590	STOML1	3' TCCCCTACAGTGGTTCTCTGGA 11233	G GGCACA
		TTCAGAGAAT GC GGA	
		AGGTCTCTTG TG CCT	
		G ACATCC	
GAM2590	LOC124216	3' CCACCACCAGTCTCTGAA 36738	A C CACA
		TTCAGAGA TGG GG GG	
		AAGTCTCT ACC CC CC	
		G A A ____	
GAM2590	LOC126302	3' TTCCTGTGCTCTCCCTC 36826	AAT C _
		GAG GG G GCACAGGAA	
		CTC CC C CGTGCCTT	
		____ TT	
GAM2590	LOC131870	3' CCTGTGCTTTCTGAA 37015	AATGGC
		TTCAGAG GGCACAGG	
		AAGTCTT TCGTGTCC	

GAM2590	LOC138399	5' CCTGTGCCCTACATCCCTGAG 37130	A A_ C
		TTCAG GA TGG GGCACAGG	

	GAGTC CT ATC CCGTGTCC	
	C AC _	
GAM2590 LOC145955 3'	TTCCCTGCTCACATTCTCTGGA 40647	GC CA
	TTCAGAGAATG GGCA GGAA	
	AGGTCTCTTAC TCGT CCTT	
	AC C_	
GAM2590 LOC149464 5'	TTTCCCACTGGAGTTCTCTGAA 40997	GG CACA
	TTCAGAGAAT CGG GGAAA	
	AAGTCTCTTG GTC CCTTT	
	AG AC__	
GAM2590 LOC150468 5'	TTCCCCAGAACCATTTTCTGAA 38977	CGGCACA
	TTCAGAGAATGG GGAA	
	AAGTCTTTTACC CCTT	
	AAGACC_	
GAM2590 LOC155066 3'	CCTACACTCCCTCTCTGAG 39541	AT C CAC
	TTCAGAGA GG GG AGG	
	GAGTCTCT CC TC TCC	
	_ C ACA	
GAM2590 LOC155179 3'	TCCCGTGGCTCGGATTCTCTGA 39560	_ GG A
G	TTCAGAGAAT GGC CAC GGA	
	GAGTCTCTTA TCG GTG CCT	
	GGC _ C	
GAM2590 LOC159053 3'	TTTCCTGTTTTCTTCATTT 42061	C C_
	GAATGG GG ACAGGAAA	
	TTTACT CT TGTCTTTT	
	T TT	
GAM2590 LOC201562 3'	TTTCACAGCACCATTTCTCAGAA 42885	A CG ACAG
	TTC GAGAATGG GC GAAA	
	AAG CTCTTACC CG CTTT	
	A A_ ACA_	
GAM2590 LOC201771 5'	TCCTGTTTTTTCATTCTC 34678	CG C
	GAGAATGG G ACAGGA	
	CTCTTACT T TGTCTT	
	TT _	
GAM2590 LOC203378 5'	TTCTGTGCCAGGCCCTGGA 43562	AGAAT _
	TTCAG GGC GGCACAGGAA	
	AGGTC CCG CCGTGTCTT	
	_ GA	
GAM2590 LOC219918 5'	CCTGCACCACCGTTTTTTGAA 44003	A C CA
	TTCAGAGA TGG GG CAGG	

		AAGTTTTT GCC CC GTCC	
		— A AC	
GAM2590	LOC220071 5'	CCTGCACCACCGTTTTTGAA 44878	A C CA
		TTCAGAGA TGG GG CAGG	
		AAGTTTTT GCC CC GTCC	
		— A AC	
GAM2590	LOC220988 3'	TCCTACGTTAGAAACCATTCTT 43685	C_____ AC
		GAGAATGG GGC AGGA	
		TTCTTACC TTG TCCT	
		AAAGA CA	
GAM2590	LOC221747 3'	TTTCCTGTGCTGTTCTC 44366	ATG
		GAGA GCGGCACAGGAAA	
		CTCT TGTCGTGTCCTTT	

GAM2590	LOC254085 5'	TTCCTGTGCCTCCCTC 45974	AAT C
		GAG GG GGCACAGGAA	
		CTC CC CCGTGTCTT	
		_____ T	
GAM2590	LOC256940 5'	TTCCTGTGCCAGTGCTGAA 46157	AGAATGGC
		TTCAG GGCACAGGAA	
		AAGTC CCGTGTCTT	
		GTGA_____	
GAM2590	LOC257471 5'	CCTGTCTCCCTCTCTGAA 45786	AT C C
		TTCAGAGA GG GG ACAGG	
		AAGTCTCT CC TC TGTCC	
		_____ C _____	
GAM2590	LOC92228 3'	TCCTGCAGTTTCTGAA 34004	A GCGGCA
		TTCAGAGA TG CAGGA	
		AAGTCTTT AC GTCCT	
		G _____	
GAM2591	SNX6 3'	AAAGAATGAAGTCTCCT 22217	TAGGGG
		AGGAGCAGTTC TCTTT	
		TCCTCGTCAAG AGAAA	
		TA_____	
GAM2591	FLJ12287 3'	ACCCCCAGACCTGCTCCTA 22752	T A
		TAGGAGCAG TCT GGGGT	
		ATCCTCGTC AGA CCCCA	
		C C	
GAM2591	WNT2B 3'	ACACCCTAGAACACTCCTA 10391	CA _
		TAGGAG GTTCTAGGG GT	

			ATCCTC CAAGATCCC CA		
			A_ A		
GAM2591	WNT2B	3'	ACACCCTAGAACACTCCTA	23692	CA _
			TAGGAG GTTCTAGGG GT		
			ATCCTC CAAGATCCC CA		
			A_ A		
GAM2591	LOC203232	3'	AAGACCCTAAAAGTCCCC	35372	A CTA
			GG GCAGTT GGGGTCTT		
			CC CGTCAA TCCCAGAA		
			_ AA_		
GAM2591	LOC220776	3'	AAAGAAGAAACTGCTCCTG	33927	_ AGGGG
			TAGGAGCAGTT CT TCTTT		
			GTCCTCGTCAA GA AGAAA		
			A _		
GAM2591	LOC253936	3'	AAGACCCTAAAAGTCCCC	45407	A CTA
			GG GCAGTT GGGGTCTT		
			CC CGTCAA TCCCAGAA		
			_ AA_		
GAM2591	LOC91138	5'	AAAAGACCCCTAAAAAGCCTA	32438	AGCAG C
			TAGG TT TAGGGGTCTTTT		
			ATCC AA ATCCCCAGAAAA		
			GA_ A		
GAM2592	MIG	3'	ATCATTTATCATATATATACAT	8243	TG C
			ATGTGT GTATGATAAA GAT		
			TACATA TATACTATTT CTA		
			TA A		
GAM2592	PRO1596	3'	ATCGTTTATCATATTGAAACAT	25294	G TG
			ATGT T GTATGATAAACGAT		
			TACA A TATACTATTTGCTA		
			A GT		
GAM2592	LOC256073	3'	ATCATTTATCATGTTACAGAT	46229	G TG C
	T		AAT TGT GTATGATAAA GAT		
			TTA ACA TGTACTATTT CTA		
			G CT A		
GAM2593	SIRT1	3'	TAGAGATCAACTTTCTCA	14542	CT
			TGAGAAAGTTGATT TCTA		
			ACTCTTTCAACTAG AGAT		
			_		
GAM2593	FLJ20725	3'	ACTCTAGAAGAATCTGTACATC	19636	GAAAGTT A
	A		TGA GATTCTTCTA AGT		

		ACT CTAAGAAGAT TCA	
		ACATGT_ C	
GAM2593	LOC122773 3'	ACTTTCAGAAAGAATAAACTTT 36710	G _ _
	CTCA	TGAGAAAGTT ATTCTT CT AAAGT	
		ACTCTTTCAA TAAGAA GA TTTCA	
		A A C	
GAM2593	LOC152200 3'	ACTCCAGATCTCAGACTTTCTC 41437	GATTCT AA
	A	TGAGAAAGTT TCT AGT	
		ACTCTTTCAG AGA TCA	
		ACTCT_ CC	
GAM2593	LOC221931 3'	ACTTTAGGCCTCAACGTCCTCA 45118	AAA TTCT
		TGAG GTTGA TCTAAAGT	
		ACTC CAACT GGATTTC	
		CTG CC_	
GAM2593	LOC91947 3'	ACTTTAGAAAAGATCATCTTC 33568	A T C_
		GAA G TGATT TTCTAAAGT	
		CTT C ACTAG AAGATTTC	
		_T AA	
GAM2594	DTR 3'	ACAGTCTGGAGAAGGTATTAGC 7658	A C AAT
	A	TG TAA ACCTTCTCCA TTGT	
		AC ATT TGGAAGAGGT GACA	
		G A CT_	
GAM2594	HLCS 3'	TTTGGGAAAAAATGTTATCA 5994	CC_ T
		TGATAACA TTC CCAA	
		ACTATTGT AAG GGTTT	
		AAAA _	
GAM2594	NORE1 3'	ACAAATTTGAATTTAATGTTGT 25440	CCTTCTC
	CA	TGATAACA CAAATTTGT	
		ACTGTTGT GTTTAAACA	
		AATTTAA	
GAM2594	AUTL1 3'	ACAAATTTAAAGATTATGTTAT 26646	CCT CC
	TA	TGATAACA TCT AAATTTGT	
		ATTATTGT AGA TTAAACA	
		ATT AA	
GAM2594	KIAA1143 3'	ACAAATTTGGTGCCACATTATC 34068	CACCTTCT
		GATAA CCAAATTTGT	
		CTATT GGTTTAAACA	
		ACACCGT_	
GAM2595	MAML1 3'	AGAATTATTTGCAATTTG 16495	_
		CAAATTGCAAA AATTCT	

			GTTTAACGTTT TTAAGA		
			A		
GAM2595	AWP1	3'	GCATTAATCTTGCAGTTT 21079	AAATTC	
			AAATTGCAA TTAATGC		
			TTTGACGTT AATTACG		
			CT____		
GAM2595	BIRC1	3'	CATTAAGAATTTCTGAATATG 10883	A G A	
			CA ATT CA AAATTCTTAATG		
			GT TAA GT TTTAAGAATTAC		
			A _ C		
GAM2595	FLJ10159	3'	CACTAAGAATTGTGATTTG 19749	TG AAA A	
			CAAAT CA ATTCTTA TG		
			GTTTA GT TAAGAAT AC		
			GT ____ C		
GAM2595	KIAA0419	3'	TGCATAGTGATTTTTGAATTTG 16260	G C A	
			CAAATT CAAAAATT TTA TGCA		
			GTTTAA GTTTT TAG GAT ACGT		
			_ T _		
GAM2595	KIAA0970	3'	TGCATTAGAGCACTTTGCAATT 17205	AA_ T	
			AATTGCAAA TTCT AATGCA		
			TTAACGTTT GAGA TTACGT		
			CAC _		
GAM2595	KIAA1546	3'	TAGGAACTTTTGCAGTTTG 33716	A_	
			CAAATTGCAAAA TTCTTA		
			GTTTGACGTTTT AAGGAT		
			CA		
GAM2595	KIAA1673	3'	CATGGTGATTTTTGCAAT 35025	CTTA	
			ATTGCAAAAATT ATG		
			TAACGTTTTTAG TAC		
			TGG_		
GAM2595	TRAD	3'	TGCATTAAGAGAAAGCAAT 13929	AAAAA	
			ATTGC TTCTTAATGCA		
			TAACG GAGAATTACGT		
			AAA_		
GAM2595	LOC158381	3'	GCATTAATCTTGCAGTTT 35175	AAATTC	
			AAATTGCAA TTAATGC		
			TTTGACGTT AATTACG		
			CT____		
GAM2595	LOC196283	3'	TGGGAATTTTGCAATTTG 42342	A	
			CAAATTGCAAAA TTCTTA		

GTTTAACGTTTT AAGGGT

GAM2596 CRIM1 3' CTTTATTA[—]AAAATCTTCCTCA 18559 GTGTC
TGAGGAAGATT TAAAG
||||||| ||||
ACTCCTTCTAA ATTC
AATT[—]

GAM2596 DFNA5 3' TCTTTAAACAGTTTTTCCTTA 10656 GTC
TGAGGAAGATTGT TAAAGA
||||||| ||||
ATTCCTTTTGACA ATTTCT
A[—]

GAM2596 GPR4 3' TCTCCAGCGATCTTCCCA 30101 A GTCTAA
TG GGAAGATTGT AGA
|| ||||| |||
AC CCTTCTAGCG TCT
[—] ACC[—]

GAM2596 S100B 3' GTTCTTTAAATGCGTTCCTCA 12956 GAT C
TGAGGAA TGTGT TAAAGAAC
||||| |||| |||||
ACTCCTT GCGTA ATTTCTTG
[—] A

GAM2596 AGPAT1 3' TTCTTTGGAACAAATCCCCCCC 26474 A AA GTG
A
TG GG GATT TCTAAAGAA
|| ||| |||||
AC CC CTAA AGGTTTCTT
C CC ACA

GAM2596 AP3M1 3' TTCTTTC[—]CAATCTTCTCA 14398 G TGTCT
TGAG AAGATTG AAAGAA
|||| ||||| ||||
ACTC TTCTAAC TTTCTT

GAM2596 C9orf7 3' GTTCCTCCGGGGCCACCTTCCT 19036 AT T AAA[—]
CA
TGAGGAAG TG GTCT GAAC
||||| || ||| |||
ACTCCTTC AC CGGG CTTG
C[—] GCCTC

GAM2596 DKFZP434F0318 3' TTCTTGACACAACCCTCCT 25146 AGA A
AGGA TTGTGTCTAA GAA
||| ||||| |||
TCCT AACACAGGTT CTT
CCC [—]

GAM2596 DKFZP434H132 5' AGACACTGAGTTTTTCCTTA 36443 [—]
TGAGGAAGATT GTGTCT
||||||| ||||
ATTCCTTTTGA CACAGA
GT

GAM2596 DKFZP566K1924 3' TCTGACACAATATCCCTCA 36522 AAG TAA
TGAGG ATTGTGTC AGA
|||| ||||| |||

ACTCC TAACACAG TCT
 CTA ____
 GAM2596 HSU79252 5' GTTCTTTTTGCTGCCATCTTCC 14958 T _ CT
 TCA TGAGGAAGAT GT GT AAAGAAC
 ||||| || || |||||
 ACTCCTTCTA CG CG TTTCTTG
 C T TT
 GAM2596 KIAA0064 5' CTTTAGACTACAGTTCCCA 16460 A AG _
 TG GGA ATTGT GTCTAAAG
 || ||| |||| |||||
 AC CCT TGACA CAGATTTC
 _ _ T
 GAM2596 KIAA0410 3' TTCTTTAGGGTCTTCC 16623 TGTG
 GGAAGAT TCTAAAGAA
 ||||| |||||
 CCTTCTG GGATTTCTT

 GAM2596 KIAA1710 5' TCTCTAGAATCTTCCT 31331 TGTG A
 AGGAAGAT TCTA AGA
 ||||| |||||
 TCCTTCTA AGAT TCT
 ____ C
 GAM2596 KIAA1853 3' TCTTGGGCATCCCCCTCA 34390 AA TTG A
 TGAGG GA TGTCTAA GA
 |||| || ||||| ||
 ACTCC CT ACGGGTT CT
 CC ____ _
 GAM2596 MGC5338 3' GTTCCTTACAATATCTTTCTCA 23498 TG CT A
 TGAGGAAGAT TGT AA GAAC
 ||||| ||| || ||||
 ACTCTTTCTA ACA TT CTG
 TA _ C
 GAM2596 OSBPL3 3' TCTTTAAGTCTATATTTTCCTC 17819 TGTGT _
 A TGAGGAAGAT CT AAAGA
 ||||| || |||||
 ACTCCTTTTA GA TTTCT
 TATCT A
 GAM2596 P37NB 5' TTCTCTGGAGAACTTCCTCA 12436 A GTG A
 TGAGGAAG TT TCTA AGAA
 ||||| || ||| ||||
 ACTCCTTC AG AGGT TCTT
 A _ C
 GAM2596 PCDH19 3' TTCCCCAGACAGGTATACTTCT 31865 _ TG_ AAA
 TCA TGAGGAAG AT TGTCT GAA
 ||||| || |||| |||
 ACTTCTTC TA ACAGA CTT
 A TGG CCC
 GAM2596 PI4KII 3' TCCTTGGTCCCAATCTTCTCA 20482 G TGT A
 TGAG AAGATTG CTAA GA
 |||| ||||| |||| ||

ACTC TTCTAAC GGTT CT
 _ CCT C
 GAM2596 RASSF2 3' TTTAGACACAAACCTC 16400 AAGA
 GAGG TTGTGTCTAAA
 ||| |||||
 CTCC AACACAGATTT
 A__
 GAM2596 LOC115286 3' TCTGAACAATTCCTCA 36314 A GTCTAA
 TGAGGA GATTGT AGA
 ||||| ||||| |||
 ACTCCT TTAACA TCT
 _ AG__
 GAM2596 LOC152195 5' TCTTTAGGGTCTACCCCA 41433 A A TGTG
 TG GG AGAT TCTAAAGA
 || || ||| |||||
 AC CC TCTG GGATTTCT
 C A ____
 GAM2596 LOC54516 3' TTCTCCAGACAAACTTCCTTA 21124 ATTG AA
 TGAGGAAG TGTCT AGAA
 ||||| ||||| |||||
 ATTCCTTC ACAGA TCTT
 AA__ CC
 GAM2597 TLR1 5' ACAGACTGCCAAATGGAA 9275 _ A
 TTTC TTT GCAGTCTGT
 ||| ||| |||||
 AAGG AAA CGTCAGACA
 T C
 GAM2597 FLJ14440 3' ACAAATGTGGAAGAAATC 26529 A GTC
 GATTTCTTT GCA TGT
 ||||| ||| |||
 CTAAAGAAG TGT ACA
 G AA_
 GAM2597 P450RAI-2 3' ACAGACTGCTCTCCAATCCCTG 21265 AC TCTTT
 A TCA GATT AGCAGTCTGT
 || ||| |||||
 AGT CTAA TCGTCAGACA
 CC CCTC_
 GAM2597 LOC200347 5' ACAGGCAAGCTAAAGAAACCTC 42806 _ A_
 GA TTTCTTTAGC GTCTGT
 || ||||| |||||
 CT AAAGAAATCG CGGACA
 CC AA
 GAM2597 LOC51716 3' GCAGAATCTAAAGAAAGCATTG 18404 CGA CAG
 A TCAA TTTCTTTAG TCTGT
 ||| ||||| |||||
 AGTT AAAGAAATC AGACG
 ACG TA_
 GAM2598 FPRL1 5' TGTTTAAACTCAAATAGA 7196 A C
 TC TATTTGAGTT AAATA
 || ||||| |||||

			AG ATAAACTCAA TTTGT		
			— A		
GAM2598	IL1RAP	3'	CAACTATTTGAACTGTTGAGTG 7939	ATTTG	A
	AT		ATCAT AGTTCAAATA TTG		
			TAGTG TCAAGTTTAT AAC		
			AGTTG C		
GAM2599	RSN	3'	TGCACCAGATGCCATTACA 8865	A_ C _	
			TGTAATG ATC GGT CA		
			ACATTAC TAG CCA GT		
			CG A C		
GAM2599	BY55	3'	GGCTTAGTATCTTTCTCATTAC 29846	ATCC C	
	A		TGTAATGA GGT ACTAAGCC		
			ACATTACT CTA TGATTCGG		
			CTTT _		
GAM2599	FLJ13340	3'	GCTTAATATTCTCATTGCA 27707	ATCC TCAC	
			TGTAATGA GG TAAGC		
			ACGTTACT CT ATTCG		
			_____ TATA		
GAM2599	KIAA0092	3'	GACCCAGGCTTCATTACA 16154	T _	
			TGTAATGAA CC GGTC		
			ACATTACTT GG CCAG		
			C AC		
GAM2599	KIAA1361	3'	CTTAGTGACCATTGTCATCA 31167	AT _____	
			TGA CC GGTCACTAAG		
			ACT GG CCAGTGATTC		
			AC TTTA		
GAM2599	KPNB3	3'	GCTTAGTGTTTTTCATTGCA 8062	TCCGGT	
			TGTAATGAA CACTAAGC		
			ACGTTACTT GTGATTCG		
			TT_____		
GAM2599	OSF-2	3'	GTCACCAGATTCATTACA 13198	C C	
			TGTAATGAATC GGT AC		
			ACATTACTTAG CCA TG		
			A C		
GAM2599	TBDN100	3'	GCTTAATATTCTCATTGCA 24698	ATCC TCAC	
			TGTAATGA GG TAAGC		
			ACGTTACT CT ATTCG		
			_____ TATA		
GAM2599	THEA	3'	GGCTTAGTGTGCAACTCAT 32953	ATCCG _	
			ATGA GT CACTAAGCC		

		TACT CG GTGATTCGG		
		CAA__ T		
GAM2599	LOC221431 3'	GCCCAATGACCGGGTTTTTCGCA 44223	AAT	CTAA
		TGT GAATCCGGTCA GC		
		ACG TTTGGGCCAGT CG		
		CT_ AACC		
GAM2599	LOC255326 3'	GCTTAAGAAAAGATCATTACA 46107	A CGG	AC
		TGTAATGA TC TC TAAGC		
		ACATTACT AG AG ATTCG		
		_ AAA A_		
GAM2600	DLG5 5'	CAGAAGGAGCGACTCCATTAA 40333	ACT	GAGA
		TTAATGGAGTT GC TCTG		
		AATTACCTCAG CG AGAC		
		___ AGGA		
GAM2600	IL2RB 3'	CAGGGGGGCAGTAACTCC 6569	GAGA	
		GGAGTTACTGC TCTG		
		CCTCAATGACG GGAC		
		GGG_		
GAM2600	FLJ14075 3'	CAGATCTCCAAGAACTC 24372	AC	C
		GAGTT TG GAGATCTG		
		CTCAA AC CTCTAGAC		
		GA _		
GAM2600	MGC4707 3'	CTCACAGCAACTCCATTAA 23562	A	C
		TTAATGGAGTT CTG GAG		
		AATTACCTCAA GAC CTC		
		C A		
GAM2600	NTN4 3'	ATTTAGCAGTAATCCATTAA 31510	G	G
		TTAATGGA TTAAGTGC AGAT		
		AATTACCT AATGACG TTTA		
		_ A		
GAM2600	LOC138429 3'	CAGACCTCATTAAGTCAATTAA 37134	G	CTGC A
		TTAATG AGTTA GAG TCTG		
		AATTAC TCAAT CTC AGAC		
		_ TA_ C		
GAM2601	DKFZp761N1114 3'	AAGTACCTACCCTACCTCA 38602	TA	CAATAA
		TGAGGTAG TG TACTT		
		ACTCCATC AT ATGAA		
		CC CC_		
GAM2601	PRO2949 3'	TATTATTGCACTTCA 20618	AGTAT	
		TGAGGT GCAATAATA		

ACTTCA CGTTATTAT

GAM2601 LOC147991 5' AAAGTATTATATTTTCTACGTC 38433 G TATGCA
A TGA GTAG ATAATACTTT

||||| |||||
ACT CATC TATTATGAAA
G TTTA_

GAM2602 RFC1 5' CTTGTATGTGTCAAAGTATACT 8819 CCG _ C
AGTATACT GAC CG TACAAG

||||| ||| |||||
TCATATGA CTG GT ATGTTT
AA_ T _

GAM2602 LOC90917 3' TGTAGTTTGACAGAGTATGCTA 32172 CGGACC
TAGTATACTC GCTACA

||||| |||||
ATCGTATGAG TGATGT
ACAGTT

GAM2603 ADH5 3' TGAAC TTTTAAGGGTCTCA 6325 GTTT A
TGAG ATTCTTAAAA TTCA

||| ||||| |||||
ACTC TGGGAATTTT AAGT
_ C

GAM2603 FPRL1 3' TTGAATTCCTGGAATAAACC 7197 TAAA
GGTTTATTCT AATTCAA

||||| |||||
CCAAATAAGG TTAAGTT
TCC_

GAM2603 PPIF 3' TTGAACCTGGGAACAAACCTCA 12285 A AAAA
TGAGGTTT TTCTTA TTCAA

||||| ||||| |||||
ACTCCAAA AAGGGT AAGTT
C CC_

GAM2603 PTP4A2 3' TGAATTTTCAGGAACCGTCA 9556 _ TTAT A
TGA GGT TCTT AAAATTCA

||| ||| |||||
ACT CCA AGGA TTTTAAGT
G _ C

GAM2603 KIAA0565 3' TTGAATTTTAAAGTAAAGCTC 33223 G C
A TGAG TTTATT TTAAAAATTCAA

||||| ||||| |||||
ACTC AAATGA AATTTTAAAGTT
G _

GAM2603 NEK1 3' TTGAATTCATGGTTAAATCTC 45885 TT TAAA
A TGAGGTTTA CT AATTCAA

||||| || |||||
ACTCTAAAT GG TTAAGTT
T_ TACC

GAM2603 RAB40C 3' GGATTATGAACAAACCTCA 22148 A TTAAA
TGAGGTTT TTC AATTC

||||| ||| |||||

ACTCCAAA AAG TTAGG
 C TA____
 GAM2603 SH3BGRL2 3' TTGAATTTTAAAAAATTTC 25534 ATTC
 TGAGGTTT TAAAAATTCAA
 ||||| |||||
 ACTTTAAA AATTTTAAAGTT
 A____
 GAM2603 STX12 3' TTGAATTTCTAAGAAGCCT 32985 TTA A
 AGGT TTCTTA AAATTCAA
 ||| ||||| |||||
 TCCG AAGAAT TTTAAGTT
 ____ C
 GAM2603 TRIP-Br2 3' AATTTTAAAGAAAAGCATCA 16481 G A
 TGA GTTT TTCTTAAAAATT
 ||| ||| |||||
 ACT CGAA AAGAATTTTAA
 A _
 GAM2603 LOC256207 3' TTGAATTTTAAAGTAAAGCTC 45623 G C
 A TGAG TTTATT TAAAAATTCAA
 ||| ||||| |||||
 ACTC AAATGA AATTTTAAAGTT
 G _
 GAM2603 LOC92597 3' TGAATTTTAAAGGCTTTCCT 34676 TTTAT
 AGG TCTTAAAAATTCA
 ||| |||||
 TCC GGAATTTTAAAGT
 TTTC_
 GAM2604 AKAP1 3' TTGTAACCATTTTCTATTTGTG 9582 TC ____ C
 C G CA GGAAAATGGT ACAA
 | || ||||| |||
 C GT TCTTTTACCA TGTT
 GT TTA A
 GAM2604 AKAP1 3' TTGTAACCATTTTCTATTTGTG 29268 TC ____ C
 C G CA GGAAAATGGT ACAA
 | || ||||| |||
 C GT TCTTTTACCA TGTT
 GT TTA A
 GAM2604 CLN5 5' ACCTTCCTGGACTGCA 13224 A AAT
 TG AGTCCAGGAA GGT
 || ||||| |||
 AC TCAGGTCCTT CCA
 G ____
 GAM2604 COL6A3 5' CCGTTCAGTTCTCCTGGGCTCC 27670 A A____
 A TG AGTCCAGGA AATGG
 || ||||| |||
 AC TCGGGTCCT TTGCC
 C CTTGAC
 GAM2604 COL6A3 5' CCGTTCAGTTCTCCTGGGCTCC 10586 A A____
 A TG AGTCCAGGA AATGG
 || ||||| |||

			AC TCGGGTCCT	TTGCC		
			C	CTTGAC		
GAM2604	CRHR2	3'	TGGCCCTTGGACTCCA	7614	A	AAAAT
			TG AGTCCAGG	GGTCA		
			AC TCAGGTTC	CCGGT		
			C	_____		
GAM2604	CYP8B1	3'	TGGAAGCCTTCCTGGATTTC	10627		AAT CA_
			TGAAGTCCAGGAA	GGT CA		
			ACTTTAGGTCCTT	CCG GT		
			_____	AAG		
GAM2604	DISC1	3'	GCTTGTTCTGGAATTCA	20739		AAT
			TGAAGTCCAGGAA	GGT		
			ACTTCAGGTCCTT	TCG		
				GT_		
GAM2604	ESPN	3'	TGTGGCCCCCGGGACCCCA	25550	AA	A AAAAT
			TG GTCC GG	GGTCACA		
			AC CAGG CC	CCGGTGT		
			CC	G C_____		
GAM2604	FABP2	3'	TGTAACCTCAAACCTCCTGGACT	5627	A	AAAT__ C
	CA		TGA GTCCAGGA	GGT ACA		
			ACT CAGGTCCT	CCA TGT		
			_____	CAAAC T A		
GAM2604	FANCC	3'	TTATTCCCCTGGACTCCG	34908	A	AA
			TG AGTCCAGG	AATGG		
			GC TCAGGTCC	TTATT		
			C	CC		
GAM2604	FER	5'	TGACCATTTTCGCTAGACTTC	11756	C	_
			GAAGTC AG	GAAAATGGTCA		
			CTTCAG TC	CTTTTACCAGT		
				A G		
GAM2604	FOX E3	3'	GTGGCCTCCTGGACTCA	14473	A	AAAT
			TGA GTCCAGGA	GGTCAC		
			ACT CAGGTCCT	CCGGTG		

GAM2604	ITPKB	3'	TCATTTTCCTAACTTCA	7983	CC	
			TGAAGT	AGGAAAATGG		
			ACTTCA	TCCTTTTACT		
				A_		
GAM2604	LFG	3'	TGTTCCCTTCCCTGACCTCA	37699	A	CA AAT TC
			TGA GTC	GGAA GG ACA		

			ACT CAG CCTT CC TGT		
			C TC ____ CT		
GAM2604	MHC2TA	3'	TGTGGCTTCCTAAAATTCA 5785	GTCC	AAAT
			TGAA AGGA GGT CACA		
			ACTT TCCT TCGGTGT		
			AAAA ____		
GAM2604	Nrap	3'	CCATGTAGTCTCCTGGGCCTCA 29238	A	AA ____
			TGA GTCCAGGA ATGG		
			ACT CGGGTCCT TACC		
			C CTGATG		
GAM2604	PTHR2	3'	TTGTGACCAGCCAGACCTCA 11482	A	CA AAAA
			TGA GTC GG TGGTCACAA		
			ACT CAG CC ACCAGTGT		
			C A_ G_		
GAM2604	PTPRO	5'	GTGACCATCTCCAGCCTTC 25015	TCCA	AA
			GAAG GGA ATGGTCAC		
			CTTC CCT TACCAGTG		
			CGA_ C_		
GAM2604	PTPRO	5'	GTGACCATCTCCAGCCTTC 25024	TCCA	AA
			GAAG GGA ATGGTCAC		
			CTTC CCT TACCAGTG		
			CGA_ C_		
GAM2604	PTPRO	5'	GTGACCATCTCCAGCCTTC 25035	TCCA	AA
			GAAG GGA ATGGTCAC		
			CTTC CCT TACCAGTG		
			CGA_ C_		
GAM2604	RAP1	3'	TGTGACCAATGAACTTTA 21047	C	GGAAAA
			TGAAGT CA TGGTCACA		
			ATTTCA GT ACCAGTGT		
			A A ____		
GAM2604	SERPINB9	3'	TGCAACCTCCTCCTCCTGGATT 10369	G	AAAT__ CA
	CA		TGAA TCCAGGA GGT CA		
			ACTT AGGTCCT CCA GT		
			_ CCTCCT AC		
GAM2604	SLA2	3'	TGCAACCTCCATCTCCTGGATT 25944	G	AAAT__ CA
	CA		TGAA TCCAGGA GGT CA		
			ACTT AGGTCCT CCA GT		
			_ CTACCT AC		
GAM2604	SLC22A2	5'	TCGTCTTCCTGGGCTTCA 29942	A	
			TGAAGTCCAGGAA ATGG		

			ACTTCGGGTCCTT TGCT		
			C		
GAM2604	SLC7A8	3'	TGACCTTTCCCTGGGCTTCA 14553	A	T
			TGAAGTCCAGG AAA GGTCA		
			ACTTCGGGTCC TTT CCAGT		
			C _		
GAM2604	SMARCA2	3'	TGTGACCAAATGGGCCTCA 9035	A	GGAAAA
			TGA GTCCA TGGTCACA		
			ACT CGGGT ACCAGTGT		
			C AA ____		
GAM2604	TRPV1	3'	TGCAACCTCCGCCTCCTGGATT 20816	A	AAAT__ CA
	CCA		TG AGTCCAGGA GGT CA		
			AC TTAGGTCCT CCA GT		
			C CCGCCT AC		
GAM2604	TRPV1	3'	TGCAACCTCCGCCTCCTGGATT 27996	A	AAAT__ CA
	CCA		TG AGTCCAGGA GGT CA		
			AC TTAGGTCCT CCA GT		
			C CCGCCT AC		
GAM2604	TRPV1	3'	TGCAACCTCCGCCTCCTGGATT 28004	A	AAAT__ CA
	CCA		TG AGTCCAGGA GGT CA		
			AC TTAGGTCCT CCA GT		
			C CCGCCT AC		
GAM2604	TRPV1	3'	TGCAACCTCCGCCTCCTGGATT 28013	A	AAAT__ CA
	CCA		TG AGTCCAGGA GGT CA		
			AC TTAGGTCCT CCA GT		
			C CCGCCT AC		
GAM2604	UNC13	3'	TGTAGCAGCCTCCTGGACTTC 13070		AAATG TC
			GAAGTCCAGGA G ACA		
			CTTCAGGTCCT C TGT		
			CCGA_ GA		
GAM2604	WNT5B	3'	TGCACCTCCCGGACTTCA 25060	A	AAAT _
			TGAAGTCC GGA GGT CA		
			ACTTCAGG CCT CCA GT		
			C ____ C		
GAM2604	WNT5B	3'	TGCACCTCCCGGACTTCA 26362	A	AAAT _
			TGAAGTCC GGA GGT CA		
			ACTTCAGG CCT CCA GT		
			C ____ C		
GAM2604	ARNTL2	3'	TGGGGCAGCCCTCAGACTTCA 21420	C_	AAAA G A
			TGAAGTC AGG TG TC CA		

			ACTTCAG TCC AC GG GT		
			AC CG__ G _		
GAM2604	C11orf11	3'	TGTGACCACCCAGCTGCA 44790	A	CCA AAAA
			TG AGT GG TGGTCACA		
			AC TCG CC ACCAGTGT		
			G ACC ____		
GAM2604	C2F	3'	TGTTTGTTCCTCCGGGACTTCA 13030	A	AA TG T
			TGAAGTCC GG AA G CA		
			ACTTCAGG CC TT T GT		
			G CC GT T		
GAM2604	Cab45	3'	GTGGCTGTCCCGGACCCCA 18278	AA	A AAA
			TG GTCC GGA TGGTCAC		
			AC CAGG CCT GTCGGTG		
			CC C ____		
GAM2604	Cab45	3'	GTGGCTGTCCCGGACCCCA 18621	AA	A AAA
			TG GTCC GGA TGGTCAC		
			AC CAGG CCT GTCGGTG		
			CC C ____		
GAM2604	CEPT1	3'	TGTAATTATCCTGGATTCA 12738	G	AAA C
			TGAA TCCAGGA TGGT ACA		
			ACTT AGGTCCT ATTA TGT		
			_ ____ A		
GAM2604	DKFZP434B205	3'	TCATCTTCCTGGACGTCA 37128	A	A
			TGA GTCCAGGAA ATGG		
			ACT CAGGTCCTT TACT		
			G C		
GAM2604	DKFZP434C128	3'	TGGCCTTCCTGGACCGCA 32375	AA	AAT
			TG GTCCAGGAA GGTCA		
			AC CAGGTCCTT CCGGT		
			GC ____		
GAM2604	DOCK3	3'	GCCGTCCTGGACTCCA 33036	A	AAA
			TG AGTCCAGGA TGGT		
			AC TCAGGTCCT GCCG		
			C ____		
GAM2604	EDR2	3'	GTGCTTTGTCTGACTCCA 30338	A	AAAT T
			TG AGTCCAGGA GG CAC		
			AC TCAGGTCCT TC GTG		
			C GTT_ _		
GAM2604	FLJ10743	3'	TGGTCTTCTCCTGGGCTCCA 20082	A	A T GT
			TG AGTCCAGGA AA G CA		

AC TCGGGTCCT TT C GT
 C C _TG
 GAM2604 FLJ13197 3' TGCAACCTCTACCTCCTGGATT 23873 G AAAT__ CA
 CA TGAA TCCAGGA GGT CA
 |||| ||||| ||| ||
 ACTT AGGTCCT CCA GT
 _ CCATCT AC
 GAM2604 FLJ22659 5' ACCTTCCTGGGCCTCA 24471 A AAT
 TGA GTCCAGGAA GGT
 ||| ||||| |||
 ACT CGGGTCCTT CCA
 C _
 GAM2604 FLJ22814 3' TGTGACCTGCCAGCTTCA 24444 CCA AAAAT
 TGAAGT GG GGT CACA
 ||||| || |||||
 ACTTCG CC CCAGTGT
 A_ GT_
 GAM2604 HHLA2 3' TTGTAACCATTTTCTGGTATCA 13939 AGT G C
 TGA CCAG AAAATGGT ACAA
 ||| ||| ||||| |||||
 ACT GGTC TTTTACCA TGTT
 AT_ _ A
 GAM2604 HSNV1 3' TGTAACCTCTGCCTCCTGGATT 18968 G AAAT__ C
 CA TGAA TCCAGGA GGT ACA
 |||| ||||| ||| |||
 ACTT AGGTCCT CCA TGT
 _ CCGTCT A
 GAM2604 KIAA0252 3' TGTTAACATTGCCTGGACTTCA 31452 AA GTC
 TGAAGTCCAGG AATG ACA
 ||||| |||| |||
 ACTTCAGGTCC TTAC TGT
 G_ AAT
 GAM2604 KIAA0416 3' GCTTTTTCCTGATCTTCA 17835 TC T
 TGAAG CAGGAAAA GGT
 |||| ||||| |||
 ACTTC GTCCTTTT TCG
 TA _
 GAM2604 KIAA0420 3' TGATCTCACCCCTGTACTTCA 31731 C AAAAT
 TGAAGT CAGG GGTCA
 ||||| |||| |||||
 ACTTCA GTCC CTAGT
 T CCACT
 GAM2604 KIAA0435 5' TGCGACCTCGGCCTCCTGGATT 16725 G AAAT__ A
 CA TGAA TCCAGGA GGTC CA
 |||| ||||| ||||| |||
 ACTT AGGTCCT CCAG GT
 _ CCGGCT C
 GAM2604 KIAA0841 3' TGCAACCTCTGCCTCCTGGATT 35364 G AAAT__ CA
 CA TGAA TCCAGGA GGT CA
 |||| ||||| ||| |||

			ACTT AGGTCCT	CCA GT		
			— CCGTCT	AC		
GAM2604	KIAA0847	3'	GTACCCTCCCTGGAGTTCA	38048	G	AAAAT C
			TGAA TCCAGG	GGT AC		
			ACTT AGGTCC	CCA TG		
			G CTC	— —		
GAM2604	KIAA1069	3'	TGATGTTCTTCCTGGAATTCA	33725	G	AATG
			TGAA TCCAGGAA	GTCA		
			ACTT AGGTCCTT	TAGT		
			A CTTG			
GAM2604	KIAA1157	3'	TGTGACCACCCTCCTCTTACT	35755	CC_	AAA
			AGT AGGA	TGGTCACA		
			TCA TCCT	ACCAGTGT		
			TTC	CCC		
GAM2604	KIAA1755	3'	TGAATTTTCCTGGCTCCA	30754	A T	GG
			TG AG	CCAGGAAAAT TCA		
			AC TC	GGTCCTTTTA AGT		
			C —	—		
GAM2604	MEF-2	3'	TGCAACCTCCGCCTCCTGGATT	32181	G	AAAT_ CA
	CA		TGAA TCCAGGA	GGT CA		
			ACTT AGGTCCT	CCA GT		
			— CCGCCT	AC		
GAM2604	MGC13053	5'	TGCAGCCTTCCTGGACT	26425		AAT CA
			AGTCCAGGAA	GGT CA		
			TCAGGTCCTT	CCG GT		
			— AC			
GAM2604	MGC9912	3'	TGCAACCTCCACCTCCTGGATT	27953	G	AAAT_ CA
	CA		TGAA TCCAGGA	GGT CA		
			ACTT AGGTCCT	CCA GT		
			— CCACCT	AC		
GAM2604	NFAT5	5'	GCGATGCCCTCGGACTTCA	28956	_	AAA G
			TGAAGTCC	AGG AT GT		
			ACTTCAGG	TCC TA CG		
			C CG_	G		
GAM2604	PDE2A	3'	ACCTTCCTGGGCCTCA	8461	A	AAT
			TGA GTCCAGGAA	GGT		
			ACT CGGGTCCTT	CCA		
			C —			
GAM2604	RAI17	3'	TGCAACCATCTCTGGGCTCA	43865	A	AAA CA
			TGA GTCCAGG	ATGGT CA		

			ACT CGGGTCT TACCA GT		
			— C — AC		
GAM2604	RBT1	3'	TGTGACCACTGGGGCCTCA 15014	A A AAAA	
			TGA GTCC GG TGGTCACA		
			ACT CGGG TC ACCAGTGT		
			C G —		
GAM2604	SERF2	5'	ACTTTGAATTCCTGGATTCA 12341	G AAT—	
			TGAA TCCAGGAA GGT		
			ACTT AGGTCCTT TCA		
			— AAGTT		
GAM2604	SS-56	3'	ACTGTCCCTTGGACTCCA 29986	A AAA	
			TG AGTCCAGG ATGGT		
			AC TCAGGTTC TGTCA		
			C CC—		
GAM2604	TTC4	3'	CCATGATGTCCTTGGACTCCA 32959	A — AA—	
			TG AGTCCA GGA ATGG		
			AC TCAGGT CCT TACC		
			C T GTAG		
GAM2604	LOC113763	3'	GTAGCTTTCCTGGGCTCCA 28805	A AAT TC	
			TG AGTCCAGGAA GG AC		
			AC TCGGGTCCTT TC TG		
			C — GA		
GAM2604	LOC124221	5'	TGTGCCCTCCTGGACTCG 36743	A AAAT T	
			TGA GTCCAGGA GG CACA		
			GCT CAGGTCCT CC GTGT		
			— CC —		
GAM2604	LOC138199	3'	TGTAACCTCAAACCTCCTGGACT 37118	A AAAT— C	
	CA		TGA GTCCAGGA GGT ACA		
			ACT CAGGTCCT CCA TGT		
			— CAAACT A		
GAM2604	LOC150113	5'	GTGGGACATCTTCCTGGATTTC 42169	A G—	
	A		TGAAGTCCAGGAA ATG TCAC		
			ACTTTAGGTCCTT TAC GGTG		
			C AG		
GAM2604	LOC152315	5'	GTGTCTTCCTGGACTCCG 39257	A AAAT T	
			TG AGTCCAGGA GG CAC		
			GC TCAGGTCCT TC GTG		
			C — T		
GAM2604	LOC152328	3'	TGACCTTCCTGGGCCTCA 39243	A AAT	
			TGA GTCCAGGAA GGTCA		

	ACT CGGGTCCTT CCAGT		
	C —		
GAM2604 LOC158527 5'	ACCTCATCCTGGACTTCA 39860	AAAT	
	TGAAGTCCAGGA GGT		
	ACTTCAGGTCCT CCA		
	ACT_		
GAM2604 LOC196500 3'	CCATTCTCTGGACTTCA 42387	AA	
	TGAAGTCCAGG AATGG		
	ACTTCAGGTCT TTACC		
	C_		
GAM2604 LOC196759 3'	TCATTCTTCCTGGACTCA 42295	A	_
	TGA GTCCAGGAA AATGG		
	ACT CAGGTCCTT TTACT		
	_ C		
GAM2604 LOC200205 3'	TTGTTTTCTCCCTGGACTTC 42738	AAAAT TC	
	GAAGTCCAGG GG ACAA		
	CTTCAGGTCC CT TGTT		
	CT__ TT		
GAM2604 LOC221463 3'	TGGGAGCCTGCCCTGGACTCCA 44205	A	AAAAT CA_
	TG AGTCCAGG GGT CA		
	AC TCAGGTCC CCG GT		
	C CGT__ AGG		
GAM2604 LOC221922 5'	TGTGTTCTCGTCCCCTGGACT 44536	AAA _T_	
	AGTCCAGG ATG G CACA		
	TCAGGTCC TGC C GTGT		
	CC_ T TT		
GAM2604 LOC254082 5'	TTGCAACCTCCGCTTCCTGGAT 46423	G	AAT__ CA
TCA	TGAA TCCAGGAA GGT CAA		
	ACTT AGGTCCTT CCA GTT		
	_ CGCCT AC		
GAM2604 LOC257354 3'	TGATCTCACCCCTGTACTTCA 45584	C	AAAAT
	TGAAGT CAGG GGTCA		
	ACTTCA GTCC CTAGT		
	T CCACT		
GAM2604 LOC257612 5'	GATCCTTCCTGGACTCCA 46741	A	AAT
	TG AGTCCAGGAA GGTC		
	AC TCAGGTCCTT CTAG		
	C C_		
GAM2604 LOC51696 3'	TGCAACCTCTGCCTCCTGGATT 18314	G	AAAT__ CA
CA	TGAA TCCAGGA GGT CA		

ACTT AGGTCCT CCA GT
 _ CCGTCT AC
 GAM2604 LOC91694 5' TGAAGGAATCTTCCTGGAGTTC 33250 G A GG_
 A TGAATCCAGGAA AT TCA
 |||| ||||| || |||
 ACTT AGGTCCTT TA AGT
 G C AGGA
 GAM2605 FLJ11850 3' GGAGCGTCATACACACA 22951 A
 TG TGTGTATGACGCTCT
 || |||||
 AC ACACATACTGCGAGG
 _
 GAM2605 RAP2B 3' ATCGGCAGCTTGACACCCAC 45860 TA A CT
 GTG TG CG CTGCCGAT
 ||| ||| |||||
 CAC AC GT GACGGCTA
 CC A TC
 GAM2605 LOC121274 3' TCAGCAGTATATACATCA 36657 ACGCT C
 TGATGTGTATG CTGC GA
 ||||| |||||
 ACTACATATAT GACG CT
 _ A
 GAM2606 GCA 3' TTTTAAATTTGAGGTA 14497 CG
 TACC CAAATTAAAGGA
 |||| |||||
 ATGG GTTTAATTTTT
 A_
 GAM2606 MEF2C 3' TTCAGACCCTTTAATAAGTGAG 8215 C AA A C
 TG TAC CGC ATTAAAGG TC GAA
 ||| ||| ||||| |||
 GTG GTG TAATTTCC AG CTT
 A AA C A
 GAM2606 Cab45 5' TCGGATCCCGAGCGCGGG 18279 AAA AAA
 CCCGC TT GGATCCGA
 |||| || |||||
 GGGCG AG CCTAGGCT
 CG_ C_
 GAM2606 Cab45 5' TCGGATCCCGAGCGCGGG 18622 AAA AAA
 CCCGC TT GGATCCGA
 |||| || |||||
 GGGCG AG CCTAGGCT
 CG_ C_
 GAM2606 FLJ14297 5' TCGCTCTGTAACCTGCGGGTA 24394 AA AA TC
 TACCCGCA TTA GGA CGA
 ||||| ||| ||| |||
 ATGGGCGT AAT TCT GCT
 CC G_ C_
 GAM2606 MRPL35 3' TTCAGATCCTTTAATGTGG 18739 AA C
 CCGCA TTAAAGGATC GAA
 |||| ||||| |||

GGTGT AATTCCTAG CTT
 — A
 GAM2607 BTBD1 3' TCAAAAACATAAATGGC 24921 CGC
 GCTA TATGTTTTTGA
 ||| |||||
 CGGT ATACAAAACT
 AA_

GAM2607 DKFZP586N0721 3' TCAAAAACACAGCTATCATAGA 17711 GC C C A
 TC ATG TA GCT TGTTTTTGA
 || ||| || |||||
 AG TAC AT CGA ACAAAAACT
 A_ T _ C

GAM2607 MGC2752 5' CAAGAACGCAGCGTGCA 38367 T A
 TGC ACGCT TGTTTTTG
 ||| ||||| |||||
 ACG TGCGA GCAAGAAC
 _ C

GAM2607 LOC146953 5' AAAGTGCAGTACGCAACGA 38285 CA TAT
 TCG TGCTACGC GTTT
 ||| ||||| |||
 AGC ACGATGCG CAAA
 A_ T_

GAM2607 LOC151647 3' CAAAAACATAGTTTCTGCA 39154 TAC_
 TGC GCTATGTTTTTG
 ||| |||||
 ACG TGATACAAAAAC
 TCTT

GAM2607 LOC152453 5' CAAAAACACAGCAAGTGGA 39275 G GCTAC A
 TC CAT GCT TGTTTTTG
 || ||| ||| |||||
 AG GTG CGA ACAAAAAC
 G AA_ C

GAM2607 LOC254431 3' CAAAAACGCTGACATGC 46291 C C TAT
 GCATG TA GC GTTTTTG
 ||||| || |||||
 CGTAC GT CG CAAAAAC
 A _ _

GAM2607 LOC254778 3' TCAAAAACAATTGAGCAT 45978 A CTA
 ATGCT CG TGTTTTTGA
 ||||| || |||||
 TACGA GT ACAAAAACT
 _ TA_

GAM2608 DNMT3B 3' CAAGTATGGCTCCTCCATATCT 13760 TG AA
 C GAGATATGGAG G ATACTTG
 ||||| ||| |||||
 CTCTATACCTC C TATGAAC
 CT GG

GAM2608 KLHL4 3' CAAGCATGGATCTCCATATTTT 21193 TGGAA A
 A TGAGATATGGAG AT CTTG
 ||||| || |||

		ACTTTATACCTC TA GAAC		
		TAGG_ C		
GAM2608	LOC153196 5'	AGTATCCACTCCATCCTCA 41588	AT	AA
		TGAG ATGGAGTGGA TACT		
		ACTC TACCTCACCT ATGA		
		C_ _		
GAM2608	LOC255096 5'	CAGGTGATCCACTCCATCCTCA 46607	AT	AA
		TGAG ATGGAGTGGA TACTTG		
		ACTC TACCTCACCT GTGGAC		
		C_ A_		
GAM2608	LOC256995 5'	AAGTAGCCTTCATATCTCA 46599		TGGAAA
		TGAGATATGGAG TACTT		
		ACTCTATACTTC ATGAA		
		CG_		
GAM2609	COL19A1 3'	AATAGGACAGATGAGTGTCAT 7591		TG_ AC
		ATGACACTT TGT CCTATT		
		TACTGTGAG ACA GGATAA		
		TAG _		
GAM2609	MEF2A 3'	AATACTGTACATAAAATGTCAT 12115	C	CC
	T	AATGACA TTTGTGTAC TATT		
		TTACTGT AAATACATG ATAA		
		A TC		
GAM2609	CITED2 3'	TAATAGGGTGTGGAATGTCGT 12727	C	TG GT
		ATGACA TT T ACCCTATTA		
		TGCTGT AG G TGGGATAAT		
		A GT_		
GAM2609	FLJ20666 3'	TAATAGGGGGGAAAATGTCA 20336	C	GTGTA
		TGACA TTT CCCTATTA		
		ACTGT AAA GGGATAAT		
		_ AGG_		
GAM2609	FLJ20666 3'	TAATAGGGGGGAAAATGTCA 19583	C	GTGTA
		TGACA TTT CCCTATTA		
		ACTGT AAA GGGATAAT		
		_ AGG_		
GAM2609	KIAA1084 3'	TAATAAAAAGATTAAAGTGTCA 17138		TGTACCC
		TGACACTTTG TATTA		
		ACTGTGAAAT ATAAT		
		TAGAAAA		
GAM2610	FUS1 3'	CTTCCATTGAGGAGCCCAGGCT 14137	CAAAA	GG
	G	CAGCC TTTT AATGGAAG		

			GTCGG	GAGG	TTACCTTC		
			ACCC_	AG			
GAM2610	HMG1	3'	TTCCAAATTTTAAGCTG	11413	CC	T	
			CAGC	AAAATTT	GGAA		
			GTCG	TTTTAAA	CCTT		
			AA	_			
GAM2610	OCLN	5'	CCATCCGAGTTTCAGGT	8379	CA	T	A
			GCC	AAATTT	GGA	TGG	
			TGG	TTTGAG	CCT	ACC	
			AC	_	_		
GAM2610	PIP5K1A	3'	TCCACTCCAGAGTTGGGT	9603	AA		A
			GCCCA	ATTTT	TGGA	TGGA	
			TGGGT	TGAGACCT	ACCT		
			_	C			
GAM2610	RXRA	3'	TTCCCAAGAATTCTGGGCTG	8874	A		GGAAT
			CAGCCCA	AATTTT	GGAA		
			GTCGGGT	TTAAGA	CCTT		
			C	AC_			
GAM2610	SLC1A4	3'	CTTCCACCATGGTTCTGGGC	8996	A	TT	AA
			GCCCA	AAT	TGG	TGGAAG	
			CGGGT	TTG	ACC	ACCTTC	
			C	GT	_		
GAM2610	STAU	3'	CTTCCATTCATTGTTTACGCTG	18914	CCA		TTTG
			CAGC	AAAT	GAATGGAAG		
			GTCG	TTTG	CTTACCTTC		
			CA_	TTA_			
GAM2610	STAU	3'	CTTCCATTCATTGTTTACGCTG	10942	CCA		TTTG
			CAGC	AAAT	GAATGGAAG		
			GTCG	TTTG	CTTACCTTC		
			CA_	TTA_			
GAM2610	STAU	3'	CTTCCATTCATTGTTTACGCTG	18926	CCA		TTTG
			CAGC	AAAT	GAATGGAAG		
			GTCG	TTTG	CTTACCTTC		
			CA_	TTA_			
GAM2610	STAU	3'	CTTCCATTCATTGTTTACGCTG	18920	CCA		TTTG
			CAGC	AAAT	GAATGGAAG		
			GTCG	TTTG	CTTACCTTC		
			CA_	TTA_			
GAM2610	WHSC1	3'	CCACTCTATTTTTTTAGGTT	17179	C	TTT	A
			AGCC	AAAA	TGGA	TGG	

		TTGG TTTT ATCT ACC		
		A TTT C		
GAM2610 WHSC1	3'	CCACTCTATTTTTTTAGGTT 28473	C TTT A	
		AGCC AAAA TGGATGG		
		TTGG TTTT ATCT ACC		
		A TTT C		
GAM2610 WHSC1	3'	CCACTCTATTTTTTTAGGTT 28460	C TTT A	
		AGCC AAAA TGGATGG		
		TTGG TTTT ATCT ACC		
		A TTT C		
GAM2610 WHSC1	3'	CCACTCTATTTTTTTAGGTT 28443	C TTT A	
		AGCC AAAA TGGATGG		
		TTGG TTTT ATCT ACC		
		A TTT C		
GAM2610 AMOTL1	3'	TCCATTCTGACATCTGGGCTG 36468	AAATT TG	
		CAGCCCA T GAATGGA		
		GTCGGGT A CTTACCT		
		CTAC_ GT		
GAM2610 BAG5	3'	CTTCCACCGTCATTTTG 11304	TT AA	
		CAAAAT TGG TGGAAG		
		GTTTTA GCC ACCTTC		
		CT _		
GAM2610 DKFZP434O047	5'	TCCCAGGTTCCAAGCCCTGGGC 17869	AAAT _	
		GCCCA TTTGGAAT GGA		
		CGGGT GAACCTTG CCT		
		CCC_ GAC		
GAM2610 GBTS1	3'	CCCCCAAACCTTGGGCTG 29728	AA AAT	
		CAGCCCAA TTTTGG GG		
		GTCGGGTT AAAACC CC		
		C_ C_		
GAM2610 HAND1	3'	TTCCACCCTTTTGGAGC 11237	_ TTTT AA	
		GC CCAAAA GG TGGAA		
		CG GGT TTT CC ACCTT		
		A _ _ C_		
GAM2610 KIAA0481	3'	CTTCCATTCCATTAGCCTTTG 35570	ATTT _	
G		CCAAA TGAATGGAAG		
		GGTTT ACCTTACCTTC		
		CCGATTT		
GAM2610 KIAA1554	3'	CTTCCATTCCCTTAAATTCTGA 45610	C A T _	
GT		GC CA AATTT GGAATGGAAG		

			TG GT TTAAA CCTTACCTTC		
			A C TTC		
GAM2610	MRPL30	5'	TTCGGAGGAAAATTTTCAGGCTG 18583	CA	GGAA
			CAGCC AAATTTT TGGA		
			GTCGG TTTAAAA GCTT		
			AC GGAG		
GAM2610	P15-2	3'	CTTCCATGTGAACTTTAGGC 20783	C A	TGGA
			GCC AAA TTT ATGGAAG		
			CGG TTT AAG TACCTTC		
			A C TG__		
GAM2610	PSMF1	3'	TCCATTCTCCTGGAGCTG 13689	_	AAATTTT
			CAGC CCA GGAATGGA		
			GTCG GGT TCTTACCT		
			A CC_____		
GAM2610	LOC115708	3'	TTCCACAGTCCTGGGCTG 36407	AA	T
			CAGCCCA ATT TGGA		
			GTCGGGT TGA ACCTT		
			CC C		
GAM2610	LOC145854	3'	TTCCAAATTTTAAGCTG 38009	CC	T
			CAGC AAAATTT GGAA		
			GTCG TTTTAAA CCTT		
			AA _		
GAM2610	LOC150967	5'	CCACCACCAGTAGCCTTGGGCT 39035	AATT_	AA_
	G		CAGCCCAA TTGG TGG		
			GTCGGGTT GACC ACC		
			CCGAT ACC		
GAM2610	LOC157624	5'	CCAGCAAGATTTTAAGCTG 41826	CC	GAA
			CAGC AAAATTTTG TGG		
			GTCG TTTTAGAAC ACC		
			AA G__		
GAM2610	LOC157918	3'	TCCACTCCAAAGTGCGT 41899	AAA	A
			GCCCA TTTTGGA TGGA		
			TGGGT GAAACCT ACCT		
			__ C		
GAM2610	LOC158956	3'	TTCCAAATTTTAAGCTG 33097	CC	T
			CAGC AAAATTT GGAA		
			GTCG TTTTAAA CCTT		
			AA _		
GAM2610	LOC197320	5'	TTCCATTCCGCGGAGCTG 42472	_	AAAATTT
			CAGC CC TGGAATGGAA		

GTCG GG GCCTTACCTT
 A C_____
 GAM2610 LOC202025 5' ATTCCAAGACCTCGGGCTG 43399 AAAA
 CAGCCC TTTTGGAAT
 ||||| |||||
 GTCGGG AGAACCTTA
 CTCC
 GAM2610 LOC206426 3' TCCACTCCAGAGTTGGGT 43120 AA A
 GCCCA ATTTTGGA TGGA
 ||||| ||||| |||||
 TGGGT TGAGACCT ACCT
 C
 GAM2610 LOC222134 5' TCCCACCATTTTGGGCTG 45170 TTT AAT
 CAGCCCCAAA TGG GGA
 ||||| ||||| |||||
 GTCGGGTTTT ACC CCT
 AC_
 GAM2610 LOC255654 5' TCCCAGGTTCCAAGCTCTGGGC 46303 AAAT
 GCCCA TTTGGAAT GGA
 ||||| ||||| |||||
 CGGGT GAACCTTG CCT
 CTC_ GAC
 GAM2610 LOC257457 5' CTTCCATTCCAGCTCTTGTGC 31376 C AATTTT
 GC CAA GGAATGGAAG
 || ||||| |||||
 CG GTT CCTTACCTTC
 T CTCGAC
 GAM2610 LOC51619 3' CTTCCCTTAAACTTTGGGCTG 18077 A AAT
 CAGCCCCAAA TTTTGG GGAAG
 ||||| ||||| |||||
 GTCGGGTTT AAAATT CCTTC
 C C_
 GAM2610 LOC91759 5' CTTCCAGTGTGAATTTTGG 33305 TGGAA
 CCAAATTT TGGAAG
 ||||| |||||
 GGTTTAAAG ACCTTC
 TGTG_
 GAM2610 LOC92539 5' CTGGAGCCAAAATTTGAGT 34503 C AA_
 GC CAAAATTTTGG TGG
 || ||||| |||||
 TG GTTTTAAAACC GTC
 A GAG
 GAM2611 ALOX15 3' CACCCTCTTCCCATGTCC 6809 A _ A
 A ATGTGGGA GAGG TG
 | ||||| |||||
 C TGTACCCT CTCC AC
 C T C
 GAM2611 AP1G1 3' CCACCCCTCCCACATTTACAGC 6799 CAC A A
 C GGT AAATGTGGGAG GG TGG
 ||| ||||| ||||| |||||

CCG TTTACACCCTC CC ACC
 ACA _ C
 GAM2611 DIA1 3' CATCCCTGTCTCATGACC 14246 CAAA T G _
 GGTCA TG GGA AGG ATG
 |||| | |||| ||||
 CCAGT AC TCCT TCC TAC
 _ _ G C
 GAM2611 DLG4 3' CCATCCTCTCCCACACACATTG 7045 TCACAAA
 C GG TGTGGGAGAGGATGG
 || |||||
 CC ACACCCTCTCCTACC
 TTACAC_
 GAM2611 LZTS1 3' CCATCCTCCCTCCACCTCAAGA 22006 ACAAAT _ A
 CC GGTC GTGG G GAGGATGG
 ||| ||| | |||||
 CCAG CACC C CTCCTACC
 AACTC_ T C
 GAM2611 RABL2A 3' CCATCCCCTCTTCTACCTCCTG 15078 CA AAT_ _
 CAACC GGT CA GTGGGAGA GGATGG
 ||| || ||||| |||||
 CCA GT CATCTTCT CCTACC
 AC CCTC CC
 GAM2611 RABL2B 3' CCATCCCCTCTTCTACCTCCTG 13945 CA AAT_ _
 CAACC GGT CA GTGGGAGA GGATGG
 ||| || ||||| |||||
 CCA GT CATCTTCT CCTACC
 AC CCTC CC
 GAM2611 SLC19A1 3' CTGCTCCACACTTGTGCC 9021 T A A
 GG CACAA TGTGGGAG GG
 || |||| ||||| ||
 CC GTGTT ACACCCTC TC
 _ C G
 GAM2611 SRR 3' CCATCCTCCTCCTTCATACC 22475 CACAA T _
 GGT ATG GGGAG AGGATGG
 ||| || |||| |||||
 CCA TAC TCCTC TCCTACC
 _ T C
 GAM2611 C11orf11 5' CCATCCTCTCCTTCCTTCTGCG 44784 CACAAATGT
 CC GGT GGGAGAGGATGG
 ||| |||||
 CCG TCCTCTCCTACC
 CGTCTTCCT
 GAM2611 C17orf31 3' CCATCCTCTTCCAACCCACGCC 18999 CACAAATG
 GGT TGGGAGAGGATGG
 ||| |||||
 CCG ACCTTCTCCTACC
 CACCCA_
 GAM2611 C20orf102 3' CACCCCCTTCCTGTCAACC 27925 C AATGT A A
 GGT ACA GGGAG GG TG
 ||| || |||| |||

		CCA TGT CCTTC CC AC		
		C _____ C C		
GAM2611	C9orf7	3' CCACCCTCTCCCTGGTGTGGCC	19032	AATGT A
		GGTCACA GGGAGAGG TGG		
		CCGGTGT CCCTCTCC ACC		
		GGT__ C		
GAM2611	FLJ12788	3' CCATCCTCTCAAGCCCCAGGAC	22872	ACAAAT GG
	C	GGTC GT GAGAGGATGG		
		CCAG CG CTCTCCTACC		
		GACCC_ AA		
GAM2611	FLJ20211	3' CCATGGGGGTCCCATTTGTGAC	19297	T AGAGG
	C	GGTCACAAATG GGG ATGG		
		CCAGTGTTTAC CCT TACC		
		_ GGGGG		
GAM2611	FLJ20718	3' CCATCCTCCCTACTCATGACT	19634	CAAAT A
		GGTCA GTGGG GAGGATGG		
		TCAGT CATCC CTCCTACC		
		ACT__ _		
GAM2611	FLJ22215	3' CTGCTCCACACCTGCGCC	46281	CA AA A
		GGT CA TGTGGGAG GG		
		CCG GT ACACCCTC TC		
		C_ CC G		
GAM2611	FLJ32752	5' CACCCTCTCCCTCTGTGCC	29481	T AATGT A
		GG CACA GGGAGAGG TG		
		CC GTGT CCCTCTCC AC		
		_ CT__ C		
GAM2611	KIAA0367	3' CCACCCCTCCACAGCCCACC	33418	CACAAA A A
		GGT TGTGGGAG GG TGG		
		CCA ACACCCTC CC ACC		
		CCCG__ C C		
GAM2611	KIAA0682	3' CCATCCTCGTCACTTGGGACC	18288	A AT GA
		GGTC CAA GTGG GAGGATGG		
		CCAG GTT CACT CTCCTACC		
		G _ G_		
GAM2611	KIAA0789	5' CATCCTCTCCCAAGCACC	31846	CACAAATG
		GGT TGGGAGAGGATG		
		CCA ACCCTCTCCTAC		
		CGA_____		
GAM2611	KIAA1862	3' CCACCCTCTCCAGAGGAC	34173	ACAAATG A
		GTC TGGGAGAGG TGG		

CAG ACCCTCTCC ACC
 GAG_____ C
 GAM2611 WBSCR21 5' TCTCCCACTTTGCAACC 25327 CA T
 GGT CAAA GTGGGAGA
 ||| ||| |||||
 CCA GTTT CACCCTCT
 AC _
 GAM2611 LOC143425 3' CATCCACACATTTGCACC 42351 CA GGAGA
 GGT CAAATGTG GGATG
 ||| ||||| |||||
 CCA GTTTACAC CCTAC
 C_ A____
 GAM2611 LOC146745 5' CCACCCTCTCTCTACCTGTCAC 38230 C AAT _ A
 C GGT ACA GTGG GAGAGG TGG
 ||| ||| ||| ||||| |||
 CCA TGT CATC CTCTCC ACC
 C C_ T C
 GAM2611 LOC152426 5' CATCCTCCTCCTATGGCC 41496 CAAATG _
 GGTCA TGGGAG AGGATG
 ||||| ||||| |||||
 CCGGT ATCCTC TCCTAC
 _____ C
 GAM2611 LOC157247 5' CCATCCCAGGGCATTGTGACC 39573 A GGGAGA
 GGTCACAA TGT GGATGG
 ||||| ||| |||||
 CCAGTGTT ACG CCTACC
 _ GGAC_
 GAM2611 LOC201182 5' CCAGCCCACTTTGTGACC 43211 T AGA
 GGTCACAAA GTGGG GG
 ||||| ||||| ||
 CCAGTGTTT CACCC CC
 _ GA_
 GAM2611 LOC201243 5' CCACCCTCTCTCTACCTGTCAC 42552 C AAT _ A
 C GGT ACA GTGG GAGAGG TGG
 ||| ||| ||| ||||| |||
 CCA TGT CATC CTCTCC ACC
 C C_ T C
 GAM2612 NEU3 3' GCAAAATGAAAATTTTGCCTT 13456 GG_
 AAGGCAAAATTTT TTGC
 ||||| ||||| |||||
 TTCCGTTTTAAAG AACG
 TAA
 GAM2612 SMP1 3' CAACCAAAAATCTATTGTGGTA 15609 AGGCAAA
 TACCA ATTTTGTGGT
 ||||| ||||| |||||
 ATGGT TAAAAACCAAC
 GTTATC_
 GAM2612 ZNF289 3' GCTGGAACTTTACCTGGTA 32550 A C A TG
 TACCA GG AAA TTTT GT
 ||||| || ||| ||||| ||

		ATGGT CC TTT AAAG CG	
		_ A C GT	
GAM2612 APOL2	5'	CAAGAGGACCCTGCCTTGGTG	25161 AAA__
		TACCAAGGCA TTTTGT	
		GTGGTTCCGT GAGAAC	
		CCCAG	
GAM2612 APOL3	5'	CAAAAGGACCCTGCCTTGGTG	15673 AAA__
		TACCAAGGCA TTTTGT	
		GTGGTTCCGT GAAAAC	
		CCCAG	
GAM2612 DKFZp434E2220	5'	ACTAATTTTGCCTTG	19109 TTT
		CAAGGCAAAA TTGGT	
		GTTCCGTTTT AATCA	
		T__	
GAM2612 FLJ10388	3'	CAATTAAATCTTGCCTT	19843 AATT
		AAGGCAA TTTGGTTG	
		TTCCGT AAATTAAC	
		CT__	
GAM2612 KIAA0367	5'	ACAGAGAATCCTGCCTTGGT	33415 AA G
		ACCAAGGCA ATTTTT GT	
		TGGTTCCGT TAAGAG CA	
		CC A	
GAM2612 KIAA0871	3'	GCAACTTTTTTGCCTTGGTG	17330 TTTTT
		TACCAAGGCAAAA GGTTGC	
		GTGGTTCCGTTTT TCAACG	
		TT__	
GAM2612 KIAA0992	3'	GCCATGAAACTTTGCCTT	18159 A _
		AAGGCAAA TTTT TGGT	
		TTCCGTTT AAAG ACCG	
		C T	
GAM2612 KIAA1028	3'	CAACCAAAACTGCCT	44157 AAA
		AGGCA TTTTGGTTG	
		TCCGT AAAACCAAC	
		C__	
GAM2612 KIAA1203	3'	GCCCTACATCTTGCCTTGGTA	35470 A TTTT
		TACCAAGGCAA AT GGT	
		ATGGTTCCGTT TA CCG	
		C CATC	
GAM2612 KIAA1954	3'	GCCATAAATTTGCCTTG	38098 T
		CAAGGCAAAATTT TGGT	

GTTCCGTTTTTAAA ACCG
 T
 GAM2612 LMOD1 3' GCTCTCCAAATTTTGCTTTAGT 14447 C TT TT_
 A TAC AAGGCAAAATT TGG GC
 ||| ||||| ||| ||
 ATG TTTCGTTTTAA ACC CG
 A _ TCT
 GAM2612 MGC26914 3' GCTGAAGAAGAATTTTGCCT 29586 GG _
 AGGCAAAATTTTT TT GC
 ||||| ||| ||
 TCCGTTTTAAGAA AG CG
 GA T
 GAM2612 PRO1617 5' GCAGAATTGATTTTGCCTTG 20665 TTTGG
 CAAGGCAAAATT TTGC
 ||||| ||| ||
 GTTCCGTTTTAG GACG
 TTAA_
 GAM2612 SKRP1 5' ACCAATCAAATTTTCGCCTT 28119 A _
 AAGGC AAATTT TTGGT
 |||| |||| ||||
 TTCCG TTAAA AACCA
 C CT
 GAM2612 SPEC1 3' CAACCAAAAATGTCT 21510 AAA
 AGGCA TTTTGGTTG
 |||| ||||| ||||
 TCTGT AAAAACCAAC
 _
 GAM2612 LOC144747 5' ACAGAAAATTTTGTCTCAGTA 37782 CA G
 TAC AGGCAAAATTTTT GT
 ||| ||||| ||| ||
 ATG TCTGTTTTTAAAAG CA
 AC A
 GAM2612 LOC158293 3' GCAACCAGCACTGCCCTGG 39806 A AAATTT
 CCA GGCA TTGGTTGC
 ||| ||| ||||| ||
 GGT CCGT GACCAACG
 C CAC_
 GAM2612 LOC162239 3' GCAACCAAAAACCTGGCTTT 40051 AAAA
 AAGGC TTTTGGTTGC
 |||| ||||| ||||
 TTTCG AAAAACCAACG
 GTC_
 GAM2613 CNTNAP2 3' ATCTGGGGTTCCTGACTGATA 15414 A TTAA
 TATCAG TT AACCCAGAT
 ||||| || ||||| ||
 ATAGTC AG TTGGGGTCTA
 _ TCC_
 GAM2613 DSCR5 5' ATTTGGCTTCAAAAATCTGA 18549 A ACC
 TCAGATTTTT AA CCAGAT
 ||||| || ||||| ||

		AGTCTAAAAA TT GGTTTA		
		C C__		
GAM2613	FOX M1	3' CTGGGGTTTTCAATTGA 22483	ATTT A	
		TCAG TT AAACCCAG		
		AGTT AA TTTGGGGTC		
		____ C		
GAM2613	OPA1	3' ATCTGAGGAAAGAAATCTGGTA 28352	AAAA C	
		TATCAGATTTTT CC CAGAT		
		ATGGTCTAAAGA GG GTCTA		
		AA__ A		
GAM2613	OPA1	3' ATCTGAGGAAAGAAATCTGGTA 28320	AAAA C	
		TATCAGATTTTT CC CAGAT		
		ATGGTCTAAAGA GG GTCTA		
		AA__ A		
GAM2613	OPA1	3' ATCTGAGGAAAGAAATCTGGTA 28336	AAAA C	
		TATCAGATTTTT CC CAGAT		
		ATGGTCTAAAGA GG GTCTA		
		AA__ A		
GAM2613	OPA1	3' ATCTGAGGAAAGAAATCTGGTA 28344	AAAA C	
		TATCAGATTTTT CC CAGAT		
		ATGGTCTAAAGA GG GTCTA		
		AA__ A		
GAM2613	OPA1	3' ATCTGAGGAAAGAAATCTGGTA 28328	AAAA C	
		TATCAGATTTTT CC CAGAT		
		ATGGTCTAAAGA GG GTCTA		
		AA__ A		
GAM2613	PCDHA11	5' CTGAAACTGAAGAATCTGGTA 20887	AAAACCC	
		TATCAGATTTTT CAG		
		ATGGTCTAAGAA GTC		
		GTCAAA_		
GAM2613	PCDHA11	5' CTGAAACTGAAGAATCTGGTA 25621	AAAACCC	
		TATCAGATTTTT CAG		
		ATGGTCTAAGAA GTC		
		GTCAAA_		
GAM2613	PTGES	3' ATCTGGAGTTTTTAAAAGGCT 11311	A C	
		AG TTTTAAAAC CCAGAT		
		TC GAAAATTTTG GGTCTA		
		G A		
GAM2613	SH2D1A	3' CTGGAGTTGAAAATCTTATA 8155	C AACC	
		TAT AGATTTTTAA CCAG		

		ATA TCTAAAAGTT	GGTC		
		T	GA__		
GAM2613	FLJ13657	3'	TCTAGGATTTTATCTGATG	24220	TTTT C C
			TATCAGA TAAAA CC AGA		
			GTAGTCT ATTTT GG TCT		
			__ A A		
GAM2613	KIAA0753	3'	TCTGGGATTTTCTCTGA	16736	TTTTT C
			TCAGA AAAA CCCAGA		
			AGTCT TTTT GGGTCT		
			CT__ A		
GAM2613	MAIL	3'	ATCTGGGATCTAGACATCTGA	25405	T AAAC
			TCAGAT TTTA CCCAGAT		
			AGTCTA AGAT GGGTCTA		
			C CTA_		
GAM2613	PELI2	3'	TCTGGGGCTTTTCTGAT	22232	TTTTT _
			ATCAGA AAAA CCCCAGA		
			TAGTCT TTTT GGGGTCT		
			__ C		
GAM2613	LOC130026	3'	ATCTGAGGTTCTATTTGAT	28818	TTTTAA C
			ATCAGAT AACC CAGAT		
			TAGTTTA TTGG GTCTA		
			TC__ A		
GAM2613	LOC200314	3'	GTCTGTTCAAAAATCTGATA	43294	A ACCC
			TATCAGATTTT AA CAGAT		
			ATAGTCTAAAAA TT GTCTG		
			C __		
GAM2613	LOC55885	3'	GGGTTACTTTAAAAATCTG	20711	__
			CAGATTTTAA ACCC		
			GTCTAAAAATTT TGGG		
			CAT		
GAM2613	LOC92465	5'	CTGGGGTTATAACTGATA	34394	ATTT A
			TATCAG TTA AACCCCAG		
			ATAGTC AAT TTGGGGTC		
			__ A		
GAM2613	LOC93259	5'	GGGCTTGGAAATCTGA	35559	AAC
			TCAGATTTTAA CCC		
			AGTCTAAAGGTT GGG		
			C__		
GAM2613	LOC96597	5'	ATCCGGGGTTCCAGCCCCTGAT	33228	ATTTTAA A
			TATCAG AACCCC GAT		
			G		

			GTAGTC	TTGGGG	CTA	
			CCCGACC_	C		
GAM2614	EDR3	5'	ATCAAAGTCTTGGGCATCGTG	46067	_ GG_	
			CGCG TG AAGACTTTGAT			
			GTGC AC TTCTGAAACTA			
			T GGG			
GAM2614	KIAA1393	3'	CAAAGCCCGCGCGCTG	35685	A AAGA	
			CA CGCGTGGG CTTTG			
			GT GCGCGCCC GAAAC			
			C _			
GAM2615	CD244	3'	GAAGTGGCTGGCAGGTTCTGCA	18526	T AA	
	C		GTGCAG GC TGCCAGCCAGTTC			
			CACGTC TG ACGGTCGGTCAAG			
			T G_			
GAM2615	EGFL5	3'	AACTAGCATGGGATGCACTGCA	41873	A G _ C	
	C		GTGCAGTGCA T CCA GC AGTT			
			CACGTCACGT A GGT CG TCAA			
			_ G A A			
GAM2615	FLJ11730	3'	AACTGGCTGGCACCAGCTTCAT	22993	C GCAA	
			GTG AGT TGCCAGCCAGTT			
			TAC TCG ACGGTCGGTCAA			
			T ACC_			
GAM2615	GOLGA1	3'	AACTGGTCCCACACGCAC	7856	A CAA CCA	
			GTGC GTG TG GCCAGTT			
			CACG CAC AC TGGTCAA			
			_ _ CC_			
GAM2615	KIAA0447	3'	GCTGCAGCATTGCACGGCAC	35494	A _	
			GTGC GTGCAATGC CAGC			
			CACG CACGTTACG GTCG			
			G AC			
GAM2615	ZAK	3'	AACTAGCTGGCATGGTAGCAC	28604	AG A C	
			GTGC TGC ATGCCAGC AGTT			
			CACG ATG TACGGTCG TCAA			
			_ G A			
GAM2615	LOC115110	3'	GAACCGTGGACACACACTGCAC	35510	CAA _ GCCA	
			GTGCAGTG TG CCA GTTC			
			CACGTCAC AC GGT CAAG			
			AC_ A GC_			
GAM2615	LOC197342	3'	GAAGTGAAGCCTGCACTGCA	42487	A_ CAGC	
			TGCAGTGCA TGC CAGTTC			

ACGTCACGT ACG GTCAAG
 CC A____
 GAM2616 IMPA1 3' TCATAGTCAATCCCA 12059 ACTC
 TGGGAT TGATTATGA
 ||||| |||||
 ACCCTA ACTGATACT

 GAM2616 PHF3 3' TTCATAATCAGATTATGCTA 17511 G C
 TGG ATA TCTGATTATGAA
 ||| ||| |||||
 ATC TAT AGACTAATACTT
 G T
 GAM2616 TTTY9 3' GTTTCATAAGTTACCCA 25680 AT CTGAT
 TGGG ACT TATGAAAC
 ||| ||| |||||
 ACCC TGA ATACTTTG
 AT _____
 GAM2616 LOC124801 3' GTCTCCTGGGGCAGAGTATGCC 36764 G A_ T A
 A TGG ATACTCTG TTA GA AC
 ||| ||||| ||| |||
 ACC TATGAGAC GGT CT TG
 G GG C C
 GAM2617 CLTCL1 3' GGTGAAGCCTTACCTGCGG 31837 C TGAT T
 CCGCAG GTA G CTTACAC
 ||||| ||| |||||
 GGCGTC CAT C GAAGTGG
 _ TC____
 GAM2617 CRKL 5' GGTGAAGACCCGTCGAGCTGCG 11708 GT_ AT
 G CCGCAGC ATG GTCTTCACC
 ||||| ||| |||||
 GGCGTCG TGC CAGAAGTGG
 AGC C_
 GAM2617 DHCR24 3' TGATGAAGGGGATACGCTG 16527 GATG C
 CAGCGTAT TCTTCA CA
 ||||| ||||| |||
 GTCGCATA GGAAGT GT
 GG_ A
 GAM2617 FZD4 3' TGGTGAGGTGACCACAGCTGC 14490 GTA ATGT
 GCAGC TG CTTACCA
 ||||| || |||||
 CGTCG AC GGAGTGGT
 AC_ CAGT
 GAM2617 SOX4 3' TGATGAAGACAGAAGGCTCCGG 9077 C GTATGA C
 CCG AGC TGTCTTCA CA
 ||| ||| ||||| |||
 GGC TCG ACAGAAGT GT
 C GAAG_ A
 GAM2617 BDG-29 3' GTGGCCATCCGCCGCGG 35820 A TAT TCT
 CCGC GCG GATG TCAC
 ||||| ||| |||||

GGCG CGC CTAC GGTG
C _ C_
GAM2617 FLJ21687 3' GGTGAAGACAAGCTGCG 24291 GTATGA
CGCAGC TGTCTTCACC
||||| |||||
GCGTCG ACAGAAAGTGG
A____
GAM2617 PCBP4 5' ACATCACCTCACGCTGCGG 21678 A____
CCGCAGCGT TGATGT
||||| |||||
GGCGTCGCA ACTACA
CTCCC
GAM2617 PIF1 3' TGAAGACAGGTGCTCCGG 30588 C TATGA
CCG AGCG TGTCTTCA
||| ||| |||||
GGC TCGT ACAGAAAGT
C GG____
GAM2617 SHARP 3' GTGAAGACAGGCTGTG 17369 GTATGA
CGCAGC TGTCTTCAC
||||| |||||
GTGTCTG ACAGAAAGTG
G____
GAM2617 LOC123096 3' GTGAAGACGACACTGGG 36722 G C ATGA
CC CAG GT TGTCTTCAC
|| ||| || |||||
GG GTC CA GCAGAAAGTG
_ A ____
GAM2617 LOC155438 3' TGGTGAAGACACTCCTGC 41768 CGTAT _
GCAG GA TGTCTTCACCA
|||| || |||||
CGTC CT ACAGAAAGTGGT
____ C
GAM2617 LOC220110 5' TGGCGAACCACACGACGCTGCG 44895 A A C_ A
G CCGCAGCGT TG TGT TTC CCA
||||| || ||| ||| |||
GGCGTCGCA GC ACA AAG GGT
_ _ CC C
GAM2617 LOC254219 5' GTGAAGACAGGTGCTCGC 46174 _ TATGA
GC AGCG TGTCTTCAC
|| ||| |||||
CG TCGT ACAGAAAGTG
C GG____
GAM2618 DHRS2 5' GAATGCACCGAGAGGAATG 12374 TG_
CATTCCTTTC GCATTC
||||| |||||
GTAAGGAGAG CGTAAG
CCA
GAM2618 GREB1 3' CATGGTTAAGGAAAGAATGCAA 35852 C GGCAT
TTGCATTC TTTCT TCATG
||||| ||||| |||||

			AACGTAAG AAAGG	GGTAC	
			_ AATT_		
GAM2618	KIAA0286	3'	CATGAATGTTTGAAAGGAA	33905	TG
			TTCCTTTC GCATTCATG		
			AAGGAAAG TGTAAGTAC		
			TT		
GAM2618	KIAA0565	5'	CATGAGAACTAGAAAGGAA	33217	CA
			TTCCTTTCTGG TTCATG		
			AAGGAAAGATC GAGTAC		
			AA		
GAM2618	PRO1600	3'	ATGAATGCCATCAATGTAA	15314	CCTTTC
			TTGCATT TGGCATT CAT		
			AATGTAA ACCGTAAGTA		
			CT____		
GAM2618	LOC148824	3'	CATGGTAAGAAAGGAATGCAA	40908	GGCAT
			TTGCATTCCTTTCT TCATG		
			AACGTAAGGAAAGA GGTAC		
			AT____		
GAM2618	LOC157292	3'	CATGAATGAGCCTCAGAAA	41775	_____
			TTTCTGG CATT CATG		
			AAAGACT GTAAGTAC		
			CCGA		
GAM2618	LOC157507	5'	ATGAAGGAAAGGGACACAA	39604	CA GG
			TTG TTCCTTTCT CAT		
			AAC AGGGAAAGG GTA		
			AC AA		
GAM2618	LOC201287	5'	CATGAGAACTAGAAAGGAA	42560	CA
			TTCCTTTCTGG TTCATG		
			AAGGAAAGATC GAGTAC		
			AA		
GAM2618	LOC254082	5'	ATGAATGTAAAAATGAA	46421	C C
			TTC TTT TGGCATT CAT		
			AAG AAA ATTGTAAGTA		
			T A		
GAM2618	LOC256207	5'	CATGAGAACTAGAAAGGAA	45618	CA
			TTCCTTTCTGG TTCATG		
			AAGGAAAGATC GAGTAC		
			AA		
GAM2619	NKX3A	3'	AAGTTAATAGAAAGTTGGCCA	12825	T TACAA
			TGGC CAACTTTCT AACTT		

			ACCG GTTGAAAGA	TTGAA		
			— TAA—			
GAM2619	WHSC1	5'	TGATAGAAAGTTAAGCCA	28478	C	TA
			TGGCT AACTTTCT	CA		
			ACCGA TTGAAAGA	GT		
			A	TA		
GAM2619	DKFZP564K1964	3'	GTTTTCAAGAAAATTGAGCCA	17805	C	AC
			TGGCTCAA TTTCTT	AAAAC		
			ACCGAGTT AAAGAA	TTTTG		
			A	C—		
GAM2619	P114-RHO-GEF	3'	AAGTTTTTAATGGAAAGTTGAG	17636		TAC—
			CCA	TGGCTCAACTTTCT	AAAAC	TT
			ACCGAGTTGAAAGG	TTTTGAA		
			TAAT			
GAM2619	LOC221042	5'	AGTCCTGTTGGTTGAGTCA	44750		TTCTT AA
			TGGCTCAACT	ACA ACT		
			ACTGAGTTGG	TGT TGA		
			T—	CC		
GAM2620	CDC7L1	3'	AAAAGAATACTTTGTAATA	9591		TTAAAG
			TATTACAAAGT	CTTTT		
			ATAATGTTTCA	GAAAA		
			TAA—			
GAM2620	OLFM1	3'	AAAGGCAAACCTTTGTA	15557		AAA
			TACAAAGTTT	GCTTTT		
			ATGTTTCAAA	CGGAAA		
			—			
GAM2620	PIGA	3'	GTAAGATTTTAAACATTTGTAA	8498	—	C
			TA	TATTACAAA GTTTAAAG	TTTTAC	
			ATAATGTTT CAAATTTT	AGAATG		
			A	—		
GAM2620	PIGA	3'	GTAAGATTTTAAACATTTGTAA	21711	—	C
			TA	TATTACAAA GTTTAAAG	TTTTAC	
			ATAATGTTT CAAATTTT	AGAATG		
			A	—		
GAM2620	PIGA	3'	GTAAGATTTTAAACATTTGTAA	21718	—	C
			TA	TATTACAAA GTTTAAAG	TTTTAC	
			ATAATGTTT CAAATTTT	AGAATG		
			A	—		
GAM2620	FLJ13984	3'	AAGACTGAACTTTGTAA	24129		AAG
			TTACAAAGTTTA	CTT		

		AATGTTTCAAGT GAA		
		CA_		
GAM2620	FLJ14621	3' GTAAAAGAAACAACTTTGTA 26582	AAAG	
		TACAAAGTTT CTTTAC		
		ATGTTTCAAA GAAAATG		
		CAAA		
GAM2620	KIAA1033	3' AAAAGTTTAAACTTTCTAATA 32229	C A	
		TATTA AAAGTTT AAGCTTTT		
		ATAAT TTTCAAA TTTGAAAA		
		C A		
GAM2620	KIAA1128	3' GCAAAAGCTTTGTGATG 33967	AAA	
		TATTACAAAGTTT GC		
		GTAGTGTTTCGAA CG		
		AA_		
GAM2620	MGC5590	3' TAAAAGCCAGAAGCATCTTGTA 23495	A__ AAA	
	ATA	TATTACAA GTTT GCTTTTA		
		ATAATGTT CGAA CGAAAAT		
		CTA GAC		
GAM2620	PDE10A	3' TAAAAGCTCGGCATTGTAAT 13463	A TAA	
		ATTACAA GTT AGCTTTTA		
		TAATGTT CGG TCGAAAAT		
		A C_		
GAM2620	TRIM2	3' AGGGTTTTAACTTTTATAAT 17597	C	
		ATTA AAAGTTTAAAGCTTT		
		TAAT TTTCAAATTTTGGA		
		A		
GAM2620	LOC146159	5' GTAAAAGCTCCTCTGTTCTTG 38075	AGTTTAA__	
	TAATA	TATTACAA AGCTTTTAC		
		ATAATGTT TCGAAAATG		
		CCTTGTCTCC		
GAM2620	LOC152559	3' AAAAGCTTTAACTTCTGCAGT 39282	A _	
		ATT CA AAGTTTAAAGCTTTT		
		TGA GT TTCAAATTCGAAAA		
		C C		
GAM2621	KIAA0884	5' AAACCAATGAAGCAATCTATTG 34770	CCAT__	
	T	GCAATAGA TTGGTTT		
		TGTTATCT AACCAAA		
		AACGAAGT		
GAM2621	LOC130507	3' AAAGCATGTGACATATTGCTA 36995	GAC T G	
		TAGCAATA CAT TG TTT		

ATCGTTAT GTG AC AAA
 ACA T G
 GAM2621 LOC221710 5' AAACCAAATTGGACTATT 44395 A _
 AATAG CCA TTTGGTTT
 ||||| ||| |||||
 TTATC GGT AAACCAA
 A T
 GAM2622 SPARC 3' CATTCTTAGCTGTA ACTTA 9088 T C
 A AGTTACAGCTAAGA TG
 | ||||| ||||| ||
 A TCAATGTCGATTCT AC
 T T
 GAM2622 FLJ12592 5' CTTTCAGTACTGTACTA 25873 T CTAAG
 TAGT ACAG ACTGAAAG
 ||||| ||||| |||||
 ATCA TGTC T GACTTTC
 _ A _
 GAM2622 FLJ25359 5' CAGCTCTCCTGTA ACTCA 29407 T CTA _
 A AGTTACAG AGA CTG
 | ||||| ||||| |||||
 A TCAATGTC TCT GAC
 C C_ C
 GAM2622 KIAA1155 3' TCAGTGGTGTAGCTGTA ACTAT 31199 AG_
 ATAGTTACAGCTA ACTGA
 ||||| ||||| |||||
 TATCAATGTCGAT T GACT
 GTGG
 GAM2622 MGC2474 3' TCAGATGGCTGTG ACTA 23420 AGA
 TAGTTACAGCTA CTGA
 ||||| ||||| |||||
 ATCAGTGTCCGGT GACT
 A _
 GAM2622 ST13 3' TCTTAAATAGTGTA ACTATA 10034 G AGACT
 TATAGTTACA CTA GA
 ||||| ||||| |||||
 ATATCAATGT GAT CT
 _ AAATT
 GAM2623 CGB 5' CCTCCTGGTGGCCTTGCCGCC 6393 A GTGAT
 GGC GCAAGGCCAT GAGG
 ||||| ||||| |||||
 CCG CGTTCCGGTG CTCC
 C GTC_
 GAM2623 GNAO1 3' CACTGCAAACCCTGCTGCCT 43720 A CCA GA
 AGGCAGCA GG TGT TG
 ||||| ||||| |||||
 TCCGTCGT CC ACG AC
 C AA_ TC
 GAM2623 MFAP3 3' CCTCTGTCAACCCTCCTGCC 12554 CA CCATG _
 GGCAG AGG TGAT GAGG
 ||||| ||||| ||||| |||||

			CCGTC TCC ACTG CTCC		
			C_ CA__ T		
GAM2623	MNT	3'	CCTCATCATCCACCCGCTGCC 21561	AA	CCAT
			GGCAGC GG GTGATGAGG		
			CCGTCG CC TACTACTCC		
			C_ ACC_		
GAM2623	SLC9A5	3'	CCTCACCCCTTGGGCTTTGCTGC 30063		ATGTGA
	C		GGCAGCAAGGCC TGAGG		
			CCGTCGTTTCGG ACTCC		
			GTTCCC		
GAM2623	SLC9A5	3'	CCTCACCCCTTGGGCTTTGCTGC 10934		ATGTGA
	C		GGCAGCAAGGCC TGAGG		
			CCGTCGTTTCGG ACTCC		
			GTTCCC		
GAM2623	SNX15	3'	CCCAGGGCCTGGCCCTACCTCC 36503	C CAA_	T GA A
	T		AGG AG GGCCA GT TG GG		
			TCC TC CCGGT CG AC CC		
			_ CATC C GG _		
GAM2623	THY1	3'	CTAAAAGCATGGCCCTGCTGCC 12976	A	GATG
			GGCAGCA GGCCATGT AG		
			CCGTCGT CCGGTACG TC		
			C AAAA		
GAM2623	CALN1	3'	TTACCTGCCCTGCTGCCT 25522	A	CAT
			AGGCAGCA GGC GTGA		
			TCCGTCGT CCG CATT		
			C TC_		
GAM2623	CDCA4	3'	CAGCGGCCCAGCCTTGCTGCC 19660	CAT	GA_
			GGCAGCAAGGC GT TG		
			CCGTCGTTCCG CG AC		
			ACC GCG		
GAM2623	CGB5	5'	CCTCCTGGTGGCCTTGCCGCC 26930	A	GTGAT
			GGC GCAAGGCCAT GAGG		
			CCG CGTTCCGGTG CTCC		
			C GTC_		
GAM2623	CGB7	5'	CCTCCTGGTGGCCTTGACGCC 26994	AG	GTGAT
			GGC CAAGGCCAT GAGG		
			CCG GTTCCGGTG CTCC		
			CA GTC_		
GAM2623	CGB8	5'	CCTCCTGGTGGCCTTGCCGCC 27045	A	GTGAT
			GGC GCAAGGCCAT GAGG		

CCG CGTTCGGTG CTCC
 C GTC__
 GAM2623 DKFZp762E1312 5' CCTCCACAGACATGGCCTTAGT 20450 CA _ GAT__
 ACCT AGG GC AAGGCCATGT GAGG
 ||| || ||||| ||||
 TCC TG TTCCGGTACA CTCC
 A_ A GACAC
 GAM2623 FLJ12783 3' CTCCCGATCTTGCTGCC 25417 CCA TGAT
 GGCAGCAAGG TG GAG
 ||||| || |||
 CCGTCGTTCT GC CTC
 A_ C__
 GAM2623 FLJ14437 3' CAAAGCATGGCCTTACCAGCT 26308 AGC_ GA
 GGC AAGGCCATGT TG
 ||| ||||| ||
 TCG TTCCGGTACG AC
 ACCA AA
 GAM2623 FLJ14810 5' CCTCATTGACCCGCGCTGCC 26634 AA CCATG
 GGCAGC GG TGATGAGG
 |||| || |||||
 CCGTCG CC GTTACTCC
 CG CA__
 GAM2623 FLJ20174 3' CCTCATCACTCTGACTCTGCCT 19268 CA GCCAT
 AGGCAG AG GTGATGAGG
 |||| || |||||
 TCCGTC TC CACTACTCC
 _ AGTCT
 GAM2623 KIAA0449 3' CCTCAGCTGTCCAGCCCTGCTG 19051 A CATGTGA_
 CCT AGGCAGCA GGC TGAGG
 ||||| || ||||
 TCCGTCGT CCG ACTCC
 C ACCTGTCG
 GAM2623 KIAA0545 3' CCTCAGGCCGTGGCCCTGCTGC 31635 A TGA
 CT AGGCAGCA GGCCATG TGAGG
 ||||| ||||| ||||
 TCCGTCGT CCGGTGC ACTCC
 C CGG
 GAM2623 KIAA1010 3' CACCCAGCCTTGCTGCCT 35670 CAT
 AGGCAGCAAGGC GTG
 ||||| ||||| |||
 TCCGTCGTTCCG CAC
 ACC
 GAM2623 KIAA1089 3' CTGGGCCAGCCTTCCTGCCT 34140 C CAT GATG
 AGGCAG AAGGC GT AGG
 |||| |||| || |||
 TCCGTC TTCCG CG TCC
 C AC_ G__
 GAM2623 KIAA1110 3' CTCTGTGTCCTTGCTGCC 30984 C TGAT
 GGCAGCAAGG CATG GAG
 ||||| |||| |||

CCGTCGTTCC GTGT CTC
 T _____
 GAM2623 KIAA1272 3' CGAATGGCCTTGTGCCT 34761 G G
 AGGCA CAAGGCCAT TG
 ||||| ||||| ||
 TCCGT GTTCCGGTA GC
 _ A
 GAM2623 KIAA1855 3' CCTCATCATGAGCCTCAACTGC 44356 CA_ CAT
 CT AGGCAG AGGC GTGATGAGG
 ||||| ||| |||||
 TCCGTC TCCG TACTACTCC
 AAC AG_
 GAM2623 MGC16279 5' TCACAGGCCTTGCCATCT 31488 CA A
 AGG GCAAGGCC TGTGA
 ||| ||||| |||||
 TCT CGTTCCGG ACACT
 AC _
 GAM2623 MGC16279 5' TCACAGGCCTTGCCATCT 26734 CA A
 AGG GCAAGGCC TGTGA
 ||| ||||| |||||
 TCT CGTTCCGG ACACT
 AC _
 GAM2623 MGC20235 3' CCTCATCACACCCTTACCTCC 29665 C C_ CCA
 GG AG AAGG TGTGATGAGG
 || || ||| |||||
 CC TC TTCC ACACTACTCC
 _ CA C_
 GAM2623 MYO18B 3' CCTTCTCTATGGCCTTGCTACC 26331 C T T
 T AGG AGCAAGGCCATG GA GAGG
 ||| ||||| ||| |||||
 TCC TCGTTCCGGTAT CT TTCC
 A _ C
 GAM2623 PGS1 5' CTCCCCACCTTGCTGCCT 23657 CCATG AT
 AGGCAGCAAGG TG GAG
 ||||| || |||
 TCCGTCGTTCC AC CTC
 _____ CC
 GAM2623 RNF36 5' CCTCACTCTGGCCTTGCTGCTT 28032 TGT _
 AGGCAGCAAGGCCA GA TGAGG
 ||||| || |||||
 TTCGTCGTTCCGGT CT ACTCC
 _____ C
 GAM2623 TM4SF11 3' CTCCCCGACCTTGCTGACT 18084 G CCATG AT
 AG CAGCAAGG TG GAG
 || ||||| || |||
 TC GTCGTTCC GC CTC
 A A_____ CC
 GAM2623 LOC115129 3' TCACAGCCCTGCTGTCT 36252 A CA
 AGGCAGCA GGC TGTGA
 ||||| || |||||

		TCTGTCGT CCG ACACT		
		C _		
GAM2623	LOC144114 5'	CCCACAGCCTTGGCCCTGCTGC 39993	A	T_ GA A
	T	GGCAGCA GGCCA GT TG GG		
		TCTGTCGT CCGGT CG AC CC		
		C TC AC _		
GAM2623	LOC146184 5'	CCTCATTAGGCCTGGCCACCT 40661	CA A	ATG
		AGG GC AGGCC TGATGAGG		
		TCC CG TCCGG ATTACTCC		
		AC G _		
GAM2623	LOC158156 3'	CTCAAAGGCCTTGCAGCC 39740	A	ATGTGA
		GGC GCAAGGCC TGAG		
		CCG CGTTCCGG ACTC		
		A AA_		
GAM2623	LOC196483 5'	TCACAGGCCTTGCCATCT 30291	CA	A
		AGG GCAAGGCC TGTGA		
		TCT CGTTCCGG ACACT		
		AC _		
GAM2623	LOC196955 5'	CCCAGACATGGCCTTCTGCCT 37933	C	GA A
		AGGCAG AAGGCCATGT TG GG		
		TCCGTC TTCCGGTACA AC CC		
		_ G_ _		
GAM2623	LOC204970 3'	CGCAGGCCGACCCTGCTGCCT 43068	A_	A
		AGGCAGCA GGCC TGTG		
		TCCGTCGT CCGG ACGC		
		CCCAG _		
GAM2623	LOC220739 3'	CCTCATTTGGGCACCTTGCTGT 44656	_	ATGT
	C	GGCAGCAAG GCC GATGAGG		
		CTGTCTGTTT CGG TTACTCC		
		CA GT_		
GAM2623	LOC221466 3'	CCTCACCCCTTTGCCTTGCTGT 44992		CATGTGA
	CT	AGGCAGCAAGGC TGAGG		
		TCTGTCGTTCCG ACTCC		
		TTTCCCC		
GAM2623	LOC255974 5'	CCTCTGTCATAGCCTATGCTGC 46556	_	CA _
	CT	AGGCAGCA AGGC TGTGAT GAGG		
		TCCGTCGT TCCG ATACTG CTCC		
		A _ T		
GAM2623	LOC51337 3'	CCCACTGCAGTCGGCCTTGCCT 18762	CA	A_ GA A
	CCT	AGG GCAAGGCC TGT TG GG		

TCC CGTTCCGG ACG AC CC
 TC CTG TC _
 GAM2623 LOC90092 5' CCTCATCAAGGCCTCCTCGCTC 30786 C A__ ATG
 CT AGG AGC AGGCC TGATGAGG
 ||| ||| |||| |||||
 TCC TCG TCCGG ACTACTCC
 _ CTCC A__
 GAM2623 LOC96652 5' CCTCATCATCCCCCTCCTGCC 32628 CA CCAT
 GGCAG AGG GTGATGAGG
 |||| ||| |||||
 CCGTC TCC TACTACTCC
 C_ CCC_
 GAM2624 PDGFRB 3' TCAATACGGTACCAAAGAT 32818 GAAAT
 ATCTT TACCGTATTGA
 |||| |||||
 TAGAA ATGGCATAACT
 ACC_
 GAM2624 RASSF1 3' TCAATAAAGATTTCAAGAT 14039 ACCG
 ATCTTGAAATT TATTGA
 ||||| ||||
 TAGAACTTTAG ATAACT
 AA_
 GAM2624 LOC157681 3' CAGGCTGGTAATCCCAAATTGA 39642 C AA TA
 TCAAT TTG ATTACCG TTG
 |||| ||| ||||| |||
 AGTTA AAC TAATGGT GAC
 _ CC CG
 GAM2624 LOC221431 3' TCAATACGATCATGATTCAAGA 44225 A C_
 T ATCTTGAA TTA CGTATTGA
 ||||| ||| |||||
 TAGAACTT AGT GCATAACT
 _ ACTA
 GAM2625 KCNA6 3' AATCATGCCCAGCTTCTGTCAT 8015 AATTG
 A TATGGCAGAAGC ATGATT
 ||||| |||||
 ATACTGTCTTCG TACTAA
 ACCCG
 GAM2625 LOC161823 3' ATCAAGTTCCTGCCATA 40030 A AA
 TATGGCAG AGC TTGAT
 ||||| ||| ||||
 ATACCGTC TTG AACTA
 C _
 GAM2626 KCNS2 3' CATCTCATAAATGTCACTCTTT 33899 A_ C T
 A TAAAGAG ACATT TATG GGATG
 ||||| |||| ||| ||||
 ATTTCTC TGTAATAC TCTAC
 AC _ _
 GAM2626 TRPM2 3' CATCCACATGCCCTCCTCCTT 9311 A ACATTC
 AAG GA TATGTGGATG
 ||| || |||||

		TTC CT GTACACCTAC		
		_ CCTCCC		
GAM2626	DKFZp434A1010	5' CATCCACAGCGTGTCTC	35345	A TCTA
		GAG ACAT TGTGGATG		
		CTC TGTG ACACCTAC		
		C CG__		
GAM2626	FLJ11383	3' TTATACAGAATATCTCTTTA	24480	AC A
		TAAAGAGA ATTCT TGTGG		
		ATTTCTCT TAAGA ATATT		
		A_ C		
GAM2626	FLJ13102	3' CATCCACACCTGGCACTCCCCT	24341	AACATT_ _
	CT	AGAG CTA TGTGGATG		
		TCTC GGT ACACCTAC		
		CCCTCAC CC		
GAM2626	KIAA0286	3' CATGGTAAAATGTTCTCT	33906	__
		AGAGAACATT CTATG		
		TCTCTTGTA GGTAC		
		AAT		
GAM2626	KIAA0737	3' CCCAGGAGTGATTTCTCTTTA	16819	_ A T
		TAAAGAGAA CATTCT TG GG		
		ATTTCTCT GTGAGG AC CC		
		TA _ _		
GAM2626	MGC3020	3' ATCCACACAGGGCTTTT	23482	AACA A
		AAGAG TTCT TGTGGAT		
		TTTTC GGGA ACACCTA		
		_ C		
GAM2626	PTP4A1	3' CATGTAGAATATGCTCTTTA	9532	AAC
		TAAAGAG ATTCTATGTG		
		ATTTCTC TAAGATGTAC		
		GTA		
GAM2626	LOC144519	3' ATCCAGGACATCTCTTTA	37758	ACAT ATG
		TAAAGAGA TCT TGGAT		
		ATTTCTCT AGG ACCTA		
		AC_ _		
GAM2627	BCL11B	3' GGACATTTAACCTTGATCTCC	23166	_
		GGAGGTTA TTAAATGTCC		
		CCTCTAGT AATTACAGG		
		TC		
GAM2627	CRHR1	3' ACATTTAGTACCCTGCAGG	10604	ACA A T
		CC GG GGT ATTAAATGT		

			GG TC CCA TGATTTACA		
			ACG _ _		
GAM2627	EHHADH	3'	ACATCTAACCTTCTAGGA	7694	AC TTAA
			TCC AGGAGGTTA ATGT		
			AGG TCTTCCAAT TACA		
			A_ C__		
GAM2627	FBXW1B	3'	GGACCAATAAACAGCCTCCT	14663	A_ AAT
			AGGAGGTT TTA GTCC		
			TCCTCCGA AAT CAGG		
			CA AAC		
GAM2627	FBXW1B	3'	GGACCAATAAACAGCCTCCT	27365	A_ AAT
			AGGAGGTT TTA GTCC		
			TCCTCCGA AAT CAGG		
			CA AAC		
GAM2627	FBXW1B	3'	GGACCAATAAACAGCCTCCT	27375	A_ AAT
			AGGAGGTT TTA GTCC		
			TCCTCCGA AAT CAGG		
			CA AAC		
GAM2627	MBL2	3'	GGACATTTTTGACTCCCT	5763	AG TT
			AGG GTTA AAATGTCC		
			TCC CAGT TTTACAGG		
			CT T_		
GAM2627	MBNL	5'	ACATTTAACTACCTGT	22023	A TTA
			ACAGG GGTTA AATGT		
			TGTCC TCAAT TTACA		
			A _		
GAM2627	PHKA2	3'	ACACTTGTGTCTCTGTGGA	5834	_ TTAT A
			TCCACAG GAGG TAA TGT		
			AGGTGTC CTCT GTT ACA		
			T GT__ C		
GAM2627	PTPRO	3'	GGACATTTAATAATGGACC	8741	AG_
			GG GTTATTAAATGTCC		
			CC TAATAATTTACAGG		
			AGG		
GAM2627	PTPRO	3'	GGACATTTAATAATGGACC	25034	AG_
			GG GTTATTAAATGTCC		
			CC TAATAATTTACAGG		
			AGG		
GAM2627	PTPRO	3'	GGACATTTAATAATGGACC	25006	AG_
			GG GTTATTAAATGTCC		

CC TAATAATTTACAGG
 AGG
 GAM2627 PTPRO 3' GGACATTTAATAATGGACC 25014 AG_
 GG GTTATTAAATGTCC
 || |||||
 CC TAATAATTTACAGG
 AGG
 GAM2627 PTPRO 3' GGACATTTAATAATGGACC 25023 AG_
 GG GTTATTAAATGTCC
 || |||||
 CC TAATAATTTACAGG
 AGG
 GAM2627 TAF11 3' ACATTTAAGATTCTCCTGTGGA 12178 TTA
 TCCACAGGAGG TTAAATGT
 ||||| |||||
 AGGTGTCCTCT AATTACA
 TAG
 GAM2627 TM4SF6 3' GGACATTTAGGGTCCCCCCTGT 9285 A TTA_
 G CACAGG GG TTAAATGTCC
 ||||| || |||||
 GTGTCC CC GATTACAGG
 C CTGG
 GAM2627 DKFZP564K0822 3' CGGACATTTAATCGGAGAACCT 45139 _____ III
 CCTGGGGA GGAGGTT ATTAAATGTCC G
 ||||| ||||| |
 CCTCCAA TAATTACAGG C
 GAGGC III
 GAM2627 FLJ10856 3' ACATTCATATAGTCTCTGTG 20217 G GT TA_
 CACAG AG TAT AATGT
 ||||| || || |||||
 GTGTC TC ATA TTACA
 _ TG TAC
 GAM2627 KIAA0087 3' GACATTTAACTGGAATCCAGGA 16559 ACA GG _
 TCC GGA TTA TTAAATGTC
 || || || |||||
 AGG CCT GGT AATTACAG
 A_ AA C
 GAM2627 KIAA0461 3' ACATTTAATAAAATGAGGG 35070 A GGAGG
 TCC CA TTATTAAATGT
 || || |||||
 GGG GT AATAATTTACA
 A AA_
 GAM2627 KIAA1319 3' GACATTTATTTCTCCTTTGGA 21868 C TTAT
 TCCA AGGAGG TAAATGTC
 ||||| |||||
 AGGT TCCTCT ATTTACAG
 T TT_
 GAM2627 KIAA1954 3' ACATTTAATGGGCACCTATGGG 38092 C AG _
 TCCA AGG GTT ATTAAATGT
 ||||| || || |||||

GGGT TCC CGG TAATTTACA
A A_ G

GAM2627 PTPRN2 3' GACATTTCCCTCCTGGGA 28369 A TTATT
TCC CAGGAGG AAATGTC
||| ||||| |||||
AGG GTCCTCC TTTACAG
_ C_

GAM2627 PTPRN2 3' GACATTTCCCTCCTGGGA 28374 A TTATT
TCC CAGGAGG AAATGTC
||| ||||| |||||
AGG GTCCTCC TTTACAG
_ C_

GAM2627 PYY2 3' GGACACCCGAGGCCTCCTGGGA 22074 A ATTAAA
TCC CAGGAGGTT TGTCC
||| ||||| |||||
AGG GTCCTCCGG ACAGG
_ AGCCC_

GAM2627 SCAMP5 3' ACATTTGGCCCTGTG 29071 AG TAT
CACAGG GT TAAATGT
||||| || |||||
GTGTCC CG GTTTACA

GAM2627 ZNF-U69274 3' GACATTCACAGCAGCTCTGTGG 15760 _AG ATTA
A TCCACAG G GTT AATGTC
||||| | ||| |||||
AGGTGTC C CGA TTACAG
T GA CAC_

GAM2627 ZNF304 3' GACATCTGTATCTCCTGTGG 21830 T TAA
CCACAGGAGGT AT ATGTC
||||||| || |||||
GGTGTCTCTA TG TACAG
_ TC_

GAM2627 LOC120856 3' GACACAGTGACCTCTGTGGA 36639 G AAA
TCCACAG AGGTTATT TGTC
||||| ||||| |||||
AGGTGTC TCCAGTGA ACAG
_ C_

GAM2627 LOC128844 5' GGACATTTTCATAGCCTCCT 37319 T_
AGGAGGTTAT AAATGTCC
||||||| |||||
TCCTCCGATA TTTACAGG
CT

GAM2627 LOC161734 3' GGACAGCAGTAACCTCT 42109 AAA
GGAGGTTATT TGTCC
||||||| |||||
TCTCCAATGA ACAGG
CG_

GAM2627 LOC219445 3' GGACATTCAAAGTGCCCTGTGG 44012 AG TA_ A
A TCCACAGG GT TT AATGTCC
||||| || || |||||

			AGGTGTCC CG AA TTACAGG	
			___ TGA C	
GAM2628	ABP1	3'	CAAGAACAGCTTCCAGAC 31614 C__ TT	
			GTC AAGT TGTTCTTG	
			CAG TTCG ACAAGAAC	
			ACC ___	
GAM2628	AKAP2	3'	CAAGAAACCTTGGGCCA 14059 TTTTG	
			TGGTCCAAG TTCTTG	
			ACCGGGTTC AAGAAC	
			CA___	
GAM2628	CETN1	3'	CAAGAGTCAACCTGGAGCA 45638 G A TTG	
			TG TCCA GTT TTCTTG	
			AC AGGT CAA GAGAAC	
			G C CT_	
GAM2628	EPB41	5'	CAAGAACAAGGAGCGGAC 10721 AAG	
			GTCC TTTTGTCTTG	
			CAGG GGAACAAGAAC	
			CGA	
GAM2628	FSTL1	3'	CAAAAACAAGATGACCA 13948 CAA C	
			TGGTC GTTTGTGTT TTG	
			ACCAG TAGAACA AAC	
			___ A	
GAM2628	GRM4	3'	CAAGAACCTGCGTCTTGGACCA 6502 TTTT__	
	T		ATGGTCCAAG GTTCTTG	
			TACCAGGTTT CAAGAAC	
			TGCGTC	
GAM2628	METTL1	3'	AAGGACTTTTGACCAT 23305 TTTT	
			ATGGTCCAAG GTTCTT	
			TACCAGGTTT CAGGAA	

GAM2628	METTL1	3'	AAGGACTTTTGACCAT 23310 TTTT	
			ATGGTCCAAG GTTCTT	
			TACCAGGTTT CAGGAA	

GAM2628	MINPP1	3'	CAAATATCTCAGTTGGACCAT 11330 _____	
			ATGGTCCAA GTTTTG	
			TACCAGGTT TAAAC	
			GA CTCTA	
GAM2628	NLGN1	5'	GGTAAATACTTGGACCAT 17229 T GTT	
			ATGGTCCAAGT TT CT	

TACCAGGTTCA AA GG
 T AT_
 GAM2628 NT5C2 3' CAAGAACAAAACCTCCAT 14526 TCCA
 ATGG AGTTTTGTTCTTG
 ||| |||||
 TACC TCAAAACAAGAAC

 GAM2628 PCSK2 3' AAGAACAATTGTCCAT 8453 TC GTT
 ATGG CAA TTGTTCTT
 ||| || |||||
 TACC GTT AACAAGAA
 T_ ____
 GAM2628 BHC80 3' CAAGAACAAGCAGAGCCCGGGC 18728 AA ____
 CA TGGTCC GTTTTGT TCTTG
 ||||| ||||| |||||
 ACCGGG CGAGACG AGAAC
 CC AACA
 GAM2628 BIRC3 3' CAAAAACAAAACACCAGGGACA 33368 _ AA____ C
 CAT ATG GTCC GTTTTGTT TTG
 ||| ||| ||||| |||
 TAC CAGG CAAAACAA AAC
 A GACCA A
 GAM2628 C20orf121 3' CAAGAACAATCAGGACCA 23629 AAGTT
 TGGTCC TTGTTCTTG
 ||||| |||||
 ACCAGG AACAAGAAC
 ACT_
 GAM2628 CASPR3 3' CAAGAAATGCTTCTTGGA CTA 27385 TTTTG_
 TGGTCCAAG TTCTTG
 ||||| |||||
 ATCAGGTT C AAGAAC
 TTCGTA
 GAM2628 CLSTN2 3' CAAGAATAGGTCCTTGGCCA 22691 T T_
 TGG CCAAG TTTGTTCTTG
 ||| ||||| |||||
 ACC GGTC GGATAAGAAC
 _ CT
 GAM2628 CRIPT 3' CAAGAACACAAGGAGCAT 36537 G AAG T
 ATG TCC TT TGTTCTTG
 ||| ||| || |||||
 TAC AGG AA ACAAGAAC
 G _ C
 GAM2628 DNAJC6 3' CAAGAACAAAACCACCA 16657 CCAA
 TGGT GTTTTGTTCTTG
 ||| |||||
 ACCA CAAAACAAGAAC
 C_
 GAM2628 FLJ10392 5' AAGAACAGAATACCA 19845 CCAA
 TGGT GTTTTGTTCTT
 ||| |||||

ACCA TAAGACAAGAA

GAM2628 FLJ20552 3' CAAGAACAAAAGCTGCTCCA 19547 TCCA
TGG AGTTTTGTTCTTG
||| |||||
ACC TCAAACAAGAAC
TCG_

GAM2628 FLJ21195 3' CAAGAAGACAACTTGAGCCA 22823 TC TTG
TGG CAAGTT TTCTTG
||| ||||| |||||
ACC GTTCAA AAGAAC
GA CAG

GAM2628 KIAA1950 3' CAAGAACAGGGCAGCTTGACC 44485 ____
GGTCCAAGTT TTGTTCTTG
||||||| |||||
CCAGGTTCTGA GACAAGAAC
CGG

GAM2628 KR18 3' CAAGAACAAAAGCTCCAT 27115 TCCA
ATGG AGTTTTGTTCTTG
||| |||||
TACC TCAAACAAGAAC

GAM2628 LAMP3 3' CAAGAACAATGACACCA 29915 CCAA _
TGGT GTT TTGTTCTTG
||| ||| |||||
ACCA CAG AACAAGAAC
____ T

GAM2628 RER1 3' CAAGAACAGTTTTGAGCCAT 13902 TC TT
ATGG CAAG TTGTTCTTG
||| ||| |||||
TACC GTTT GACAAGAAC
GA T_

GAM2628 SCYA28 3' AAGTGGACTTGGCCAT 21249 T TGTT
ATGG CCAAGTTT CTT
||| ||||| |||
TACC GGTTGAGG GAA
____ T____

GAM2628 STK39 3' CAAGAACAAGCAAATGCCA 14892 CCAA T
TGGT GTTT GTTCTTG
||| ||| |||||
ACCG CGAA CAAGAAC
TAAA _

GAM2628 TNK1 3' AGGGGCCCACTGGACCAT 10134 A TTT
ATGGTCCA GT GTTCTT
||||||| || |||||
TACCAGGT CA CGGGGA
_ CAC

GAM2628 LOC132880 5' CAAGGATAACCTGGGCCA 37029 A TT
TGGTCCA GT TGTTCTTG
||||||| || |||||

ACCGGGT CA ATAGGAAC
 C _
 GAM2628 LOC147138 5' CAAGAATGTGCTGGAC 38307 A TT
 GTCCA GT TGTTCTTG
 ||||| || |||||
 CAGGT CG GTAAGAAC
 _ T_
 GAM2628 LOC147727 5' CAAGAATGGCTTGAATCA 38380 C TT
 TGGT CAAGTT GTTCTTG
 |||| ||||| |||||
 ACTA GTTCGG TAAGAAC
 A _
 GAM2628 LOC155081 3' AGAAGAACCTGGACCAT 39542 A TG
 ATGGTCCA GTTT TTCT
 ||||| |||| ||||
 TACCAGGT CAAG AAGA
 C _
 GAM2628 LOC201245 3' AGGGGCCACACTGGACCAT 42228 A TTT
 ATGGTCCA GT GTTCTT
 ||||| || |||||
 TACCAGGT CA CGGGGA
 _ CAC
 GAM2628 LOC202802 3' AGAAGAACCTGGACCAT 42987 A TG
 ATGGTCCA GTTT TTCT
 ||||| |||| ||||
 TACCAGGT CAAG AAGA
 C _
 GAM2628 LOC222228 3' AGAAGAACCTGGACCAT 45273 A TG
 ATGGTCCA GTTT TTCT
 ||||| |||| ||||
 TACCAGGT CAAG AAGA
 C _
 GAM2628 LOC222233 3' AGAAGAACCTGGACCAT 45242 A TG
 ATGGTCCA GTTT TTCT
 ||||| |||| ||||
 TACCAGGT CAAG AAGA
 C _
 GAM2628 LOC57406 3' AAGCAGCCACCTTGGACCAT 21837 TTTT _
 ATGGTCCAAG GTT CTT
 ||||| || ||||
 TACCAGGTTT CGA GAA
 CAC_ C
 GAM2628 LOC92568 3' CAAGAACAAAAACCA 34575 CCAAG
 TGGT TTTTGTCTTG
 |||| |||||
 ACCA AAAACAAGAAC
 A____
 GAM2629 HGF 3' ACCAATAAATCATCAAACA 45217 GC GACGA
 TG TTGATGAT GTTGGT
 || ||||| |||||

			AC AACTACTA TAACCA		
			A_ AA__		
GAM2629	RFX2	3'	ACCGTCACCATCAAGCCA 6269	A	A
			TGGCTTGATG TGACG GT		
			ACCGAACTAC ACTGC CA		
			C _		
GAM2629	FLJ12934	3'	TACCAACTTAGTCATCAAGCC 23178		GAC
			GGCTTGATGAT GAGTTGGTA		
			CCGAACTACTG TTCAACCAT		
			A__		
GAM2629	FLJ13868	3'	ACCAACCCATCAACATCAAGCC 22954	A	CGA
			GGCTTGATG TGA GTTGGT		
			CCGAACTAC ACT CAACCA		
			A ACC		
GAM2629	PEG10	3'	CACCTTACCATCATCATGCCA 17425	T	AC T
			TGGC TGATGATG GAG TG		
			ACCG ACTACTAC TTC AC		
			T CA C		
GAM2629	UPLC1	3'	ACCTAAGCCATCATCAACCA 19283	C	ACGAGTT
			TGG TTGATGATG GGT		
			ACC AACTACTAC CCA		
			_ CGAAT__		
GAM2629	LOC149271	3'	ACTCAGTCATCATCAACCCA 38674	C	_
			TGG TTGATGATGAC GAGT		
			ACC AACTACTACTG CTCA		
			C A		
GAM2629	LOC90333	3'	ACCACTTATTCACCATCAAGC 31218	A	C_ T
			GCTTGATG TGA GAGT GGT		
			CGAACTAC ACT TTCA CCA		
			C TA _		
GAM2630	GTF2H1	3'	TCAACCATCAGGAAACAGTTGT 11793		GTATG A
	CA		TGACAA TTCT ATGGTTGA		
			ACTGTT AGGA TACCAACT		
			GACAA C		
GAM2630	VAPB	3'	TCAACCATTACTCACACTT 11133	A	TTC
			AAGT TG TAATGGTTGA		
			TTCA AC ATTACCAACT		
			C TC_		
GAM2630	C1orf27	5'	CCACAGAACATGCCTGCCA 19509	A A	AA
			TG CA GTATGTTCT TGG		

			AC GT CGTACAAGA ACC		
			C C C_		
GAM2630	SURB7	3'	GACCAGAACATACTT 10465	AAT	
			AAGTATGTTCT GGTT		
			TTCATACAAGA CCAG		
GAM2631	AK2	3'	GCTACCCAGCACATGCCA 15076	T CA AA	
			TGGCATGT GC GG GGC		
			ACCGTACA CG CC TCG		
			_ A_ CA		
GAM2631	FKRP	3'	AGACCAGCCTCGGCAACATGCC 23591	_ AA C	
	A		TGGCATGTTGCC AGG GG CT		
			ACCGTACAACGG TCC CC GA		
			C GA A		
GAM2631	PPP1R3A	3'	AGGGTTTTAGTCAACATGCCAT 8564	CCAG G	
	A		TATGGCATGTTG GAAG CCT		
			ATACCGTACAAC TTTT GGA		
			TGA_ G		
GAM2631	SLC14A2	5'	AGGCCTCCCCAGCAATGTG 14006	CA A	
			CATGTTGC GG AGGCCT		
			GTGTAACG CC TCCGGA		
			AC C		
GAM2631	SNX9	3'	GAGGCCTAAGTGGCAACATGGC 18331	G A_____ AAGG	
	ATA		TG CATGTTGCC GG C		
			AC GTACAACGG CC G		
			G TGAIIIT GGAA		
GAM2631	C1orf34	3'	AGGGATTAACAAGATGCCATA 30434	G CCAGG GG	
			TATGGCAT TTG AA CCT		
			ATACCGTA AAC TT GGA		
			G AA_ AG		
GAM2631	DKFZP564O1664	3'	AGACCTTCCTGAGGCTGCC 25101	T GC C	
			GGCA GTT CAGGAAGG CT		
			CCGT CGG GTCCTTCC GA		
			_ A_ A		
GAM2631	MGC16186	5'	AGACCTCCCCAGCAATGTG 26160	CA A C	
			CATGTTGC GG AGG CT		
			GTGTAACG CC TCC GA		
			AC C A		
GAM2631	TESK2	3'	AGGCCTTCCTAGTTAGGGCCA 31648	ATGTT C	
			TGGC GC AGGAAGGCCT		

ACCG TG TCCTTCGGA
 GGAT_ A
 GAM2631 LOC150157 5' GAGGCCTAGACGGCACATGCCA 41144 T C_____ AAGG
 TA TGGCATGT GC AGG C
 ||||| || || |
 ACCGTACA CG TCC G
 _ GCAGAI|| GGAA
 GAM2631 LOC201685 3' AGGCCTTTCCCAACATGCCA 43384 CCA
 TGGCATGTTG GGAAGGCCT
 ||||| |||||
 ACCGTACAAC CTTTCCGGA
 C_
 GAM2631 LOC253150 3' GCCTTTCTTGGCTGGCAACACA 45732 GCA _____
 CA TG TGTTGCCAG GAAGGC
 || ||||| |||||
 AC ACAACGGTC TTTCCG
 AC_ GGTTG
 GAM2632 FLJ10996 3' AGTTCCTACTGCACAAGT 21126 C T
 ACTTGTGCAG AG AACT
 ||||| || |||||
 TGAACACGTC TC TTGA
 A C
 GAM2633 CCNDBP1 5' GTCCGTGCAGCACTAACGTA 27398 AA ACA
 TACGTTGGT CTGCA GAC
 ||||| |||| |
 ATGCAATCA GACGT CTG
 C_ GC_
 GAM2633 COL6A3 3' CTGTTGCAGGCAAATGTA 10588 GGTA
 TACGTT CTGCAACAG
 |||| |
 ATGTAA GACGTTGTC
 ACG_
 GAM2633 COL6A3 3' CTGTTGCAGGCAAATGTA 27672 GGTA
 TACGTT CTGCAACAG
 |||| |
 ATGTAA GACGTTGTC
 ACG_
 GAM2633 GYG 3' GTCTGTTACAGTTGCTAG 10338 C
 TTGGTAACTG AACAGAC
 ||||| |||||
 GATCGTTGAC TTGTCTG
 A
 GAM2633 BDG-29 3' GTCTGTTGTTACCCACGTA 35819 T ACT
 TACGT GGTA GCAACAGAC
 |||| |||| |||||
 ATGCA CCAT TGTTGTCTG
 C _
 GAM2633 FLJ20275 3' TCTGTTGATTGCCAAC 19323 CTG
 GTTGGTAA CAACAGA
 ||||| |||||

			CAACCGTT GTTGTCT		
			A__		
GAM2633	HBP1	3'	CTGCTGCAGTTACCATG 14560	T	A
			CGT GGTAAGTCA CAG		
			GTA CCATTGACGT GTC		
			__ C		
GAM2633	HIC2	3'	GTCTGGTCCTTACCAAC 32530	CT	AA
			GTTGGTAA GC CAGAC		
			CAACCATT TG GTCTG		
			CC __		
GAM2633	MAN1	3'	CTGTTGCAAGAGTGAATGTA 15617	G	TAAC
			TACGTT G TGCAACAG		
			ATGTAA T ACGTTGTC		
			G GAGA		
GAM2633	MGC16142	5'	TCTGTTGCATGACAAACGT 26509	G	AAC
			ACGTT GT TGCAACAGA		
			TGCAA CA ACGTTGTCT		
			A GT__		
GAM2633	MGC2827	3'	GTCCGTTGCAGTTTCACCAAAT 23426	__ __	A
	GTA		TACGTT GGT AACTGCAAC GAC		
			ATGTAA CCA TTGACGTTG CTG		
			A CT C		
GAM2633	TTC4	3'	TCTGCTGCAGTTACCACAGC 32961	__	A
			GT TGGTAAGTCA CAGA		
			CG ACCATTGACGT GTCT		
			AC C		
GAM2633	LOC150606	3'	GTCTACCAGGGCCAACGTA 41235	AA	CAAC
			TACGTTGGT CTG AGAC		
			ATGCAACCG GAC TCTG		
			G_ CA__		
GAM2633	LOC91813	5'	TCTGTCACTGCCACCGTA 33401	T	AC CA
			TACG TGGTA TG ACAGA		
			ATGC ACCGT AC TGTCT		
			C C_ __		
GAM2634	ATP2A2	3'	TGCAAAATGTCATAGCT 7403	A	AAACC
			AGTTATGA CAT TTGCA		
			TCGATACT GTA AACGT		
			__ A__		
GAM2634	CRTAP	3'	TTGTCTTCCCATGTTTCATAGC 13064		AAACCTT
	T		AGTTATGAACAT GCAA		

		TCGATACTTGTA	TGTT		
		CCCCTTC			
GAM2634	RNTRE	3' TTGCTATGTTTCATAATT	16189		AACCTT
		AGTTATGAACATA	GCAA		
		TTAATACTTGTAT	CGTT		
GAM2634	TBX5	5' TTTGTGTCTTATGTTTCATCAC	28015	T	ACCT
		GTATGAACATAA	TGCAAA		
		CATACTTGTATT	GTGTTT		
		C	CT__		
GAM2634	TBX5	5' TTTGTGTCTTATGTTTCATCAC	5691	T	ACCT
		GTATGAACATAA	TGCAAA		
		CATACTTGTATT	GTGTTT		
		C	CT__		
GAM2634	DCLRE1A	5' TTGCCAATATGTTTCATTAC	34284	T	AACCTT
		GTATGAACATA	GCAA		
		CATACTTGTAT	CGTT		
		T	AAC__		
GAM2634	ELOVL2	3' TGCAAGATTTTCATAATT	19389		C AAAC
		AGTTATGAAAT	CTTGCA		
		TTAATACTT	TA GAACGT		
		T	__		
GAM2634	FLJ13110	3' TGTAATGTTTCATGTCATAACT	23224		A A C
		AGTTATGACAT	AAC TTGCA		
		TCAATACT	GTA TTG AATGT		
		_	C T		
GAM2634	LOC200339	3' TTGCAAGGTCTTCCGTTATAAC	43303		ACATAA
	T	AGTTATGA	ACCTTGCAA		
		TCAATATT	TGGAACGTT		
		GCCTTC			
GAM2634	LOC257407	3' TGCAAGGTGCTGCCTAACT	46338		TGAA TAA
		AGTTA	CA ACCTTGCA		
		TCAAT	GT TGGAACGT		
		CC__	CG_		
GAM2634	LOC92997	3' TGCAAGGTGCTGCCTAACT	35222		TGAA TAA
		AGTTA	CA ACCTTGCA		
		TCAAT	GT TGGAACGT		
		CC__	CG_		
GAM2635	B3GALT2	5' CTCTCATATACCACTACTGGA	9872		GCTTCTTCA
		TCCAGTAGTGG	AGAG		

			AGGTCATCACC	TCTC	
			ATATAC____		
GAM2635	LARGE	3'	AAGAAGCCCACCACTAGG	11127	_ A
			CC AGT GTGGGCTTCTT		
			GG TCA CACCCGAAGAA		
			A C		
GAM2635	LARGE	3'	AAGAAGCCCACCACTAGG	28599	_ A
			CC AGT GTGGGCTTCTT		
			GG TCA CACCCGAAGAA		
			A C		
GAM2635	MLC1	3'	CTCTTGAGAGCCCCACCCCTG	17524	TA C T
			CAG GTGGG TTCT CAAGAG		
			GTC CACCC GAGA GTTCTC		
			CC C _		
GAM2635	MLC1	3'	CTCTTGAGAGCCCCACCCCTG	29218	TA C T
			CAG GTGGG TTCT CAAGAG		
			GTC CACCC GAGA GTTCTC		
			CC C _		
GAM2635	NXT1	5'	CTCTTCCCGTGCCCCCTACCAGA	14909	CA T TTCTTC
			TC GTAG GGGC AAGAG		
			AG CATC CCCG TTCTC		
			AC _ TGCCC_		
GAM2635	PDYN	3'	CTCTTGAAGAACTGACTTCCTG	23653	T_ G C
			CAG AGT GG TTCTTCAAGAG		
			GTC TCA TC AAGAAGTTCTC		
			CT G _		
GAM2635	RAD52	3'	TCTTGAAGACAACTCTG	28649	T GGGCT
			CAG AGT TCTTCAAGA		
			GTC TCA AGAAGTTCT		
			_ AC__		
GAM2635	RAD52	3'	TCTTGAAGACAACTCTG	28657	T GGGCT
			CAG AGT TCTTCAAGA		
			GTC TCA AGAAGTTCT		
			_ AC__		
GAM2635	RAD52	3'	TCTTGAAGACAACTCTG	28665	T GGGCT
			CAG AGT TCTTCAAGA		
			GTC TCA AGAAGTTCT		
			_ AC__		
GAM2635	SORCS1	3'	CTGGGCAAAGCCCACTAT	27485	CT A
			GTAGTGGGCTT TC AG		

TATCACCCGAA GG TC
 AC G
 GAM2635 C21orf93 5' CTCCCGAAGGCCTCACCTCTG 29741 TA _ TT AA
 CAG GTG GGC CTTC GAG
 ||| ||| ||| ||| |||
 GTC CAC CCG GAAG CTC
 TC T _ CC
 GAM2635 DKFZP434H132 5' CTCCTACCCAGGCCCACTG 36448 A CTTCAA
 G CCA GT GTGGGCTT GAG
 ||||| ||||| |||
 GGTCA CACCCGGA CTC
 C CCCATC
 GAM2635 FOXH1 5' CTCAGGAGAAGCCCCCACTA 10011 _ AA
 TAGT GGGCTTCTTC GAG
 ||| ||||| |||
 ATCA CCCGAAGAGG CTC
 CC A_
 GAM2635 KIAA1468 5' CTCTTGAAAAGAGAGCTC 44099 _ _
 GGGCT TCT TCAAGAG
 ||||| ||| |||||
 CTCGA AGA AGTTCTC
 G AA
 GAM2635 TIX1 3' CTCCTGAAGAAAAAGCCTAT 30928 _ A
 GTGGGCT TCTTCA GAG
 ||||| ||||| |||
 TATCCGA AGAAGT CTC
 AAA C
 GAM2635 LOC148759 3' CTCCCAAAGGCAGCCCACCAC 40904 A _ CAA
 GT GTGGGCT TCTT GAG
 || ||||| ||| |||
 CA CACCCGA GGAA CTC
 C C ACC
 GAM2635 LOC153937 5' CTCCTGAAAAAGTGCTGCCTCC 39447 TA_TG_ C A
 TG CAG G G GCTT TTCA GAG
 ||| | ||| ||| |||
 GTC C C TGAA AAGT CTC
 CTC GT G A C
 GAM2635 LOC200845 5' CTCTTGAAAGACGCATCACTGGA 42863 AGTGG T
 TCCAGT GC TCTTCAAGAG
 ||||| || ||||| |||
 AGGTCA CG AGAAGTTCTC
 CTA_ C
 GAM2635 LOC220776 3' CTTGAAGAAACCCAGGGC 33932 AG C
 GT TGGG TTCTTCAAG
 || ||| ||||| |||
 CG ACCC AAGAAGTTC
 GG A
 GAM2636 NCOA6 5' AGACCCCTGAATATTTATATCA 15286 TAAA_ A_
 GT ATTGATATAA AGG TCT
 ||||| ||| |||

			TGACTATATT	TCC AGA		
			TATAAG	CC		
GAM2636	SLC1A3	3'	TAGATCCTCTGATATACAATTA	10385	_	AATAAA
			TAATTG ATAT	AGGATCTA		
			ATTAAC TATA	TCCTAGAT		
			A	GTC__		
GAM2636	GFPT1	3'	ATCCTTATTTATATATCAGTTA	7817	A	_
			TAATTGATATA TAAA	AGGAT		
			ATTGACTATAT ATTT	TCCTA		
			_	AT		
GAM2636	GRIN3A	3'	AGACTTCCTTATTTATCAATTA	28527	T	AA _
			TAATTGATA AATA	AGGA TCT		
			ATTAAC TAT	TCCT AGA		
			_	TC		
GAM2636	KIAA1674	3'	TAGATCCTTTTACATCATCA	34115	ATAA	
			TGAT	TAAAAGGATCTA		
			ACTA	ATTTTCCTAGAT		
			CTAC			
GAM2636	LOC51125	3'	TTGTTTTATTATAGCAATTA	18182	A	G
			TAATTG TATAATAAAA	GA		
			ATTAAC ATATTATTTT	TT		
			G	G		
GAM2637	PTGS1	3'	AGATATAACATTCAGTTCC	6671	_	TTT
			GGAAC TATGT	TATATCT		
			CCTTGA TTACA	ATATAGA		
			C	_		
GAM2637	PTGS1	3'	AGATATAACATTCAGTTCC	27892	_	TTT
			GGAAC TATGT	TATATCT		
			CCTTGA TTACA	ATATAGA		
			C	_		
GAM2637	STAT1	3'	AGAAACATCAGTTACTCT	14230	G	A
			AGAG AACT	ATGTTTTT		
			TCTC TTGA	TACAAAGA		
			A	C		
GAM2637	VBP1	3'	ATAAATGTATTAGTTCATCT	9398	G	TT
			AGA GAACTAATG	TTTAT		
			TCT CTTGATTAT	AAATA		
			A	GT		
GAM2637	ARHE	3'	AGATATTTTGGACCAGTTCCTT	11667	AAT	TTT_
	T		AGAGGAACT	GTT ATATCT		

TTTCTTGA CAG TATAGA
 C__ TTTT
 GAM2637 FLJ10139 3' AAAAACATTATTCCTCT 19734 C
 AGAGGAA TAATGTTTTT
 ||||| |||||
 TCTCCTT ATTACAAAAA

 -
 GAM2637 KIAA1655 3' GGATTCAAACCCAGTTCCTC 33090 AAT TTAT
 GAGGAACT GTTT ATCT
 ||||| ||| |||
 CTCCTTGA CAAA TAGG
 CC_ CT_
 GAM2637 NY-REN-25 3' AGATATAAAAACAACCTCC 30414 ACTAA
 GGA TGTTTTTATATCT
 || |||||
 CCT ACAAAAATATAGA
 CA_
 GAM2637 RoXaN 3' AGATCACAAGACCAGTTCCTC 24599 AAT TAT
 GAGGAACT GTTT ATCT
 ||||| ||| |||
 CTCCTTGA CAGAA TAGA
 C__ CAC
 GAM2638 FOXO1A 3' AGACACAAGAACAATCTTTGCT 7756 CT A_ C
 A TGGCAAAGA TTG CTTG GTCT
 ||||| ||| ||| |||
 ATCGTTTCT AAC GAAC CAGA
 _ AA A
 GAM2638 RS1 3' AGACACAGGGTAGTCTTTGCTA 5873 TTGA C
 TGGCAAAGACT CTTG GTCT
 ||||| ||| |||
 ATCGTTTCTGA GGAC CAGA
 TG_ A
 GAM2638 CDH26 5' AGACGCAATTTGGCCTTGCCA 22370 A ACT TG C
 TGGCAA G T A TTGCGTCT
 ||||| | | |||||
 ACCGTT C G T AACGCAGA
 _ C_ GT T
 GAM2638 ZER6 3' TGCCAGAAATCTTTGCCA 31747 C GACTT
 TGGCAAAGA TTT GCG
 ||||| ||| |||
 ACCGTTTCT AAG CGT
 A AC_
 GAM2638 LOC196527 3' ACACACCAAAGTCTCTGCCA 42397 A ACT C
 TGGCA AGACTTTG TG GT
 ||||| ||||| || ||
 ACCGT TCTGAAAC AC CA
 C C_ A
 GAM2638 LOC220954 3' ACACATTATTAGGCCTTTGCCA 44736 A TGACT C
 TGGCAAAG CTT TG GT
 ||||| ||| || ||

			ACCGTTTC GGA AC CA		
			C TTATT A		
GAM2639	ADAM11	3'	CTGGACCATCGCTGCCTGCCA 22241	T	A
			TGGCA GCAGCGATGGTT CGG		
			ACCGT CGTCGCTACCAG GTC		
			C _		
GAM2639	BACH1	3'	CACCGTGGGTCACCAATGCCA 6857	GCAGC	GG
			TGGCAT GAT TTACGGTG		
			ACCGTA CTG GGTGCCAC		
			ACCA_ _		
GAM2639	CRAT	5'	CACCACAGCCATCGCCACTGCC 10151	_ CA	AC
	A		TGGCA TG GCGATGGTT GGTG		
			ACCGT AC CGCTACCGA CCAC		
			C _ CA		
GAM2639	KCND2	5'	CACCGTAACCACTGCACATCA 14607	CA	CGA
			TGG TGCAG TGGTTACGGTG		
			ACT ACGTC ACCAATGCCAC		
			AC _		
GAM2639	TGFBR2	3'	CACCGTAGGGCATGCTGATACC 9237	C G G G _	
	A		TGG AT CAGC ATG T TACGGTG		
			ACC TA GTCG TAC G ATGCCAC		
			A _ _ G G		
GAM2639	KIAA0628	3'	CACCTGTGTAACCACCGCC 16674	ATGCAGCGA	_
	A		TGGC TGGTTAC GGTG		
			ACCG ACCAATG CCAC		
			CCACC_ TGT		
GAM2639	KIAA0960	3'	CACTTCCTCATCACTGCAGCCA 44516	A C	TTAC
			TGGC TGCAG GATGG GGTG		
			ACCG ACGTC CTACT TCAC		
			_ A CCT_		
GAM2639	LOC150776	3'	ACCGCAGACCGCAAGCCA 31672	A	AGCGAT A_
			TGGC TGC GGTT CGGT		
			ACCG ACG CCAG GCCA		
			A _ AC		
GAM2640	BCL11B	3'	GGCCGGTTTCCGCACTGCCACA 23168	CA	TCCAA A
			TGTGGCAG CGG GG CC		
			ACACCGTC GCC CC GG		
			AC TTTGG _		
GAM2640	DRG2	3'	CCTTGGGTGCCCCACA 7075	CA	GGT
			TGTGG GCAC CCAAGG		

		ACACC CGTG GGTTC	
		C_ _	
GAM2640 LFG	3'	GGACCCAGGCCAGCTGCCACA 37694	AC CAA A
		TGTGGCAGC GGTC GG CC	
		ACACCGTCG CCGG CC GG	
		A_ AC_ A	
GAM2640 NEO1	3'	GTCCTTGGTGTCTCCACA 8318	C C GT
		TGTGG AG ACG CCAAGGAC	
		ACACC TC TGT GGTTCCTG	
		_ T _	
GAM2640 RAP1GA1	3'	GGACCCTCCAGTTCTGCCACA 8799	C _
		TGTGGCAG AC GGTCC	
		ACACCGTC TG CCAGG	
		T ACCTC	
GAM2640 SLC19A1	5'	GGGTCCTTCCAACACCGCTACA 9024	AGCAC_ TCC
		TGTGGC GG AAGGACCC	
		ACATCG CC TTCCTGGG	
		CCACAA _	
GAM2640 SOX15	5'	GGTCTGGCCCGCCTGCCACA 13827	CA T AG
		TGTGGCAG CGG CCA GACC	
		ACACCGTC GCC GGT CTGG	
		C_ C _	
GAM2640 TNFRSF8	3'	GGACCCTCCTGGTGCTGCCCA 6910	T _
		TG GGCAGCAC GGTCC	
		AC CCGTCGTG CCAGG	
		_ GTCCTC	
GAM2640 UBE2V1	3'	GGTCCTCAGCCCTGCCAC 9373	CAC CCA
		GTGGCAG GGT AGGACC	
		CACCGTC CCG TCCTGG	
		_ AC_	
GAM2640 UBE2V1	3'	GGTCCTCAGCCCTGCCAC 22772	CAC CCA
		GTGGCAG GGT AGGACC	
		CACCGTC CCG TCCTGG	
		_ AC_	
GAM2640 UBE2V1	3'	GGTCCTCAGCCCTGCCAC 22525	CAC CCA
		GTGGCAG GGT AGGACC	
		CACCGTC CCG TCCTGG	
		_ AC_	
GAM2640 ARTN	5'	GGACCCCGTGCTGCCTCA 27661	T _
		TG GGCAGCAC GGTCC	

AC CCGTCGTG CCAGG
 T CC
 GAM2640 C20orf18 3' GGATCCGCTGCACCGTCTGCCA 25276 C C A_ _
 CA TGTGGCAG ACGGT CA GGA CC
 ||||| ||||| || ||| ||
 ACACCGTC TGCCA GT CCT GG
 _ C CG A
 GAM2640 CDT1 5' GGGCCCCCGCATCGCGCCGC 38067 T A A CCAA_ A
 CCA TG GGC GC CGGT GG CCC
 || ||| || |||| || |||
 AC CCG CG GCTA CC GGG
 _ C C CGCCCC C
 GAM2640 CECR7 5' TCATGAGACCGTGCTGCACA 38880 G _ A
 TGTG CAGCACGGTC CA GG
 ||| ||||| || ||
 ACAC GTCGTGCCAG GT CT
 _ A A
 GAM2640 CHST8 5' GTCCCCGCTGCTGCCAC 22818 _ TCCAA
 GTGGCAGCA CGG GGAC
 ||||| || ||||
 CACCGTCGT GCC CCTG
 C _
 GAM2640 DKFZP434H132 5' GTCCTTGACCCAGCTGGCCCA 36450 T _ AC
 TG GGC AGC GGTCCAAGGAC
 || ||| || ||||| |||||
 AC CCG TCG CCAGGTTCTG
 _ G AC
 GAM2640 DLL1 3' GGTCTCGACGCCTGCCGACA 12134 _ CACG CA
 TGT GGCAG GTC AGGACC
 ||| |||| || |||||
 ACA CCGTC CAG TCCTGG
 G CG_ C_
 GAM2640 FLJ10242 3' GGTCTTAAAGCATTTGCTGCC 19776 CG_ CC_
 A TGGCAGCA GT AAGGACC
 ||||| || |||||
 ACCGTCGT CG TTCCTGG
 TTA AAA
 GAM2640 FLJ12076 5' GGGTCCCTTCTGCGCTGCCGCA 24826 A TCCAA
 TGTGGCAGC CGG GGACCC
 ||||| || |||||
 ACGCCGTCG GTC CCTGGG
 C TTC_
 GAM2640 MYT1 3' GGCCCCGACCCATCACTGCCA 10877 CAC_ CAA A
 CA TGTGGCAG GGTC GG CC
 ||||| ||| || ||
 ACACCGTC CCAG CC GG
 ACTAC CCC _
 GAM2640 TAO1 3' GGCCCTCAGACCTGCCACA 11191 GCAC CA A
 TGTGGCA GGTC AGG CC
 ||||| ||| ||| ||

ACACCGT CCAG TCC GG
 _____ AC C
 GAM2640 ZNF282 3' CCTGCTGTGCTCCACA 42992 C CCA
 TGTGG AGCACGGT AGG
 ||||| ||||| ||
 ACACC TCGTGTCTG TCC

 GAM2640 LOC112868 3' GGGCCCTGGTGCTGCCAC 36083 _____
 GTGGCAGCAC GGTCC
 ||||| |||||
 CACCGTCGTG CCGGG
 GTC
 GAM2640 LOC126661 5' CCTGCCGCTCCCCTGCCACA 36850 CA_____ CCA
 TGTGGCAG CGGT AGG
 ||||| ||||| ||
 ACACCGTC GCCG TCC
 CCCTC _____
 GAM2640 LOC130470 5' GGTCTTGTGCGGGCACCACA 36990 CA A GTC
 TGTGG GC CG CAAGGACC
 ||||| ||||| |||||
 ACACC CG GC GTTCCTGG
 A_ G _____
 GAM2640 LOC150095 5' GGGTCCTTGCGCGCGTCCACA 41130 CAGC _
 TGTGG ACGGT CCAAGGACCC
 ||||| ||||| |||||
 ACACC TGCCG GGTTCTGGG
 _____ C
 GAM2640 LOC158267 3' GGTCTTGTGATAGGCACCACA 39794 CA ACG _
 TGTGG GC GTC CAAGGACC
 ||||| ||||| |||||
 ACACC CG TAG GTTCCTGG
 A_ GA_ T
 GAM2640 LOC163682 3' GGTCTTGGGTCTGCCACA 42097 GCAC GT A
 TGTGGCA G CCA GGACC
 ||||| | |||||
 ACACCGT C GGT CCTGG
 _____ TG _
 GAM2640 LOC204804 3' GGGTCCTTGTCTGCTGCCCA 43100 T CG TC
 TG GGCAGCA G CAAGGACCC
 ||||| ||||| |||||
 AC CCGTCGT C GTTCCTGGG
 _____ TT
 GAM2640 LOC256933 5' GGGCCCTCCCCTGCTGCCAC 46226 C TCCA A
 GTGGCAGCA GG AGG CCC
 ||||| ||||| |||||
 CACCGTCGT CC TCC GGG
 C C_____ C
 GAM2641 AXIN1 3' ACCCCACCATGCCAC 30512 T AC
 GTG GCATGGTGG GGT
 ||||| ||||| |||||

CAC CGTACCACC CCA

GAM2641	AXIN1	3'	CTGCACCACCACCGACAC	30516	GCA	AC	A
			GTGT TGGTGG GGT CAG				
			CACA GCCACC CCA GTC				
			___ A_ C				
GAM2641	FGF5	3'	GTCTGTGCACACATGCACAC	27002	GTG	T	
			GTGTGCATG GACGG AC				
			CACACGTAC CTGTC TG				
			ACA _				
GAM2641	FGF5	3'	GTCTGTGCACACATGCACAC	10775	GTG	T	
			GTGTGCATG GACGG AC				
			CACACGTAC CTGTC TG				
			ACA _				
GAM2641	GSPT1	5'	TCTCTGTCCACCACACAC	7884	CA	TAC	
			GTGTG TGGTGGACGG AGA				
			CACAC ACCACCTGTC TCT				

GAM2641	MIR16	3'	GTGTTGCCACCATGCAC	18746	A	GG	
			GTGCATGGTGG C TAC				
			CACGTACCACC G GTG				
			_ TT				
GAM2641	TRPS1	3'	CTGTACATACACATGCACAC	15353	G	GACG	
			GTGTGCATG TG GTACAG				
			CACACGTAC AC CATGTC				
			_ ATA_				
GAM2641	WHSC1	3'	TCTGCACCTAAACCCATAC	17187	CAT	GGAC	A
			GTGTG GGT GGT CAGA				
			CATAC CCA CCA GTCT				
			___ AAT_ C				
GAM2641	WHSC1	3'	TCTGCACCTAAACCCATAC	28451	CAT	GGAC	A
			GTGTG GGT GGT CAGA				
			CATAC CCA CCA GTCT				
			___ AAT_ C				
GAM2641	WHSC1	3'	TCTGCACCTAAACCCATAC	28468	CAT	GGAC	A
			GTGTG GGT GGT CAGA				
			CATAC CCA CCA GTCT				
			___ AAT_ C				
GAM2641	ARHU	3'	ACCCATGCACACTCATGCACAC	22180	_	GA	_
			GTGTGCATG GTG C GGT				

		CACACGTAC CAC G CCA	
		T AC TAC	
GAM2641	CARD9	3' ACCACCCCCATGCACAC 22747	T AC
		GTGTGCATGG GG GGT	
		CACACGTACC CC CCA	
		_ CA	
GAM2641	CTNNBIP1	3' GTCCTCCACCATGCAC 21545	C T
		GTGCATGGTGGG GG AC	
		CACGTACCACCT CC TG	
		- -	
GAM2641	FLJ12960	3' TACACCCACATGCACAC 23918	G ACG
		GTGTGCATG TGG GTA	
		CACACGTAC ACC CAT	
		_ CA_	
GAM2641	FLJ13441	3' GTCTGCACCACATACATGGACA 23396	G _ GAC A
	C	GTGT CATG GTG GGT CAGAC	
		CACA GTAC TAC CCA GTCTG	
		G A A_ C	
GAM2641	FLJ20452	3' CTGTCCACACATGCACAC 19489	-
		GTGTGCATG GTGGACGG	
		CACACGTAC CACCTGTC	
		A	
GAM2641	KIAA0329	3' ACCCACGCACATGCACAC 16875	_ GAC
		GTGTGCATG GTG GGT	
		CACACGTAC CGC CCA	
		A AC_	
GAM2641	KIAA1126	3' CTGATTTCCTCCATGCACAC 35608	T C A
		GTGTGCATGG GGA GGT CAG	
		CACACGTACC CCT TTA GTC	
		T _ -	
GAM2641	KIAA1550	3' ACCTATGCTCATGCACAT 33065	_ GAC
		GTGTGCATG GTG GGT	
		TACACGTAC CGT CCA	
		T AT_	
GAM2641	KIAA1918	3' GTCCACACCACTCACCACACAT 36216	CA AC ACA
	AC	GTGTG TGGTGG GGT GAC	
		CATAC ACCACT CCA CTG	
		AC CA CAC	
GAM2641	KIAA1970	3' GTCTTCCCTCCATGCACAC 36754	T AC T
		GTGTGCATGG GG GG AC	

			CACACGTACC CC TC TG		
			T CT _		
GAM2641	RNPS1	3'	GTCCGTGCACCGATGCACAC 27903	_	G T
			GTGTGCAT GGTG ACGG AC		
			CACACGTA CCAC TGCC TG		
			G G _		
GAM2641	RNPS1	3'	GTCCGTGCACCGATGCACAC 13538	_	G T
			GTGTGCAT GGTG ACGG AC		
			CACACGTA CCAC TGCC TG		
			G G _		
GAM2641	LOC124976	3'	ACCTCCCATCCATGCACAC 36779	_	AC
			GTGTGCATGG TGG GGT		
			CACACGTACC ACC CCA		
			T CT		
GAM2641	LOC147054	5'	CTGTAGGACACACACACACAC 40791	CA _	GACGG
			GTGTG TG GTG TACAG		
			CACAC AC CAC ATGTC		
			AC A AGG__		
GAM2641	LOC147817	3'	CTGTGTATCCACCATGCAGAC 38386	G	CGG
			GT TGCATGGTGG TACAG		
			CA ACGTACCACCT GTGTC		
			G AT_		
GAM2641	LOC149345	5'	GCCCCACCATGCCAC 38714	T	AC
			GTG GCATGGTGG GGT		
			CAC CGTACCACC CCG		
			_ C_		
GAM2641	LOC153346	3'	CTGTGCACACATACACAC 41617	C _	G
			GTGTG ATG GTG ACGG		
			CACAC TAC CAC TGTC		
			A A G		
GAM2641	LOC220018	5'	GCCTGAGGCCACCATGCCAC 44855	T	AC__
			GTG GCATGGTGG GGT		
			CAC CGTACCACC CCG		
			_ GGAGT		
GAM2642	CYLN2	3'	GTGTGGCCGCCCCGGGTG 9425	TAA	
			CACCCG CGGCCACAC		
			GTGGGC GCCGGTGTG		
			CC_		
GAM2642	TRPM2	5'	GAGGTTGTTACCATATG 9312	C	CCAC
			CGTAA GG ACGACCTC		

			GTATT CC TGTTGGAG		
			A AT__		
GAM2642	UNC5C	3'	GTCTGTGGCCGTCCAGGTG 9820	CGTA	C
			CACC ACGGCCACA GAC		
			GTGG TGCCGGTGT CTG		
			ACC_ _		
GAM2642	ABTB1	5'	AGGTCGTTCGGCTCGGGT 26272	TAAC	AC
			ACCCG GGCC ACGACCT		
			TGGGC TCGG TGCTGGA		
			_____ CT		
GAM2642	ARFD1	3'	AGGTCATGCTGTTACAGGTG 7371	C	CACAC
			CACC GTAACGGC GACCT		
			GTGG CATTGTCG CTGGA		
			A TA__		
GAM2642	C20orf59	3'	GTGTGGCCGTCAGGGTG 22625	GTA	
			CACCC ACGGCCACAC		
			GTGGG TGCCGGTGTG		
			AC_		
GAM2642	DKFZp566H0824	5'	AGGTCGTGCAGCCAGTGGC 18974	A _	CA
			GT AC GGC CACGACCT		
			CG TG CCG GTGCTGGA		
			G A AC		
GAM2642	KIAA0173	5'	GAGACCGTGTGGCCATGATGTG 16040	_ AAC	AC
	G		CC CGT GGCCACACG CTC		
			GG GTA CCGGTGTGC GAG		
			T GTA CA		
GAM2642	MNAB	5'	AGGTCGTGTAAGAGCCATGCG 20821	AC C__	
			CGTA GGC ACACGACCT		
			GCGT CCG TGTGCTGGA		
			A_ AGAA		
GAM2642	LOC125268	3'	CGTGGGAGCCGTGCGGGTG 37451	A CA_	
			CACCCGTA CGGC CACG		
			GTGGGCGT GCCG GTGC		
			_ AGG		
GAM2642	LOC256158	5'	GAGATCGTGTGGCTGAAGG 46626	GTAA	C
			CC CGGCCACACGA CTC		
			GG GTCGGTGTGCT GAG		
			AA__ A		
GAM2643	ACATN	3'	TTTGCCTTGTCAATGTATTTA 11109	C T	CAA
			TAAATGCA TG ACAG GCAAA		

			ATTTATGT AC TGTT CGTTT		
			A _ C__		
GAM2643	CCND1	3'	TTTGCTTGCTCATATGCAT 27603	C AC	
			ATGCA TGT AGCAAGCAAA		
			TACGT ATA TCGTTCGTTT		
			_ C_		
GAM2643	CD4	3'	TTTGCTTACTTTGCATTTG 6219	CT C	
			TAAATGCA GTA AGCAAG		
			GTTTACGT CAT TCGTTT		
			TT _		
GAM2643	DDEF2	3'	TTTGACAGTGCACTTA 9970	A ACA	
			TAA TGCACGTGT GCAAG		
			ATT ACGTGACA CGTTT		
			C _		
GAM2643	GPR87	5'	TTTGCTTACAGTGCAATCA 23388	A C	
			A ATGCACTGTA AGCAAG		
			A TACGTGACAT TCGTTT		
			C _		
GAM2643	KPNA1	3'	TTTGCTTGCCTTGCGCA 39151	ACT CA	
			TGC GTA GCAAGCAAA		
			ACG CGT CGTTCGTTT		
			_ TC		
GAM2643	NFATC1	3'	TGCTGCCTTACACAGTGCAATTT 12817	ACA__ A	
			AAATGCACTGT GCA GCA		
			TTTACGTGACA CGT CGT		
			CATTC _		
GAM2643	RPP30	3'	TGCAAATACATGCATTTA 13123	C CA_	
			TAAATGCA TGTA GCA		
			ATTTACGT ACAT CGT		
			_ AAA		
GAM2643	SACS	3'	TGTTGTACTCAGTGCAATTTA 45497	_	
			TAAATGCACT GTACAGCA		
			ATTTACGTGA CATGTTGT		
			CT		
GAM2643	ARHU	3'	CTTAATGCACAGTGCATT 22182	A GC	
			AATGCACTGT CA AAG		
			TTACGTGACA GT TTC		
			C AA		
GAM2643	BIRC1	3'	TTGCTTGTGGTAACCATTTA 10888	CACTG A	
			TAAATG TAC GCAAGCAA		

ATTTAC ATG TGTTCGTT
 CA__ G
 GAM2643 CECR1 3' TTTGCTTACAACGCAGTGCGTT 18887 ACAGC
 TA TAAATGCACTGT AAGCAAA
 ||||| |||||
 ATTTGCGTGACG TTCGTTT
 CAACA
 GAM2643 FLJ14437 3' TTGCACAGTGCACTTA 26312 A ACA
 TAA TGCAGTGT GCAA
 ||| ||||| |||
 ATT ACGTGACA CGTT
 C _
 GAM2643 KIAA1940 3' TTTGCTTGCTGGGAGGC 39011 A GTA
 GC CT CAGCAAGCAAA
 || || |||||
 CG GA GTCGTTCGTTT
 _ GG_
 GAM2643 ODZ2 3' GCAAATACAGGTGCATTTA 35096 _ CA_
 TAAATGCAC TGTA GC
 ||||| ||| ||
 ATTTACGTG ACAT CG
 G AAA
 GAM2643 PPIL2 3' TTGCCTGCTGCCTGCATCC 15651 A CTGTA A
 A ATGCA CAGCA GCAA
 | |||| |||| ||||
 C TACGT GTCGT CGTT
 C CC__ C
 GAM2643 LOC121441 3' TTTGCCTACATGGTGTATTTA 36660 ACA_
 TAAATGCACTGT GCAAG
 ||||| |||||
 ATTTATGTGGTA CGTTT
 CATC
 GAM2643 LOC145945 5' CTTGCTGTGAGACCATT 40631 CA G
 AAATG CT TACAGCAAG
 |||| || |||||
 TTTAC GA GTGTCGTTT
 CA _
 GAM2643 LOC222008 3' TTGCTTGTGAACAATGCTTTTA 45128 T C ACA
 TAAA GCA TGT GCAAGCAA
 |||| ||| |||||
 ATTT CGT ACA TGTTCGTT
 T A AG_
 GAM2644 AK3 5' AAGTTCCCGGGGCTTCCTCC 15072 A _
 GGAGGAAG CTCGG AACTT
 ||||| ||||| |||||
 CCTCCTTC GGGCC TTGAA
 G C
 GAM2644 ALEX3 5' AGTCCCACAGCCTTCCTCC 18712 A C_ A
 GGAGGAAG CT GG ACT
 ||||| || |||

			CCTCCTTC GA CC TGA	
			C CA C	
GAM2644 EHD2	3'	GAATAAAGCCAAGGCTTCTTCC	15965	A C AA C
		GGAGGAAG CT GG CTT ATTC		
		CCTTCTTC GA CC GAA TAAG		
		G A _ A		
GAM2644 LILRB4	3'	AATGAAGCCTTCTTCC	13715	ACTCGGAA
		GGAGGAAG CTTCATT		
		CCTTCTTC GAAGTAA		
		C _		
GAM2644 NXF2	5'	GGTTCCAAGTCTTCTTCC	22589	C
		GGAGGAAGACT GGAAGT		
		CCTTCTTCTGA CCTTGG		
		A		
GAM2644 TP53BP2	5'	GAACGAAGTTCGCTTCTTCCTT	11894	CT G A
	C	GGAGGAAGA CG AACTTC TTC		
		CTTCCTTCT GC TTGAAG AAG		
		TC _ C		
GAM2644 CYYR1	3'	AATGAAGTTCAGATTCCCTTC	27511	AA C G
		GGAGG GA TC GAACTTCATT		
		CTTCC CT AG CTTGAAGTAA		
		_ T A		
GAM2644 FLJ20507	3'	GAAGGTCATCCAAGTTTCCTCC	30221	A C A _
		GGAGGA GACT GGA CTTC		
		CCTCCT TTGA CCT GAAG		
		_ A ACTG		
GAM2644 FLJ20507	3'	GAAGGTCATCCAAGTTTCCTCC	19513	A C A _
		GGAGGA GACT GGA CTTC		
		CCTCCT TTGA CCT GAAG		
		_ A ACTG		
GAM2644 HT010	5'	GAGGCCCGGTCTTCCTCC	20539	T AA
		GGAGGAAGAC CGG CTTC		
		CCTCCTTCTG GCC GGAG		
		_ CC		
GAM2644 KIAA0247	3'	AATGAAAAGCCTTCCTTC	16370	A CGGAAC
		GGAGGAAG CT TTCATT		
		CTTCCTTC GA AAGTAA		
		C A _		
GAM2644 KIAA0453	3'	AATGAAGCTAATCTTCTTCC	34227	CTC AA
		GGAGGAAGA GG CTTCATT		

		CCTTCTTCT TC GAAGTAA	
		AA_ _	
GAM2644 KIAA0574	3'	GTGCCCAGAGCCTTCCTCC 34345	A _ A_
		GGAGGAAG CTC GG AC	
		CCTCCTTC GAG CC TG	
		C A CG	
GAM2644 KIAA0711	3'	GAATGAGCTTGAGCCTTCCTCC 16958	A AAC
		GGAGGAAG CTCGG TTCATTC	
		CCTCCTTC GAGTT GAGTAAG	
		C C_	
GAM2644 KIAA1786	3'	AATGACTGATCCTTCCTCC 32843	AC AACT
		GGAGGAAG TCGG TCATT	
		CCTCCTTC AGTC AGTAA	
		CT _	
GAM2644 PABPC5	3'	AATAAAGTGATTTCCTCC 28095	G TCGGA C
		GGAGGAA AC ACTT ATT	
		CCTCCTT TG TGAA TAA	
		A _ A	
GAM2644 PRDM10	5'	AATGAAGCCAGCTCTTCCTC 21494	_ C AA
		GAGGAAGA CT GG CTTCATT	
		CTCCTTCT GA CC GAAGTAA	
		C _ _	
GAM2644 PRO1617	5'	AATGCTGTCAAGTTTCCTCC 20663	CG A TT
		GGAGGAAGACT GA C CATT	
		CCTCCTTTTGA CT G GTAA	
		A_ _ TC	
GAM2644 PTPRU	3'	GAATGAAGTCACCTCGCCCCC 28400	AAGACTC A_
TCT		GGAGG GG ACTTCATTC	
		TCTCC CC TGAAGTAAG	
		CCCCGCT AC	
GAM2644 PTPRU	3'	GAATGAAGTCACCTCGCCCCC 28405	AAGACTC A_
TCT		GGAGG GG ACTTCATTC	
		TCTCC CC TGAAGTAAG	
		CCCCGCT AC	
GAM2644 PTPRU	3'	GAATGAAGTCACCTCGCCCCC 12255	AAGACTC A_
TCT		GGAGG GG ACTTCATTC	
		TCTCC CC TGAAGTAAG	
		CCCCGCT AC	
GAM2644 RAP140	3'	AATGAAGTCATCCCTTCTCC 17551	AG ACTC _
		GG GAAG GGA ACTTCATT	

		CC CTTC CCT TGAAGTAA		
		CT ____ AC		
GAM2644	RNF38	3' GAATGAGAAAAGCCTTCTTCC 23062	A	CGGAAC
		GGAGGAAG CT TTCATTC		
		CCTTCTTC GA GAGTAAG		
		C AAA__		
GAM2644	LOC144347	3' GATGCCCCTCTGAGCCTTCCTC 37723	A	ACTT
	C	GGAGGAAG CTCGGA CATT		
		CCTCCTTC GAGTCT GTAG		
		C CCCC		
GAM2644	LOC148581	5' GAAGTGCCCAAGTCTTCCTTC 38567	C	A_
		GGAGGAAGACT GG ACTTC		
		CTTCCTTCTGA CC TGAAG		
		A CG		
GAM2644	LOC197259	3' AATGAAGTCTCTTTCCCC 42470	A	ACTC GA
		GG GGAAG G ACTTCATT		
		CC CCTTT C TGAAGTAA		
		- ____ TC		
GAM2644	LOC93268	5' AGGAATCAAGTCTTCCCC 35586	A	C AA
		GG GGAAGACT GG CTT		
		CC CCTTCTGA CT GGA		
		- A AA		
GAM2645	SCA7	5' CTATGTGACTGTCCCTATCTTA 5885	A_	TTC
		TAAGGTAG GCAG TCACATAG		
		ATTCTATC TGTC AGTGTATC		
		CC ____		
GAM2645	KIAA1028	3' ATGTCAGTCTACCTTA 44156	GCAGTT	C
		TAAGGTAGA CT ACAT		
		ATTCCATCT GA TGTA		
		____ C		
GAM2645	LOC148254	3' CTATGTGAGAACAAATACCTT 38500	GAGCA	
		AAGGTA GTTCTCACATAG		
		TTCCAT CAAGAGTGTATC		
		AAA__		
GAM2645	LOC256306	3' ATGTACTCACACTGCTCTTCCT 46234	T	TCTC__
		AGG AGAGCAGT ACAT		
		TCC TCTCGTCA TGTA		
		T CACTCA		
GAM2646	ASTN	3' AGTGGCCTGAACACACACCTTC 34362	GCAAGAAAA	
	A	TGAGGGTGTG CCACT		

			ACTTCCACAC	GGTGA	
			ACAAGTCC_		
GAM2646	GALGT	5'	GGGTCCCCACACCCTCA	7213	CAAGAAA A
			TGAGGGTGTGG	ACC C	
			ACTCCCACACC	TGG G	
			CCC_____		
GAM2646	KIAA0442	3'	AGTGACTTCACACACACCTCA	17841	_ GC AAAAC
			TGAGG GTGTG AAG	CACT	
			ACTCC CACAC TTC	GTGA	
			A AC A_____		
GAM2646	LZTR1	3'	GTGGCTCCTGCCACACCC	13639	A AAA
			GGGTGTGGCA GA	CCAC	
			CCCACACCGT CT	GGTG	
			C C_____		
GAM2646	NOS1	3'	GTGGTTTCCTCGGCCCTC	6232	_T CAAGA
			GAGGGT G GG	AAACCAC	
			CTCCCG C CC	TTTGGTG	
			G T _____		
GAM2646	PCDH11X	3'	TTTCTTACACTAACCGTCA	26797	G _ GC
			TGA GGT GTG AAGAAA		
			ACT CCA CAC TTCTTT		
			G AT A_		
GAM2646	PCDH11X	3'	TTTCTTACACTAACCGTCA	26812	G _ GC
			TGA GGT GTG AAGAAA		
			ACT CCA CAC TTCTTT		
			G AT A_		
GAM2646	PCDH11Y	3'	TTTCTTACACTAACCGTCA	26831	G _ GC
			TGA GGT GTG AAGAAA		
			ACT CCA CAC TTCTTT		
			G AT A_		
GAM2646	SMAC	5'	AGTGATCCTCCCGCCTTGCCCT	29048	T AA AAAC
			AGGGTG GGC GA	CACT	
			TCCCGT CCG CT	GTGA	
			T CC CCTA		
GAM2646	UVRAG	3'	GTGGTCTCCTTACATCT	9395	CA AAA
			GGGTGTGG AGA	CCAC	
			TCTACATT TCT	GGTG	
			CC _____		
GAM2646	ADAM9	3'	TGGTTTTCTTAAATACCTACA	9907	A GGC
			TG GGGTGT AAGAAAACCA		

AC TCCATA TTCTTTTGGT
 A AA_
 GAM2646 AP3M1 3' AGCAGTTTTCTTACCTTTGCCT 14396 T_ C CA
 GGGTG GG AAGAAAAC CT
 ||||| || ||||| ||
 TCCGT CC TTCTTTTG GA
 TT A AC
 GAM2646 AQP10 3' GGGTTTTCTGACCCTCA 27841 GTGG A A
 TGAGGGT CA GAAAACC C
 ||||| || ||||| |
 ACTCCA GT CTTTGG G
 C
 GAM2646 CDT1 5' TGGCCTGCCGCACCCCA 38070 A A AAAA
 TG GGGTGTGGCA G CCA
 || ||||| | |||
 AC CCCACGCCGT C GGT
 C _ C_
 GAM2646 CHSY1 3' AGTGGTTTTCTTACATAGGACT 17172 GG_ GC
 C GAG TGTG AAGAAAACCACT
 ||| ||| |||||
 CTC ATAC TTCTTTTGGTGA
 AGG A_
 GAM2646 DKFZp434E2220 3' TGGTTTTCTGTTTGTCCCTC 19113 TGT A
 GAGGG GGCA GAAAACCA
 ||||| ||| |||||
 CTCCC TTGT CTTTGGT
 TGT C
 GAM2646 DKFZP434L1435 5' AGTGACCCTTCTCCACCCCC 44265 T CA AAC_
 GGG GTGG AGAA CACT
 ||| ||| ||| |||
 CCC CACC TCTT GTGA
 C _ CCA
 GAM2646 DKFZP434L1435 5' AGTGACCCTTCTCCACCCCC 46701 T CA AAC_
 GGG GTGG AGAA CACT
 ||| ||| ||| |||
 CCC CACC TCTT GTGA
 C _ CCA
 GAM2646 DKFZP434L1435 5' AGTGACCCTTCTCCACCCCC 46663 T CA AAC_
 GGG GTGG AGAA CACT
 ||| ||| ||| |||
 CCC CACC TCTT GTGA
 C _ CCA
 GAM2646 DRIL2 3' GTTTTCTGCCACACCCCA 13190 A A
 TG GGGTGTGGCA GAAAAC
 || ||||| |||||
 AC CCCACACCGT CTTTGG
 C _
 GAM2646 FLJ13195 3' AGTGGCTCTTAAAAACACCCTC 23204 GGC_ AAA
 A TGAGGGTGT AAGA CCACT
 ||||| ||| |||||

ACTCCCACA TTCT GGTGA
 AAAA C__
 GAM2646 FLJ14547 3' GTGGTTTTCTTGCTCCC 26560 TGT
 GGG GGCAAGAAAACCAC
 ||| |||||
 CCC TCGTTCTTTTGGTG

 GAM2646 FLJ20079 3' AGTGATTCTCCTGCCTCACCT 19166 T A A C
 CA TGAGGGTG GGCA GA AA CACT
 ||||| ||| || || |||
 ACTCCCAC CCGT CT TT GTGA
 T C C A
 GAM2646 FLJ20342 3' AGCAGTCTTCTTGCTCAGCCT 19397 G T A CA
 C GAGG TG GGCAAGAA AC CT
 ||| || ||||| || ||
 CTCC AC CCGTTCTT TG GA
 G T C AC
 GAM2646 FLJ20519 3' GTGGTCTTCTTGCTTCAT 19538 T_ A
 GTG GGCAAGAA ACCAC
 ||| ||||| |||||
 TAC CCGTTCTT TGGTG
 TT C
 GAM2646 FLJ22169 3' TGGGCTTGCCACAGCCCCA 23526 A _ AAAA
 TG GGG TGTGGCAAG CCA
 || ||| ||||| |||
 AC CCC ACACCGTTC GGT
 _ G G__
 GAM2646 KIAA0561 3' TGGCTTTCCCACTCTGTGCCTC 32768 ____ T CAA A
 A TGAGG G GTGG GAAA CCA
 |||| | ||| |||||
 ACTCC C CACC CTTT GGT
 GTGT T _ C
 GAM2646 KIAA0779 3' TGGCTTTCTTGTCCCTTA 41502 TGTG A
 TGAGGG GCAAGAAA CCA
 ||||| ||||| |||
 ATTCCC TGTTCCTT GGT
 _ C
 GAM2646 KIAA1396 3' AGTGACCCTCCCACCTCATTCT 31544 T CAA AAAC
 CA TGAGGGTG GG GA CACT
 ||||| || || |||
 ACTCTTAC CC CT GTGA
 T ACC CCCA
 GAM2646 KIAA1553 3' AGTGATTTTCTTAATACCTT 44140 GGC C
 AGGGTGT AAGAAAA CACT
 ||||| ||||| |||||
 TTCCATA TTCTTTT GTGA
 A_ A
 GAM2646 KIAA1602 3' AGCGGCCCTCCCCACTGCCCTC 32276 _ CA AAAA A
 GAGGGT GTGG AG CC CT
 ||||| ||||| || |||

CTCCCG CACC TC GG GA
 T CC CC__ C
 GAM2646 LASP1 3' TTTTCTTACACACCCCA 12805 A GC
 TG GGGTGTG AAGAAAA
 || ||||| |||||
 AC CCCACAC TTCTTTT
 C A_
 GAM2646 MAPK8IP3 3' AGTGATCCTCTCTCAAACCACA 27217 A CA__ AAAC__
 CCCCCA G GGGTGTGG AGA CACT
 | ||||| ||| ||||
 C CCCACACC TCT GTGA
 C AAAC CTCCTA
 GAM2646 NUDT12 3' AGTGATCTCAATACCACACCCT 25446 CAAGAAAAC
 CA TGAGGGTGTGG CACT
 ||||| ||||
 ACTCCACACC GTGA
 ATA ACTCTA
 GAM2646 PMX2B 3' AGTGACTTTCTCGCACCC 10014 GCA AC
 GGGTGTG AGAAA CACT
 ||||| |||| ||||
 CCCACGC TCTTT GTGA
 __ CA
 GAM2646 PRO2389 3' AGTGGTCTCCTTACGTGCTCAC 31879 _ ____ AAA
 ACCC GGGTGTG GCA AG ACCACT
 ||||| ||| || |||||
 CCCACAC CGT TC TGGTGA
 T GCAT CTC
 GAM2646 SIMRP7 3' AGTGACTTTCTTCAATGCCACA 44369 ____ AC
 CCC GGGTGTGGCA AGAAA CACT
 ||||| |||| ||||
 CCCACACCGT TCTTT GTGA
 AACT CA
 GAM2646 TCF-3 3' TGGTTTCCTCCCAACCCCG 25307 A G CA A
 TG GGGT TGG AG AAACCA
 || |||| ||| || |||||
 GC CCCA ACC TC TTTGGT
 C _ C_ C
 GAM2646 TUBB5 3' TTCCCTGCCTCACCCTCA 12732 T A_
 TGAGGGTGT GGCA GAA
 ||||| |||| |||
 ACTCCAC CCGT CTT
 T CC
 GAM2646 ZNF31 3' AGTGGTTCTCCTACTTTCTCA 32421 T CAA A
 TGAGGG GTGG GA AACCCT
 ||||| |||| || |||||
 ACTCTT CATC CT TTGGTGA
 T __ C
 GAM2646 ZNF317 3' AGTGACTTCCCCGGTATCCACT 35634 TG_ AA__ AAC
 CTCA TGAGGGTGT GC GAA CACT
 ||||| || ||| ||||

ACTCTCAC TG CTT GTGA
 CTA GCCC CA_
 GAM2646 LOC130644 3' AGCGGTGATGAGCTCCACACCC 37302 A CAAGAAA_ A
 CCA TG GGGTGTGG ACC CT
 || ||||| ||||
 AC CCCACACC TGG GA
 C TCGAGTAG C
 GAM2646 LOC149650 3' TGGTTTTCTTCCTC 38798 TGT CAA
 GAGGG GG GAAAACCA
 |||| || |||||
 CTCCT TC CTTTTGGT

 GAM2646 LOC150776 3' AGTGGCTCTCCTGATTCTTCA 31674 TGT_ CA AAA
 TGAGGG GG AGA CCACT
 |||| || ||| ||||
 ACTTCT CC TCT GGTGA
 TAGT _ C_
 GAM2646 LOC256158 5' GGCTCTGGCCACACCCTCA 46630 A AAA
 TGAGGGTGTGGC AGA CC
 ||||| ||| ||
 ACTCCACACCG TCT GG
 G C_
 GAM2646 LOC90841 3' GTTTTCTAAGCCACCCTCA 32112 GT A_
 TGAGGGT GGC AGAAAC
 |||| ||| |||||
 ACTCCCA CCG TCTTTTG
 _ AA
 GAM2646 LOC92609 3' AGTGACCCTCCTGCCTCAGCCT 36060 G T A AAAC
 C GAGG TG GGCA GA CACT
 ||| || ||| || |||
 CTCC AC CCGT CT GTGA
 G T C CCA
 GAM2647 NRAP 3' CCATCAGCAAAGACGAGCCTC 12832 AGTTT A
 GAGGT TCTTTGCT ATGG
 |||| ||||| |||
 CTCCGA AGAAACGA TACC
 GC_ C
 GAM2647 LOC115294 3' CCATCAGCAACCTCAGACCAAC 36144 A A TCT_ A
 CC G GGTT GTTT TTGCT ATGG
 | ||| ||| |||| |||
 C CCAA CAGA AACGA TACC
 _ C CTCC C
 GAM2648 PROML1 3' ATCTGGTGTCCAGCATGGATG 12633 C C T_
 CA CCAT CT ACACCAGAT
 || ||| || |||||
 GT GGTA GA TGTGGTCTA
 A C CC
 GAM2648 FLJ13052 3' ATCTGAACACAGAAGGTGTGAA 23282 CA CTTACAC
 TTCACACC TC CAGAT
 ||||| || |||

			AAGTGTGG AG GTCTA		
			A_ ACACAA_		
GAM2648	HSPC063	5'	GTAAAAGATGGGTGTGAA 15439	C_	
			TTCACACCCATC TTAC		
			AAGTGTGGGTAG AATG		
			AA		
GAM2648	PSMD12	3'	TGAGATGAATTGGTGTGAA 8683	_____ C	
			TTCACACC CATC TTA		
			AAGTGTGG GTAG AGT		
			TTAA _		
GAM2648	LOC158055	3'	ATCTGGTGCAAAGCTCTGTGA 39702	CCCATC A_	
			TCACA CTT CACCAGAT		
			AGTGT GAA GTGGTCTA		
			CTC___ AC		
GAM2649	PRKCB1	3'	CAATTTATTTTCCGCAGCA 34902	A CT	
			TGTT CGGAAAATA TTG		
			ACGA GCCTTTTAT AAC		
			C TT		
GAM2649	SLC16A2	3'	TCATGATTTTCCGTTACA 13273	T ACTT	
			TGT ACGGAAAAT TGA		
			ACA TGCCTTTTA ACT		
			T GT__		
GAM2649	MGC4415	3'	TGTCCTGGCCTCTCCGTGACA 25573	AAATA TT	
			TGTTACGGA CT GACA		
			ACAGTGCCT GG CTGT		
			CTCC_ TC		
GAM2649	LOC126669	3'	TTGTCTCCTATTTTCCATAAC 37161	C TACTTT	
			GTTA GGAAAA GACAA		
			CAAT CCTTTT CTGTT		
			A TATCCT		
GAM2649	LOC195977	3'	CAGGGCATTTCGCAAC 42299	A A	
			GTT CGGAAAAT CTTTG		
			CAA GCCTTTTA GGGAC		
			C C		
GAM2649	LOC51026	3'	TCAAGTGTATTTTCTGTAACA 18143	_	
			TGTTACGGAAAATAC TTTGA		
			ACAATGTCTTTTATG GAACT		
			T		
GAM2649	LOC91565	3'	TGCCAAACTGTTTTCCACGACA 33025	AC C A	
			TGTT GGAAAATA TTTG CA		

ACAG CCTTTTGT AAAC GT
 CA C C
 GAM2650 MGC10960 3' TTCTGTGTAACAGGCCAC 26386 AA C
 GTG CTGTTACGCG GAA
 ||| ||||| |||
 CAC GACAATGTGT CTT
 CG _
 GAM2650 LOC220514 3' TTCAGTTTAACAGTTCCTTTAA 30324 T C GC
 TTAAAG GAACTGTTA GC GAA
 ||||| ||||| || |||
 AATTTC CTTGACAAT TG CTT
 _ T A_
 GAM2651 ADD2 3' TTGTTTAATGCTCAGGGCAG 18942 A ATGA
 CT CCCT ATTAAACAA
 || ||| |||||
 GA GGGA TAATTTGTT
 C CTCG
 GAM2651 ADD2 3' TTGTTTAATGCTCAGGGCAG 18945 A ATGA
 CT CCCT ATTAAACAA
 || ||| |||||
 GA GGGA TAATTTGTT
 C CTCG
 GAM2651 ADD2 3' TTGTTTAATGCTCAGGGCAG 18950 A ATGA
 CT CCCT ATTAAACAA
 || ||| |||||
 GA GGGA TAATTTGTT
 C CTCG
 GAM2651 ADD2 3' TTGTTTAATGCTCAGGGCAG 18937 A ATGA
 CT CCCT ATTAAACAA
 || ||| |||||
 GA GGGA TAATTTGTT
 C CTCG
 GAM2651 ATRX 3' TTTAATTGGGTGGGG 28688 TATG
 CCCTACCC AATTAAA
 ||||| |||||
 GGGGTGGG TTAATTT
 _
 GAM2651 ATRX 3' TTTAATTGGGTGGGG 6099 TATG
 CCCTACCC AATTAAA
 ||||| |||||
 GGGGTGGG TTAATTT
 _
 GAM2651 PRKAR1A 3' TTTACATTTTAGGGTGGGTA 8609 T T _
 TACCC ACCCTA GAAT TAAA
 |||| ||||| ||| |||
 ATGGG TGGGAT TTTA ATTT
 _ _ C
 GAM2651 SIAT4C 3' TTTAATTAAGGGGTAGG 12958 ATG
 CCTACCCT AATTAAA
 ||||| |||||

GGATGGGG TTAATTT
AA_
GAM2651 DKFZP434L187 5' TTGGTTCCTAGAGTAGAGTA 34128 C C T
TAC CTAC CTA GAATTAA
||| ||| ||| |||||
ATG GATG GAT CTTGGTT
A A C
GAM2651 FLJ11506 3' TTGTTCTAGGAATGAGGGTAGG 23970 ATGAA _
CCTACCCT TTA AACAA
||||| ||| |||||
GGATGGGA GAT TTGTT
GTAAG C
GAM2651 FLJ23878 3' TTGGGCCAGAAGGTAGGGTA 29593 CTA AA
TACCCTACC TG TTAA
||||| || |||||
ATGGGATGG AC GGTT
AAG CG
GAM2651 KIAA0649 3' TGTTC AATTTTGTAGGGTG 16775 CCTAT A
TACCCTAC GAATT AACAA
||||| ||||| |||||
GTGGGATG TTAA TTGT
T____ C
GAM2651 KIAA1238 3' TTAAACATAGGGTGAGTA 35217 CC AA
TAC TACCCTATG TTAA
||| ||||| ||||| |||||
ATG GTGGGATAC AATT
A_ AA
GAM2651 ZNF84 3' TAATTCATAGAGTAGAGTG 9480 C C
TAC CTAC CTATGAATTA
||| ||| ||||| |||||
GTG GATG GATACTTAAT
A A
GAM2651 LOC152328 3' TGTTTAATTCTAGATATAGGG 39244 CC_ T
CCCTA CTA GAATTAAACA
||||| ||| ||||| |||||
GGGAT GAT CTTAATTTGT
ATA _
GAM2651 LOC255533 5' TTGTTCAAATATTAGAGTTAGG 46333 _C TGAATTA
GTA TACCCTA C CTA AACAA
||||| ||| ||||| |||||
ATGGGAT G GAT TTGTT
T A TATAAAC
GAM2652 A1BG 3' TCAAGTGATTCTCGTGC 28278 CATT C
GCAT GAGAATCACT GA
||| ||||| ||||| |||||
CGTG CTCTTAGTGA CT
____ A
GAM2652 ADAMTS4 3' TTCAAGTGATTCTCATGC 11570 TCAT C
GCA TGAGAATCACT GAA
||| ||||| ||||| |||||

			CGT	ACTCTTAGTGA	CTT		
			_____	A			
GAM2652	AHR	3'	TCAAGTGATTCTCTTGC	7334	TCATT	C	
			GCA	GAGAATCACT	GA		
			CGT	CTCTTAGTGA	CT		
			T_____	A			
GAM2652	ATP6V1A1	3'	TCAAGTGATTCTCCTGC	7410	TCATT	C	
			GCA	GAGAATCACT	GA		
			CGT	CTCTTAGTGA	CT		
			C_____	A			
GAM2652	BRIP1	3'	TCAAGTGATTCTCCTGC	25756	TCATT	C	
			GCA	GAGAATCACT	GA		
			CGT	CTCTTAGTGA	CT		
			C_____	A			
GAM2652	CHRNA4	3'	TCAAGTGATTCTCCTGC	6404	TCATT	C	
			GCA	GAGAATCACT	GA		
			CGT	CTCTTAGTGA	CT		
			C_____	A			
GAM2652	COX15	3'	TTCAAGCGATTCTCATGC	27793	TCAT	A C	
			GCA	TGAGAATC	CT GAA		
			CGT	ACTCTTAG	GA CTT		
			_____	C A			
GAM2652	CYP2B6	3'	TCAAGTGATTCTCCTGC	6415	TCATT	C	
			GCA	GAGAATCACT	GA		
			CGT	CTCTTAGTGA	CT		
			C_____	A			
GAM2652	FCAR	3'	TCAAGTGATTCTTGTGC	28424	CATT	C	
			GCAT	GAGAATCACT	GA		
			CGTG	TTCTTAGTGA	CT		
			_____	A			
GAM2652	FCAR	3'	TCAAGTGATTCTTGTGC	7728	CATT	C	
			GCAT	GAGAATCACT	GA		
			CGTG	TTCTTAGTGA	CT		
			_____	A			
GAM2652	FCAR	3'	TCAAGTGATTCTTGTGC	28428	CATT	C	
			GCAT	GAGAATCACT	GA		
			CGTG	TTCTTAGTGA	CT		
			_____	A			
GAM2652	FCAR	3'	TCAAGTGATTCTTGTGC	28426	CATT	C	
			GCAT	GAGAATCACT	GA		

			CGTG	TTCTTAGTGA	CT		
			_____	A			
GAM2652	FCAR	3'	TCAAGTGATTCTTGTGC	28430	CATT	C	
			GCAT	GAGAATCACT	GA		
			CGTG	TTCTTAGTGA	CT		
			_____	A			
GAM2652	FZD4	3'	TTCAAGTGATTCTCCTGCCAC	14491	_ TCATT	C	
			GTG CA	GAGAATCACT	GAA		
			CAC GT	CTCTTAGTGA	CTT		
			C C_____	A			
GAM2652	G6PC	3'	TTCAAGCGATTCTCATGTCTCA	5659	CAT T	A C	
			TG	CAT GAGAATC	CT GAA		
			AC	GTA CTCTTAG	GA CTT		
			TCT	_	C A		
GAM2652	GPR56	5'	TTCAAGTGATTCTCATGC	12240	TCAT	C	
			GCA	TGAGAATCACT	GAA		
			CGT	ACTCTTAGTGA	CTT		
			_____	A			
GAM2652	M11S1	3'	TCGAGTTATTCAATGAT	12519	AATC		
			ATCATTGAG	ACTCGA			
			TAGTAACTT	TGAGCT			
			AT_____				
GAM2652	MAK	3'	TCAAGTGATTCTCCTGC	12530	TCATT	C	
			GCA	GAGAATCACT	GA		
			CGT	CTCTTAGTGA	CT		
			C_____	A			
GAM2652	MEF2A	5'	TCAAGTGATTCTCGTAC	12117	ATCATT	C	
			GTGC	GAGAATCACT	GA		
			CATG	CTCTTAGTGA	CT		
			_____	A			
GAM2652	MHC2TA	3'	TCAAGTGATTCTCCTGC	5781	TCATT	C	
			GCA	GAGAATCACT	GA		
			CGT	CTCTTAGTGA	CT		
			C_____	A			
GAM2652	MPL	3'	TCAAGCGATTCTTGTGC	11851	CATT	A C	
			GCAT	GAGAATC	CT GA		
			CGTG	TTCTTAG	GA CT		
			_____	C A			
GAM2652	NCOA6	5'	TCAAGTGATTCTCTTGC	15292	TCATT	C	
			GCA	GAGAATCACT	GA		

			CGT CTCTTAGTGA CT			
			T_____A			
GAM2652	PDE6B	3'	TCAAGCGATTCTCGTGC 5829	CATT	A C	
			GCAT GAGAATC CT GA			
			CGTG CTCTTAG GA CT			
			_____C A			
GAM2652	PIK3CD	3'	TCAAGTGATTCTTCTTGC 11464	TCATT	C	
			GCA GAGAATCACT GA			
			CGT TTCTTAGTGA CT			
			TC_____A			
GAM2652	POU2AF1	3'	TCAAGTGATTCTCCTGC 12893	TCATT	C	
			GCA GAGAATCACT GA			
			CGT CTCTTAGTGA CT			
			C_____A			
GAM2652	PRKR	3'	TCAAGTGATTCTCCTGC 8646	TCATT	C	
			GCA GAGAATCACT GA			
			CGT CTCTTAGTGA CT			
			C_____A			
GAM2652	RBBP9	3'	TTCAAGTGATTCTCATCTCAGC 34747	ATCAT	C	
			GC TGAGAATCACT GAA			
			CG ACTCTTAGTGA CTT			
			ACTCT A			
GAM2652	SCD	3'	TTCAAGTGACACATTAATGATA 11498	GC	GAA_ C	
	AAC		GT ATCATTGA TCACT GAA			
			CA TAGTAATT AGTGA CTT			
			AA ACAC A			
GAM2652	TBXA2R	3'	TCAAGCGATTCTCGTGC 6728	CATT	A C	
			GCAT GAGAATC CT GA			
			CGTG CTCTTAG GA CT			
			_____C A			
GAM2652	TMC1	5'	TCAAGTGATTCTCCTGC 28934	TCATT	C	
			GCA GAGAATCACT GA			
			CGT CTCTTAGTGA CT			
			C_____A			
GAM2652	TNFRSF10B	3'	TCAAGCGATTCTCGTGC 9938	CATT	A C	
			GCAT GAGAATC CT GA			
			CGTG CTCTTAG GA CT			
			_____C A			
GAM2652	TRAF5	3'	TCAAGTGATTCTCCTGC 10968	TCATT	C	
			GCA GAGAATCACT GA			

			CGT	CTCTTAGTGA	CT		
			C_____	A			
GAM2652	VHL	3'	TTCAAGTGATTCTCCTGGCTCA	6165	CA TT	C	
	C		GTG TCA GAGAATCACT	GAA			
			CAC GGT CTCTTAGTGA	CTT			
			TC C_	A			
GAM2652	ARHGAP9	5'	TCAAGTGATTCTTGTGC	26248	CATT	C	
			GCAT GAGAATCACT	GA			
			CGTG TTCTTAGTGA	CT			
			_____	A			
GAM2652	ASB16	3'	TCAAGCGATTCTTGTGC	28108	CATT	A C	
			GCAT GAGAATC	CT GA			
			CGTG TTCTTAG	GA CT			
			_____	C A			
GAM2652	BA108L7.2	3'	TCAAGTGATTCTCTTGC	25241	TCATT	C	
			GCA GAGAATCACT	GA			
			CGT CTCTTAGTGA	CT			
			T_____	A			
GAM2652	C6orf5	3'	TCAAGTGATTCTTCTGC	17782	TCATT	C	
			GCA GAGAATCACT	GA			
			CGT TTCTTAGTGA	CT			
			C_____	A			
GAM2652	CHRA1	3'	TCAAGTGATTCTCCTGC	18907	TCATT	C	
			GCA GAGAATCACT	GA			
			CGT CTCTTAGTGA	CT			
			C_____	A			
GAM2652	COLEC12	3'	TCAAGTGATTCTCCTGC	25071	TCATT	C	
			GCA GAGAATCACT	GA			
			CGT CTCTTAGTGA	CT			
			C_____	A			
GAM2652	CYLC2	3'	TCAAGTGATTCTCCTGC	7019	TCATT	C	
			GCA GAGAATCACT	GA			
			CGT CTCTTAGTGA	CT			
			C_____	A			
GAM2652	DKFZp434A2417	3'	TTCAAGTGATTCTCCTGC	32865	TCATT	C	
			GCA GAGAATCACT	GAA			
			CGT CTCTTAGTGA	CTT			
			C_____	A			
GAM2652	DKFZP434D146	3'	TCAAGTGATTCTCCTGC	17873	TCATT	C	
			GCA GAGAATCACT	GA			

		CGT CTCTTAGTGA CT			
		C_____A			
GAM2652	DKFZp547H025 3'	TCAAGTGATTCTTGTGC	21374	CATT	C
		GCAT GAGAATCACT GA			
		CGTG TTCTTAGTGA CT			
		_____A			
GAM2652	DKFZP564G092 5'	TCAAGTGATTCTCCTGC	17877	TCATT	C
		GCA GAGAATCACT GA			
		CGT CTCTTAGTGA CT			
		C_____A			
GAM2652	EVI5 3'	AGTGAAGTGAGATGATGCAT	12208	GAGAA	
		GTGCATCATT TCACT			
		TACGTAGTAG AGTGA			
		AGTGA			
GAM2652	FLJ12687 3'	TCAAGTGATTCTCGTGC	24446	CATT	C
		GCAT GAGAATCACT GA			
		CGTG CTCTTAGTGA CT			
		_____A			
GAM2652	FLJ13188 3'	TTCAAGTGATTCTCATGC	22608	TCAT	C
		GCA TGAGAATCACT GAA			
		CGT ACTCTTAGTGA CTT			
		_____A			
GAM2652	FLJ14957 3'	TCAAGTGATTCTCCTGC	26683	TCATT	C
		GCA GAGAATCACT GA			
		CGT CTCTTAGTGA CT			
		C_____A			
GAM2652	FLJ20034 3'	TCAAGTGATTCTCCTGC	19137	TCATT	C
		GCA GAGAATCACT GA			
		CGT CTCTTAGTGA CT			
		C_____A			
GAM2652	FLJ22002 3'	TCAAGTGATTCTCCTGC	24248	TCATT	C
		GCA GAGAATCACT GA			
		CGT CTCTTAGTGA CT			
		C_____A			
GAM2652	FLJ22531 5'	TTCAAGTGATTCTCATGC	23947	TCAT	C
		GCA TGAGAATCACT GAA			
		CGT ACTCTTAGTGA CTT			
		_____A			
GAM2652	FLJ22794 3'	TCAAGCGATTCTTATGC	44036	CATT	A C
		GCAT GAGAATC CT GA			

			CGTA	TTCTTAG	GA	CT		
			_____	C	A			
GAM2652	FLJ31153	3'	TCAAGT	GATTCTCCTGC	29414	TCATT		C
			GCA	GAGAATCACT	GA			
			CGT	CTCTTAGTGA	CT			
			C_____	A				
GAM2652	FLJ32865	3'	TCAAGT	GATTCTCCTGC	29431	TCATT		C
			GCA	GAGAATCACT	GA			
			CGT	CTCTTAGTGA	CT			
			C_____	A				
GAM2652	GP5	3'	TTCAAGT	GATTCTCATGC	10822	TCAT		C
			GCA	TGAGAATCACT	GAA			
			CGT	ACTCTTAGTGA	CTT			
			_____	A				
GAM2652	GTPBG3	3'	TCAAGT	GATTCTCCTGC	26334	TCATT		C
			GCA	GAGAATCACT	GA			
			CGT	CTCTTAGTGA	CT			
			C_____	A				
GAM2652	HRH4	3'	TCAAGC	GATTCTTGTGC	22262	CATT	A	C
			GCAT	GAGAATC	CT	GA		
			CGTG	TTCTTAG	GA	CT		
			_____	C	A			
GAM2652	HSMPP8	3'	TCAAGT	GATTCTCCTGC	44904	TCATT		C
			GCA	GAGAATCACT	GA			
			CGT	CTCTTAGTGA	CT			
			C_____	A				
GAM2652	KIAA0472	5'	TCAAGT	GATTCTTCTGC	35582	TCATT		C
			GCA	GAGAATCACT	GA			
			CGT	TTCTTAGTGA	CT			
			C_____	A				
GAM2652	KIAA0513	5'	TCAAGT	GATTCTCCTGC	16360	TCATT		C
			GCA	GAGAATCACT	GA			
			CGT	CTCTTAGTGA	CT			
			C_____	A				
GAM2652	KIAA0555	3'	TTCAAGT	GATTCTCCTGC	16686	TCATT		C
			GCA	GAGAATCACT	GAA			
			CGT	CTCTTAGTGA	CTT			
			C_____	A				
GAM2652	KIAA0557	3'	TCAAGT	GATTCTCCTGC	38210	TCATT		C
			GCA	GAGAATCACT	GA			

			CGT	CTCTTAGTGA	CT		
			C_____	A			
GAM2652	KIAA0836	3'	TCAAGT	GATTCTGATGCA	32248	TTGA	C
			TGCATCA	GAATCACT	GA		
			ACGTAGT	CTTAGTGA	CT		
			_____	A			
GAM2652	KIAA0924	3'	TCAAGT	GATTCTCCTGC	17066	TCATT	C
			GCA	GAGAATCACT	GA		
			CGT	CTCTTAGTGA	CT		
			C_____	A			
GAM2652	KIAA1028	3'	TCAAGT	GATTCTCCTGC	44163	TCATT	C
			GCA	GAGAATCACT	GA		
			CGT	CTCTTAGTGA	CT		
			C_____	A			
GAM2652	KIAA1373	3'	TTCAAGCG	ATTCTCATGC	35129	TCAT	A C
			GCA	TGAGAATC	CT GAA		
			CGT	ACTCTTAG	GA CTT		
			_____	C A			
GAM2652	KIAA1473	3'	TCAAGT	GATTCTCCTGC	34997	TCATT	C
			GCA	GAGAATCACT	GA		
			CGT	CTCTTAGTGA	CT		
			C_____	A			
GAM2652	KIAA1617	3'	TCAAGT	GATTCTCCTGC	43944	TCATT	C
			GCA	GAGAATCACT	GA		
			CGT	CTCTTAGTGA	CT		
			C_____	A			
GAM2652	KIAA1712	3'	TCAAGT	GATTCTTGTGC	33539	CATT	C
			GCAT	GAGAATCACT	GA		
			CGTG	TTCTTAGTGA	CT		
			_____	A			
GAM2652	KIAA1737	3'	TTCAAGT	GATTCTCCTGCCAC	33449	_ TCATT	C
			GTG CA	GAGAATCACT	GAA		
			CAC GT	CTCTTAGTGA	CTT		
			C C_____	A			
GAM2652	KIAA1826	3'	AGTGATTCT	GATACAC	33376	C TTGA	
			GTG ATCA	GAATCACT			
			CAC TAGT	CTTAGTGA			
			A _____				
GAM2652	MGC4638	3'	TCAAGT	GATTCTTCTGC	25558	TCATT	C
			GCA	GAGAATCACT	GA		

			CGT	TTCTTAGTGA	CT		
			C_____	A			
GAM2652	MRPL44	3'	TTCAAGCGATTCTCGTGGC	23228	ATCAT	A	C
			GC	TGAGAATC	CT	GAA	
			CG	GCTCTTAG	GA	CTT	
			GT_____	C	A		
GAM2652	NDP52	3'	TCAAGCGATTCTCATGC	12445	TCAT	A	C
			GCA	TGAGAATC	CT	GA	
			CGT	ACTCTTAG	GA	CT	
			_____	C	A		
GAM2652	NXN	3'	TCAAGTGATTCTCCTGC	22812	TCATT	C	
			GCA	GAGAATCACT	GA		
			CGT	CTCTTAGTGA	CT		
			C_____	A			
GAM2652	PRO0529	5'	TCAAGTGATTCTCCTGC	15300	TCATT	C	
			GCA	GAGAATCACT	GA		
			CGT	CTCTTAGTGA	CT		
			C_____	A			
GAM2652	PRO2955	3'	TCAAGTGATTCTCCTGC	20622	TCATT	C	
			GCA	GAGAATCACT	GA		
			CGT	CTCTTAGTGA	CT		
			C_____	A			
GAM2652	PSTPIP2	3'	TCAAGTGATTCTCCTGC	23683	TCATT	C	
			GCA	GAGAATCACT	GA		
			CGT	CTCTTAGTGA	CT		
			C_____	A			
GAM2652	RAB33B	3'	TCAAGTGATTCTCCTGC	25330	TCATT	C	
			GCA	GAGAATCACT	GA		
			CGT	CTCTTAGTGA	CT		
			C_____	A			
GAM2652	SCAND2	3'	TCAAGTGATTCTCCTGC	22577	TCATT	C	
			GCA	GAGAATCACT	GA		
			CGT	CTCTTAGTGA	CT		
			C_____	A			
GAM2652	SCYA22	3'	TCAAGTGATTCTCTTGC	43716	TCATT	C	
			GCA	GAGAATCACT	GA		
			CGT	CTCTTAGTGA	CT		
			T_____	A			
GAM2652	SIRPB1	3'	TCAAGTGATTCTCCTGC	12710	TCATT	C	
			GCA	GAGAATCACT	GA		

			CGT	CTCTTAGTGA	CT		
			C_____	A			
GAM2652	SLC6A14	3'	TCAAGTGATTCTCCTGC	14104	TCATT	C	
			GCA	GAGAATCACT	GA		
			CGT	CTCTTAGTGA	CT		
			C_____	A			
GAM2652	SNAP91	3'	TTCAAGTGATTCTGAAGGCAC	16871	ATCA	G	C
			GTGC	TTAGAATCACT	GAA		
			CACG	AA	TCTTAGTGA	CTT	
			G_____	G	A		
GAM2652	TCL6	5'	TCAAGTGATTCTTCTGC	15769	TCATT	C	
			GCA	GAGAATCACT	GA		
			CGT	TTCTTAGTGA	CT		
			C_____	A			
GAM2652	TCL6	5'	TCAAGTGATTCTTCTGC	21762	TCATT	C	
			GCA	GAGAATCACT	GA		
			CGT	TTCTTAGTGA	CT		
			C_____	A			
GAM2652	TCL6	5'	TCAAGTGATTCTTCTGC	14845	TCATT	C	
			GCA	GAGAATCACT	GA		
			CGT	TTCTTAGTGA	CT		
			C_____	A			
GAM2652	TCL6	5'	TCAAGTGATTCTTCTGC	21771	TCATT	C	
			GCA	GAGAATCACT	GA		
			CGT	TTCTTAGTGA	CT		
			C_____	A			
GAM2652	TERA	3'	TCAAGTGATTCTCCTGC	22205	TCATT	C	
			GCA	GAGAATCACT	GA		
			CGT	CTCTTAGTGA	CT		
			C_____	A			
GAM2652	TU12B1-TY	3'	TCAAGTGATTCTCCTGC	18650	TCATT	C	
			GCA	GAGAATCACT	GA		
			CGT	CTCTTAGTGA	CT		
			C_____	A			
GAM2652	USP3	5'	TCAAGTGATTCTTCTGC	43172	TCATT	C	
			GCA	GAGAATCACT	GA		
			CGT	TTCTTAGTGA	CT		
			C_____	A			
GAM2652	ZNF338	3'	TTCAAGCGATTCTCATGC	22634	TCAT	A	C
			GCA	TGAGAATC	CT	GAA	

		CGT	ACTCTTAG GA CTT		
		_____	C A		
GAM2652	LOC113675 5'	TCAAGTGATTCTCCTGC	28796	TCATT	C
		GCA	GAGAATCACT GA		
		CGT	CTCTTAGTGA CT		
		C_____	A		
GAM2652	LOC126364 3'	TCAAGTGATTCTCCTGC	37272	TCATT	C
		GCA	GAGAATCACT GA		
		CGT	CTCTTAGTGA CT		
		C_____	A		
GAM2652	LOC135293 3'	TCAAGTGATTCTCCTGC	37497	TCATT	C
		GCA	GAGAATCACT GA		
		CGT	CTCTTAGTGA CT		
		C_____	A		
GAM2652	LOC143241 5'	TCAAGTGATTCTCCTGC	29036	TCATT	C
		GCA	GAGAATCACT GA		
		CGT	CTCTTAGTGA CT		
		C_____	A		
GAM2652	LOC144524 5'	TTCAAGTGATTCTCCTGCGC	40435	TCATT	C
		GTGCA	GAGAATCACT GAA		
		CGCGT	CTCTTAGTGA CTT		
		C_____	A		
GAM2652	LOC144776 5'	TCAAGTGATTCTCCTGC	37788	TCATT	C
		GCA	GAGAATCACT GA		
		CGT	CTCTTAGTGA CT		
		C_____	A		
GAM2652	LOC145757 5'	TCAAGTGATTCTCCTGC	37974	TCATT	C
		GCA	GAGAATCACT GA		
		CGT	CTCTTAGTGA CT		
		C_____	A		
GAM2652	LOC146050 3'	TCAAGTGATTCTCCTGC	38056	TCATT	C
		GCA	GAGAATCACT GA		
		CGT	CTCTTAGTGA CT		
		C_____	A		
GAM2652	LOC146894 3'	TCAAGTGATTCTTCTGC	29784	TCATT	C
		GCA	GAGAATCACT GA		
		CGT	TTCTTAGTGA CT		
		C_____	A		
GAM2652	LOC147817 3'	TCAAGTGATTCTCCTGC	38388	TCATT	C
		GCA	GAGAATCACT GA		

		CGT	CTCTTAGTGA	CT		
		C_____	A			
GAM2652	LOC148189 5'	TCAAGCGATTCTTATGC	38485	CATT	A	C
		GCAT	GAGAATC	CT	GA	
		CGTA	TTCTTAG	GA	CT	
		_____	C	A		
GAM2652	LOC148198 3'	TCAAGTGATTCTCCTGC	35000	TCATT		C
		GCA	GAGAATCACT	GA		
		CGT	CTCTTAGTGA	CT		
		C_____	A			
GAM2652	LOC149171 5'	TCGAGTGATTCTCCTGC	38668	TCATT		
		GCA	GAGAATCACTCGA			
		CGT	CTCTTAGTGAGCT			
		C_____				
GAM2652	LOC149267 3'	GGGCCTTCTCAATGAGCAC	28833	A		TCA
		GTGC	TCATTGAGAA	CTC		
		CACG	AGTAACTCTT	GGG		
		_____	CC_			
GAM2652	LOC149478 3'	TCAAGCGATTCTCGTGC	38755	CATT	A	C
		GCAT	GAGAATC	CT	GA	
		CGTG	CTCTTAG	GA	CT	
		_____	C	A		
GAM2652	LOC149577 3'	TCAAGTGATTCTCCTGC	41023	TCATT		C
		GCA	GAGAATCACT	GA		
		CGT	CTCTTAGTGA	CT		
		C_____	A			
GAM2652	LOC149711 3'	TCAAGTGATTCTCCTGC	41075	TCATT		C
		GCA	GAGAATCACT	GA		
		CGT	CTCTTAGTGA	CT		
		C_____	A			
GAM2652	LOC150054 5'	TCAAGTGATTCTCCTGC	41126	TCATT		C
		GCA	GAGAATCACT	GA		
		CGT	CTCTTAGTGA	CT		
		C_____	A			
GAM2652	LOC150696 3'	TCAAGCGATTCTCATGC	29530	TCAT	A	C
		GCA	TGAGAATC	CT	GA	
		CGT	ACTCTTAG	GA	CT	
		_____	C	A		
GAM2652	LOC151057 3'	TCAAGTGATTCTCCTGC	41295	TCATT		C
		GCA	GAGAATCACT	GA		

		CGT	CTCTTAGTGA	CT		
		C_____	A			
GAM2652	LOC152300 3'	TCAAGT	GATTCTCCTGC	39252	TCATT	C
		GCA	GAGAATCACT	GA		
		CGT	CTCTTAGTGA	CT		
		C_____	A			
GAM2652	LOC152925 3'	TCAAGT	GATTCTTATGC	39336	CATT	C
		GCAT	GAGAATCACT	GA		
		CGTA	TTCTTAGTGA	CT		
		_____	A			
GAM2652	LOC157858 5'	TCAAGT	GATTCTCCTGC	41869	TCATT	C
		GCA	GAGAATCACT	GA		
		CGT	CTCTTAGTGA	CT		
		C_____	A			
GAM2652	LOC169611 3'	TCAAGT	GATTCTCCTGC	40286	TCATT	C
		GCA	GAGAATCACT	GA		
		CGT	CTCTTAGTGA	CT		
		C_____	A			
GAM2652	LOC196264 3'	TCAAGC	GATTCTTGTGC	42337	CATT	A C
		GCAT	GAGAATC	CT GA		
		CGTG	TTCTTAG	GA CT		
		_____	C A			
GAM2652	LOC196411 3'	TCAAGT	GATTCTCCTGC	42365	TCATT	C
		GCA	GAGAATCACT	GA		
		CGT	CTCTTAGTGA	CT		
		C_____	A			
GAM2652	LOC199725 5'	TCAAGT	GATTCTCCTGC	43243	TCATT	C
		GCA	GAGAATCACT	GA		
		CGT	CTCTTAGTGA	CT		
		C_____	A			
GAM2652	LOC199906 3'	TCAAGT	GATTCTCTTGC	42658	TCATT	C
		GCA	GAGAATCACT	GA		
		CGT	CTCTTAGTGA	CT		
		T_____	A			
GAM2652	LOC200169 5'	TCAAGC	GATTCTTGTGC	43286	CATT	A C
		GCAT	GAGAATC	CT GA		
		CGTG	TTCTTAG	GA CT		
		_____	C A			
GAM2652	LOC200860 3'	TCAAGT	GATTCTCCTGC	43356	TCATT	C
		GCA	GAGAATCACT	GA		

		CGT	CTCTTAGTGA	CT		
		C_____	A			
GAM2652	LOC201411 3'	TCAAGTGATTCTCCTGC	31529	TCATT		C
		GCA	GAGAATCACT	GA		
		CGT	CTCTTAGTGA	CT		
		C_____	A			
GAM2652	LOC201696 3'	TCAAGTGATTCTCCTGC	31626	TCATT		C
		GCA	GAGAATCACT	GA		
		CGT	CTCTTAGTGA	CT		
		C_____	A			
GAM2652	LOC202908 5'	TCAAGTGATTCTCCTGC	42998	TCATT		C
		GCA	GAGAATCACT	GA		
		CGT	CTCTTAGTGA	CT		
		C_____	A			
GAM2652	LOC203197 3'	TTCAAGTGATTCTCATGC	43014	TCAT		C
		GCA	TGAGAATCACT	GAA		
		CGT	ACTCTTAGTGA	CTT		
		_____	A			
GAM2652	LOC220064 3'	TCAAGTGATTCTCCTGC	44869	TCATT		C
		GCA	GAGAATCACT	GA		
		CGT	CTCTTAGTGA	CT		
		C_____	A			
GAM2652	LOC220963 3'	TTCAAGTGATTCTGATAACAC	43960	C_ TTGA		C
		GTG ATCA	GAATCACT	GAA		
		CAC TAGT	CTTAGTGA	CTT		
		AA _____	A			
GAM2652	LOC221174 5'	TCAAGTGATTCTCCTGC	44912	TCATT		C
		GCA	GAGAATCACT	GA		
		CGT	CTCTTAGTGA	CT		
		C_____	A			
GAM2652	LOC222031 3'	TCAAGTGATTCTCCTGC	45136	TCATT		C
		GCA	GAGAATCACT	GA		
		CGT	CTCTTAGTGA	CT		
		C_____	A			
GAM2652	LOC257017 5'	TCAAGTGATTCTCCTGC	46498	TCATT		C
		GCA	GAGAATCACT	GA		
		CGT	CTCTTAGTGA	CT		
		C_____	A			
GAM2652	LOC57107 3'	TCAAGTGATTCTCCTGC	21652	TCATT		C
		GCA	GAGAATCACT	GA		

CGT CTCTTAGTGA CT
 C_____ A
 GAM2652 LOC90591 3' TCAAGTGATTCTCCTGC 31761 TCATT C
 GCA GAGAATCACT GA
 ||| ||||| ||
 CGT CTCTTAGTGA CT
 C_____ A
 GAM2652 LOC91115 3' TCAAGTGATTCTTCTGC 32400 TCATT C
 GCA GAGAATCACT GA
 ||| ||||| ||
 CGT TTCTTAGTGA CT
 C_____ A
 GAM2652 LOC91291 5' TCAAGTGATTCTCCTGC 32630 TCATT C
 GCA GAGAATCACT GA
 ||| ||||| ||
 CGT CTCTTAGTGA CT
 C_____ A
 GAM2653 BACH2 3' CCTCCAACCACGGGCTGTTTA 22378 C CTAA
 A AACAGCCCGTG GGAGG
 | ||||| ||||
 A TTGTCGGGCAC CCTCC
 T CAA_
 GAM2653 CDKN2C 5' CCTCCTTAAACTCTGCCGTT 6928 A CC_ GC
 AAC GC GT TAAGGAGG
 ||| || |||||
 TTG CG CA ATTCCTCC
 C TCT AA
 GAM2653 CXCL16 3' CCTCCTTAGCAGGTGCCGT 22599 A _ G
 AC GC CC TGCTAAGGAGG
 || || |||||
 TG CG GG ACGATTCCTCC
 C T _
 GAM2653 EIF2S3 3' CCTCCAGGCTGAAAGACTGTTG 7111 CCCGT_ AA
 TA TACAACAG GCT GGAGG
 ||||| || ||||
 ATGTTGTC CGG CCTCC
 AGAAAGT A_
 GAM2653 IGFBP3 3' CCTCCTTAGCACAATGT 6198 GCCC
 ACA GTGCTAAGGAGG
 ||| |||||
 TGT CACGATTCCTCC
 AA_
 GAM2653 MEL 3' CCTCCTTAAGCTGCTGT 11845 CCGT _
 ACAGC GCT AAGGAGG
 |||| || |||||
 TGT CG CGA TTCCTCC
 T_ A
 GAM2653 OSR1 3' CCTCCTTTTTTTGGACTTTGTA 11589 C C TGCT
 TACAA AG CCG AAGGAGG
 |||| || || |||||

ATGTT TC GGT TTCCTCC
 _ A TTTT
 GAM2653 SLC7A6 3' CCTCCTCACTCAGGCTGTTGTA 10127 C__ CTA
 TACAACAGCC GTG AGGAGG
 ||||| || |||||
 ATGTTGTCGG CAC TCCTCC
 ACT ____
 GAM2653 TFEB 5' CCTCACAGGCTGTTGTG 44239 C CTA
 TACAACAGCC GTG AGG
 ||||| || ||
 GTGTTGTCGG CAC TCC
 A ____
 GAM2653 C11orf25 3' CCTTAGCACAAATCTATTGTA 25400 C CCC
 TACAA AG GTGCTAAGG
 |||| || |||||
 ATGTT TC CACGATTCC
 A TAA
 GAM2653 C16orf5 3' CCCAGCTGACAGGCTGTTG 15052 C __ AA A
 CAACAGCC GT GCT GG GG
 ||||| || || ||
 GTTGTCTGG CA CGA CC CC
 A GT __ _
 GAM2653 DKFZP566K1924 5' CCTCCTGCCCGGGGCTGTT 36520 _ T TA
 AACAGCCC G GC AGGAGG
 ||||| || |||||
 TTGTCTGGG C CG TCCTCC
 G C ____
 GAM2653 DPYSL4 3' CCTCCTTAGCATTTTCTTTTGT 13141 C CCC
 A TACAA AG GTGCTAAGGAGG
 |||| || |||||
 ATGTT TC TACGATTCCTCC
 T TTT
 GAM2653 FLJ00024 3' CCTTTGTCCACGGGCTATTG 31889 C CTAA
 CAA AGCCCGTG GGAGG
 || ||||| ||||
 GTT TCGGGCAC TTTCC
 A CTG_
 GAM2653 FLJ11383 3' CCTCCTTGTTGACTGCTGTT 24476 CCGT_ T
 AACAGC GC AAGGAGG
 |||| || |||||
 TTGTCTG TG TTCCTCC
 TCAGT ____
 GAM2653 FLJ13114 3' CCCCTTACCCTGCTGTTGT 23749 CCGTGC A
 ACAACAGC TAAGG GG
 ||||| |||| ||
 TGTTGTCTG ATTCC CC
 TCCC__ _
 GAM2653 FLJ32865 3' CCTCCCCAGCCAGCTCCTGTCT 29425 _ CCC _ AA
 GTA TACA ACAG GT GCT GGAGG
 |||| || || |||||

ATGT TGTC CG CGA CCTCC
 C CT_ AC CC
 GAM2653 HEF1 3' CTCCCTGGGGCTGTTCA 13111 C GTGC A
 A AACAGCCC TA GGAG
 | ||||| || ||||
 A TTGTCGGG GT CCTC
 C ____ C
 GAM2653 IAN4L1 5' CCTCCTTAAGTGGTCTGCTCA 20416 C C__ GC_
 A AGC CGT TAAGGAGG
 | || | |||||
 A TCG GCG ATTCCTCC
 C TCT TCA
 GAM2653 KIAA1260 5' CCTCCTTGCAATGGGCTG 30157 _ T
 CAGCCCGT GC AAGGAGG
 ||||| || |||||
 GTCGGGTA CG TTCCTCC
 A _
 GAM2653 MGC12837 3' CCTCCTTAGCCCCACTGGT 26452 C ____
 GCC GT GCTAAGGAGG
 || | |||||
 TGG CA CGATTCCTCC
 T CCC
 GAM2653 N4BP3 3' CCTCCTTACCTTGGAAGCCCT 32933 CA ____ TGC
 TGTA TACAA GC CCG TAAGGAGG
 |||| | || |||||
 ATGTT CG GGT ATTCCTCC
 CC AAC TCC
 GAM2653 NFAT5 5' CTCCTCCAGCTGTTGT 28955 CCG CTA
 ACAACAGC TG AGGAG
 ||||| || ||||
 TGTGTGCG AC TCCTC
 ____ C_
 GAM2653 PPP1R16B 3' CCTCCTTAGACTGAGCTGT 30772 C TG
 ACAGC CG CTAAGGAGG
 |||| | |||||
 TGTGCG GT GATTCCTCC
 A CA
 GAM2653 SS18L1 3' CCTCCTCATGCAGTGTGTA 32560 GCC CTA
 TACAACA CGTG AGGAGG
 |||| | ||||
 ATGTTGT GTAC TCCTCC
 GAC ____
 GAM2653 STX1B2 3' CCCCTTCACCGGGGCTGTTGTG 27455 ____ CT A
 TACAACAGCCC GTG AAGG GG
 ||||| || |||| |
 GTGTTGTCGGG CAC TTCC CC
 GC ____
 GAM2653 VPS4B 5' CCTCCCCAGTTTGAGGGCTGTT 11293 GT__ AA
 AACAGCCC GCT GGAGG
 ||||| || ||||

	TTGTCGGG TGA CCTCC		
	AGTT CC		
GAM2653 LOC144871 3'	CCTAGCCACAGCTGTTGTA 40469	CC _ A	
	TACAACAGC GTG CTA GG		
	ATGTTGTCG CAC GAT CC		
	A_ C _		
GAM2653 LOC158987 3'	CCTCCAGCAGCACGGATGCTG 42046	_ AA_	
	CAGC CCGTGCT GGAGG		
	GTCG GGCACGA CCTCC		
	TA CGA		
GAM2653 LOC201164 3'	CCTCCCTGCGGGCTGCTGTG 42529	A CTAA	
	TACA CAGCCCGTG GGAGG		
	GTGT GTCGGGCGT CCTCC		
	C C_		
GAM2653 LOC255308 3'	CCTCCAGGCTGAAGGACTGTTG 45354	C GT_ AA	
TA	TACAACAG CC GCT GGAGG		
	ATGTTGTC GG CGG CCTCC		
	A AAGT A_		
GAM2653 LOC256821 5'	CCTCTTTGTCAACCGCATGT 46638	_ CCG C	
	ACA GC TG TAAGGAGG		
	TGT CG AC GTTTCTCC		
	A CCA T		
GAM2654 ZNF215 3'	GACATTTGCCTTAGGAACTTAA 14911	_ G CA	
CTCT	AGAGTTAA TC TA GCAAATGTC		
	TCTCAATT AG AT CGTTTACAG		
	CA G TC		
GAM2654 FLJ21820 3'	ACATTGCCATACATTAACCTCT 22452	C CA A	
	AGAGTTAAT GTA GCAA TGT		
	TCTCAATTA CAT CGTT ACA		
	_ AC _		
GAM2654 STRBP 5'	GACATTTGCTATATTGACGCT 20418	A CGTAC	
	AG GTTAAT AGCAAATGTC		
	TC CAGTTA TCGTTTACAG		
	G TA_		
GAM2654 LOC149302 5'	GACATTTGCCATCTAGGTACTC 38707	TA GTACA_	
T	AGAGT ATC GCAAATGTC		
	TCTCA TGG CGTTTACAG		
	_ ATCTAC		
GAM2655 AP1GBP1 3'	GCACATTAGCTCCGCTCA 27880	_ _	
	TGAGCGGA CTAATG GT		

		ACTCGCCT GATTAC CG	
		C A	
GAM2655	LOC158055 3'	GCACCAGGGCCAATCTGCTCA 39705	CTAA A_
		TGAGCGGA TGGT TGGTGC	
		ACTCGTCT ACCG ACCACG	
		A__ GG	
GAM2656	ABCA1 3'	ACTGAAAGCAAATGCTTTGTGA 12011	GAC GA
		TCACAAAG TTGTT TAGT	
		AGTGTTTC AACGA GTCA	
		GTA AA	
GAM2656	HLA-G 3'	ACTGAGTGGCAAGTCCCTTTGT 7906	_ A_
	GA	TCACAAAGG ACTTGTTG TAGT	
		AGTGTTTCC TGAACGGT GTCA	
		C GA	
GAM2656	DKFZp761F2014 3'	ACTATTCTTGAGTCCTTTG 21457	GTT_
		CAAAGGACTT GATAGT	
		GTTTCCTGAG TTATCA	
		GTTC	
GAM2656	KIAA1463 3'	ACTAAAAGCCACTTTGTGA 35768	GACTT GA
		TCACAAAG GTT TAGT	
		AGTGTTTC CGA ATCA	
		AC__ AA	
GAM2656	MGC2488 3'	GTCATAAGTCCTTTGTGA 23473	T
		TCACAAAGGACTTGT GAT	
		AGTGTTTCCTGAATA CTG	
		-	
GAM2656	MGC2560 3'	CTATGGTACTTTGTGATT 25466	G TGTG
		AATCACAAAG ACT ATAG	
		TTAGTGTTTC TGG TATC	
		A _____	
GAM2656	SYT13 3'	CAACTAGTCCTTGTGATT 44886	A T
		AATCACAA GGACT GTTG	
		TTAGTGTT CCTGA CAAC	
		- T	
GAM2656	LOC113523 3'	ACTATCAAAGGGCCCTTCAGGA 36150	ACA A TG
		TC AAGG CT TTGATAGT	
		AG TTCC GG AACTATCA	
		GAC C GA	
GAM2656	LOC147343 5'	ACCATCATGTCTTCCTTTGTG 40830	CTTGT A
		CACAAAGGA TGAT GT	

		GTGTTTCCT ACTA CA	
		TCTGT C	
GAM2656	LOC150245 3'	CTGAAGCACCTTTGTGA 41161	ACT GA
		TCACAAAGG TGTT TAG	
		AGTGTTTCC ACGA GTC	
		___ A_	
GAM2656	LOC220477 5'	ACCATCCCAAGTCCTTTGT 37407	TT A
		ACAAAGGACTTG GAT GT	
		TGTTTCCTGAAC CTA CA	
		C_ C	
GAM2656	LOC254700 3'	ATTGACAAGCCCTTCTGAT 46037	CA A TG
		ATCA AAGG CTTGT AT	
		TAGT TTCC GAACA TA	
		C_ C GT	
GAM2657	ABCC3 3'	GCCTCCCTCGCTCCCTGCTCCT 21292	A AC TCTGT_
	C	GAGGAGCA G AGCG GC	
		CTCCTCGT C TCGC CG	
		_CC TCCCTC	
GAM2657	CELSR2 3'	GCACTCATGCCCTGCTCCT 7107	A ACA CT
		AGGAGCA G GCGT GTGC	
		TCCTCGT C CGTA CACG	
		C CT	
GAM2657	FXVD6 3'	CACATGGCCATCTGCTCCTC 22548	A CA GTC
		GAGGAGCA GA GC TGTG	
		CTCCTCGT CT CG ACAC	
		AC GT	
GAM2657	HNF4A 3'	CACTTGGGGGCACCTTGCTCCTC 6072	ACA G T_
		GAGGAGCAAG GC TC GTG	
		CTCCTCGTTC CG GG CAC	
		CA_ G TT	
GAM2657	NRL 3'	TGCACAGGGTGCTCCTGCCACC 12838	A_ A CA G
	TC	GAGG GCA GA GC TCTGTGCA	
		CTCC CGT CT TG GGACACGT	
		AC C CG _	
GAM2657	PACE 3'	CACCGTCCGCCCTGCTCCTC 8422	A ACA TCT_
		GAGGAGCA G GCG GTG	
		CTCCTCGT C CGC CAC	
		C CTGC	
GAM2657	RAD52 3'	TGCACAGACAGCACCTCCTC 28658	CAAGACA _
		GAGGAG GC GTCTGTGCA	

		CTCCTC	CG CAGACACGT	
		CCA_____A		
GAM2657	RIMS1	5'	GCCGCCGCCGCTGCTCCTC 35957	A ACA TC T
			GAGGAGCA G GCG TG GC	
			CTCCTCGT C CGC GC CG	
			GC C_ _	
GAM2657	RNH	5'	CACAGACCCCCTTGCTCC 29993	ACAGC
			GGAGCAAG GTCTGTG	
			CCTCGTTC CAGACAC	
			CCC_	
GAM2657	RNH	5'	CACAGACCCCCTTGCTCC 8844	ACAGC
			GGAGCAAG GTCTGTG	
			CCTCGTTC CAGACAC	
			CCC_	
GAM2657	SLC7A7	5'	CGCTACTGTCCTGTCCTC 10121	G A CGTCT
			GAGGA CA GACAG GTG	
			CTCCT GT CTGTC CGC	
			_ C AT_	
GAM2657	SLC7A7	5'	TGCGGGCTGCCTCACCTCCTC 10122	CA_ A GT
			GAGGAG AG CAGC CTGTG	
			CTCCTC TC GTCG GCGT	
			CAC C _	
GAM2657	USP6	5'	CACATCACCGCCTTGTTCTC 43809	ACA TC_
			GAGGAGCAAG GCG TGTG	
			CTCCTTGTTT CGC ACAC	
			_ CACT	
GAM2657	DKFZP434O047	5'	CACATCGCTGCCTTGTTCTC 17862	A TC
			GAGGAGCAAG CAGCG TGTG	
			CTCCTTGTTT GTCGC ACAC	
			C T_	
GAM2657	FLJ22814	3'	TGCACAGACGGCGGCATCCTC 24443	_ AAGACAG
			GAGGA GC CGTCTGTGCA	
			CTCCT CG GCAGACACGT	
			A GCG_	
GAM2657	FLJ23416	3'	CAGGCTCCCTGCTCCTC 25960	A_ CAGC
			GAGGAGCA GA GTCTG	
			CTCCTCGT CT CGGAC	
			CC _	
GAM2657	FLJ23519	5'	CACAGACCCCCTTGCTCC 34307	ACAGC
			GGAGCAAG GTCTGTG	

			CCTCGTTC CAGACAC		
			CCC__		
GAM2657	KCNG3	5'	TGCACAGAGGCCCCGCCCCC 28437	A A	AAGACA G
			G GG GC GC TCTGTGCA		
			C CC CG CG AGACACGT		
			C _ CCC__ G		
GAM2657	KIAA1464	3'	CACTGCCTGCCTTGCTCC 33879	A C	CT
			GGAGCAAG CAG GT GTG		
			CCTCGTTC GTC CG CAC		
			C _ T_		
GAM2657	KIAA1674	3'	CAGATCCCATCCTGCTCCTC 34104	A	CAGC
			GAGGAGCA GA GTCTG		
			CTCCTCGT CT TAGAC		
			C ACCC		
GAM2657	KIAA1674	3'	CAGATCCCATCCTGCTCCTC 34105	A	CAGC
			GAGGAGCA GA GTCTG		
			CTCCTCGT CT TAGAC		
			C ACCC		
GAM2657	KIAA1674	3'	CAGATCCCATCCTGCTCCTC 34106	A	CAGC
			GAGGAGCA GA GTCTG		
			CTCCTCGT CT TAGAC		
			C ACCC		
GAM2657	KIAA1674	3'	CAGATCCCATCCTGCTCCTC 34107	A	CAGC
			GAGGAGCA GA GTCTG		
			CTCCTCGT CT TAGAC		
			C ACCC		
GAM2657	KIAA1674	3'	CAGATCCCATCCTGCTCCTC 34108	A	CAGC
			GAGGAGCA GA GTCTG		
			CTCCTCGT CT TAGAC		
			C ACCC		
GAM2657	KIAA1674	3'	CAGATCCCATCCTGCTCCTC 34109	A	CAGC
			GAGGAGCA GA GTCTG		
			CTCCTCGT CT TAGAC		
			C ACCC		
GAM2657	MAP2K3	5'	GCCGCCGCCGCTGCTCCTC 29714	A ACA	TC T
			GAGGAGCA G GCG TG GC		
			CTCCTCGT C CGC GC CG		
			_ GC_ C_ _		
GAM2657	MGC2474	3'	AGACAGCATCTTGCTCCTC 23415	CA	_
			GAGGAGCAAGA GC GTCT		

			CTCCTCGTTCT CG CAGA		
			A_ A		
GAM2657	MGC3047	3'	TGCACCTCTCCTGTCTGTGCTC 26138	_	CGTCT
		CTC	GAGGAGCA AGACAG GTGCA		
			CTCCTCGT TCTGTC CACGT		
			G CTCTC		
GAM2657	MGC5391	3'	AGAACACTGCCTTGTTCC 26471	A C _	
			GGAGCAAG CAG GT CT		
			CCTTGTTT GTC CA GA		
			C A A		
GAM2657	NIFU	5'	CGCAGACGCGCCCGGCCCTC 33436	A	AAGACA
			GAGG GC GCGTCTGTG		
			CTCC CG CGCAGACGC		
			C CCCC_G		
GAM2657	SDC3	3'	TGCACAGACACCATTGCC 16091	A	GACAGC
			GG GCAA GTCTGTGCA		
			CC CGTT CAGACACGT		
			_ ACCA_		
GAM2657	TOB2	3'	TGCTGCTCCCTGCTCCTC 45771	A_ _	
			GAGGAGCA GA CAGCG		
			CTCCTCGT CT GTCGT		
			CC C		
GAM2657	LOC142927	3'	TGCACAGGTCATCCCGCTCCC 37569	A	AA CA GT
			G GGAGC GA GC CTGTGCA		
			C CCTCG CT TG GACACGT		
			_ CC AC _		
GAM2657	LOC144571	5'	TGCAACATGCCCTTGCTCC 40444	ACA	CTG
			GGAGCAAG GCGT TGCA		
			CCTCGTTC CGTA ACGT		
			CC_ CA_		
GAM2657	LOC145195	3'	CACAGCCTGGCCTGCTCCTC 40512	AGA	C T
			GAGGAGCA CAG G CTGTG		
			CTCCTCGT GTC C GACAC		
			CCG _ _		
GAM2657	LOC146782	5'	CACATCGCCGCTTGTTCTC 37524	ACA	TC
			GAGGAGCAAG GCG TGTG		
			CTCCTTGTTT CGC ACAC		
			CGC T_		
GAM2657	LOC148709	5'	CACTCCACTGCCTGCTCCTC 38579	A A	CGTCT
			GAGGAGCA G CAG GTG		

		CTCCTCGT C GTC CAC	
		_ C ACCT_	
GAM2657	LOC149478 5'	GCACCGCATTCTGCTCCTC 38753	A CA TCT
		GAGGAGCA GA GCG GTGC	
		CTCCTCGT CT CGC CACG	
		_ TA _	
GAM2657	LOC170395 5'	CAGATCCCATCCTGCTCCTC 37543	A CAGC
		GAGGAGCA GA GTCTG	
		CTCCTCGT CT TAGAC	
		C ACCC	
GAM2657	LOC170395 5'	CAGATCCCATCCTGCTCCTC 37541	A CAGC
		GAGGAGCA GA GTCTG	
		CTCCTCGT CT TAGAC	
		C ACCC	
GAM2657	LOC170395 5'	CAGATCCCATCCTGCTCCTC 37542	A CAGC
		GAGGAGCA GA GTCTG	
		CTCCTCGT CT TAGAC	
		C ACCC	
GAM2657	LOC195977 3'	TGCACAGGCTCCCTGCTGCCC 42303	A A A C__
		GG GCA G CAG GTCTGTGCA	
		CC CGT C GTC CGGACACGT	
		_ _ _ CCT	
GAM2657	LOC256158 5'	TGCCCTCCAACGCCCTGCTCCT 46634	A ACA C T__
	C	GAGGAGCA G GCGT TG GCA	
		CTCCTCGT C CGCA AC CGT	
		_ C_ _ CTCC	
GAM2657	LOC257054 5'	GCACCGTCTGCTCCTC 45782	A AGCGTCT
		GAGGAGCA GAC GTGC	
		CTCCTCGT CTG CACG	
		_ C_	
GAM2657	LOC90019 5'	TGCACAGAACCCTCGCCCCCT 28877	A A ACAGCG
		AGG GC AG TCTGTGCA	
		TCC CG TC AGACACGT	
		C C CCA__	
GAM2658	HNRPK 3'	TTCATAGGTGTTCTGCATTTGA 7918	T C CAC
		TCAAATGC AGAGC ACC GAA	
		AGTTTACG TCTTG TGG CTT	
		_ _ ATA	
GAM2658	HNRPK 3'	TTCATAGGTGTTCTGCATTTGA 25282	T C CAC
		TCAAATGC AGAGC ACC GAA	

		AGTTTACG TCTTG TGG CTT	
		— — ATA	
GAM2658	IFITM2	5' TGGCCAGCTCTGCATTTGA 13143	T CAC
		TCAAATGC AGAGC CCA	
		AGTTTACG TCTCG GGT	
		— ACC	
GAM2658	RPE	5' TCGTGGGTAACCTTGCTTTTGG 31157	T TA CC
		TCAAA GC GAG ACCCACGA	
		GGTTT CG TTC TGGGTGCT	
		T — AA	
GAM2658	C20orf140	3' TGGGGACAGAAGCTCCAGCATT 29444	A CA_____
	TG	CAAATGCT GAGC CCCA	
		GTTTACGA CTCG GGGT	
		C AAGACAG	
GAM2658	CNOT4	3' TTGTTGATCCAGCATTTGA 14965	A GC CCC
		TCAAATGCT GA CA ACGA	
		AGTTTACGA CT GT TGTT	
		C A_ —	
GAM2658	KIAA1348	3' TCATGAGTTGCTGTGGCATT 34031	G C C C
		AAATGCTA AGC AC CA GA	
		TTTACGGT TCG TG GT CT	
		G T A A	
GAM2658	KIAA1577	5' CGCGGGTGGCCCCTCTGGCAT 32210	— A
		ATGCTAGA GCCACCC CG	
		TACGGTCT CGGTGGG GC	
		CCC C	
GAM2658	MGC2835	3' CGTGGGTGGCTCTCCTTTTG 23504	TGCT
		CAAA AGAGCCACCCACG	
		GTTT TCTCGGTGGGTGC	
		TCC_	
GAM2658	LOC146823	3' TTCATGATGCTTCTAGCATTGG 40751	A C CC C
	A	TC AATGCTAGAG CA CA GAA	
		AG TTACGATCTT GT GT CTT	
		G C A_ A	
GAM2658	LOC149302	5' CGTGGCAGCCCAGCATTTGG 38704	AGA CAC
		TCAAATGCT GC CCACG	
		GGTTTACGA CG GGTGC	
		CC_ AC_	
GAM2658	LOC164397	3' GGTGGCTCTGCACTTGA 40154	A T
		TCAA TGC AGAGCCACC	

AGTT ACG TCTCGGTGG
 C _
 GAM2659 ALDH3B1 3' TGCCTGACAACCCTTCT 44001 T CTGTT A
 AGAAG GGTT TCA GCA
 ||||| ||| |||
 TCTTC CCAA AGT CGT
 _ C _ C
 GAM2659 ATBF1 5' TGCTCCTGACCAGACCACCTC 13750 A TT _
 GA GTGGTTCTG TCA AGCA
 || ||||| ||| |||
 CT CACCGAGAC AGT TCGT
 C C _ CC
 GAM2659 AXIN1 3' GCTTGGCACCCTTC 30519 TCT TT
 GAAGTGGT GT CAAGC
 ||||| || |||||
 CTTCACCA CG GTTCG
 _ _
 GAM2659 BCL9 3' TTTGGTACAAAACCACTC 10526 A C T
 GA GTGGTT TGT TCAAG
 || ||||| ||| |||||
 CT CACCAA ACA GGTTT
 _ A T
 GAM2659 CPSF6 3' TGCTATCAAACCACTTCT 13870 C TTTCA
 AGAAGTGGTT TG AGCA
 ||||| || |||
 TCTTCACCAA AC TCGT
 _ TA _
 GAM2659 POU4F1 3' CTTCTATCAGAACCAATTCT 12899 G TTTC
 AGAA TGGTTCTG AAG
 ||| ||||| |||
 TCTT ACCAAGAC TTC
 A TATC
 GAM2659 SOX4 3' TTTGCTTGAAGAGACCCCCT 9078 T T G
 AG GG TCT TTTCAAGCAAA
 || || ||| |||||
 TC CC AGA GAAGTTCGTTT
 C C _
 GAM2659 TLX1 3' TTTGCCCTGGGAAACCCCTTCT 12047 T CTG TT A_
 AGAAG GGTT T CA GCAAA
 ||||| ||| | || |||||
 TCTTC CCAA A GT CGTTT
 C _ GG CC
 GAM2659 CXorf1 3' TTTGCTTAAACAGAGCCCAC 11057 _ C
 GTGG TTCTGTTT AAGCAAA
 ||| ||||| |||||
 CACC GAGACAAA TTCGTTT
 C A
 GAM2659 DC-TM4F2 3' TTTGCCATAGCTCAGACCACTT 25200 T TTTCAA_
 CT AGAAGTGGT CTG GCAAA
 ||||| || |||||

TCTTCACCA GAC CGTTT
 _ TCGATAC
 GAM2659 DKFZP566N034 3' TTTGCTCAAAAGGAGACCATTC 39064 G T G CA_
 T AGAA TGGT CT TTT AGCAAA
 |||| |||| || ||||
 TCTT ACCA GA GAA TCGTTT
 _ _ G AAC
 GAM2659 FLJ10597 3' TGCTGAGAACCATTCT 19954 A TGTT A
 AG AGTGGTTC TCA GCA
 || |||| || ||||
 TC TTACCAAG AGT CGT
 C _ _ _
 GAM2659 FLJ12687 3' TTTGCTTGGGTTTGACCACT 24449 CTGT
 AGTGGTT TTCAAGCAAA
 |||| |||| ||||
 TCACCAG GGGTTCGTTT
 TTT_
 GAM2659 FLJ23323 5' TTTGCTTAATATTACAGAACCA 23956 G TTC_
 GTTCT AGAA TGGTTCTGT AAGCAAA
 |||| |||| |||| ||||
 TCTT ACCAAGACA TTCGTTT
 G TTATAA
 GAM2659 FLJ23399 5' CTTGAAACCAGGCACTTT 23009 G CT
 GAAGTG TT GTTTC AAG
 |||| || |||| ||||
 TTTCAC GA CAAAGTTC
 G C_
 GAM2659 GOLPH3 3' TGCTCGGGGTGAACCATCT 22688 G T TT A
 AGAA TGGTTC G TC AGCA
 |||| |||| | || ||||
 TCTT ACCAAG T GG TCGT
 _ _ GG C
 GAM2659 KIAA1130 3' TGGAATAAAACCACTTCT 31288 C
 AGAAGTGGTT TGTTTCA
 |||| || |||| ||||
 TCTTCACCAA ATAAGGT
 A
 GAM2659 KIAA1287 3' CTTGAAACAGACCTCTTC 38326 T T
 GAAG GGT CTGTTTCAAG
 |||| || |||| ||||
 CTTC CCA GACAAAGTTC
 T _
 GAM2659 KIAA1434 3' TTTGCTTGTCTGAAACACCTC 34492 A G TGTTT
 GA GTG TTC CAAGCAAA
 || |||| || |||| ||||
 CT CAC AAG GTTCGTTT
 C A TCT_
 GAM2659 KIAA1493 3' CTTGAAACCCTATTTCT 32088 TTCT
 AGAAGTGG GTTTC AAG
 |||| || |||| ||||

TCTTTATC CAAAGTTC
 C____
 GAM2659 MGC11352 5' TTTGCCATAGCTCAGACCACTT 32358 T TTTCAA_
 CT AGAAGTGGT CTG GCAAA
 ||||| ||| ||||
 TCTTCACCA GAC CGTTT
 _ TCGATAC
 GAM2659 PRPF8 3' TGCAGACACAGAACCACCTC 30690 A T AA
 GA GTGGTTCTGT TC GCA
 || ||||| || |||
 CT CACCAAGACA AG CGT
 C C A_
 GAM2659 SRCRB4D 3' GCTCTGCAGACCACCTCT 28029 A T TTCA
 AGA GTGGT CTGT AGC
 || |||| ||| |||
 TCT CACCA GACG TCG
 C _ TC_
 GAM2659 LOC112616 3' TGCTTCTAGAACCACCTC 28774 A TTTC
 GA GTGGTTCTG AAGCA
 || ||||| ||||
 CT CACCAAGAT TTCGT
 C C_
 GAM2659 LOC135763 3' TGCAGCAGAACCCCTCCT 28885 A T TCAA
 AG AG GGTCTGTT GCA
 || || ||||| |||
 TC TC CCAAGACGA CGT
 C C _
 GAM2659 LOC150279 3' TGCTTGAACAGGCCTCTCCT 38900 A T T T
 AG AG GGT CTGTT CAAGCA
 || || || |||| |||||
 TC TC CCG GACAA GTTCGT
 C T _ _
 GAM2659 LOC151516 5' CTTAAAAAAGACCATTCT 39129 T G C
 AGAAGTGGT CT TTT AAG
 ||||| || ||| |||
 TCTTTACCA GA AAA TTC
 _ A A
 GAM2659 LOC152215 3' TTGCCTAAAACAGTAGCTTT 39225 GGTT CAA
 GAAGT CTGTTT GCAA
 |||| |||| |||
 TTTCG GACAAA CGTT
 AT_ ATC
 GAM2659 LOC152313 5' CTGGGGACAAAATCACTCCT 41475 A C TT A
 AG AGTGGTT TGT C AG
 || |||| ||| |||
 TC TCACTAA ACA G TC
 C A GG G
 GAM2659 LOC158434 5' TTTGAAACAAGACCACTTCT 41990 TC
 AGAAGTGGT TGTTTCAAG
 ||||| |||||

		TCTTCACCA ACAAAGTTT		
		GA		
GAM2659	LOC167147 5'	TTGCCCCAAGAGCCACTTC 40227		GTTTCAA
		GAAGTGGTTCT GCAA		
		CTTCACCGAGA CGTT		
		ACCC__		
GAM2659	LOC220776 3'	TTTGCTTGAACAGCCCTCTTCT 33940		T TT T
		AGAAG GG CTGTT CAAGCAAA		
		TCTTC CC GACAA GTTCGTTT		
		T C_ _		
GAM2659	LOC221002 3'	CTTGAAACAGTGTCTGTCT 43973		AGT TT
		AGA GG CTGTTTCAAG		
		TCT CT GACAAAGTTC		
		GT_ GT		
GAM2659	LOC221935 3'	TGCCCAAAGCCACTTCT 44502		C TTTCAA
		AGAAGTGGTT TG GCA		
		TCTTCACCGA AC CGT		
		A C_____		
GAM2659	LOC254228 3'	TTTGCCTTTGCGAACCATTTC 45922		T TTCAA
		GAAGTGGTTC GT GCAAA		
		CTTTACCAAG CG CGTTT		
		_ TTTC_		
GAM2659	LOC255645 3'	CTTGCCCAGAACTACTTCT 46220		TTT
		AGAAGTGGTTCTG CAAG		
		TCTTCATCAAGAC GTTC		
		CC_		
GAM2659	LOC51619 3'	TGCTGCAGAACCACATC 18079	A	TTCA
		GA GTGGTTCTGT AGCA		
		CT CACCAAGACG TCGT		
		A _____		
GAM2659	LOC92573 5'	CTTGTAACAGAACACCTCT 34597	A G	T
		AGA GTG TTCTGTT CAAG		
		TCT CAC AAGACAA GTTC		
		C _ T		
GAM2660	AQP1 3'	ATTCACCCACTCCCTTGAAGTT 5959	_	A ATC
		AGCT CAAGGGA TGG GAAT		
		TTGA GTTCCCT ACC CTTA		
		A C CA_		
GAM2660	DLST 3'	GACTCACATTGCCTTGAGCTT 7644	G _ _	
		AAGCTCAAGG AATG GA TC		

		TTCGAGTTCC TTAC CT AG		
		G A C		
GAM2660	DNASE1L1	5' TCAGTCCTCCCTTGACTT	13569	C AT C
		AAG TCAAGGGA GGAT GA		
		TTC AGTTCCTT CCTG CT		
		— — A		
GAM2660	HOXD4	5' GATTCATTCTCCCTTGAGCT	15980	—
		AGCTCAAGGGA ATGGATC		
		TCGAGTTCCTT TACTTAG		
		CT		
GAM2660	LOH11CR2A	5' ATCCAAGTCCCTTGAGTCC	15984	A AA—
		A GCTCAAGGG TGGAT		
		C TGAGTTCCC ACCTA		
		C CGTCA		
GAM2660	C14orf4	5' GACTCGCGTTCCCTCCAGC	33445	CA — —
		GCT AGGGAATG GA TC		
		CGA TCCCTTGC CT AG		
		CC G C		
GAM2660	FLJ21791	3' GATCCATCCCTTGAGCT	30809	A
		AGCTCAAGGGA TGGATC		
		TCGAGTTCCTT ACCTAG		
		—		
GAM2660	KIAA0449	3' GACTCTGTCCCTTGAGCT	19052	A —
		AGCTCAAGGG ATGGA TC		
		TCGAGTTCCC TGTCT AG		
		C C		
GAM2660	TUBB5	3' TGGCTCCCCTTTGAGC	12731	AAT —
		GCTCAAGGG GGA TCG		
		CGAGTTTCC CCT GGT		
		— C		
GAM2660	LOC163782	3' GATCACTCCCTTGCTT	39965	T ATG
		AAGC CAAGGGA GATC		
		TTCG GTTCCCT CTAG		
		— CA—		
GAM2660	LOC221922	5' GGCCATTCTCCTGAGCT	44535	A A
		AGCTCA GGGGAATGG TC		
		TCGAGT CTCTTACC GG		
		C —		
GAM2660	LOC254848	5' TCGATGTCCCTGACTT	46382	C A ATGG
		AAG TCA GGA ATCGA		

TTC AGT CCCT TAGCT
 _ _ G_
 GAM2660 LOC255452 5' TCGATTTGTCCCCTAGCTT 46577 CA A TG
 AAGCT AGGG A GATCGA
 |||| ||| | ||||
 TTCGA TCCC T TTAGCT
 _ C GT
 GAM2660 LOC93496 3' GATTTATTCCCTTGACTT 35866 C
 AAG TCAAGGGAATGGATC
 || |||||
 TTC AGTTCCTTATTTAG
 _
 GAM2661 F8 3' TCCAATTAACTTAACTCTTAC 5618 C C TT
 C GG AAGAGTTAAG TA TTGGA
 || ||||| || ||||
 CC TTCTCAATTC AT AACCT
 A A TT
 GAM2661 DKFZP434L187 5' CCATTCTTAACTCATGCCA 34120 A CTATTT
 TGGCA GAGTTAAG TGG
 |||| ||||| ||
 ACCGT CTCAATTC ACC
 A TT_
 GAM2661 FLJ13262 3' CCGCACTTAACTCTTACC 24431 C CTATTT
 GG AAGAGTTAAG TGG
 || ||||| ||
 CC TTCTCAATTC GCC
 A AC_
 GAM2661 HNRPA3 3' TCCAAAATAACCTAACTGCAGC 12324 AAG AGC
 GC AGTTA TATTTTGG
 || |||| |||||
 CG TCAAT ATAAAACCT
 ACG CCA
 GAM2661 KIAA1437 5' CCACTGTGGCTCATCTCTTGCC 30383 TTA TT
 A TGGCAAGAG AGCTAT TGG
 ||||| |||| ||
 ACCGTTCTC TCGGTG ACC
 TAC TC
 GAM2661 PCSK7 3' CCAAATAAAAACCTTCCA 11074 C A AAGC
 TGG AAG GTT TATTTTGG
 ||| ||| |||||
 ACC TTC CAA ATAAAACC
 _ _ AA_
 GAM2661 LOC129676 5' CCAACAAGCTTAACACCCACCA 37283 CAAGA ATT
 TGG GTTAAGCT TTGG
 || ||||| ||
 ACC CAATTCGA AACC
 ACCCA AC_
 GAM2661 LOC148918 5' TCCGCTGCCCACCTCTTGCCA 38613 TTAA TATTT
 TGGCAAGAG GC TGG
 ||||| || |||

ACCGTTCTC CG GCCT
 CACC TC___
 GAM2661 LOC164832 3' TCCAAAATGGGACGCTTGCCA 40110 A AAG
 TGGCAAG GTT CTATTTTGGA
 ||||| ||| |||||
 ACCGTTC CAG GGTA AACCT
 G ___
 GAM2661 LOC220988 3' TCCAAAATAACCTAACTGCAGC 43684 AAG AGC
 GC AGTTA TATTTTGGA
 || ||||| |||||
 CG TCAAT ATAA AACCT
 ACG CCA
 GAM2662 DPYSL3 3' GCACTGCCCTTGGGACTTCCG 7073 A TCA A
 TG GA TC CCAAGG CAGTGC
 || || |||||
 GC CT AG GGTTC CCGTCACG
 _ TC_ _
 GAM2662 FANCC 3' CATTGTTAGTGTAATCTCA 34905 CAT CAAG
 TGAGAT CAC GGCAGTG
 ||||| ||| |||||
 ACTCTA GTG TTGTTAC
 AT_ A___
 GAM2662 FLJ13055 3' CACTGCCCCCATGCCTCA 22943 AT CACCAA
 TGAG CAT GGCAGTG
 |||| ||| |||||
 ACTC GTA CCGTCAC
 C_ CCC___
 GAM2662 KIAA0352 3' GCACTGCCCTGGTGGGATTCA 16823 A A A
 TGAG TC TCACCA GGCAGTGC
 |||| || ||||| |||||
 ACTT AG GGTGGT CCGTCACG
 _ _ C
 GAM2662 KIAA1136 3' GCACTGCTAACTTAATGCATCC 43884 A _ CACCAAG
 CA TG GAT CAT GGCAGTGC
 || ||| ||| |||||
 AC CTA GTA TCGTCACG
 C C ATTCAA_
 GAM2662 KR18 5' CACTGCCCCCTGACGACCT 27116 A A CCAA
 AG TC TCA GGCAGTG
 || ||| ||| |||||
 TC AG AGT CCGTCAC
 C C CC___
 GAM2662 MGC16386 3' CACTGCCTGGATGCATCTCA 27958 _ ACCAA
 TGAGAT CATC GGCAGTG
 ||||| ||||| |||||
 ACTCTA GTAG TCCGTCAC
 C G___
 GAM2662 PISD 3' CAGGCTGGAATGATCTCA 15654 CA AGG AG
 TGAGATCAT CCA GC TG
 ||||| ||| || ||

			ACTCTAGTA GGT CG AC		
			A_ _ G_		
GAM2662	TA-PP2C	3'	ACTCCCAGTGATGATCT 29281	CAA	C
			AGATCATCAC GGG AGT		
			TCTAGTAGTG CCC TCA		
			A_ _		
GAM2662	LOC136288	3'	GCTGGCCTGGTGTATGCCA 37100	A T	A G
			TG GA CATCACCA GG CAGT		
			AC CT GTAGTGGT CC GTCG		
			C _ _ G		
GAM2662	LOC203392	5'	GCGCTTGGTGACGATCCCA 43042	A A	G
			TG GATC TCACCAAG GC		
			AC CTAG AGTGGTTC CG		
			C C G		
GAM2662	LOC64116	3'	CAAAGCCCCAACAATGATCTCA 22713	CACCAA	AG
			TGAGATCAT GGGC TG		
			ACTCTAGTA CCG AC		
			ACAA_ AA		
GAM2663	RAP1	3'	ATTGTGACCAATGAACCTTA 21045	CAA_	
			TAAAGTTCAT TACAAT		
			ATTTCAAGTA GTGTTA		
			ACCA		
GAM2663	FLJ22029	3'	CTAACATGAGAGATGAACTT 24505	AATACA	
			AAGTTCATC ATGTTAG		
			TTCAAGTAG TACAATC		
			AGAG_		
GAM2664	HS2ST1	3'	TGCAAATTCTGTTTCCAACCTTG 14580	GAATTT	T
	A		TCAAGT AC GAATTTGCA		
			AGTTCA TG CTAAACGT		
			ACCTT_ T		
GAM2664	MTMR2	3'	TGCAAATTCTGTAATTTCACT 18245	T T	
			AGTGAA TTAC GAATTTGCA		
			TCACTT AATG CTAAACGT		
			T T		
GAM2664	STCH	3'	CAAATTCAGTATCCT 13833	T ATT	
			AG GA TACTGAATTTG		
			TC CT ATGACTTAAAC		
			_ _ _		
GAM2664	DKFZP761E2110	3'	GCAAATTAGGATCACTTGA 25225	ATTTA	A
			TCAAGTGA CTGA TTTGC		

AGTTCACT GATT AAACG
 AG_____
 GAM2664 KIAA0009 3' AAATTCAGAAAATTCACCTGA 16021 A A
 TCA GTGAATTT CTGAATTT
 ||| ||||| |||||
 AGT CACTTAAA GACTTAAA
 C A
 GAM2664 KIAA0795 5' CAAATTCAGTGCCCACCGGA 24584 AA AATT
 TC GTG TACTGAATTTG
 || ||| |||||
 AG CAC GTGACTTAAAC
 GC CC_
 GAM2664 KIAA1348 3' TGCAAATTTGATAATTCTCCTG 34032 AGT TAC
 A TCA GAATT TGAATTTGCA
 ||| ||||| |||||
 AGT CTTAA GTTTAAACGT
 CCT TA_
 GAM2664 SLC1A7 3' TGCAAATTCAGTGTTAACT 13491 GAATT
 AGT TACTGAATTTGCA
 ||| |||||
 TCA GTGACTTAAACGT
 ATT_
 GAM2664 LOC203197 3' TGCAAATTGCTTTCCAAACTCA 43012 A ACTG_
 CTTGA TCAAGTGA TTT AATTTGCA
 ||||| ||| |||||
 AGTTCACT AAA TTAAACGT
 C CCTTTCG
 GAM2664 LOC221692 3' TGCAAATTAAAGAACTACTTGA 44300 AA ACTG
 TCAAGTG TTT AATTTGCA
 ||||| ||| |||||
 AGTTCAT AGA TTAAACGT
 CA AA_
 GAM2664 LOC257464 5' TGCAAATTTGGTCATCTACTCG 43170 A A TT TG
 A TC AGTG AT AC AATTTGCA
 || |||| || || |||||
 AG TCAT TA TG TTAAACGT
 C C C_ GT
 GAM2664 LOC92719 3' ATTCAGTTAATTCACCTGA 34846 T
 TCAAGTGAATT ACTGAAT
 ||||| |||||
 AGTTCACTTAA TGACTTA
 T
 GAM2665 AGRP 5' GCCCTGCCATATAAGCCA 6806 A C
 TG CTTATG GGTAGGGC
 || ||||| |||||
 AC GAATAT CCGTCCCG
 C A
 GAM2665 CHL1 3' TTGCCCCTCGTGATAAGTCA 13399 _ _ A
 TGACTTAT GCG GT GGGCAA
 ||||| ||| || |||||

ACTGAATA TGC CA CCCGTT
 G T _
 GAM2665 DKFZp761A132 3' TGCCCCGCATAGGCCA 26077 A TAG
 TG CTTATGCGG GGCA
 || ||||| |||
 AC GGATACGCC CCGT
 C _
 GAM2665 FLJ10375 5' GGCTGCCCCATATAAGTCA 19838 CGGTA A
 TGACTTATG GGGCA CC
 ||||| ||| ||
 ACTGAATAT CCCGT GG
 A _ C
 GAM2665 FLJ11726 3' TGGGTGCGCCCTACAAGAGAGT 24529 ATGCG A
 ACTT GTAGGGC ACCCA
 ||| ||||| |||||
 TGAG CATCCCG TGGGT
 AGAA _ C
 GAM2665 KIAA1956 3' TGGACTGCCCTGTATCTAAGTC 38364 TGCG AC
 GACTTA GTAGGGCA CCA
 ||||| ||||| |||
 CTGAAT TGTCCCGT GGT
 CTA _ CA
 GAM2665 MGC12217 5' GGCTGCCCCATATAAGTCA 26517 CGGTA A
 TGACTTATG GGGCA CC
 ||||| ||| ||
 ACTGAATAT CCCGT GG
 A _ C
 GAM2665 LOC51622 3' TGTCCACCTCATAAGTCA 17885 C A
 TGACTTATG GGT GGGCA
 ||||| ||| |||||
 ACTGAATAC CCA CCTGT
 T _
 GAM2665 LOC93082 3' TGGGTTGCCTCCCACAAGTC 28767 A C TA
 GACTT TG GG GGGCAACCCA
 |||| || || |||||
 CTGAA AC CC TCCGTTGGGT
 C _ _
 GAM2666 APG5L 3' CTTCTGATCTAGATTTGAA 11262 GACTA
 TTCAAA TAGATCAGAAG
 ||||| |||||
 AAGTTT ATCTAGTCTTC
 AG _
 GAM2666 CR1 3' GCTTCATAAAGTCTTTGAA 6174 A GATCA
 TTCAAAGACT TA GAAGC
 ||||| || |||||
 AAGTTTCTGA AT CTTCG
 A A _
 GAM2666 NCOA6 5' CTGATCTATGTGTTTGAG 15290 G T
 TTCAAA AC ATAGATCAG
 ||||| || |||||

GAGTTT TG TATCTAGTC
 G _
 GAM2666 PRDX3 3' AGCTTCTGATCAACGGTCCTGA 36303 AA ATA
 A TTCA GACT GATCAGAAGCT
 |||| ||| ||||||||
 AAGT CTGG CTAGTCTTCGA
 C_ CAA
 GAM2666 RAG1 3' AGCTTCTGCATACAGTCTT 6036 A GAT
 AAGACT TA CAGAAGCT
 ||||| || |||||||
 TTCTGA AT GTCTTCGA
 C AC_
 GAM2666 VANG2 3' GCTTCCATAGTCTTTG 35482 AGATCA
 CAAAGACTAT GAAGC
 ||||||| ||||
 GTTTCTGATA CTTCTG
 C_____
 GAM2666 CAP350 3' AGCTTCTATGGTTCATAGTCTT 16769 AG _
 TG CAAAGACTAT ATCA GAAGCT
 ||||||| ||| |||||
 GTTTCTGATA TGGT CTTCTG
 CT AT
 GAM2666 DKFZP434I092 3' AGCTCTTCAACTATGTCTTTGA 33671 T ATC_ A
 A TTCAAAGAC ATAG AGA GCT
 ||||||| ||| ||| |||
 AAGTTTCTG TATC TCT CGA
 _ AACT _
 GAM2666 FLJ10874 3' AGCCTCTGACATGCTCTTTGA 20219 C AGA A
 TCAAAGA TAT TCAGA GCT
 |||||| ||| ||||| |||
 AGTTTCT GTA AGTCT CGA
 C C_ C
 GAM2666 FLJ11383 5' CTTCTAATCATTTTTTTTGAA 24477 CT A C
 TTCAAAGA AT GAT AGAAG
 |||||| || ||| |||||
 AAGTTTTT TA CTA TCTTC
 TT _ A
 GAM2666 KIAA0459 3' GGCTCTGACCTATGTCTTTGAA 30576 T A A
 TTCAAAGAC ATAG TCAGA GCT
 ||||||| |||| ||||| |||
 AAGTTTCTG TATC AGTCT CGG
 _ C _
 GAM2666 KIAA0599 3' AGCCTCTGATCTTCCCTTGAA 37851 A_ CTAT A
 TTCAA GA AGATCAGA GCT
 |||| || ||||||| |||
 AAGTT CT TCTAGTCT CGA
 CC _____ C
 GAM2666 KIAA0669 3' TGACCTATAATCTTTGAA 16627 C A
 TTCAAAGA TATAG TCA
 ||||||| ||||| |||

AAGTTTCT ATATC AGT
 A C
 GAM2666 KIAA1317 3' AGCTTCTGACTCTTTCTT 41621 CTAT _
 AAGA AGA TCAGAAGCT
 ||| ||| |||||
 TTCT TCT AGTCTTCGA
 T__ C
 GAM2666 LOC158722 3' AGCTTCTGAGCTACCTTT 39888 ACTA A
 AAAG TAG TCAGAAGCT
 ||| ||| |||||
 TTTC ATC AGTCTTCGA
 C__ G
 GAM2666 LOC169026 3' AGCTTCCGCTTTTATCTTTGAA 40263 CTAT ATCA
 TTCAAAGA AG GAAGCT
 ||||| || |||||
 AAGTTTCT TC CTTCGA
 ATTT GC__
 GAM2667 CASP8AP2 3' AGAAGCTTCAAATTCCTCA 14430 C G G
 TGAGGAATT TGAA G TTCT
 ||||| ||| | |||
 ACTCCTTAA ACTT C AAGA
 _ _ G
 GAM2667 LIFR 3' TAGTGA CTCAGAATCCTCA 8105 A AGG _
 TGAGGA TTCTGA GTT CTA
 ||||| ||||| ||| |||
 ACTCCT AAGACT CAG GAT
 _ _ T
 GAM2667 NDRG3 3' AGAACCCATTTCTCA 25721 TCTGAA
 TGAGGAAT GGGTTCT
 ||||| |||||
 ACTCTTTA CCAAGA

 GAM2667 PKD2 3' AATTTTGCAGAATTCCTC 30176 A
 GAGGAATTCTG AGGGTT
 ||||| |||||
 CTCCTTAAGAC TTTTAA
 G
 GAM2667 C16orf5 3' GGCCCTCAGA ACTCTCA 15055 AA A
 TGAGG TTCTGA GGGTT
 |||| ||||| |||||
 ACTCT AAGACT CCCGG
 C_ _
 GAM2667 FLJ22635 3' GGCCCCTTCAGAATTCCTCA 24718 TT
 TGAGGAATTCTGAAGGG C
 ||||| ||||| |||
 ACTCCTTAAGACTTCCC G
 CG
 GAM2667 KIAA0391 3' ATTAGTTAAAATTCCTCA 16135 C AG
 TGAGGAATT TGA GGT
 ||||| ||| |||

ACTCCTTAA ATT TTA
 A GA
 GAM2667 KIAA1340 3' TAGATCAACATTCCTCA 34297 TC AGGGT
 TGAGGAAT TGA TCTA
 ||||| || |||
 ACTCCTTA ACT AGAT
 CA ____
 GAM2667 KIAA1576 3' TGTCCAGCTCCTAGAAATTCCTC 32777 AA CT
 A TGAGGAATTCTG GGGTT ACA
 ||||| ||| |||
 ACTCCTTAAGAT CTCGA TGT
 C_ CC
 GAM2667 MGC13033 5' GCATCTTCAGAATCCCCCA 25461 A A _
 TG GG ATTCTGAAGG GT
 || || ||||| ||
 AC CC TAAGACTTCT CG
 C C A
 GAM2667 PACSIN2 3' TAGAACCTTAGGTAGAACTCC 14099 A AA__
 GGA TTCTG GGGTTCTA
 || ||| |||||
 CCT AAGAT TCCAAGAT
 C GGAT
 GAM2667 PRO2015 5' AACCCGAATTCCTCA 20583 TGAA
 TGAGGAATTC GGGTT
 ||||| |||
 ACTCCTTAAG CCCAA

 GAM2667 Rpo1-2 3' TGTATCGTCTTCAGACTCCTCA 21107 AT GTTC
 TGAGGA TCTGAAGG TACA
 |||| | ||||| |||
 ACTCCT AGACTTCT ATGT
 C_ GCT_
 GAM2667 STI2 3' TGTA AAATAGACAGAATTCC 42878 AAGG C
 GGAATTCTG GTT TACA
 ||||| || |||
 CCTTAAGAC TAA ATGT
 AGA_ A
 GAM2667 LOC140214 5' AGCTCTCAAAATTCCTCA 37399 C A
 TGAGGAATT TGA GGGTT
 ||||| || |||
 ACTCCTTAA ACT CTCGA
 A _
 GAM2667 LOC142927 3' ATTCTTTAGAAATCCCCCA 37566 A A
 TG GG ATTCTGAAGGGT
 || || ||||| |||
 AC CC TAAGATTTCTTA
 C C
 GAM2667 LOC150311 5' TAGGCATTTTCCAGAATTCCTC 38928 A _
 A TGAGGAATTCTG AGGGT TCTA
 ||||| ||| |||

		ACTCCTTAAGAC TTTTA GGAT		
		C C		
GAM2667	LOC158267 3'	AGCTCCTGAATTCCTCA 39791	TGAA	
		TGAGGAATTC GGGTT		
		ACTCCTTAAG CTCGA		
		TC__		
GAM2667	LOC219445 5'	AGCTGTCTCAGAATTCCTC 44010	AG_	
		GAGGAATTCTGA GGT		
		CTCCTTAAGACT TCGA		
		CTG		
GAM2667	LOC220514 3'	TAGAACCTTAGGTAGAACTCC 30323	A AA__	
		GGA TTCTG GGGTTCTA		
		CCT AAGAT TCCAAGAT		
		C GGAT		
GAM2667	LOC90841 3'	ACCTTCCCCAGAACCCTCA 32110	AA A__	
		TGAGG TTCTG AGGGT		
		ACTCC AAGAC TTCCA		
		C_ CCC		
GAM2667	LOC93259 5'	ACCCCCAGAATTTCTCA 35555	AA	
		TGAGGAATTCTG GGGT		
		ACTCTTTAAGAC CCCA		
		CC		
GAM2668	ZF 3'	TGACAAAAATATGGTGTCTATAA 22192	G TTCC__	
	TA	TGTTATGG ATTAT GTCA		
		ATAATACT TGGTA CAGT		
		G TAAAAA		
GAM2668	LOC114984 5'	AGTGACGGTGGGATCCACAACA 36219	ATG ATTT	
		TGTT GGATT CCGTCACT		
		ACAA CCTAG GGCAGTGA		
		CA_ GGT_		
GAM2669	BAP1 3'	AAGCCAGGTCTTCTCTCT 11022	AC	
		AGAGAGAAGATCTG GCTT		
		TCTCTCTTCTGGAC CGAA		
		—		
GAM2669	D12S2489E 5'	AAGAATCAAGATCTTCCCTCT 14290	A _ CG	
		AGAG GAAGATCT GA CTT		
		TCTC CTTCTAGA CT GAA		
		C A AA		
GAM2669	DTNA 3'	AAGTTGTTGATCAGACCCTTCT 26837	A_ _ CTT	
	CT	AGAGAAG TCTGA CG GCTT		

			TCTCTTC AGACT GT TGAA	
			CC A TGT	
GAM2669	DTNA	3'	AAGTTGTTGATCAGACCCTTCT 26842	A_ _ CTT
	CT		AGAGAAG TCTGA CG GCTT	
			TCTCTTC AGACT GT TGAA	
			CC A TGT	
GAM2669	DTNA	3'	AAGTTGTTGATCAGACCCTTCT 26847	A_ _ CTT
	CT		AGAGAAG TCTGA CG GCTT	
			TCTCTTC AGACT GT TGAA	
			CC A TGT	
GAM2669	DTNA	3'	AAGTTGTTGATCAGACCCTTCT 7079	A_ _ CTT
	CT		AGAGAAG TCTGA CG GCTT	
			TCTCTTC AGACT GT TGAA	
			CC A TGT	
GAM2669	EFNB2	3'	AGGTAGGTCAGATCCCCCTC 10294	AA_ G T
			GAG GATCTGAC CT GCTT	
			CTC CTAGACTG GA TGGA	
			CCC _ _	
GAM2669	FOXF1	3'	GAGCTCAGATCTCCCTC 7185	A A C
			GAG GA GATCTGA GCTT	
			CTC CT CTAGACT CGAG	
			C _ _	
GAM2669	HPS1	3'	AGGCCCCAGATCCTTCTCTCT 5692	_ AC
			AGAGAGAAG ATCTG GCTT	
			TCTCTCTTC TAGAC CGGA	
			C CC	
GAM2669	PRKG2	3'	AAGCAAGAAATATTTTCTCTC 12939	CTGACG
			GAGAGAAGAT CTTGCTT	
			CTCTCTTTTA GAACGAA	
			TAAA_	
GAM2669	ZNF216	3'	GAGGATCAGACCTTCTTTC 12620	A CG
			GAGAGAAG TCTGA CTT	
			CTTTCTTC AGACT GAG	
			C AG	
GAM2669	ABCA10	5'	AAGTGCTTCAAATACTTCTCTC 27823	_ C C TT
	T		AGAGAGAAG AT TGA GC GCTT	
			TCTCTCTTC TA ACT CG TGAA	
			A A T _	
GAM2669	FLJ12425	3'	AAGCAAGTTGGTGACCTTCCTC 41561	A A TGAC
	T		AGAG GAAG TC GCTTGCTT	

			TCTC CTTC AG TGAACGAA		
			_ C TGGT		
GAM2669	FLJ12484	3'	AAGCAAGCGAGGGACTTCACTC 23015	A A	GA
		T	AGAG GAAG TCT CGCTTGCTT		
			TCTC CTTC AGG GCGAACGAA		
			A _ GA		
GAM2669	FLJ12484	3'	AAGCAAGCGAGGGACTTCACTC 34513	A A	GA
		T	AGAG GAAG TCT CGCTTGCTT		
			TCTC CTTC AGG GCGAACGAA		
			A _ GA		
GAM2669	FLJ13441	3'	CAAAGTCACCTTTCTCTC 23390	ATC	GC
			GAGAGAAG TGAC TTG		
			CTCTCTTT ACTG AAC		
			CC_ A_		
GAM2669	FLJ22195	3'	AAGCAGTCAGCCTTCTCTC 22996	AT	_
			GAGAGAAG CTGAC GCTT		
			CTCTCTTC GACTG CGAA		
			C_ A		
GAM2669	KIAA0472	3'	AAGCAAAGACCTTTCTCT 35573	A A	GAC
			AGAGAGA G TCT GCTT		
			TCTCTTT C AGA CGAA		
			_ C AA_		
GAM2669	KIAA0794	3'	AGCAAGTCACCTTCCTTCT 39176	A	ATC GC
			AGAG GAAG TGAC TTGCT		
			TCTT CTTC ACTG AACGA		
			C C_ _		
GAM2669	PAK6	5'	AGGTCCCAGGTCTTCCCTCT 21387	A	AC
			AGAG GAAGATCTG GCTT		
			TCTC CTTCTGGAC TGGA		
			C CC		
GAM2669	RAI17	3'	AGCAAACCATTTCTCTC 43856	ATC	ACGC
			GAGAGAAG TG TTGCT		
			CTCTCTTT AC AACGA		
			_ CA_		
GAM2669	RHO6	3'	AAGCCCCAGACCCCTTCTCT 15819	A_	AC
			AGAGAAG TCTG GCTT		
			TCTCTTC AGAC CGAA		
			CCCC CC		
GAM2669	LOC155006	3'	AAGCAAGTGCATAACCTTCTC 39522	ATC_	A
			GAGAAG TG CGCTTGCTT		

		CTCTTC AC GTGAACGAA		
		CAAT _		
GAM2669	LOC199926 5'	AAGCAAGCATATATTCTCTCTC 43258	A	TCTGAC
	T	AGAGAGA GA GCTTGCTT		
		TCTCTCT CT CGAACGAA		
		_ TATATA		
GAM2669	LOC202316 5'	AAGCAAGCATATATTCTCTCTC 43422	A	TCTGAC
	T	AGAGAGA GA GCTTGCTT		
		TCTCTCT CT CGAACGAA		
		_ TATATA		
GAM2669	LOC219899 3'	GGGCCAGAACTTCTCTCT 43992	A	AC
		AGAGAGAAG TCTG GCTT		
		TCTCTCTTC AGAC CGGG		
		A _		
GAM2670	ATP5B 5'	CCAATTCTAAATGCCCTGGA 30005	A	CATTTTC
		TC CAGGGCATT ATTGG		
		AG GTCCCGTAA TAACC		
		_ ATCT__		
GAM2670	ISL1 3'	GAAATGAATGCTCCATGA 7959	CA	
		TCA GGGCATTCATTTT		
		AGT CTCGTAAGTAAAG		
		AC		
GAM2670	TRIM 3'	CCAATGGGCAATAGCCC 18529	_	CATT
		GGGC ATT TTCATTGG		
		CCCG TAA GGGTAACC		
		A C__		
GAM2670	ARHGEF15 3'	CCAATGAAAACGGCCGCCT 17317	AT	A
		GGGC TC TTTTCATTGG		
		TCCG GG AAAAGTAACC		
		CC C		
GAM2670	KIAA0326 3'	CCAACGAAGGGGGTGCCCTGT 32158	A	A
		ACAGGGCATTCTTTTC TTGG		
		TGTCCCGTGGG GGAAG AACC		
		_ C		
GAM2670	KIAA0416 3'	CCAATAAAAATGAGCCCTATG 17833	C	AT C
		CA AGGGC TCATTTT ATTGG		
		GT TCCCG AGTAAAA TAACC		
		A _ A		
GAM2671	MGC15705 3'	ATCTCAGGCTGGGAAGA 26499	A	C
		TCTTCCTA GTC GAGAT		

AGAAGGGT CGG CTCTA
 _ A
 GAM2671 LOC153561 3' CTCTGATGTTCAAGAGTA 39401 A _ AA_ C
 CCA TG TACTCTTC CT GTC GAG
 || ||||| || ||| ||
 AC ATGAGAAG GA TAG CTC
 C T CTTG T
 GAM2671 LOC223073 5' ATCTCCCTAAGGAAGAGT 45315 A TCC
 ACTCTTCCT AG GAGAT
 ||||| || ||||
 TGAGAAGGA TC CTCTA
 A C_
 GAM2671 LOC255231 3' ATCTCGGAATGGAAAAAGATCA 45672 ACTC TAAG
 TGAT TTCC TCCGAGAT
 ||| ||| |||||
 ACTA AAGG AGGCTCTA
 GAAA TA_
 GAM2672 DXYS155E 3' GTCCTTTAAGATCAAACTCA 11542 C AGTAA
 TGAGT TTT TTAAAGGAC
 |||| ||| |||||
 ACTCA AAA AATTCCTG
 _ CTAG_
 GAM2672 MLLT2 3' TCCTTTAATTTCAAGGTCTCA 12572 T TAGT
 TGAG CTT AAATTAAAGGA
 ||| ||| |||||
 ACTC GGA TTAAATTCCT
 T C_
 GAM2672 DKFZP761E2110 3' TCCTTTAAAAATTCCAAAGCTC 25227 T AGTAA_
 A TGAG CTTT TTAAAGGA
 ||| ||| |||||
 ACTC GAAA AATTCCT
 _ CCTTAA
 GAM2672 PIK3R4 5' TCCTAACCTTACTAAAGACCA 31149 A ATTAA
 TG GTCTTTAGTAA AGGA
 || ||||| |||
 AC CAGAAATCATT TCCT
 _ CCAA_
 GAM2672 TMPRSS5 3' GTCCTCTTTCTCACTAGAGACT 25055 AAATTAA
 CA TGAGTCTTTAGT AGGAC
 ||||| |||
 ACTCAGAGATCA TCCTG
 CTCTTTC
 GAM2672 LOC129011 3' TCCTTTAATTTACCTGAT 36966 TTTA
 GTC GTAAATTAAAGGA
 ||| |||||
 TAG CATTTAATTCCT
 TC_
 GAM2672 LOC132235 5' CCTTCCACTAAGGACTCA 37481 AAATT
 TGAGTCTTTAGT AAAGG
 ||||| |||

	ACTCAGGAATCA	TTTCC	
	CC__		
GAM2672 LOC144363	3' TCCTCTAACTTAATAGGACTTA	37731	TAG A A
	TGAGTCTT TAA TTA AGGA		
	ATTCAGGA ATT AAT TCCT		
	TA_ C C		
GAM2672 LOC144571	3' TCCTTTAATCCTGGCTCA	40443	TTT TAA
	TGAGTC AG ATTAAAGGA		
	ACTCGG TC TAATTCCT		
	__ C__		
GAM2673 SLC4A7	3' CTAATAAAGGATCATGAGGAA	9669	T ATAAGA
	TTCCTCAT GA TTATTAG		
	AAGGAGTA CT AATAATC		
	_ AGGA__		
GAM2673 LEC3	3' GAACTCATTTCATGAGGAA	17570	T A A
	TTCCTCAT GAAT AG TT		
	AAGGAGTA CTTA TC AG		
	_ C A		
GAM2673 MGC2835	3' ATCTTCCCAATGAGGAA	23502	AAT
	TTCCTCATTG AAGAT		
	AAGGAGTAAC TTCTA		
	CC_		
GAM2673 LOC196264	3' ATCCCATTAATGAGGAA	42332	G AA
	TTCCTCATT AAT GAT		
	AAGGAGTAA TTA CTA		
	A CC		
GAM2673 LOC202460	5' AGTGATTTATTCCATAAGGAA	42980	C T A
	TTCCT AT GAATA GATTATT		
	AAGGA TA CTTAT TTAGTGA		
	A C _		
GAM2674 BCL10	5' CTTCTCAGGTTGCTTCTTACAC	10008	C TA_ GG
A	TGTG AAGA AACC TGAGAAG		
	ACAC TTCT TTGG ACTCTTC		
	A TCG _		
GAM2674 CLDN14	5' GCTGAGTCCTCTTGCACA	29310	TAA _
	TGTGCAAGA AC CGGT		
	ACACGTTCT TG GTCG		
	CC_ A		
GAM2674 GNPI	3' TCTTGAGAGTCCTTCTTGCACA	11967	TAA CGG
	TGTGCAAGA AC TGAGA		

		ACACGTTCT	TG	GTTCT		
		TCC	AGA			
GAM2674	OTC	5'	TTCTCTATCATCTTGCAC	6133	AAACC	_
			GTGCAAGAT	GGT	GAGAA	
			CACGTTCTA	CTA	CTCTT	
			_____	T		
GAM2674	RERE	3'	CTCTTCCATTTTGCACA	14406	AAACC	T_
			TGTGCAAGAT	GG	GAG	
			ACACGTTTTA	CC	CTC	
			_____	TT		
GAM2674	ASPN	5'	CTCATCTTTTCTTCTTACACA	19224	C	TA CC
			TGTG AAGA	AA	GGTGAG	
			ACAC TTCT	TT	CTACTC	
			A	TC	TT	
GAM2674	C12orf22	3'	CTCCTACTTATCTTGCTCA	25127	T	ACC T
			TG GCAAGATAA	GG	GAG	
			AC CGTTCTATT	TC	CTC	
			T	CA_	_	
GAM2674	CASP9	3'	CTCACCCCTGCCTTATCTTGCAC	6900	ACC_	
			GTGCAAGATAA	GGTGAG		
			CACGTTCTATT	CCACTC		
			CCGTC			
GAM2674	DKFZP434J193	3'	CTCCTTAAATTTATCTTCACA	35165	C	CC_ T
			TGTG AAGATAAA	GG	GAG	
			ACAC TTCTATTT	TC	CTC	
			_____	AAAT	_	
GAM2674	DKFZP564B1162	5'	TCTTTCCTCTTGCACA	25338	TAAACC	T
			TGTGCAAGA	GG	GAGA	
			ACACGTTCT	CC	TTCT	
			_____	T		
GAM2674	FLJ10997	3'	CTTGAGGCTCATCTTGCACA	20283	AAA	GG
			TGTGCAAGAT	CC	TGAG	
			ACACGTTCTA	GG	GTTC	
			CTC	A_		
GAM2674	FLJ12903	3'	CTTATTGAACTTATTTTGCACA	22979	AC_	
			TGTGCAAGATAA	CGGTGAG		
			ACACGTTTTATT	GTTATTC		
			CAA			
GAM2674	FLJ13189	3'	CTTCCCACCTTCCATTCTTGCAC	24331	TAAACC	A
	A		TGTGCAAGA	GGTG	GAAG	

ACACGTTCT TCAC CTTC
 TACCT_ C
 GAM2674 FLJ13615 5' TTCTCATCATCCTGAACA 24764 G A AAACC
 TGT CA GAT GGTGAGAA
 ||| || ||| |||||
 ACA GT CTA CTACTCTT
 A C ____
 GAM2674 FLJ22169 3' TCTCTCCGCTTCTTGCACA 23525 TAAAC T
 TGTGCAAGA CGG GAGA
 ||||| ||| |||
 ACACGTTCT GCC CTCT
 TC__ T
 GAM2674 GIT2 3' CTCCTTTATCTTGCA 27685 ACC T
 TGCAAGATAA GG GAG
 ||||| ||| |||
 ACGTTCTATT TC CTC
 ____ -
 GAM2674 GIT2 3' CTCCTTTATCTTGCA 27698 ACC T
 TGCAAGATAA GG GAG
 ||||| ||| |||
 ACGTTCTATT TC CTC
 ____ -
 GAM2674 GIT2 3' CTCCTTTATCTTGCA 16603 ACC T
 TGCAAGATAA GG GAG
 ||||| ||| |||
 ACGTTCTATT TC CTC
 ____ -
 GAM2674 KIAA0430 3' TTTCCCATCTTGCA 21153 AAACC T
 GTGCAAGAT GG GAGA
 ||||| ||| |||
 CACGTTCTA CC CTTT
 ____ -
 GAM2674 KIAA1789 5' CTCCTGCTTATCTTGCACA 33310 AC T
 TGTGCAAGATAA CGG GAG
 ||||| ||| |||
 ACACGTTCTATT GTC CTC
 C_ _
 GAM2674 KIAA1805 3' TCTTGTTTTTTTATCTTGCCCA 39001 T CC TG
 TG GCAAGATAAA GG AGA
 || ||||| ||| |||
 AC CGTTCTATTT TT TCT
 C TT GT
 GAM2674 MGC15631 3' TCTCACCGTGTGCTCGCCA 26495 T A A AAC
 TG GC AG TA CGGTGAGA
 || ||| ||| |||||
 AC CG TC GT GCCACTCT
 _ C _ GT_
 GAM2674 MGC5139 5' CTCAAAAAAGTTCACTTGCACA 36676 ATA CGG_
 TGTGCAAG AAC TGAG
 ||||| ||| |||

		ACACGTTC TTG ACTC	
		AC_ AAAAA	
GAM2674	PPP1R10	5' TTCCACCTATCTTGCCCA 8580	T AACC A
		TG GCAAGATA GGTG GAA	
		AC CGTTCTAT CCAC CTT	
		C _ _ C	
GAM2674	RAB35	3' TTCTCACCGACTCTCCAC 13735	CA TAAAC
		GTG AGA CGGTGAGAA	
		CAC TCT GCCACTCTT	
		C_ CA_	
GAM2674	TRIM26	3' CCAGGTTCTTCTTGCACA 9499	TA_ _
		TGTGCAAGA AACC GG	
		ACACGTTCT TTGG CC	
		TCC A	
GAM2674	LOC137964	5' CTCAGTCTCACTTGCACA 37111	ATAAAC
		TGTGCAAG CGGTGAG	
		ACACGTTC GTCAGTC	
		ACTC_	
GAM2674	LOC144110	3' CTCCCCTTTTTCATCTGCACA 37680	A _ CC T
		TGTGCA GAT AAA GG GAG	
		ACACGT CTA TTT CC CTC	
		_ C TT C	
GAM2674	LOC146226	5' CTCTCGGCTCATTTTGCACA 40663	AAA T
		TGTGCAAGAT CCGG GAG	
		ACACGTTTTA GGCT CTC	
		CTC _	
GAM2674	LOC157922	3' CTTCTCACCTCGCCCCCTTGCA 41889	ATAAACC
	CA	TGTGCAAG GGTGAGAAG	
		ACACGTTC CCACTCTTC	
		CCCCGCT	
GAM2674	LOC158125	5' CTCTCCAGGCTTCCTTGCACA 39730	ATAAA _ T
		TGTGCAAG CC GG GAG	
		ACACGTTC GG CC CTC	
		CTTC_ A T	
GAM2674	LOC221773	3' CTCATGGAGTCATCTTGCACA 43764	AAA_ G
		TGTGCAAGAT CCG TGAG	
		ACACGTTCTA GGT ACTC	
		CTGA _	
GAM2674	LOC257494	3' CCAGGTTCTTCTTGCACA 46686	TA_ _
		TGTGCAAGA AACC GG	

		ACACGTTCT TTGG CC	
		TCC A	
GAM2675	PCDHA9	5' CTCTTACACTAGAATCCT 15210	ACTA
		AGGATTCTAGT TAAGGG	
		TCCTAAGATCA ATTCTC	
		C__	
GAM2675	PCDHA9	5' CTCTTACACTAGAATCCT 25602	ACTA
		AGGATTCTAGT TAAGGG	
		TCCTAAGATCA ATTCTC	
		C__	
GAM2675	SRD5A1	3' CTCCCCCTATAGGGCTGGAATC 6715	TA A
	T	GGATTCTAG CTATA GGGGAG	
		TCTAAGGTC GATAT CCCCTC	
		GG C	
GAM2675	ARPP-19	3' CTCAGATAGTACTGAACCCT 13420	A T AA
		AGG TTC AGTACTAT GGG	
		TCC AAG TCATGATA CTC	
		C _ GA	
GAM2675	ATP6V1B2	3' CTCCAAATAATACACAGAATCC 7414	A_ C AA
	T	AGGATTCT GTA TAT GGGG	
		TCCTAAGA CAT ATA CCTC	
		CA A AA	
GAM2675	C1orf34	3' CCCCTCTGCCAGGATCCT 30436	A CTATA
		AGGATTCT GTA AGGGG	
		TCCTAGGA CGT TCCCC	
		C C__	
GAM2675	FLJ13912	3' CTTGTACAGAACCAAGAATCCT 23029	A A _
		AGGATTCT GT CT ATAAG	
		TCCTAAGA CA GA TGTTC	
		C A CA	
GAM2675	FLJ20511	3' CCCTTTAATACAGAACCCCT 19527	A A CTA
		AGG TTCT GTA TAAGGGG	
		TCC AAGA CAT ATTTCCC	
		C _ A__	
GAM2675	HCA127	3' CTCCCACATATACTAAAATTCT 20756	C C AAG
		AGGATT TAGTA TAT GGGAG	
		TCTTAA ATCAT ATA CCCTC	
		A _ CA_	
GAM2675	LOC254057	3' CTCCCCCTCTAGAATACCAGGA 46345	A _ TAA
	TCCT	AGGATTCT GTA CTA GGGGAG	

TCCTAGGA CAT GAT CCCCTC
 C AA CTC
 GAM2675 LOC92935 3' CCCCCAAACTTATCAGAATCCT 35132 A CTATAA
 AGGATTCT GTA GGGG
 ||||| || |||
 TCCTAAGA TAT CCCC
 C TCAAAC
 GAM2676 KNSL1 3' ATAAGAACTGTACTCTTCTCA 10862 AT GTAAC
 TGA AGAG GTTCTTAT
 || ||| |||||
 ACT TCTC CAAGAATA
 CT ATGT_
 GAM2676 KIAA0254 3' ATAAGAGTCCCCACCTCTACTC 16505 A AACG_
 GA TAGAGGT TTCTTAT
 || ||||| |||||
 CT ATCTCCA GAGAATA
 C CCCCT
 GAM2676 SULT1C2 5' AGAGTGCTGCCTCTATCCA 13351 A A
 TG ATAGAGGTA CGTTCT
 || ||||| |||||
 AC TATCTCCGT GTGAGA
 C C
 GAM2676 LOC144519 5' AAGAACACCTACCTCTAT 37755 AC_
 ATAGAGGTA GTTCTT
 ||||| |||||
 TATCTCCAT CAAGAA
 CCA
 GAM2677 PAICS 3' AATGTATTAGTGAAT 13162 ATT
 ATTCACTA ATGCGTT
 ||||| |||||
 TAAGTGAT TATGTAA

 GAM2677 KIAA0844 3' TAACCAGAGCTTAGCAAATGGG 17284 CA TTA_ C
 A TCCCAT CTAA TG GTTA
 ||||| ||| || |||
 AGGGTAA GATT AC CAAT
 AC CGAG _
 GAM2677 LOC126669 3' AACTGCTAGAAAATGGGAG 37153 CA ATTAT _
 CTCCCAT CT A GC GTT
 ||||| ||| || |||
 GAGGGTAA GAT CG CAA
 AA _____ T
 GAM2677 LOC145644 5' ACAGTAATAATGGGAG 32289 CACTA GC
 CTCCCAT ATTAT GT
 ||||| ||||| ||
 GAGGGTAA TAATG CA
 _____ A_
 GAM2677 LOC90829 5' GCAATTGTGAATGGGAG 32055 T TA
 CTCCCATTCAC AAT TGC
 ||||| ||| |||

GAGGGTAAGTG TTA ACG

GAM2678 JAG2 3' TTTGTAAATGTGTACATAT 8008 T
ATAT TACATATTTACAAA
|||||
TATA ATGTGTAAATGTTT
C
GAM2678 MAB21L1 3' TTGAAATGTTATTTAAATATAT 12114 C__ A
TCA TGAATATATTTA ATATTT CAA
|||||
ACTTATATAAAT TGTAAA GTT
TTAT
GAM2678 MTM1 3' TTTGTAAATGCTGTAAATATTT 5793 T _
CA TGAA ATATTTACA TATTTACAAA
|||||
ACTT TATAAATGT GTAAATGTTT
C
GAM2678 VHL 3' TTTGTAAATATGTGACATTC 6166 ATAT
GAAT TTACATATTTACAAA
|||||
CTTA AGTGTATAAATGTTT
C__
GAM2678 ANKT 3' TTGTAAATATTCCTGTATTC 18500 TTTAC
GAATATA ATATTTACAA
|||||
CTTATGT TATAAATGTT
CCT__
GAM2678 DKFZP761L0424 3' TTTGTAAATATATAAATATA 43892 C
TATATTTA ATATTTACAAA
|||||
ATATAAAT TATAAATGTTT
A
GAM2678 FLJ10852 3' TAAATATGTAAAAAATATTTA 21118 A_
TGAATAT TTTACATATTTA
|||||
ATTTATA AAATGTATAAAT
AA
GAM2678 FLJ22054 3' TTGTAAATATGTCTGTAATATT 45320 _ TT
AATAT AT ACATATTTACAA
|||||
TTATA TG TGTATAAATGTT
A TC
GAM2678 FLJ23259 3' TTTGTAAATATATATATATATT 24064 T C
AATATAT TA ATATTTACAAA
|||||
TTATATA AT TATAAATGTTT
T A
GAM2678 HSMPP8 3' TTTGTAAATATGCTGTAGTCA 44906 A TTTA
TGA TATA CATATTTACAAA
|||||

ACT ATGT GTATAAATGTTT
 G C___
 GAM2678 KIAA1014 3' TTGTAAATTTGTATATATG 32572 T T
 TATAT TACA ATTTACAA
 ||||| ||||| |||||
 GTATA ATGT TAAATGTT
 T T
 GAM2678 MGC35558 3' GTGAGTCTAAATATATTCA 29618 CAT
 TGAATATATTTA ATTTAC
 ||||| |||||
 ACTTATATAAAT TGAGTG
 C___
 GAM2678 Spir-1 3' TTGTAAATACTGTAATATATTT 32309 T _
 A TGAATATATT ACA TATTTACAA
 ||||| |||||
 ATTTATATAA TGT ATAAATGTT
 _ C
 GAM2678 ZFD25 3' TTTGTAGATGTATAATTACATT 18326 A T C
 CA TGAAT TA TTA ATATTTACAAA
 ||||| |||||
 ACTTA AT AAT TGTAGATGTTT
 C T A
 GAM2678 LOC157503 3' TGTAAATATATATATTCA 41816 TTAC
 TGAATATAT ATATTTACA
 ||||| |||||
 ACTTATATA TATAAATGT

 GAM2678 LOC201475 3' TTGTAAATATGCATATATGCA 42579 A TTA
 TG ATATAT CATATTTACAA
 || ||||| |||||
 AC TATATA GTATAAATGTT
 G C___
 GAM2678 LOC221814 5' TTTGGGTATATGTACATACATT 45098 A T TTA
 CA TGAAT TAT TACATAT CAAA
 ||||| ||||| |||||
 ACTTA ATA ATGTATA GTTT
 C C TGG
 GAM2679 BTEB1 3' TATGCTTTTAGTTAACATCATT 6871 CA T _
 AT ATAATGAT TTA CTA AGCATA
 ||||| ||||| |||||
 TATTACTA AAT GAT TCGTAT
 C_ T TT
 GAM2679 NPAT 3' TATACTTAGATATAGTGCATTG 33387 ATCAT C
 T ATAATG TATCTAAG ATA
 ||||| ||||| |||||
 TGTTAC ATAGATTC TAT
 GTGAT A
 GAM2679 PRO0641 5' ATGCCGTAATGTCATTAT 15401 T CTAA
 ATAATGA CATTAT GCAT
 ||||| ||||| |||||

TATTACT GTAATG CGTA
 _ C_
 GAM2679 RAB14 3' TATGCTTAAATAGATC 18450 AT C
 GATC TAT TAAGCATA
 |||| |||||
 CTAG ATA ATTCGTAT
 _ A
 GAM2679 WNT2B 3' ATGCTTAACAGATCATT 10392 ATTATC
 TAATGATC TAAGCAT
 ||||| |||||
 ATTACTAG ATTCGTA
 ACA_
 GAM2679 WNT2B 3' ATGCTTAACAGATCATT 23693 ATTATC
 TAATGATC TAAGCAT
 ||||| |||||
 ATTACTAG ATTCGTA
 ACA_
 GAM2679 LOC221060 3' TATGCTAAGATGATTATTAT 44769 TTA A
 ATAATGATCA TCT AGCATA
 ||||| |||||
 TATTATTAGT AGA TCGTAT
 _ A
 GAM2680 ADAM10 3' CCAATGTACATACCTTGTTATA 6767 ATA _
 TATAACAAG TATGTG TGG
 ||||| |||||
 ATATTGTTT ATACAT ACC
 C_ GTA
 GAM2680 CACNG2 5' TCATACATATATCCATTATA 12724 CAA
 TATAA GATATATGTGTGG
 |||| |||||
 ATATT CTATATACATACT
 AC_
 GAM2680 FBXL3A 3' TTACACATACACCTGTTATA 14458 AGATA
 TATAACA TATGTGTGG
 ||||| |||||
 ATATTGT ATACACATT
 CCAC_
 GAM2680 HGF 3' TCACCATGTATCCTGCAATA 45227 AA A T
 TAT CA GATATATG GTGG
 || ||||| |||||
 ATA GT CTATGTAC CACT
 AC C _
 GAM2680 PYGB 3' CACACATCTTGCTATG 8765 A TATA
 TATA CAAGA TGTGTG
 |||| |||||
 GTAT GTTCT ACACAC
 C _
 GAM2680 DKFZp564K142 3' CCCACATATGCCTGTTA 25806 A A T
 TAACA G TATATGTG GG
 |||| | ||||| ||

		ATTGT C GTATACAC CC	
		_C _	
GAM2680 KIAA0429	5'	CCGCACTCATCCTGTTATA 16470	A ATAT
		TATAACA GAT GTGTGG	
		ATATTGT CTA CACGCC	
		C CT_	
GAM2680 KIAA1691	3'	CCACTTCATATTTGTTATA 44465	GAT T_
		TATAACAA ATATG GTGG	
		ATATTGTT TATAC CACC	
		__ TT	
GAM2680 MGC3248	3'	ACCACACAATTACTTTTATA 26233	C A TA
		TATAA AAG TA TGTGTGGT	
		ATATT TTC AT ACACACCA	
		_ _ TA	
GAM2680 MMD	3'	TTACCATGTTTCATCTTGGCAT 30077	AA ATAT TG
A		TAT CAAGAT G TGGTAA	
		ATA GTTCTA T ACCATT	
		CG CTT_ GT	
GAM2680 PMAIP1	3'	TTATACATATTACCTTGTTATA 22103	AT_
		TATAACAAG ATATGTGTGG	
		ATATTGTTT TATACATATT	
		CAT	
GAM2680 PRO0611	5'	CCATGTCATGTATCTCATTATA 15303	CA _
		TATAA AGATATATG TGTGG	
		ATATT TCTATGTAC GTACC	
		AC T	
GAM2680 SE57-1	3'	TACCTTGATTACATATGTTGTT 24891	AG T__
A		TAACA ATATATGTG GGTA	
		ATTGT TGTATACAT CCAT	
		_ TAGTT	
GAM2680 LOC127255	3'	TTACCAAATATATAACTT 29775	A G
		AAG TATATGT TGGTAA	
		TTC ATATATA ACCATT	
		A A	
GAM2681 FLJ13456	3'	CGAATGTTAATGTCTAAGACA 32797	A TTCT C
		TGTC TA ACA TAACATTGG	
		ACAG AT TGT ATTGTAAGC	
		A C_ A	
GAM2681 KIAA1979	5'	GAATGTGAAGAATGTGACA 42590	ACACTA
		TGTCATATTCT ACATTC	

			ACAGTGTAAGA	TGTAAG		
			AG_____			
GAM2681	MGC32104	3'	AATGTAAAGAATATGACA	29501	ACACTA	
			TGTCATATTCT	ACATT		
			ACAGTATAAGA	TGTAA		
			AA_____			
GAM2682	FCAR	5'	TGTCGTAAGAATATCTGTC	7729	TTCCA	A
			GAT	ATATTCTTAC ACA		
			CTG	TATAAGAATG TGT		
			TC_____	C		
GAM2682	FCAR	5'	TGTCGTAAGAATATCTGTC	28429	TTCCA	A
			GAT	ATATTCTTAC ACA		
			CTG	TATAAGAATG TGT		
			TC_____	C		
GAM2682	FCAR	5'	TGTCGTAAGAATATCTGTC	28431	TTCCA	A
			GAT	ATATTCTTAC ACA		
			CTG	TATAAGAATG TGT		
			TC_____	C		
GAM2682	FCAR	5'	TGTCGTAAGAATATCTGTC	28434	TTCCA	A
			GAT	ATATTCTTAC ACA		
			CTG	TATAAGAATG TGT		
			TC_____	C		
GAM2682	FCAR	5'	TGTCGTAAGAATATCTGTC	28435	TTCCA	A
			GAT	ATATTCTTAC ACA		
			CTG	TATAAGAATG TGT		
			TC_____	C		
GAM2682	FCAR	5'	TGTCGTAAGAATATCTGTC	28425	TTCCA	A
			GAT	ATATTCTTAC ACA		
			CTG	TATAAGAATG TGT		
			TC_____	C		
GAM2682	FCAR	5'	TGTCGTAAGAATATCTGTC	28427	TTCCA	A
			GAT	ATATTCTTAC ACA		
			CTG	TATAAGAATG TGT		
			TC_____	C		
GAM2682	PRKACA	3'	TGTTGTAAACATATTTGAAAAC	8599	A C TC	
	TA		TAG TTTC AATAT TTACAACA			
			ATC AAAG TTATA AATGTTGT			
			A T CA			
GAM2682	YWHAH	3'	TGTTGATCTATGGGAAATCTA	9440	A TTCTTA	
			TAGATTTCC ATA CAACA			

		ATCTAAAGG TAT	GTTGT		
		G CTA__			
GAM2682	ZNF10	3' TTGTAAGAGGATATCTA	17697	T AATAT	
		TAGAT TCC TCTTACAA			
		ATCTA AGG AGAATGTT			
		T ____			
GAM2682	DC8	3' TTGTGGTTTATTGGAACCTA	17752	AT TT T	
		TAG TTCCAATA CT ACAA			
		ATC AAGGTTAT GG TGTT			
		C_ TT _			
GAM2682	DCLRE1A	3' TGTGGGCACCTGGAAATCTA	34283	ATATT	
		TAGATTTCCA CTTACA			
		ATCTAAAGGT GGGTGT			
		CCAC_			
GAM2682	FLJ10704	3' GTTGCGTATTGGAAATT	20035	TCTTA	
		GATTTCCAATAT CAAC			
		TTAAAGGTTATG GTTG			
		C____			
GAM2682	FLJ23151	3' TGTAAGCTGGAAATTTA	24136	ATATT	
		TAGATTTCCA CTTACA			
		ATTTAAAGGT GAATGT			
		C____			
GAM2682	NUP160	3' TAAGAAAAAATTGGAAATC	42328	A__	
		GATTTCCAAT TTCTTA			
		CTAAAGGTTA AAGAAT			
		AAA			
GAM2682	LOC151996	5' TGTGATCTGGAAATCTA	41417	ATATTC	
		TAGATTTCCA TTACA			
		ATCTAAAGGT AGTGT			
		CT____			
GAM2682	LOC221596	5' AAGAAATCTGGAAATCTA	44173	ATA	
		TAGATTTCCA TTCTT			
		ATCTAAAGGT AAGAA			
		CTA			
GAM2682	LOC256073	3' TTGTAAGGATCATGGGAAATCT	46231	AAT_	
	A	TAGATTTCC ATTCTTACAA			
		ATCTAAAGG TAGGAATGTT			
		GTAC			
GAM2683	GNS	3' ATCAAAAATACTAACATCA	7855	CC GA	
		TGATG TAGTATTT GAT			

ACTAC ATCATAAA CTA
 A_ AA
 GAM2683 MTM1 3' ATCTCAAATACAGTAGTAT 5789 _ A
 ATGC CT GTATTTGAGAT
 |||| || |||||
 TATG GA CATAAACTCTA
 AT _
 GAM2683 C11orf21 3' ATATCTCAAACACCAGCATCA 15425 CTA A
 TGATGC GT TTTGAGATAT
 ||||| || |||||
 ACTACG CA AAACCTCTATA
 AC_ C
 GAM2683 C20orf38 3' CGAAACTAAGCATCATA 20322 C A
 TATGATGC TAGT TTTG
 ||||| ||| |||
 ATACTACG ATCA AAGC
 A _
 GAM2683 DREV1 3' CAAATACTTAGCACCATA 18107 A CT
 TATG TGC AGTATTTG
 |||| ||| |||||
 ATAC ACG TCATAAAC
 C AT
 GAM2683 FLJ10493 3' ATATTTTAGATATAAACATCAT 19884 CCTA
 A TATGATG GTATTTGAGATAT
 ||||| |||||
 ATACTAC TATAGATTTTATA
 AAA_
 GAM2684 CHS1 3' CAAATAATGATAAAGTCTATTTC 5526 G GATG
 A TGAA TAGA ATCATTATTTG
 |||| ||| |||||
 ACTT ATCT TAGTAATAAAC
 _ GAAA
 GAM2684 HOXC11 3' CAAATCACGCATCTCTACT 30209 ATCATT
 AGTAGAGATG ATTTG
 ||||| |||
 TCATCTCTAC TAAAC
 GCAC_
 GAM2684 MAPK14 3' CAAGTGATATCACCTCTCTTCA 7001 T A C
 TGAAG AGAG TGAT ATTATTTG
 |||| ||| ||| |||||
 ACTTC TCTC ACTA TAGTGAAC
 _ C _
 GAM2684 MAPK14 3' CAAGTGATATCACCTCTCTTCA 29105 T A C
 TGAAG AGAG TGAT ATTATTTG
 |||| ||| ||| |||||
 ACTTC TCTC ACTA TAGTGAAC
 _ C _
 GAM2684 MAPK14 3' CAAGTGATATCACCTCTCTTCA 29112 T A C
 TGAAG AGAG TGAT ATTATTTG
 |||| ||| ||| |||||

			ACTTC TCTC ACTA TAGTGAAC		
			— C —		
GAM2684	CHL1	3'	AAATAAAAGTTCTACTTCA	13390	ATGATCA
			TGAAGTAGAG TTATTT		
			ACTTCATCTT AATAAA		
			GAA_____		
GAM2684	MGC14289	3'	AGTGATCATCCCACCTCA	27946	A AGA
			TGA GT GATGATCATT		
			ACT CA CTACTAGTGA		
			C CC_		
GAM2684	MYH10	3'	CAAATAATGATCAATGCTATTT	34261	AGA
	CA		TGAAGTAG TGATCATTATTTG		
			ACTTTATC ACTAGTAATAAAC		
			GTA		
GAM2684	USP10	3'	CAAATAATGAAGATCTCTCCTT	31983	T GA
	CA		TGAAG AGAGAT TCATTATTTG		
			ACTTC TCTCTA AGTAATAAAC		
			C GA		
GAM2684	LOC145368	3'	CAAATAATGAAGATCTCTCCTT	37827	T GA
	CA		TGAAG AGAGAT TCATTATTTG		
			ACTTC TCTCTA AGTAATAAAC		
			C GA		
GAM2684	LOC150423	3'	CAAATAATGAAGATCTCTCCTT	38967	T GA
	CA		TGAAG AGAGAT TCATTATTTG		
			ACTTC TCTCTA AGTAATAAAC		
			C GA		
GAM2684	LOC152343	3'	AGTGATCATTCCACCTCA	39261	A A A
			TGA GT GAG TGATCATT		
			ACT CA CTT ACTAGTGA		
			C C _		
GAM2684	LOC197358	3'	CAAATAATGATCATACATCTTC	42506	TAGAG
	A		TGAAG ATGATCATTATTTG		
			ACTTC TACTAGTAATAAAC		
			TACA_		
GAM2685	MAGEB4	3'	TTAGAAATTTAAAATAACTC	8176	G AA
			GAG TATTTTAAAT TCTAA		
			CTC ATAAAATTTA AGATT		
			A A_		
GAM2685	CLDN1	3'	TAGCATACTTAAAATATCTCT	22083	A AT
			AGAGGTATTTTAA TA CTA		

			TCTCTATAAAATT AT GAT		
			C AC		
GAM2685	RBM7	3'	GGAAGTTAAAATATCTCT 18178	ATAA	
			AGAGGTATTTTAA TCT		
			TCTCTATAAAATT AGG		
			GA__		
GAM2685	LOC92497	5'	AGAATTTAAAACACCTCT 34460	A AA	
			AGAGGT TTTTAAAT TCT		
			TCTCCA AAAATTTA AGA		
			C _		
GAM2686	CANX	3'	TCATTTGCAATTCATGTAA 42277	TAAATAT	
			TTAC ATTGCAAATGA		
			AATG TAACGTTTACT		
			TACT__		
GAM2686	NCOA6IP	3'	GCAATATATTTTGTAAATA 24227	T	
			TATTAC AAATATATTGC		
			ATAATG TTTATATAACG		
			T		
GAM2686	EPLIN	3'	TGCAATATTTTAGTAATA 18497	T	
			TATTACTAAA ATATTGCA		
			ATAATGATTT TATAACGT		
			_		
GAM2686	LOC253970	3'	TCATCTGCAATATTTGG 46172	AT A	
			CTAAATAT TGCA ATGA		
			GGTTTATA ACGT TACT		
			_ C		
GAM2686	LOC57826	3'	TCATTTGCAGAAGTTAGTAA 22162	ATATA	
			TTACTAA TTGCAAATGA		
			AATGATT GACGTTTACT		
			GAA__		
GAM2687	FANCF	3'	TAATCCATGAAGGCCATCTTG 22924	TAAAC C	
			CAAG CC TCATGGATTA		
			GTTC GG AGTACCTAAT		
			TACC_ A		
GAM2687	FLJ10895	3'	AATCCATGATTTATACTCAGAA 21157	A_ AACCCC	
			TTC AGTA TCATGGATT		
			AAG TCAT AGTACCTAA		
			AC ATTT__		
GAM2687	GPT2	3'	ATGAGGGGTTCCCTTGAA 28521	TA	
			TTCAAG AACCCCTCAT		

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AAGTTC TTGGGGAGTA
CC
GAM2687 KIAA1676 3' TAATCCATGAGAGGTGTTT 44728 _ _
AAAC CC CTCATGGATTA
||||| || |||||
TTTG GG GAGTACCTAAT
T A
GAM2687 LOC200609 5' TAATCCATGAATATACTT 43332 AACCCC
AAGTA TCATGGATTA
||||| |||||
TTCAT AGTACCTAAT
ATA__
GAM2688 F2RL3 3' AGGGGGATCCCATCTCTACACA 10080 A A A G
TG TG TAGAGATG GA TT TTCT
|| ||||| || |||
AC ACATCTCTAC CT AG GGGA
_ C _ G
GAM2688 FLJ10520 3' AACTTGTCTCATCTCCACACA 19903 A A ATT
TG TGT GAGATGAGA GTT
|| || ||||| |||
AC ACA CTCTACTCT CAA
_ C GTT
GAM2688 KIAA0451 3' GGCGAACTCATCTCTAC 16808 AA
GTAGAGATGAG TTGTT
||||||| ||||
CATCTCTACTC AGCGG
A_
GAM2688 SFRS11 3' ATTCCCACATCTACATCA 11157 GA A
TGATGTAGA TG GAAT
||||||| || |||
ACTACATCT AC CTTA
AC C
GAM2688 LOC149271 5' AGAACATTCAACCATCTCTACA 38675 A_ T
TG TAGAGATG GAAT GTTCT
||||||| ||| ||||
ACATCTCTAC CTTA CAAGA
CA _
GAM2688 LOC255196 5' AGAAACCCTCATCTCTAC 46411 AATTG
GTAGAGATGAG TTCT
||||||| |||
CATCTCTACTC AAGA
CCA__
GAM2689 EP300 5' CCTCTAGAGCCGCGAGTTCTC 7148 G T CC
GAGAACTCG C GCTC AGAGG
||||||| | ||| ||||
CTCTTGAGC G CGAG TCTCC
_ C A_
GAM2689 HMOX1 3' CCTCCAAAAGCCCTGAGTTTCA 7910 A CT CCCA
TGAGA CTCGG GCT GAGG
||||| |||| ||| ||||

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ACTTT GAGTC CGA CTCC
 _ C_ AAAC
 GAM2689 RXRA 3' CCTCTGGGAAGGACAGCC 8867 _ _
 GGCTG C TCCCAGAGG
 ||||| | |||||
 CCGAC G AGGGTCTCC
 A GA
 GAM2689 TNFSF15 3' CTCTGCCACCGAGTTC 11601 C CTCC
 GAACTCGG TG CAGAG
 ||||| || |||||
 CTTGAGCC AC GTCTC
 _ C _
 GAM2689 VAT1 3' CCTCTGGGCTTGACCAGTTCCC 13067 A C CT CT
 A TG GAACT GG G CCCAGAGG
 || ||||| || | |||||
 AC CTTGA CC T GGGTCTCC
 C _ AG TC
 GAM2689 DGKZ 3' CCCTGGTCTTCGGCCGGGT 9720 CTC_ A
 ACTCGGCTG CCAG GG
 ||||| |||||
 TGGGCCGGC GGTC CC
 TTCT _
 GAM2689 DKFZP434F0318 3' CCTCTGGGTCTCTCTCCAAGTCC 25140 A C CTGCT_
 T AG ACT GG CCCAGAGG
 || ||||| |||||
 TC TGA CC GGGTCTCC
 C A TCTCCT
 GAM2689 FLJ20034 3' CCTCCAAGAGCCTCATTTTCA 19131 CTC G CCCA
 TGAGAA GGCT CT GAGG
 ||||| ||||| |||||
 ACTTTT CCGA GA CTCC
 ACT _ AC _
 GAM2689 FLJ20188 3' CCTCTGGGAAGCCTAGTTCCCA 19276 A C GC
 TG GAACT GGCT TCCCAGAGG
 || ||||| ||||| |||||
 AC CTTGA CCGA AGGGTCTCC
 C T _
 GAM2689 KIAA1317 5' CCTCTGGCTCGCACCGGCTC 41626 AAC C TC_
 GAG TCGG TGC CCAGAGG
 || ||||| ||||| |||||
 CTC GGCC ACG GGTCTCC
 _ _ CTC
 GAM2689 KIAA1813 5' CCTCTGGGAGGCAGGAG 34811 GG _
 CTC CTGC TCCCAGAGG
 || ||||| ||||| |||||
 GAG GACG AGGGTCTCC
 _ G
 GAM2689 KRTAP1-5 3' CCTCTGGACCACTAACAAGTTC 25698 C_ C CTC
 TCA TGAGAACT GG TG CCAGAGG
 ||||| ||||| ||||| |||||

ACTCTTGA TC AC GGTCTCC
 ACAA _ CA_
 GAM2689 MAGE-E1 3' CCTCTGGGGCCTGCGAGCC 25104 _ ____
 GGCT GC TCCCAGAGG
 |||| || |||||
 CCGA CG GGGGTCTCC
 G TCC
 GAM2689 moblak 3' CTCCCAGCCGAGCCCTCA 28306 AA CTCCCA
 TGAG CTCGGCTG GAG
 |||| ||||| ||
 ACTC GAGCCGAC CTC
 CC C____
 GAM2689 MYH10 3' CCATCGCCAGCCGGGCCCTCA 34262 AA CTCCCA _
 TGAG CTCGGCTG GA GG
 |||| ||||| ||
 ACTC GGGCCGAC CT CC
 CC CG____ A
 GAM2689 TBC1D2 5' CCCTGGGAGCAGAGGCCCTTCT 20465 CTC ____ A
 AGAA GGCT GCTCCCAG GG
 |||| |||| ||||| ||
 TCTT CCGG CGAGGGTC CC
 C__ AGA _
 GAM2689 TNK1 3' CCCTGCTCCAGCCAGTTCTCA 10135 C CTCC A
 TGAGAACT GGCTG CAG GG
 ||||| |||| ||||
 ACTCTTGA CCGAC GTC CC
 C CTC_ _
 GAM2689 LOC146774 3' GGAGCCAGGGCCGAGTCCTC 38235 A ____
 GAG ACTCGGCT GCTCC
 |||| ||||| ||||
 CTC TGAGCCGG CGAGG
 C GAC
 GAM2689 LOC150290 3' CCCTGGGAGCATCAGTGTCTCCTC 38931 A TC_ C A
 A TGAG AC GG TGCTCCCAG GG
 |||| || ||||| ||
 ACTC TG CT ACGAGGGTC CC
 C TGA _ _
 GAM2689 LOC155064 5' CCTCCGGGAGCCTGGGT 39528 CT A
 ACTCGG GCTCCC GAGG
 |||| ||||| ||||
 TGGGTC CGAGGG CTCC
 _ C
 GAM2689 LOC256477 5' CCTCCCCGACCGAGTTCTCA 46535 C TCCCA
 TGAGAACTCGG TGC GAGG
 ||||| |||| ||||
 ACTCTTGAGCC ACG CTCC
 _ CCC_
 GAM2689 LOC257465 3' CCTAGGAGCAGTGTTTCA 39666 A TCG C A
 TGAGA C GCTGCTCC AG G
 |||| | ||||| || |

			ACTTT G	TGACGAGG TC C		
			_____	A _		
GAM2690	COX11	3'	TGACTATTCAATACCATA	10596	T	_
			TAT GTATTGAATAG CG			
			ATA CATAACTTATC GT			
			C	A		
GAM2690	CEGP1	3'	ACGTGCCACTCAATACAA	21958		ATA
			TTGTATTGA GCGTGT			
			AACATAACT CGTGCA			
			CAC			
GAM2690	KIAA1061	3'	ACCCACATTCCCCAATCAATA	35264	T	AATAGC
			TATTG ATTG GTGTGGGT			
			ATAAC TAAC TACACCCA			
			_ CCCT_			
GAM2690	KIAA1211	3'	ACCCACACACCATTTCAGAACA	34159	A	AGC
			TGT TTGAAT GTGTGGGT			
			ACA GACTTA CACACCCA			
			A CCA			
GAM2690	LOC163231	5'	ACCCACACACTCAGTACAATG	40093		ATA C
			TATTGTATTGA G GTGTGGGT			
			GTAACATGACT C CACACCCA			
			_____	A		
GAM2691	C8orf13	3'	ACGCAAACCTCTCCACCGA	39651	A	TGTTATA
			TCGG TGGG TTTGCGT			
			AGCC ACCT AAACGCA			
			_ CTC_			
GAM2691	PP35	3'	CAAATACCAACATCCATCC	13871		A_
			GGATGGATGTT TATTTG			
			CCTACCTACAA ATAAAC			
			CC			
GAM2691	LOC200014	3'	AACACAAATACAGTATCCA	42686	A	C
			TGGATGTT TATTTG GTT			
			ACCTATGA ATAAAC CAA			
			C A			
GAM2692	FBXW1B	3'	TGTACCAATTTCTTTTAA	14667		C_
			TTAAA AAATTGGTACA			
			AATTT TTTAACCATGT			
			TC			
GAM2692	FBXW1B	3'	TGTACCAATTTCTTTTAA	27369		C_
			TTAAA AAATTGGTACA			

AATTT TTTAACCATGT
 TC
 GAM2692 FBXW1B 3' TGTACCAATTTCTTTTAA 27379 C_
 TTAAA AAATTGGTACA
 |||| |||||
 AATTT TTTAACCATGT
 TC
 GAM2692 PLAGL1 3' TTTGTACCAAATTTAATGA 8531 G CAAA
 TC ATTAAA TTGGTACAAA
 || |||| |
 AG TAATTT AACCATGTTT
 _ A_
 GAM2692 C1orf17 3' TTTTGTGGTGTGTTTGTGTTAATA 33856 G TT G
 GA TC ATTAACAAA G TACAAAA
 || ||||| |
 AG TAATTTGTTT T GTGTTTT
 A TG G
 GAM2692 DKFZp434A2417 3' TTTGTAATCATTTTTGTTTAAC 32866 A T_ _
 TGA TCG TTAAACAAA TGGT ACAA
 || ||||| ||
 AGT AATTTGTTT ACTA TGTTT
 C TT A
 GAM2692 FLJ10607 3' TTTTGTATATTTTTGTTTCATC 37836 T TTG
 GAT AAACAAA GTACAAAA
 || |||| |
 CTA TTTGTTT TATGTTTT
 C TTA
 GAM2692 FLJ20202 3' TTGTACCAATTTTAGTC 19290 CAA
 GATTAAA ATTGGTACAA
 |||| |
 CTGATT TAACCATGTT
 _
 GAM2692 FLJ31101 3' TTTGCATTGACTGTTTAATC 19688 AA TG A
 GATTAAACA T GT CAAA
 ||||| | ||
 CTAATTTGT A TA GTTT
 C_ GT C
 GAM2692 KIAA0979 3' TGTAGCAAATTTGTTTAATC 17390 _ G
 GATTAAACAAATT G TACA
 ||||| |
 CTAATTTGTTTAA C ATGT
 A G
 GAM2692 NAV3 3' TTTTATACCAATTATTAGTC 17092 ACA C
 GATTAA AATTGGTA AAAA
 |||| ||||| ||
 CTGATT TTAACCAT TTTT
 A_ A
 GAM2692 PAK7 3' TTTGTACCACAGTATTAATCG 34512 _ AAAT
 CGATTAA AC TGGTACAAA
 |||| | |||||

		GCTAATT TG ACCATGTTT	
		A AC__	
GAM2692	SEC14L1	3' TGTACCAATTAAAGGATTGA 8907	AAACA
		TCGATT AATTGGTACA	
		AGTTAG TTAACCATGT	
		GAAA_	
GAM2693	ARCN1	3' ACATTTTGTAACCCTGTAAA 7365	TTGATT
		TTTACAG CAAAATGT	
		AAATGTC GTTTTACA	
		CCAAT_	
GAM2693	B3GALT2	5' ACACTTTGGATACTGTGAA 9869	TG A
		TTTACAGT ATTCAAA TGT	
		AAGTGTCA TAGGTTT ACA	
		— C	
GAM2693	ENC1	3' ACATTTTGAGGTTTTGTAAA 9695	TTGA
		TTTACAG TTCAAAATGT	
		AAATGTT GAGTTTTACA	
		TTG_	
GAM2693	EPS8	3' ACATTTGAATGAACTGTAAA 10741	G A
		TTTACAGTT ATTCAAA TGT	
		AAATGTCAA TAAGTTT ACA	
		G _	
GAM2693	FABP2	3' ACATCTTGAACCTGGTTGTGAA 5621	TT A A
		TTTACAG G TTCAA ATGT	
		AAGTGTT T AAGTT TACA	
		GG C C	
GAM2693	LPL	3' ACATTTTATTTATTAGCTGTAA 5748	TC__
	A	TTTACAGTTGAT AAAATGT	
		AAATGTGATTA TTTTACA	
		TTTA	
GAM2693	NR4A2	3' ACATTTTCTCAATTGTAAA 12853	TTC
		TTTACAGTTGA AAAATGT	
		AAATGTAACT TTTTACA	
		C_	
GAM2693	PARK2	3' ACATTTGGCTCCACTGTAAA 10902	T TT A
		TTTACAGT GA CAAA TGT	
		AAATGTCA CT GTTT ACA	
		C CG _	
GAM2693	PARK2	3' ACATTTGGCTCCACTGTAAA 15149	T TT A
		TTTACAGT GA CAAA TGT	

			AAATGTCA CT GTTT ACA		
			C CG _		
GAM2693	PARK2	3'	ACATTTGGCTCCACTGTAAA 15156	T TT A	
			TTTACAGT GA CAAA TGT		
			AAATGTCA CT GTTT ACA		
			C CG _		
GAM2693	UBE2V1	3'	ACATCTAACTCAACTGTGAA 22764	TTCAAA	
			TTTACAGTTGA ATGT		
			AAGTGTCAACT TACA		
			CAATC_		
GAM2693	UBE2V1	3'	ACATCTAACTCAACTGTGAA 22517	TTCAAA	
			TTTACAGTTGA ATGT		
			AAGTGTCAACT TACA		
			CAATC_		
GAM2693	UBE2V1	3'	ACATCTAACTCAACTGTGAA 9365	TTCAAA	
			TTTACAGTTGA ATGT		
			AAGTGTCAACT TACA		
			CAATC_		
GAM2693	DKFZP566F2124	3'	ACATTTTGTATCTTGTA 17886	TT T	
			TTTACAG GAT CAAAATGT		
			AAATGTT CTA GTTTTACA		
			_ T		
GAM2693	FLJ11726	3'	ACATTTGTTTAACTGTGAA 24523	TT A	
			TTTACAGTTGA CAAA TGT		
			AAGTGTCAATT GTTT ACA		
			TT _		
GAM2693	KIAA0335	3'	ACATATGTCAACTGTAA 16728	TCAAA	
			TTACAGTTGAT ATGT		
			AATGTCAACTG TACA		
			TA__		
GAM2693	NETO1	3'	ACATTTTGAGATTA 29068	_	
			CAGTTGAT TCAAAATGT		
			GTCAATTA AGTTTACA		
			G		
GAM2693	NTT73	3'	ACATTTTGAAATAATGTAA 19821	G A	
			TTACA TTG TTCAAAATGT		
			AATGT AAT AAGTTTACA		
			_ A		
GAM2693	R3HDM	5'	ACATCCTGGCTGACAACTGTGA 17658	AT__ AA	
	A		TTTACAGTTG TCA ATGT		

			AAGTGTCAAC GGT TACA AGTC CC	
GAM2693	SS18L1	3'	ACATTTTAGATAACTGTGAA 32557 TTTACAGTTG T AAAATGT AAGTGTCAAT A TTTTACA _ GA	A TC
GAM2694	ARL4	5'	GCGTAGAAACGCCTGCCAA 12299 TTGGCA CGTT TTGCGT AACCGT GCAA GATGCG CC A	AA _
GAM2694	MSN	3'	CAAAATGACATTTTGCCAAA 30227 TTTGGCAAA CGTTTTG AAACCGTTT GTAAAC TACA	_____
GAM2694	NCOA6	5'	ACAAAAACATTTGCCAA 15285 TTGGCAAA GTTTT GT AACCGTTT CAAAA CA A A_	C GC
GAM2694	NDP	3'	ATGTGAAACATGTTGCCAAA 5805 TTTGGCAA GTTT CGT AAACCGTT CAAA GTA GTA GT	AC_ TG
GAM2694	SHOC2	3'	GCTTAAACATTTGCCAA 14305 TTGGCAAA GTTTTG GT AACCGTTT CAAAAT CG A T	C C
GAM2694	SSPN	3'	GTAAGTGGATCACTTGCCAAA 11536 TTTGGCAA TT C TTAC AAACCGTT AG G AATG CACT GT_	ACGT TG G
GAM2694	SUV39H2	3'	TGTTTCAAGACATTTGCCAAA 23977 TTTGGCAAA GTTTTG ACA AAACCGTTT CAGAAC TGT A TT_	C CGTT
GAM2694	TRIM37	3'	TAGCCCAAAACAGTTGCCAAA 17616 TTTGGCAA GTTTTG GTTA AAACCGTT CAAAAC CGAT GA C	AC C
GAM2694	ZNF137	3'	TGTAAACTCACACTTGCCAAA 9495 TTTGGCAA GTTTTGCG 	AC_____

			AAACCGTT	CAAAATGT		
			CACACT			
GAM2694	ATP10D	3'	TGTAACATTTGCCAAA	36203	C	T
			TTTGGCAA	GTTT GCG		
			AAACCGTTT	CAAA TGT		
			A	_		
GAM2694	C2orf6	3'	TGGAAGACTTGCCAAA	20143	AC	G
			TTTGGCAA	GTTTT CG		
			AAACCGTT	CAGAA GT		
			_	G		
GAM2694	ELL2	3'	TGTTTTGAAATGTTTGCCAAA	14370		CGTT
			TTTGGCAAACGTTTTG	ACA		
			AAACCGTTTGTAAAGT	TGT		
			TT	_		
GAM2694	FUSIP1	3'	TGTAATTGAGAAAATGTTCCACC	13412	CA	G_ _
	AAA		TTTGG AACGTTTT	CG TTACA		
			AAACC	TTGTAAAA GT AATGT		
			AC	GA T		
GAM2694	KIAA0495	5'	TGCAAACGTTTCCAAA	31365	C	T
			TTTGG AAACGTTT	GCG		
			AAACC	TTTGCAA CGT		
			-	-		
GAM2694	NET-6	3'	TTGTAACAGCAACTTGTCAAA	15743	ACGTT	_
			TTTGGCAA	TTGC GTTACAA		
			AAACTGTT	AACG CAATGTT		
			C	_	A	
GAM2694	LOC150517	5'	TGCAAACCATGTTTGCCAAA	38986		_
			TTTGGCAAACGT	TTTGCG		
			AAACCGTTTGTA	AAACGT		
			CC			
GAM2694	LOC253228	3'	CAAAATGACATTTTGCCAAA	45914		_____
			TTTGGCAA	CGTTTTG		
			AAACCGTTT	GTAAAC		
			TACA			
GAM2694	LOC256946	3'	TGTAATTGAGAAAATGTTCCACC	45362	CA	G_ _
	AAA		TTTGG AACGTTTT	CG TTACA		
			AAACC	TTGTAAAA GT AATGT		
			AC	GA T		
GAM2694	LOC56959	5'	ATGCAAAGACTTGCCAAA	39838	ACG	
			TTTGGCAA	TTTTGCGT		

		AAACCGTT GAAACGTA		
		CA_		
GAM2694	LOC93550	3' GACTCTAAAAGATTTGCCAAA 35932	CG	C_
		TTTGGCAA TTTTG GTT		
		AAACCGTTT AAAAT CAG		
		AG CT		
GAM2695	YES1	3' CATGTTTTTAATGGTAAACTG 11912	C	TGCTAT
		TAG TTACCATTA ACATG		
		GTC AATGGTAAT TGTAC		
		A TTT__		
GAM2695	KIAA0721	3' ATGTACTTATGGTAAGCTA 22317		TATGCTA
		TAGCTTACCAT TACAT		
		ATCGAATGGTA ATGTA		
		TTC__		
GAM2695	KIAA0721	3' ATGTACTTATGGTAAGCTA 45924		TATGCTA
		TAGCTTACCAT TACAT		
		ATCGAATGGTA ATGTA		
		TTC__		
GAM2695	LOC158088	3' GCATATTTGGTGGTAACCTA 41918	C	__
		TAG TTACCAT TATGC		
		ATC AATGGTG ATACG		
		C GTTT		
GAM2696	ING1	3' TCCAAATGAACCTGCACTTGTT 12061	A__	GAG C
	ATA	TATAACAG TAGG CAT TGGA		
		ATATTGTT GTTC GTA ACCT		
		CAC AA_ A		
GAM2696	MAP3K9	3' TCCAGGTGCCCCACCTATTT 30460	GA__	
		AGATAGG GCATCTGGA		
		TTTATCC CGTGGACCT		
		ACCC		
GAM2696	P2RY1	3' TCCAAACACCTCTCTGTTGTA 8412	T	GAGCATC
		TATAACAGA AGG TGGA		
		ATGTTGTCT TCC ACCT		
		C ACAA__		
GAM2696	SLC7A8	3' CCAAGACCCTATCTGTTCA 14551	T	AGCA _
		A AACAGATAGGG TCT GG		
		A TTGTCTATCCC AGA CC		
		C ____ A		
GAM2696	C20orf12	5' TCCAGATGTCAACATATATTAT 19960		CAGATAGG G
	A	TATAA GA CATCTGGA		

		ATATT	CT	GTAGACCT		
		ATATACAA	_			
GAM2696	COLEC10	3'	CCAGATGTTTTACCAGTC	13144	A	___
			GAT GG GAGCATCTGG			
			CTG CC TTTGTAGACC			
			A AT			
GAM2696	ZNF387	3'	CCAGATGGATCTGTTA	16175	AGGGAG	
			TAACAGAT CATCTGG			
			ATTGTCTA GTAGACC			
			G_____			
GAM2696	LOC133584	3'	CCAGAGCCTGTCTGCTATA	37044	A	GAGCA
			TATA CAGATAGG TCTGG			
			ATAT GTCTGTCC AGACC			
			C G_____			
GAM2697	BCL11B	3'	TTTTTGTTAGTGAATTTGGAAA	23171	G	ACT
			TTT CAAATTCATAA AGA			
			AAA GTTTAAGTGATT TTT			
			G GTT			
GAM2697	ITGAV	3'	TAGCTTTAGTGAATTTCAA	7975	C	_
			TTTG AAATTCATAA CTA			
			AAAC TTTAAGTGATTT GAT			
			_ C			
GAM2697	SPON1	3'	ATCTAGACGTTCAAGTTTGCAA	31298		CACTAAA
	A		TTTGCAAATT CTAGAT			
			AAACGTTTGA GATCTA			
			ACTTGCA			
GAM2697	ADNP	3'	ATCTAGTTTACCTAGCAAA	17646	AAATTCAC	
			TTTGC TAACTAGAT			
			AAACG ATTTGATCTA			
			ATCC_____			
GAM2697	ATP6M8-9	3'	TCTGTTTAATGAATTTGGAAA	12328	G	C T
			TTT CAAATTCA TAAAC AGA			
			AAA GTTTAAGT ATTTG TCT			
			G A _			
GAM2697	KIAA0830	3'	TATCCAGTCACAGTGAATTTG	34545	AA_	A
			CAAATTCAT ACT GATA			
			GTTTAAGTGA TGA CTAT			
			CAC C			
GAM2697	LOC135932	5'	CTGGCAGGAAATTTGCAAA	37498	CA	AAA
			TTTGCAAATT CT CTAG			

			AAACGTTTAA GA GGTC		
			AG C__		
GAM2697	LOC154760	5'	CTGGCAGGAAATTTGCAAA 41724	CA AAA	
			TTTGCAAATT CT CTAG		
			AAACGTTTAA GA GGTC		
			AG C__		
GAM2697	LOC91266	5'	TGGTGTTAGTGAATTTTGCAAA 32605	_ _	
			TTTGCAAA TTCACTAA ACTA		
			AAACGTTT AAGTGATT TGGT		
			T G		
GAM2698	ADRB3	3'	TCCCATGGGATTCCCCGGCTGT 5462	GA __ AGA	
	GAC		GTCACAGC GG TC ATGGGA		
			CAGTGTGC CC AG TACCCT		
			GC CTT GG_		
GAM2698	AVPR1A	5'	CCCAAACCCCGCTGTGA 6374	A CAGAA	
			TCACAGCG GGT TGGG		
			AGTGTCGC CCA ACCC		
			C A__		
GAM2698	BCL2	3'	CCCAGTCCCTCGCTGCACA 6253	CA TCA A	
			TGT CAGCGAGG GA TGGG		
			ACA GTCGCTCC CT ACCC		
			C_ __ G		
GAM2698	BCL7A	3'	CCCACCTTCGCTGGAACA 21991	CA TCAGAA	
			TGT CAGCGAGG TGGG		
			ACA GTCGCTTC ACCC		
			AG C__		
GAM2698	MYCL2	3'	TCCCACTCTCAATGCTGTGAC 11857	AGGTC A	
			GTCACAGCG AGA TGGGA		
			CAGTGTCTGT TCT ACCCT		
			AAC__ C		
GAM2698	SYN3	3'	TCCCATTTTCCTTCACCGTGAC 28593	AGC TC	
	A		TGTCAC GAGG AGAATGGGA		
			ACAGTG CTTC TTTTACCCT		
			CCA C_		
GAM2698	SYN3	3'	TCCCATTTTCCTTCACCGTGAC 28595	AGC TC	
	A		TGTCAC GAGG AGAATGGGA		
			ACAGTG CTTC TTTTACCCT		
			CCA C_		
GAM2698	SYN3	3'	TCCCATTTTCCTTCACCGTGAC 9584	AGC TC	
	A		TGTCAC GAGG AGAATGGGA		

			ACAGTG CTTC TTTTACCCT		
			CCA C_		
GAM2698	ECE2	3'	CCCACCATTCACTGTGACA 16197	C	GTCAGAA
			TGTCACAG GAG TGGG		
			ACAGTGTC CTT ACCC		
			A ACC_		
GAM2698	FLJ31952	3'	CCCATTCTGACCCCTGAC 29498	CAGCGA	
			GTCA GGTGAGAAATGGG		
			CAGT CCAGTCTTACCC		
			CC_		
GAM2698	HSOBRGRP	3'	CCCACTCTGGACCCAGGACA 18970	ACAGCGA	_ A
			TGTC GGTC AGA TGGG		
			ACAG CCAG TCT ACCC		
			GAC_ G C		
GAM2698	MYT1L	5'	CCCACCCCTGGCTGTGAC 33184	G	TCAGAA
			GTACACAGC AGG TGGG		
			CAGTGTGTCG TCC ACCC		
			G CC_		
GAM2698	TUSP	3'	TCCCATTCTAAAAGTGTGGACA 21535	ACA	GAGGTC
			TGTC GC AGAATGGGA		
			ACAG TG TCTTACCCT		
			GTG AAAA_		
GAM2698	LOC145225	3'	CCCACTTTGTCCTGTGACA 40525	C	GGT A
			TGTCACAG GA CAGA TGGG		
			ACAGTGTC CT GTTT ACCC		
			_ _ C		
GAM2699	ATP1A2	3'	CTCCCAAAGGCTGTCAT 6365	_	TCTTT
			ATGA AGCCTTTG GGAG		
			TACT TCGGAAAC CCTC		
			G _		
GAM2699	CASP8	3'	TGGAGACAAAGGCATCAT 27208	A	TT
			ATGA GCCTTTGTCT G		
			TACT CGGAAACAGA T		
			A GG		
GAM2699	CLCN3	3'	CCACAACAAAGGCTCAT 7565	A	CTT
			ATGA GCCTTTGT TGG		
			TACT CGGAAACA ACC		
			_ AC_		
GAM2699	COLQ	3'	ATCTCCAAGGTGAGGT 12231	TGT	
			GCCTT CTTTGGAGAT		

			TGGAG GGAACCTCTA		
			T__		
GAM2699	COLQ	3'	ATCTCCAAGGTGAGGT 27851	TGT	
			GCCTT CTTTGGAGAT		
			TGGAG GGAACCTCTA		
			T__		
GAM2699	COLQ	3'	ATCTCCAAGGTGAGGT 27854	TGT	
			GCCTT CTTTGGAGAT		
			TGGAG GGAACCTCTA		
			T__		
GAM2699	COLQ	3'	ATCTCCAAGGTGAGGT 27857	TGT	
			GCCTT CTTTGGAGAT		
			TGGAG GGAACCTCTA		
			T__		
GAM2699	COLQ	3'	ATCTCCAAGGTGAGGT 27860	TGT	
			GCCTT CTTTGGAGAT		
			TGGAG GGAACCTCTA		
			T__		
GAM2699	COLQ	3'	ATCTCCAAGGTGAGGT 27863	TGT	
			GCCTT CTTTGGAGAT		
			TGGAG GGAACCTCTA		
			T__		
GAM2699	GP9	5'	CCTGACCAAAGGCTTCA 5683	_ TTT	
			TGAAGCCTTTG TC GG		
			ACTTCGGAAC AG CC		
			C T__		
GAM2699	ICA1	3'	TATCTGCCTTAGACAAAGGCT 22739	TT _	
			AGCCTTTGTCT GG AGATA		
			TCGGAACAGA CC TCTAT		
			TT G		
GAM2699	RBMX	3'	TATCTCCAACCTCCTAAAGGCT 33858	TCT__	
	T		AAGCCTTTG TTGGAGATA		
			TTCGGAAT AACCTCTAT		
			CCTTC		
GAM2699	ZNF255	5'	CACTGAACAAAGGCTTCA 12348	_ TT	
			TGAAGCCTTTGT C TG		
			ACTTCGGAACA G AC		
			A TC		
GAM2699	ZNF268	3'	TATCTTTCAAGACAAAACCTC 31501	AGCC TG	
	AT		ATGA TTTGTCTT GAGATA		

		TACT	AAACAGAA	TTCTAT		
		CCAA	CT			
GAM2699	C20orf97	3'	TATCCCTGTGCCAAAGGCTCCA	22139	A	TCTTT A
			TG AGCCTTTG	GG GATA		
			AC TCGGAAAC	CC CTAT		
			C	CGTGT _		
GAM2699	C8orf13	3'	ATCTCCAAAGAGCCTCTTCA	39652		CCTTTG
			TGAAG	TCTTTGGAGAT		
			ACTTC	AGAAACCTCTA		
			TCCG_			
GAM2699	FLJ13224	3'	CTCCAAGACAAAACCTTC	24178	CC	T
			GAAG	TTTGTCTT GGAG		
			CTTC	AAACAGAA CCTC		
			A_	_		
GAM2699	FLJ20209	3'	ATCTCCAAGGTAGACCTCA	41404	AGCC	T
			TGA	TTTG CTTTGGAGAT		
			ACT	AGAT GGAACCTCTA		
			CC_	_		
GAM2699	KIAA0217	3'	CTCCAAGACGAGGGCCTCAT	33281	A	T
			ATGA	GCCTTTGTCTT GGAG		
			TACT	CGGGAGCAGAA CCTC		
			C	_		
GAM2699	KIAA0980	3'	TTCCAGAAAAGGCTTCA	24811		GTC
			TGAAGCCTTT	TTTGGAG		
			ACTTCGGAAA	AGACCTT		

GAM2699	KIAA1130	3'	TATCTCCGAGCAAAGCCTCCA	31286	A C	CT
			TG AG	CTTTGT TTGGAGATA		
			AC TC	GAAACG AGCCTCTAT		
			C C	_		
GAM2699	KIAA1204	3'	CCATAGATAAAAAGCCTCAT	34314	A C	T
			ATGA	GC TTTGTCT TGG		
			TACT	CG AAATAGA ACC		
			C A	T		
GAM2699	KIAA1281	5'	ATCTCCAAAGAAAAGTTCAT	42962	GC	G
			ATGAA	CTTT TCTTTGGAGAT		
			TACTT	GAAA AGAAACCTCTA		

GAM2699	KIAA1727	3'	ATCTCTAAAGCAAAGCCTCA	32029	A C	T
			TGA	GC TTTG CTTTGGAGAT		

ACT CG AAAC GAAATCTCTA
 C A _
 GAM2699 KIAA1879 3' CTCCAGCACAGCTTCA 36416 CTT CT
 TGAAGC TGT TTGGAG
 ||||| ||| |||||
 ACTTCG ACA GACCTC
 _ C_
 GAM2699 KIAA1938 3' CTCCAAACTTTCAACTTCA 44278 CCT TC_
 TGAAG TTG TTTGGAG
 ||||| ||| |||||
 ACTTC AAC AAACCTC
 _ TTTC
 GAM2699 NR6A1 3' CACAGACAAAGAGCCCAT 27186 AA _ T
 ATG GC CTTTGTCT TG
 ||| || ||||| ||
 TAC CG GAAACAGA AC
 C_ A C
 GAM2699 NR6A1 3' CACAGACAAAGAGCCCAT 27180 AA _ T
 ATG GC CTTTGTCT TG
 ||| || ||||| ||
 TAC CG GAAACAGA AC
 C_ A C
 GAM2699 NR6A1 3' CACAGACAAAGAGCCCAT 7232 AA _ T
 ATG GC CTTTGTCT TG
 ||| || ||||| ||
 TAC CG GAAACAGA AC
 C_ A C
 GAM2699 P2RX1 3' CTCCATAGGGAAAGGCTTC 33354 G T
 GAAGCCTTT TCT TGGAG
 ||||| ||| |||||
 CTTTCGAAA GGA ACCTC
 G T
 GAM2699 RNAC 3' TATCTCCATGAGAAAATTCAT 12345 GCCTTTG _
 ATGAA TCTT TGGAGATA
 |||| ||| |||||
 TACTT AGAG ACCTCTAT
 AAA_ T
 GAM2699 U5-116KD 3' ATCTCCCAAGAGGCTTCA 10436 TTTG T
 TGAAGCC TCTT GGAGAT
 ||||| ||| |||||
 ACTTCGG AGAA CCTCTA
 _ C
 GAM2699 LOC146909 3' TGTCTCTAACACAGGCCCA 38272 AA T CTT
 TG GCCT TGT TGGAGATA
 || ||| ||| |||||
 AC CGGA ACA ATCTCTGT
 CC C _
 GAM2699 LOC152445 5' TATCTCCAAAAACCATCTTCAT 41510 CCTTT C
 ATGAAG GT TTTGGAGATA
 ||||| || |||||

TACTTC CA AAACCTCTAT
TAC__ A
GAM2699 LOC158476 5' CTCCAAAAGGATAGCTGCCAT 41998 A_ CTT _
ATG AGC TGTCT TTGGAG
||| ||| |||| |||||
TAC TCG ATAGG AACCTC
CG ____ AA
GAM2699 LOC223009 5' ATCTCCAGGCCCAAACTTC 45313 CC TC
GAAG TTTG TTTGGAGAT
|||| ||| |||||
CTTC AAAC GGACCTCTA
A_ CC
GAM2699 LOC256158 5' ATCTCCAAAGACGACCCCTT 46618 CCT
AAG TTGTCTTTGGAGAT
||| |||||
TTC AGCAGAAACCTCTA
CCC
GAM2699 LOC257444 3' ATCTCCAGTTGTAAAGCTCA 39479 A C TCT_
TGA GC TTTG TTGGAGAT
||| ||| |||||
ACT CG AAAT GACCTCTA
_ _ TGTT
GAM2699 LOC56267 3' TATCTCCAACCTCCTAAAGGCT 21229 TCT_
T AAGCCTTTG TTGGAGATA
||||||| |||||
TTCGGAAAT AACCTCTAT
CCTTC
GAM2700 GJA1 3' TACTCAACAGCCTTATTC 5679 A A
GAG TAAGGCT TTGAGTA
||| ||||| |||||
CTT ATTCCGA AACTCAT
_ C
GAM2700 RABIF 3' ACTCAGCTCCATCTCCAA 8780 AA ATT
TTGGAGAT GGCT GAGT
||||||| ||| |||
AACCTCTA TCGA CTCA
CC ____
GAM2700 C20orf108 3' TACCCATGTCAGTTATCTCCA 28089 _ TAT A
TGGAGATAA GGC TG GTA
||||||| ||| || |||
ACCTCTATT CTG AC CAT
GA T__ C
GAM2701 FGF5 3' CAATCCAACCTGTACTGGCCA 10771 AT
TG TAGTACAGTTGGATTG
|| |||||
AC GTCATGTCAACCTAAC
CG
GAM2701 FGF5 3' CAATCCAACCTGTACTGGCCA 26998 AT
TG TAGTACAGTTGGATTG
|| |||||

AC GTCATGTCAACCTAAC
 CG
 GAM2701 LOC122830 3' CTGACTGTACTATCCACTGA 36706 A AT TG
 TCA TG TAGTACAGT G
 ||| || ||||| |
 AGT AC ATCATGTCA C
 C CT GT
 GAM2701 LOC90333 3' CAATTGAGTATATAATCATTGA 31221 GTA____
 TCAATGATTA CAGTTG
 ||||| |||||
 AGTTACTAAT GTTAAC
 ATATGA
 GAM2702 HUNK 3' ATCATCTAAGACCATCTCT 15944 ACCC _
 AGAGATGG TAG TGAT
 ||||| ||| ||||
 TCTCTACC ATC ACTA
 AGA_ T
 GAM2702 HABP2 3' AATATCACCAGGCTTCTTCT 10341 T C A
 AGA GGA CCT GTGATATT
 ||| ||| ||| |||||
 TCT CTT GGA CACTATAA
 T C C
 GAM2702 KIAA1023 3' AGTGTCCAGTGCCCATCTCT 19085 ACC AGT
 AGAGATGG CT GATATT
 ||||| || |||||
 TCTCTACC GA CTGTGA
 CGT C____
 GAM2702 OR2C3 3' TATCACTAGAGTTACCTCT 37176 A C
 AGAG TGGAC CTAGTGATA
 ||| |||| |||||
 TCTC ACTTG GATCACTAT
 C A
 GAM2702 TERA 3' AATATGGATCATCTCT 22203 A CTAGTG
 AGAGATGG CC ATATT
 ||||| || |||||
 TCTCTACT GG TATAA
 A _____
 GAM2702 LOC147949 3' ATATTTCTGGAATCCACCTCT 38422 A CC T
 AGAG TGGA CTAG GATAT
 ||| ||| ||| |||||
 TCTC ACCT GGTC TTATA
 C AA T
 GAM2702 LOC155179 3' AGTGTCCAGTGCCCATCTCT 39553 ACC AGT
 AGAGATGG CT GATATT
 ||||| || |||||
 TCTCTACC GA CTGTGA
 CGT C____
 GAM2702 LOC158267 3' AATATCACACCTCCACTC 39790 A CCCTA
 GAG TGGA GTGATATT
 ||| ||| |||||

			CTC ACCT CACTATAA		
			CCA__		
GAM2702	LOC90161	3'	ATAATACCACTAGGGCCTCT	30901	T A A
			AGA GG CCCTAGTG TATTAT		
			TCT CC GGGATCAC ATAATA		
			__ C		
GAM2703	C5orf3	3'	GTGTTTCGTGTCTACCATA	20763	A AAA
			TAT GTA ACGAAACAC		
			ATA CAT TGCTTTGTG		
			C CTG		
GAM2703	FLJ21870	3'	GGCTGCCCCGTTTTTACTA	23281	AAA C
			TAGTAAAAACG CA CC		
			ATCATTTTTGC GT GG		
			CCC C		
GAM2703	MGC2452	5'	ACGGGTGTGTTTGCTATA	26364	AACGAA
			TATAGTAAA ACACCCGT		
			ATATCGTTT TGTGGGCA		
			G__		
GAM2704	CALU	3'	TGTCATTGAAAGTGCCTTTAA	6888	A ATACGG
			TTAAAGGCA CT GACA		
			AATTTC CGT GA CTGT		
			__ AAGTTA		
GAM2704	LASS2	3'	CCCAGTTGCCTTTAA	33624	ATAC
			TTAAAGGCAACT GGG		
			AATTTC CGTTGA CCC		
			__		
GAM2704	LOC51339	3'	CGTATGGATGCTAGTGCCTTTA	18769	A__
			A TTAAAGGCA CTATACG		
			AATTTC CGT GGTATGC		
			GATCGTA		
GAM2705	AMPD3	3'	GTTGGAAGCCAAATGTACT	6089	CAAC A__
			AGTGCATT TGG CCGAC		
			TCATGTAA ACC GGTG		
			__ GAA		
GAM2705	BSN	3'	TCAGGTATGGGCTGAATGCA	9519	A_ G _
			TGCATTCA CTG ACC GA		
			ACGTAAGT GGT TGG CT		
			CG A A		
GAM2705	NPAT	3'	TCAGTCCAGTTGAAGAATTG	33388	GTGCA C
			CAA TTCAACTGGAC GA		

			GTT AAGTTGACCTG CT		
			AAG__ A		
GAM2705	OTOR	3'	TTCAGTTGAATAACTTG 21367	GC	
			CAAGT ATTCAACTGGA		
			GTTCA TAAGTTGACTT		
			A_		
GAM2705	SYT1	3'	GTTCTGAATGCACTT 12171	ACT	
			AAGTGCATTCA GGAC		
			TTCACGTAAGT CTTG		

GAM2705	T	5'	CGGCCAAATGCGCTCGT 9154	A CAAC A	
			AC AGTGCATT TGG CCG		
			TG TCGCGTAA ACC GGC		
			C _____		
GAM2705	YES1	3'	TCAGGGACTTGAATGCACTT 11916	CTGGA _	
			AAGTGCATTCAA CC GA		
			TTCACGTAAGTT GG CT		
			CAG__ A		
GAM2705	ARHGEF10	3'	GTCCAGTTAGCATGATTTG 30305	G TC_	
			CAAGT CAT AACTGGAC		
			GTTTA GTA TTGACCTG		
			_ CGA		
GAM2705	CD109	3'	TCAGAATGAATGCAGTTGT 28572	G A_	
			ACAA TGCATTCA CTGG		
			TGTT ACGTAAGT GACT		
			G AA		
GAM2705	FLJ12934	3'	GTCTGAGTTAAATGCACTT 23177	C _	
			AAGTGCATT AACT GGAC		
			TTCACGTAA TTGA TCTG		
			A G		
GAM2705	KIAA0014	3'	GTCGGTCTCTGAGAAAGCACCT 16117	A A AACT	
	G		CA GTGC TTC GGACCGAC		
			GT CACG AAG TCTGGCTG		
			C A AGTC		
GAM2705	KIAA0092	3'	TCAGTGTTAAGTGCAGTTGT 16157	CA__	
			ACAAGTGCATT ACTGG		
			TGTTACGTGA TGA CT		
			ATTG		
GAM2705	KIAA0318	3'	CCAGTAGAGAAATGCACTT 34185	__ A	
			AAGTGCAT TC ACTGG		

TTCACGTA AG TGACC
 AAG A
 GAM2705 KIAA1219 3' TCATGTTGAATGCATTTGT 30760 _
 ACAAGTGCATTCAAC TGG
 |||||
 TGTTTACGTAAGTTG ACT
 T
 GAM2705 LRP1B 3' GTTGCCGACTGCACTTG 20640 T AACT A
 CAAGTGCA TC GG CCGAC
 ||||| || |||||
 GTTCACGT AG CC GGTG
 C _ _
 GAM2705 TRIP-Br2 3' CGGCCCCGGGATGCACT 16487 CAA A
 AGTGCATT CTGG CCG
 ||||| ||| |||
 TCACGTAG GGCC GGC
 _ C
 GAM2705 TUBGCP3 3' GTCGGAGTCGAATGCATTTGT 13013 A GGA
 ACAAGTGCATTC ACT CCGAC
 ||||| ||| |||||
 TGTTTACGTAAG TGA GGCTG
 C _
 GAM2705 LOC158014 5' TGAGCCAAATGCACTAGT 39696 A CAAC AC
 AC AGTGCATT TGG CG
 || ||||| ||| ||
 TG TCACGTAA ACC GT
 A _ GA
 GAM2705 LOC202908 5' CCAGTTGAAGCACCTGT 42996 A A
 ACA GTGC TTCAACTGG
 ||| ||| |||||
 TGT CACG AAGTTGACC
 C _
 GAM2705 LOC90719 5' GTCGGTCCAGTCCTTGCCT 31948 T TTCA
 AG GCA ACTGGACCGAC
 || ||| |||||
 TC CGT TGACCTGGCTG
 _ TCC_
 GAM2706 DACH 3' CCACCTTTTGTGTTTG 28035 TCTAGT
 TAAAC CAAAAGGTGG
 ||||| |||||
 GTTTG GTTTTCCACC
 TT_
 GAM2706 SERPINB9 3' CCACCTTTATTTAAAGTT 10362 C TCA
 AACT TAG AAAGGTGG
 ||| ||| |||||
 TTGA ATT TTTCCACC
 A TA_
 GAM2706 C20orf139 5' GCCACCTTCAAGAGCCCAGA 41107 AAA AGTCAA
 TCT CTCT AAGGTGGC
 ||| ||| |||||

			AGA GAGA TTCCACCG		
			CCC AC_____		
GAM2706	FLJ13769	3'	CCACCTTGTAGAGGCTAGA 24590	AA	GTCAA
			TCTA CTCTA AAGGTGG		
			AGAT GAGAT TTCCACC		
			CG G_____		
GAM2706	FLJ32734	5'	GCCACCTTCTGTGGAGT 29496	GT	A
			ACTCTA CA AAGGTGGC		
			TGAGGT GT TTCCACCG		
			___ C		
GAM2706	KIAA0494	3'	GCCACCTTTTAACTTGTTTG 16590	TCT	C
			TAAAC AGT AAAAGGTGGC		
			GTTTG TCA TTTTCCACCG		
			T___ A		
GAM2706	KIAA1775	3'	CACTGACTAGAATCTGGA 26942	AAC	AAAG
			TCTA TCTAGTCA GTG		
			AGGT AGATCAGT CAC		
			CTA _____		
GAM2706	MGC2749	3'	GCCACCTCGGGAAGAGTTTA 23499	AG	AAA
			TAAACTCT TC AGGTGGC		
			ATTTGAGA GG TCCACCG		
			AA GC_		
GAM2706	MGC3178	3'	CCCTAACTAGAGTTCTAGA 25131	_	CAAAA T
			TCTA AACTCTAGT GG GG		
			AGAT TTGAGATCA TC CC		
			C A_____		
GAM2706	LOC146229	3'	GCCACCTTTTCCTGGGAACCTG 38111	AAC_	TC
	GA		TCTA TCTAG AAAAGGTGGC		
			AGGT GGGTC TTTTCCACCG		
			CCAA C_		
GAM2706	LOC147040	3'	ACCTGACTGGAGCTCAGA 38287	AAA	AAA
			TCT CTCTAGTCA GGT		
			AGA GAGGTCAGT CCA		
			CTC _____		
GAM2706	LOC154881	3'	CCACCTTTTGGAGATTTA 39496	C	AG
			TAAA TCT TCAAAAGGTGG		
			ATTT AGA GGTTTTCCACC		

GAM2706	LOC155036	5'	CCACTTGGCTAGAGTTCAGA 41753	A	AAA
			TCT AACTCTAGTCA GGTGG		

AGA TTGAGATCGGT TCACC
 C _____
 GAM2706 LOC253681 3' ACCTGACTGGAGCTCAGA 45605 AAA AAA
 TCT CTCTAGTCA GGT
 ||| ||||| |||
 AGA GAGGTCAGT CCA
 CTC _____
 GAM2707 TMEPAI 3' AGTTTTGAAGTTCTAGCCACT 21404 A GTT_ C
 GGT GC GC TCAAAACT
 ||| || || |||||
 TCA CG TG AGTTTTGA
 C ATCT A
 GAM2707 FLJ13769 3' TTTTGAGGCAAAGTTCAGT 24598 GGT G
 GC AGC TTGCCTCAAAA
 || ||| |||||
 TG TTG AACGGAGTTTT
 AC_ A
 GAM2707 KIAA1915 3' TAGTTTTGAAACTCGTGCC 36272 G TTGCC
 GGTA CG TCAAAACTA
 |||| || |||||
 CCGT GC AGTTTTGAT
 _ TCAA_
 GAM2707 MGC12217 3' AGTTTTGAGGTTATGCAC 26516 A T
 GT GCGT GCCTCAAAACT
 || |||| |||||
 CA CGTA TGGAGTTTTGA
 _ T
 GAM2707 LOC152503 5' AGTCTCTGCTGGACAACGCTAG 41516 GG _ T_ AA_
 C GC TAGCGTTG CC CA ACT
 || ||||| || || |||
 CG ATCGCAAC GG GT TGA
 _ A TC CTC
 GAM2707 LOC153914 5' AGCTTTAAGGTGTTACCCT 39436 C GTT C A
 AG GGTAGC GCCT AAA CT
 || ||||| |||| ||| ||
 TC CCATTG TGGA TTT GA
 _ _ A C
 GAM2707 LOC253430 5' AGTTTTGAAACAGTTAC 46044 _ GCC
 GTAGC GTT TCAAAACT
 |||| || |||||
 CATTG CAA AGTTTTGA
 A _____
 GAM2707 LOC91496 5' TGAGGCAAGACTTCGACT 32921 _ T CG
 AG CGG AG TTGCCTCA
 || ||| || |||||
 TC GCT TC AACGGAGT
 A _ AG
 GAM2707 LOC92096 3' TAGTTTTGAAAGCCTCACCTCT 33777 C _ C GCC
 AG GGT AG GTT TCAAAACTA
 || ||| || |||||

		TC CCA TC CGA AGTTTTGAT	
		T C _ A__	
GAM2708 RDX	3'	TGCCAAAGCACTTACACCA 8811	GAG A AA
		TGGTGTA GGTG TTTT CA	
		ACCACAT TCAC GAAA GT	
		_ _ CC	
GAM2708 AKT3	3'	TCACCAAAATTTCTACACCA 11959	_____
		TGGTGTAGAG GGTGA	
		ACCACATCTT CCACT	
		TAAAA	
GAM2708 KIAA1091	3'	GAGATCACCTCCTACACCA 34540	AG
		TGGTGTAG GGTGATTTT	
		ACCACATC CCACTAGAG	
		CT	
GAM2708 MO25	3'	TTAAAATGGCAGTCTACATCA 18418	GG G
		TGGTGTAGA GT ATTTTAA	
		ACTACATCT CG TAAAATT	
		GA G	
GAM2708 LOC155061	3'	TGTTAAAATAAAACCTAACCA 39538	GTAG GTG_
		TGGT AGG ATTTTAACA	
		ACCA TCC TAAAATTGT	
		A__ AAAA	
GAM2709 TOX	3'	TCACTTGAGCATGTAATA 16328	CG GGAC
		TATTACAT GT CAAGTGA	
		ATAATGTA CG GTTCACT	
		_ A__	
GAM2709 FLJ14153	3'	TCACTTAGGGATGTAAT 22941	GGTGGA _
		ATTACATC CC AAGTGA	
		TAATGTAG GG TTCACT	
		_ _ A	
GAM2710 NBS1	3'	AGGCTGGCCTCTACAT 34434	T CCGG
		ATGTAGAG CC AGCTT	
		TACATCTC GG TCGGA	
		C _	
GAM2710 FLJ20127	3'	GAGCAGAGAATCTACATTA 19220	G CCCGGA
		TAATGTAGA TC GCTT	
		ATTACATCT AG CGAG	
		A AGA__	
GAM2710 LOC150503	5'	TAAGTTTGTGAAAATCTACATT 38985	GTCCCCG
		A TAATGTAGA GAGCTTA	

ATTACATCT TTTGAAT
 AAAAGTG
 GAM2710 LOC150504 5' TAAGTTTGTGAAAATCTACATT 29850 GTCCCCG
 A TAATGTAGA GAGCTTA
 ||||| |||||
 ATTACATCT TTTGAAT
 AAAAGTG
 GAM2710 LOC221410 3' AAGCTCCAGAAGGTTCTATTA 44194 T T CC__
 A GTAGAG CC GGAGCTT
 | ||||| || |||||
 A TATCTT GG CCTCGAA
 T _ AAGA
 GAM2710 LOC90408 5' GCTCCTGCGGAAATCTACATTA 31397 G_ C_
 TAATGTAGA TCC C GGAGC
 ||||| ||| |||||
 ATTACATCT AGG G CCTCG
 AA C T
 GAM2711 ETS2 3' TCTGGCTGTTTGAGATTCTC 11749 T GAT
 GA GAATT GGCAGCCAGA
 || |||| |||||
 CT CTTAG TTGTCGGTCT
 _ AGT
 GAM2711 MASP1 3' CTGACCACTTATCAAACCCATC 29159 AA_ ____ _
 GG CCGATG TTGA TGG CAG
 ||||| ||| |||||
 GGCTAC AACT ACC GTC
 CCA ATT C A
 GAM2711 TIMM23 3' GGCTGCCATCCCGTCTAGGA 30199 GAT ATT
 TCC GA GATGGCAGCC
 ||| || |||||
 AGG CT CTACCGTCGG
 AT_ GCC
 GAM2711 AMOT 3' CTGATGCCAATTCATC 28412 TGA GC
 GATGAAT TGGCA CAG
 ||||| ||||| |||
 CTA CTTA ACCGT GTC
 _ A_
 GAM2711 CENTA2 3' CTGGCTGCCACCACATC 20442 AAT AT
 GATG TG GGCAGCCAG
 ||||| || |||||
 CTAC AC CCGTCGGTC
 C_ _
 GAM2711 DKFZP434O047 5' CTGACCACCACTTATCGGA 17864 AT A _
 TCCGATGA TG TGG CAG
 ||||| || ||| |||
 AGGCTATT AC ACC GTC
 C_ C A
 GAM2711 FLJ11078 3' CTGGCTGCGAGTCCATCCGA 20309 C AATT G_
 TC GATG GAT GCAGCCAG
 || |||| ||| |||||

AG CTAC CTG CGTCGGTC
 C ____ AG
 GAM2711 FLJ11274 3' TCCAGCCTGCCATTCCATC 20401 AATT _ CA
 GATG GATGGCAG C GA
 ||| ||||| | ||
 CTAC TTACCGTC G CT
 C ____ C AC
 GAM2711 FLJ21603 3' TCTGGCTGCATAACTCACAGGA 24119 GA A ATG
 TCC TGA TTG GCAGCCAGA
 || ||| || |||||
 AGG ACT AAT CGTCGGTCT
 AC C A ____
 GAM2711 KIAA1077 5' GGCTGCCGGCGCTCCTCGGA 36096 T ATTGA
 TCCGA GA TGGCAGCC
 |||| || |||||
 AGGCT CT GCCGTCGG
 C CGCG_
 GAM2711 LOC150150 5' TCTGGCTGAATATCCACTGGA 41138 A AATT G_
 TCCG TG GATG CAGCCAGA
 ||| || ||| |||||
 AGGT AC CTAT GTCGGTCT
 C ____ AA
 GAM2711 LOC254381 5' TCTGGCTGCCAAAGCCATGAGA 46544 CG AA GA
 TC ATG TT TGGCAGCCAGA
 || ||| || |||||
 AG TAC AA ACCGTCGGTCT
 AG CG ____
 GAM2712 BCAT1 3' TTTTCTTTGTGGCAGTCA 32898 AG G
 TGACT CG AAAGAAAG
 |||| || |||||
 ACTGA GT TTTCTTTT
 CG G
 GAM2712 DDEF1 3' AGTTTTCTTTTCATCCCAGC 29962 ____ AA
 GC GGA GAAAGAAAAC
 || ||| |||||
 CG CCT TTTTCTTTGA
 AC AC
 GAM2712 HLCS 3' AGTTTTCTCTCTCCAGTC 5989 AGC A A
 GACT GGAA GA AGAAAAC
 ||| ||| || |||||
 CTGA CCTT CT TCTTTTGA
 ____ _ C
 GAM2712 PDE4B 3' AGTCTTCCTTCTTTCTTGGGC 8465 ____ A A
 GC GGAAAGAA GAA ACT
 || ||||| ||| |||
 CG TCTTTCTT CTT TGA
 GGT C C
 GAM2712 SH3GL2 3' AGTTTTCTTCCTCCTTGCTA 8965 ____ AA A
 TAGC GGA GAA GAAAAC
 ||| ||| || |||||

			ATCG CCT CTT CTTTGA			
			TT CC _			
GAM2712 SSPN	3'	TCTTCTTTCCTGTTAGTC	11538	_	A	
		GACTAGC GGAAAGAA GA				
		CTGATTG CCTTTCTT CT				
		T _				
GAM2712 TACC1	3'	TTTTCTTTCCAGCCAGTTA	12970	A	_	
		TGACT GC GGAAAGAAAG				
		ATTGA CG CCTTTCTTTT				
		C A				
GAM2712 TRIM	3'	CTTTCTTTCCAGTCA	18530	AGC		
		TGACT GGAAAGAAAG				
		ACTGA CCTTTCTTTC				
		—				
GAM2712 AP1S2	3'	CTTTCTTTCCATGGCA	10003	A	GC	
		TG CTA GGAAAGAAAG				
		AC GGT CCTTTCTTTC				
		_ A_				
GAM2712 DIO2	3'	AGTTCTCTTTCTTAGTCCCTAA	15165	C	C	_ A
TC		GA TAG GGA AAGAAAGA AACT				
		CT ATC CCT TTCTTTCT TTGA				
		A _ GA C				
GAM2712 DIO2	3'	AGTTCTCTTTCTTAGTCCCTAA	6455	C	C	_ A
TC		GA TAG GGA AAGAAAGA AACT				
		CT ATC CCT TTCTTTCT TTGA				
		A _ GA C				
GAM2712 DKK2	3'	TTTCGGTTTTTCTGCCAGCCA	15776	A	A	AAA
		TG CT GCGGAAAG GAAA				
		AC GA CGTCTTTT CTTT				
		C C GG_				
GAM2712 EPB41L1	3'	AGTTCCCCCTCTTTCTGGGTCA	34937	AG		AAGAA
		TGACT CGGAAAGA AACT				
		ACTGG GTCTTTCT TTGA				
		— CCCCC				
GAM2712 GIT2	3'	AGTTTTCTTTCTTTCCTTGTC	16599	TAGC		
		GAC GGAAAGAAAGAAAAC				
		CTG CCTTTCTTTCTTTTGA				
		TT_				
GAM2712 GIT2	3'	AGTTTTCTTTCTTTCCTTGTC	27681	TAGC		
		GAC GGAAAGAAAGAAAAC				

CTG CCTTTCTTTCTTTTGA
 TT__
 GAM2712 GIT2 3' AGTTTTCTTTCTTTCCTTGTC 27694 TAGC
 GAC GGAAAGAAAGAAAAC
 ||| |||||
 CTG CCTTTCTTTCTTTTGA
 TT__
 GAM2712 KIAA1571 3' AGTTTTCTTTCTTTTAAAGC 30564 ____
 GC GGAAAGAAAGAAAAC
 || |||||
 CG TTTTCTTTCTTTTGA
 AAA
 GAM2712 NPTXR 3' AGGTGTCCCTCCCCTGCTAGTC 27732 AAA AA AAA
 A TGACTAGCGG GA GA CT
 ||||| || ||
 ACTGATCGTC CT CT GA
 CC_ CC GTG
 GAM2712 NPTXR 3' AGGTGTCCCTCCCCTGCTAGTC 15584 AAA AA AAA
 A TGACTAGCGG GA GA CT
 ||||| || ||
 ACTGATCGTC CT CT GA
 CC_ CC GTG
 GAM2712 PHYHIP 3' TCTTCTTCTCTTGGCA 16513 A C GA
 TG CTAG G AAGAAAGA
 || ||| | |||||
 AC GGTT C TTCTTTCT
 _ _TC
 GAM2712 PSR 3' AGTTTTCTTTCTCCAGATGCTA 32498 GAA__
 TAGCG AGAAAGAAAAC
 |||| |||||
 ATCGT TCTTTCTTTTGA
 AGACC
 GAM2712 SLC38A4 3' AGTTTTCTTTCTTCACAGTCA 19757 AGCG A
 TGACT GAA GAAAGAAAAC
 |||| || |||||
 ACTGA CTT CTTTCTTTTGA
 CA_ _
 GAM2712 LOC151414 3' AGTTTTCTTTCTTGCTTGAAG 39108 ____ AAA
 T ACT AGCGG GAAAGAAAAC
 || |||| |||||
 TGA TCGTT CTTTCTTTTGA
 AGT C_
 GAM2712 LOC199704 3' TCTCCCTTCTGCTGTCA 42604 T A AA
 TGAC AGCGGAA G AGA
 |||| ||||| | |||
 ACTG TCGTCTT C TCT
 _ _CC
 GAM2712 LOC201771 5' AGTCCTCTTTCTTTATCCTTAG 34677 C ____ AA
 CTAG GGA AAGAAAGA ACT
 |||| || ||||| |||

GATT CCT TTCTTTCT TGA
 _ AT CC
 GAM2712 LOC206426 3' GTTTTCTTTCCCCTCATC 43119 CT C AAA
 GA AG GG GAAAGAAAAC
 || || || |||||
 CT TC CC CTTTCTTTTG
 AC _ _
 GAM2712 LOC90843 3' CTTTCTTTCTGTTAGCA 32117 A
 TG CTAGCGGAAAGAAAG
 || |||||
 AC GATTGTCTTTCTTTC
 _
 GAM2713 XT3 3' GGCTTCCCAGCCGCTCA 21447 A C
 TGAGCG CT GGGAAGTT
 |||| || |||||
 ACTCGC GA CCCTTCGG
 C _
 GAM2713 BRPF3 3' TGACACAACCTTCCCAGCTC 44346 GACTC A
 GAGC GGGAAGTTGT TCA
 ||| ||||| |||
 CTCG CCCTTCAACA AGT
 A _ C
 GAM2713 FLJ10661 3' ACAGCTTCCCGAGTCATTCA 19993 C
 TGAG GACTCGGGAAGTTGT
 ||| |||||
 ACTT CTGAGCCCTTCGACA
 A
 GAM2713 FLJ11856 5' CGGCTCCCGAGTCGCCCA 23735 A A
 TG GCGACTCGGGA GTTG
 || ||||| |||
 AC CGCTGAGCCCT CGGC
 C _
 GAM2713 GFR 3' TGATACAACCTGTGACATCA 14644 GCGACT AAG
 TGA CGGG TTGTATCA
 || ||| |||||
 ACT GTCC AACATAGT
 ACAGT_ _
 GAM2713 GRIN3A 3' GATACAACCTCCCGATC 28535 C A
 GA TCGGG AGTTGTATC
 || ||| |||||
 CT AGCCC TCAACATAG
 _ C
 GAM2713 KIAA1219 3' CAAGTTTCCCAAGTCCTCA 30756 C C _
 TGAG GACT GGGAAG TTG
 ||| ||| ||||| |||
 ACTC CTGA CCCTTT AAC
 _ A G
 GAM2713 LOC202934 3' ATACAACCTACCCTCATCA 43452 GC CTC _
 TGA GA GGG AAGTTGTAT
 ||| || ||| |||||

		ACT CT CCC TTCAACATA		
		A_ _ _ A		
GAM2713	LOC255465	3' ATACAACCTTACCCTCATCA	46446	GC CTC _
		TGA GA GGG AAGTTGTAT		
		ACT CT CCC TTCAACATA		
		A_ _ _ A		
GAM2713	LOC51193	5' CAGCCTCCCGAGTAGCTCA	18454	G A
		TGAGC ACTCGGGA GTTG		
		ACTCG TGAGCCCT CGAC		
		A C		
GAM2714	ALDH3B2	3' CACACGCGCACTTCCACCTC	6356	A TTG
		GAG TGGAAGTGC GTGTG		
		CTC ACCTTCACG CACAC		
		C CG_		
GAM2714	BACH2	3' GCACACCTCTCCCATCCA	22379	A A TGCTT
		TG GATGG AG GGTGTGC		
		AC CTACC TC CCACACG		
		_ C T_		
GAM2714	C5R1	3' CACACCATCTTTCCATCCCA	7471	A TGCT
		TG GATGGAAG TGGTGTG		
		AC CTACCTTT ACCACAC		
		C CT_		
GAM2714	COL6A2	3' CACACCCGCTCCACCTGCA	27727	_ A A CTT
		TG AG TGGA GTG GGTGTG		
		AC TC ACCT CGC CCACAC		
		G C _ _		
GAM2714	DHFR	3' CGCACACCTGTATTCCCATCT	6448	A TT
		AGATGG AGTGC GGTGTGCG		
		TCTACC TTATG CCACACGC		
		C T_		
GAM2714	PFN2	3' CAAAAGCACTTCCTCCCA	8487	A T GG
		TG GA GGAAGTGCTT TG		
		AC CT CCTTCACGAA AC		
		C _ AA		
GAM2714	PFN2	3' CAAAAGCACTTCCTCCCA	27580	A T GG
		TG GA GGAAGTGCTT TG		
		AC CT CCTTCACGAA AC		
		C _ AA		
GAM2714	CYP2A7	5' CACAGCCCACTTCCATCTCA	6414	CT _
		TGAGATGGAAGTG TGG TGTG		

ACTCTACCTTCAC ACC ACAC
 — G
 GAM2714 CYP2A7 5' CACAGCCACACTTCCATCTCA 24957 CT _
 TGAGATGGAAGTG TGG TGTG
 ||||| ||| |||
 ACTCTACCTTCAC ACC ACAC
 — G
 GAM2714 KIAA0310 3' CGCACACTGTGCCTCCCTCCTC 39709 AT A T T
 A TGAG GG AG GC TGGTGTGCG
 ||| || || |||||
 ACTC CC TC CG GTCACACGC
 CT C _ T
 GAM2714 KIAA1280 5' CACACCATCTCCATCTC 34548 AGTGCT
 GAGATGGA TGGTGTG
 ||||| |||||
 CTCTACCT ACCACAC
 CT____
 GAM2714 MGC2452 5' CCAAGCACTTCCCACCTCA 26367 AT_
 TGAG GGAAGTGCTTGG
 ||| |||||
 ACTC CCTTCACGAACC
 CAC
 GAM2714 NESHBP 5' CACACCAAACCTGCTCCCA 17727 A C_
 TGG AGTG TTGGTGTG
 ||| ||| |||||
 ACC TCGT AACCACAC
 C CCA
 GAM2714 LOC131034 5' CACACCAACCACCTCCACTTCA 28314 A A C
 TGAG TGGA GTG TTGGTGTG
 ||| ||| ||| |||||
 ACTT ACCT CAC AACCACAC
 C C C
 GAM2714 LOC196500 3' CACACTCACCTCCACCTT 42386 A A CTT
 GAG TGGA GTG GGTGTG
 ||| ||| ||| |||||
 TTC ACCT CAC TCACAC
 C C _
 GAM2714 LOC256158 5' CCAAACACTTCCAGCTCA 46620 A C
 TGAG TGGAAGTG TTGG
 ||| ||||| |||
 ACTC ACCTTCAC AACC
 G A
 GAM2715 AP1B1 3' CTGCACCACCCACTTGCA 6796 A
 TGCAAG TGGGTGGTGCGG
 ||||| |||||
 ACGTTC ACCCACCACGTC
 —
 GAM2715 COL6A2 3' ACACCCGCTCCACCTGCA 27724 AGATG T
 TGCA GGTGG GCGGGTGT
 ||| ||||| |||||

ACGT CCACC CGCCCACA
 _____ T
 GAM2715 CREBBP 3' CACACCCACACATCTATCT 10603 _ C
 AGATGGGTG GTG GGGTGTG
 ||||| || |||||
 TCTATCTAC CAC CCCACAC
 A A
 GAM2715 ERBB2 3' CACACCCACTTTGTCCATTTGC 10744 A TG TGC
 A TGCA GATGGG G GGGTGTG
 ||| |||| | |||||
 ACGT TTACCT T CCCACAC
 _ GT TCA
 GAM2715 FASN 3' CACACCCAGCGCCCCCGCA 10314 AAGAT G GC
 TGC GGGT GT GGGTGTG
 || ||| || |||||
 ACG CCCG CG CCCACAC
 CCC_ G A_
 GAM2715 ITGAL 3' ACACTTCCACCACCCTGCA 7968 AGAT CG
 TGCA GGGTGGTG GGTGT
 ||| ||||| |||||
 ACGT CCCACCAC TCACA
 _____ CT
 GAM2715 PMM2 3' CACACGTGCTACCCACCCGCA 35677 AAGA T G
 TGC TGGGTGG GCG GTGTG
 ||| ||||| || |||||
 ACG ACCCACT CGT CACAC
 CCC_ _ G
 GAM2715 APOL4 3' CACACCCACACCCTATTCT 24974 _ C
 ATGGGT GGTG GGGTGTG
 ||||| ||| |||||
 TACTTA CCAC CCCACAC
 TC A
 GAM2715 FLJ11106 5' CACAGAGACCAGCCATCTTGCA 20317 G GCGG
 TGCAAGATGG TGGT GTG
 ||||| ||| |||
 ACGTTCTACC ACCA CAC
 G GAGA
 GAM2715 FLJ20699 3' CATCCACCACCCTTCTTACA 19617 C T GC
 TG AAGA GGGTGGT GGGTG
 || ||| ||||| |||||
 AC TTCT CCCACCA CCTAC
 A T _
 GAM2715 KIAA1028 3' CACAGTACCACCCATCT 44158 GG
 AGATGGGTGGTGC GTG
 ||||| ||||| |||
 TCTACCCACCATG CAC
 A_
 GAM2715 KIAA1161 5' CACACCCGCACCATGTACTCCC 39750 CA A G
 A TG AG TG GTGGTGCGGGTGTG
 || || || ||||| |||||

AC TC AT TACCACGCCACAC
 CC _ G
 GAM2715 KIAA1303 3' CACAGCCCACCTCCCCGCA 32832 AA_ T T GG
 TGC GA GGGTGG GC GTG
 ||| || ||||| || |||
 ACG CT CCCACC CG CAC
 CCC _ _ A_
 GAM2715 KIAA1866 3' CACACCCACCACTCCCATC 30555 T C_
 GATGGG GGTG GGGTGTG
 ||||| ||| |||||
 CTACCC TCAC CCCACAC
 _ CA
 GAM2715 PV1 3' CACACCCGCACCCGCGCCTC 25349 T _ _
 GA GG GTGG TGCGGGTGTG
 || || ||| |||||
 CT CC CGCC ACGCCCACAC
 _ G C
 GAM2715 SEC14L1 3' CACACCCACACCACCACTGTC 8901 A ____ C
 TGCA TGCA GA TGGGTGGTG GGGTGTG
 ||| || ||||| |||||
 ACGT CT ACCCACCAC CCCACAC
 _ GTC A
 GAM2715 LOC149832 5' ACACTGCCACCACCCTGCA 41078 AGAT CG
 TGCA GGGTGGTG GGTGT
 ||| ||||| |||||
 ACGT CCCACCAC TCACA
 ____ CG
 GAM2715 LOC151521 3' CACACTTCCACTCCACCTCA 41366 _ _ CG
 TG GGTGG TG GGTGTG
 || |||| || |||||
 AC CCACC AC TCACAC
 T TC CT
 GAM2715 LOC200325 5' CACCACCACCCACCGCTGCA 43287 AGA_ GCG
 TGCA TGGGTGGT GGTG
 ||| ||||| |||
 ACGT ACCCACCA CCAC
 CGCC ____
 GAM2715 LOC90593 3' CACACCAAAACCATCTGTA 31764 A GGTGCG
 TGCA GATGGGT GGTGTG
 ||| ||||| |||||
 ATGT CTACCCA CCACAC
 _ AAA____
 GAM2715 LOC93259 5' CATCACCACCCACCCTGTC 35556 _ _ CG
 GAT GGGTGG TG GGTG
 ||| ||||| || |||
 CTG CCCACC AC CTAC
 T C CA
 GAM2716 CELSR2 3' CTGGGGGGCCTGCCCTCA 7106 ATGA A
 TGAG CAGGCTTC TTAG
 ||| ||||| |||

ACTC GTCCGGGG GGTC
 CCC_ _
 GAM2716 ERAP140 3' CTCCTTTTCTGCCATCATCTCA 37085 CA TTCATTA
 TGAGATGA GGC GAAG
 ||||| || ||||
 ACTCTACT CCG CTC
 A_ TCTTC_
 GAM2716 FLJ13910 3' CTTCTGCAAAGCGTATCATCTC 23055 CAG CAT
 A TGAGATGA GCTT TAGAAG
 ||||| || |||||
 ACTCTACT CGAA GTCTTC
 ATG AC_
 GAM2716 HCA127 3' TCATTAGAAGCTCCTACCCTCA 20759 C_ G_ ATTA
 TCTCA GATGA AG CTC GA
 |||| || |||| ||
 CTACT TC GAAG CT
 CCCA CTC|| ATTA
 GAM2716 KIAA1009 3' CTTCTAGTGTACCCATCATCCA 17052 A CA CTT
 TG GATGA GG CATTAGAAG
 || |||| || |||||
 AC CTACT CC GTGATCTTC
 _ AC AT_
 GAM2716 Kv6.3 3' TCTCTGAGCCTGTCTCCCA 28566 A T T TT
 TG GA GACAGGCT CA AGA
 || || ||||| || ||||
 AC CT CTGTCCGA GT TCT
 C _ _ C_
 GAM2716 PRO0365 5' CTTCTAATGAAAACCTTGGTCAT 15389 _ GC
 CTT GAGATGAC AG TTCATTAGAAG
 ||||| || |||||
 TTCTACTG TC AAGTAATCTTC
 GT AA
 GAM2716 LOC152742 3' CTTCTAATGGTGACTTCCATCT 41544 AC GCT
 CA TGAGATG AG TCATTAGAAG
 ||||| || |||||
 ACTCTAC TC GGTAATCTTC
 CT AGT
 GAM2717 ZNF265 3' ATTTTGTGTCATTTCCAAA 11940 C T
 TTTGGAAA GAC AAAAT
 ||||| || ||||
 AAACCTTT CTG TTTA
 A T
 GAM2717 RBM9 3' CTTTAATTCTTTTGTTCCTCAA 15597 A CTAA
 TTTGGAA CGA AATTAAAG
 ||||| || |||||
 AAACCTT GTT TTAATTC
 _ TTC_
 GAM2717 TCF6L1 3' TCTTTAATTTTACATTTCC 9189 CGAC
 GGAAA TAAAATTAAAGA
 |||| |||||

CCTTT ATTTTAATTTCT
 AC__
 GAM2717 LOC120526 3' CTCCAATCTTGGTCCGTATTTTC 36622 __ _ A AA
 CAAA TTTGGAA ACG ACTAA ATT AG
 ||||| || ||||| || ||
 AAACCTT TGC TGGTT TAA TC
 TA C C CC
 GAM2717 LOC202266 3' TCTTTAAAGACCCTGTTTCCAA 43420 ACTAAAA
 A TTTGGAAACG TTAAAGA
 ||||| |||||
 AAACCTTTGT AATTTCT
 CCCAGA_
 GAM2718 BACH2 5' TTTCTGATCATTTGCAGCTGT 22383 AATA C
 ACAGC TGAA GATCAGAAA
 |||| ||| |||||
 TGTCTG GTTT CTAGTCTTT
 AC__ A
 GAM2718 KIF5C 3' TCTGATCGTTCTGAAGCTTGC 10857 TAT__
 GCAA GAACGATCAGA
 ||| |||||
 CGTT CTTGCTAGTCT
 CGAAGT
 GAM2718 PHKA2 3' TCTGGAACATTTGCTGTA 5836 T AACGA
 TACAGCAA ATG TCAGA
 ||||| || |||||
 ATGTCGTT TAC GGTCT
 _ AA__
 GAM2718 BRD3 3' TCTGTGGTTCATATTACT 14298 C G T
 AG AATATGAAC A CAGA
 || ||||| |||||
 TC TTATACTTG T GTCT
 A G_
 GAM2718 C1orf28 3' TTCTGATTTTTTCATTGCT 23732 AT C
 AGCA ATGAA GATCAGAA
 ||| ||||| |||||
 TCGT TACTT TTAGTCTT
 _ T
 GAM2718 DCOHM 3' CTGATTGGTGTGCTGTA 25846 GAA
 TACAGCAATAT CGATCAG
 ||||| |||||
 ATGTCGTTGTG GTTAGTC
 _
 GAM2718 FLJ10726 3' TTCTAGTTCCATTGCTGTA 20060 AT GATC
 TACAGCAAT GAAC AGAA
 ||||| ||| |||||
 ATGTCGTTA CTTG TCTT
 C_ A__
 GAM2718 FLJ20986 5' TTCTGAATAGCATTTGCTGTA 23730 T AACGA
 TACAGCAA ATG TCAGAA
 ||||| ||| |||||

		ATGTCGTT TAC AGTCTT	
		_ GATA_	
GAM2718	FLJ22004	3' TTTCTAAAGGCTATATTGCTGT 24818	AACGATC
	A	TACAGCAATATG AGAAA	
		ATGTCGTTATAT TCTTT	
		CGGAAA_	
GAM2718	FLJ23129	3' TCTGATTGTGAATACTGCT 24120	A GA
		AGCA TAT ACGATCAGA	
		TCGT ATA TGTTAGTCT	
		C AG	
GAM2718	KIAA0459	3' TGAGGCCATTCATATTCTGTA 30580	C CGA_
		TACAG AATATGAA TCA	
		ATGTC TTATACTT AGT	
		_ ACCGG	
GAM2718	MAP4K3	3' TTTCTGTGAAACTTCATATTGC 9684	CGAT_
	TG	CAGCAATATGAA CAGAAA	
		GTCGTTATACTT GTCTTT	
		CAAAGT	
GAM2718	MGC2217	3' TTTCTAATAAATGATTGCTGTA 23590	ATGAACG C
		TACAGCAAT AT AGAAA	
		ATGTCGTTA TA TCTTT	
		GTAAA_ A	
GAM2718	PCDH17	3' TTTCTGATCACTCTCAGACTGT 15815	CAATAT AC
		ACAG GA GATCAGAAA	
		TGTC CT CTAGTCTTT	
		AGACT_ CA	
GAM2718	STX6	3' TCGTTTCCCATTTGCTGTA 12421	AT_
		TACAGCAAT GAACGA	
		ATGTCGTTA TTTGCT	
		CCC	
GAM2718	LOC145624	5' TTTCTGATCATGGTATGTGCT 40550	A AAC_
		AGCA TATG GATCAGAAA	
		TCGT GTAT CTAGTCTTT	
		_ GGTA	
GAM2718	LOC146909	3' TTCTGATCCTTTATTTCTGC 38274	AT_ C
		GCA ATGAA GATCAGAA	
		CGT TATTT CTAGTCTT	
		CTT C	
GAM2718	LOC152742	3' TTCTGATCATCACTGCTG 41546	ATA AC
		CAGCA TGA GATCAGAA	

GTCGT ACT CTAGTCTT
 C__ A_
 GAM2718 LOC158435 3' TCTGGTCGTCCTCACTGCT 28847 ATA __
 AGCA TGA ACGATCAGA
 ||| ||| |||||
 TCGT ACT TGCTGGTCT
 C__ CC
 GAM2718 LOC219649 3' TTTCTGATCAATTATCGGC 44670 AAT AC
 GC ATGA GATCAGAAA
 || ||| |||||
 CG TATT CTAGTCTTT
 GC_ AA
 GAM2718 LOC219940 3' CTGATATCTTGCTGTA 44831 TAT ACG
 TACAGCAA GA ATCAG
 ||||| || |||
 ATGTCGTT CT TAGTC
 __ A_
 GAM2718 LOC93613 3' TTTCTGGCCCTTATTGCTG 35998 TGAACGA
 CAGCAATA TCAGAAA
 ||||| |||||
 GTCGTTAT GGTCTTT
 TCCC__
 GAM2719 SERPINB9 3' ACAATGACCAGGTTGGACTGTT 10358 A TTAA__
 TAA TTGAACAGT TCG TCATTGT
 ||||| || |||||
 AATTTGTCA GGT AGTAACA
 _ TGGACC
 GAM2719 TCTE1L 3' ACAATAATTAATAATTGTTCAA 35141 ATC C
 TTGAACAGT GTTAAT ATTGT
 ||||| ||||| |||||
 AACTTGTTA TAATTA TAACA
 A__ A
 GAM2719 KIAA0318 3' ACAATGATTTGTACTGTCTAA 34182 A CGTT
 TTG ACAGTAT AATCATTGT
 || ||||| |||||
 AAT TGT CATG TTAGTAACA
 C T__
 GAM2720 FCMD 3' TAATTCAATGGCAAT 13576 TAC
 ATTGCCATTG AATTA
 ||||| |||||
 TAACGGTAAC TTAAT
 __
 GAM2720 TEM8 3' TGGGCAAAACCTGTACAATGAC 25921 C ATTA__
 AA TTG CATTGTACA CCCA
 || ||||| |||||
 AAC GTAACATGT GGGT
 A CCAAAAC
 GAM2720 THBD 3' GGGCAATGATGGCAAT 5922 GTACA A
 ATTGCCATT ATT CCC
 ||||| ||| |||

		TAACGGTAG	TAA GGG		
		_____ C			
GAM2720	VAPB	3'	TGAGTAATGCCACAATGGCA	11134	ACA C
			TGCCATTGT ATTAC CA		
			ACGGTAACA TAATG GT		
			CCG A		
GAM2720	WARS	3'	TGGGTAATTGGTGCTGGC	33414	TT _
			GCCA GTAC AATTACCCA		
			CGGT CGTG TTAATGGGT		
			_ G		
GAM2720	FLJ20802	5'	TGGGTGCAACAATGGCAATG	19676	ACAAT
			CATTGCCATTGT TACCCA		
			GTAACGGTAACA GTGGGT		
			AC_		
GAM2720	FLJ22087	5'	GGTAATTGTTGATGAACAGCA	22614	_ T
			TGC CATTG ACAATTACC		
			ACG GTAGT TGTTAATGG		
			ACAA _		
GAM2720	KIAA1497	5'	TGGGCAATTGTAACACAATGGC	33531	_ A
	AA		TTGCCATTGT ACAATT CCCA		
			AACGGTAACA TGTTAA GGGT		
			CAA C		
GAM2720	P66	3'	TGGACAATTTGGGTGGCAGTGT	21849	GTAC AC
			ACATTGCCATT AATT CCA		
			TGTGACGGTGG TTAA GGT		
			GT_ CA		
GAM2720	LOC152274	3'	GGTAACTGTCGGCAATGT	39232	ATT T A
			ACATTGCC G ACA TTACC		
			TGTAACGG C TGT AATGG		
			_ _ C		
GAM2720	LOC157247	5'	TGGGCCTGGTACATGGCAATG	39577	T AATTA
			CATTGCCAT GTAC CCCA		
			GTAACGGTA CATG GGGT		
			_ GTCC_		
GAM2720	LOC199986	3'	GGTAATTGTTCGTGGCA	43274	TGT
			TGCCAT ACAATTACC		
			ACGGTG TGTTAATGG		
			CT_		
GAM2720	LOC90750	3'	TGAGTAATTTGTACAGTCAAT	31971	CC _ C
			ATTG ATTGTACAA TTAC CA		

		TAAC TGACATGTT AATG GT	
		___ T A	
GAM2721	FLNB	3' CGTTTCAGTCCCTTCCTTGGT 31142	AATCCC A
		ATCAAG GA CTGAAACG	
		TGGTTC CT GACTTTGC	
		CTTCC_ _	
GAM2721	SLC4A7	3' TCAGGTTCAAGTTCTTGA 9671	CCC _
		TCAAGAAT GAAC TGA	
		AGTTCTTG CTTG ACT	
		AA_ G	
GAM2721	FLJ10704	3' CAGGCTTCATGGATTCTTGA 20031	C_ _
		TCAAGAATCC GAA CTG	
		AGTTCTTAGG CTT GAC	
		TA CG	
GAM2721	KIAA0229	3' CATTTCTGGGGTTCCCGAT 44398	AA _ C
		ATC GAATCCC GAA TG	
		TAG CTTGGGG CTT AC	
		CC T T	
GAM2721	SNAP29	3' CACCTCAGGGATTCTGAT 11185	A _ AC
		ATCA GAATCCC GA TG	
		TAGT CTTAGGG CT AC	
		_ A CC	
GAM2721	LOC89932	3' CGTCTCCTGGGTTCTTGAT 30490	T AACT A
		ATCAAGAA CCCG GA ACG	
		TAGTTCTT GGGT CT TGC	
		_ C_ C	
GAM2722	ATRX	3' TGTTTTATAAACAACATCAA 6097	C
		TTGATG TGTTTATGAAGCA	
		AACTAC ACAAATATTTTGT	
		A	
GAM2722	ATRX	3' TGTTTTATAAACAACATCAA 28686	C
		TTGATG TGTTTATGAAGCA	
		AACTAC ACAAATATTTTGT	
		A	
GAM2722	FKBP1B	3' CACTGCCTCATGGCATCA 27642	GTTT A A
		TGATGCT ATGA GCA TG	
		ACTACGG TACT CGT AC	
		_ C C	
GAM2722	DKFZp761H2121	5' TGGATCACAAACAGCACAA 28739	A A AG
		TTG TGCTGTTT TGA CA	

			AAC ACGACAAA ACT GT		
			— C AG		
GAM2722	MGC2452	5'	CATTGCTTCAACACAGCA	26366	TTA
			TGCTGT TGAAGCAATG		
			ACGACA ACTTCGTTAC		
			CA_		
GAM2722	TCFL5	3'	TCATTACTTCATGTGTCA	13383	TGTTT C
			TGATGC ATGAAG AATGA		
			ACTGTG TACTTC TTACT		
			_____ A		
GAM2722	LOC152313	3'	TCATGAGAACAGCACCAA	41477	A _
			TTG TGCTGT TTATGA		
			AAC ACGACA AGTACT		
			C AG		
GAM2723	GABPB1	5'	AATAGCGCCCTGTGCAGCTGA	11759	AAT_
			TTAGCTGCACAG CTATT		
			AGTCGACGTGTC GATAA		
			CCGC		
GAM2723	RGS5	3'	GTAATAGATTTCCAGCTAA	9678	CACA
			TTAGCTG GAATCTATTAC		
			AATCGAC TTTAGATAATG		
			C_		
GAM2723	FBXO24	3'	TAACAGATACGGGCAGCTAG	14464	ACAGA A
			TTAGCTGC ATCT TTA		
			GATCGACG TAGA AAT		
			GGCA_ C		
GAM2723	FLJ13852	3'	GGTGGCTCCGTGCAGCTA	23342	A AT TATT
			TAGCTGCAC GA C ACC		
			ATCGACGTG CT G TGG		
			C CG_		
GAM2723	FLJ20202	3'	GGGTTGAGCTCTGTGCAGT	19289	AT ATT
			GCTGCACAGA CT ACCC		
			TGACGTGTCT GA TGGG		
			C_ GT_		
GAM2723	FLJ23519	3'	AGTATGAATTCTGTGCAGCTA	25972	_ _
			TAGCTGCACAGAAT C TATT		
			ATCGACGTGTCTTA G ATGA		
			A T		
GAM2723	GABPB2	5'	AATAGCGCCCTGTGCAGCTGA	7794	AAT_
			TTAGCTGCACAG CTATT		

AGTCGACGTGTC GATAA
 CCGC
 GAM2723 GFR 3' TAGTTTCTGTACAACTGA 14640 C C T
 TTAG TG ACAGAA CTA
 |||| || ||||| |||
 AGTC AC TGTCTT GAT
 A A T
 GAM2723 SEC15B 3' TAATTTTTCTATGCAGCTA 33127 C TCT
 TAGCTGCA AGAA ATTA
 ||||| ||| |||
 ATCGACGT TCTT TAAT
 A TT_
 GAM2723 LOC253782 3' GGTAATAGCATATTACAGCTGA 45799 CACAGAAT
 TTAGCTG CTATTACC
 ||||| |||||
 AGTCGAC GATAATGG
 ATTATAC_
 GAM2724 NUMB 3' TCAATCGAAATATGCTCTA 9833 _
 TAGAGCATATTTTG TGG
 ||||| |||
 ATCTCGTATAAAGC ACT
 TA
 GAM2724 DKFZp434E1822 5' GTACCAGCATATGCTCTGA 33984 T TG
 TTAGAGCATAT TTG GC
 ||||| ||| ||
 AGTCTCGTATA GAC TG
 C CA
 GAM2724 ELF4 3' GCCACGGAAACAACCTCTAA 7123 CATA
 TTAGAG TTTTGTGGC
 |||| |||||
 AATCTC AAGGCACCG
 AACA
 GAM2724 FLJ10656 3' TGCCAGTATCTGCTCTAA 19991 T TTTG
 TTAGAGCA AT TGGCA
 ||||| || |||
 AATCTCGT TA ACCGT
 C TG_
 GAM2724 KIAA1728 3' TGATGCCATTGATATATCTAA 33950 GC TT C
 TTAGA ATATT GTGGCA CA
 |||| |||| ||||| ||
 AATCT TATAG TACCGT GT
 A_ T_ A
 GAM2724 LOC154877 3' GTGCCACAAAATAAAGCTC 41744 A_
 GAGC TATTTTGTGGCAC
 ||| |||||
 CTCG ATAAAACACCGTG
 AA
 GAM2724 LOC54103 3' TGAAATAAAATATGCTTTAA 45210 GG
 TTAGAGCATATTTTGT CA
 ||||| ||| ||

AATTTTCGTATAAAATA GT
 AA
 GAM2725 FGF5 3' ATCAATGGTTTAACAGTTATCC 10770 T CTCTC C
 A TG GATAACTG CTAT GAT
 || ||||| ||| |||
 AC CTATTGAC GGTA CTA
 _ AATTT A
 GAM2725 FGF5 3' ATCAATGGTTTAACAGTTATCC 26997 T CTCTC C
 A TG GATAACTG CTAT GAT
 || ||||| ||| |||
 AC CTATTGAC GGTA CTA
 _ AATTT A
 GAM2725 SOST 3' AGGGAGCAGCCATCACA 24917 AA T
 TGTGAT CTGCTC CCT
 ||||| ||||| |||
 AACTA GACGAG GGA
 CC _
 GAM2725 KIAA1870 3' GGTTCAGTGAGCAGTTATCAC 26711 TCCT__
 A TGTGATAACTGCTC ATC
 ||||| ||||| |||
 AACTATTGACGAG TGG
 TGACGT
 GAM2726 DKFZp761B0514 3' ACATCACAATAATCTGGGAC 26048 G _ T
 GTC CAGAT TGTGAT GT
 ||| |||| ||||| ||
 CAG GTCTA AACTA CA
 G ATA _
 GAM2726 KIAA1028 3' GTATTACACAAAATCTGGACT 44162 G G AT
 AGTC CAGATT TG TGTAATAC
 |||| ||||| || |||||
 TCAG GTCTAA AC ACATTATG
 _ A _
 GAM2726 PRO2831 3' TTGCATACAATCTGAACT 20612 CG AT
 AGT CAGATTGTG TGTA
 ||| ||||| |||||
 TCA GTCTAACAT ACGTT
 AA _
 GAM2726 LOC200734 3' TACTATTAACAATCTGTAAC 42841 CG _ T
 GT CAGATTGT GAT GTA
 || ||||| ||| |||
 CA GTCTAACA TTA CAT
 AT A T
 GAM2726 LOC219940 3' GTATTACAACATCACTGCGCT 44833 T ATT A
 AG CGCAG GTG TTGTAATAC
 || |||| ||| |||||
 TC GCGTC TAC AACATTATG
 _ AC _ _
 GAM2727 CTBP2 5' TCATGCACGCAGACTCCTGCAA 7010 A A_ CA
 TTGCAGGA TT CG TATGA
 ||||| || || |||||

		AACGTCCT AG GC GTACT		
		C AC AC		
GAM2727	DKFZP434O125 3'	TCATATTTATTCCTGCA	32405	TACGC
		TGCAGGAAT ATATGA		
		ACGTCCTTA TATACT		
		TT__		
GAM2727	KIAA0546 3'	ATCATATACGTAAGTATAGTTC	35329	_____ C III
		CTCAA AGGAAT TACG ATATGA T		
		TCCTTG ATGC TATACT A		
		ATATGA A III		
GAM2727	LRRN3 5'	TCATGCTGCTATTCCTGCAA	34402	TAC _
		TTGCAGGAAT GCA TATGA		
		AACGTCCTTA CGT GTACT		
		T__ C		
GAM2727	Rpo1-2 3'	TCATATAGTGGGATCATGCAA	21106	G A TA _
		TTGCA GA T CGC ATATGA		
		AACGT CT A GTG TATACT		
		A _ GG A		
GAM2727	Rpo1-2 3'	TCATATAGTGGGATCATGCAA	25936	G A TA _
		TTGCA GA T CGC ATATGA		
		AACGT CT A GTG TATACT		
		A _ GG A		
GAM2727	LOC145623 3'	TCATTGTGTCAATTCCTGCAA	40547	_ T
		TTGCAGGAATT ACGCA ATGA		
		AACGTCCTTAA TGTGT TACT		
		C _		
GAM2727	LOC157695 3'	TCATATGTTTGTCTTGCAA	41833	TAC
		TTGCAGGAAT GCATATGA		
		AACGTTCTTG TGTATACT		
		TT_		
GAM2727	LOC221042 5'	TCAAGTGCCATTCCTGCAA	44758	TAC A
		TTGCAGGAAT GCAT TGA		
		AACGTCCTTA CGTG ACT		
		C__ A		
GAM2728	HDGF 3'	AGTGCTCAAGGCCAGCTT	10831	___ C
		AAGCTGGC GA GTACT		
		TTCGACCG CT CGTGA		
		GAA _		
GAM2728	IGFBP4 3'	CATGTACTACGTGCCAGCT	7274	G C
		AGCTGGC ACGTA TATATG		

		TCGACCG TGCAT ATGTAC		
		— C		
GAM2728	PLN	5' CATATTTGGCTGCCAGCTT 8537	AC	ACT
		AAGCTGGCG GT ATATG		
		TTCGACCGT CG TATAC		
		— GTT		
GAM2728	PPP1CB	3' CATATAGTATTACCCAACT 8557	C	CGAC
		AG TGG GTACTATATG		
		TC ACC TATGATATAC		
		A CAT_		
GAM2728	SLC22A3	3' ATAATATGTAGCCAGTTT 22502	G	C
		AAGCTGGC ACGTA TAT		
		TTTGACCG TGTAT ATA		
		A A		
GAM2728	DKFZP434H132	5' TGTGTACGCCGCCAGCT 17763	A	T
		AGCTGGCG CGTAC ATA		
		TCGACCGC GCATG TGT		
		C —		
GAM2728	FLJ22833	3' CATATAGTAACATGCAGT 23120	G	ACG
		GCTG CG TACTATATG		
		TGAC GT ATGATATAC		
		— ACA		
GAM2728	KIAA1821	3' CATATTTGTGTCCTCGCCAGCT 35552	CG_	T_
		AGCTGGCGA TAC ATATG		
		TCGACCGCT GTG TATAC		
		CCT TT		
GAM2728	MGC22014	3' TGTAGTACATGGCCAACTT 32225	C	GAC
		AAG TGGC GTACTATA		
		TTC ACCG CATGATGT		
		A GTA		
GAM2728	LOC90829	5' CATATGGCTAGCCAGCTT 32054	GAC	GTA
		AAGCTGGC CTATATG		
		TTCGACCG GGTATAC		
		ATC__		
GAM2729	FCMD	3' CCAATTTTAATGACACTAA 13573	C	AT
		TTAGTG TATTA GAGTTGG		
		AATCAC GTAAT TTAAACC		
		A —		
GAM2729	KERA	3' CTTCCATAGCTTATTAACACTA 13908	CTA	—
	A	TTAGTG TTAATGAGT TGGAAG		

			AATCAC AATTATTCG ACCTTC		
			____ AT		
GAM2729	VANGL2	3'	TCCAACCTCTCTAAGCACTAA 35485	AT AT	
			TTAGTGCT TA GAGTTGGA		
			AATCACGA AT CTCAACCT		
			____ CT		
GAM2730	FGF2	3'	GCTATAAAGCAAGAAAGTAAAC 7740	A_ CCG_	
	A		TGTTTACTTTTT CT GGC		
			ACAAATGAAAGA GA TCG		
			AC AATA		
GAM2730	SCML1	3'	TTTAGAGTAAAAAATAAGCA 13593	C CG	
			TGTTTA TTTTACTC GG		
			ACGAAT AAAAATGAG TT		
			A AT		
GAM2730	TTN	3'	GCCACAGCAAAAAGTAAA 28504	A CCG	
			TTTACTTTTT CT GGC		
			AAATGAAAAA GA CCG		
			C CA_		
GAM2730	TTN	3'	GCCACAGCAAAAAGTAAA 28509	A CCG	
			TTTACTTTTT CT GGC		
			AAATGAAAAA GA CCG		
			C CA_		
GAM2730	TTN	3'	GCCACAGCAAAAAGTAAA 28519	A CCG	
			TTTACTTTTT CT GGC		
			AAATGAAAAA GA CCG		
			C CA_		
GAM2730	FLJ10830	3'	TCCTAAATAAAAAGTAAACA 20184	CTCC	
			TGTTTACTTTTTA GGG		
			ACAAATGAAAAAT CCT		
			AAAT		
GAM2730	KIAA1116	3'	GCAGTGAGTAAAAAAGAAACA 17041	AC CGG	
			TGTTT TTTTACTC GC		
			ACAAA AAAAATGAG CG		
			GA TGA		
GAM2730	Rpo1-2	3'	GCCACGTTGAAGTAAAAACAAA 21104	AC C_ _	
	CA		TGTTT TTTTACT CG GGC		
			ACAAA AAAAATGA GC CCG		
			C_ AGTT A		
GAM2730	Rpo1-2	3'	GCCACGTTGAAGTAAAAACAAA 25934	AC C_ _	
	CA		TGTTT TTTTACT CG GGC		

		ACAAA AAAAATGA GC CCG		
		C_ AGTT A		
GAM2730	LOC158987 3'	GCTGAGGAAAAAGTAAACA 42049	A CG	
		TGTTTACTTTTT CTC GGC		
		ACAAATGAAAAA GAG TCG		
		G _		
GAM2730	LOC93613 5'	GCCACGGTAAAAGCAAACA 35995	A TACT _	
		TGTTT CTTTT CCG GGC		
		ACAAA GAAAA GGC CCG		
		C T_ A		
GAM2731	LOC152328 3'	GAAC TTTGAACGATCCCA 39242	AA TACG	
		TGGGATC TCA GAGTC		
		ACCCTAG AGT TTCAAG		
		CA _		
GAM2732	FLJ20701 3'	AAGTGAACACACTCTATGTCA 19621	A _ CTA	
		TGACATAGA TG GT TGCTT		
		ACTGTATCT AC CA GTGAA		
		C A A_		
GAM2732	P5-1 3'	CAAAGCTGGCATCCTCCTATGT 13495	AAT _ T	
	CA	TGACATAG GGT CTA GCTTTG		
		ACTGTATC CTA GGT CGAAAC		
		CTC C _		
GAM2732	LOC149705 3'	AAAGCAATATTCTGTGTCA 41051	GTCTA	
		TGACATAGAATG TGCTTT		
		ACTGTGTCTTAT ACGAAA		
		A _		
GAM2733	BCL7A 3'	TGTCTATTTCTGCACTTC 21996	_ _	
		GAAGTGCAG AGG AGACA		
		CTTCACGTC TTT TCTGT		
		C A		
GAM2733	BRF1 3'	CTTGAAGGTCCTCTGCCTCCA 7257	A T GACAA	
		TG AG GCAGAGGA CAAG		
		AC TC CGTCTCCT GTTC		
		C _ GGAA_		
GAM2733	CAPZA1 3'	CTCATTGTCTCCTTCCCAT 35948	CA CA	
		GTG GAGGAGACAA AG		
		TAC TTCCTCTGTT TC		
		CC AC		
GAM2733	FGF23 3'	TCTCGCTGTCTCCCTCTGTGC 21795	TG _ ACA	
		G CAGAGG AGACA AGA		

C GTCTCC TCTGT TCT
 GT C CGC
 GAM2733 OCRL 3' TCCTGGATCACTCCTTTGCACT 5820 A ACAA_ A
 CCA TG AGTGCAGAGGAG CA GA
 || ||||| || ||
 AC TCACGTTTCCTC GT CT
 C ACTAG C
 GAM2733 OCRL 3' TCCTGGATCACTCCTTTGCACT 7307 A ACAA_ A
 CCA TG AGTGCAGAGGAG CA GA
 || ||||| || ||
 AC TCACGTTTCCTC GT CT
 C ACTAG C
 GAM2733 SKI 3' TCTTCGGCTCCTCTGCAC 8991 ACAAC
 GTGCAGAGGAG AAGA
 ||||| ||||
 CACGTCTCCTC TTCT
 GGC__
 GAM2733 SMP1 3' TCTTGTTGTCTCTTCCTCTTCA 15612 TGCA
 TGAAG GAGGAGACAACAAGA
 |||| |||||
 ACTTC CTTCTCTGTTGTTCT
 TC__
 GAM2733 SORCS3 3' TCCTGTTGTCTGTCACTT 17365 CA GG A
 AAGTG GA AGACAACA GA
 |||| || ||||| ||
 TTCAC CT TCTGTTGT CT
 A_ G_ C
 GAM2733 TNFRSF10B 3' GTTGTCCCCTGCACTTC 9937 A A
 GAAGTGCAG GG GACAAC
 ||||| || |||||
 CTTCACGTC CC CTGTTG
 - -
 GAM2733 BRAG 3' TCTTGTTGCGATCGCTAACCTC 16943 A GC AG GA_
 A TGA GT AG GA CAACAAGA
 ||| || || |||||
 ACT CA TC CT GTTGTTCT
 C A_ G_ AGC
 GAM2733 DCLRE1A 3' TCTTGTTGTCTGTGGCACTT 34282 AGAGG
 AAGTGC AGACAACAAGA
 |||| |||||
 TTCACG TCTGTTGTTCT
 GTG__
 GAM2733 DKFZP434P0111 3' TGCTCCTCTGCCCTCA 33459 A T A
 TGA G GCAGAGGAG CA
 ||| ||||| ||
 ACT C CGTCTCCTC GT
 _C _
 GAM2733 FLJ22944 3' TGCCTTTCTGCACTGTCA 24783 _ G A
 TGA AGTGCAGAG AG CA
 ||| ||||| || ||

ACT TCACGTCTT TC GT
 G _ C
 GAM2733 FLJ23022 5' TGTCCCTCTGCACTCCA 24648 A A
 TG AGTGCAGAGG GACA
 || ||||| ||||
 AC TCACGTCTCC CTGT
 C _
 GAM2733 JAM1 3' CTTATTTGTCTTCTACACCCCA 29330 AA CAG C_
 TG GTG AGGAGACAA AAG
 || || ||||| ||||
 AC CAC TCTTCTGTT TTC
 CC A_ TA
 GAM2733 JAM1 3' CTTATTTGTCTTCTACACCCCA 29341 AA CAG C_
 TG GTG AGGAGACAA AAG
 || || ||||| ||||
 AC CAC TCTTCTGTT TTC
 CC A_ TA
 GAM2733 JAM1 3' CTTATTTGTCTTCTACACCCCA 18863 AA CAG C_
 TG GTG AGGAGACAA AAG
 || || ||||| ||||
 AC CAC TCTTCTGTT TTC
 CC A_ TA
 GAM2733 JAM1 3' CTTATTTGTCTTCTACACCCCA 29322 AA CAG C_
 TG GTG AGGAGACAA AAG
 || || ||||| ||||
 AC CAC TCTTCTGTT TTC
 CC A_ TA
 GAM2733 JAM1 3' CTTATTTGTCTTCTACACCCCA 29351 AA CAG C_
 TG GTG AGGAGACAA AAG
 || || ||||| ||||
 AC CAC TCTTCTGTT TTC
 CC A_ TA
 GAM2733 KIAA1322 3' CTTGGGGTGCTCTGCACTCCA 36027 A GAG AA
 TG AGTGCAGAG AC CAAG
 || ||||| || ||||
 AC TCACGTCTC TG GTTC
 C G_ GG
 GAM2733 MYLE 3' TGCCTCCCTGCACTTCA 15235 A A
 TGAAGTGCAG GGAG CA
 ||||| |||| ||
 ACTTCACGTC CCTC GT
 _ C
 GAM2733 LOC118738 3' TCTTGTTGATTTGCTGCCTCCA 37195 A T AG GA
 TG AG GCAG GA CAACAAGA
 || || || || |||||
 AC TC CGTC TT GTTGTTCT
 C _ GT A_
 GAM2733 LOC142913 5' CTTGCCATCTCCTTTTCACTTC 37564 C CAA
 GAAGTG AGAGGAGA CAAG
 ||||| ||||| ||||

	CTTCAC TTTCCTCT GTTC		
	T ACC		
GAM2733 LOC144519 5'	TCTTGCCACCTCCTCTGCAC 37761	ACAA	
	GTGCAGAGGAG CAAGA		
	CACGTCTCCTC GTTCT		
	CACC		
GAM2733 LOC145501 3'	TCACCTAAGCTGCACTTCA 37884	___ A	
	TGAAGTGCAG AGG GA		
	ACTTCACGTC TCC CT		
	GAA A		
GAM2733 LOC148930 3'	TCTTAGAAGCCTCCCCTGACTT 38621	G A ACAAC_	
CA	TGAAGT CAG GGAG AAGA		
	ACTTCA GTC CCTC TTCT		
	_ C CGAAGA		
GAM2733 LOC166206 5'	TTGTCTCTGCAGTTCA 40209	G GGA	
	TGAA TGCAGA GACAA		
	ACTT ACGTCT CTGTT		
	G ___		
GAM2733 LOC200227 3'	CTTGTTCTCTGCCTTCA 42746	T AGACA	
	TGAAG GCAGAGG ACAAG		
	ACTTC CGTCTCT TGTTT		

GAM2733 LOC221466 3'	TTGTTGCCTGCACTCA 44999	A AGGAGA	
	TGA GTGCAG CAACAA		
	ACT CACGTC GTTGTT		
	_ C ___		
GAM2733 LOC254531 5'	CTTGTTGCTGCCCCACACTCCA 45539	A CAGA _ A	
	TG AGTG GG AG CAACAAG		
	AC TCAC CC TC GTTGTTC		
	C ACC_ G _		
GAM2733 LOC91097 5'	TTGTCCCCTGACCTCA 32371	A G A A	
	TGA GT CAG GG GACAA		
	ACT CA GTC CC CTGTT		
	C _ _ _		
GAM2733 LOC91689 3'	CTTGTTGGACTTCCCCACTCCA 27156	A CA AGA	
	TG AGTG GAGG CAACAAG		
	AC TCAC CTTC GTTGTTC		
	C CC AG_		
GAM2734 B4GALT1 3'	AACCAAGGGAAATACTGCT 7243	___	
	AGCAGTAT CTTGGTT		

		TCGTCATA GAACCAA		
		AAGG		
GAM2734	CRHR1	3' ACCAAGGGCCCTCACTCA	10605	A A_ AGTA
		TGAG TGA GC TCTTGGT		
		ACTC ACT CG GGAACCA		
		_ CC _		
GAM2734	VHL	3' AACTTACACTGTTTCATCTCA	6155	ATCTT
		TGAGATGAAGCAGT GGTT		
		ACTCTACTTTGTCA TCAA		
		CAT_		
GAM2734	CDKL2	5' AACCATATGCATTTACCTCA	10069	A CA CT
		TGAG TGAAG GTAT TGGTT		
		ACTC ACTTT CGTA ACCAA		
		C A_ T_		
GAM2734	FLJ11117	3' ACCAAGACCTCATCTACA	20325	_ AGCAGTA
		TG AGATGA TCTTGGT		
		AC TCTACT AGAACCA		
		A CC_		
GAM2734	FLJ12649	3' AACCTCCGCCTCCTCATCTCA	23832	A C TATCTT
		TGAGATGA G AG GGTT		
		ACTCTACT C TC CCAA		
		C CGCCT		
GAM2734	FLJ13081	3' AACCAAGACACTACATTGTCT	24236	TG AGC A
		AGA A AGT TCTTGGTT		
		TCT T TCA AGAACCAA		
		GT ACA C		
GAM2734	FLJ22794	3' AACCAAAACTTGTTTCATCTCA	44021	GC ATC
		TGAGATGAA AGT TTGGTT		
		ACTCTACTT TCA AACCAA		
		GT A_		
GAM2734	KIAA0084	3' AACCAAGGCTGCTGTTTCATCCC	33803	A G _
	A	TG GATGAA CAGTA TCTTGGTT		
		AC CTACTT GTCGT GGAACCAA		
		C _ C		
GAM2734	LOC155179	3' AACCAGGATTTGCTCGATCTCA	39550	GA T
		TGAGAT AGCAG ATCTTGGTT		
		ACTCTA TCGTT TAGGACCAA		
		GC _		
GAM2734	LOC90092	5' AGACACTGCTTCTTCTCA	30780	T A
		TGAGA GAAGCAGT TCT		

		ACTCT CTTCGTCA AGA	
		T C	
GAM2735 PDYN	3'	TCATGCAGATAGTATACACATC 23654	A _ TATT
A		TGATGTGTG TACTA CT TGA	
		ACTACACAT ATGAT GA ACT	
		_ A CGT_	
GAM2735 BHC80	3'	TCAAATAAGCAGTATTTAATCA 18730	GTGT A
		TGAT GATACT CTTATTTGA	
		ACTA TTATGA GAATAAACT	
		AT_ C	
GAM2735 C20orf50	5'	TCAAACAATATTTATCACACAT 34719	CTACTTA
		ATGTGTGATA TTTGA	
		TACACACTAT AAACT	
		TTATAAC	
GAM2735 LOC151760	5'	TGAGCACATCACACATCA 41389	ACTA
		TGATGTGTGAT CTTA	
		ACTACACACTA GAGT	
		CAC_	
GAM2736 TEM8	3'	TCAGCACATCAGTCATATGCCC 25919	A C ACT
A		TG GTATA GACTGATG TTGA	
		AC CGTAT CTGACTAC GACT	
		C A AC_	
GAM2736 FLJ13612	3'	CAAAGTCATGGCCATACTCA 24860	ACGA G
		TGAGTAT CT ATGACTTTG	
		ACTCATA GG TACTGAAAC	
		CC_ _	
GAM2736 KIAA0534	3'	TCAAAACCCATTTGCCGTATAC 35386	ACT AC_
T		AGTATACG GATG TTTGA	
		TCATATGC TTAC AAACT	
		CGT CCA	
GAM2736 PRO2214	5'	TCAAAGTTAACACCTATACTCA 20589	CGAC A
		TGAGTATA TG TGACTTTGA	
		ACTCATAT AC ATTGAAACT	
		CC_ A	
GAM2736 LOC149721	3'	TCTCAGTCATATGCCCA 38813	A C T
		TG GTATA GACTGA GA	
		AC CGTAT CTGACT CT	
		C A _	
GAM2736 LOC153883	3'	TCAAAGTCATTTTGGACACATC 39430	GTATA CT
A		TGA CGA GATGACTTTGA	

		ACT GTT TTA	CTGAACT		
		ACACA T_			
GAM2737	RIG	3' TACAATCATGTGCAACTTT	13107	AT A	
		AAAGTTGTG TGA TTGTA			
		TTTCAACGT ACT AACAT			
		GT _			
GAM2737	LOC85479	5' CAAGAAAATCACAACTTGA	26957	A	GAA
		TCAA GTTGTGATT TTG			
		AGTT CAACACTAA AAC			
		_ AAG			
GAM2738	SMT3H1	3' TTGCCTCTCCCCTGCTCA	30127	C A AA	
		TGAGCAGG GA GA CAA			
		ACTCGTCC CT CT GTT			
		C _ CC			
GAM2738	FLJ23071	5' CAATTACCTCTTTTTTGCTC	24844	C	AAC
		GAGCAGG GAAGA AATTG			
		CTCGTTT TTTCT TTAAC			
		_ CCA			
GAM2738	KIAA0332	3' TGTTTTTCTCCCCTGCTCA	31423	C _	
		TGAGCAGG GA AGAAACA			
		ACTCGTCC CT TTTTGT			
		C C			
GAM2738	PRSC	3' TCAACTTTTAGCCTGCTCA	13350	G	AACAA
		TGAGCAGGC AAGA TTGA			
		ACTCGTCCG TTTT AACT			
		A C_			
GAM2738	LOC256158	5' TCAGGCCTCTTCGCCTGCCA	46631	A	AACAA
		TG GCAGGCGAAGA TTGA			
		AC CGTCCGCTTCT GACT			
		_ CCG_			
GAM2739	TEM8	3' TCAGCACATCAGTCATATGCCC	25919	A C	ACT
	A	TG GTATA GACTGATG TTGA			
		AC CGTAT CTGACTAC GACT			
		C A AC_			
GAM2739	FLJ13612	3' CAAAGTCATGGCCATACTCA	24860	ACGA G	
		TGAGTAT CT ATGACTTTG			
		ACTCATA GG TACTGAAAC			
		CC_ _			
GAM2739	KIAA0534	3' TCAAAACCCATTTGCCGTATAC	35386	ACT	AC_
	T	AGTATACG GATG TTTGA			

	TCATATGC	TTAC	AAACT	
	CGT	CCA		
GAM2739	PRO2214	5'	TCAAAGTTAACACCTATACTCA	20589 CGAC A
			TGAGTATA TG TGACTTTGA	
			ACTCATAT AC ATTGAAACT	
			CC__ A	
GAM2739	LOC149721	3'	TCTCAGTCATATGCCCA	38813 A C T
			TG GTATA GACTGA GA	
			AC CGTAT CTGACT CT	
			C A _	
GAM2739	LOC153883	3'	TCAAAGTCATTTTTTGACACATC	39430 GTATA CT
			TGA CGA GATGACTTTGA	
			ACT GTT TTACTGAAACT	
			ACACA T_	